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The characterisation of the cell surface of *Staphylococcus aureus* in the search for new therapeutic targets.

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ithreeinstitute

CERTIFICATE OF ORIGINAL AUTHORSHIP

I, Kate Harvey, certify that the work in this thesis has not previously been submitted for a degree nor has it been submitted as part of requirements for a degree except where fully acknowledged within the text.

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Declaration

All data collected, analysed, and presented in this thesis is the work of the author unless clearly specified. Chapters 2-4 have been prepared for publication as described at the beginning of the relevant chapter. Chapter 4 is written verbatim from the papers it is made up of. The author declares no conflict of interest in this thesis or the data it contains.

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List of Abbreviations

General

Methicillin resistant *Staphylococcus aureus*	MRSA
Hospital-acquired methicillin resistant *Staphylococcus aureus*	HA-MRSA
Community-acquired methicillin resistant *Staphylococcus aureus*	CA-MRSA
Vancomycin intermediate *Staphylococcus aureus*	VISA
Vancomycin resistant *Staphylococcus aureus*	VRSA
Hospital acquired infection	HAI
United States	US
Small colony variant	SCV
Wild type	WT
Heparin	HP
Heparan sulfate	HS
Microbial surface components recognising adhesive matrix molecules	MSCRAMMs
Secretable expanded repertoire adhesive molecules	SERAM
Glycosaminoglycan	GAG
Proteoglycan	PG
Deoxyribonucleic acid	DNA
Ribonucleic acid	RNA
Gene ontology	GO
Extracellular deoxyribonucleic acid	eDNA
Glyceraldehyde 3-phosphate dehydrogenase	GAPDH
Centers for Disease Control and Prevention	CDC
Open reading frame	ORF
Intensive care unit	ICU
Single nucleotide polymorphism	SNP
Post-translational modifications	PTMs
Horizontal gene transfer	HGT
Colony forming units	CFU
Extracellular matrix	ECM
Whole cell lysate	WCL
Excreted cytosolic proteins	ECP
Elongation factor thermo unstable	Ef-Tu
Major histocompatibility complex class II analog protein	MAP
Short linear motif	SLiM
Protein-protein interaction	PPI

Method-related

Immuno-fluorescence microscopy	IFM
1-Dimensional sodium dodecyl sulfate polyacrylamide gel electrophoresis	1D-SDS-PAGE
2-Dimensional polyacrylamide gel electrophoresis	2D-PAGE
Difference in-gel electrophoresis	DIGE
Liquid chromatography	LC

Reversed-phase chromatography	RPLC
High pressure liquid chromatography	HPLC
Isobaric peptide tags for relative and absolute quantitation	iTRAQ
Isotope-coded affinity tags	ICAT
Stable isotope labels with amino acids in cell culture	SILAC
Hydrophilic interaction liquid chromatography	HILIC
Mass spectrometry	MS
Tandem mass spectrometry	MS/MS
Imaging mass spectrometry	IMS
Matrix assisted laser desorption/ionisation	MALDI
Electrospray ionisation	ESI
Electrospray droplet impact	EDI
Automated direct infusion	ADI
Time-of-flight	TOF
Strong cation exchange	SCX
Polymerase chain reaction	PCR
Semi-quantitative real-time polymerase chain reaction	sqrtPCR
Intelligent data acquisition	IDA

Solutions

Dithiothreitol	DTT
Acetonitrile	ACN
Trifluoroacetic acid	TFA
Sodium dodecyl sulfate	SDS
Phosphate buffered saline	PBS
Tryptic soy broth	TSB

Units used

Molar	M
Litre	L
Gram	g
Kilogram	kg
Second	s
Hour	h
Millimetres squared	mm^2
Nano	n
Milli	m
Micro	μ
Hertz	Hz
Kilo Dalton	kDa
Dalton	Da
Relative centrifugal force	rcf

Degrees celsius	°C
Potential of hydrogen	pH
Weight per volume	w/v
Optical density	OD
Parts per million	ppm
Molecular weight	MW
Amino acid	aa

Abstract

Staphylococcus aureus is a Gram-positive pathogen which causes a wide range of afflictions including endocarditis, osteomyelitis, cellulitis, toxic shock syndrome, and necrotising pneumonia. *S. aureus* is a leading cause of hospital-acquired infections and has rapidly acquired resistance to multiple antimicrobials. As such, it was deemed a serious threat by the Centers for Disease Control and Prevention (CDC) in 2013 indicating urgent attention is required to control this pathogen [1]. Currently there are no efficacious vaccines available to treat infections caused by *S. aureus*. With resistance being noted against every class of antibiotic currently available, the development of an alternative therapeutic would not only relieve morbidities, mortalities, and the associated economic burden, but also reduce the selective pressures that drive antibiotic resistance.

To better understand how *S. aureus* interacts with the human host and presents antigens that interact with key host cell receptors, a better understanding of which proteins are displayed on the cell surface is required. This dissertation presents an analysis of the surface proteome of *S. aureus* and describes several potential novel adhesins. Enzymatic cell shaving and surface protein biotinylation were used to catalogue proteins on the cell surface and identify regions within molecules that are surface accessible. Our approaches included methods that maintained protein size context (SDS-PAGE), providing an insight into the extent of surface protein processing. We also characterised heparin-binding proteins in *S. aureus* and interrogated the data in light of our surface proteome studies. This approach enabled us to gain insight into novel binding characteristics used by surface-accessible proteins that could not be predicted using reverse vaccinology and other hypothesis-directed approaches commonly used to develop potential vaccine candidates. Ascertaining the repertoire of heparin-binding proteins was considered important as these proteins are bacterial virulence

factors that facilitate adherence, colonisation, and invasion of target host cells. By coupling these data with other proteomic and bioinformatics techniques, a number of proteins of interest were identified. This includes Elongation Factor Tu, which was found to be surface exposed and highly processed, a finding that has not been seen before in *S. aureus*.

The data presented in the following chapters contributes significantly to the rapidly evolving field of *S. aureus* proteomics. These data will aid in the development of future therapeutic strategies and highlights a number of proteins for further therapeutic investigation.

Chapter 1. Introduction to *Staphylococcus aureus* proteomics

1.1 *Staphylococcus aureus*

1.1.1 General background

Staphylococcus aureus is an opportunistic pathogen that persists within the nasal cavity of approximately 20-35 % [2,3] of healthy individuals globally, with a further 60 % being colonised at some point in their life [3] and an additional 12.8 % of individuals being exclusively throat carriers [4]. *S. aureus* can colonise both humans and other animals [5], and be transferred between different hosts species [6-9]. Complications attributed to *S. aureus* can arise when there is an imbalance in normal flora or the immune system, allowing it to transition from a commensal to a pathogen. These complications can develop in part due to the ability of *S. aureus* to form biofilms (local infections), or transition to a blood-borne infection known as bacteraemia; a systemic infection that can introduce *S. aureus* toxins into the bloodstream (systemic infection) [10]. Armed with the knowledge that *S. aureus* can quickly acquire resistance to a range of antimicrobials, treating such infections has now become both challenging and costly. The annual healthcare burden of *S. aureus* in the US is now estimated to be between $6-9 billion US dollars [11], with the median treatment cost averaging between $16 000 and $34 000 for susceptible and resistant strains, respectively [12]. In the European Union, hospital acquired methicillin resistant *S. aureus* (HA-MRSA) infection involves an added cost of € 380 million annually [13]. In Iceland and Norway alone, MRSA is responsible for 44 % of hospital acquired infections (HAIs)[14]. *S. aureus* is also one of the most prevalent infections seen in intensive care units (ICU) worldwide [15]. Although MRSA infections are currently following a downward trend [1,13], with antibiotic resistance on the rise, other resistant forms of *S. aureus* are likely to become a major health issue over the next few decades. This is part of a broader problem with the rise in antimicrobial resistance (AMR) affecting many leading pathogens, particularly Gram negatives such that the Review on Antimicrobial Resistance estimates that if current trends prevail antimicrobial resistant bacteria may claim more people by 2050 (10 million) than the number that currently die of cancer (8.2 million) [16]. As the virulence, resistance, and cost of treatment of *S. aureus* rises, there is a desperate need to understand mechanisms of pathogenesis and identify surface-accessible proteins that can be effectively targeted by different arms of the immune response or therapeutics.

There has been a significant effort to characterise the genomes of susceptible, resistant, and clinical isolate strains of *S. aureus* and numerous strains such as Newman, Mu50, SH1000, and COL have been studied intensively [17-23]. Genomic sequence analyses show that the *S. aureus* genome encodes for approximately 2 600 proteins [24]. With the advent of the post-genomic era, there have also been many proteomic studies undertaken to better understand the biology of *S. aureus* (discussed in Section 1.2). Although a great deal is known about this pathogen, there are still no effective vaccines, nor any antibiotics that it hasn't developed resistance to. Hence there is still a need for a deeper understanding of *S. aureus* and how it causes disease in order to develop novel and effective therapies.

1.1.2 Pathogenicity

S. aureus is responsible for a range of infections in the human host varying from benign, localised skin infections to life-threatening systemic infections [25]. These include endocarditis, osteomyelitis, cellulitis, toxic shock syndrome, and necrotising pneumonia [19,26,27]. Before the discovery of antibiotics (penicillin), *S. aureus* infections had a mortality rate of 80 % [28]. Today, we are facing the prospect of a return to the pre-antibiotic era, with antibiotic resistance continuing to rise [29]. The mortality rate of methicillin resistant *S. aureus* (MRSA) has been noted to have surpassed that of AIDS in America [30,31]. Further, MRSA kills more than emphysema, Parkinson's, HIV/AIDS, and homicide combined in the US [32]. Hence, this bacteria is of escalating medical concern as it remains a major cause of both nosocomial [17] and community-based infections throughout the world [17,19,33]. This is partly due to the high adaptability of *S. aureus,* which is able to switch from commensal to pathogenic bacterium as a consequence of the repertoire of virulence factors that can be expressed to enhance infection and disease [34,35]. A large proportion of the *S. aureus* genome (22 %) [36] is able to undergo horizontal gene transfer. This can involve the exchange of virulence, fitness and, resistance genes [7,37] thus exacerbating the issues faced by these pathogenic, resistant *S. aureus* strains [21,37,38]. The role of phage inducible and related chromosomal islands (PICIs and PRCIs) have also been recognised to play an important role in lateral acquisition of virulence and drug resistance gene in *S. aureus* [39-41].

1.1.2.1. Virulence factors

S. aureus is an opportunistic pathogen that can reside in the host without causing disease, but can also quickly cause disease in immunocompromised individuals (e.g. lowered immunity or an open wound). This bacterium has been said to possess the broadest range, scope, and frequency of virulence factors when compared to other common bacterial pathogens [42]. As a commensal, *S. aureus* is an efficient coloniser and has evolved an impressive arsenal of sophisticated adherence proteins that recognise host molecules that promote adherence to host cells. The major class of adhesion molecules in microbes are known as "microbial surface components recognising adhesive matrix molecules" (MSCRAMMs) [43]. These molecules include proteins, lipoteichoic acids, and teichoic acids [44]. Various proteins in *S. aureus* have been noted to be part of this family and have been shown to be important for biofilm formation, host adhesion, and internalisation of the bacteria [43,45,46]. This group of virulence factors, the adhesins, is described more in Section 1.1.2.2.

Following colonisation, *S. aureus* can secrete a variety of molecules that are harmful to the host, known as exotoxins. Exotoxins include enterotoxins (exotoxins released in the intestine), nucleases, lipases, proteases, collagenases, glycosidases, hyaluronidases, and haemolysins. Due to their importance in infection these elements have previously been reviewed [47-51]. These proteins, in part, function by facilitating *S. aureus* to successfully scavenge for nutrients [47]. The secretion of such toxins can result in serious clinical symptoms, such as toxic shock syndrome in the host. This syndrome is caused by the release of super antigens by *S. aureus* species which results in a host cytokine storm [11]. The secretion of such toxins results in systemic effects without the bacteria itself spreading throughout the host. The rapid toxicity that *S. aureus* can induce in the host can result in a mortality rate of 5-30 % [11]. Another major class of toxins produced by *S. aureus* are haemolysins which lyse red blood cells, of which there are 4 types (α, β, γ and δ), with different strains expressing different haemolysins [47].

Not only does *S. aureus* secrete toxins that cause direct harm to the host, but they also produce immunomodulatory proteins. By binding, or even mimicking host proteins, this bacterium can effectively ‘hide’ from the host’s immune cells allowing it to proliferate. One example of this is the IgG-binding surface protein of *S. aureus* which binds host IgG, hence avoiding immune recognition [52]. Another example of this is the major histocompatibility complex (MHC) class II analog protein (MAP) which mimics the host MHC class II protein inhibiting the host T-cell response [53,54]. *S. aureus* has evolved the ability to express many such immunomodulatory proteins, allowing the bacteria to avoid the host immune response

[55-57]. This added layer of complexity within the host-pathogen interaction landscape needs to be better understood for intelligent vaccine design [55]. The virulence factor group that this thesis will investigate is surface proteins that aid in host adhesion.

1.1.2.2. Adhesins

One major component of host-pathogen interactions is the ability of bacteria to adhere to host surfaces. Most infections require the initial successful adhesion of bacteria to the host. Adhesion to the host is modulated by surface adhesion proteins that the bacteria express. The topic of surface adhesins in *S. aureus* has been investigated by several groups with a number of reviews being published [45,58-68]. It is believed that the adherence of *S. aureus* to host receptors occurs via adhesin families including MSCRAMMs which are covalently anchored to the cell wall [43,58,62,69], and non-covalently surface-associated adhesins such as the secretable expanded repertoire adhesive molecules (SERAM) [45,70]. These proteins bind to host ligands including fibrinogen, fibrin, and collagen. In most cases, specific *S. aureus* proteins have been identified to bind to a specific host ligand, and are often named after this function [71]. For the proteins that have been identified as adhesins thus far, studies have shown that they contribute to successful *S. aureus* infection by executing cellular attachment, cellular invasion, and prosthetic attachment via host ligands [58,71]. *S. aureus* cells with truncated adhesins or expression deficient mutants have been shown to delay, or lack, the ability to invade host cells and/or cause disease [72-76].

Currently there are over 20 MSCRAMMs that have been described in *S. aureus* [58], although it is likely there are other adhesive proteins residing on the surface that are yet to been characterised. This is because there have been no global proteomic studies of adhesins in *S. aureus* (such as pull-down studies using host ligands and *S. aureus* lysates), and *S. aureus* adhesins are known to be promiscuous (one protein capable of having multiple adhesive functions) [58,77]. Further, 50 % of the *S. aureus* proteome is hypothetical, containing conserved and unique hypothetical proteins whose function(s) remain unknown [78]. Hence, much more research needs to be conducted in this area, especially using global proteomic approaches involving pull-downs of whole cell lysates (WCL). The combination of mass spectrometry coupled with affinity chromatography represents systems approaches to uncover putative adhesins [79].

1.1.2.3. Glycosaminoglycans

One major group of host molecules that *S. aureus* utilises for adhesion to host cells, including macrophages and epithelial cells, are glycosaminoglycans (GAGs) [80]. These highly sulphated macromolecules decorate the surface of host cells as well as the extracellular matrix (ECM). There are multiple GAGs that can be presented on the surface of host cells, each harbouring a net negative charge [80]. The interaction between the pathogen protein/s and the host GAGs can either be specific or promiscuous (one pathogen protein may bind many GAGs, or vice versa leading to functional redundancy) [81]. Many adhesive properties of bacterial proteins can be highly redundant, and indeed this extends to *S. aureus* [58]. This makes blocking adhesins more challenging and needs to be kept in mind for future vaccine design [82].

One GAG of interest that interacts with *S. aureus* is heparin (HP). HP is a highly sulphated GAG that can be presented as a proteoglycan (PG, a GAG linked to a core protein) [83] and is produced and released from host basophils and mast cells [84]. As it is commercially available, it is one of the most commonly used GAGs in research studies [85]. Due to the physical properties of HP, it is an extremely useful molecule as it mimics the highly sulphated side-chains of GAGs [86]. Hence it is not only used to study ligand interactions in its own right, but to study interactions with various GAGs. Due to variations in the number of monosaccharide units, its mass can range from 15-20 kDa [81]. Heparin appears to be an important factor in the infection cycle of *S. aureus* as it not only facilitates binding, but it also aids in biofilm formation [87-89].

Heparan sulfate (HS) is a closely related, albeit less sulphated GAG. *S. aureus* captures HS on its surface in a dose-dependent manner [90] and HS mediates intestinal cell adhesion and invasion by *S. aureus* [91,92]. Further, co-incubation of enterocytes and *S. aureus* with HP and heparosan (the precursor to HP) blocks the adhesion of the bacteria to the enterocytes [93]. Only a few proteins have been implicated in HP and HS-binding in *S. aureus* thus far [90,94,95], and their identities and features that promote binding to HP remain poorly understood.

1.1.3 Moonlighting proteins

The work of Garrod [96], and Beadle and Tatum [97] led to the original concept that each gene encodes for a single protein and that each protein has one function. With this concept in mind, genomic data and derived amino acid sequences have been used to predict the function (and localisation) of proteins using bioinformatic techniques. Bioinformatics was coined in the 1970s as “the study of informatic processes in biotic systems” [98,99]. Once a set of proteins have been identified, they are often annotated using programs that attempt to predict their function, cellular location, and functional/structural domains through algorithms based on sequence homology with proteins whose function has been experimentally determined. Furthermore, there are also public databases which use experimentally verified data to determine protein localisation [100] and function (NCBI and UniProt) [101,102]. This use of bioinformatics in proteomics has followed the trend from its use in genomics with its demand soaring with the advent of large-scale proteomic studies. The advantage of bioinformatics is that it offers a quick, often semi-automatic process whereby biological relevance can be added to protein data (eg. protein identification and function from spectra obtained from mass spectrometry). Unfortunately, as many bioinformatics predictions are often genome-centric, they commonly fail to grasp the full complexity of the proteome (which is much more complex than the genome) [103]. These concepts have governed how we assign function to genes in genome sequence datasets. These algorithms influence how protein function is assigned but these prediction tools do not take into account the fact that often proteins are multifunctional and many have evolved moonlighting functions that cannot easily be predicted from a bioinformatics viewpoint [104].

By the 1980s, the idea that one protein could have more than one function (moonlighting) was presented by various publications (for eukaryotic cells) and later followed by moonlighting proteins being found in prokaryotes in the 1990s [105]. Moonlighting proteins are defined as proteins with multiple functions, although this excludes multifunctionality due to splice variants, gene fusions, families of homologous proteins, promiscuous enzyme activity, or proteolysis [106,107]. It should be noted that although proteolysis may result in multifunctional cleavage products derived from a single open reading frame (predicted protein), it does not fall under the current definition for moonlighting (Figure 1.1). Further, this concept of moonlighting does not include proteins that have the same function in different cellular locations [106]. Moonlighting proteins are often transported to other locations, a process known as “geographical moonlighting” [52,108]. This may result in proteins being found in non-predicted locations, and can impact the interpretation of proteomic datasets, especially that of the secretome (proteins secreted from the cell to the external environment) and surface proteome (proteins found on the cell surface) [109]. Bioinformatics is used to characterise such proteins, but as the predictions are often based on the translated genome, they cannot predict moonlighting capabilities, including geographical moonlighting which may place a classically cytosolic protein on the surface of the cell. There are no well described moonlighting motifs that would be able to be captured using prediction algorithms. Short linear motifs (SLiMs) that localise to surface-exposed, non-conserved regions within what are otherwise structurally-constrained molecules are thought to promote multifunctional behaviour [52,110,111]. These motifs have usually acquired a single point mutation, often enriching for positively charged amino acids within the sequence, profoundly altering the multifunctional behaviour of a SLiM and are hard to predict. Attempts to predict patterns in characterised moonlighting proteins to try and determine their distinctive features [112,113] has been problematic. Further, a number of researchers have proposed using multiple analyses to determine moonlighting possibilities from large-scale datasets [114,115]. These analyses are relatively new, and would still need to be validated through experimental data. For these reasons proteomic techniques, including mass spectrometry-coupled experiments, remain a “go-to” technology for the identification of potential moonlighting proteins [108].

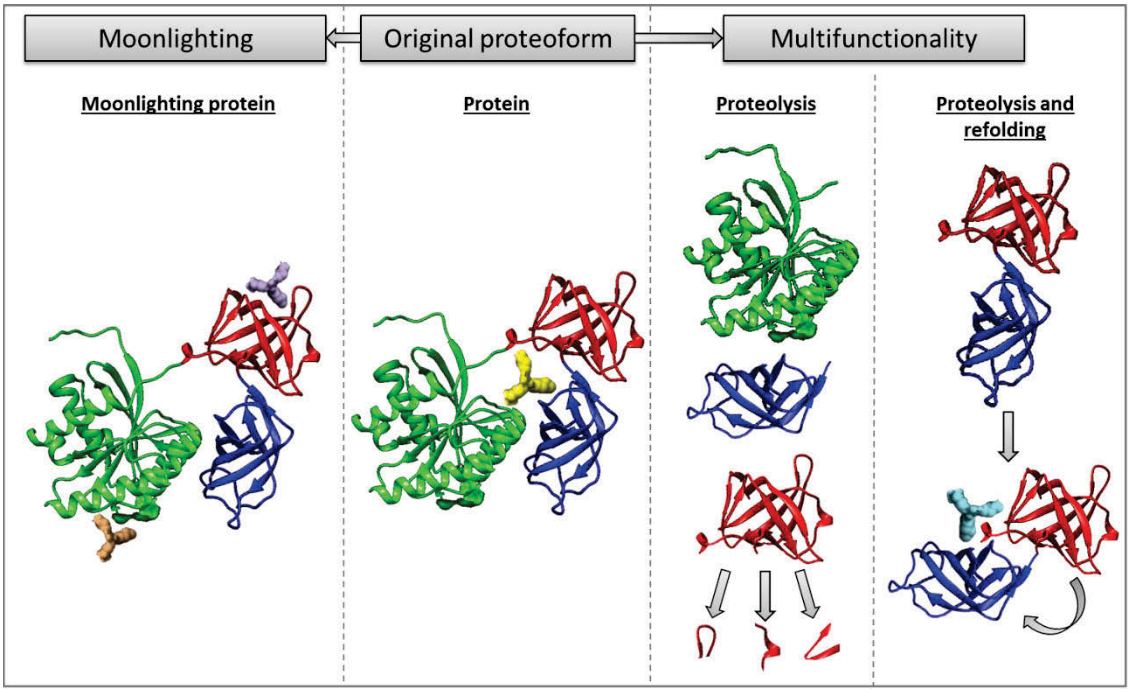


Figure 1.1 Potential mechanisms for the acquisition of multifunctional properties in proteins. The function of the original proteoform is dependent on its tertiary structure. The left panel depicts a true moonlighting protein, with active sites that are distinct from its canonical active site (see purple and orange substrate it can interact with). True moonlighting proteins need to maintain the tertiary structure required for its canonical role and does not acquire a secondary active site as a result of proteolysis. Protein multifunctionality is shown on the two right panels. Firstly, proteolysis may release domains that are functional in their own right (green, blue and red domains), or essentially recycle amino acids resulting in the release of SLiMs or other “hot spots” (smaller, red protein fragments at the bottom of the “proteolysis” panel). The rightmost panel shows how the cleavage product may respond to proteolysis by refolding, culminating in a new active site for that proteolysis product. This allows a new substrate to bind, shown in blue.

Bacterial moonlighting proteins have now been identified in a wide range of species, both pathogenic and commensal. The characterisation of protein moonlighting is a rapidly emerging field with proteins that have canonical functions in the cytosol being reported to have diverse functions on the cell surface and extracellular environment. As such, a number of reviews have recently been published in this area [44,52,107,112,113,116]. Moonlighting proteins have been identified in *S. aureus*, including: enolase [117], glyceraldehyde 3-phosphate dehydrogenase (GAPDH) [118], autolysin [119], and triosephosphate isomerase [120]. Many of these proteins perform their canonical function in the cytosol and are therefore predicted to be cytosolic (via bioinformatics algorithms). As with many bacterial moonlighting proteins [113], these *S. aureus* moonlighting proteins are metabolic enzymes. This means that each of these molecules is an ancient protein with a well-defined 3D-structure that enables it to execute its canonical function. Hence, any evolutionary mechanism that has allowed these proteins to become multifunctional cannot perturb canonical function including changes to the active site, as this would render the protein inefficient as a metabolic enzyme. The trend of many enzymes being discovered as moonlighting proteins is interesting as it goes directly against some of the moonlighting definitions as the current moonlighting definition doesn't include promiscuous enzymes [106,107]. The multifunctional capabilities of enzymes has long been known in both eukaryotes and prokaryotes [112,121-123] and is just one key reason why the definition of moonlighting may need to be adapted in the future to include multifunctional enzymes.

The presence of such proteins on the surface of *S. aureus* has, for a long time, been dismissed [124-127]. It is still poorly understood how classically cytosolic proteins that moonlight get to the external face of the bacterium [128,129] and this mechanism is usually described as "non-classical secretion". Non-classical secretion describes the secretion of any protein, or protein product, that cannot be accounted for by a known secretion pathway. Interestingly, non-classical secretion of proteins is linked to virulence in the closely related *Staphylococcus epidermidis* [130]. In many other pathogens, moonlighting proteins are involved in pathogenesis [131,132] (for example, an in-depth list of moonlighting functions of Ef-Tu can be seen in Chapter 4), however the secondary function of moonlighting proteins can be difficult to determine from its sequence or structure [104]. Therefore it is important to identify potential moonlighting proteins to target for functional assays. If the moonlighting function is important for survival or pathogenesis, the protein could make for a potential therapeutic target. Indeed, moonlighting proteins have been identified as therapeutic targets in other prokaryotes including GAPDH [133], α-enolase in *Streptococcus sobrinus* [134] and *Streptococcus suis* [135], arginine deiminase in *Streptococcus pyogenes* [136], trigger factor in *S. pyogenes* [136], macrophage infectivity potentiator proteins in *Legionella pneumophila* [137], and fructose-bisphosphate aldolase in *Streptococcus pneumoniae* [138] and *Neisseria meningitides* [139]. Hence, employing strategies to discover novel potential surface moonlighting proteins in *S. aureus* may aid in better understanding the pathogenesis of this bacterium and guide therapeutic target development [Jeffery 2015]. Further, such proteins may play important, yet to be characterised roles, in the virulence of *S. aureus*.

1.1.3.1. Protein degradation

Post-translational modifications (PTMs) of proteins are a widely employed mechanism to expand the functional proteome (Figure 1.2), modifications include (but are not limited to) phosphorylation, methylation, and acetylation [140]. PTMs identified in *S. aureus* include: cysteine phosphorylation [141], hydroxymethylation of asparagine and glutamine [142], oxidation, methionine clipping, acetylation, formylation, and proteolysis [143]. The protein modification that this dissertation will focus on is endogenous proteolysis, hereby referred to as protein cleavage. Proteins are cleaved for a number of reasons including natural degradation (including amino acid recycling), to release signal peptides, to activate a protein, or to cleave the protein for a yet known function [144]. A protein may be cleaved in one specific location, or a number of times across the amino acid chain, further, sequential cleavage can occur with sequential amino acids being cleaved (also known as “clipping”) [145].

S. aureus produces proteases which have been shown to be able to cleave both endogenous and exogenous proteins. Proteases encoded for in the *S. aureus* genome include cysteine proteases, metalloproteases, serine proteases, and staphopain [146,147]. A number of its secreted proteases have been described as major virulence factors [148,149], with expression levels varying between strains [146]. Although there has been much research into *S. aureus* proteases, it appears there is still more to learn as the current knowledge on proteases doesn't account for all staphylococcal proteolysis.

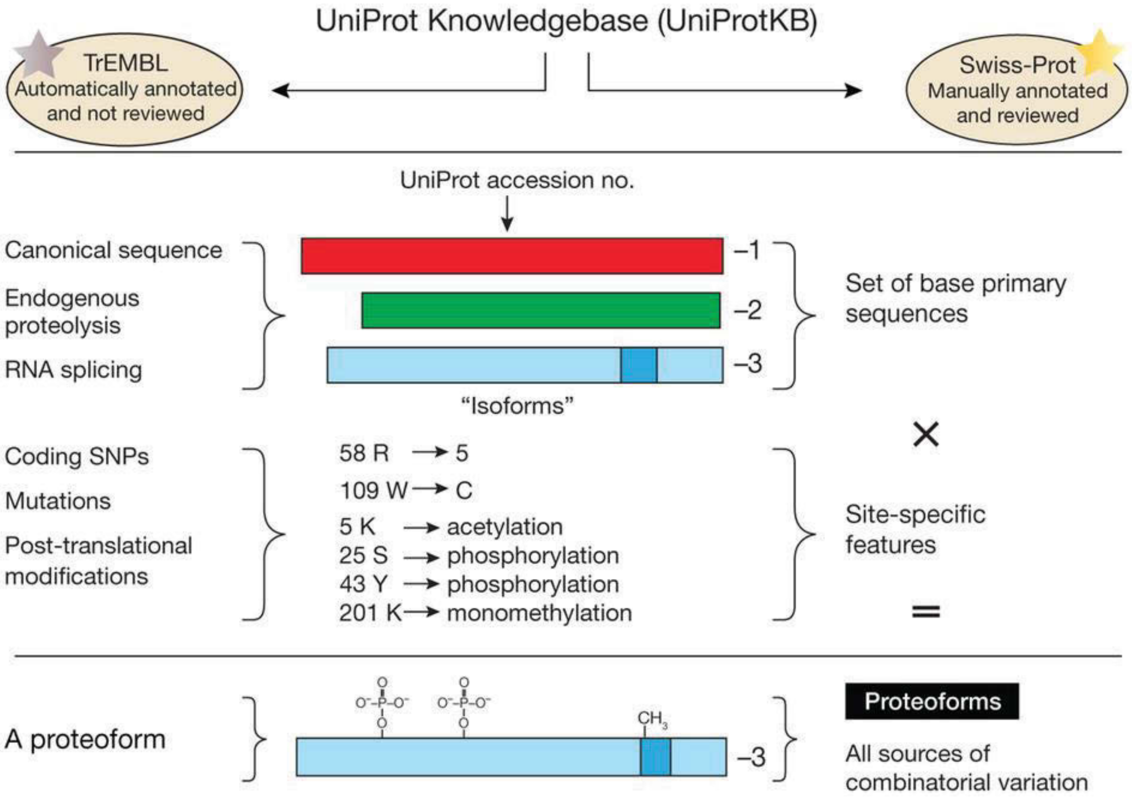


Figure 1.2 Schematic description of proteoforms.

Figure taken from Smith et al. 2013 [150]. Shows that one sequence (represented by a single UniProt accession number) may be modified in a number of ways. Endogenous proteolysis and RNA splicing affects a region of the protein, reducing the amino acid chain. Further to this, single amino acids can be modified in a number of site-specific modifications. Any combination, or number of these modifications may occur in a single protein increasing the proteoform potential from that one canonical sequence.

Protein cleavage events are not entirely uncommon in *S. aureus* [151-153], although the consequence of this, or the function of the cleavage products has not yet been investigated. With the identification of novel cleavage events in *S. aureus*, novel proteases have also been implicated in this proteolysis [152]. As such findings are quite recent, it appears we are only beginning to scratch the surface of *S. aureus* PTMs, including cleavage. Available data [154,155] from gel-based proteomic databases shows that *S. aureus* proteins can be found across a broad mass range, removed from their predicted position [156,157]. Indeed, many gel-based proteomic analyses of *S. aureus* appear to have identified cleavage (protein migrating at a different MW), but this is not investigated [156-160]. These abnormally migrating proteins are not usually discussed, and are often only seen on interrogation of the raw data. If they are mentioned, there is usually a brief sentence dedicated to their appearance, but no insight is given to peptide coverage or potential cleavage sites.

These abnormally migrating proteins may be migrating as such due to methodological anomalies. These include gel shifting, which is the observed unusual migration of proteins, and protein degradation during sample preparation [161,162]. The use of SDS in sample preparation can also interfere with migration as a protein’s ability to bind SDS can influence its migration in the gel [162]. Sample degradation can become an issue as it may obscure analysis of biologically relevant protein degradation (cleavage). As intact proteins are usually desired for in-gel methods, steps are taken to reduce protein degradation during sample preparation. The addition of protease inhibitors is often used to cease the activity of the naturally occurring proteases in the cell sample [163]. Further steps such as controlling temperature, denaturing the sample, and adding reagents to inhibit degradation should also be employed [161,163]. When endeavouring to analyse protein cleavage, it is important that steps are taken to inhibit protein degradation post-cell harvest so that a true snapshot of the proteoforms at the harvest time-point is seen.

1.2 *Staphylococcus aureus* proteomics

The post-genomic era of *S. aureus* started in 2001 [25] when the genomes of two *S. aureus* strains were first sequenced [22]. Since then, the proteomic analysis of *S. aureus* has been enabled. Using genome sequencing information, it has been estimated that the *S. aureus* genomes encodes for 2600-2900 proteins [164], with around half of these proteins being hypothetical [165]. This follows the trend that for many self-replicating organisms, protein function remains poorly understood [166].

The investigation of the entire *S. aureus* proteome presents researchers with a challenging task. As the proteome is defined as the complete set of proteins expressed under any one condition [167], this would include cytosolic proteins, membrane proteins, surface proteins, and secreted proteins. The isolation of each of these sub-sets of proteins may demand different methodologies, each coming with their own challenges. Hence, researchers often focus on one sub-set at a time. “Proteome” investigations of *S. aureus* are usually restricted to cytosolic proteins (i.e. collecting cells by centrifugation, lysing cells, removing membrane debris, and analysing the remaining proteins) or those proteins most easily solubilised by commonly used chaotropes (urea, thiourea) and surfactants (SDS, CHAPS) [168-171]. Unfortunately, such analyses overlook important sub-proteomes such as secretomes, surface proteomes, and membrane proteomes.

In 2009, Becher and colleagues aimed to extensively study the entire proteome of *S. aureus* [172] under standard laboratory conditions using two time-points (covering exponential and stationary growth). An unprecedented total of 1700 proteins were identified, with 1450 of these being quantified [172]. Their methodology covered 65 % of the predicted COL strain proteome, and to date, this remains the most extensive (protein identification wise) proteomics study published for *S. aureus*. However, this study did not include the analysis of protein expression in biofilms, any host-induced stress (e.g. cells grown in the presence of a host cell line), or host-mimicking media. Given the lack of environmental factors tested and the rapid increase in mass spectrometry sensitivity since this publication, it is likely there are many more proteins that could be identified in studies today.

1.2.1 *S. aureus* surface proteome

There have been several investigations into surface-associated proteins in *S. aureus* [124-127,153,172-177] (Table 1.1). Currently the methods of trypsin shaving and biotinylation seem to be the preferred method for isolating surface proteins. On top of whole cell (intact) surface analysis, membrane and cell wall extracts have also been isolated for surface studies. There have also been a number of studies investigating specific surface-associated proteins, but this chapter will only cover non-targeted approaches.

Currently, nine *S. aureus* strains have been analysed in surface proteome studies (COL [and mutants derived from this strain], USA300, RN6390, VP32, C2355, HIP5827, Phillips, ATCC 29213, and Newman) (Table 1.1). It is important that a wide range of strains are used for analysis due to the high proteomic variation noted among different strains. The high variability in the genomic data, enabled by the large variable portion of the *S. aureus* genome (see Section 1.1.2), indicates the potential variation that proteomic analysis can encounter. Dreisbach et al. applied trypsin shaving to 4 different strains of *S. aureus,* finding an overlap of less than 10 % in surface protein identifications [173]. A fifth strain (NCTC 8325) was excluded from further data analysis due to the limited overlap of identified proteins with RN6390 (a closely related strain) [173]. 87 proteins were identified on the surface of NCTC 8325, while only 39 were identified in RN6390, with an overlap of 21 proteins between the two related strains. To account for the increase of surface proteins in strain NCTC 8325, the authors concluded that NCTC 8325 was more susceptible to lysis, hence releasing more false "surface" proteins [173]. This may be due to the fact that many proteins with known functions in the cytosol were found in this NCTC 8325 surface proteome dataset. Although, when compared to the other strains analysed, the other surface proteomes still contained proteins with known functions in the cytosol. Even though lysis was not investigated, NCTC 8325 was omitted from further analysis. These studies highlight the fact that *S. aureus* proteomes are highly heterologous [173,178], but it also exemplifies a major issue within the field of surface proteomics (not just in *S. aureus*), where researchers attribute unexpected protein localisation(s) to cell lysis without any investigation into, or evidence, of lysis.

Many surface proteome studies include controls to check for, and account for cell lysis within their data. There are several techniques that can be used including CFU counts, microscopy, control incubation buffers (without enzyme), and quantitative gel analysis (and Western blots) of cytosolic marker proteins. The issue with many of these techniques is that they do not account for complete cell lysis during the growth of the cells where cellular contents are able to re-attach to the cell surface. Exploding cell lysis is now being more widely accepted as part of the natural growth cycle in many bacteria, and a way of providing "public goods" (including proteins) to the surrounding cells [179]. Hence, there may need to be a shift in how surface proteome data is interpreted. It is important to place more weight in experimental data over bioinformatic assessment of what should or should not be on the cell surface. It is common practice in surface proteome studies to analyse the experimental data with a variety of bioinformatics tools to show that the protein identified is predicted to be surface exposed.

Often, if the protein isn’t predicted to be surface exposed it is often exempted from further analysis. This is a classic case where dogma reinforces scientific prejudice. Unfortunately this workflow places more belief in the bioinformatic prediction over experimental data, leading to the loss of potentially important information. For example, enolase has been shown to be a surface exposed protein in *S. aureus* where it has a secondary (moonlighting) role as a plasminogen and collagen I binding protein [117]. If analysis was based on bioinformatics algorithms e.g. PSORTb, there is every likelihood that research would ignore the potential of this molecule playing a role in pathogenesis [180].

Among the *S. aureus* surface proteome studies, a large number of classically cytosolic proteins are consistently found on the surface of the cell (even with controls in place). For example, Solis et al. notes that Proteinase K shaving resulted in no lysis, although this method resulted in 55 out of the 79 (69.7 %) total identified proteins predicted to be of cytosolic origin [125]. Ventura et al. found more than half of their surface proteins (63 out of 113, 55.8 %) to be predicted to be classically cytosolic [124] and attributed their presence to cell lysis, despite equivalent colony forming units per mL (CFU/mL) before, and after, trypsin treatment [124]. Interestingly, Dreisbach et al. also found unexpected (cytosolic) proteins on the surface, and discussed the idea of moonlighting proteins in relation to this [173,181]. The phenomena of proteins being excreted to the surface (and extracellular area) of *S. aureus* that aren’t predicted to be surface exposed or excreted has recently been reviewed [182]. *S. aureus* has a number of well-defined secretion systems at its deposal for the transport of proteins, such as the secretory (Sec) and twin-arginine (Tat) pathways [164]. The signal motifs associated with these secretion systems are known, however they are not located in these extracytosolic cytosolic proteins. Ebner [182] discusses a number of mechanisms (for cell lysis hypothesis see Section 2.4) to explain cytosolic proteins being present on the surface or secretome, these include the Sec and twin arginine (Tat) pathway, ESAT-6 secretion system, holing-antiholin system, the action of prophages, impact of peptidoglycan structure, autolysins [183], and protein release upon cell division (from the septa) [129]. This highlights the complexity in characterising the surface proteome of an organism.

Proteins on the surface of the bacteria have evolved to interact with host molecules, and it is an important sub-proteome, especially in regards to pathogenesis. As they are exposed to the host immune system, they are under evolutionary selective pressure to avoid recognition, or even neutralise the host immune response [184]. The surface proteome is also a large repository of virulence factors, and a better understanding of how these are presented to the host is still needed. Investigation of the surface proteome has led to important discoveries such as the presence of novel leukotoxins that lyse human polymorphonuclear cells, on the surface of strain USA300 [124]. Given the large numbers of cytosolic proteins on the surface that have not yet been investigated, and the ability of *S. aureus* to produce moonlighting proteins, it is likely there is still more to the surface proteome story of *S. aureus*. Surface proteins are vital to host-pathogen interactions, and proteomics offers a tool in which to identify novel surface proteins whose functions remain to be elucidated [185,186]. Further, proteomic strategies also provide a faster way of efficiently discovering new vaccine candidates (when compared to standard biological assays) [187]. As we are in desperate need of a new way to combat resistant *S. aureus*, proteomics may hold the key to unlocking a new therapeutic.

Table 1.1 Surface proteome studies of *S. aureus*.

Publication	Method summary	Strain	Surface proteins identified in publication	Notes
Monteiro et al. 2015 **[177]**	1h Trypsin shaving → LC-MS/MS	C2355	236 proteins	
Hempel et al. 2011 **[126]**	15min Trypsin shaving → LC-MS/MS 1h biotinylation → 1D-SDSPAGE → LC-MS/MS	COL	246 proteins 246 proteins	Also tested under iron-limited conditions.
Driesbach et al. 2010 **[173]**	45min Trypsin shaving → LC-MS/MS	RN6390 Newman USA300 COL	39 59 24 47 96 total	
Hempel et al. 2010 **[127]**	2h Biotinylation → 1D-SDS-PAGE → LC-MS/MS	COL WT COL ΔsigB	309 proteins in growing (exponential phase) 441 proteins in non-growing (stationary phase)	Quantification of proteins
Solis et al. 2010 **[125]**	15min Trypsin shaving → LC-MS/MS 15min Proteinase K shaving → LC-MS/MS	COL	67 (reduced to 40 with false-positive results) 79 (reduced to 69 with false-positive results) 132 (104 final total)	Only trypsin false positive control data applied to all data sets (including Proteinase K).
Ventura et al. 2010 **[124]**	1h Trypsin shaving → HILIC/SCX → RPLC → MS/MS	USA300 (strain LAC)	113	
Becher et al. 2009† **[172]**	2h Biotinylation → 1D-SDS-PAGE → LC-MS/MS Membrane extract→ → 1D-SDS-PAGE → LC-MS/MS Membrane extract → 15h Proteinase K shaving → 6h Chymotrypsin Digestion → LC-	COL	Biotinylation results: 146 cell surface-associated proteins were identified Other results not disclosed	Part of a global study, not declared as surface proteome study.

	MS/MS			
Glowalla et al. 2009† **[174]**	Cell wall preparation → 2D-PAGE (pH 3-10, pH 4-7) → (proteins of interest) → MALDI-TOF	ATCC 29213	39 proteins* *immunogenic spots cut of of 2D-PAGE gel and Identified	Immunogenic proteins of interest were identified using western blotting.
Wolff et al. 2008† **[176]**	15h Proteinase K shaving of membrane → 6h Chymotrypsin digest → RPC-MS/MS Membrane preparation → 1D-SDSPAGE → in gel trypsin digest (12 slices) → RPC-MS/MS Membrane preparation → chymotryptic-tryptic digestion→ SCX chromatography (12 fractions) → RPC-MS/MS	COL	121, 118, 112, 122, 132, and 135 proteins (six replicates) =182 493 and 526 proteins (2 replicates) =572 289 and 262 proteins (2 replicates) =321	68 proteins identified in all three methods. Total of 271 integral and 86 peripheral membrane proteins identified.
Gatlin et al. 2006† **[153]**	4hs enzymatic cell wall digestion (CWDS) → LC fractionation → 2D-PAGE 24cm (pH 4-7) → In gel trypsin digest → nano-ESI-LC-MS/MS and MALDI-TOF TOF 4hs enzymatic cell wall digestion (CWDS) → DEAE LC fractionation → SCX fractionation → trypsin digest → LC-MS/MS 4hs non-enzymatic cell wall digestion (neCWS) CWDS, WCL (loaded separately) → 2D-PAGE 24cm (pH 4-7) → In gel trypsin digest → nano-ESI-LC-MS/MS and MALDI-TOF TOF	VP32	144 proteins of interest. 284 total Full data not shown	*The cell envelope is defined here as encompassing the cell surface, the cell wall, and extracytoplasmic cell membrane components.

	30min Biotinylation → CWDS prepared as above → biotinylated proteins isolated with avidin → nano-ESI-LCMS/MS.	HIP5827 (biotin)		
Nandakumar et al. 2005† **[175]**	4 cell wall preparations: i) enzymatic treatment with lysostaphin for 30min ii) Boiling in the presence of SDS, iii) extraction with LiCl, and iv) extraction using ProteoPrep membrane extraction Kit (PROT-MEM, Sigma). → 2D -PAGE (pH 3-10) → in-gel trypsin digest → MALDI-TOF	Phillips	36 proteins identified, many proteins spots not analysed.	Different numbers of reproducibly displayed protein spots shown in each method: i). 121 spots ii). 101 spots iii). 85 spots iv). numbers for ProteoPrep not shown.

Includes publications studying the cell surface, cell membrane, and cell wall of *S. aureus*. As cell membrane and cell wall studies may not identify truly exposed surface proteins, studies that include these analyses have been marked with a †.

1.3 The resistance apocalypse

S. aureus has a reputation as a highly variable, rapidly evolving pathogen [21,25], swiftly developing resistance to all classes of antibacterial drugs. Strains develop resistance to the same antibiotic independently, leading to a range of different, resistant strains evolving concurrently [18]. *S. aureus* possesses mobile genetic elements that have the ability to undergo horizontal gene transfer (HGT), to spread resistance or survival genes [188]. These genotypic changes can lead to phenotypic changes, but phenotypic changes can also result as a direct response to the host environment or antibiotic exposure. By living in a biofilm, where various microbial species can co-exist within an exopolysaccharide matrix [189], *S. aureus* can increase its resilience to antimicrobial agents [190].

S. aureus can also persist intracellularly as small colony variants (SCVs) [191] a phenotype that is only recently being appreciated as it was long ignored, due to the belief that the SCV phenotype was non-virulent [192]. The pharmaceutical industry's interest and successful discovery of new classes of antibiotics has slowed in the past few decades adding to the urgency in this research area [193,194]. Hence, *S. aureus* infections are now very difficult to treat and can result in a chronic infection and even death.

1.3.1 Lack of current therapeutics

With the discovery of penicillin, *S. aureus* was initially well-controlled, but it only took two years for *S. aureus* to develop resistance to it [6]. Currently, *S. aureus* strains have been found to be resistant to all commercially available antibiotics such as penicillin, methicillin, and vancomycin [21]. Although invasive MRSA was found to be declining in a 2013 US based study [1], the frequency of Vancomycin intermediate *S. aureus* (VISA) and Vancomycin resistant

S. aureus (VRSA) (vancomycin being a later line of defence than methicillin) has been reported as increasing in 2015 [195]. Strains resistant to last-line antibiotics have been identified across the world [196]. To compound this issue, no new classes of antibiotics have been implemented for use with *S. aureus* infections in over three decades [196]. As the development of antibiotics has slowed down, and *S. aureus* is known to quickly develop resistance, other therapeutic mechanisms are being investigated. These include phage therapy, quorum sensing inhibitors, and most commonly, vaccination strategies [197].

1.3.2 Beyond antibiotics: the vaccine race

Despite much research and multiple trials, there has been no successful vaccine to date that can provide protection against *S. aureus* [196]. For such a problematic pathogen, the discovery of a successful vaccine would represent an enormous contribution to human health. The shift towards preventative measures over treatment has been shown to also save money, with studies investigating general preventative practice against *S. aureus* infections [198,199]. The implementation of vaccines would also lower the selective pressure in the spread of antimicrobial resistance [200], allowing antibiotics to be used only in extreme cases. Many researchers have found vaccine candidates [43,201-209], but all clinical trials have failed or been suspended before being completed. Due to the barrage of research in this area a number of review articles have been published in the last couple of years summarising these efforts to date [195,196,210-212]. Currently, there are several potential therapeutic targets that are undergoing phase two trials, with none in phase three [211].

Many of these candidates are targeting surface molecules that have been identified by targeted, hypothesis-driven approaches including reverse vaccinology. The evolvement of the "omics" studies in *S. aureus*, namely genomics, transcriptomics, and proteomics in the post-genomic era have provided comprehensive datasets to initiate vaccinology investigations [196]. Specifically, the use of large-scale genomic data to drive vaccine discovery is known as "reverse vaccinology" (RV). RV offers a rapid, streamlined approach to identifying potential new vaccine targets using *in silico* methods [213]. This technique has been fruitful in providing new vaccine targets [214]. However, as this is essentially a bioinformatic pipeline used to select targets for testing from genomic data, it carries forward all of the downsides of genomic-based bioinformatic predictions. Hence such pipelines are limited by the quality of the omics data and prediction algorithms. As discussed above, there are still many flaws in bioinformatics predictions of protein data, and as therapeutic agents commonly target proteins, this can result in incorrect or missed antigen targeting.

There are a number of features that are desirable in a vaccine including a target that is specific to the pathogen, but expressed across all strains, an easily accessible target, a target that is expressed during infection, and also a target that is "essential" to the bacterium's survival or ability to compete. Further, as bacteria can easily adapt and regulate various proteins or may not translate various genes, vaccines based on a single protein/gene or cell component may not be successful [196,215]. Indeed, most reviews recommend the investigation and trials of multivalent vaccines against *S. aureus* [42,195,196,210,216-220], although some argue against the proven efficacy of multivalent vaccines [221]. Such issues and the lack of success with vaccine development in *S. aureus* have been discussed and reviewed [42,195,196,210,212,215-222]. Although *S. aureus* is an extensively studied pathogen, there are still many areas that lack examination that may be the reason behind the many failed vaccine trials. One particular area that will be discussed in this dissertation is the underestimation of functional redundancy in *S. aureus*. This issue within vaccine development has now been realised [195,218,222], but the full scale of functional redundancy in *S. aureus* is yet to be determined. By better understanding the repertoire of compensatory proteins *S. aureus* holds in its arsenal, more effective vaccine candidates may be identified for future testing.

1.4 Project Aims

Aim 1: Characterise surface proteins in *S. aureus*.

Aim 1 is addressed in **Chapter 2**, where the analysis of *S. aureus* surface proteins is described. Using biotinylation and trypsin shaving, over 700 proteins were identified on the surface of *S. aureus* SH1000. By using these two methods, this allowed for surface-exposed regions of the proteins to be mapped, cleavage fragments retained on the surface identified, and further evidence for surface localization to be obtained.

Aim 2: Determine the repertoire of proteins *S. aureus* possesses that bind heparin.

Chapter 3 aimed to identify proteins from *S. aureus* that have the potential to bind the archetype GAG, HP. As HP is used to mimic host GAGs and DNA, proteins identified may have various roles as putative adhesins. This dataset identified over 600 proteins that were retained in the HP column. These proteins represent putative HP-binding proteins, and are deemed as novel putative adhesins in *S. aureus*. This dataset was compared to the surface proteome dataset (**Chapter 2**), as adhesins that are also surface exposed represent novel targets for therapeutic intervention. This dataset comprises of the first ever global study of HP-binding proteins in *S. aureus*.

Aim 3: Characterise the novel *S. aureus* surface moonlighting protein, Ef-Tu.

As many classically cytosolic proteins were identified in the surface proteome analysis of *S. aureus* (outlined in **Chapter 2**), the third aim presented in this thesis was to characterize a surface moonlighting protein of interest. Although data was consolidated for a number of surface moonlighting proteins, Ef-Tu was of particular interest as it was also found to be a highly cleaved protein that was retained by HP affinity chromatography (**Chapter 3**). Therefore, the third aim, presented here as **Chapter 4**, was to further characterise Ef-Tu in *S. aureus* to gain a better understanding of how Ef-Tu has evolved to be a surface exposed, potential adhesin.

Overall investigation techniques

For the analysis presented in this thesis, *S. aureus* strain SH1000 was used as the essential genes list for this strain [223], and the genome of the parent strain, *S. aureus* NCTC 8325 had been published [17]. Throughout these chapters, various major experimental themes were used to acquire and analyse the data presented.

The vast majority of proteomic experiments use a peptide-centric approach where peptides are derived by specific enzymatic cleavage of mature proteoforms, known as ‘shotgun’ or ‘bottom-up’ techniques [25,224]. By analysing peptides, MS instrument sensitivity is increased and fragmentation spectra easier to interpret, allowing for greater proteome coverage. The major limitation to greater proteome coverage by shotgun MS methods lies in the sample complexity and its dynamic range [224] which can hinder the identification of low abundance proteins if no pre-fractionation is utilised. Sample complexity and dynamic range [224] refers to the number of proteins in a sample and the range of concentrations at which they are present. The dynamic range, or the difference in concentration between least abundant protein and most abundant protein, in cellular samples can be as large as six orders of magnitude (10^6), and even higher in plasma (10^{10} – 10^{12}) [225]. In *Leptospira interrogans*, proteomic analysis showed that the dynamic range in this species was 1:40,000 [226]. This results in peptides derived from high-abundance proteins masking the presence of the peptides derived from the low-abundance proteins and hence decreasing proteome coverage and the sequence coverage of individual proteoforms. As samples often include multiple proteins at various concentrations, the more a sample is fractionated and simplified, the higher the statistical likelihood of the instrument detecting the peptide becomes (especially important for peptides of low abundance). Consequently extensive pre-fractionation before LC-MS/MS analysis of a sample is often encouraged [227]. However, there needs to be a practical balance with the amount of fractions created, as more samples increases instrument and analysis time [228]. One should also be aware that the data gathered from LC-MS/MS experiments may be limited by the quality of the database that is being searched. As data (MS spectra) is mapped back to the database (usually genome-based theoretical protein sequences), annotation errors in the database can cause misidentification [228].

By fractionating the sample on the protein level with a gel-based technique, the mass context of a proteoform is preserved as all peptides from a proteoform, possibly created from a larger precursor proteoform, are present in the same MS sample (a specific gel slice/spot). Two major gel electrophoresis methods are 2-dimensional polyacrylamide gel electrophoresis (2D-PAGE) and 1-Dimensional sodium dodecyl sulfate polyacrylamide gel electrophoresis (1D-SDS-PAGE) (Figure 1.3). 2D-PAGE separates proteins in two orthogonal dimensions, usually by isoelectric point (pI) followed by mass [224]. By separating proteins in 2-dimensions it is possible to see individual protein isoforms on the gels (seen as dots – refer to Figure 1.3). This particular method can be very useful as it can indicate endogenous proteolysis, hereby referred to as cleavage [229].

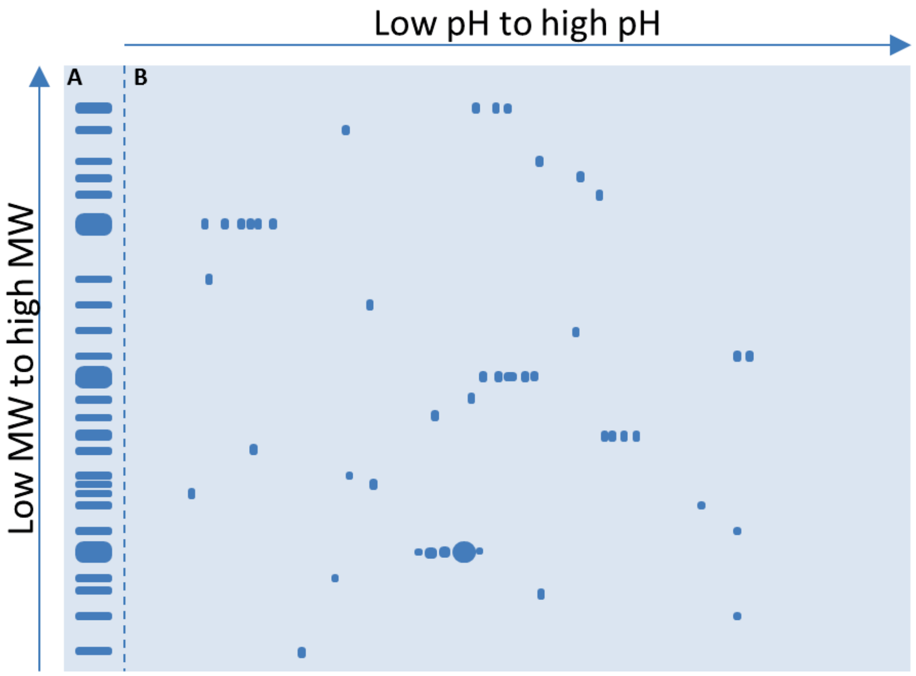


Figure 1.3 Gel electrophoresis for separation of a protein sample.

A. 1D-SDS-PAGE where proteins are separated by MW. This generates proteins that migrate as “bands” down the gel, in a complex sample (eg. a whole cell lysate [WCL]), individual protein bands may be indistinguishable and one band may contain a number of proteins. **B.** When proteins are separated out by 2D-PAGE, proteins (or proteoforms) appear as “spots” throughout the gel. This lowers sample complexity as what might appear as one band in 1D-SDS-PAGE may be separated out into several protein spots. Proteoforms may also be distinguished in this method as various isoforms of the one protein may cause a trail (PTMs may cause a slight shift in the pH of the protein).

Cleavage is one type of post-translational modification, resulting in proteoforms, that has the ability to expand the capacity of a genome [166]. Proteoforms can arise from a number of modifications not predicted by the genome (open reading frame - ORF), including alternate splicing, and post-translational modifications (PTMs) (Figure 1.2). As PTMs play a role in bacterial pathogenesis [186] they were named a major focus of future proteomic research in 2013 [230]. Hence many of the proteomic experiments undertaken and presented in this thesis employ in-gel electrophoresis for its ability to study cleavage events in proteins. Although cleavage is known to occur in *S. aureus* [151-153], there has yet to be a global study of this, and therefore the data presented here contributes to the first global study of cleavage in this pathogen.

The use of complementary methods to analyse the surface proteome dataset allowed for the preservation of mass context within the biotinylation dataset, and the trypsin shaving technique allowed for the approximate mapping of surface exposed residues within proteins (Figure 1.4). Knowing which regions are exposed within the protein in vital to therapeutic design. These two techniques (trypsin shaving and biotinylation) also resulted in a more robust dataset, helping build evidence for surface exposure. Utilising these two complementary methods have rarely been used for the analysis of the *S. aureus* surface proteome (see Table 1.1). Hence, many other previous studies lack the depth of coverage and characterisation of surface proteins that these methods allow. This was a robust, global approach which included 2 methodologies (surface trypsin shaving and surface biotinylation), all of which were analysed as biological triplicates. By also analysing biotinylated proteins via both 1D-SDS-PAGE and 2D-PAGE, more protein coverage information was obtained in this study. Further separating proteins in a second dimension results in each MS sample (a specific gel slice/spot) having reduced sample complexity, increasing chance of peptide selection, fractionation and hence, protein identification. Biotinylation coupled gel electrophoresis allowed for the identification of post-translational modifications such as endoproteolytic cleavage, specifically identifying cleavage products that reside on the cell surface. As no previous analyses have focused on the cleavage products on the surface of *S. aureus*, this is a layer of complexity that has yet to be realised in surface proteome studies until now.

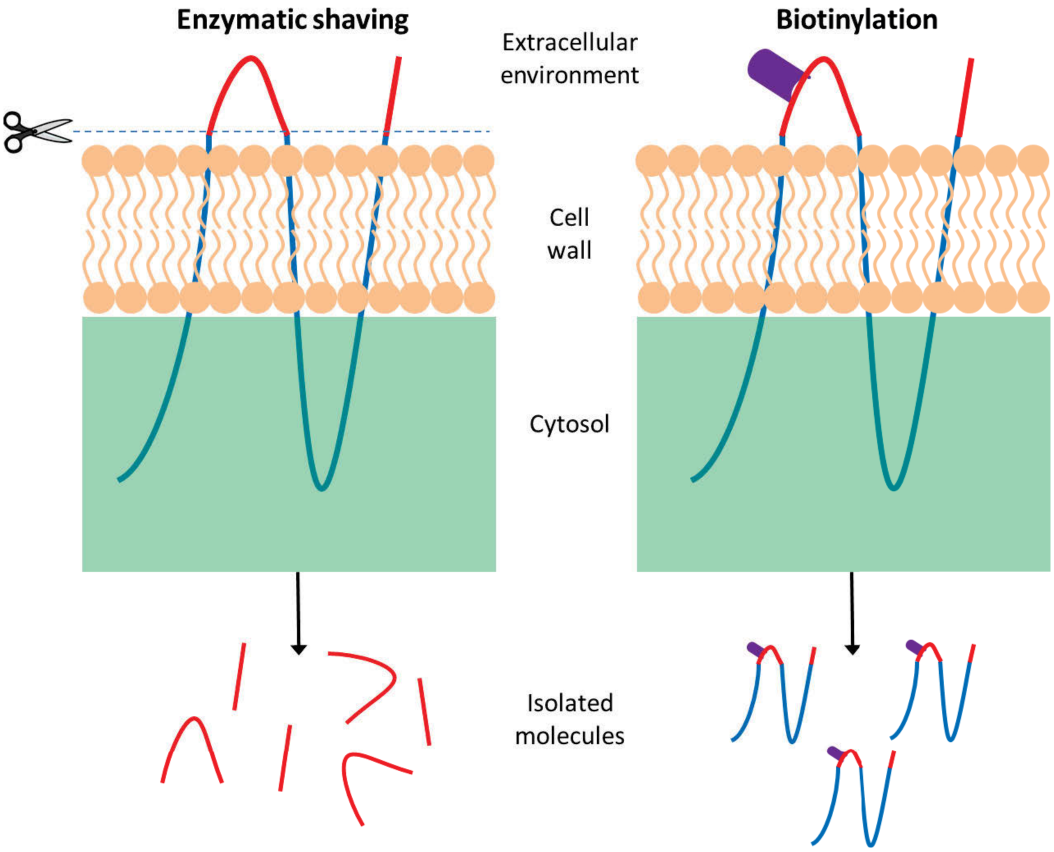


Figure 1.4 Difference between what portion of a surface protein can be isolated using different methodologies.

Both methodologies require a portion of the protein to be accessible to the reagent. The left side shows enzymatic cell surface shaving, where whole cells are treated with an impermeable enzyme that has the ability to cleave proteins. Enzymes used in cell shaving, typically trypsin, cut at specific residues. This method releases peptides that are surface exposed and accessible to the enzyme, but if there is an external loop (∧), two cut sites need to be made to release that portion of the protein. On the other hand, when whole cells are incubated with a membrane impermeable reagent such as NHS-biotin (shown on the right), the biotin (⬟) tags any accessible sites (primary amines) on the protein. These proteins then need to be isolated by lysing the cells and using affinity chromatography to separate out tagged (surface) proteins. This results in the isolation of intact proteins, or proteoforms that are presented on the surface.

The next methodological theme followed was to give more weight to experimental data than bioinformatics predictions. Often data is ignored if the bioinformatics predictions do not match experimental data (eg. bioinformatically predicted cytosolic proteins found in surface proteome data). In these datasets, those proteins that were identified in our surface proteome studies, but bioinformatically predicted to reside in the cytosol were not excluded from further analyses in this study. This theme extended to the HP-binding experiments. Proteins identified in this study may not have specific binding motifs, but were including in the analyses as they may be novel adhesins and contain uncharacterised motifs. Indeed, the identification of cleavage events relied on the experimental data as cleavage events are not able to be predicted by perusing genomic data.

All these experimental approaches were non-reductionist so as to not bias a particular outcome (although each method has distinct advantages and disadvantages). By coupling in-gel techniques with off-gel, peptide-centric analytic techniques, proteoform mass context could be maintained (allowing for proteoform identification) while still exploiting the sensitively that peptide analysis provides. This use of on-and-off gel techniques has previously been recommended in the literature [167,231,232]. This resulted in large, global datasets for *S. aureus* surface proteins and potential adhesins. As host-pathogen interactions in *S. aureus* involve a large number of proteins, using a global approach meant that this complexity and functional redundancy are likely to be exposed during the analysis.

Overarching aims

The overall aim of this thesis is to present data that can guide the selection of novel targets for future research into therapeutics against the human pathogen, *S. aureus*. The following chapters include data on the novel findings in regards to surface proteins, adhesins, and protein processing and presentation, mainly on the surface of *S. aureus*. These new findings may assist in the development and design of future therapeutic agents.

Chapter 2. The surface proteome of *Staphylococcus aureus*

Declaration

This chapter is being prepared for manuscript submission in combination with Chapter 3 (Putative HP-binding proteins of *Staphylococcus aureus*). All data obtained and analysis performed has been done by the author unless otherwise specified. Neo-N-termini analysis was performed and analysed by N. Strange. Rabbit anti-DnaK antibodies and control (zero time) bleeds were produced by D. Stipic in association with The Elizabeth Macarthur Agricultural Institute (EMAI).

2.1 Introduction

S. aureus is a major cause of both nosocomial and community acquired infections. This bacterium is part of the ESKAPE (*Enterococcus faecium*, *S. aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumanni*, *Pseudomonas aeruginosa*, and *Enterobacter* species) group of pathogens as it is a major problem in hospitals and can be multi-drug resistant [233]. Multi-drug resistant (MDR) infections were declared in the top three threats to global public health in 2016 [234]. Resistant strains of *S. aureus* pose a huge financial burden on the healthcare system, as they cost approximately double to treat in comparison to susceptible *S. aureus* strains [12]. These increased costs result in Hospital acquired MRSA (HA-MRSA) costing the European Union an additional € 380 billion dollars annually [13]. Not only does MDR *S. aureus* cause a huge financial burden, but the morbidity and mortality rate are also increasingly concerning. In the US, MRSA kills more than emphysema, Parkinson’s Disease, HIV/AIDS, and homicide, combined [32], and *S. aureus* remains a prominent cause of both nosocomial[17], and community-based infections worldwide [17,19,33].

S. aureus can display resistance to all classes of clinically-relevant antibiotics. Hence, there is an urgent need to develop vaccines against *S. aureus*. This preventative measure is expected to result in lowered mortality rates and associated costs [198,199], and it would also lower the burden on antibiotic use, decreasing selection for resistance and reserving antibiotics for extreme cases [200]. All vaccine trials to date against *S. aureus* have failed to demonstrate acceptable levels of protective efficacy [196]. In order to produce an efficacious vaccine, a better understanding of how *S. aureus* causes disease and colonises biotic surfaces is needed. Importantly, key antigens that enable this pathogen to adhere and proliferate in a host need to be identified and characterised. One major class of antigens that are investigated for therapeutic benefits are the surface proteins of bacteria [202,235]. Surface exposed proteins tend to be accessible and play a key role in binding host receptors, sensing environmental cues, disarming immune effector molecules, invading host cells, and are often the first point of interaction with the host's immune system [187].

Surface proteins are defined as proteins that, even in part, are exposed on the surface of the bacteria. They can be tethered to the membrane by an N-terminal lipid anchor (e.g. lipoproteins) or pass through a lipid membrane several times via transmembrane domains. Proteins can associate with the membrane by non-covalent interactions (eg. ionic association to the surface), while other can covalently bond to the cell wall (eg. by a sortase if the protein contains a LPXTG signal) (Figure 2.1) [61,181,236,237]. The *S. aureus* surface proteome has been analysed using a variety of proteomic tools (Table 1.1). The analysis in this chapter incorporated two complementary methods, trypsin shaving and surface biotinylation, a combination which is uncommon in the *S. aureus* literature (Table 1.1). By using this combination, the data obtained can start to build not only a picture of what proteins are on the surface of *S. aureus*, but also how they are exposed; ie. what portion of the protein is exposed and if there are cleaved protein products on the surface (Section 1.4, Figure 1.4). Further, separation of the biotinylated proteins using SDS-PAGE allowed for the application of in-gel analysis allowing mass context of extracted proteins to be observed.

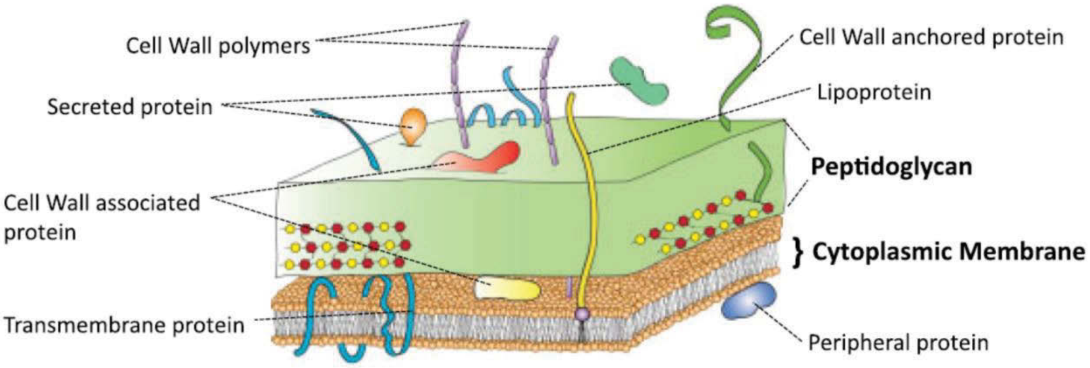


Figure 2.1 Association of proteins with the (Gram positive) bacterial cell surface.
Figure taken from Solis et al., 2011 [238]. There are 4 major classes of surface proteins, which are depicted above. These proteins may be bound to (lipoproteins) or transverse through (membrane proteins) the cell membrane. Proteins can interact with the cell wall with either covalent or non-covalent bonding.

Often, a large number of cytosolic proteins are identified in surface proteome analyses. For example, Gatlin et al. stated that over 200 of the proteins identified as part of their study did not contain any motifs or signals responsible for the surface localisation of those identified proteins [153]. Another surface study found 55.8 % of proteins identified were predicted to have a cytoplasmic location [124]. Dreisbach et al. summarised this phenomena in a 2011 review [181] where she showed the amount of cytosolic proteins in the collected surface data across a range of publications (Figure 2.2). The significant white panel in Figure 2.2.B shows that cytoplasmic proteins are identified in abundance on the surface of *S. aureus*. Interestingly, these proteins are often deemed to be contamination due to cell lysis or regular cell turnover

[124-127]. Therefore, this collection of proteins is usually excluded from further analysis. However, cellular integrity is usually also investigated in such analysis and no significant cellular death, lysis, or debris is reported [125]. For example, when Solis et al. used Proteinase K to shave cells, this resulted in no lysis, although this still resulted in 55 out of the total of 79 (55.7 %) of the identified proteins predicted to be cytosolic [125]. Due to this common issue, control methods have been adapted by some researchers including the use of a false-positive control where cells are incubated in the buffer without enzyme (trypsin or proteinase K) [125]. Any peptides identified in the false-positive experiment are subtracted from the surface proteome dataset. Even with this false positive method adjusting the data, still over 50 % of surface proteins identified are proteins that perform their canonical function in the cytosol [125] [181]. Despite their best efforts to account for “false positives”, this method doesn’t account for the phenomena of surface re-association (by cytosolic proteins). As this has been shown to occur in *S. aureus* [239,240], and such proteins shouldn’t be excluded from surface proteome dataset lists. The importance of such classically cytosolic proteins on the surface of *S. aureus* has yet to be fully explored (some classically cytosolic proteins have already been investigated [117,118,120]) and further information on how they are displayed will help with the future characterisation of such possible moonlighting proteins and novel therapeutic targets.

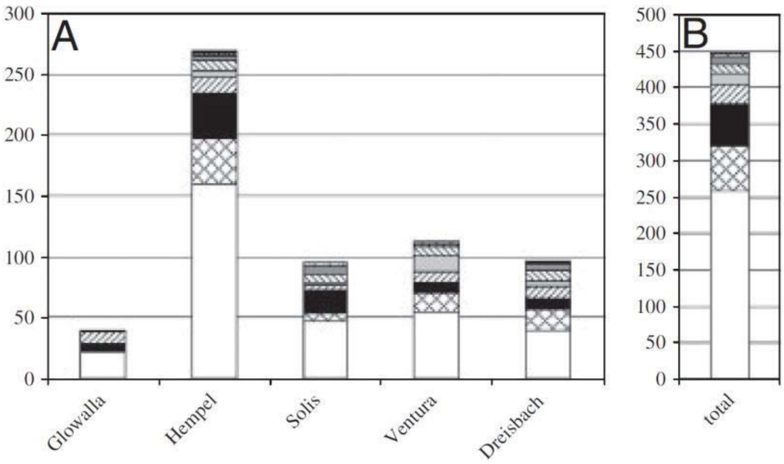


Figure 2.2 Graph representing the amount cytosolic proteins identified on the surface of *S. aureus*.

A. The amount of proteins predicted to be cytosolic (white bar) identified in five different *S. aureus* surfaceome studies [124,125,127,173,174] figure taken from Dreisbach et al. 2011 [181]. This set of summary data **B**. Shows that over 50 % of the proteins identified across these listed surface studies are predicted to be cytosolic.

A number of surface moonlighting proteins from *S. aureus* are predicted to be cytosolic. Currently, online databases of moonlighting proteins [241,242] state that four *S. aureus* proteins have been assigned moonlighting functions, these are; enolase [117], GAPDH [118], autolysin [119], and triosephosphate isomerase [120]. As the phenomena of surface moonlighting is now seen to be widespread amongst prokaryotes [44,52,107,113,116], and with increasing numbers of surface moonlighting proteins being identified in other bacteria, this sub-population of previously largely ignored surface proteins may prove to be important novel therapeutic targets.

The *S. aureus* proteome is extremely variable, and as such, there is no one strain, growth phase, or phenotype that can represent the entire *S. aureus* proteome. This variability extends to the surface proteome [181], with different strains (Newman, COL, RN6390, and USA300) having a surface proteome overlap of less than 10 % (under the same growth conditions) [173]. As the repertoire of proteins expressed on the surface of (and secreted by) *S. aureus* changes with growth phases [64,172], all phases should be investigated. Further, proteomic investigations should be reflective of the life forms found in infectious states and should include lifestyle variations such as L-forms (cell wall deficient), SCVs [243-245], biofilms, and co-cultured bacteria [186]. Unfortunately, due to their tendency to readily revert to the normal form [246,247] and the complex variables involved, these studies are not common [248]. Currently the focus of surface proteome studies has been on planktonic, exponential phase cells [64], although limiting analysis to one growth phase (*in vitro*) may neglect identifying other proteins with the ability to remain on the surface (eg. proteins that are excreted and re-associate with the surface at a later growth phase). As expression profiles can change *in vivo*, it is important to identify all possible proteins that possess the capability of adhering to the *S. aureus* surface. The complexity of protein expression in bacteria is further compounded by post translational-modifications. These modifications that occur within proteins (after synthesis) can produce multiple proteoforms from a single open reading frame (ORF) (See Section 1.1.3.1) [150]. Such modifications can include methylation, glycosylation, oxidation, acetylation, phosphorylation and proteolytic processing to name a few. This is best demonstrated in the reduced genome porcine pathogen, *Mycoplasma hyopneumoniae*, whose genome contains only approximately 700 ORFs, yet it has been shown to exploit protein processing to increase its proteoform complexity [86]. Currently there has been limited analysis of protein modifications of the *S. aureus* surface proteome with most analysis focussing on expression levels and protein identification [181]. However, surface protein G (SasG) has been shown to have successive N-termini cleavage events [249]. Although this protein plays an important role in biofilm formation, the role of these protein processing events are still unknown. It is possible that other proteins residing on the surface of *S. aureus* are also a target of processing events. The implementation of in-gel proteomics will allow for the analysis of surface protein processing in this dataset presented, which has previously not been a focus of *S. aureus* surface proteome studies.

This chapter aims to characterise the surface proteome of *S. aureus* SH1000 using two complementary methods including in-gel and off-gel proteomic techniques. As part of this analysis, methodology developments were also made regarding the incubation period of *S. aureus* with trypsin and biotinylation. The application of gel-based techniques allows for the non-reductionist analysis of protein cleavage on the surface of *S. aureus*. This combination of methodologies, and the inclusion of predicted cytosolic proteins results in one of the most comprehensive surface proteome datasets yet to be presented.

2.2 Material and methods

2.2.1 Cell growth

S. aureus SH1000 cells were grown overnight in TSB (Oxoid, Hampshire UK) from a single colony. The next day, these cells were diluted to an optical density (OD_{595}) of 0.05 in TSB in a baffled flask. Cells were grown with intermediate shaking (210 rpm) at 37 °C until early stationary phase. OD_{595} was checked intermittently to ensure cell growth.

2.2.2 Live/dead staining

To ensure cell wall integrity Live/dead staining (Invitrogen, Life Technologies, Waltham MA, USA) was utilised. 1mL was taken from a 50 mL culture of freshly harvested cells, or 100 µL was taken from trypsin shaved cells, or biotinylated cells (equivalent volumes). Cells were pelleted by centrifugation for 30 s at 17000 rcf. Supernatant was removed carefully and the cell pellet was resuspended in 1 mL of 0.9 % NaCl saline solution to wash cells. Cells were centrifuged again at 17000 rcf for 30 s. Cells were washed a total of three times before staining. To stain the cells, the pellet was resuspended in 1 mL of 0.9 % saline solution and Syto 9 and propidium iodide were added to a final concentration of 10 µM and 30 µM, respectively. Samples were incubated in the dark for 15 min. 3 µL of each sample was placed on an agarose pad microscope slide, and sealed with a coverslip for immediate fluorescence microscopy analysis. A cover slip was secured onto the slide and cells were visualised using fluorescent microscopy on a Zeiss Axioplan 2 fluorescence microscope (Carl Zeiss, Oberkochen, Germany) using the 100 x objective. Light was used from a high pressure mercury lamp with 100 W power which passed through filter set 02 (Carl Zeiss). Phase-contrast and fluorescence microscopy was used to capture cell images as previously published [250], with the following modifications; Syto 9 was excited at 488 nm and Propidium iodide at 561 nm, emission were collected at 500-550 nm, and 570-620 nm, respectively. Images were captured using an AxioCam MRm (Carl

Zeiss) camera. This microscope was linked to the AxioVision 4.5 (Carl Zeiss) program for image analysis.

2.2.3 Cell harvest

Cultures were poured into 50mL tubes containing protease inhibitors (Complete, Roche Diagnostics, Basel, Switzerland) and centrifuged at 3 220 rcf for 10 min at 4 °C. Supernatant was removed and cells to be biotinylated were washed three times in ice-cold PBS and protease inhibitors. Cells that were going to be enzymatically shaved (with trypsin) were washed twice in ice cold PBS and protease inhibitors, followed by twice in ice cold PBS to remove protease inhibitors. Cells were pelleted by centrifugation at 3 220 rcf for 10 min at 4 °C and the washing solution was removed.

2.2.4 Surface trypsin shaving

Cell pellets were resuspended in pre-warmed PBS (37 °C) and (50 µg/µL) pre-dissolved trypsin (from porcine pancreas, Sigma, St. Louis MO, USA), mixed and incubated for either 30 min, or 1 min. The trypsin shaving reaction was stopped by cooling the solution rapidly on ice. Shaved cells were pelleted by centrifugation at 3 220 rcf for 10 min at 4 °C. The supernatant was carefully removed and further centrifuged at 21 000 rcf for 10 min to remove any debris. The supernatant was carefully removed to a new Eppendorf tube. 1 µL of MS-grade trypsin (1 µg/µL) was added to each sample and samples were incubated at 37 °C overnight with mixing. Samples were reduced and alkylated using 5 mM of tributylphosphine (TBP) and 20 mM of acrylamide monomers, respectively, the reaction was then quenched using 10 mM dithiothreitol (DTT).

2.2.5 Solid phase extraction of peptides

Sample containing shaved peptides (from Section 2.2.4) was desalted and peptides were concentrated using a solid phase extraction C18 column (Oasis, Waters, Milford MA, USA). Column was activated by passed 100 % Acetonitrile (ACN) through it, it was then washed using 2 % ACN/0.2 % TFA. Before the peptide sample was added, the peptide sample was acidified with a final concentration of 0.1 % TFA. The entire sample was run through the column. Column was washed with 2 % ACN/ 0.2 % TFA. Peptides were eluted in 150 µL of 50 % ACN, 0.2 % TFA. Sample was placed in evaporator to remove excess ACN.

2.2.6 Preparation of surface biotinylated proteins

S. aureus cells were washed (see Section 2.2.3) before the addition of EZ-link sulfo-NHS-biotin (Thermo Fisher Scientific, Waltham MA, USA) at a final concentration of 2mM. Cells were biotinylated for 1 min on ice with gentle agitation. The reaction was quenched by the addition of Tris-HCl pH 7.2 to a final concentration 50 mM and the sample was incubated for 10 min. Cells were washed with ice cold PBS to remove any excess biotin. The centrifuged pellet after washing was then collected for lysis.

2.2.7 Cell disruption of biotinylated cells

The cell pellet was freeze dried overnight and added to a pre-cooled metal canister. Pellets were bead-milled 15 times for 1 min each with resting in liquid nitrogen in between. Cell debris was washed out of the canister with 1.5 mL of 7 M urea, 2 M thiourea, 1 % (w/v) C7bZ0, 40 mM Tris-HCl (pH 8.8), and 50 mM LiCl. The solution was probe sonicated 20 times for 30 s at high intensity to shear any DNA and further lyse cells. Insoluble material was pelleted by centrifuging the cells at 21 000 rcf for 15 min at 4 °C. The supernatant was collected and the proteins reduced and alkylated using 5mM tributylphosphine (TBP) and 10 mM acrylamide monomers, respectively for a minimum of 90 min at room temperature and then the reaction was quenched by adding DTT to a final concentration of 10 mM and incubating for a further 30 min. Protein was precipitated out of the solution by adding 5 volumes of acetone and incubating overnight at -20 °C. Precipitated protein was collected by pelleting with centrifugation at 3 220 rcf for 10 min at 4 °C, with the acetone supernatant being removed to waste. The protein pellet was resuspended in 1mL of 7 M urea, 2 M thiourea, 1 % (w/v) C7bZ0.

2.2.8 Affinity chromatography (streptavidin)

To isolate biotinylated surface proteins from the whole cell lysate (see Section 2.2.7) was run through an affinity chromatography system. 250 µL of the sample described in Section 2.2.7 was mixed with 30 µL of buffer A (20 mM sodium phosphate, 0.15 M NaCl, pH 7.5) and centrifuged for 10 min, at 21 000 rcf to remove any remaining debris. Sample supernatant was carefully removed to a fresh 0.5 mL tube. A 1 mL HiTrap Streptavidin HP (GE healthcare, Chicago IL, USA) column was attached to an ÄTKA pure LC separations module (GE Healthcare) and the system was equilibrated for 5 min with buffer A. The sample was manually injected into the sample loop, ready for application to the streptavidin column. The sample was passed through the column with 100 % buffer A. The column was washed extensively with buffer A for 30 min at a flow rate of 0.5 mL min^{-1}. Biotinylated proteins were eluted off the column with the application of buffer B (elution buffer, 8 M guanidine-HCl, pH 1.5) at 0.5 mL min^{-1} for 40 min. The elution profile was monitored at A=280 nm, and fractions were collected in 2 mL intervals using a Fraction collector F9-R (GE healthcare).

2.2.9 Protein Preparation for Gel Electrophoresis

Fractions collected from the ÄTKA pure system were pooled into 3 groups; flow through, wash, and elutions. Samples were neutralized by the addition of 5 M NaOH, until they reached ~7 pH. Each of these samples were concentrated using a 3 kDa cut-off filter (Pall, Port Washington NY, USA). Excess guanidine (buffer B) was diluted out during this phase by adding water to the top chamber (to the newly concentrated sample) and re-filtering it several times. Samples were further concentrated by placing in a speedvac evaporating chamber. If protein samples precipitated due to the addition of water and evaporation, a small amount of 5 mM Tris / 0.1 % SDS (protein preparation for 1D-SDS-PAGE) or UTC_7 (protein preparation for 2D-PAGE) was added.

2.2.10 1D-PAGE of surface biotinylated proteins

Samples were prepared and run as previously described in [79]. Briefly, 15 µL of 2x sample buffer (4 % w/v SDS, 20 % glycerol, 125 mM Tris-HCl pH 6.8, and 0.02 % w/v Bromophenol Blue) was added to the entire concentrated protein sample (15 µL) and protein was boiled for 5 min, then centrifuged at 21 000 rcf for 5 min. Elution samples from the three biological replicates (30 µL) were electrophoresed on a 4-12 % Criterion™ TGX™ 1D-SDS-PAGE gel (Bio-Rad, Hercules CA, USA) in Tris-glycine-SDS buffer (0.025 M Tris, 0.192 M glycine, 0.1 % SDS from Bio-Rad), fixed with 50 mL of 40 % methanol / 10 % acetic acid solution, and visualized by staining with 50 mL 1 X Flamingo fluorescent gel stain (Bio-Rad), imaged and overstained with Coomassie Blue G-250 (Sigma) [251]. Excess Coomassie stain was removed from the gel by washing the gel in 1 % acetic acid solution.

2.2.11 2D-PAGE of surface biotinylated proteins

250 µg of protein was passively loaded onto 11 cm pH 3-10 IPG strips (BioRad) by rehydrating the strip in the presence of the sample diluted in UTC_7. Focusing was performed in a Bio-Rad Protean IEF cell unit set at 20 ˚C and 50 µA current limit (per strip) with the following program: 4 h slow ramp up to 4000 V, 4 h linear ramp up to 10000 V, followed by 10000 V until at least 100 kVh were reached. Following IEF, the strips were equilibrated for 20 min with equilibration solution (2 % SDS, 6 M urea, 250 mM Tris-HCl pH 8.5, 0.0025 % [w/v] bromophenol blue) before loading the strip onto a gel and running the second-dimension SDS-PAGE. Second-dimension SDS-PAGE was run as described for 1D-SDS-PAGE in Section 2.2.10.

2.2.12 Avidin Western blot

Samples eluted from the avidin column, as well as positive and negative controls and Precision Plus Protein™ Dual Standards (Bio-Rad), were run on 1D-SDS PAGE (without fixing) ready for transferral onto PVDF (Polyvinylidene fluoride, Millipore, Burlington MA, USA) membrane for Western blotting [252]. In preparation, the PVDF membrane was submerged in 100 % methanol for 2 min and transferred to Buffer 2 (25 mM Tris, 20 % methanol) before the transfer. Once the 1D-SDS PAGE run was completed, the 1D-SDS PAGE gel was submerged in MilliQ water for 2 min and then transferred into a tray with Buffer 1 (40 mM Amino-caproic acid, 25 mM Tris, 10 % methanol, 0.05 % SDS) for 5 min for equilibration. During this, the western blot stack was assembled in the following order: two pieces of blotting filter paper (BioRad) pre-soaked in buffer 1 (40 mM Amino-caproic acid, 25 mM Tris, 10 % methanol, 0.05 % SDS) were placed on the cathode side of the electroblotting cassette (Thermo Fisher Scientific), on top of this the 1D-SDS PAGE gel was carefully placed followed by the PVDF membrane, then a single blotting filter paper (BioRad) pre-soaked in buffer 2 (25 mM Tris, 20 % methanol, 0.05 % SDS), on top of this stack two pieces of blotting filter paper (BioRad) pre-soaked in buffer 3 (300 mM Tris) was carefully placed. The entire stack was set up ensuring no air bubbles were present throughout. The anode end of the electroblotting cassette was placed on top of the stack ready for voltage to be applied.

Proteins were transferred onto the PVDF membrane using the Owl HEP-1 Semi Dry Electroblotting Cassette (Thermo Fisher Scientific) attached to a power-pack (BioRad). A constant voltage of 300 mA was applied for 30 min. After the run was completed the PVDF membrane was incubated in Ponceau S (in 1 % acetic acid) to confirm that protein transfer was successful. Once transfer was confirmed, the Ponceau S was washed off the membrane with MilliQ water. Blocking solution (5 % skim milk, 0.1 % tween 20 in PBS) was then added to prevent non-specific binding. This was incubated for 60 min with gentle rocking. The membrane was washed three times by adding 50 mL of the wash solution (0.1 % tween 20 in PBS), rocking for 10 min, and then discarding the wash solution off the membrane. The membrane was then probed with ExtrAvidin- HRP (Sigma) at a concentration of 1:5000 for 60 min with gentle rocking. The membrane was washed again three times as described above, and the wash solution was discarded off the membrane. The membrane was developed with the addition of pre-dissolved DAB (3,3’-Diaminobenzidine) and urea hydrogen peroxidase tablet (Sigma) in 5 mL of MilliQ water. A duplicate gel was fixed and stained as described in Section 2.2.10.

2.2.13 Protein Preparation for LC-MS/MS

2.2.13.1. Trypsin shaved peptides

Samples from Section 2.2.5 were centrifuged at 21 000 rcf for 10 min. 15 µL of the supernatant was removed and added to an auto-sampler vial ready to load onto the LC-MS/MS system (Section 2.2.14).

2.2.13.2. In gel protein digestion from 1D-SDS-PAGE

A total of 14 bands were cut at the same molecular weight (MW) for each biological replicate (As shown in Figure A.1 of Appendix A). Gel slices were diced into approximately 1 mm^2 cubes and added to a 0.5 mL tube. Pieces were washed in 50 mM NH_4HCO_3, de-stained with 50 mM NH_4HCO_3 / 50 % ACN, and then dehydrated with 100 % ACN (all solutions added with enough volume of liquid to cover gel pieces). ACN was removed, and excess ACN was evaporated off. In-gel digestion was carried out with trypsin (12.5 ng/µL trypsin in 100 mM NH_4HCO_3) incubated at 4 °C for 30 min, followed by 37 °C overnight. Peptides were further extracted from the gel using sonication, and the liquid solution containing peptides was transferred to a new 0.5 mL tube. Gel pieces were covered with 50 % ACN / 0.2 % TFA and sonicated again to extract remaining peptides from the gel, this liquid solution was added to the 0.5 mL tube containing previously extracted peptides. Samples were concentrated in an evaporator to remove ACN.

Samples were desalted and peptides were concentrated using a solid phase extraction C18 100 µL OMIX pipette tip (Agilent). The tip was activated by pipetting 30 µL of 100 % ACN 5 times, all liquid was discarded into waste. The OMIX pipette tip was then washed 5 times with 30µL 2 % ACN/0.2 % TFA. The OMIX pipette tip was then used to pipette the peptide sample up and down a number of times to allow peptides to bind to the C18-derived monolith. Again, the OMIX pipette tip was washed 5 times with 40 µL 2 % ACN/0.2 % TFA. The OMIX pipette tip was then placed in a 0.5 mL tube with 40 µL of 50 % ACN/2 % FA and the solution was pipetted up and down a number of times to elute the peptides off the tip, and into solution. Sample was placed in evaporator to remove excess ACN and reduce sample volume to 15 µL.

2.2.13.3. In gel protein digestion from 2D-PAGE

Any visible gel spots were excised using a pipette tip of varying size, depending on the size of the spot. The gel spot was deposited into a 0.5 mL tube. Gel pieces were treated as described in Section 2.2.13.2, albeit without the OMIX tip step.

2.2.14 LC-MS/MS

Peptides were analysed using LC-MS/MS as previously described [79]. Samples (10 µL) were loaded onto a C8 Cap Trap column (Michrom, Auburn CA, USA) using an Eksigent AS-1 autosampler connected to a Tempo nanoLC system (Eksigent, Dublin CA, USA) at 20 µL min^{-1} with MS buffer A (2 % ACN / 0.2 % formic acid). The trapping column was washed for 180 s. Peptides were washed off the trapping column (300 nL min^{-1}) onto a PicoFrit column (75 µm × 150 mm) packed with Magic C18AQ resin (5 micron particles; Michrom), and into the source of a QSTAR elite hybrid quadrupole-time-of-flight mass spectrometer (Applied Biosystems, Foster City CA, USA /MDS Sciex, Framingham MA, USA) using the following program: 5−30 % MS buffer B (98 % ACN / 0.2 % formic acid) over 30 min, 30−80 % MS buffer B over 5 min, and 80 % MS buffer B for 2 min, 80−5 % for 3 min. Eluting peptides were ionized from the Picofrit column at 2300 V. An Intelligent Data Acquisition (IDA) experiment was performed, with a mass range of 350−1500 Da continuously scanned for peptides of charge state 2+ to 5+ with an intensity of more than 30 counts/scan and a resolution >12 000. Selected peptides were fragmented, and the product ion fragment masses were measured over a mass range of 100–1500 Da. The mass of the precursor peptide was then excluded for 120 s.

2.2.14.1. LC-MS/MS for 1D biotinylation samples

Samples (5 µL) were loaded at 300 nl/min with MS buffer A (2 % ACN + 0.2 % Formic Acid) using an Eksigent 415 autosampler connected to a 415 nanoLC system (Eksigent), by direct injection onto a PicoFrit column (75 µm x 150 mm; New Objective, Woburn MA, USA) packed with C18AQ resin (1.9 m, 200 Å, Dr Maisch, Germany). Peptides were eluted from the column and into the source of a 6600 TripleTOF hybrid quadrupole-time-of-flight mass spectrometer (Sciex, CA) using the following program: 2-35 % MS buffer B (80 % ACN + 0.2 % Formic Acid) over 30 min, 35-95 % MS buffer B over 9 min, 95 % MS buffer B for 9 min, 80-2 % for 2 min. The eluting peptides were ionised at 2300 V. An Intelligent Data Acquisition (IDA) experiment was performed, with a mass range of 350-1500 Da continuously scanned for peptides of charge state 2 +-5 + with an intensity of more than 400 counts/s. Up to 50 candidate peptide ions per cycle were selected and fragmented and the product ion fragment masses measured over a mass range of 100-2000 Da. The mass of the precursor peptide was then excluded for 15 s.

2.2.15 Protein identification

MS data files were searched against a *S. aureus* NCTC 8325 database derived from the published genome, the non-redundant protein database from NCBI, and common contaminants database using Mascot Daemon (v 2.4, provided by the Australian Proteomics Computational Facility, hosted by the Walter and Eliza Hall Institute for Medical Research Systems Biology Mascot Server). Searches were conducted with the following parameters: Fixed modifications: none. Variable modifications: Deamidation (NQ), propionamide (C), and oxidation (M). This setting searches for deamidation of asparagine (N) and glutamine (Q), the addition of propionamide to cysteine (C) (alkylation modification), and the oxidation of methionine (M), respectively. For biotinylated protein samples, the following variable modifications were included in the search parameters: Biotin (K) and Biotin (N-term). Enzyme: semitrypsin. Number of allowed missed cleavages: 3. Peptide mass tolerance: 100 ppm. MS/MS mass tolerance: 0.2 Da. Charge state: 2+, 3+ and 4+. Search parameters for samples that were run on the 6600 TripleTOF were the same except for the following changes: peptide mass tolerance: 50 ppm, MS/MS mass tolerance: 0.1 Da.

Proteins were deemed positively identified if significantly scoring peptides (E-value > 0.05) were found in two or more replicates. The "score" mentioned hereon, if otherwise not specified, is the protein or peptide score assigned by Mascot. For 2D-PAGE protein identification, proteins were identified if peptides were found that had an E-value > 0.05. If proteins of interest were analysed in more depth, each protein was identified by a number of unique peptides that scored significantly (E-value > 0.05). If there was insufficient evidence for protein identification (eg. one peptide identified significantly) peptide spectra were manually inspected to determine the likelihood of this peptide, and hence, protein identification being true.

2.2.16 DnaK antibody growth assays

A single colony of *S. aureus* SH1000 Δspa Δsbi was grown overnight in TSB in appropriate antibiotics and diluted the next day to approximately 10^3 CFU/mL in TSB. 120 µL of TSB was added to appropriate wells (wells that would have cells and antibodies added), 135 µL of TSB was added to positive (normal growth) control wells (with 15 µL of cells later added), 150 µL of TSB was added to blank wells in a 96 well microtitre plate. 15 µL of DnaK antibodies and zero-bleeds (antibody control) (produced by D. Stipic in conjunction with the Elizabeth Macarthur Agricultural Institute [EMAI] with ethics approval [AEC project no. M12/11]) were mixed into wells to final concentrations of 1:10 (other antibodies and combinations were tested, but will not be presented here). Finally, 15 µL of the prepared cells were added and mixed into the wells and the plate was immediately incubated at 37 °C with intermediate shaking in a plate reader (Powerwave HT Bio Tek, Winooski VT, USA). Plates were read every half-hour to measure the optical density (OD) at 595 nm over 24 h. Plates were also examined by eye on completion of the time-course for any macroscopic phenotypic changes.

2.2.17 Bioinformatic Analysis

Bioinformatic analysis on protein results was performed using the following open-source software and resources: Protein sequences were obtained from UniProt, using the *S. aureus* NCTC 8325 protein data as the default for all *S. aureus* protein analysis (http://www.uniprot.org/) [101]. As all proteins were identified from an uploaded *S. aureus* NCTC 8325 database derived from the genome [253], proteins were manually matched to their UniProt number, or manually annotated. Protein location was predicted using PSORTb v3.0 [180]; and predicted MW and pI for proteins, and protein fragments was obtained from ProtParam via ExPASy (http://web.expasy.org/protparam/) [254] [255].

2.3 Results

2.3.1 Live-Dead staining

For each replicate within a treatment, over 400 cells were counted and scored as either "live" (staining green with syto9) or "dead" (staining red with propidium iodide). Over 99 % of the cells were scored as live after the 30 min incubation with trypsin, the 1 min incubation with trypsin and after 1 min incubation in the biotinylation solution (Figure 2.3). Interestingly, as part of the optimisation experiments (data not shown), cells were also stained after 2 h of incubation in the biotinylation solution and over 99 % were scored as live. Cells were also stained before the incubation period to determine if any cell death seen was due to the incubation, or part of the harvested culture. These counts showed that prior to incubation 99.5 % of cells were seen as "live", showing no significant difference (Appendix A, Table A.1). It should also be noted that in these images no obvious cellular debris or eDNA was observed. This result shows the resistance of *S. aureus* cells to lysis during biotinylation incubations.

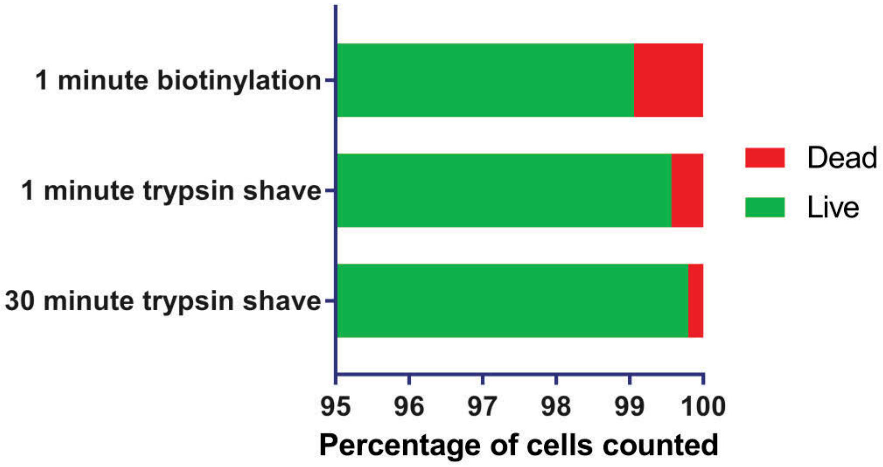


Figure 2.3 Live-dead staining results after incubation periods used in these experiments. This graph has been adjusted to show a range between 95 % and 100 % of cells as the dead portion of cells (shown as red) is otherwise difficult to see (with the x-axis from 0-100 %). All methodologies used resulted in less than 1 % cell lysis being detected.

2.3.2 Cell surface trypsin shaving

2.3.2.1. Thirty min trypsin shaving protocol

Initially, *S. aureus* cells were incubated with trypsin for 30 min which resulted in the identification of 98 proteins by LC-MS/MS (Table 2.1). This timing was based on previous literature where *S. aureus* has been treated with trypsin for 1 h [124,177], 45 min [173] and 15 min [125,126]. Proteins were scored when they were identified in two or more replicates.

2.3.2.2. One min trypsin shaving protocol

S. aureus cells were incubated for 1 min with trypsin resulted in the identification of 145 proteins (Table 2.1) in two or more replicates. This reduction in the incubation time was implemented to limit stress and cellular turnover, as the average doubling time of *S. aureus* is around 30 min.

2.3.2.3. Comparison of trypsin incubation times

The 1 min incubation technique identified 71 (42 %) unique proteins (proteins not identified in the 30 min incubation), and had 74 protein identifications in common (43.8 %) with the 30 min technique (Figure 2.4). As both experiments followed the same methodology, it is possible that a protein identified in two replicates in one experiment (eg. 30 min) and only found in one replicate in another (1 min) may be truly surface exposed, and the evidence for this is supported by the two 30 min replicates. These differences can also be due to the stochastic nature of the mass spectrometer during the selection and fragmentation phases, leading to variations in replicates. Hence, the number of proteins identified that were unique to each experiment (comparing 30 min incubation to 1 min incubation) were examined to see if they were present in one replicate in the other incubation period. Of the 24 (14.2 %) unique proteins identified in the 30 min trypsin shaving experiment, 16 of these were identified once in the 1 min experiment (Figure 2.5). Of the 71 unique proteins identified in the 1 min experiment, 29 of these were found once in the 30 min experiment (Figure 2.5). Taking these numbers into account the total overlap between experiments can be seen as 119 proteins (119 from 199, 59.8%, Figure 2.5). There were also 30 proteins that were identified in one replicate from each trypsin shaving experiment (two biological replicates in total). Therefore the total number of proteins that were present in at least 2 biological replicates across shaving experiments was 199.

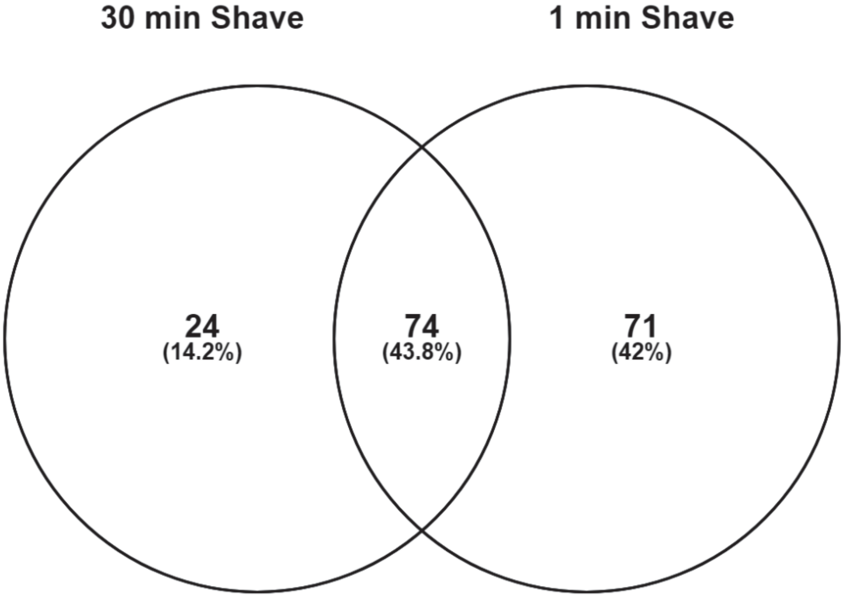


Figure 2.4 Venn diagram comparing proteins identified in the 30 min and 1 min trypsin shaving experiment.

Diagram showing the overlap between proteins identified in the 30 min and 1 min trypsin incubation (found in two or more replicates). A total of 98 proteins were identified using the 30 min trypsin shaving methodology. On the other hand, 145 proteins were identified in the 1 min trypsin shaving methodology. These two methodologies identified 74 proteins (43.8 %) in common.

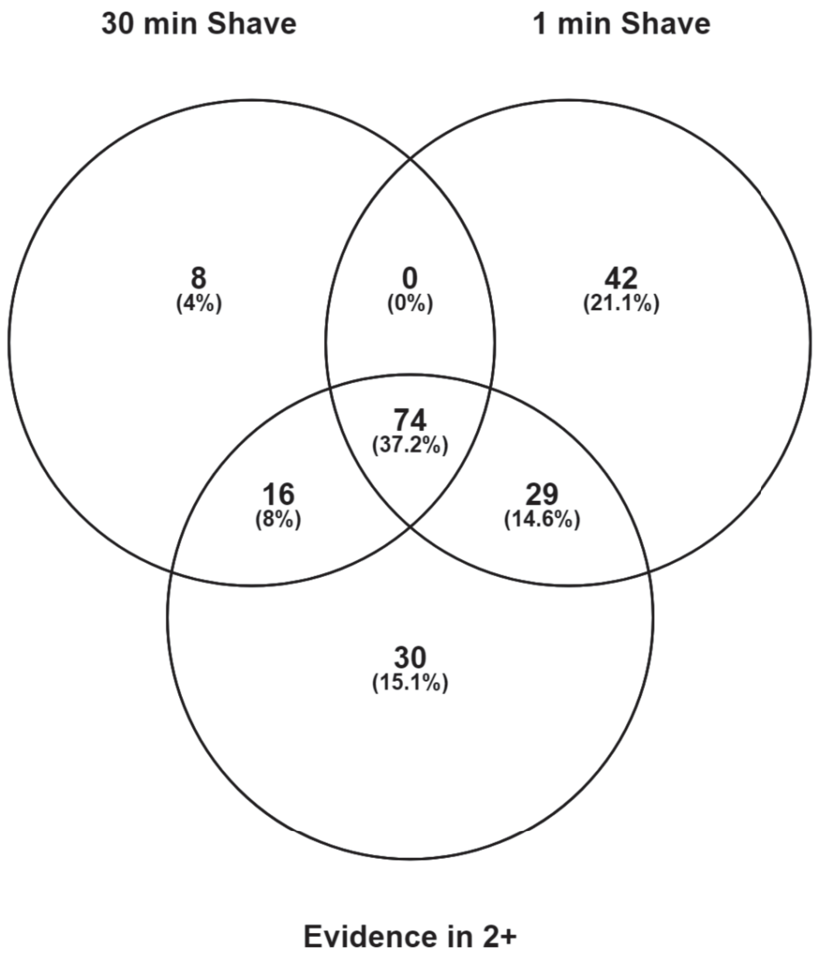


Figure 2.5 Venn diagram including all proteins identified in 2 or more replicates

Diagram showing the overlap between proteins identified in the 30 min and 1 min trypsin incubation (found in two or more replicates), and proteins found in two or more replicates when all six replicates (both shaving incubations) were analysed together (evidence in 2+).

2.3.3 Cell surface Biotinylation

2.3.3.1. No natively biotinylated proteins were identified in *S. aureus* SH1000

A western blot of a whole cell lysate of *S. aureus* probed with avidin-HRP was performed to determine if *S. aureus* contains natively biotinylated proteins. No biotinylated proteins were observed in this blot from the whole cell lysate (negative control, that had not been treated with biotin), nor in the wash lane from the LC. The wash cycle on the AKTA pure LC system was also extended 30 min to ensure all none-bound proteins were removed from the column before starting the elution gradient.

2.3.3.2. 1D-SDS-PAGE analysis of surface biotinylated proteins

Across all 14 slices of the biotinylated proteins, a total of 725 proteins were identified as surface biotinylated proteins in *S. aureus* SH1000 (Table 2.1, for slice location see Appendix A Table A.2). Of this, 107 proteins (14.8 %) were also identified in at least one of the shaving replicates (i.e. 30 min trypsin shave, or 1 min trypsin shave, Figure 2.6). Using the biotinylation methodology, 618 proteins (78.5 % of all surface proteins) were uniquely identified. Across all three experimental methodologies, 47 proteins (6 %) were identified (Figure 2.6).

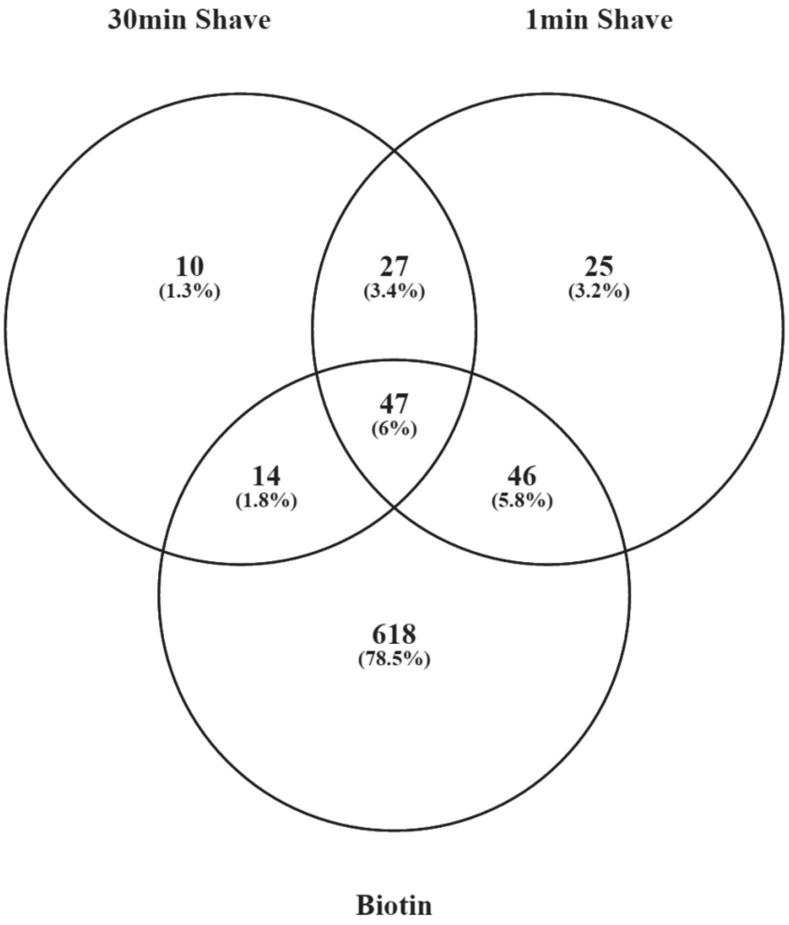


Figure 2.6 Venn diagram showing overlap of protein identifications across the three experiments.

The 30 min trypsin shaving experiment resulted in the identification of 98 proteins, 61 of which were also found in the 1D-SDS-PAGE surface biotinylation experiment. The 1 min trypsin shaving experiment resulted in the identification of 145 proteins, 93 of which were also identified in the 1D-SDS-PAGE surface biotinylation experiment (and 74 of which were shared with the other trypsin shaving experiment as previously stated). The 1D-SDS-PAGE surface biotinylation experiment resulted in 618 (78.5%) unique protein identifications.

Table 2.1 787 Proteins identified as surface exposed in *S. aureus* SH1000.

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88196002	Q2FWF5	(3R)-hydroxymyristoyl-ACP dehydratase	Cytoplasmic	16071			X
88195002	Q2FZ02	(dimethylallyl)adenosine tRNA methylthiotransferase	Cytoplasmic	58894			X
88195537	Q2FXJ7	1-acyl-sn-glycerol-3-phosphate acyltransferase domain-containing protein	Cytoplasmic	23059			X
88196500	Q2FV67	1-pyrroline-5-carboxylate dehydrogenase	Cytoplasmic	56832			X
88194312	Q2G0M8	2-amino-3-ketobutyrate coenzyme A ligase	Cytoplasmic	42864			X
88194032	Q2G1C0	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	Unknown	26640			X
88194028	Q2G2C4	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	Cytoplasmic	25198			X
88194671	Q2FZS6	2-isopropylmalate synthase	Unknown	43647	X	X	
88195143	Q2FYM1	2-oxoglutarate dehydrogenase E1 component	Cytoplasmic	105277			X
88195664	Q2G2T1	3~-5~ exoribonuclease YhaM	Cytoplasmic	35756			X
88195210	Q2FYF9	30S ribosomal protein S1	Cytoplasmic	43261	X	X	X
542123276	N/A	30S ribosomal protein S10	Cytoplasmic^	11569	X	X	X
88196137	Q2FW31	30S ribosomal protein S11	Cytoplasmic	13873	X		X
88194307	P0A0H0	30S ribosomal protein S12	Cytoplasmic	15277	X		X
88196138	Q2FW30	30S ribosomal protein S13	Cytoplasmic	13711	X		X
161353519	Q2FW19	30S ribosomal protein S14	Cytoplasmic	7295			X
88194983	Q2G2Q1	30S ribosomal protein S15	Cytoplasmic	10602			X
88194945	Q2FZ45	30S ribosomal protein S16	Cytoplasmic	10229			X
88196153	Q2FW15	30S ribosomal protein S17	Cytoplasmic	10169			X
88194149	Q2G111	30S ribosomal protein S18	Cytoplasmic	9304			X
88196158	Q2FW10	30S ribosomal protein S19	Cytoplasmic	10609			X
88195395	Q2FXY6	30S ribosomal protein S20	Cytoplasmic	9016	X		X
88195384	Q2FXZ7	30S ribosomal protein S21	Cytoplasmic	6968			X
88196156	Q2FW12	30S ribosomal protein S3	Cytoplasmic	24085	X	X	X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88195529	Q2FXK6	30S ribosomal protein S4	Cytoplasmic	22999	X		X
88196145	Q2FW23	30S ribosomal protein S5	Cytoplasmic	17732	X		X
88194147	Q2G113	30S ribosomal protein S6	Cytoplasmic	11588	X	X	X
88194308	P48940	30S ribosomal protein S7	Cytoplasmic	17783		X	X
88196148	Q2FW20	30S ribosomal protein S8	Cytoplasmic	14822	X	X	X
88196129	Q2FW39	30S ribosomal protein S9	Cytoplasmic	14821	X	X	X
88196546	Q2FV21	3-methyl-2-oxobutanoate hydroxymethyltransferase	Unknown	28222			X
88194678	Q2FZR9	3-oxoacyl- synthase	Cytoplasmic Membrane	43712			X
88194677	Q2FZS0	3-oxoacyl-(acyl carrier protein) synthase III	Cytoplasmic	33858			X
88194937	Q2FZ53	3-oxoacyl-(acyl-carrier-protein) reductase	Cytoplasmic	25870			X
88194087	Q2G170	5~-nucleotidase	Unknown	33331		X	
88194300	Q2G0P0	50S ribosomal protein L1	Cytoplasmic	24693	X	X	X
88194301	Q2G0N9	50S ribosomal protein L10	Cytoplasmic	17699	X	X	X
88194299	P0A0F4	50S ribosomal protein L11	Cytoplasmic	14865			X
88196130	Q2FW38	50S ribosomal protein L13	Unknown	16323			X
88196152	Q2FW16	50S ribosomal protein L14	Cytoplasmic	13127			X
88196143	P0A0F8	50S ribosomal protein L15	Unknown	15587	X		X
88196155	Q2FW13	50S ribosomal protein L16	Cytoplasmic	16232	X		X
88196135	Q2FW33	50S ribosomal protein L17	Cytoplasmic	13739	X		X
88196146	Q2FW22	50S ribosomal protein L18	Cytoplasmic	13089			X
88194948	Q2FZ42	50S ribosomal protein L19	Cytoplasmic	13354	X	X	X
88196159	P60430	50S ribosomal protein L2	Cytoplasmic	30136	X	X	X
88195485	Q2FXQ1	50S ribosomal protein L20	Cytoplasmic	13678			X
88195458	Q2FXS8	50S ribosomal protein L21	Unknown	11326	X		X
88196157	Q2FW11	50S ribosomal protein L22	Cytoplasmic	12827	X	X	X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88196160	Q2FW08	50S ribosomal protein L23	Cytoplasmic	10599	X		X
88194261	Q2G0S0	50S ribosomal protein L25/general stress protein Ctc	Cytoplasmic	23773	X	X	X
88195456	Q2FXT0	50S ribosomal protein L27	Cytoplasmic	10308			X
88194930	Q2FZ60	50S ribosomal protein L28	Cytoplasmic	6973			X
88196154	Q2FW14	50S ribosomal protein L29	Cytoplasmic	8085	X		X
88196162	Q2FW06	50S ribosomal protein L3	Cytoplasmic	23703	X		X
88196144	P0A0G2	50S ribosomal protein L30	Cytoplasmic	6550	X		X
88196024	Q2FWD8	50S ribosomal protein L31 type B	Cytoplasmic	9717			X
88195058	Q2FYU6	50S ribosomal protein L33	Cytoplasmic	5928			X
88195359	Q2FY22	50S ribosomal protein L33	Cytoplasmic	5869			X
88195486	Q2FXQ0	50S ribosomal protein L35	Cytoplasmic	7692			X
88196161	Q2FW07	50S ribosomal protein L4	Unknown	22451			X
88196150	Q2FW18	50S ribosomal protein L5	Cytoplasmic	20254	X	X	X
88196147	Q2FW21	50S ribosomal protein L6	Cytoplasmic	19774	X	X	X
88194302	P48860	50S ribosomal protein L7/L12	Cytoplasmic	12704	X		X
88193838	Q2G2T3	50S ribosomal protein L9	Cytoplasmic	16629			X
88194138	Q2G122	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	Cytoplasmic	85023			X
88195582	Q2FXG2	6,7-dimethyl-8-ribityllumazine synthase	Cytoplasmic	16386			X
88196101	Q2G2D5	6-phospho-beta-galactosidase	Cytoplasmic	54516			X
88195507	Q2FXM8	6-phosphofructokinase	Cytoplasmic	33376			X
88195316	Q2FY60	6-phosphogluconate dehydrogenase	Cytoplasmic	51770			X
88194605	Q2FZY7	ABC transporter ATP-binding protein	Cytoplasmic	28257			X
88195832	Q2FWW9	ABC transporter ATP-binding protein	Cytoplasmic Membrane	32931			X
88195119	Q2FYP2	ABC transporter ATP-binding protein	Cytoplasmic	60219			X
88196059	Q2FWA1	ABC transporter ATP-binding protein	Cytoplasmic Membrane	28987			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88194089	Q2G167	ABC transporter ATP-binding protein	Cytoplasmic Membrane	24967			X
88195682	Q2FX86	ABC transporter permease	Cytoplasmic Membrane	53089			X
88194402	Q2G2D8	ABC transporter substrate-binding protein	Cytoplasmic Membrane	35049			X
88195935	Q2FWM4	accessory gene regulator protein A	Cytoplasmic	24238			X
88195934	Q2FWM5	accessory gene regulator protein C	Cytoplasmic Membrane	47953			X
88194390	Q2G2U9	accessory regulator A	Cytoplasmic	14709			X
88193886	Q2G1N7	accessory regulator-like protein	Cytoplasmic	29871			X
88195520	Q2FXL5	acetate kinase	Cytoplasmic	44015	X		X
88193901	Q2G1M1	acetoin reductase	Cytoplasmic	27199			X
88195952	Q2FWK6	acetolactate synthase large subunit	Cytoplasmic	64450			X
88195333	Q2FY43	acetyl-CoA carboxylase biotin carboxylase subunit	Cytoplasmic	50017			X
88195508	Q2FXM7	acetyl-CoA carboxylase carboxyltransferase subunit alpha	Cytoplasmic	35048			X
88195509	Q2FXM6	acetyl-CoA carboxylase subunit beta	Cytoplasmic	31851			X
88196556	Q2FV14	acetyl-CoA synthetase	Cytoplasmic	59711			X
88195075	Q2FYS9	aconitate hydratase	Cytoplasmic	98908			X
88194939	Q2FZ51	acyl carrier protein	Cytoplasmic	8544	X		X
88195132	Q2FYM9	acylphosphatase	Cytoplasmic	10154			X
88196355	Q2FVJ6	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	Cytoplasmic	51372			X
88196141	Q2FW27	adenylate kinase	Cytoplasmic	23959			X
88195807	Q2G2S0	adenylosuccinate lyase	Cytoplasmic	49572			X
88193840	Q2G1S3	adenylosuccinate synthetase	Cytoplasmic	47549			X
88195010	Q2FYZ4	aerobic glycerol-3-phosphate dehydrogenase	Cytoplasmic	62349			X
88195971	Q9ZAH5	alanine racemase	Cytoplasmic*	42796			X
88195427	Q2FXV9	alanyl-tRNA synthetase	Cytoplasmic	98459			X
88193945	Q2G1J0	aldehyde dehydrogenase	Cytoplasmic	53626			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88196026	Q2FWD6	aldehyde dehydrogenase	Cytoplasmic	51937			X
88195822	Q2FWX9	aldehyde dehydrogenase	Cytoplasmic	51709			X
88195500	Q2FXN6	alkaline phosphatase synthesis transcriptional regulatory protein	Cytoplasmic	27105			X
88196094	Q2FW66	alkaline shock protein 23	Unknown	19180	X	X	X
88194163	P0A0B7	alkyl hydroperoxide reductase subunit C	Cytoplasmic	20963	X	X	X
88194162	O05204	alkyl hydroperoxide reductase subunit F	Cytoplasmic Membrane	54687		X	X
88196119	Q2FW50	alpha-acetolactate decarboxylase	Unknown	26207			X
88194768	Q2FZI9	amidophosphoribosyltransferase	Cytoplasmic	54363			X
88196382	Q2FVG8	amino acid ABC transporter ATP-binding protein	Cytoplasmic Membrane	46145			X
88196337	Q2FVL4	amino acid ABC transporter ATP-binding protein	Cytoplasmic Membrane	27224			X
88196037	Q2FWC4	aminobenzoyl-glutamate utilization protein B	Cytoplasmic	42932			X
88195775	Q2FX14	aminopeptidase PepS	Cytoplasmic	47088			X
88194607	Q2FZY5	aminotransferase	Cytoplasmic	46590			X
88195093	Q2FYR9	anthranilate synthase component I	Cytoplasmic	54077	X	X	
88196590	Q2FUX7	arginine deiminase	Cytoplasmic	46885			X
88195327	Q2FY49	arginine repressor	Cytoplasmic	17087			X
88194381	Q2G0F8	arginyl-tRNA synthetase	Cytoplasmic	62342			X
88195188	Q2FYH6	asparaginyl-tRNA synthetase	Cytoplasmic	49127			X
88194906	Q2FZ75	aspartate carbamoyltransferase catalytic subunit	Cytoplasmic	33237			X
88195049	Q2FYV5	aspartate kinase	Cytoplasmic	51971			X
88195799	Q2FWY9	aspartyl/glutamyl-tRNA amidotransferase subunit A	Cytoplasmic	52788	X		X
88195798	Q2FWZ0	aspartyl/glutamyl-tRNA amidotransferase subunit B	Cytoplasmic	53623			X
88195441	Q2FXU5	aspartyl-tRNA synthetase	Cytoplasmic	66587			X
88196493	Q2FV74	ATP-dependent Clp protease ATP-binding subunit ClpC	Cytoplasmic*	77789			X
88194551	Q2G036	ATP-dependent Clp protease proteolytic subunit	Cytoplasmic	21500			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88195804	Q53727	ATP-dependent DNA helicase PcrA	Cytoplasmic	84021			X
88195479	Q2FXQ7	ATP-dependent protease ATP-binding subunit ClpX	Cytoplasmic	46269			X
88194962	Q2FZ28	ATP-dependent protease ATP-binding subunit HslU	Cytoplasmic	52282			X
88194961	Q2FZ29	ATP-dependent protease peptidase subunit	Cytoplasmic	19560			X
88194219	Q2G0U9	autolysin	Cell wall	35814	X	X	
88193983	Q2G1F2	azoreductase	Cytoplasmic	23338	X	X	X
88195293	Q2FY83	bacteriophage integrase	Unknown	47452			X
88195764	Q2FX25	bacteriophage L54a antirepressor	Cytoplasmic	30155		X	
88194148	Q2G112	bacteriophage L54a single-stranded DNA binding protein	Cytoplasmic	18528			X
88196560	Q2FV10	betaine aldehyde dehydrogenase	Cytoplasmic	54589			X
88195550	Q2G248	bifunctional 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase	Cytoplasmic	40593			X
88194761	Q2FZJ6	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	Cytoplasmic	30824			X
88194750	Q2FZK7	bifunctional autolysin	Extracellular	137300	X	X	
88194139	Q2G121	bifunctional homocysteine S-methyltransferase/5,10-methylenetetrahydrofolate reductase	Cytoplasmic	68436			X
88194771	Q2FZI6	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	Cytoplasmic	54314		X	X
161353523	Q2FXT8	bifunctional preprotein translocase subunit SecD/SecF	Cytoplasmic Membrane	84201			X
88194904	Q2FZ77	bifunctional pyrimidine regulatory protein PyrR/uracil phosphoribosyltransferase	Cytoplasmic	19843			X
88194794	Q2G2A4	branched-chain alpha-keto acid dehydrogenase subunit E2	Cytoplasmic	46326	X	X	X
88194316	Q2G0M4	branched-chain amino acid aminotransferase	Cytoplasmic	40062			X
88193938	Q2G1J7	cap5L protein/glycosyltransferase	Cytoplasmic	46547			X
88194909	Q2FZ72	carbamoyl phosphate synthase large subunit	Cytoplasmic	117112			X
88194908	Q2FZ73	carbamoyl phosphate synthase small subunit	Cytoplasmic	40369			X
88195548	Q2G295	catabolite control protein A	Cytoplasmic	36038			X
88195057	Q2FYU7	catalase	Cytoplasmic	54908	X		X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88196503	Q2FV64	cation transporter E1-E2 family ATPase	Cytoplasmic Membrane	86690			X
88196504	Q2FV63	cation transporter E1-E2 family ATPase	Cytoplasmic	7232	X		
88194890	Q2FZ91	cell division protein	Cell wall*	50182			X
88194891	O07325	cell division protein	Cytoplasmic	52902			X
88194892	Q2FZ89	cell division protein FtsZ	Cytoplasmic	41012	X	X	X
88194884	Q2FZ97	cell division protein MraZ	Cytoplasmic	17226			X
88194955	Q9ZNI1	cell wall hydrolase	Cytoplasmic Membrane	41729	X		
88194313	Q2G0M7	chaperone protein HchA	Cytoplasmic	32156	X	X	X
88195925	Q2FWN4	chaperonin GroEL	Cytoplasmic	57629			X
88196559	Q2FV11	choline dehydrogenase	Cytoplasmic Membrane	63570			X
88193824	Q2G2H5	chromosomal replication initiation protein	Cytoplasmic	51934			X
88194572	Q2G015	clumping factor	Cell wall	96392	X		
88196585	Q2FUY2	clumping factor B	Cell wall	93540	X	X	
88194665	O52582	coenzyme A disulfide reductase	Cytoplasmic	49259			X
88196660	Q2FUQ9	cold shock protein	Cytoplasmic	8417	X		
88195129	Q2FYN2	cold shock protein	Cytoplasmic	7317	X		X
88195392	Q2FXY9	coproporphyrinogen III oxidase	Cytoplasmic	42814			X
88196031	Q2FWD1	CTP synthetase	Cytoplasmic	59945			X
88194648	Q2FZU9	cyclophilin-type peptidyl-prolyl cis-trans isomerase	Cytoplasmic	21605			X
88194292	Q2G2M6	cysteinyl-tRNA synthetase	Cytoplasmic	53652			X
228937973	Q2FYF5	cytidylate kinase	Cytoplasmic	24580			X
88194785	Q2FZH2	cytochrome d ubiquinol oxidase subunit II	Cytoplasmic Membrane	38921	X		
88194636	Q2FZV6	cytosol aminopeptidase	Cytoplasmic	54095			X
88195533	Q2FXK1	D-3-phosphoglycerate dehydrogenase	Cytoplasmic	57583			X
88195564	Q2FXI0	D-alanine aminotransferase	Cytoplasmic	31874			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88194626	Q2FZW6	D-alanine--poly(phosphoribitol) ligase subunit 1	Cytoplasmic	54636			X
88195984	Q2FWH3	D-alanyl-alanine synthetase A	Cytoplasmic	40205			X
88195982	Q2FWH5	DEAD-box ATP dependent DNA helicase	Cytoplasmic	56907			X
88195931	Q2FWM8	delta-hemolysin	Extracellular	5006	X	X	
88193913	Q2G224	deoxyribose-phosphate aldolase	Cytoplasmic	23458			X
88196042	Q2FWB9	deoxyribose-phosphate aldolase	Cytoplasmic	23313			X
88195495	Q2FXP1	dephospho-CoA kinase	Cytoplasmic	23578			X
88195158	Q2FYK6	dihydrofolate reductase	Cytoplasmic	18239			X
88194795	Q2G2A3	dihydrolipoamide dehydrogenase	Cytoplasmic	49451	X		X
88195142	Q2FYM2	dihydrolipoamide succinyltransferase	Cytoplasmic	46644			X
88194907	Q2FZ74	dihydroorotase	Cytoplasmic	46342			X
88194274	Q2G0Q7	dihydropteroate synthase	Cytoplasmic	29504			X
88195565	Q2FXH9	dipeptidase PepV	Cytoplasmic	52791			X
88196221	Q2FVW4	D-isomer specific 2-hydroxyacid dehydrogenase NAD binding domain-containing protein	Cytoplasmic	34653			X
88196464	Q2FVA3	D-lactate dehydrogenase	Cytoplasmic	34782			X
88193829	Q2G2Q0	DNA gyrase subunit A	Cytoplasmic	99290			X
88193828	Q2G274	DNA gyrase subunit B	Cytoplasmic	72495			X
88195397	Q2FXY4	DNA internalization-related competence protein ComEC/Rec2	Cytoplasmic Membrane	82812			X
88195497	Q2FXN9	DNA polymerase I	Cytoplasmic	99133			X
88194974	Q2G1Z8	DNA polymerase III PolC	Cytoplasmic	162357			X
88195511	Q9F1K0	DNA polymerase III subunit alpha superfamily protein	Cytoplasmic	122888			X
88193825	Q2G2H4	DNA polymerase III subunit beta	Cytoplasmic	41888			X
88194241	Q2G2X1	DNA polymerase III subunit delta~	Cytoplasmic	32158			X
161353534	Q2G243	DNA repair protein RadA	Cytoplasmic	49832			X
88195464	P31337	DNA repair protein RadC	Unknown	24119	X		

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88195326	Q2FY50	DNA repair protein RecN	Cytoplasmic	64282			X
88194958	Q2FZ32	DNA topoisomerase I	Cytoplasmic	79277			X
88196165	Q2FW03	DNA topoisomerase III	Cytoplasmic	81500			X
88195080	Q2FYS4	DNA topoisomerase IV subunit A	Cytoplasmic	90942			X
88195079	Q2FYS5	DNA topoisomerase IV subunit B	Cytoplasmic	74318			X
88195207	Q2FYG2	DNA-binding protein HU	Cytoplasmic	9620	X	X	X
88195297	Q2FY79	DNA-binding response regulator	Cytoplasmic	28143			X
88196136	Q2FW32	DNA-directed RNA polymerase subunit alpha	Cytoplasmic	34990			X
161353532	P47768	DNA-directed RNA polymerase subunit beta	Cytoplasmic	133136	X		X
88194305	Q2G0N5	DNA-directed RNA polymerase subunit beta~	Cytoplasmic	134190	X		X
88196032	Q2FWD0	DNA-directed RNA polymerase subunit delta	Cytoplasmic	20868			X
88195189	Q2FYH5	DnaQ family exonuclease/DinG family helicase	Cytoplasmic	104152			X
88194047	Q2G1A5	D-ribose pyranase	Cytoplasmic	15156			X
88194053	Q2G199	drug transporter	Cytoplasmic Membrane	49025			X
88195217	Q2FYF1	elastin binding protein	Cytoplasmic Membrane*	53190	X	X	X
88194309	Q2G0N1	elongation factor G	Cytoplasmic	76564	X	X	X
88194967	Q2FZ23	elongation factor Ts	Cytoplasmic	32474			X
88194310	Q2G0N0	elongation factor Tu	Cytoplasmic	43077	X	X	X
88196270	Q2G2W1	EmrB/QacA family drug resistance transporter	Cytoplasmic Membrane	70932			X
88195365	Q2FY16	endonuclease IV	Cytoplasmic	33138			X
88194286	Q2G0P5	endopeptidase	Cytoplasmic	90981		X	X
88194704	Q2FZQ3	enoyl-(acyl carrier protein) reductase	Cytoplasmic Membrane	28005			X
88196375	Q2FVH5	epimerase/dehydratase	Cytoplasmic	31173			X
88194541	Q2G046	excinuclease ABC subunit A	Cytoplasmic	105303			X
88194661	Q2FZT6	exonuclease RexB	Cytoplasmic	134420			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88194575	Q2G012	extracellular matrix and plasma binding protein	Cell wall	38461	X		
88196009	Q2FWE8	F0F1 ATP synthase subunit alpha	Cytoplasmic	54550			X
88196011	Q2G2F8	F0F1 ATP synthase subunit B	Cytoplasmic Membrane	19527			X
88196007	Q2FWF0	F0F1 ATP synthase subunit beta	Cytoplasmic Membrane	51368		X	X
88196012	Q2G2F6	F0F1 ATP synthase subunit C	Cytoplasmic Membrane	6975			X
88196010	Q2FWE7	F0F1 ATP synthase subunit delta	Cytoplasmic	20486			X
161353520	Q2FWE9	F0F1 ATP synthase subunit gamma	Unknown	32086			X
88195790	Q2FWZ8	ferritin	Cytoplasmic	19576	X		X
88194324	Q2G0L5	fibrinogen-binding protein SdrC	Cell wall	107731	X	X	
88194325	Q2G0L4	fibrinogen-binding protein SdrD	Cell wall	146000	X	X	
88194856	Q2FZC2	fibrinogen-binding protein-like protein	Extracellular	12589	X		
88196438	P14738	fibronectin-binding protein	Cell wall	108659	X		
88194650	Q2FZU7	FMN oxidoreductase	Cytoplasmic	42083			X
88193997	Q2G1D8	formate acetyltransferase	Cytoplasmic	84808			X
88193954	Q2G1I1	formate dehydrogenase	Cytoplasmic	38094			X
88195544	Q2G296	formate--tetrahydrofolate ligase	Cytoplasmic	59819			X
88196252	Q2FVT2	formimidoylglutamase	Cytoplasmic	34491			X
88194472	Q2G238	fructose 1-phosphate kinase	Unknown	32553			X
88194473	Q2G239	fructose specific permease	Cytoplasmic Membrane	68670			X
88196553	Q2FV17	fructose-1,6-bisphosphate aldolase	Unknown	33034	X	X	X
88196029	Q2FWD3	fructose-bisphosphate aldolase	Cytoplasmic	30817			X
88195674	Q2FX94	fumarate hydratase	Cytoplasmic	51075			X
88195528	Q2FXK7	GAF domain-containing protein	Cytoplasmic	17100			X
88196106	Q2G2R0	galactose-6-phosphate isomerase subunit LacB	Cytoplasmic	18939			X
88195354	Q2FY27	glucokinase	Cytoplasmic	35056		X	

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88196443	Q2G208	gluconate operon transcriptional repressor	Cytoplasmic	26578			X
88196060	Q2FWA0	glucosamine--fructose-6-phosphate aminotransferase	Cytoplasmic	65809			X
88195310	Q2FY66	glucose-6-phosphate 1-dehydrogenase	Cytoplasmic	56929			X
88194657	Q2FZU0	glucose-6-phosphate isomerase	Cytoplasmic	49791			X
88194652	Q2FZU5	glutamate dehydrogenase	Cytoplasmic	45731			X
88194852	Q2FZC6	glutamate racemase	Unknown	29679			X
88194226	Q2G0U2	glutamate synthase large subunit	Cytoplasmic Membrane	166244			X
161353522	Q2G283	glutamate-1-semialdehyde aminotransferase	Cytoplasmic	46727			X
88195472	Q2FXR4	glutamate-1-semialdehyde aminotransferase	Cytoplasmic	46359			X
88194281	Q2G0Q0	glutamine amidotransferase subunit PdxT	Cytoplasmic	20617			X
88195018	Q2FYY6	glutamine synthetase	Cytoplasmic	50808			X
88194290	Q2G241	glutamyl-tRNA synthetase	Cytoplasmic	56253			X
88195014	Q2FYZ0	glutathione peroxidase	Unknown	18106			X
88195494	Q2FXP2	glyceraldehyde 3-phosphate dehydrogenase 2	Cytoplasmic	36956			X
88194555	Q2G032	glyceraldehyde-3-phosphate dehydrogenase	Cytoplasmic	36258	X	X	X
88195007	Q2FYZ7	glycerol uptake operon antiterminator regulatory protein	Cytoplasmic	20437			X
88194935	Q2FZ55	glycerol-3-phosphate acyltransferase PlsX	Cytoplasmic	35408			X
88194820	Q2FZF9	glycerophosphoryl diester phosphodiesterase	Cytoplasmic	34712			X
88194594	Q2FZZ8	glycine cleavage system protein H	Cytoplasmic	14084			X
88195342	Q2FY34	glycine dehydrogenase subunit 1	Cytoplasmic	49685			X
88195341	Q2FY35	glycine dehydrogenase subunit 2	Cytoplasmic	54748			X
88194554	Q2G033	glycolytic operon regulator	Cytoplasmic	37187			X
88195373	Q2FY08	glycyl-tRNA synthetase	Cytoplasmic	53586			X
88194173	Q2G0Y6	GMP synthase	Cytoplasmic	58194			X
88194328	Q2G0L1	GTP cyclohydrolase	Cytoplasmic	33461			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88195445	Q2FXU1	GTP pyrophosphokinase	Cytoplasmic	83642			X
88195209	Q2FYG0	GTP-binding protein EngA	Cytoplasmic Membrane	48949			X
161353525	Q2FY06	GTP-binding protein Era	Cytoplasmic Membrane	34249			X
88195394	Q2FXY7	GTP-binding protein LepA	Cytoplasmic Membrane	68132			X
88194808	Q2G1Y6	GTP-binding protein TypA	Cytoplasmic Membrane	69152			X
88194145	Q2G115	GTP-dependent nucleic acid-binding protein EngD	Cytoplasmic	40570			X
88195060	Q2FYU4	guanosine 5~-monophosphate oxidoreductase	Cytoplasmic	36093			X
88194318	Q2G0M2	haloacid dehalogenase-like hydrolase	Cytoplasmic	24977			X
88195390	Q2FXZ1	heat shock protein GrpE	Cytoplasmic	23994			X
88194348	Q2G0J1	heme peroxidase	Unknown	29371			X
88193943	Q2G1J2	heme-degrading monooxygenase IsdI	Cytoplasmic	12783			X
88195203	Q2FYG6	heptaprenyl diphosphate syntase component II	Cytoplasmic	35563			X
88196650	Q2FUR9	high affinity nickel transporter	Cytoplasmic Membrane	37806	X	X	
88193831	Q2G2P7	histidine ammonia-lyase	Cytoplasmic	56041			X
88194498	Q2G087	histidinol-phosphate aminotransferase	Unknown	39763			X
88195442	Q2FXU4	histidyl-tRNA synthetase	Cytoplasmic	48252			X
88195867	Q2G1W8	HK97 family phage major capsid protein	Cytoplasmic	47152	X	X	
88195250	Q2FYC7	HK97 family phage portal protein	Unknown	47657			X
88196491	Q2FV76	HMG-CoA synthase	Cytoplasmic	43178			X
88195452	Q2FXT4	Holliday junction DNA helicase RuvB	Cytoplasmic	37695			X
88195050	Q2FYV4	homoserine dehydrogenase	Unknown	46845			X
88194542	Q2G045	HPr kinase/phosphorylase	Cytoplasmic	34461			X
88193973	Q2G1G2	HsdR family type I site-specific deoxyribonuclease	Cytoplasmic	109159			X
88194272	Q2G0Q9	Hsp33-like chaperonin	Cytoplasmic	31802			X
88196115	Q59801	hyaluronate lyase	Extracellular	91928			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88193837	Q2G2T6	hypothetical protein SAOUHSC_00015	Cytoplasmic	73735			X
88193846	Q2G253	hypothetical protein SAOUHSC_00025	Cell wall	83373	X	X	X
88193869	Q2G1Q4	hypothetical protein SAOUHSC_00049	Unknown	121654			X
88193895	Q2G1M8	hypothetical protein SAOUHSC_00080	Cytoplasmic	71906			X
88193909	Q2G260	hypothetical protein SAOUHSC_00094	Cell wall	21834		X	
88193953	Q2G1I2	hypothetical protein SAOUHSC_00141	Unknown	13971			X
88193956	Q2G1H9	hypothetical protein SAOUHSC_00144	Cytoplasmic	273308			X
88193995	Q2G1E0	hypothetical protein SAOUHSC_00185	Cytoplasmic Membrane	61009			X
88194007	Q2G1C8	hypothetical protein SAOUHSC_00197	Cytoplasmic	44701			X
88194009	Q2G1C6	hypothetical protein SAOUHSC_00199	Unknown	58840			X
88194010	Q2G1C5	hypothetical protein SAOUHSC_00200	Cytoplasmic Membrane	42156			X
88194034	Q2G1B8	hypothetical protein SAOUHSC_00227	Cytoplasmic Membrane	66034			X
88194035	Q2G1B7	hypothetical protein SAOUHSC_00228	Cytoplasmic	66272			X
88194041	Q2G1B1	hypothetical protein SAOUHSC_00234	Cytoplasmic	26997	X	X	
88194063	Q2G189	hypothetical protein SAOUHSC_00257	Extracellular	11029			X
88194064	Q2G188	hypothetical protein SAOUHSC_00258	Cytoplasmic Membrane	114754			X
88194073	Q2G179	hypothetical protein SAOUHSC_00268	Cytoplasmic	68275			X
88194110	Q2G146	hypothetical protein SAOUHSC_00309	Cytoplasmic	37753			X
88194112	Q2G144	hypothetical protein SAOUHSC_00311	Cytoplasmic	10391			X
88194113	Q2G143	hypothetical protein SAOUHSC_00312	Cytoplasmic	16289			X
88194115	Q2G141	hypothetical protein SAOUHSC_00314	Unknown	16162			X
88194120	Q2G136	hypothetical protein SAOUHSC_00319	Cytoplasmic	39147			X
88194155	Q2G105	hypothetical protein SAOUHSC_00356	Unknown	21293	X	X	X
88194156	Q2G104	hypothetical protein SAOUHSC_00357	Cytoplasmic	10782	X		
88194167	Q2G0Z2	hypothetical protein SAOUHSC_00369	Cytoplasmic	35591			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88194169	Q2G0Z0	hypothetical protein SAOUHSC_00371	Cytoplasmic	15113			X
88194195	Q2G0X3	hypothetical protein SAOUHSC_00400	Unknown	56512			X
88194220	Q2G0U8	hypothetical protein SAOUHSC_00428	Cytoplasmic Membrane	9993			X
88194224	Q2G0U4	hypothetical protein SAOUHSC_00433	Cytoplasmic Membrane	41633			X
88194234	Q2G0T4	hypothetical protein SAOUHSC_00444	Unknown	11590			X
88194265	Q2G0R6	hypothetical protein SAOUHSC_00480	Cytoplasmic	45082			X
88194266	Q2G0R5	hypothetical protein SAOUHSC_00481	Cytoplasmic	9850			X
88194271	Q2G0R0	hypothetical protein SAOUHSC_00486	Cytoplasmic Membrane	77764	X		X
88194273	Q2G0Q8	hypothetical protein SAOUHSC_00488	Cytoplasmic	32955	X	X	X
88194283	Q2G0P8	hypothetical protein SAOUHSC_00502	Cytoplasmic	17830			X
88194293	Q2G2M4	hypothetical protein SAOUHSC_00512	Cytoplasmic	15711			X
88194294	Q2G2M3	hypothetical protein SAOUHSC_00513	Cytoplasmic	27190			X
88194315	Q2G0M5	hypothetical protein SAOUHSC_00535	Unknown	36030			X
88194322	Q2G0L8	hypothetical protein SAOUHSC_00542	Cytoplasmic	31821			X
88194323	Q2G0L7	hypothetical protein SAOUHSC_00543	Unknown	20899			X
88194331	Q2G0K8	hypothetical protein SAOUHSC_00552	Cytoplasmic	28449			X
88194332	Q2G0K7	hypothetical protein SAOUHSC_00553	Cytoplasmic	22422		X	X
88194355	Q2G0I4	hypothetical protein SAOUHSC_00581	Cytoplasmic	48386			X
88194356	Q2G0I3	hypothetical protein SAOUHSC_00582	Cytoplasmic	15788			X
88194375	Q2G0G4	hypothetical protein SAOUHSC_00605	Unknown	18403			X
88194386	Q2G0F3	hypothetical protein SAOUHSC_00616	Cytoplasmic*	30906			X
88194387	Q2G0F2	hypothetical protein SAOUHSC_00617	Unknown	18582	X	X	
88194404	Q2G2L2	hypothetical protein SAOUHSC_00637	Cytoplasmic Membrane	28007			X
88194414	Q2G2E5	hypothetical protein SAOUHSC_00647	Cytoplasmic Membrane	64010			X
88194422	Q2G0E9	hypothetical protein SAOUHSC_00656	Unknown	21247			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88194428	Q2G0E2	hypothetical protein SAOUHSC_00663	Cytoplasmic	19267			X
88194439	Q2G0D1	hypothetical protein SAOUHSC_00674	Unknown	16707			X
88194440	Q2G0D0	hypothetical protein SAOUHSC_00675	Cytoplasmic	26304	X		X
88194450	Q2G0C0	hypothetical protein SAOUHSC_00685	Extracellular	15179			X
88194451	Q2G0B9	hypothetical protein SAOUHSC_00686	Cytoplasmic	11317			X
88194453	Q2G0B7	hypothetical protein SAOUHSC_00688	Cytoplasmic	20875			X
88194455	Q2G0B5	hypothetical protein SAOUHSC_00690	Unknown	26671			X
88194459	Q2G0B1	hypothetical protein SAOUHSC_00694	Cytoplasmic	17079			X
88194470	Q2G0A0	hypothetical protein SAOUHSC_00705	Unknown	17739			X
88194471	Q2G240	hypothetical protein SAOUHSC_00706	Cytoplasmic	28455			X
88194477	Q2G2T8	hypothetical protein SAOUHSC_00712	Cytoplasmic	32339			X
88194482	Q2G2G0	hypothetical protein SAOUHSC_00717	Unknown	16035			X
88194493	Q2G093	hypothetical protein SAOUHSC_00728	Cytoplasmic Membrane	74353	X	X	
88194520	Q2G065	hypothetical protein SAOUHSC_00756	Cytoplasmic	41771			X
88194525	Q2G060	hypothetical protein SAOUHSC_00762	Cytoplasmic Membrane	38504	X		
88194530	Q2G055	hypothetical protein SAOUHSC_00767	Cytoplasmic	22199			X
88194549	Q2G038	hypothetical protein SAOUHSC_00788	Unknown	36238			X
88194578	Q2G009	hypothetical protein SAOUHSC_00819	Cytoplasmic	7370	X		
88194589	Q2G1T3	hypothetical protein SAOUHSC_00831	Unknown	15330			X
88194591	Q2G001	hypothetical protein SAOUHSC_00833	Cytoplasmic	20736			X
88194593	Q2FZZ9	hypothetical protein SAOUHSC_00835	Cytoplasmic	13591			X
88194596	Q2FZZ6	hypothetical protein SAOUHSC_00838	Cytoplasmic	33479			X
88194603	Q2FZY9	hypothetical protein SAOUHSC_00845	Unknown	7014	X		X
88194606	Q2FZY6	hypothetical protein SAOUHSC_00848	Cytoplasmic	48519			X
88194609	Q2FZY3	hypothetical protein SAOUHSC_00851	Cytoplasmic	52498			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88194620	Q2FZX2	hypothetical protein SAOUHSC_00863	Cytoplasmic	10175			X
88194621	Q2FZX1	hypothetical protein SAOUHSC_00864	Cytoplasmic	16781			X
88194622	Q2FZX0	hypothetical protein SAOUHSC_00865	Unknown	27928			X
88194630	Q2FZW2	hypothetical protein SAOUHSC_00873	Cytoplasmic	8735	X	X	
88194632	Q2FZW0	hypothetical protein SAOUHSC_00875	Cytoplasmic Membrane	39374			X
88194635	Q2FZV7	hypothetical protein SAOUHSC_00878	Cytoplasmic Membrane	44077	X		X
88194663	Q2FZT4	hypothetical protein SAOUHSC_00906	Cytoplasmic	33093			X
88194674	Q2FZS3	hypothetical protein SAOUHSC_00917	Unknown	19138			X
88194708	Q2FZP9	hypothetical protein SAOUHSC_00951	Cytoplasmic	19314	X		X
88194721	Q2FZN6	hypothetical protein SAOUHSC_00964	Cytoplasmic	6672	X		
88194729	Q2FZM8	hypothetical protein SAOUHSC_00972	Cytoplasmic	11187			X
88194746	Q2FZL1	hypothetical protein SAOUHSC_00989	Cytoplasmic	43163			X
88194780	Q2FZH7	hypothetical protein SAOUHSC_01027	Unknown	20077			X
88194787	Q2FZG9	hypothetical protein SAOUHSC_01035	Cytoplasmic	62630			X
88194788	Q2FZG8	hypothetical protein SAOUHSC_01036	Cytoplasmic	8746	X		X
88194791	Q2FZG5	hypothetical protein SAOUHSC_01039	Unknown	23861	X		
88194805	Q2G2G7	hypothetical protein SAOUHSC_01054	Cytoplasmic	24004			X
88194810	Q2G1Y7	hypothetical protein SAOUHSC_01061	Unknown	18569			X
88194829	Q2FZE9	hypothetical protein SAOUHSC_01081	Cell wall	38722	X	X	
88194838	Q2FZE0	hypothetical protein SAOUHSC_01091	Unknown	26897			X
88194867	Q2FZB4	hypothetical protein SAOUHSC_01123	Unknown	8625			X
88194877	Q2FZA4	hypothetical protein SAOUHSC_01135	Unknown	4493	X	X	
88194878	Q2FZA3	hypothetical protein SAOUHSC_01136	Unknown	4453	X	X	
88194879	Q2FZA2	hypothetical protein SAOUHSC_01137	Cytoplasmic	27189			X
88194880	Q2FZA1	hypothetical protein SAOUHSC_01138	Unknown	16991			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88194898	Q2FZ83	hypothetical protein SAOUHSC_01158	Cytoplasmic	23500			X
88194913	Q2G1U2	hypothetical protein SAOUHSC_01174	Unknown	14849			X
88194926	Q2FZ64	hypothetical protein SAOUHSC_01187	Cytoplasmic Membrane	74317			X
88194931	Q2FZ59	hypothetical protein SAOUHSC_01192	Unknown	13377			X
88194932	Q2FZ58	hypothetical protein SAOUHSC_01193	Unknown	60477			X
88194977	Q2G2D1	hypothetical protein SAOUHSC_01244	Cytoplasmic	11033			X
88194978	Q2G2C9	hypothetical protein SAOUHSC_01245	Unknown	11530			X
88194985	Q2FZ19	hypothetical protein SAOUHSC_01252	Cytoplasmic	58753			X
88194988	Q2FZ16	hypothetical protein SAOUHSC_01255	Cytoplasmic	48588			X
88194989	Q2FZ15	hypothetical protein SAOUHSC_01256	Unknown	49878			X
88194997	Q2FZ07	hypothetical protein SAOUHSC_01264	Cytoplasmic	8156			X
88194998	Q2FZ06	hypothetical protein SAOUHSC_01265	Cytoplasmic	29856			X
88194999	Q2FZ05	hypothetical protein SAOUHSC_01266	Cytoplasmic	64515			X
88195053	Q2FYV1	hypothetical protein SAOUHSC_01323	Cytoplasmic	29803			X
88195067	Q2FYT7	hypothetical protein SAOUHSC_01338	Cytoplasmic Membrane	11016			X
88195077	Q2FYS7	hypothetical protein SAOUHSC_01349	Cytoplasmic	11489			X
88195092	Q2FYS0	hypothetical protein SAOUHSC_01365	Cytoplasmic	37832			X
88195110	Q2FYQ2	hypothetical protein SAOUHSC_01383	Cytoplasmic	69241			X
88195118	Q2FYP3	hypothetical protein SAOUHSC_01391	Cytoplasmic	34177			X
88195134	Q2FYM7	hypothetical protein SAOUHSC_01408	Unknown	43381			X
88195141	Q2FYM3	hypothetical protein SAOUHSC_01415	Cytoplasmic	30066			X
88195150	Q2FYL4	hypothetical protein SAOUHSC_01425	Cytoplasmic	19834			X
88195157	Q2FYK7	hypothetical protein SAOUHSC_01433	Cytoplasmic	30626			X
88195161	Q2FYK3	hypothetical protein SAOUHSC_01437	Cytoplasmic	42896			X
88195162	Q2FYK2	hypothetical protein SAOUHSC_01438	Unknown	9401	X		X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88195168	Q2FYJ6	hypothetical protein SAOUHSC_01447	Cell wall	1029310	X	X	X
88195173	Q2FYJ1	hypothetical protein SAOUHSC_01454	Unknown	33381			X
88195174	Q2FYJ0	hypothetical protein SAOUHSC_01455	Unknown	133025			X
88195179	Q2FYI5	hypothetical protein SAOUHSC_01462	Cytoplasmic	13143			X
88195193	Q2G254	hypothetical protein SAOUHSC_01476	Cytoplasmic	12187			X
88195194	Q2G257	hypothetical protein SAOUHSC_01477	Cytoplasmic Membrane	24566		X	
88195215	Q2FYF3	hypothetical protein SAOUHSC_01499	Cytoplasmic	36713			X
88195279	Q2FY98	hypothetical protein SAOUHSC_01567	Cytoplasmic	13653			X
88195305	Q2FY71	hypothetical protein SAOUHSC_01594	Cytoplasmic	33485			X
88195321	Q2FY55	hypothetical protein SAOUHSC_01610	Cytoplasmic	16211			X
88195332	Q2FY44	hypothetical protein SAOUHSC_01622	Unknown	13265			X
88195339	Q2FY37	hypothetical protein SAOUHSC_01629	Cytoplasmic	31861			X
88195340	Q2FY36	hypothetical protein SAOUHSC_01630	Unknown	14794			X
88195358	Q2FY23	hypothetical protein SAOUHSC_01650	Cytoplasmic Membrane	20987			X
88195366	Q2FY15	hypothetical protein SAOUHSC_01659	Cytoplasmic	51049			X
88195371	Q2FY10	hypothetical protein SAOUHSC_01664	Cytoplasmic	30765			X
88195380	Q2FY01	hypothetical protein SAOUHSC_01673	Cytoplasmic	34892			X
88195382	Q2FXZ9	hypothetical protein SAOUHSC_01676	Cytoplasmic	35160	X		X
88195401	Q2G298	hypothetical protein SAOUHSC_01695	Cytoplasmic	13474			X
88195402	Q2G297	hypothetical protein SAOUHSC_01696	Cytoplasmic	22449			X
88195407	Q2FXX9	hypothetical protein SAOUHSC_01701	Cytoplasmic Membrane	20207			X
88195421	Q2FXW5	hypothetical protein SAOUHSC_01716	Cytoplasmic	47625			X
88195426	Q2FXW0	hypothetical protein SAOUHSC_01721	Unknown	10297			X
88195432	Q2FXV4	hypothetical protein SAOUHSC_01727	Cytoplasmic	42458			X
88195433	Q2FXV3	hypothetical protein SAOUHSC_01728	Cytoplasmic	37960			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88195434	Q2FXV2	hypothetical protein SAOUHSC_01729	Unknown	5652	X		
88195435	Q2FXV1	hypothetical protein SAOUHSC_01730	Extracellular	6678	X		X
88195439	Q2FXU7	hypothetical protein SAOUHSC_01735	Cytoplasmic	28623			X
88195447	Q2FXT9	hypothetical protein SAOUHSC_01744	Unknown	85557			X
88195469	Q2FXR7	hypothetical protein SAOUHSC_01768	Unknown	21403			X
88195483	Q2FXQ3	hypothetical protein SAOUHSC_01782	Cytoplasmic	22932			X
88195502	Q2FXN3	hypothetical protein SAOUHSC_01802	Cytoplasmic	32371			X
88195514	Q2FXM1	hypothetical protein SAOUHSC_01814	Unknown	15216			X
88195516	Q2FXL9	hypothetical protein SAOUHSC_01816	Cytoplasmic	39529			X
88195519	Q2FXL6	hypothetical protein SAOUHSC_01819	Cytoplasmic	18464	X		X
88195521	Q2FXL4	hypothetical protein SAOUHSC_01821	Cytoplasmic	35924			X
88195525	Q2FXL0	hypothetical protein SAOUHSC_01825	Cytoplasmic	42339			X
88195532	Q2FXK2	hypothetical protein SAOUHSC_01832	Cytoplasmic	42823			X
88195538	Q2FXJ6	hypothetical protein SAOUHSC_01838	Cytoplasmic Membrane	45775			X
88195542	Q2FXJ2	hypothetical protein SAOUHSC_01843	Cell wall	100886	X	X	X
88195552	Q2G245	hypothetical protein SAOUHSC_01854	Cell wall	55058			X
88195553	Q2G247	hypothetical protein SAOUHSC_01855	Cytoplasmic	17991	X	X	X
88195555	Q2FXI9	hypothetical protein SAOUHSC_01857	Cytoplasmic Membrane	144568			X
88195556	Q2FXI8	hypothetical protein SAOUHSC_01858	Cytoplasmic	21676			X
88195557	Q2FXI7	hypothetical protein SAOUHSC_01859	Cytoplasmic	33049			X
88195558	Q2FXI6	hypothetical protein SAOUHSC_01860	Cytoplasmic	11848	X		X
88195559	Q2FXI5	hypothetical protein SAOUHSC_01861	Cytoplasmic	39758			X
88195566	Q2FXH8	hypothetical protein SAOUHSC_01869	Unknown	15724			X
88195570	Q2FXH4	hypothetical protein SAOUHSC_01873	Cell wall	238046			X
88195571	Q2FXH3	hypothetical protein SAOUHSC_01874	Unknown	11337			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88195579	Q2FXG5	hypothetical protein SAOUHSC_01882	Cytoplasmic	31845			X
88195581	Q2FXG3	hypothetical protein SAOUHSC_01884	Cytoplasmic	38006			X
88195586	Q2FXF8	hypothetical protein SAOUHSC_01890	Unknown	57541			X
88195592	Q2FXF2	hypothetical protein SAOUHSC_01897	Unknown	19141			X
88195602	Q2FXE2	hypothetical protein SAOUHSC_01907	Cytoplasmic	31452			X
88195603	Q2G1W5	hypothetical protein SAOUHSC_01908	Unknown	35031	X		X
88195626	Q2FXD2	hypothetical protein SAOUHSC_01931	Cytoplasmic	163164			X
88195657	Q2G2F3	hypothetical protein SAOUHSC_01964	Cytoplasmic	19536			X
88195660	Q2G2F0	hypothetical protein SAOUHSC_01968	Unknown	15935			X
88195661	Q2G2T0	hypothetical protein SAOUHSC_01969	Unknown	13204			X
88195665	Q2G2S8	hypothetical protein SAOUHSC_01974	Cytoplasmic	114351			X
88195666	Q2G2S7	hypothetical protein SAOUHSC_01975	Cytoplasmic	46196			X
88195668	Q2FXA0	hypothetical protein SAOUHSC_01977	Cytoplasmic	13302	X	X	X
88195669	Q2FX99	hypothetical protein SAOUHSC_01978	Cytoplasmic Membrane	42669			X
88195670	Q2FX98	hypothetical protein SAOUHSC_01979	Cytoplasmic	17787			X
88195678	Q2FX90	hypothetical protein SAOUHSC_01987	Cytoplasmic	22330			X
88195680	Q2FX88	hypothetical protein SAOUHSC_01989	Cytoplasmic Membrane	42406			X
88195687	Q2G280	hypothetical protein SAOUHSC_01999	Cell wall*	17249			X
88195701	P0A0K3	hypothetical protein SAOUHSC_02013	Cytoplasmic	18620			X
88195702	Q2G2H1	hypothetical protein SAOUHSC_02014	Cytoplasmic	6301			X
88195718	Q2FX66	hypothetical protein SAOUHSC_02031	Cytoplasmic	37017			X
88195776	Q2FX13	hypothetical protein SAOUHSC_02093	Unknown	7582	X		
88195778	Q2FX11	hypothetical protein SAOUHSC_02096	Cytoplasmic	10316			X
88195779	Q2FX10	hypothetical protein SAOUHSC_02097	Cytoplasmic Membrane	45576			X
88195830	Q2FWX1	hypothetical protein SAOUHSC_02150	Unknown	21902			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88195831	Q2FWX0	hypothetical protein SAOUHSC_02151	Cytoplasmic Membrane	28121		X	
88195838	Q2FWW3	hypothetical protein SAOUHSC_02158	Cytoplasmic	48089			X
88195895	Q2FWQ9	hypothetical protein SAOUHSC_02221	Cytoplasmic	29420			X
88195902	Q2FWQ2	hypothetical protein SAOUHSC_02228	Unknown	7899			X
88195929	Q2FWN0	hypothetical protein SAOUHSC_02258	Cytoplasmic Membrane	23989			X
88196035	Q2FWC6	hypothetical protein SAOUHSC_02372	Cytoplasmic	25839			X
88196036	Q2FWC5	hypothetical protein SAOUHSC_02373	Cytoplasmic	45618			X
88196044	Q2FWB7	hypothetical protein SAOUHSC_02381	Cytoplasmic	16681	X	X	X
88196050	Q2FWB1	hypothetical protein SAOUHSC_02387	Unknown	24017			X
88196065	Q2FW95	hypothetical protein SAOUHSC_02404	Cell wall	262863			X
88196081	Q2FW79	hypothetical protein SAOUHSC_02425	Unknown	10000			X
88196088	Q2FW72	hypothetical protein SAOUHSC_02434	Cytoplasmic	67169	X	X	
88196090	Q2FW70	hypothetical protein SAOUHSC_02436	Cytoplasmic	76040			X
88196096	Q2FW64	hypothetical protein SAOUHSC_02443	Cytoplasmic Membrane	20787			X
88196099	Q2G2D7	hypothetical protein SAOUHSC_02447	Cytoplasmic	36244			X
88196100	Q2G2D6	hypothetical protein SAOUHSC_02448	Unknown	33165			X
88196123	Q2FW46	hypothetical protein SAOUHSC_02471	Cytoplasmic	56116			X
88196124	Q2FW45	hypothetical protein SAOUHSC_02472	Cytoplasmic	44072			X
88196171	Q2FVZ7	hypothetical protein SAOUHSC_02523	Cytoplasmic	6390	X		
88196173	Q2FVZ5	hypothetical protein SAOUHSC_02525	Cytoplasmic Membrane	114631			X
88196179	Q2FVY9	hypothetical protein SAOUHSC_02532	Cytoplasmic	13978			X
88196210	Q9F0R1	hypothetical protein SAOUHSC_02566	Cytoplasmic	13660			X
88196212	Q2G270	hypothetical protein SAOUHSC_02568	Cytoplasmic	12526			X
88196214	Q2G2J4	hypothetical protein SAOUHSC_02570	Unknown	75957			X
88196218	Q2G1W0	hypothetical protein SAOUHSC_02574	Cytoplasmic	40717			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88196227	Q2FVV7	hypothetical protein SAOUHSC_02584	Cytoplasmic	30365			X
88196242	Q2FVU2	hypothetical protein SAOUHSC_02600	Cytoplasmic	20070			X
88196246	Q2FVT8	hypothetical protein SAOUHSC_02604	Cytoplasmic	31715			X
88196250	Q2FVT4	hypothetical protein SAOUHSC_02608	Cytoplasmic	34996			X
88196271	Q2G2W5	hypothetical protein SAOUHSC_02630	Cytoplasmic Membrane	23010			X
88196305	Q2FVN7	hypothetical protein SAOUHSC_02665	Unknown	15904			X
88196306	Q2FVN6	hypothetical protein SAOUHSC_02666	Unknown	13331			X
88196310	Q2FVN2	hypothetical protein SAOUHSC_02670	Cell wall*	16295			X
88196329	Q2G1U9	hypothetical protein SAOUHSC_02689	Unknown	17408			X
88196339	Q2FVL2	hypothetical protein SAOUHSC_02699	Unknown	28886		X	X
88196364	Q2FVI6	hypothetical protein SAOUHSC_02724	Unknown	25784	X		
88196385	Q2FVG5	hypothetical protein SAOUHSC_02747	Unknown	23785			X
88196386	Q2FVG4	hypothetical protein SAOUHSC_02750	Cytoplasmic Membrane	60601			X
88196391	Q2FVF9	hypothetical protein SAOUHSC_02755	Cytoplasmic	39168			X
88196392	Q2FVF8	hypothetical protein SAOUHSC_02756	Unknown	10642			X
88196406	Q2FVE4	hypothetical protein SAOUHSC_02770	Unknown	30984			X
161353518	Q2FVE2	hypothetical protein SAOUHSC_02772	Cytoplasmic	26173			X
88196414	Q2FVD5	hypothetical protein SAOUHSC_02778	Cytoplasmic	24589			X
88196426	Q2FVC3	hypothetical protein SAOUHSC_02790	Unknown	109832	X		X
88196433	Q2G2B2	hypothetical protein SAOUHSC_02798	Cell wall	178419	X	X	
88196446	Q2G2L6	hypothetical protein SAOUHSC_02812	Cytoplasmic	15982	X		X
88196449	Q2FVB9	hypothetical protein SAOUHSC_02815	Cytoplasmic Membrane	47595		X	
88196454	Q2FVB4	hypothetical protein SAOUHSC_02820	Cytoplasmic Membrane	25788			X
88196456	Q2FVB2	hypothetical protein SAOUHSC_02822	Cytoplasmic	76127			X
88196461	Q2FVA6	hypothetical protein SAOUHSC_02827	Cytoplasmic	10541			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88196462	Q2FVA5	hypothetical protein SAOUHSC_02828	Unknown	30041			X
88196477	Q2FV90	hypothetical protein SAOUHSC_02844	Cytoplasmic	36824			X
88196497	Q2FV70	hypothetical protein SAOUHSC_02866	Cytoplasmic Membrane	90352			X
88196509	Q2FV58	hypothetical protein SAOUHSC_02880	Cytoplasmic Membrane	42517		X	
88196514	Q2FV53	hypothetical protein SAOUHSC_02886	Cytoplasmic	19129			X
88196527	Q2FV40	hypothetical protein SAOUHSC_02899	Cytoplasmic	38170		X	X
88196528	Q2FV39	hypothetical protein SAOUHSC_02900	Cytoplasmic	30986			X
88196540	Q2FV27	hypothetical protein SAOUHSC_02912	Cytoplasmic	16928			X
88196562	Q2FV08	hypothetical protein SAOUHSC_02935	Cytoplasmic	21729			X
88196600	Q2G220	hypothetical protein SAOUHSC_02980	Unknown	20717			X
88196601	Q2FUW9	hypothetical protein SAOUHSC_02982	Cell wall	70889			X
88196609	Q2FUW1	hypothetical protein SAOUHSC_02990	Cell wall	227909		X	X
88196611	Q2FUV9	hypothetical protein SAOUHSC_02992	Extracellular	16733			X
88196613	Q2FUV7	hypothetical protein SAOUHSC_02994	Unknown	13013			X
88196640	Q2FUS9	hypothetical protein SAOUHSC_03022	Unknown	18643	X	X	X
88196651	Q2FUR8	hypothetical protein SAOUHSC_03034	Cytoplasmic	30419			X
542123273	N/A	hypothetical protein SAOUHSC_1307a	Unknown^	7495			X
88194270	Q2G0R1	hypoxanthine phosphoribosyltransferase	Cytoplasmic	20142			X
88196248	Q2FVT6	imidazolonepropionase	Cytoplasmic	45011			X
88196515	Q2FV52	immunodominant antigen A	Extracellular	24188	X	X	
88196593	Q2FUX3	immunodominant antigen B	Extracellular	19358	X	X	
88196346	Q2FVK5	immunoglobulin G-binding protein Sbi	Unknown	50040	X	X	
88193965	Q2G1H0	indolepyruvate decarboxylase	Cytoplasmic	60501			X
88194172	Q2G0Y7	inosine-5~-monophosphate dehydrogenase	Cytoplasmic	52818	X	X	X
88194806	Q2G2G4	inositol monophosphatase family protein	Cytoplasmic	30453			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88195501	Q2FXN4	isocitrate dehydrogenase	Cytoplasmic	46394			X
88194899	Q2FZ82	isoleucyl-tRNA synthetase	Cytoplasmic	104820			X
88196108	P0A0Q0	lactose phosphotransferase system repressor	Cytoplasmic	29869			X
88195645	Q2FXB3	lantibiotic epidermin biosynthesis protein EpiB	Cytoplasmic Membrane	117561			X
88195572	Q2FXH2	leucyl-tRNA synthetase	Cytoplasmic	91728			X
88196625	Q2FUU5	lipase	Extracellular	76629		X	
88194101	Q2G155	lipase	Extracellular	76341			X
88195796	Q2FWZ2	lipid kinase	Cytoplasmic	34865			X
88194720	Q2FZN7	lipoyltransferase and lipoate-protein ligase	Cytoplasmic	37904			X
88196549	Q2G1Y5	L-lactate dehydrogenase	Cytoplasmic	34399			X
88194016	Q2G218	L-lactate dehydrogenase	Cytoplasmic	29429			X
88196288	Q2FVQ4	L-lactate permease	Cytoplasmic Membrane	56606			X
88194278	Q2G0Q3	lysyl-tRNA synthetase	Cytoplasmic	56684			X
88196053	Q2FWA8	lytic regulatory protein	Cytoplasmic Membrane	40640			X
88196554	Q2FV16	malate:quinone oxidoreductase	Cell wall*	55964	X	X	X
88196287	Q2FVQ5	malate:quinone oxidoreductase	Cell wall*	54779			X
88195820	Q2FWY1	manganese-dependent inorganic pyrophosphatase	Cytoplasmic	34047			X
88196064	Q2FW96	mannitol-1-phosphate 5-dehydrogenase	Cytoplasmic	40912			X
88194748	Q2FZK9	MarR family transcriptional regulator	Cytoplasmic	16440			X
88195515	Q2FXM0	metal-dependent hydrolase	Cytoplasmic	25234			X
88195101	Q2FYR1	methicillin resistance factor	Cytoplasmic	49645			X
88195100	Q2FYR2	methicillin resistance factor FemA	Cytoplasmic	49093			X
88195087	P0A084	methionine sulfoxide reductase A	Unknown	19598			X
88195155	P0A088	methionine sulfoxide reductase B	Cytoplasmic	16267	X		
88194922	Q2FZ68	methionyl-tRNA formyltransferase	Cytoplasmic	34190			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88194248	Q2G1R9	methionyl-tRNA synthetase	Cytoplasmic	74838			X
88196492	Q2FV75	methylated-DNA--protein-cysteine methyltransferase	Cytoplasmic	18934			X
88195840	Q2FWW1	MHC class II analog protein	Cytoplasmic Membrane	65534	X	X	
88195389	Q2FXZ2	molecular chaperone DnaK	Cytoplasmic	66321	X	X	X
88196193	Q2FVX5	molybdenum ABC transporter permease	Cytoplasmic Membrane	24847			X
88196188	Q2FVY0	molybdopterin biosynthesis protein MoeA	Cytoplasmic	44988			X
88196190	Q2FVX8	molybdopterin precursor biosynthesis MoaB	Cytoplasmic	18489			X
88196187	Q2FVY1	molybdopterin-guanine dinucleotide biosynthesis protein MobB	Cytoplasmic	18557			X
88195946	Q2FWL3	MutS domain-containing protein	Cytoplasmic Membrane	61283			X
88194221	Q2G0U7	MutT/nudix family protein	Cytoplasmic	15044			X
88194475	Q2G2U0	N-acetylglucosamine-6-phosphate deacetylase	Cytoplasmic	43103			X
88193969	Q2G1G6	N-acetylmuramic acid-6-phosphate etherase	Cytoplasmic	32231			X
88196599	Q2G222	N-acetylmuramoyl-L-alanine amidase	Extracellular	69212	X	X	
88194096	Q2G160	N-acetylneuraminate lyase	Cytoplasmic	33022			X
88195812	Q2G236	NAD synthetase	Cytoplasmic	30678			X
88195208	Q2FYG1	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	Cytoplasmic	36048			X
88195803	Q2G1Y0	NAD-dependent DNA ligase	Cytoplasmic	75035			X
88195510	Q2FXM5	NADP-dependent malic enzyme	Cytoplasmic	44206			X
88194121	Q2G135	NADPH-dependent FMN reductase	Cytoplasmic	21301			X
88194742	Q2FZL5	naphthoate synthase	Cytoplasmic	30406			X
88194828	Q2FZF0	neurofilament protein	Cell wall	72148	X	X	X
88195202	Q2FYG7	nucleoside diphosphate kinase	Cytoplasmic	15787			X
88194853	Q2FZC5	nucleoside-triphosphatase	Cytoplasmic	21390			X
88194694	Q2G1U3	oligoendopeptidase F	Cytoplasmic	69776			X
88195104	Q2FYQ8	oligopeptide ABC transporter ATP-binding protein	Cytoplasmic Membrane	26241		X	

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88194685	Q2FZR2	oligopeptide ABC transporter substrate-binding protein	Cell wall*	64487			X
88194237	Q2G232	Orn/Lys/Arg decarboxylase	Cytoplasmic	50989			X
88194651	Q2FZU6	ornithine--oxo-acid transaminase	Cytoplasmic	43390			X
88194911	Q2FZ70	orotate phosphoribosyltransferase	Cytoplasmic	22029			X
88194910	Q2FZ71	orotidine 5~-phosphate decarboxylase	Cytoplasmic	25580			X
88194142	Q2G118	ParB family chromosome partioning protein	Cytoplasmic	32836			X
88194887	Q2FZ94	penicillin-binding protein 1	Cytoplasmic Membrane	82657			X
88195184	Q2FYI0	penicillin-binding protein 2	Cytoplasmic Membrane	80377	X		
88195360	Q2FY21	penicillin-binding protein 3	Cytoplasmic Membrane	77190			X
88195317	Q2FY59	peptidase T	Cytoplasmic	40235			X
88196022	Q2FWE0	peptide chain release factor 1	Cytoplasmic	40325			X
88194713	Q2FZP4	peptide chain release factor 3	Cytoplasmic	59564			X
88194262	Q2G0R9	peptidyl-tRNA hydrolase	Cytoplasmic	21689			X
88193889	Q2G1N4	periplasmic binding protein	Cytoplasmic Membrane	36721			X
88196282	Q2FVR0	permease domain-containing protein	Cytoplasmic Membrane	39456			X
88195864	Q2FWT7	phage head-tail adaptor	Unknown	13072			X
88196598	Q2G221	phage infection protein	Cytoplasmic Membrane	108649			X
88195856	Q2FWU5	phage minor structural protein	Cytoplasmic	143656	X	X	X
88195239	Q2FYC8	phage tail tape meausure protein	Extracellular	225925			X
88195719	Q2FX65	phage tape measure protein	Cytoplasmic Membrane	125734			X
88195871	Q2FWT4	phage terminase large subunit	Cytoplasmic Membrane	65249			X
88195922	Q2G2N7	phage terminase small subunit	Cytoplasmic	22208			X
88194839	Q2FZD9	phenylalanyl-tRNA synthetase subunit alpha	Cytoplasmic	40081			X
88194840	Q2FZD8	phenylalanyl-tRNA synthetase subunit beta	Cytoplasmic	88866			X
88195861	Q2FWU0	phi PVL orf 13-like protein	Unknown	34917		X	X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88195112	Q2FYQ0	phosphate transporter ATP-binding protein	Cytoplasmic Membrane	32134			X
88194781	Q2FZH6	phosphocarrier protein HPr	Cytoplasmic	9490	X	X	X
88194996	Q2FZ08	phosphodiesterase	Cytoplasmic	58477			X
88195605	Q2G1W2	phosphoenolpyruvate carboxykinase	Cytoplasmic	59340			X
88194782	Q2FZH5	phosphoenolpyruvate-protein phosphotransferase	Cytoplasmic	63179			X
88196066	P0C0V7	phosphoglucosamine mutase	Cytoplasmic	49234			X
88194556	Q2G031	phosphoglycerate kinase	Cytoplasmic	42575	X		X
88194558	Q2G029	phosphoglyceromutase	Cytoplasmic	56389			X
88196343	Q2FVK8	phosphoglyceromutase	Unknown	26663			X
88194341	Q2G0J8	phosphomethylpyrimidine kinase	Unknown	29838			X
88193918	Q2G1L7	phosphonate ABC transporter substrate-binding protein	Unknown	34978			X
88194559	Q2G028	phosphopyruvate hydratase	Cytoplasmic	47088	X	X	X
88194772	Q2FZI5	phosphoribosylamine--glycine ligase	Cytoplasmic	45820			X
88194763	Q2FZJ4	phosphoribosylaminoimidazole carboxylase ATPase subunit	Cytoplasmic Membrane	42466			X
88194762	Q2FZJ5	phosphoribosylaminoimidazole carboxylase catalytic subunit	Cytoplasmic Membrane	14733			X
88194769	Q2FZI8	phosphoribosylaminoimidazole synthetase	Cytoplasmic	36994			X
88194764	Q2FZJ3	phosphoribosylaminoimidazole-succinocarboxamide synthase	Cytoplasmic	26676			X
88194766	Q2FZJ1	phosphoribosylformylglycinamidine synthase I	Cytoplasmic	24511			X
88194767	Q2FZJ0	phosphoribosylformylglycinamidine synthase II	Cytoplasmic	79486			X
88194765	Q2FZJ2	phosphoribosylformylglycinamidine synthase PurS	Cytoplasmic	9915			X
88194349	Q2G0J0	phosphotransacetylase	Cytoplasmic	34930		X	X
88194984	Q2FZ20	polynucleotide phosphorylase/polyadenylase	Cytoplasmic	77314			X
88194531	O06446	preprotein translocase subunit SecA	Cytoplasmic	95900			X
88195449	Q2FXT7	preprotein translocase subunit YajC	Cytoplasmic Membrane	9665			X
88195491	Q2FXP5	primosomal protein DnaI	Cytoplasmic	35613			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88195336	Q2FY40	proline dipeptidase	Cytoplasmic	39313			X
88194973	Q2G1Z4	prolyl-tRNA synthetase	Cytoplasmic	63823			X
88193885	P02976	protein A	Cell wall	56403	X	X	
88194111	Q2G145	PTS system ascorbate-specific transporter subunit IIC	Cytoplasmic Membrane	47382	X		
88196596	Q2FUX0	PTS system fructose-specific transporter subunit IIABC	Cytoplasmic Membrane	69838			X
88196480	Q2FV87	PTS system glucose-specific transporter subunit IIABC	Cytoplasmic Membrane	74368			X
88196103	Q2G2R5	PTS system lactose-specific transporter subunit IIA	Cytoplasmic	11363			X
88196061	Q2FW99	PTS system mannitol-specific protein	Cytoplasmic Membrane	55030			X
88196063	Q2FW97	PTS system mannitol-specific transporter subunit IIA	Cytoplasmic	15533			X
88193970	Q2G1G5	PTS system transporter	Cytoplasmic Membrane	50632			X
88195154	Q2FYL0	PTS system transporter subunit IIA	Cytoplasmic	17949			X
88194254	Q2G0S7	pur operon repressor	Cytoplasmic	30376			X
88196043	Q2FWB8	purine nucleoside phosphorylase	Cytoplasmic	25892			X
88195596	Q2FXE8	putative translaldolase	Unknown	25689	X	X	X
88194280	Q2G0Q1	pyridoxal biosynthesis lyase PdxS	Cytoplasmic	31972	X		X
88196040	Q2FWC1	pyrimidine-nucleoside phosphorylase	Unknown	46279			X
88195308	Q2FY68	pyrroline-5-carboxylate reductase	Cytoplasmic	28740			X
88194813	Q2G2C1	pyruvate carboxylase	Cytoplasmic	128467			X
88194792	Q2FZG4	pyruvate dehydrogenase complex, E1 component subunit alpha	Cytoplasmic	41357	X	X	X
88194793	Q2G2A5	pyruvate dehydrogenase complex, E1 component subunit beta	Cytoplasmic	35224	X	X	X
88195506	Q2FXM9	pyruvate kinase	Cytoplasmic	63063	X	X	X
88196481	Q2FV86	pyruvate oxidase	Cytoplasmic Membrane	63717			X
88194758	Q2FZJ9	quinol oxidase AA3 subunit II	Cytoplasmic Membrane	41750			X
228937974	Q2FZ09	recombinase A	Cytoplasmic	37633		X	X
88194845	Q2FZD3	recombination and DNA strand exchange inhibitor protein	Cytoplasmic	88606			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
161353524	Q2FXU8	recombination factor protein RarA	Cytoplasmic	47221			X
88195699	Q2G2G9	recombination regulator RecX	Cytoplasmic	32221			X
88195943	Q2FWL6	redox-sensing transcriptional repressor Rex	Cytoplasmic	23584			X
88194256	Q2G0S5	regulatory protein SpoVG	Cytoplasmic	11271			X
88193839	Q2G1S4	replicative DNA helicase	Cytoplasmic	52538			X
88194480	Q2G2G2	response regulator	Cytoplasmic	26841			X
88194046	Q2G1A6	ribokinase	Cytoplasmic	32429			X
88194940	Q2FZ50	ribonuclease III	Cytoplasmic	27904			X
88194507	Q2G078	ribonucleotide-diphosphate reductase subunit alpha	Cytoplasmic	82552			X
88194508	Q2G077	ribonucleotide-diphosphate reductase subunit beta	Cytoplasmic	37489			X
88194259	Q2G0S2	ribose-phosphate pyrophosphokinase	Cytoplasmic	35262			X
88195673	Q2FX95	ribosomal large subunit pseudouridine synthase D	Cytoplasmic	31421			X
88195478	Q2FXQ8	ribosome biogenesis GTP-binding protein YsxC	Unknown	22671			X
88194969	Q2FZ21	ribosome recycling factor	Cytoplasmic	20341	X		X
88194928	Q2FZ62	ribulose-phosphate 3-epimerase	Cytoplasmic	23557			X
88195369	P0A0J0	RNA polymerase sigma factor RpoD	Cytoplasmic	42145			X
88195604	Q2G1W4	S-adenosylmethionine synthetase	Cytoplasmic	43614			X
88196215	Q2G2J2	secretory antigen	Extracellular	29309	X	X	
88194479	Q2G2U1	sensor histidine kinase SaeS	Cytoplasmic Membrane	39717			X
88195527	Q2FXK8	septation ring formation regulator EzrA	Cytoplasmic*	66206			X
88194291	Q2G2M7	serine acetyltransferase	Cytoplasmic	23740			X
88196017	Q2FWE5	serine hydroxymethyltransferase	Cytoplasmic	45144			X
88194715	Q2FZP2	serine protease HtrA	Unknown	87036	X		
88195635	Q2FXC3	serine protease SplB	Extracellular	26081			X
88195965	Q2FWJ3	serine-protein kinase RsbW	Cytoplasmic	19170			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88193832	P95689	seryl-tRNA synthetase	Cytoplasmic	48609			X
88194660	Q2FZT7	signal peptidase IB	Cell wall*	17587			X
88194944	Q2FZ46	signal recognition particle protein	Cytoplasmic Membrane	50672			X
88194942	Q2FZ48	signal recognition particle-docking protein FtsY	Cytoplasmic Membrane	46561			X
161353531	Q2G0K6	SIS domain-containing protein	Unknown	19546			X
88194941	Q2FZ49	SMC domain-containing protein	Cytoplasmic	136665			X
88196038	Q2FWC3	S-ribosylhomocysteinase	Cytoplasmic	17502			X
88194564	Q2G023	SsrA-binding protein	Cytoplasmic	17745			X
88195808	Q2G2R8	staphopain thiol proteinase	Extracellular	44235	X		
88195966	P60070	STAS domain-containing protein	Cytoplasmic	12197			X
88194850	Q2FZC8	succinate dehydrogenase flavoprotein subunit	Cytoplasmic*	65462			X
88194851	Q2FZC7	succinate dehydrogenase iron-sulfur subunit	Cytoplasmic*	30563			X
88194954	Q2FZ36	succinyl-CoA synthetase subunit alpha	Cytoplasmic	31522			X
88194953	Q2FZ37	succinyl-CoA synthetase subunit beta	Cytoplasmic	42030			X
88195939	Q2FWM0	sucrose operon repressor	Cytoplasmic	35477	X	X	
88195938	Q2FWM1	sucrose-6-phosphate hydrolase	Cytoplasmic	57892			X
88194182	Q2G0X7	superantigen-like protein	Extracellular	40156	X		
88193908	Q2G261	superoxide dismutase	Extracellular	23026			X
88195361	P0A0J3	superoxide dismutase	Extracellular	22697			X
88196104	P0A011	tagatose 1,6-diphosphate aldolase	Cytoplasmic	36573			X
88195858	Q2FWU3	tail length tape measure protein	Cytoplasmic Membrane	169851			X
88194030	Q2G1C2	teichoic acid biosynthesis protein TagB	Cytoplasmic Membrane	60146			X
88195522	Q2FXL3	thiol peroxidase	Unknown	17994		X	X
88194846	Q2FZD2	thioredoxin	Cytoplasmic	11433	X		X
88194592	Q2G000	thioredoxin	Cytoplasmic	12133	X		X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88194546	Q2G041	thioredoxin reductase	Cytoplasmic	33595		X	X
88195051	Q2FYV3	threonine synthase	Cytoplasmic	37846			X
88195489	Q2FXP7	threonyl-tRNA synthetase	Cytoplasmic	74441			X
88194298	Q2G0P2	transcription antitermination protein	Cytoplasmic	20651	X		X
88195331	Q2FY45	transcription antitermination protein NusB	Unknown	15052			X
88195419	Q2FXW7	transcription elongation factor GreA	Cytoplasmic	17732			X
88196025	Q2FWD7	transcription termination factor Rho	Cytoplasmic	49939			X
88194963	Q2FZ27	transcriptional repressor CodY	Cytoplasmic	28737			X
88194263	Q2G0R8	transcription-repair coupling factor	Cytoplasmic	134135			X
88195066	Q2FYT8	transketolase	Unknown	68317			X
88196140	Q2FW28	translation initiation factor IF-1	Cytoplasmic	8274	X		
88194979	Q2G2D0	translation initiation factor IF-2	Cytoplasmic	77823	X		X
88195487	Q2FXP9	translation initiation factor IF-3	Cytoplasmic	20200			X
88194215	Q2G0V3	trans-sulfuration enzyme family protein	Cytoplasmic	41253			X
88195480	Q2FXQ6	trigger factor	Cytoplasmic	48579	X	X	X
88194557	Q2G030	triosephosphate isomerase	Cytoplasmic	27275			X
88194959	Q2FZ31	tRNA (uracil-5-)-methyltransferase Gid	Cytoplasmic	48341			X
88195012	Q2FYZ2	tRNA delta(2)-isopentenylpyrophosphate transferase	Cytoplasmic	35845			X
161353516	Q2FUQ3	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA	Cytoplasmic	70072			X
88194690	Q2FZQ7	tryptophanyl-tRNA synthetase	Cytoplasmic	36886			X
88193841	Q2G2U6	two-component response regulator	Cytoplasmic	27175			X
88195539	Q2FXJ5	tyrosyl-tRNA synthetase	Cytoplasmic	47568			X
88194516	Q2G069	UDP-N-acetylenolpyruvoylglucosamine reductase	Cytoplasmic	33776			X
88196003	Q2FWF4	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Cytoplasmic	44913			X
88196079	Q2FW81	UDP-N-acetylglucosamine pyrophosphorylase	Cytoplasmic	44866			X

GI ID	Uniprot	Protein	PSORTb	MW (Da)	1 min shave	30 min shave	Biotin
88195554	Q2FXJ0	UDP-N-acetylmuramate--L-alanine ligase	Cytoplasmic	49157			X
88194889	Q2FZ92	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	Cytoplasmic	49813			X
88195789	Q2FWZ9	UDP-N-acetylmuramyl tripeptide synthetase	Cytoplasmic	49235	X		X
88194970	Q2G1Z7	undecaprenyl pyrophosphate synthase	Cytoplasmic	29829			X
88195149	Q2FYL5	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	Cytoplasmic Membrane	39672			X
88196016	Q2FWE6	uracil phosphoribosyltransferase	Cytoplasmic	23035			X
88194342	Q2G0J7	uracil-DNA glycosylase	Cytoplasmic	24922			X
88196205	Q2G2K5	urease subunit alpha	Cytoplasmic	61741			X
88194968	Q2FZ22	uridylate kinase	Cytoplasmic	26128			X
88196249	Q2FVT5	urocanate hydratase	Cytoplasmic	60595			X
88195655	Q2FXA3	uroporphyrinogen decarboxylase	Cytoplasmic	39327			X
88196436	Q2G1T6	UTP-glucose-1-phosphate uridylyltransferase	Cytoplasmic	29440			X
88195468	Q2FXR8	valyl-tRNA synthetase	Cytoplasmic	101660			X
88194170	Q2G0Y9	xanthine phosphoribosyltransferase	Cytoplasmic	20871			X

Proteins are listed alphabetically. An “X” denotes the identification of that protein in two or more replicates within that experimental method. Locations shown are the result of PSORTb bioinformatics predict tool [180]. Shaded proteins were determined to be essential to *S. aureus* SH1000 using a Transposon-Mediated Differential Hybridisation (TMDH) library [223]. ^This GI ID is not linked to a Uniprot ID, so the FASTA file was downloaded from the NCBI website (https://www.ncbi.nlm.nih.gov/protein) [102] and then entered into PSORTb. *Predicted to have more than one location by PSORTb [180], in which case the highest scoring location is shown.

2.3.3.3. 2D- PAGE analysis of surface biotinylated proteins

2D-PAGE analysis of biotinylated proteins was conducted to further analyse the surface proteome. By reducing complexity (separating out proteoforms, and proteins of similar MW) there is a greater chance of enhanced peptide coverage proteins (compared to a 1D-SDS-PAGE slice), within each protein identification. This is due to the stochastic nature of the mass spectrometer as well as the competition between peptides for fragmentation, giving each peptide a greater chance to be selected for fragmentation. As a number of proteins were found migrating at a lower MW than their annotated MW, this method was implemented to gain more evidence of cleavage fragments that reside on the surface of *S. aureus*. This analysis also provided more in-depth information regarding surface exposed proteoforms. 223 individual spots were excised and trypsin digested for analysis and protein identification. From this, over 300 proteins were identified with the cut-offs described in Section 2.2.15. This number discrepancy occurs as multiple proteins were identified in a number of spots, indicating that sample complexity can be further reduced. As these proteins were separated out on a 3-10 pI gradient, smaller gradients could be used for this purpose in the future.

2.3.4 A large number of predicted cytosolic proteins are consistently found on the surface of *S. aureus*

Predicted cellular location of identified surface proteins was determined using PSORTb [180]. This prediction model was used to highlight the limiting factors in such algorithms and because this is how many publications determine if proteins reside on the surface [256]. For proteins not included in the UniProt database, eg. 30S ribosomal protein S10, their FASTA sequence was retrieved from NCBI [102] for PSORTb analysis. Manual analysis was carried forward for all unassigned identifications. The lack of annotation within UniProt highlights the need for experimental data to verify gene products and correct online databases.

For the 30 min trypsin incubation, PSORTb determined that of the proteins identified, 52 (53 %) were predicted to be cytoplasmic, 14 (14 %) were predicted to be cell wall located, 14 (14 %) were unknown, 11 (11 %) were predicted to be located within the cytoplasmic membrane, and 7 (7 %) were predicted to be located extracellularly (Figure 2.7). A similar cellular location pattern was predicted for proteins identified in the 1 min trypsin shave: 87 (60 %) proteins were predicted to be cytoplasmic, 22 (15 %) unknown, 15 (10 %) cell wall associated, 11 (8 %) cytoplasmic membrane associated, and 10 (7 %) extracellularly located (Figure 2.8). Although more protein identifications were made using the 1 min incubation technique, this technique led to the identification of a higher number of proteins predicted to locate to the cytosol, cytoplasmic membrane, cell wall, extracellular, and unknown locations (non-classical surface proteins).

The 1D-SDS-PAGE analysis of biotinylated proteins resulted in the identification of 725 proteins, of which 520 (72 %) were predicted to be cytoplasmic, 97 (13 %) were unknown, 82 (11 %) were predicted to be located within the cytoplasmic membrane, 16 (2 %) were predicted to be located in the cell wall, and 10 (2 %) were predicted to be located extracellularly (Figure 2.9). This was the highest percentage of predicted cytoplasmic proteins across any methodology executed. When all data was combined, a total of 536 (68 %) of the IDs were predicted to reside in the cytosol of *S. aureus* (Figure 2.10), with 6 of these predicted to have multiple locations.

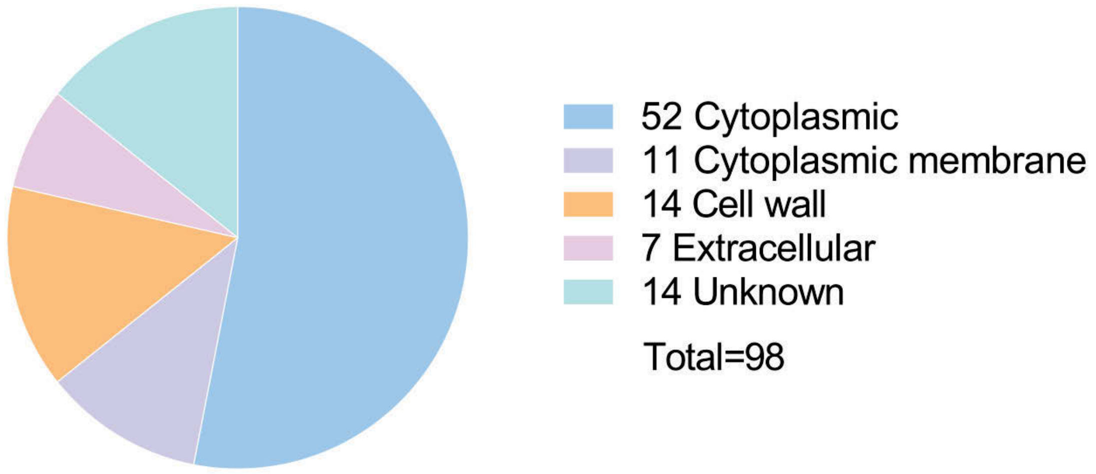


Figure 2.7 PSORTb predicted locations of proteins identified in the 30 min trypsin shave experiment.

A majority (52, 53%) of identified proteins in the 30 min trypsin shave experiment were predicted to reside in the cytosol via the PSORTb algorithm [180].

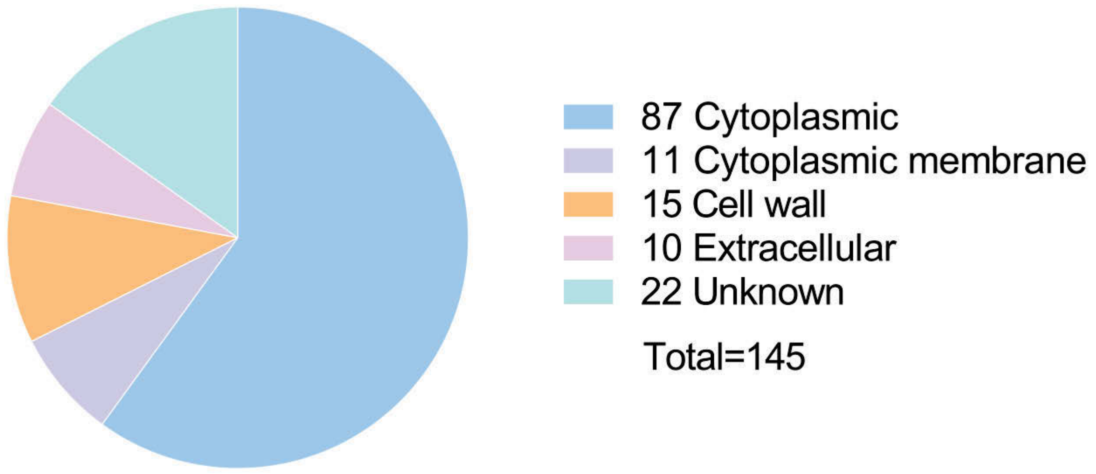


Figure 2.8 PSORTb predicted locations of proteins identified in the 1 min trypsin shave experiment.

The majority (87, 60%) of proteins identified in the 1 min trypsin shave experiment were predicted to be cytosolic via the PSORTb algorithm [180].

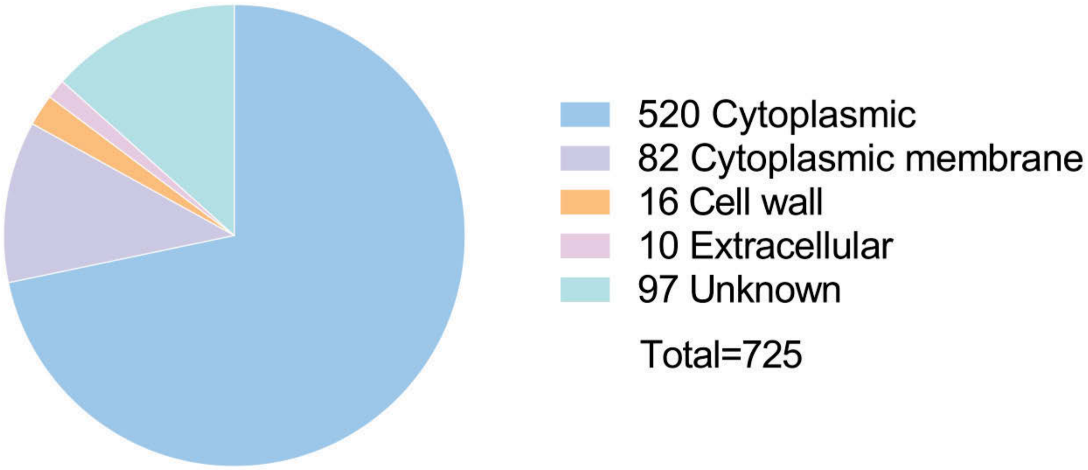


Figure 2.9 PSORTb predicted locations of proteins identified in the biotinylation experiment.

The majority (520, 72%) of proteins identified in the biotinylation experiment were predicted to be cytosolic via the PSORTb algorithm [180].

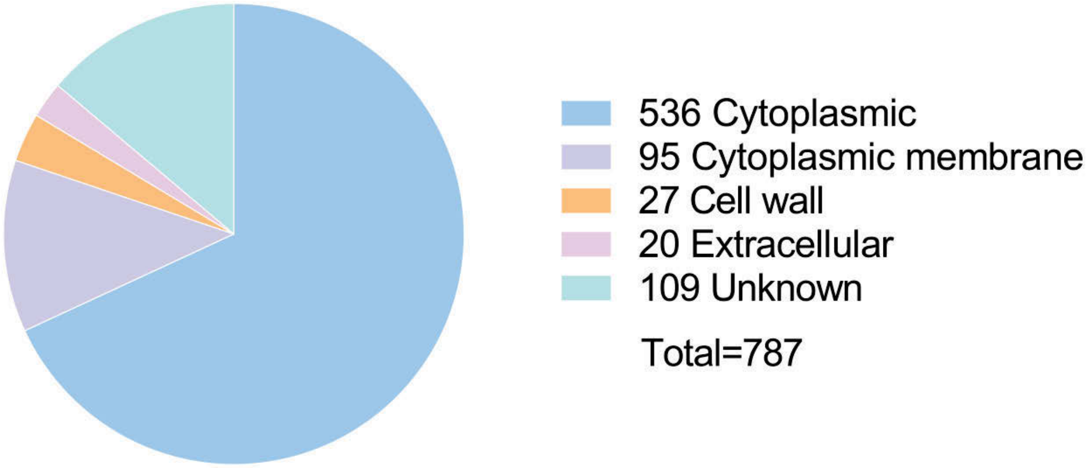


Figure 2.10 PSORTb predicted locations of proteins identified across all surface methodologies.

Again, the majority (536, 68%) of proteins identified across all experiments were predicted to be cytosolic via the PSORTb algorithm [180].

2.3.5 Proteins derived from essential genes were surface exposed

Proteins that were not previously identified as surface exposed (novel surface proteins) and proteins that are essential in *S. aureus* [223] were highlighted as potential novel therapeutic targets. Essential proteins (determined by Chaudhuri et al. [223] using a Transposon-Mediated Differential Hybridisation [TMDH] library) that were identified as part of the surface proteome are shown in a grey shaded colour in Table 2.1. A number of proteins were identified to fulfil these criteria including the previously well-studied DnaK, and Ef-Tu proteins (for analysis of Ef-Tu see Chapter 4). Many hypothetical proteins were also identified on the surface, some also being deemed essential (Table 2.1) indicating the need for a better understanding of the *S. aureus* proteome.

2.3.5.1. DnaK

DnaK was identified in all three methodologies, as well as in protein spots separated by 2D-PAGE of surface biotinylated proteins. Despite being identified on the surface, no predicted transmembrane domains were identified by TMpred for this protein [257]. In the 1D-SDS-PAGE analysis, DnaK was found migrating across a wide MW range. The 3-10 pH 2D-PAGE analysis resulted in 4 spots where DnaK was found migrating below its predicted MW of 66 kDa (Figure 2.11). It should also be noted that DnaK was identified at the predicted MW (66 kDa) indicating the intact protein is also surface exposed (identified in spots 5 and 8 in Figure 2.11). As DnaK was the top hit for spot 5, and given the density of spot 5, it may suggest that the full length protein resides on the surface in greater quantity than its cleavage products (seen as spots 41, 47, 152, 198, and 210 in Figure 2.11). Multiple proteins were identified in spot 5 and other quantitative methods are needed to validate this observation. This result also indicates that 2D SDS-PAGE methods have insufficient resolving power to separate *S. aureus* surface proteins. Only two spots (174 and 25, see Figure 2.12) were identified where DnaK was migrating below 66 kDa in the WCL 2D-PAGE sample. DnaK contains a trypsin insensitive region (region of protein lacking in lysine or arginine residues for trypsin to cleave) near its C-terminus (underlined in green in Figure 2.13) which may have caused the lack of identified peptides in that region.

Analysis of neo N-termini (conducted by N. Strange) also provides evidence that DnaK (66 kDa) is proteolytically processed in *S. aureus* SH1000. From the 2D-PAGE analysis of surface biotinylated proteins, a spot with a mass of approximately 30 kDa (spot 210, Figure 2.11) generated protein coverage spanning DnaK, indicating this protein being cleaved into two similarly sized fragments (Figure 2.13). These are most likely produced by cleavage events at sites ^{251}ISL↓PFI^{256}, and/or ^{275}FEE↓LSD^{280} near the middle of the DnaK protein sequence (Figure

2.13). A possible N-terminal cleavage event may also have occurred at site ^{12}TNS↓CTV^{17}, identified as part of the N-terminal analysis (by N. Strange). As the C-terminus region was not identified in this spot, there are two possible reasons as to why it was not identified. Firstly, there is a large trypsin insensitive region (of 30 amino acids) in the C-terminus from amino acid 572 - 601 (underlined in green in Figure 2.13) which would lead to difficulties in peptide identification. Secondly, this region may have been removed by a series of cleavage events. Indeed one possible cleavage site was identified at ^{590}QNN↓DST^{595} (Figure 2.13), as well as evidence for proteolytic cleavage (underlined in green in figure Figure 2.13, peptides listed in Table 2.2) was seen in the surface shotgun analysis (trypsin shave data). To aid in estimating amino acid coverage of the cleaved fragments, potential cleavage fragments were analysed by ProtParam [254,255] to determine their predicted MW and pI (Table 2.3). The most plausible explanation is highlighted in grey in Table 2.3. For the C-terminal fragment, the possibility that matches best to the migration includes the removal of the C-terminus at amino acid 575 (Table 2.3), which is also the start of the predicted clipping event (Table 2.2).

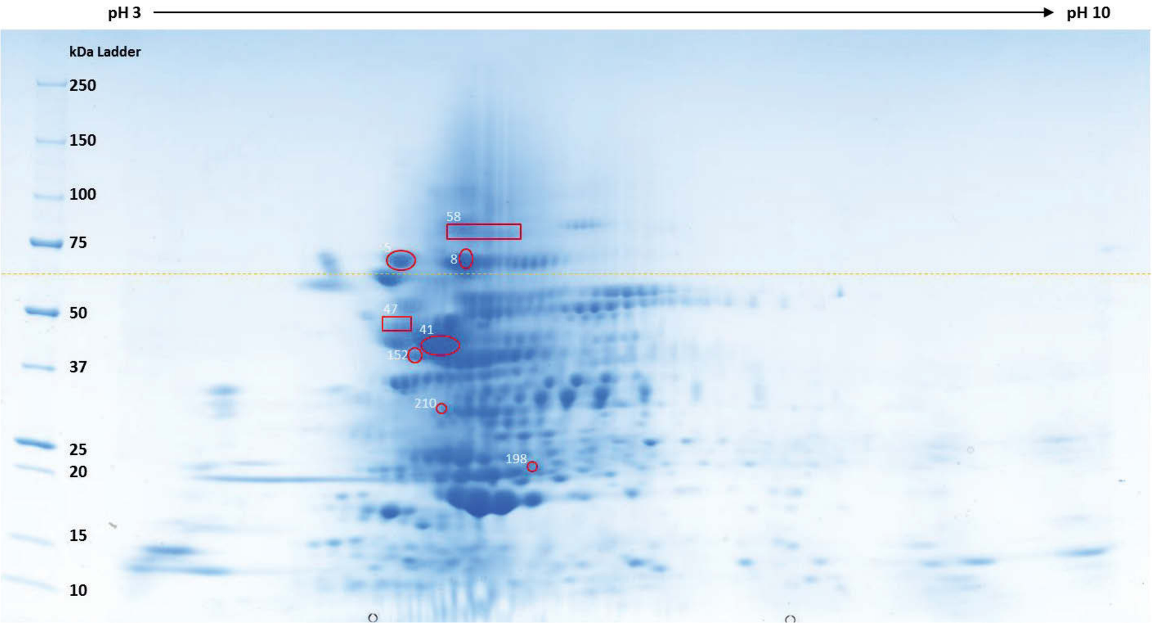


Figure 2.11 3-10 2D-PAGE of *S. aureus* surface biotinylated proteins.

Red sections and spot numbers indicate where DnaK was identified. Yellow broken line indicates where DnaK is expected to migrate to on gel (66 kDa). This gel identified five potential cleavage fragments of DnaK (spots 41, 47, 152, 198, and 210) which were found below 66 kDa. The three spots where DnaK were identified around and over 66 kDa are numbered 5, 8, and 58.

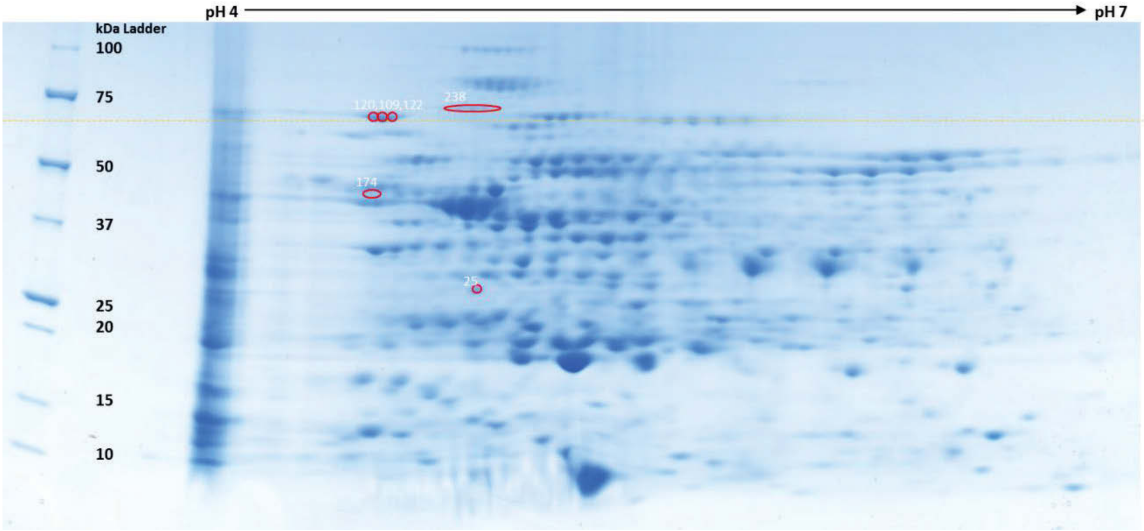
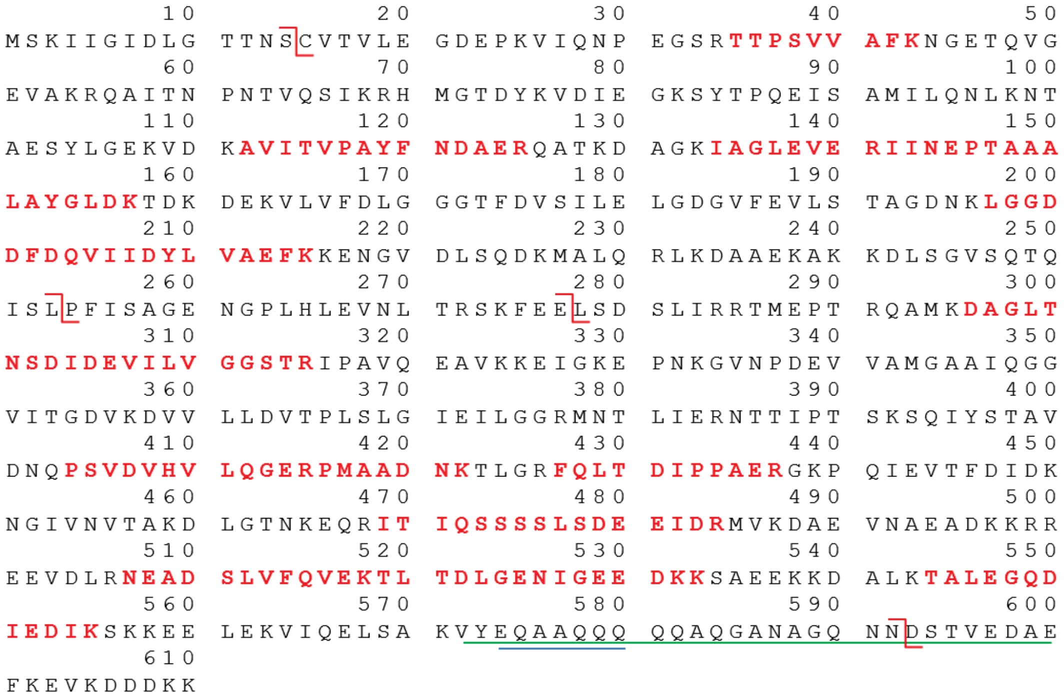


Figure 2.12 4-7 2D-PAGE of *S. aureus* WCL proteins.

Red circles and spot numbers indicate where DnaK was identified. Yellow broken line indicates where DnaK is expected to migrate to on gel (66 kDa). This gel identified two potential cleavage fragments of DnaK (spots 174 and 25) which were found below 66 kDa. Spots where DnaK was found near and above the line are numbered 120, 109, 122, and 238 (from left to right).



```
        10         20         30         40         50
MSKIIGIDLG TTNSCVTVLE GDEPKVIQNP EGSRTTPSVV AFKNGETQVG
        60         70         80         90        100
EVAKRQAITN PNTVQSIKRH MGTDYKVDIE GKSYTPQEIS AMILQNLKNT
       110        120        130        140        150
AESYLGEKVD KAVITVPAYF NDAERQATKD AGKIAGLEVE RIINEPTAAA
       160        170        180        190        200
LAYGLDKTDK DEKVLVFDLG GGTFDVSILE LGDGVFEVLS TAGDNKLGGD
       210        220        230        240        250
DFDQVIIDYL VAEFKKENGV DLSQDKMALQ RLKDAAEKAK KDLSGVSQTQ
       260        270        280        290        300
ISLPFISAGE NGPLHLEVNL TRSKFEELSD SLIRRTMEPT RQAMKDAGLT
       310        320        330        340        350
NSDIDEVILV GGSTRIPAVQ EAVKKEIGKE PNKGVNPDEV VAMGAAIQGG
       360        370        380        390        400
VITGDVKDVV LLDVTPLSLG IEILGGRMNT LIERNTTIPT SKSQIYSTAV
       410        420        430        440        450
DNQPSVDVHV LQGERPMAAD NKTLGRFQLT DIPPAERGKP QIEVTFDIDK
       460        470        480        490        500
NGIVNVTAKD LGTNKEQRIT IQSSSSLSDE EIDRMVKDAE VNAEADKKRR
       510        520        530        540        550
EEVDLRNEAD SLVFQVEKTL TDLGENIGEE DKKSAEEKKD ALKTALEGQD
       560        570        580        590        600
IEDIKSKKEE LEKVIQELSA KVYEQAAQQQ QQAQGANAGQ NNDSTVEDAE
       610
FKEVKDDDKK
```

Figure 2.13 DnaK protein sequence showing tryptic peptides generated from spot 210.

All peptides identified are shown as red amino acid residues. Semi tryptic cleavage sites identified that may be relevant to these cleavage fragments are indicated by ⌊. A trypsin insensitive region occurs near the C-terminal end of this protein and is shown underlined in green. There was putative evidence that amino acid clipping event (Table 2.2) takes place in this region as indicated underlined in blue. Although, there was not enough data gathered on this to definitively say this was a cleavage event.

Table 2.2 Proteolytic clipping evidence in the C-terminus of DnaK.

^{572}VYE.Q.AA.QQ.QQQ^{582}			
Amino acid range	**E-value**	**Score**	**Peptide identified**
575–602	1.40E^{+02}	1	**E.Q**AAQQQQQAQGANAGQNNDSTVEDAEFK.E
558–575	1.20E^{+02}	4	K.KEELEKVIQELSAKVYE**Q.A**
578–605	1.20E^{+02}	4	**A.Q**QQQQAQGANAGQNNDSTVEDAEFKEVK.D
580–602	19	12	**Q.Q**QQAQGANAGQNNDSTVEDAEFK.E

Semi-tryptic peptides identified in shotgun surface analysis (trypsin shave experiments) that indicate the possibility of a clipping event at the C-terminal region of DnaK (aa 574-580). Semi-tryptic cleavage site indicated in bold, semi-tryptic residues were identified in the N-and –C-termini of the peptides.

Table 2.3 Predicted MW and pI of possible fragments in spot 210.

Amino acid range		Number of amino acids	MW	Theoretical pI
N-terminus	1-253	253	27289.76	4.69
N-terminus	1-277	277	29956.73	4.71
N-terminus	15-277	263	28525.06	4.70
C-terminus	278-574	297	32505.58	4.67
C-terminus	278-592	315	34342.44	4.67
C-terminus	278-610	333	36422.63	4.61
C-terminus	403-610	207	23083.37	4.56

All predictions were calculated using ProtParam [254,255]. A number of possible cleavage fragments are represented in this data, and that could explain the peptide coverage presented in Figure 2.13. The most likely cleavage fragments are shaded in grey.

2.3.5.2. Confirmation that DnaK resides on the surface of *S. aureus*

A crude growth assay was performed to observe whether the antibodies raised (antibodies produced by D. Stipic in conjunction with EMAI) against a recombinantly expressed poly-histidine-tagged version of DnaK in *Escherichia coli*, were able to disrupt the growth of *S. aureus* cells. The resulting growth curves were unusual (extremely high error bars) in the sample treated with anti-DnaK antibodies (data not shown). Upon inspection, *S. aureus* cells were observed to aggregate only when anti-DnaK antibodies were added (Figure 2.14), this was not observed with the addition of other antibodies tested (data not shown). These aggregates were clearly visible and most anti-DnaK treated wells contained a major group of aggregates, rather than multiple smaller clusters (Figure 2.14). This suggests that the aggregation effect of these antibodies was rather strong. Hence the presence of this antibody appears to affect the phenotype of *S. aureus* SH1000 *in vitro*, and should be further investigated.

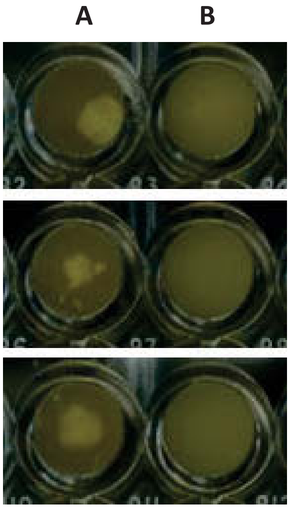


Figure 2.14 Small scale growth assays with antibodies to DnaK.
A. *S. aureus* cells grown in the presence of anti-DnaK, with wells showing the aggregation of cells. Cellular aggregation was in no distinct pattern, although there appeared to be a major aggregate of cells in each well (not micro-aggregates) **B.** *S. aureus* cells grown in the presence of pre-immunisation (zero-bleed, negative control serum), with wells showing the normal cloudy appearance as is expected of *S. aureus* SH1000. The three rows represent biological replicates.

2.4 Discussion

The data presented in this chapter represents one of the most comprehensive surface proteome studies in *S. aureus* to date. *S. aureus* cells were analysed for surface-exposed proteins using surface trypsin shaving and the biotinylation method. From this analysis, a total of 787 proteins were identified on the surface of *S. aureus*. This is a significantly larger number compared to previous surface studies (Table 1.1). This is, in-part, due to the protein count including all staphylococcal proteins identified in two or more replicates in any methodology, and not excluding proteins that aren't predicted to have a surface localisation.

This research also resulted in the finding that current trends in trypsin and biotin incubation periods for *S. aureus* can be dramatically reduced. Initially, cells were incubated with trypsin for 30 min based on the incubation times in the literature ranging from 15-60 min [124-126,173,177]. As the doubling time for *S. aureus* is approximately 30 min, it was realised that this incubation time is not ideal as this is equivalent to an entire cell cycle in the organism. As trypsin incubations occur at 37 °C, it is feasible that some metabolic activity may be occurring in/on the bacterial cell. This could impact the proteomic data as the cell may start responding to the environment (as cells are incubated in nutrient poor PBS, this can trigger stress). To limit artefacts arising from cell division events (possibly releasing cytoplasmic proteins or membrane vesicles (MVs) [258]), cellular turnover/stress resulting in cell lysis, and protease activity during the incubation period the trypsin incubation period was reduced to 1 min. This had no adverse effects on the data obtained or, as expected, the live-dead staining results (with the live cell count remaining above 99 %).

The biotinylation incubation period used in earlier studies was also questioned here. Previously, *S. aureus* had been incubated in biotin from 30 min to 2 h (Table 1.1) [126,127,153,172]. Again, as the doubling time of *S. aureus* is around 30 min, these incubation periods were not ideal. Given that more physically sensitive species had been incubated with biotin for a shorter time period (as little as 30 s) [259], this time reduction was also applied to *S. aureus*. It should be noted that a biotinylation time-course was conducted (data not shown) and proteins were analysed with an avidin blot (as per Section 2.2.12) to determine if there was any visible change in biotinylated proteins identified, and between 1 min and 2 h, no change was observed. Therefore the biotinylation methodology was continued using a 1 min incubation time. From this data, it is now suggested that incubation times be reduced for future trypsin and biotinylation surface protein experiments in *S. aureus*.

A large number of classically cytosolic proteins were identified in this dataset (536, 68%). Cell lysis was controlled for as much as possible by reducing incubation periods and cell death was monitored during these incubations using fluorescence microscopy [124-127] If a significant number of cells happen to lyse during the incubation period, the proteins that are released can come into contact with the various reagents, likely leading to their identification in the surface proteome dataset. Hence the identification of “false positive” surface proteins may occur. As cell lysis is an important feature of surface proteome studies, it is generally assessed, or controlled for in a number of ways (Figure 2.15). These include: checking for lysis of cells using microscopy (live-dead staining) or CFU cell counts (agar plates) [124], checking for the appearance of false positives in the incubation solution (cells incubated in buffer without trypsin) [125,126], or checking for a cytosolic marker protein in the surface proteome via Western blotting [173].

Unfortunately, many of these "controls" do not take into account the natural cell cycle of bacterial populations. Many of the controls would not be able to detect lysis during growth (eg. live-dead staining), and other controls (eg. Western blotting) do not take into account this natural cell turnover and the presence of classically cytosolic proteins that moonlight on the surface of the bacterial cell (Figure 2.15). There is a turnover rate within bacterial communities as cells die, cell wall components are shed, and are broken down [260]. The complexity of bacterial autolysis is only starting to be truly understood, as it was previously seen as merely an end-stage event, it is now appreciated to be a highly complex, regulated process similar to what occurs in eukaryotic programmed cell death [260]. In fact, this process has been suggested to be integral to bacterial development [261], as a protection strategy [262], and as a way of removing damaged cells [261,263-265]. Programmed cell death releases various "public goods", helping the greater bacterial community [179]. There are various death mechanisms/modes that have been described in prokaryotes [266] all of which may result in the redistribution of cytosolic proteins for non-canonical functions. Recently, "exploding cell lysis" was described and directly linked to the extracytosolic distribution of cytosolic proteins [179]. Further, *S. aureus* produces MVs which are able to package up proteins and release them to the extracytosolic space [267] (Figure 2.15). These issues complicate the efforts to define the surface proteome and the secretome, but suggest that proteins have evolved to be more multifunctional than is currently appreciated.

The presence of classically cytosolic proteins on the cell surface may also be due to yet-discovered excretion mechanisms. Pasztor et al. [183] published that the Staphylococcal major autolysin (*Atl*) protein is involved in the excretion of cytoplasmic proteins. Ebner et al. [129] suggests that cytosolic proteins may hitchhike on the Sec-excretion machinery as the classically cytosolic proteins they studied had a similar excretion pattern to proteins known to be excreted by the Sec pathway. Interestingly their findings go against the cell lysis (during growth) hypothesis [153] as the abundance of the studied cytosolic protein did not constantly increase in secretions, rather a bell-shape curve for excreted cytosolic protein (ECP) concentration was observed [129]. It also appears that proteases are not responsible for enabling translocation of proteins, as *S. aureus* cells grown in the presence of protease inhibitors also had the same pattern of localisation and excretion of the studied ECPs [129]. Gatlin et al. [153] suggests a number of other potential mechanisms including ABC transporters and twin-arginine-translocation (Tat) pathways. It is clear that we still do not fully understand protein translocation in bacteria.

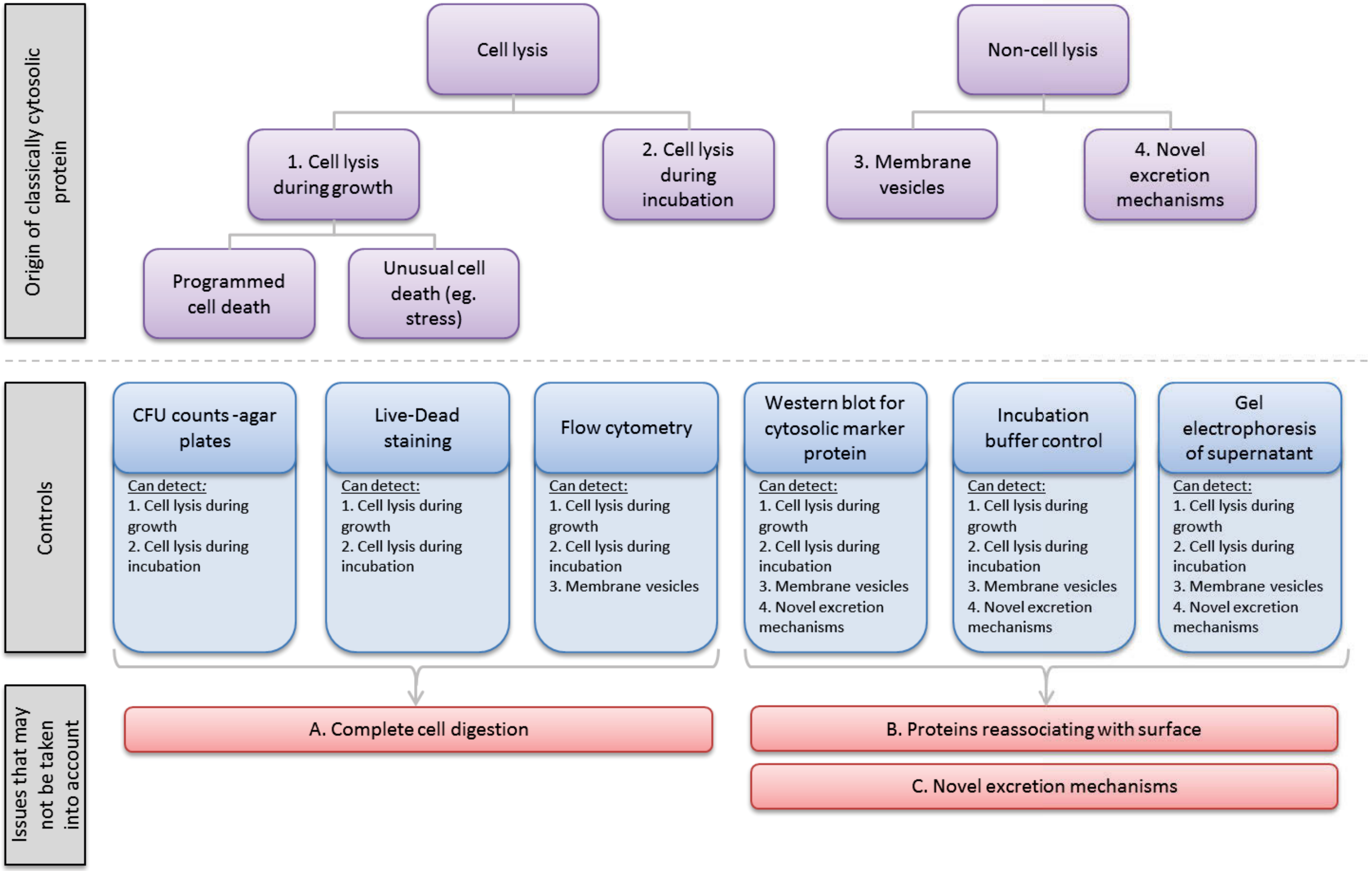


Figure 2.15 Possible causes for the presence of classically cytosolic proteins on the surface of *S. aureus*, and controls used in surface proteome analysis.

In this complete dataset, a total of 536 (68% of proteins identified on the surface of *S. aureus* cells) *S. aureus* proteins were predicted to by cytosolic via PSORTb [180]. This is interesting in regard to the experimental set-up and controls put in place. Firstly, live-dead staining was utilised to ensure large numbers of compromised cells were absent before and after incubation with trypsin or biotin. This indicates that cells were not lysed during these incubations. Secondly, as mentioned, live-dead staining would not account for cells that have been completely decomposed during the growth phase, leaving room for cytosolic proteins to reassociate onto the surface of live cells. Cells were washed thoroughly before incubation with trypsin or biotin, indicating that proteins that reassociate onto the cell surface of living cells do so with sufficient avidity to resist removal by washing. This suggests that cytosolic proteins have evolved over time to retain the ability to re-adhere to cell surfaces. Re-association of proteins to the cell surface has previously been described, and this has specifically been shown in *S. aureus* for classically cytoplasmic proteins [240]. Hence, cytosolic proteins in this dataset remained in the presented data for further investigation.

Within most proteomic studies of surface or secreted proteins, a number of classically cytosolic proteins are found (in the raw data) although they are not always presented in the results. It has been calculated that approximately one quarter of identified proteins across secretome studies in *Bacillus subtilis* and *S. aureus* are predicted to be cytosolic [129]. This phenomenon extends to all previous surface proteome studies in *S. aureus* (some shown in Figure 2.2). For example, of the 309 proteins identified on the surface of exponential phase cells by Hempel et al., 209 of these were predicted to be cytosolic (68 %) and of the 441 proteins identified in the stationary phase sample as surface proteins, 314 of these were predicted to be cytosolic (71 %) [127]. Indeed, this is an ongoing pattern and by looking more closely at previous *S. aureus* surface studies (including supplementary data); there is further experimental evidence of annotated cytosolic proteins being detected extracellularly, on the cell surface.

We compared the list of surface proteins identified in this study with a list of essential proteins in *S. aureus* SH1000 [223]. From this, a total of 211 proteins found on the surface were also found to be essential (shaded proteins in Table 2.1), and 177 of these were predicted to be cytosolic. These include *S. aureus* moonlighting (multifunctional) proteins; phosphopyruvate hydratase (enolase) [117], GAPDH [118], and triosephosphate isomerase [120]. Within this dataset resides a large number of ribosomal proteins. Ribosomal proteins have consistently been identified on the surface of bacterial cells [113,268,269]. Ribosomal proteins have also previously been described as anchorless cell wall proteins [130,269] and surface moonlighters in bacteria [113,270,271]. In *S. aureus* specifically, they have been found in secretome studies [159,178], and studies of *S. aureus* immunogens [272].

As cell wall-associated proteins are known to exhibit moonlighting roles [58], cytosolic proteins on the surface may moonlight as important virulence factors [123]. In the closely related *S. epidermidis*, non-classical protein secretion has been linked to virulence [130]. In this chapter, many non-classically secreted *S. aureus* proteins were identified on the surface (Table 2.1). DnaK was selected as a protein of interest (among other proteins, including Ef-Tu which is discussed in Chapter 4) because it was identified on the surface of *S. aureus* SH1000 across all three experimental procedures (Table 2.1). On the surface it was present as a full-length proteoform (at 66 kDa) and was identified in 1D-SDS-PAGE migrating as a cleaved protein product between 65-15 kDa and below 10 kDa (in two or more replicates). These cleavage products were further supported by the 2D-PAGE biotin data which showed DnaK present in protein spots with the molecular weight of 48, 43, 40, 30, and 21 kDa (see Appendix A Figure A.2).

DnaK is of particular interest as it is essential [223], highly conserved across bacteria [273], and belongs to the functional category (Clusters of Orthologous Groups of proteins [COG]) of post-translational modification, protein turnover, chaperones [274]. Proteins that reside within this COG often display moonlighting capabilities [113]. When inspecting surface data from previous studies more closely (supplementary data), DnaK has been identified on the surface of *S. aureus* in 7 of the 9 studies that analyse global surface data (Table 2.4). This protein has been found to be a moonlighting protein in a number of bacterial species [275-284]. Recombinant DnaK bound plasminogen and actin with the average dissociation constant [K_d] of 160±25 nM and 614±133 nM across three replicates, respectively [285] indicating a novel moonlighting role for this protein in *S. aureus*. Further, as shown in Chapter 3, DnaK is a putative GAG adhesin, although it was only identified to bind to HP with weak-medium (eluting between 0.5-1M NaCl) affinity (see Appendix B Table B.2). This protein has been shown to be important to the *S. aureus* stress response and the pathogen's survival in infection models [286] as well as biofilm formation and host cell adhesion [287]. The addition of anti-DnaK antibody to *S. aureus* SH1000 cells causes them to clump extensively (as shown in Section 2.3.5.2). Not only does this indicate that the targeting of DnaK affects cells (which should be further investigated regarding whether it decreases virulence), but it also provides another layer of evidence that that a subpopulation of DnaK molecules reside on the surface of *S. aureus*. Hence DnaK may prove to be a useful vaccine target in *S. aureus*. Indeed, this protein has already been suggested as a vaccine target in a number of other bacterial species [273] and has been tested as a vaccine candidate with varied efficacy [288-290]. As DnaK has not shown consistent protection, it should be considered as part of a multivalent strategy, or may also be useful for species-specific (*S. aureus*) therapeutics. As there is a human homologue to this protein, heat shock protein 70 (Hsp70), cross reactivity must be avoided when targeting the bacterial homologue. This issue has previously been investigated and the results found several "hot spots" that are unique to the bacterial DnaK sequence that may be targeted [273].

Table 2.4 Previous *S. aureus* surface studies that identified DnaK.

Publication	**Nandakumar 2004**	**Gatlin 2006**	**Wolff 2008**	**Glowalla 2009**	**Becher 2009**	**Dreisbach 2010**	**Hempel 2010**	**Solis 2010**	**Ventura 2010**	**Hempel 2011**	**Monteiro 2015**
DnaK found	Y	N/A	Y	N/A	Y	Y	Y	N	N	Y	Y
Reference	[175]	[153]	[176]	[174]	[172]	[173]	[127]	[125]	[124]	[126]	[177]

"Y" indicates DnaK was found in the (raw) data, "N" indicates DnaK was not found. "N/A" means that the full surface data was not analysed, or was not disclosed. DnaK has previously been found in 7 of the 9 surface publications that have full data analysed and disclosed. Cell wall and cell membrane studies have been included in this table.

2.5 Conclusion

By studying the surface proteome of *S. aureus* SH1000 using three complementary methodologies, a total of 787 proteins were reproducibly identified. As expected, a large number of these proteins (68 %) were predicted to be cytosolic [180]. Often, these proteins are regarded as “contaminants” despite being reported on the surface of a wide variety of bacterial species. We have retained these molecules in our list of surface accessible proteins as they are likely to be performing unique functions in this location. By retaining such potential surface moonlighting proteins in the dataset, an even greater number of potential therapeutic targets are available for investigation. DnaK was investigated further and was determined to be presented on the surface of *S. aureus* as both a full length protein, and as cleavage fragments. Incubating *S. aureus* cells with anti-DnaK antibodies caused uncharacteristic clumping, further supporting a location on the surface. This disruption to the normal phenotype indicates that targeting DnaK may cause adverse side effects to *S. aureus* cells, and hence DnaK may be considered a novel therapeutic target (as part of a multivalent strategy).

Further, this study demonstrated that the incubation periods for proteomic surface analysis (either with enzymes or labelling agents), should be reduced. Both the treatment of cells with trypsin and with NHS-biotin was reduced to 1 min for this study with no adverse effects on the identified proteins. With the issue of cell lysis a common concern to investigators of surface proteomes, reducing incubation times is highly recommended for any future surface proteome studies in bacterial cells.

Chapter 3.Putative heparin-binding proteins of *Staphylococcus aureus*

Declaration

Data presented in this chapter was acquired and analysed by the author, unless specified otherwise. The N-termini data presented here was obtained by N. Strange, and has been acknowledged in-text.

3.1 Introduction

S. aureus is an opportunistic pathogen of great concern to the health industry and greater public. It is known to quickly acquire resistance to the antibiotics it faces, and all current vaccines developed to control this pathogen have failed [42,216]. Therefore, a greater understanding of the pathogenesis pathway, and new targets for this pathogen are needed. *S. aureus* can cause a range of diseases, from mild skin infections to life-threatening toxic shock syndrome [25]. Surface proteins that bind host molecules are critical in the early stages of colonisation of the host, cell invasion, and the long term establishment of disease. *S. aureus* adheres to both abiotic and biotic surfaces [291,292] and is also renowned for causing chronic, persistent, and reoccurring infections due to its ability to form biofilms [291,293] and survive as an intracellular, albeit dormant, pathogen [192,294-296]. Due to the importance of surface adhesins in infections caused by *S. aureus*, this area has been investigated by several groups, and a number of reviews have appeared on the subject [45,58-66].

MSCRAMMs (Microbial Surface Components Recognising Adhesive Matrix Molecules) are molecules on the surface of bacteria that, as the name suggests, can recognise and interact with various host matrix molecules [43]. For this reason, they are seen as important virulence factors in pathogenic bacteria. More recently due to protein structure research, the term was revised to include proteins with structural and mechanistic similarities, with binding mediated by two adjacent subdomains, each containing IgG-like folds [58,297]. Growth stage and strain variation play an important role in determining the range of MSCRAMMs that are expressed on the cell surface [43]. The ligands described for MSCRAMMs in *S. aureus* are often limited to fibrinogen, fibrin, and collagen. Heparin (HP) is a negatively-charged glycosaminoglycan that has been used to mimic the highly sulfated regions of PGs that decorate the surfaces of a wide range of host epithelial surfaces and other cell types [86,298]. These highly sulfated regions are also known to be targeted by MSCRAMMs [81,299] and HP-binding ability is another trait of MSCRAMMs [43]. HP is one of several naturally occurring glycosaminoglycans (GAGs) in the host [300].

Glycosaminoglycans (GAGs) are highly sulphated macromolecules that decorate the surface of host cells. GAGs are often targeted by pathogens to enable cellular adhesion, invasion, and colonization [301]. The enzymatic removal of GAGs from host cell surfaces decreases the ability of bacteria to colonise, emphasising the importance of GAGs in establishing bacterial infection [302-304]. GAGs play a role in *S. aureus* adhesion to a range of host cell types including epithelial cells and macrophages [80]. There are numerous naturally occurring GAGs which are classified according to their structure [81]. HP can be linked to a core protein, becoming a PG, whereas the closely related heparan sulfate (HS) has multiple different core proteins and is less sulphated than HP [83]. The units of HP and HS can be differentially sulfated (Figure 3.1), with HS usually having only 30 % of its sequence sulfated [305]. Due to variations in the number of monosaccharide units, HP and HS range in molecular weight from 15-20 kDa [81]. In the host, HP was first identified as an anticoagulant in the bloodstream [300], and is now known to play a role in various cell-signalling, cell growth and differentiation pathways [81]. HP is also used *in vitro* as an archetypal GAG to assess the ability of molecules to bind GAGs [86,259,298,306]. GAG-protein binding is still poorly understood and multiple mechanisms may underlie the interaction such as hydrogen bonding, ionic bonding, hydrophobic or electrostatic interactions [81]. The ability for a pathogen to have a repertoire of proteins capable of non-specific interactions with GAGs increases its infectivity potential (Figure 3.2). Host PGs/GAGs also have these promiscuous binding characteristics (due to non-specific electrostatic-based binding sites, and multiple binding sites in one PG) compounding the infection issue [307]. Pathogenic and commensal bacteria are presented with numerous options when wanting to bind to host PGs. Binding is multifactorial and redundant because many proteins contribute to binding interactions with host cell surfaces As such, blocking one bacterial adhesin is unlikely to be sufficient to prevent host cell adherence. Hence, studying and inhibiting such interactions requires a global approach (rather than identifying one protein of interest).

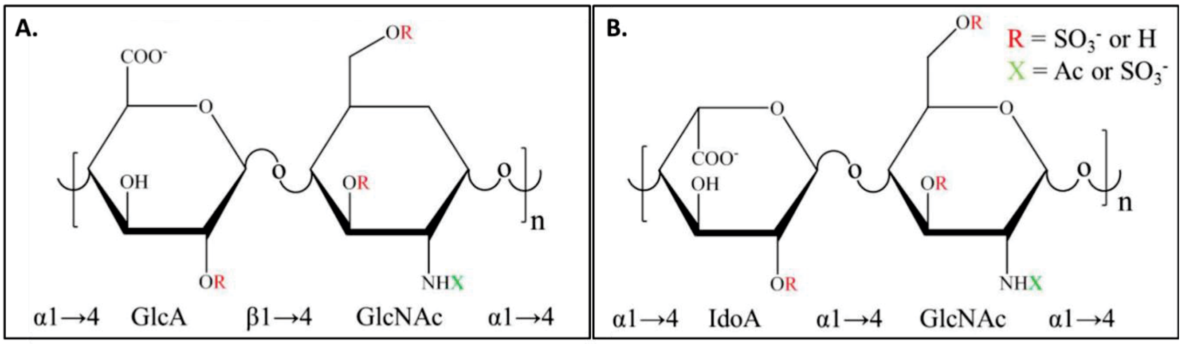


Figure 3.1 Structure of the heparan sulfate and heparin disaccharide units.

Figure adapted from Farrugia et al. 2015 [305]. **A.** The disaccharide unit of heparan sulphate (HS). **B.** The disaccharide unit of heparin (HP). The variable regions in the structure are shown as “R” and “X”.

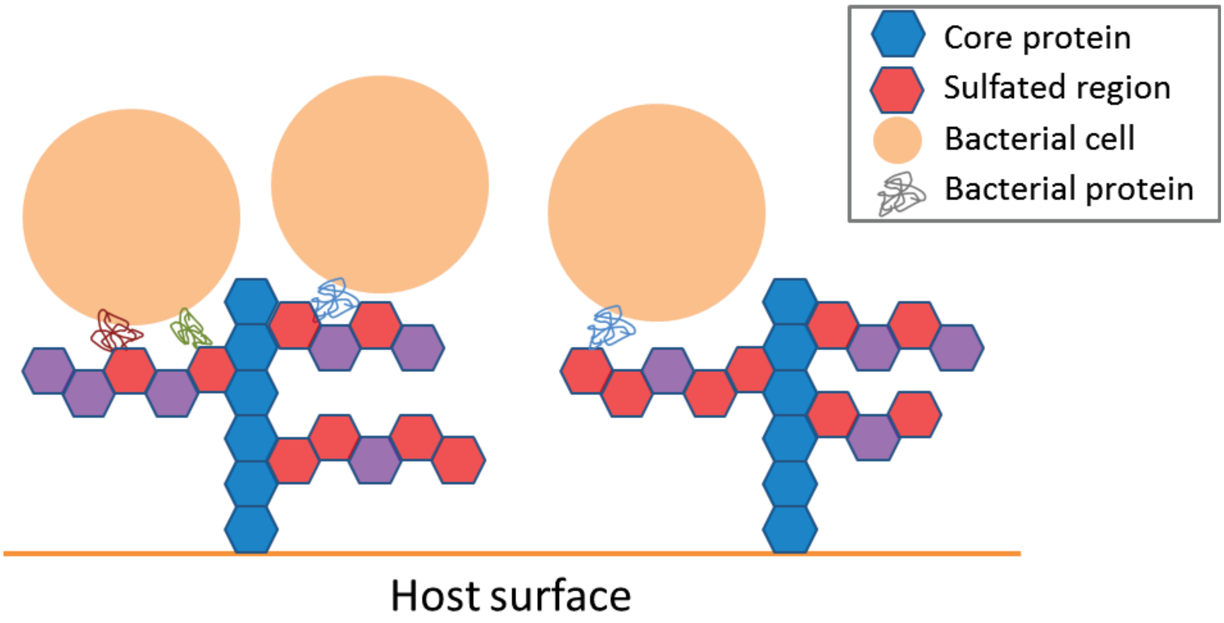


Figure 3.2 Diagram is depicting bacterial surface proteins interacting with proteoglycans (PG) on the host cell surface.

The chained glycosaminoglycans (GAGs) are linked to a core protein (shown as blue hexagons), this structure is collectively known as a PG. One protein can be linked to multiple GAG chains and different GAGs. The length of these GAG chains and the sulfated regions (shown as red hexagons) are variable. The clustering of these sulfated regions is responsible for the negative charge carried by GAGs. These negative charges are often associated with non-specific electrostatic interactions, allowing GAG chains to bind to different (bacterial) proteins (as shown in the figure). As PGs have multiple side GAG chains, it is also possible that each of these chains, and specific regions within them, have this binding capacity. This promiscuous, non-specific interaction means that one PG may have the ability to bind a number of bacterial proteins (different bacterial proteins shown by different colours). Further, one bacterium may have more than one protein capable of binding the GAG chain. This two-fold effect: the host PG having many (bacterial) protein binding sites, as well as invading bacteria displaying multiple GAG-binding proteins results in a complex interplay between the commensal/pathogen and the host. Diagram not drawn to scale.

Early studies showed that HS binds to the surface of *S. aureus* in a dose-dependent manner [90]. HS PGs mediate intestinal cell adhesion and invasion by *S. aureus*, and this interaction can be blocked by pre-incubation of the bacterial cells with HP [91,92]. Pre-treatment with HP and heparosan (the precursor to HP) also blocks the adhesion of *S. aureus* to enterocytes [93]. So far, only three *S. aureus* proteins have been shown to bind HS and HP. A 60 kDa and a 66 kDa protein (unknown identification) were found to bind HS and HP, although their full sequence is unknown [90]. The third is a smaller, uncharacterised staphylococcal protein, of only 17 kDa which binds HP [95]. Although other proteins were seen in gel electrophoresis results in these publications [90,95], these three proteins were the only ones investigated. Sequence alignments [94] of the identified peptides within these proteins returned minimal homologous proteins, suggesting that HP/HS-binding proteins, that are likely to be crucial to staphylococcal disease, remain to be elucidated.

Other than acting as a receptor for bacterial adhesion, HP has also been shown to promote biofilm formation by *S. aureus* [87], adding greater emphasis to this molecule's role in facilitating *S. aureus* virulence. This element of HP's role appears to be conserved across strains and is based on biofilm dispersion, not the increase of initial cellular attachment to the host, nor an overall increase in bacterial cell growth [87]. The study by Shanks et al., was implemented due to the frequent use of sodium HP in catheters and the formation of biofilms in such devices. HP-stimulated biofilms acquired the same increase in antibiotic resistance observed in native biofilms and the presence of HP increased *S. aureus* attachment to abiotic surfaces [87], increasing the likelihood of catheter related blood stream infections (compared to low concentration citrate or antimicrobial-containing citrate solution) [308]. Interestingly, the increase in cell-to-cell interaction (biofilm formation) was not seen when protein synthesis was inhibited by the addition of chloramphenicol [87]. This indicates that HP related biofilm stimulation is not mediated by HP alone/directly and may be mediated by protein interactions on the cell surface of *S. aureus*.

Despite these known relationships between HP invasion, and biofilm formation, there has yet to be a global analysis of proteins with the ability to bind HP in *S. aureus*. With little known about HP-binding proteins in *S. aureus*, and with the implications of HP-binding now clear, there is a need to characterise putative HP-binding proteins in *S. aureus*. As we are now able to analyse large proteomic datasets and identify multiple proteins with good sequence coverage within a bacterial sample, we can now identify numerous *S. aureus* proteins that possess the potential to bind HP and other host GAGs. Agarose columns containing immobilised HP are available to study putative protein-HP interactions [309]. GAGs carry a strong negative charge [80], and electrostatic interactions between HP and positively charged residues on bacterial proteins can be disrupted with the addition of an increasing concentration of NaCl which carries a positive charge when ionised in solution, outcompeting the protein for HP-binding. A NaCl gradient was used to segregate proteins that bind to HP into those that elute from the HP-agarose column at NaCl concentrations less than 500 mM (weak affinity), 0.5-1 M (medium affinity), and 1+ M (high affinity) sub-populations. Further, as the proteomics tools utilised to study these proteins maintains mass context (SDS-PAGE fractionation and in-gel enzymatic digestion allowed for the estimation of the approximate mass of that protein or protein fragment that was identified at a specific migration distance in the gel), this allowed for the identitification of different proteoforms (derived from the same ORF) that retain the ability to bind HP. This is important because analysis of proteoforms can be a powerful method to delineate binding domains to particular regions of the protein. Many bacterial proteins are modified post-translationally and mature proteoforms cannot be reliably predicted from gene sequence (ORF).

With many unexpected findings in the identities of proteins in the surfaceome study in Chapter 2, it is now important to investigate what subset of proteins in the surfaceome bind HP. One area that has been neglected in *S. aureus* studies is global adhesive studies, specifically involving glycosaminoglycans. For this reason, this chapter covers the first global study of HP-binding proteins in the human pathogen, *S. aureus*.

3.2 Material and methods

3.2.1 Cell Growth

S. aureus SH1000 cells were grown overnight in TSB (Oxoid) from a single colony. The next day, these cells were diluted to an optical density (OD_{595}) of 0.05 in TSB in a baffled flask. Cells were grown with intermediate shaking (210 rpm) at 37 °C until early stationary phase. OD_{595} was checked intermittently to ensure cell growth.

3.2.2 Cell Lysis and Protein Harvest

Cultures were poured into 50 mL tubes containing one pre-dissolved protease inhibitor tablet (Complete; Roche Diagnostics®) and centrifuged at 3 220 rcf for 10 min at 4 °C. The supernatant was removed, and cells were washed three times in ice-cold PBS containing protease inhibitors. The cell pellet was freeze-dried overnight and added to a pre-cooled metal canister. Dried cell pellets were bead-milled for 1 min with cooling in liquid nitrogen in between, this was repeated 15 times. Cell debris was washed out and resuspended in 1.5 mL of 10 mM sodium phosphate, pH 7 (buffer A). The solution was sonicated 4 times for 30 s at high intensity to shear any DNA and further lyse cells. Insoluble material was pelleted by centrifuging the lysate at 21 000 rcf for 15 min at 4 °C. 250 µL of the supernatant was removed and 30 µL of 10 mM sodium phosphate was added, this was further centrifuged for 10 min, 21 000 rcf. 260 µL of the supernatant was loaded into an auto-sampler vial ready for HP affinity chromatography.

3.2.3 Affinity Chromatography

Using a Waters 2690 Alliance LC separations module, the sample was loaded at 0.5 mL min^{-1} onto a 1 mL HiTrap Heparin HP column (GE healthcare) in buffer A. The elution gradient was run at 0.5 mL min^{-1} as follows: protein sample was loaded onto the HP column and the column was washed thoroughly with buffer A for 20 min; weakly binding proteins were eluted off with an increasing gradient from 0-50 % buffer B (10 mM sodium phosphate, 2 M sodium chloride, pH 7) for 25 min; then medium binding proteins were eluted using a gradient from 50-100 % buffer B for 10 min; followed by any strongly binding proteins that were eluted off using 100 % buffer B for 5 min. The elution profile was monitored at A = 220 and 280 nm with a Waters 996 photodiode array detector, and fractions were collected in 2 min intervals (1 mL) using a Waters fraction collector III.

3.2.4 Protein Preparation for Gel Electrophoresis

Fractions collected off the HP column were pooled into 5 groups; flow through, wash, and elutions 1-3. Elution 1 contains proteins eluted up to 0.5 M NaCl, elution 2 contains proteins eluted in 0.5-1 M NaCl, and elution 3 contains proteins that eluted above 1 M NaCl. Samples were reduced and alkylated using 5 mM of tributylphosphine and 20 mM of acrylamide monomers, respectively, and the reaction quenched using 10 mM dithiothreitol. Each of these pooled elution samples (E_1-E_3) were concentrated using a 3 kDa cut-off filter. Salt was diluted out during this phase by adding water to the top chamber (to the newly concentrated sample) and re-filtering it several times.

3.2.5 1D-SDS-PAGE One-Dimensional Gel Electrophoresis

As described in Section 2.2.10.

3.2.6 Two-Dimensional Gel Electrophoresis

Cells for Whole cell lysates (WCL) were grown, washed, and lysed, as per Section 2.2.1, 2.2.3, 2.2.7. 2D-PAGE gel of surface biotinylated and whole cell lysate proteins was performed as described in Section 2.2.11. With IPG strips (BioRad) of pH 4-7 and 6-11 used for WCL samples.

3.2.7 Protein Preparation for LC-MS/MS

Bands were cut at the same molecular weight (MW) for each biological replicate (As shown in Appendix B Figure B.1). The bands were cut based on protein density i.e. not equal size sections throughout the lane. A total of 27 protein bands were cut from each replicate representing the three salt elution concentrations. Gel slices were diced into approximately 1 mm^2 cubes and added to a 0.5 mL tube. Pieces were washed in 50 mM $NH_4HCO_{3,}$ de-stained with 50 mM NH_4HCO_3 / 50 % ACN, and then dehydrated with 100 % ACN (all solutions added with enough volume of liquid to cover gel pieces). ACN was removed, and excess ACN was evaporated off. In-gel digestion was carried out with trypsin (12.5 ng/µL trypsin in 100 mM NH_4HCO_3) incubated at 4 °C for 30 min, followed by 37 °C overnight. Peptides were further extracted from the gel using sonication, and the liquid solution containing peptides was transferred to a new 0.5 mL tube. Gel pieces were covered with 50 % ACN / 0.2 % TFA and sonicated again to extract remaining peptides from the gel, this liquid solution was added to the 0.5 mL tube containing previously extracted peptides. Peptides were concentrated to an approximate volume of 15 µL using an evaporator for subsequent LC-MS/MS analysis as described in [79].

Peptides extracted from 1D-SDS-PAGE were analysed using LC-MS/MS as previously described [79]. Samples (10 µL) were loaded onto a C8 Cap Trap column (Michrom) using an Eksigent AS-

1 autosampler connected to a Tempo nanoLC system (Eksigent) at 20 µL min^{-1} with MS buffer A (2 % ACN +0.2 % formic acid). The trapping column was washed for 180 s. Peptides were washed off the column (300 nL min–1) onto a PicoFrit column (75 µm × 150 mm) packed with Magic C18AQ resin (5 micron particles; Michrom), and into the source of a QSTAR elite hybrid quadrupole-time-of-flight mass spectrometer (Applied Biosystems/MDS Sciex) using the following program: 5–30 % MS buffer B (98 % ACN +0.2 % formic acid) over 30 min, 30–80 % MS buffer B over 5 min, and 80 % MS buffer B for 2 min, 80–5 % for 3 min. Eluting peptides were ionized from the Picofrit column at 2300 V. An Intelligent Data Acquisition (IDA) experiment was performed, with a mass range of 350–1500 Da continuously scanned for peptides of charge state 2+ to 5+ with an intensity of more than 30 counts/scan and a resolution >12 000. Selected peptides were fragmented, and the product ion fragment masses were measured over a mass range of 100– 1500 Da. The mass of the precursor peptide was then excluded for 120 s.

3.2.8 Protein identification

MS data files were searched against a *S. aureus* NCTC 8325 database derived from the published genome, and common contaminants database using Mascot Daemon (v 2.4, provided by the Australian Proteomics Computational Facility, hosted by the Walter and Eliza Hall Institute for Medical Research Systems Biology Mascot Server). Searches were conducted with the following parameters: Fixed modifications: none. Variable modifications: Deamidation (NQ), propionamide (C), and oxidation (M). Enzyme: semitrypsin. Number of allowed missed cleavages: 3. Peptide mass tolerance: 100 ppm. MS/MS mass tolerance: 0.2 Da. Charge state: 2+, 3+ and 4+. Proteins were deemed positively identified if significantly scoring peptides (E-value > 0.05) were found, and the protein was identified in two or more replicates at the same molecular mass slice in SDS-PAGE.

3.2.9 Bioinformatic Analysis

Bioinformatic analysis on protein results was performed using the following open-source software and resources: Protein sequences were obtained from UniProt, using the *S. aureus* NCTC 8325 protein data as the default for all *S. aureus* protein analysis (http://www.uniprot.org/) [101]; protein location was predicted using PsortB v3.0 [180]; functional categories of the identified proteins were predicted using Panther Gene Ontology [310], and predicted MW and pI for proteins, and protein fragments was obtained from ProtParam via ExPASy (http://web.expasy.org/protparam/) [254] [255]. ScanProsite [311] was used to search proteins for the following specific motifs; the two HP-binding consensus sequences [312] X-[HRK]-[HRK]-[HRK]-X-X-[HRK]-X and X-[HRK]-[HRK]-X-[HRK]-X, the heparan sulfate-binding motif [313] X-[HRK]-X-[HRK]-[HRK]-X, and motifs for clusters of basic residues X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X and X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X. Where HRK refers to histidine, arginine, and lysine, respectively (as per the IUPAC amino acid code), and X refers to any amino acid. Numbers in parentheses indicates the number range of repeating amino acids that will be searched, eg. X(1,4) will search for X, XX, XXX, or XXXX.

3.3 Results

3.3.1 Potential heparin-binding proteins identified in *S. aureus*

Six hundred thirty-one *S. aureus* proteins bound to the HP-agarose column, accounting for just over 20 % of the theoretical proteome. A total of 519 proteins were identified in E_1 (0-0.5 M NaCl), 423 in E_2 (0.5-1 M NaCl), and 67 in E_3 (1 + M NaCl) (Appendix B Tables B1-3). These salt gradients are proportional to K_d values, as such, proteins seen as interacting with high affinity (eluted in 1 + M NaCl) would have a K_d value in the range of 10^{-7} - 10^{-9} M [85]. This conversion relies on the assumption that the protein-HP interaction is an ionic one, which may not be correct in all cases, however it is a useful conversion for comparisons [85]. Some proteins were identified in multiple salt fractions, most likely due to multiple cleavage fragments (from the same protein) binding at different affinities. Each elution had a distinct protein profile, and the banding profiles were reproducible across each of the three replicates (Figure 3.3). Six hundred thirty-one out of a total of 1020 proteins (61.9 %) were identified in two or more replicates (within one protein slice). As expected, the highest protein overlap was seen between E_1 and E_2 at 318 (50.4 %) proteins, with only 45 (7.1 %) proteins being found in all three elutions (Figure 3.4). Only 7 (1.1 %) proteins identified were unique to E_3, while 14 (2.2 %) were shared only with E_2, and as expected, none were shared only with E_1. Within the three elution profiles, proteins were also found in more than one slice (MW range). It is important to note that the list of proteins that elute from the column can only be regarded as putative HP-binding proteins. Further studies are needed to confirm the binding interaction between the candidate proteins and HP using a number of biochemical and biophysical approaches.

A number of previously known adhesins were identified in this dataset (for full protein list see Appendix B Tables B1-3), including elastin-binding protein and extracellular matrix-binding protein ebh (for information on the latter see Section 3.3.4) [45]. In the highest salt elution, many unexpected proteins were identified, such as ribosomal proteins (see Section 3.3.4). In line with this, the most striking difference in the gel profile indicates that most proteins in the 1+ M NaCl elution were migrating below 35 kDa (Figure 3.3), indicating a bias towards a smaller MW. All proteins in this elution contained at least one HP binding, HS binding, or basic residue clustering motif that was searched as per Section 3.2.9 (see Appendix B Item B.1). Of the proteins in the 1+ M NaCl elution, 84 (53.8 %) carried evidence of nucleic acid-binding capacity (see Appendix B Tables B1-3). The implications of this are discussed in Section 3.4.5.

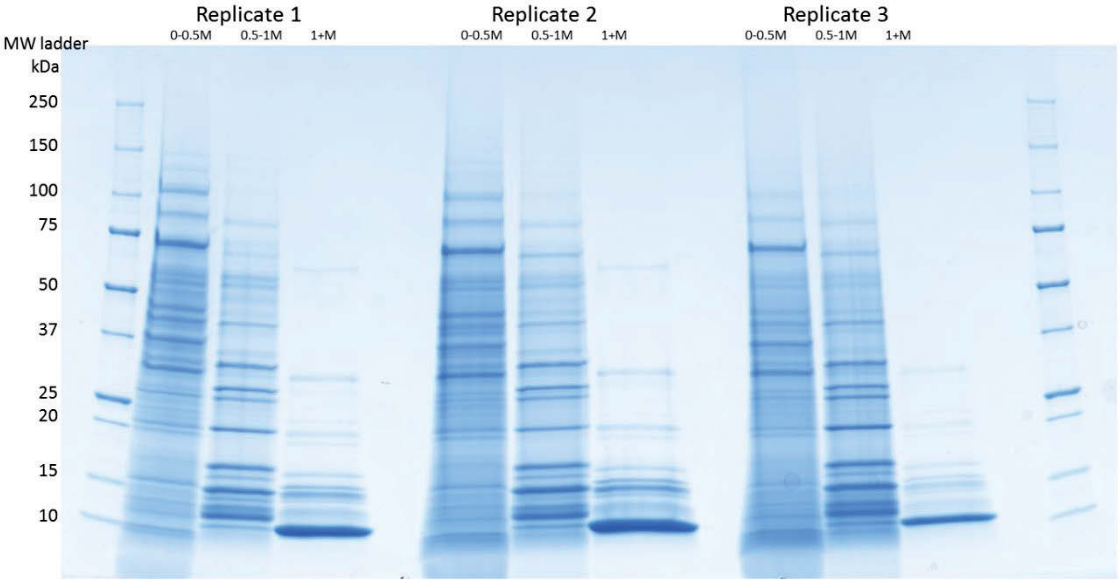


Figure 3.3 1D-SDS-PAGE gel of *S. aureus* putative heparin-binding proteins.

Biological replicates of putative HP-binding proteins from *S. aureus*. The protein elution gradient was divided into three pools: E_1 0-0.5 M NaCl, E_2 0.5-1 M NaCl, and E_3 1+ M NaCl, showing a different protein profile for each elution. See Figure B.1 in Appendix B for protein slice information (how the gel was cut for peptide extraction).

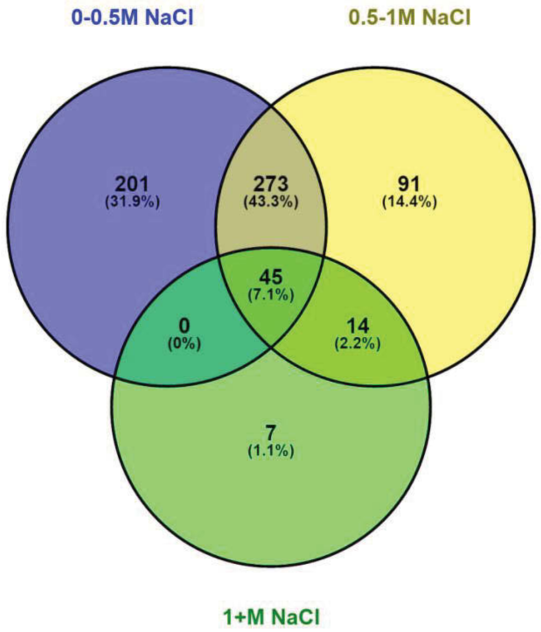


Figure 3.4 Venn diagram showing the overlap of *S. aureus* proteins identified across the three elutions (0-0.5 M, 0.5-1 M and 1 M+ NaCl).
To be “identified”, proteins needed to be found at the same molecular mass when separated by SDS-PAGE in two or more replicates.

3.3.2 Novel potential *S. aureus* adhesins identified

Of the total number of proteins identified (631) in this study, only 93 proteins (14.7 %) were predicted to have binding functionality using Panther Gene Ontology predictions (Appendix B Table B.4) [310]. Many proteins which have canonical functions in glycolysis were recovered from HP-agarose columns including pyruvate kinase, glyceraldehyde-3-phosphate-dehydrogenase, and fructose biphosphate aldolase. A large number of proteins with roles in protein translation were also identified including a number of ribosomal proteins. Most of the identified proteins (448, 71 %) have a canonical function in the cell cytosol (Figure 3.5). These putative HP-binding proteins identified from the HP-agarose column may represent a subset of moonlighting adhesins that assemble on the *S. aureus* cell surface. We interrogated our surfaceome dataset (presented in Chapter 2) to determine which surface proteins were retained during HP-agarose chromatography.

3.3.3 Identification of cleavage products binding heparin

Of the proteins identified to bind to HP, 186 (29 %) were found to electrophorese at a lower molecular weight than predicted from their gene sequence (Figure 3.6). This may indicate that the protein contains unusual motifs that cause aberrent gel migration [314] or are modified postranslationally either by the addition or remove of functional groups or by proteolysis. At the highest salt elution, a total of 19 (29 %) proteins identified appeared at a lower molecular weight than expected during SDS-PAGE. Furthermore, some proteoforms were found to bind HP with an apparent higher affinity (different elution) than the full length, parent form of the protein. To investigate this we selected a subset of proteins and mapped cleavage sites within the molecule.

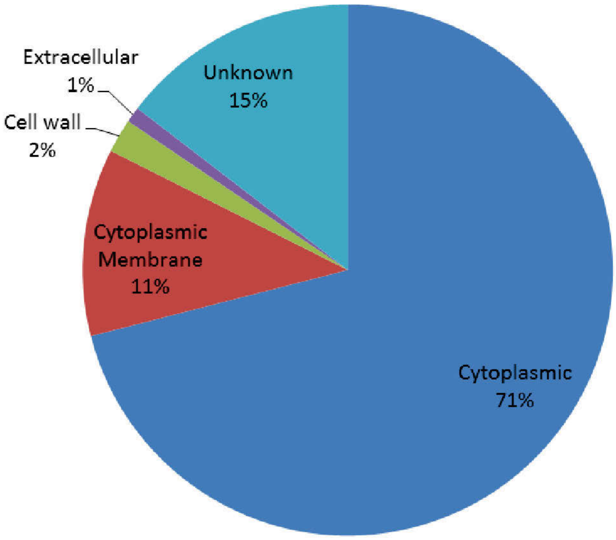


Figure 3.5 Predicted cellular locations of identified proteins.

Predicted locations were determined using PsortB v3.0 [180]. The majority of the proteins identified (448, 71 %) in this analysis were predicted to reside within the cytoplasm of the bacteria.

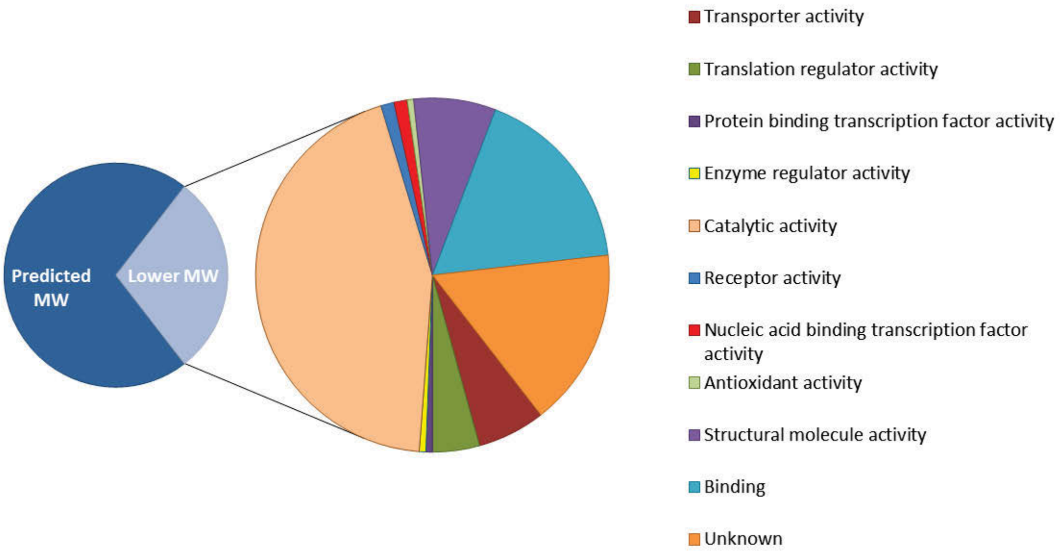


Figure 3.6 Functions of cleaved proteins identified.

Proteins found in HP elutions (in two or more replicates) were analysed for the presence of proteolysis. Proteins were deemed to have undergone proteolysis if they were migrating at a lower molecular weight on the 1D-SDS-PAGE gel to that predicted from their gene sequence. 186 proteins (29 % of HP-binding proteins) were found to have undergone proteolysis. These proteins were analysed for their functional category using GO annotations [310], it appears that a large amount of *S. aureus* catalytic proteins are proteolytically processed.

3.3.4 Cleaved proteins bind heparin at high salt concentrations

Several cleavage products were found to bind HP at salt concentrations much higher than the native physiological conditions of 150 mM. Among these, one of the most processed molecules appears to be extracellular matrix-binding protein ebh (hypothetical protein SAOUHSC_01447). Ebh has a molecular weight of over 1000 kDa and comprises of 9535 amino acids. Remarkably, tryptic peptides spanning the entire length of this protein were found migrating at approximately 10 kDa at the highest salt elution. With coverage mapped throughout the length of the protein, this indicated that this protein is cleaved at least 100 times to produce fragments of about 10 kDa length. Investigating all semi-tryptic (N-and C-terminal) and neo-N-terminal labelled peptides (Neo-N-terminal labelled peptides identified by J. Steele and N. Strange) revealed that this molecule is processed throughout its length. A total of 2065 N-terminal cleavage events were identified, and 694 C-terminal events (evidence for each of these sites had to be found in at least 3 biological samples, either labelled or semi-tryptic) (Figure 3.7). Even with this large number of sites no such processing patterns were identified. However, as shown in Figure 3.7, there does appear to be “hot spots” for processing of this molecule (areas with higher black colour density). HP-binding motifs were also identified in this molecule, and when overlapping motifs were combined, this resulted in 90 predicted HP-binding domains (shown as dark blue regions in Figure 3.7).

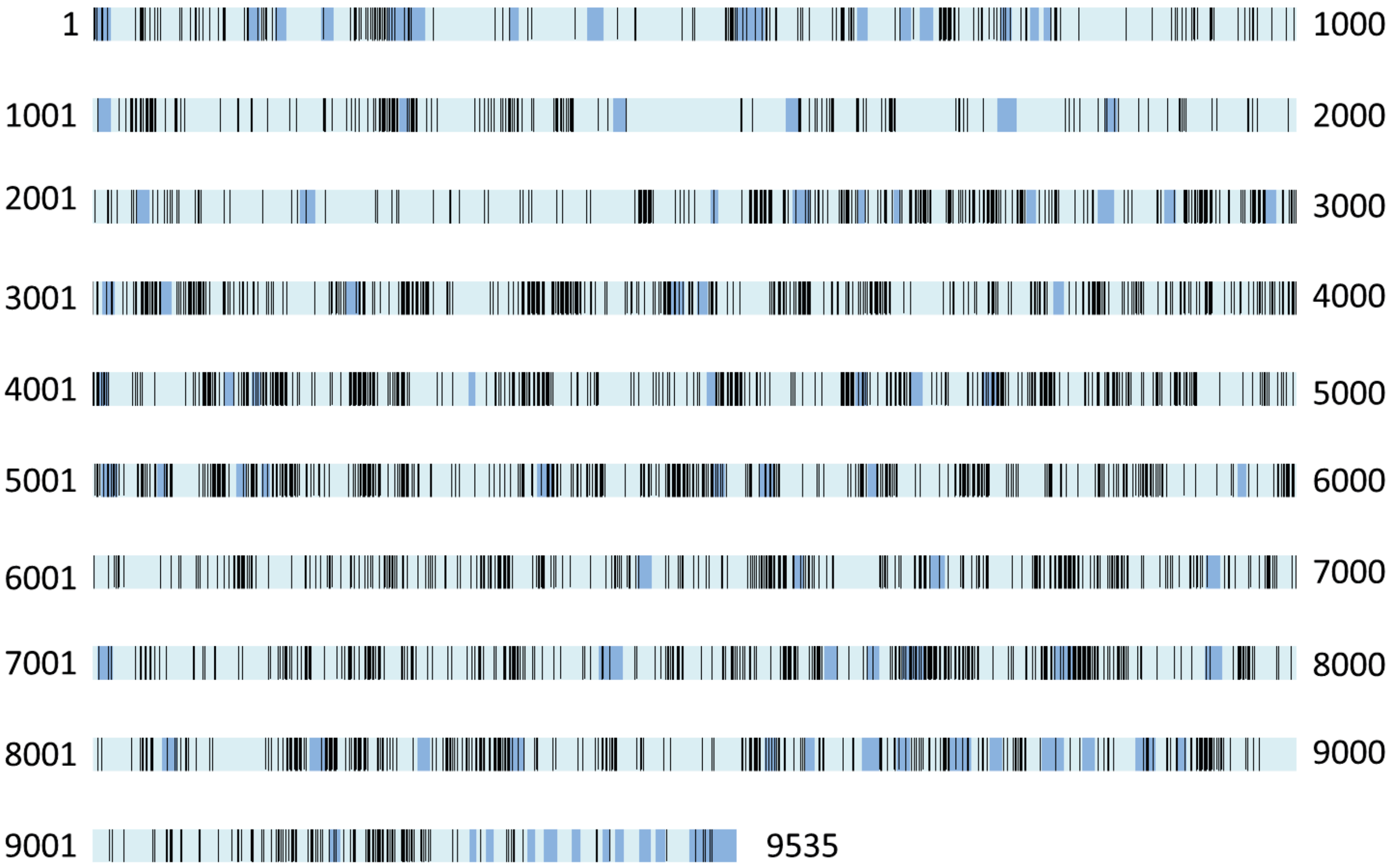


Figure 3.7 Cleavage sites identified in extracellular matrix-binding protein ebh (hypothetical protein SAOUHSC_01447).

This large protein is represented as 9 bars, each representing 1000 amino acids (except the ninth bar which ends at amino acid 9535). Each black vertical line represents a possible cleavage site determined by the presence of a semi-tryptic peptide, or neo-N-termini labelling. Darker blue regions represent predicted 90 putative HP-binding domains predicted as described in Section 3.2.9.

A number of ribosomal proteins were also found to bind HP with high affinity (Table 3.1), while migrating at a lower than predicted MW. 30S ribosomal protein S7 (predicted mass of 17.8 kDa) was found migrating at a lower MW (as far down as 1-10 kDa, slice 3 - see Figure B.1 in Appendix B) in the HP-binding elutions 1D-PAGE gels. Peptide matches from these low MW slices match to the majority of the protein, but do not include the first 40 amino acids (Figure 3.8). To determine if this was due to peptide detection bias, or fragmentation issues in the N-terminus, the peptide coverage for this protein was also checked within its predicted molecular range. As an example, in slice 5 (which has a MW range of 17-25 kDa) a peptide was identified that matched to amino acids 10-21 (within the previously undetected N-terminus of the protein) with this peptide being found in all three replicates. This indicates that the first 40 amino acids are not likely identified in the low MW slices as they are not present in the sample due to (pre-tryptic) enzymatic removal. These observations were supported from N-terminome experiments (data obtained by N. Strange, Table 3.2). These experiments identified a number of novel N-termini within this protein, including novel N-termini at amino acid 42. When 30S ribosomal protein S7 was identified below its predicted MW, the peptide coverage begins at amino acid 42. This same coverage was also found when surface proteins were biotinylated and run on a 2D-PAGE gel (pink bars in Figure 3.8, for gel image and spot location see Figure B.2 in Appendix B).

Table 3.1 30S and 50S ribosomal proteins found in the 1 M+ NaCl elution.

GI ID	Uniprot ID	Protein	MW (kDa)	Slices found in (Heparin 1D-SDS-PAGE)	Found below predicted MW	PSORTb	1 min shave	30 min shave	Biotin
88195529	Q2FXK6	30S ribosomal protein S4	22999	4, 5		Cytoplasmic	X		X
88196145	Q2FW23	30S ribosomal protein S5	17732	6		Cytoplasmic	X		X
88194147	Q2G113	30S ribosomal protein S6	11588	2, 7		Cytoplasmic	X	X	X
88194308	P48940	30S ribosomal protein S7 †	17783	3*, 4, 5, 6, 7	X	Cytoplasmic		X	X
88196129	Q2FW39	30S ribosomal protein S9 †	14821	1, 2, 3*, 4, 5, 6, 7	X	Cytoplasmic	X	X	X
88196137	Q2FW31	30S ribosomal protein S11	13873	2, 3, 4, 5, 6, 7		Cytoplasmic	X		X
88194307	P0A0H0	30S ribosomal protein S12	15277	5, 6, 7		Cytoplasmic	X		X
88196138	Q2FW30	30S ribosomal protein S13	13711	6, 7		Cytoplasmic	X		X
161353519	Q2FW19	30S ribosomal protein S14	7295	7		Cytoplasmic			X
88194983	Q2G2Q1	30S ribosomal protein S15	10602	7		Cytoplasmic			X
88194945	Q2FZ45	30S ribosomal protein S16	10229	7		Cytoplasmic			X
88196153	Q2FW15	30S ribosomal protein S17	10169	7		Cytoplasmic			X
88194149	Q2G111	30S ribosomal protein S18	9304	2, 3, 5, 6, 7		Cytoplasmic			X
88195395	Q2FXY6	30S ribosomal protein S20	9016	2, 3, 5, 7		Cytoplasmic	X		X
88195384	Q2FXZ7	30S ribosomal protein S21	6968	7		Cytoplasmic			X
88196159	P60430	50S ribosomal protein L2	30136	3*, 4, 5*	X	Cytoplasmic	X	X	X
88196162	Q2FW06	50S ribosomal protein L3	23703	4, 7*	X	Cytoplasmic	X		X
88196161	Q2FW07	50S ribosomal protein L4	22451	5		Unknown			X
88196147	Q2FW21	50S ribosomal protein L6	19774	5		Cytoplasmic	X	X	X
88196130	Q2FW38	50S ribosomal protein L13	16323	6		Unknown			X
88196143	P0A0F8	50S ribosomal protein L15	15587	5, 6		Unknown	X		X
88196155	Q2FW13	50S ribosomal protein L16	16232	5, 6		Cytoplasmic	X		X

88196135	Q2FW33	50S ribosomal protein L17	13739	1, 4, 5, 6		Cytoplasmic	X		X
88196146	Q2FW22	50S ribosomal protein L18	13089	2, 3, 5, 6, 7		Cytoplasmic			X
88194948	Q2FZ42	50S ribosomal protein L19	13354	6, 7		Cytoplasmic	X	X	X
88195485	Q2FXQ1	50S ribosomal protein L20	13678	2, 6, 7		Cytoplasmic			X
88195458	Q2FXS8	50S ribosomal protein L21	11326	1, 2, 3, 4, 5, 6, 7		Unknown	X		X
88196157	Q2FW11	50S ribosomal protein L22	12827	2, 3, 4, 5, 6, 7		Cytoplasmic	X	X	X
88196160	Q2FW08	50S ribosomal protein L23	10599	7		Cytoplasmic	X		X
88196151	Q2FW17	50S ribosomal protein L24	11529	4, 5, 6		Cytoplasmic			
88194261	Q2G0S0	50S ribosomal protein L25	23773	4, 7*	X	Cytoplasmic	X	X	X
88195456	Q2FXT0	50S ribosomal protein L27	10308	7		Cytoplasmic			X
88194930	Q2FZ60	50S ribosomal protein L28	6973	2, 3, 5, 6, 7		Cytoplasmic			X
88196154	Q2FW14	50S ribosomal protein L29	8085	2, 4, 5		Cytoplasmic	X		X
88195486	Q2FXQ0	50S ribosomal protein L35	7692	2, 3, 5, 6, 7		Cytoplasmic			X
88196139	Q2FW29	50S ribosomal protein L36	4302	3		Cytoplasmic			

S. aureus NCTC 8325 ribosomal proteins binding to HP at 1M+, showing which gel slices they were identified in (see Figure B.1 in Appendix B). An “X” in the 6th column denotes that this protein was migrating in the SDS-PAGE gel at a lower MW than predicted.

*Protein is migrating at a lower-than predicted MW in this slice.

† Proteins selected for further cleavage analysis.

For full table (including if the protein is known to bind nucleic acids) see Appendix B Table B1-3.

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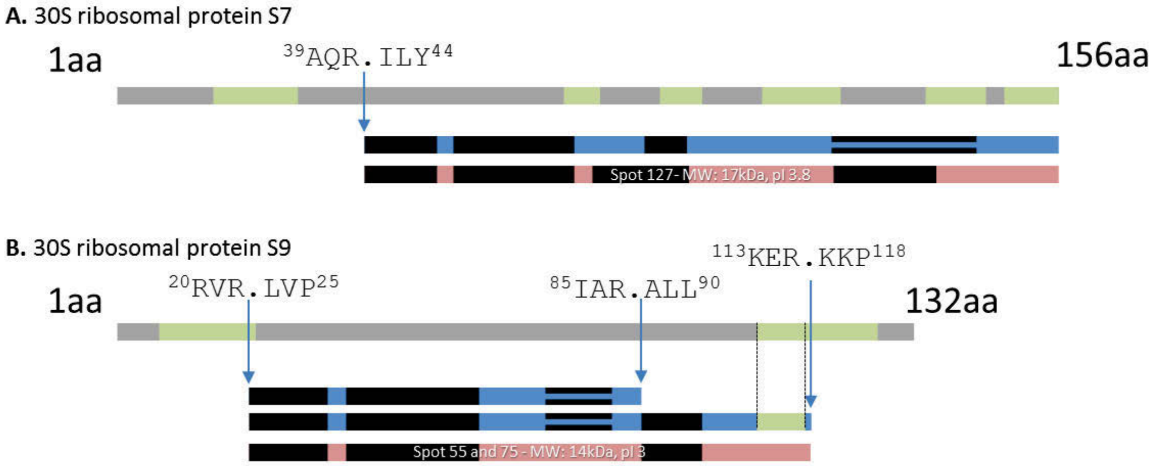

Figure 3.8 Cleavage maps of ribosomal proteins S7 and S9 which have fragments retained in the heparin column.

A. Cleavage map of 30S ribosomal protein S7, showing the full-length protein (top grey bar), the fragments found in the HP elution (1 M+ NaCl) and 2D-PAGE of surface biotinylated proteins. Predicted fragments based on peptide coverage and N-terminal analysis are shown by the blue and pink bars for HP-binding proteins and surface biotinylated proteins (gel image and spot location shown in Appendix B Figure B.2), respectively. Tryptic peptides identified are indicated by the black bars, double black bars indicate limited evidence for that peptide. Arrows indicate predicted cleavage sites within the protein based on the neo-N-termini analysis. Green bars in the full-length protein depict putative HP motifs identified (see Table 3.3). Within 30S ribosomal protein S7, both sets of peptides do not match to any of the first 40 amino acids of the protein. The N-terminal analysis identified a cleavage event, creating a neo-N-termini at amino acid 42, where these fragments are predicted to start. **B**. Cleavage map of 30S ribosomal protein S9, showing the two possible fragments found in the HP elution (1 M+ NaCl), one migrating below 10 kDa (23-87 aa) and another migrating around 10 kDa (23-115 aa - larger blue fragment). This larger fragment was also identified as a spot in a 2D-PAGE of surface biotinylated proteins (pink bar, for gel image and spot location see Appendix B Figure B.3). This larger fragment also retains one HP-binding motif (depicted as a green bar) from aa 107-114, see Table 3.3.

Table 3.2 N-termini identified that maps to cleavage products of 30S ribosomal protein S7 and 30S ribosomal protein S9 found during gel electrophoresis analysis.

Neo-N-termini Position	Dimethyl Labelled peptide sequence	Rep 1		Rep 2		Rep 3	
	30S ribosomal protein S7	**Score**	**E-value**	**Score**	**E-value**	**Score**	**E-value**
42	R. ILYSAFDLVEQR. S	104	5.20E^{-09}	90	1.30E^{-07}	92	7.30E^{-08}
		88	2.20E^{-07}	86	3.20E^{-07}	82	7.30E^{-07}
		100	1.30E^{-08}	90	1.20E^{-07}	67	2.40E^{-05}
				65	3.60E^{-05}	57	2.50E^{-04}
				85	4.00E^{-07}	66	3.00E^{-05}
				75	4.10E^{-06}	98	1.90E^{-08}
	30S ribosomal protein S9	**Score**	**E-value**	**Score**	**E-value**	**Score**	**E-value**
23	R. LVPGEGNITVNNR. D	85	4.1E^{-07}	77	2.4E^{-06}	85	3.3E^{-07}
		56	0.00029	74	4.3E^{-06}	66	2.5E^{-05}
		11	9.1			58	0.00019
		5	38			29	0.13
88	R. ALLEADPEYR. G	74	5.4E^{-06}	74	5.7E^{-06}	73	6.4E^{-06}
		55	0.00038	72	9.1E^{-06}	62	7.5E^{-05}
116	R. KKPGLKAAR. R	18	0.18	44	0.00031	21	0.054
		38	0.0014	34	0.0023		

This data was acquired by N. Strange according to [285], with data collated by the author. For a peptide to be considered, it needed to be identified in two or more replicates, with an E-value of less than 0.05 as assigned by Mascot (using MudPIT scoring).

Table 3.3 Putative heparin-binding motifs found in 30S ribosomal protein S7 and 30S ribosomal protein S9.

30S ribosomal protein S7	
aa range	Motif
	X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
17 - 26:	iHns..Klvt.Kl
20 - 30:	sKlvt.Klin.Ki
108 - 120:	aRlrgeKtmedRl
135 - 144:	vKk...RedthKm
148 - 156:	nKafa.Hy...Rw
	X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
75 - 80:	vKa.R..Rv
91 - 97:	vRpeR..Rt
108 - 115:	aRl.RgeKt
135 - 139:	vK..K..Re
	X-[HRK]-X-[HRK]-[HRK]-X
75 - 80:	vKaRRv
30S ribosomal protein S9	
	X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
8 - 16:	yRgtg.Rr...Kn
12 - 21:	gRr...KnsvaRv
14 - 23:	rKnsvaRv...Rl
107 - 118:	tRdprmKerk.Kp
110 - 122:	pRmkerKkpglKa
115 - 126:	rKkpglKaar.Rs
	X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
12 - 16:	gR..R..Kn
107 - 114:	tRdpRm.Ke
110 - 117:	pRm.KerKk
112 - 118:	mKerK..Kp
120 - 126:	lKaaR..Rs
	X-[HRK]-X-[HRK]-[HRK]-X
112 - 117:	mKeRKk

Sequences for both proteins were searched using ScanProsite [311] with the following motifs; the HP-binding consensus sequences [312] X-[HRK]-[HRK]-[HRK]-X-X-[HRK]-X and X-[HRK]-[HRK]-X-[HRK]-X, the heparan sulfate-binding motif [313] X-[HRK]-X-[HRK]-[HRK]-X, and motifs for clusters of basic residues X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X and X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X. A total of 10 putative HP-binding motifs were identified in 30S ribosomal protein S7, and 12 for 30S ribosomal protein S9. Not all motifs were represented in each protein, and some identified motifs had overlapping regions within the protein.

Another ribosomal protein that could be mapped with clear peptide coverage patterns was 30S Ribosomal protein S9 (14.8 kDa). This protein was found in all slices of the 1 M+ elution lane, a fragment of approximately 7 kDa was found migrating below 10 kDa (slice 3). There also appears to be a slightly larger fragment of around 10 kDa (slice 2) which includes peptides defining the C-terminal amino acids (Figure 3.8). This indicates that the HP-binding capacity depends on the central amino acids of this protein, as they are consistently identified in the 1 M+ elution. Further, this larger fragment ranging from amino acid 23-115 (Figure 3.8) was also identified in spots cut and digested from a 2D-PAGE gel of surface biotinylated proteins. Again, peptide coverage to the full length of the protein was identified in the expected MW range in slice 6 (15-17 kDa). N-terminome data (obtained by N. Strange) identified multiple neo-N-termini in 30S Ribosomal protein S9 (Table 3.2), with three of these sites mapping to peptide coverage shown in the lower MW fragments. For the two fragments described above, peptide coverage started at amino acid 23, which was also found to be a novel N-terminal site. The lack of C-terminal coverage could also be explained by a neo-N-terminal site at amino acid position 88 (in the smaller 7 kDa fragments), and another neo-N-terminal site at amino acid position 116 (in the larger 10 kDa fragment).

These two ribosomal proteins were searched for putative HP-binding motifs, resulting in the identification of 10 sequences in 30S ribosomal S7 and 12 sequences in 30S ribosomal protein S9 (Table 3.3). Some of these sequences overlapped in their amino acid coverage resulting in six distinct regions with putative HP-binding domains in 30S ribosomal S7 and two regions in 30S ribosomal protein S9 with putative HP-binding domains. The cleavage site mapped to 30S ribosomal S7 (^{39}AQR↓ILY^{44}) did not disrupt any of these motifs, and motifs were mapped to within the cleavage products identified in the HP elutions. On the other hand, the two HP-binding regions identified for 30S ribosomal protein S9 were disrupted by the two cleavage events identified, but there are some individual motifs (ranging from aa 107-114, see Figure 3.8 and Table 3.3) that would not be affected by these cleavage events. Interestingly, none of these motifs are included within the smaller cleavage fragment (aa 23-87). This indicates that these fragments may be binding to HP by a yet undetermined mechanism. Further studies are required to confirm these observations.

3.4 Discussion

With the importance of GAGs to infectious disease, it is vital to understand the interactions between bacteria and host GAGs. Although GAGs have been implied in *S. aureus* infection [80,91-93], as well as biofilm formation [87], at the start of this study, there had yet to be a global study in *S. aureus* to determine the repertoire of putative GAG-binding proteins it possesses. The data presented indicates that there are a large number of proteins in *S. aureus* that need to be further investigated as putative novel adhesins.

3.4.1 *S. aureus* retains high functional redundancy in adhesin proteins

These results indicate that *S. aureus* has 631 proteins that have the potential to bind HP and, by inference, other highly sulphated glycosaminoglycans during host colonization and invasion. This high number indicates functional redundancy within the *S. aureus* proteome, and may explain the success of *S. aureus* as a colonising pathogen. This functional redundancy has already been shown in the adhesive ability of *S. aureus* [58,64,315-317]. This is also supported by recent research identifying over 100 HP-binding proteins in the *S. aureus* cell wall and supernatant fraction [89]. Of these identified proteins by Mishra et al. [89], 75 % were also identified in Section 3.3.1 with discrepancies being most likely due to difference in cell fractions tested and in strains (see Appendix B Table B.5). These data support previous suggestions [42,202,216-218,318-321] that therapeutic strategies against *S. aureus* should be multi-faceted, as another protein may be able to rescue or replace the function of the single, targeted protein. While these proteins identified may bind various GAGs, it is also possible that these proteins bind DNA as HP columns have been shown to identify DNA-binding proteins [309], and indeed many predicted DNA-binding proteins were identified in the analysis of HP-binding proteins described here (Table B.1-3 in Appendix B). This supports the previous findings from Mishra et al. showing a distinct overlap between DNA-binding and HP-binding proteins in *S. aureus* [89]. It is also important to note that some proteins and cleavage fragments may be retained on the column as part of a complex, i.e. not directly binding to HP. As this experiment harvested proteins under native conditions, these native protein complexes may have been present. This non-specific binding could account for the high number of identification made in this study. Further analysis is needed to confirm which proteins bind directly to HP and those that form a complex where only one or a few proteins interact directly with HP.

3.4.2 Proteins from key metabolic pathways have moonlighting capabilities as potential adhesins

Proteins that form part of two major biochemical pathways; the glycolytic pathway and the translational pathway were heavily represented in our putative HP-binding datasets. Bacterial proteins belonging to the glycolytic pathway are known to display moonlighting functions and several recent reviews have focussed on this [44,112,113]. Ribosomal proteins also feature prominently in studies of bacterial moonlighting proteins [270], and in eukaryotes the glycolytic pathway often contains moonlighting proteins [121]. The multifunctionality of glycolytic proteins in *S. aureus* has been reported; a secondary function has already been assigned to GAPDH [118], triosephosphate isomerase (TPI) [120,322,323], and enolase [117,324] indicating moonlighting is likely widespread amongst the glycolytic pathway proteins in *S. aureus*. Enolase and GAPDH have already been implicated in *S. aureus* biofilm development [239,240] and HP-binding [89]. There is yet no specific evidence for moonlighting roles for ribosomal proteins in *S. aureus*, although proteins within the translational pathway, such as Ef-Tu are well described multifunctional proteins (see Chapter 4).

3.4.3 Cleaved protein products of *S. aureus* were retained by heparin affinity chromatography

In this analysis 186 proteins (29 %) were identified at a lower MW than their predicted MW. This could indicate database issues (protein prediction based on genomic data alone), gel migration variabilities, protein modification, and specifically, the cleavage of proteins in *S. aureus*. A number of proteins migrating below their predicted MW were investigated and it was apparent, in most cases, that peptide coverage only mapped to a portion of the protein. This portion of the protein had a predicted MW closer to where the protein was found in the gel than the predicted MW of the full-length protein. There were some instances where there was peptide coverage throughout the protein, but the protein was migrating at a dramatically lower MW. This includes extracellular matrix-binding protein ebh, which had peptide matches throughout the length of the protein, indicating that the entire protein, or the majority of it, was present in that particular gel slice. As the protein was migrating at a 100 fold lower MW, it is unlikely that the intact protein was present (it was never identified migrating >100 kDa in any proteomic analysis described). N-terminal analysis (J. Steele and N. Strange, unpublished data) found multiple neo-N-termini in this protein, but given its large length, there was not enough evidence to deduce the start and end of the (at least) 100 novel fragments that would collectively migrate at ~10 kDa. In *S. aureus,* this protein binds fibronectin [318] and its homologue in the closely related *S. epidermidis* is essential for biofilm formation [325]. Evidence for the cleavage of this protein was found in the exoproteome of two *S. aureus* isolates, but it appears to be different fragments to the ones observed in the 1 M+ elution as they are migrating at approximately 42 kDa [151]. Notably this protein was found in the other elution lanes (0-1 M NaCl) at a variety of MWs (1-100 kDa). It is possible that this protein is differentially processed and exported, with the smaller fragments (10 kDa) having an especially high affinity for HP-binding (>1 M NaCl). This extreme example of protein processing highlights the potential that proteins may be used as decoys upon invasion (eg. adsorbing host antibodies) and that proteins may be cleaved to increase the function(s) of a single ORF (different fragments can localise to different areas, and may be individually functional). This particular finding warrants further investigation into the cleavage mechanisms and biological potential of this protein and its fragments.

3.4.4 Novel cleavage sites in ribosomal proteins identified

Many ribosomal proteins (Table 3.1) were found to bind HP with high affinity (>1 M NaCl), with some of these proteins also being present at a lower molecular weight than their predicted MW. 30S Ribosomal protein S7 (17.8 kDa) was identified in slices 3-7 which covers a range from 1-37 kDa. At lower MW slices, this protein was found to be missing its N-terminal portion. This lack of N-terminal amino acids could be explained by the neo-N-termini at amino acid 42, giving the new fragment a length of 115 aa (from aa 42 to aa 156) (Figure 3.8). A similar cleaving of the N-terminal aa was found in 30S Ribosomal protein S9, with fragments missing the first 22 aa. The cleavage event within the N-terminal portion of ribosomal proteins in *S. aureus* has been identified once before in 50S ribosomal protein L27 [152]. The N-terminal extension, which is not present in Gram-negative bacteria, was found to be cleaved by a novel cysteine protease in *S. aureus*, with this cleavage event also found in other firmicutes [152]. Within the HP and N-terminal analysis, evidence for this cleavage event was observed, but is not strong enough to definitively prove the event. As this data only recently identified ribosomal cleavage and a novel protease in *S. aureus* [152], and with the data presented in this chapter showing more evidence of ribosomal cleavage, it is likely there is still more to be discovered in regards to ribosomal biology in Staphylococci. It also highlights that there is much to learn in regards to Staphylococcal proteases. No common motifs or responsible protease was identified with this data. Others have reported the possibility of unknown proteases in *S. aureus* [143].

Our data suggests that N- and C-terminal extensions of ribosomal proteins may have a unique biological function, but further studies are needed to determine this. Cytosolic peptide excretion is a known phenomenon that is potentially retained across Firmicutes [326]. The ability to cleave proteins and release short N- and C-terminal peptides into the surrounding environment may hold many implications for bacterial pathogenesis. Indeed, many ribosomal proteins were identified by the cell surface analysis (Table 3.1), in some instances as a truncated protein (Figure 3.8). As these proteins are surface exposed, it is possible that the cleavage of their N-or-C-terminal region results in the release of this short peptide into the surrounding environment, as already described in *Lactococcus lactis* [326]. Ribosomal proteins have been shown to be cell wall associated in bacteria, despite lacking a signal peptide, hence they have been seen by some as novel anchorless surface proteins [130]. In *S. aureus* they have also been identified in MVs [258,267], one mechanism by which they may reach the extracellular space. As non-classical protein secretion has been linked to virulence in other staphylococci species [130], it is important to further study these ribosomal proteins that are both presented on the surface of *S. aureus*, and that may bind host GAGs.

3.4.5 Implications of results on biofilm formation

Biofilm formation in *S. aureus* has been shown to develop in a protein-dependant manner [327-331], with proteases [328,332] and DNases [333-336] inhibiting biofilm formation and aiding in biofilm eradication. Similarly, the adhesion of *S. aureus* to the glycosaminoglycan, heparan sulfate has also been shown to be proteinaceous [90]. Two molecules that have been implicated in Staphylococcal biofilm formation are HP and eDNA. HP increases biofilm formation in a protein synthesis-dependant manner, where the addition of protein synthesis inhibitors also inhibited the biofilm stimulation seen from the added HP [87]. Further, proteins on the surface of *S. aureus* have been shown to bind HP, incorporating it into their biofilm structure [89]. This study also implied that HP can even be used as a substitute for eDNA by *S. aureus* cells [89]. As suggested in the data in this chapter, it appears that *S. aureus* takes advantage of already evolved DNA-binding proteins to enable binding to HP and eDNA to enhance biofilm formation, a hypothesis that is consistent with the work of other researchers [89].

eDNA has been reported extensively in *S. aureus* biofilms [239,333,335-339] (Figure 3.9). HP columns can be used to identify DNA-binding proteins due to the characteristic similarities (including a negative charge) between HP and DNA [309]. For this reason, proteins that bind HP columns, especially with high affinity, above physiological conditions (high salt) may have a role in biofilm formation in *S. aureus*. Further to implication in host colonization and infection, the identified proteins may bind host GAGs, HS on implants, or native eDNA leading to an increase in *S. aureus* biofilm formation, host colonisation, and antibiotic resistance. The extracellular matrix of *S. aureus* biofilms is derived from a mixture of eDNA and cytoplasmic proteins [239,240,293,337-340] and electrostatic interactions between cytoplasmic proteins and eDNA is thought to tether cells together in *S. aureus* and mixed-species biofilms [239]. These electrostatic interactions have also been observed for *S. aureus* and glycosaminoglycan interactions [90], further giving weight to the hypothesis that certain glycosaminoglycans may substitute for eDNA in biofilms [89].

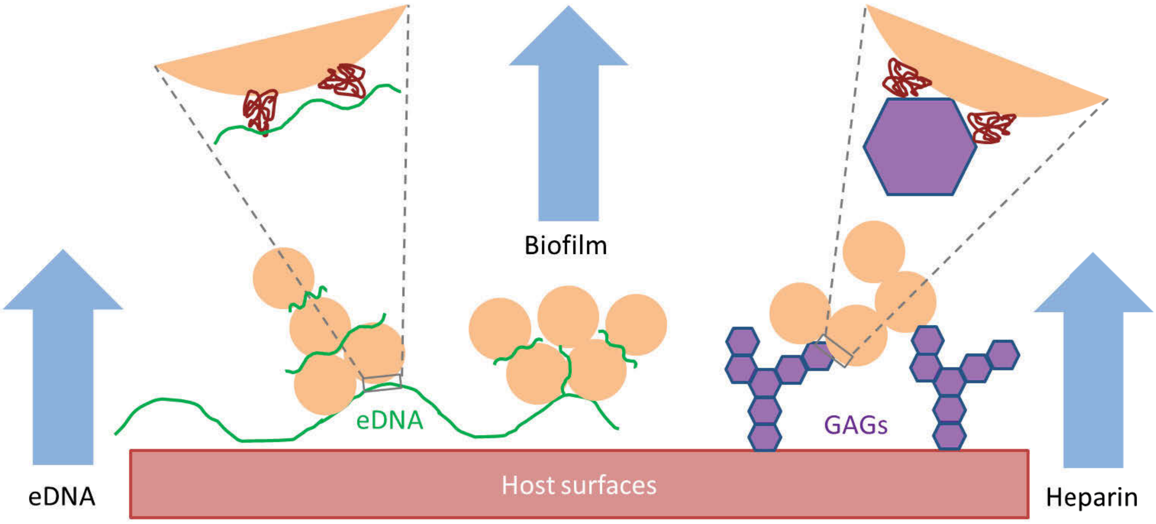

Figure 3.9 Diagram showing the ability of eDNA and GAGs (such as HP) aiding in the attachment of bacteria to host surfaces.

Both these elements have been shown to have a positive impact on *S. aureus* biofilm development and expansion. The ability for surface proteins (shown in red) to bind these two elements allows for bacterial attachment and biofilm development. Both eDNA and HP carry a strong negative charge, with many proteins exploiting electrostatic interactions allowing them to bind. Figure not to scale.

In order to bind to HP (or eDNA) many of the identified proteins contain HP motifs, clusters of basic residues, or are known DNA-binding proteins. Electrostatic interactions with negatively charged eDNA and HP, require a net positive charge from the interacting protein. As an example, this was shown in Table 3.3 which lists the HP motifs and clusters of basic residues identified within two of the ribosomal proteins which were found to bind HP (for full analysis of all proteins found in the 1 M+ elution see Appendix Item B.1). This accumulation of positive residues could be selected for by the identified cleavage events (negatively charged regions removed) or conversely, smaller positive regions may be cleaved to increase the functional binding capacity (based on electrostatic interactions) of that one protein. Given the extensive cleaving of the ebh protein shown in Figure 3.7, it is hypothesised that this protein may be recycled for its binding capabilities. Such events may release a number of smaller, “sticky” peptides the bacterium may use to bind HP or eDNA and establish biofilms. Further, the accumulation of positive residues in classically cytosolic proteins is an evolutionary trait [111] seen in other organism and may be selected for in *S. aureus* to establish infections while exploiting is relatively small genome (recycling classically cytosolic proteins as adhesins). This accumulation of positive residues may occur in discrete locations within the protein, allowing for a specific span of aas to have a positive charge. This section of aas may be isolated and utilised by the pathogen by cleaving off the surrounding peptides. This accumulation of residues may result in a positive bias in only a portion of the protein, without enormously affecting the overall charge of the protein.

Many proteins identified to interact with HP at a high affinity, are already known to interact with DNA in the cytosol, for example, DNA binding protein HU. The role of DNA, specifically extracellular DNA has been investigated in biofilm formation [333,338,341-349]. The ability for proteins on the surface of bacteria to bind eDNA and form a matrix for biofilm formation may be another function of these identified proteins and, again, the reason why so many proteins have maintained their evolved DNA-binding motifs. Indeed, DNA binding protein HU is an important protein for biofilm formation in *S. aureus*, with antibodies against this protein eradicating already establish biofilms [350]. This protein was also identified in the cell wall fraction with the ability to bind HP in *S. aureus* [89]. In the closely related *Streptococcus intermedius*, it plays a role in biofilm formation where it is suggested to bind eDNA in biofilms [341].

Interestingly, we identified a large number of ribosomal proteins in this dataset, and this may also be due to their ability to bind DNA, a finding that is supported by Mishra et al. [89]. This binding capacity is likely due to the DNA-binding motifs within ribosomal proteins that were discovered decades ago [351]. It is believed this is a possible side-effect of the ribosomal unit evolution, that ribosomal proteins may have evolved from other (DNA-binding) proteins [351]. This interaction is best described for 30S ribosomal protein S16 in *E. coli* which is able to bind and cleave DNA [352]. Perhaps ribosomal proteins have maintained their DNA-binding capabilities due to evolutionary pressures to be exploited by *S. aureus* during biofilm formation. The identification of such DNA-binding proteins indicates that this protocol may identify DNA-binding proteins that are important to biofilm formation in *S. aureus* that have previously not yet been identified.

Many proteins identified in this HP-binding dataset have been shown to be upregulated in the extracellular space during biofilm formation including ribosomal proteins, Glyceraldehyde-3-phosphate dehydrogenase, FtsZ, Elongation factor Tu, and Pyruvate kinase [240]. These proteins are classically cytosolic, but there are many ways in which they may get to the surface of the bacteria, including, re-association [353] sometimes in a pH-dependant manner [117,240], explosive cell lysis [179] or excretion via an unknown mechanism. The phenomena of the excretion of cytoplasmic proteins in *S. aureus* has been investigated [129], where cytosolic protein association with the cell septa was shown, yet there still appears to be an unknown mechanism/s involved. The issue remains, that for these proteins to be useful in biofilm formation they need to be surface accessible. Previous studies have found numerous classically cytosolic proteins on the surface of *S. aureus*, including 30S Ribosomal protein S7 [124,126] and 30S Ribosomal protein S9 [124-126,173]. This was supported by our surfaceome data (Chapter 2) showing these two proteins present on the surface of *S. aureus* SH1000. The ability to present these proteins on the surface may be an energy efficient way of exploiting their multi-functionality.

3.5 Conclusion

S. aureus causes a range of diseases in the human host which results in a large economic burden throughout the world [198]. This bacterium rapidly acquires resistance to antibiotics, with MRSA deemed a serious threat by the CDC in 2013 [1]. The ability of this bacterium to colonise and invade a range of host tissues, and form biofilms makes it a successful pathogen. Many adhesins have been identified on the surface of *S. aureus*, but targeting single adhesins has yet to lead to a successful vaccine (or therapeutics to block host colonisation) [42,216-218]. One sub-population of host molecules that bacteria exploit for adhesion upon infection are the GAGs. GAGs have been shown to play a specific role in *S. aureus* infection for a range of host cells [80]. Unfortunately, the binding of *S. aureus* to GAGs is one area that is relatively poorly understood. Hence, this chapter aimed to identify putative GAG-binding proteins in *S. aureus* by using an affinity enrichment protocol coupled with SDS-PAGE and mass spectrometry.

This data indicates, for the first time, the potential repertoire of *S. aureus* GAG-binding proteins. This extensive list of proteins may be important in PG and eDNA binding within the host. Some of the proteins identified were also found in our surface proteome analysis showing that they are accessible to the host. A number of proteins were also found to bind the archetypal GAG, HP, as cleaved products, with some cleaved proteins having a higher affinity for HP than their parent protein. This adds to our knowledge of *S. aureus* colonisation and invasion of the host. These proteins now present a new list of candidate proteins to further study for their potential therapeutic capabilities.

Chapter 4.Elongation factor Tu is highly processed and surface exposed

Chapter Declaration

This chapter consists of two manuscripts, one draft manuscript and one published manuscript. One manuscript is a review on the roles of Ef-Tu and another data paper on the role of Ef-Tu as a moonlighting protein on the surface of three pathogenic bacteria. The relevant sections from the manuscripts have been amalgamated as Chapter 4 with some sections submitted verbatim, as they have been thoroughly reviewed and one has been accepted for publication (see below). Extra detail and data has been added, where relevant. All data shown in this chapter was obtained and analysed by the author unless specified.

First paper details:

Title: "Elongation factor Tu is a multifunctional and processed moonlighting protein."

Authors: Michael Widjaja†, Kate Louise Harvey†, Lisa Hagemann†, Iain James Berry, Veronica Maria Jarocki, Benjamin Bernard Armando Raymond, Jessica Leigh Tacchi, Anna Gründel, Joel Ricky Steele, Matthew Paul Padula, Ian George Charles, Roger Dumke, Steven Philip Djordjevic

† These authors contributed equally to this work

Author contributions: M.W. acquired data and analysed it for M. pneumoniae except those listed for I.J.B. and L.H. K.L.H. acquired data and analysed it for S. aureus except data for the N-terminome that was acquired by J.R.S., M.W. and K.H. prepared all figures and tables except those listed for L.H. and A.G. M.W., K.L.H., R.D. and I.G.C. assisted with drafting the manuscript. A.G. produced the recombinant Ef-Tu of M. pneumoniae and the guinea pig antiserum. L.H. acquired binding data for A549 cells and most host proteins, performed plasminogen binding and activation studies, conducted experiments with recombinant antisera, and prepared figures with A.G. I.J.B. acquired N-terminome data for M. pneumoniae and M. hyopneumoniae, and I.J.B. and M.W. analysed it. I.J.B. assisted with the preparation of cleavage maps. VMJ performed the SLiM analysis and prepared figures. B.B.A.R. and J.L.T. acquired and analysed surfaceome data for M. hyopneumoniae. M.P.P. oversaw the acquisition mass spectrometry data and assisted with data interpretation. S.P.D. initiated this study, assisted in writing the manuscript, and secured funding. R.D. supervised the binding studies performed by L.H. and A.G. and secured funding. I.G.C. provided intellectual input and reviewed drafts of the manuscript. All authors reviewed and approved the manuscript.

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Draft paper details:

"Elongation factor thermo unstable (Ef-Tu) and its role in microbial pathogenesis"

Authors: Kate Louise Harvey, and Steven Philip Djordjevic.

Author contributions: K.L.H wrote the manuscript and S.P.D. edited the manuscript

This paper is in its final draft stage, pending further revision for submission.

4.1 Introduction

Elongation factor Thermo unstable (Ef-Tu) is one the most abundant proteins in bacteria [354,355], comprising up to 6 % of the total protein expressed in *E. coli* [354] and as high as 10 % of the total protein expressed in *Mycoplasma pneumoniae* [355]. It functions as an essential and universally conserved GTPase that ensures translational accuracy by catalysing the reaction that adds the correct amino acid to a growing nascent polypeptide chain [356]. After the incoming aminoacyl-tRNA docks with the mRNA, GTPase activity induces a conformational change releasing Ef-Tu from the ribosome [356-358]. Ef-Tu is considered to be an ancient molecule that is comprised of domains that are highly conserved in phylogenetically diverse prokaryotes [359]. In *E. coli*, Ef-Tu is comprised of three functional domains known as domain I (amino acids 1 - 200), domain II (amino acids 209 - 299) and domain III (amino acids 301 - 393) [360]. Domain I forms a helix structure with Rossmann fold topology, a structural motif found in proteins that bind nucleotides, while domains II and III largely comprise of beta sheets [356,361]. The GTP/GDP binding domains are housed in domain I, while domains I and II are needed for nucleotide exchange. Domains II and III physically adjust to form an amino acid tRNA binding site [356,358]. Ef-Tu sequences derived from phylogenetically diverse species share considerable sequence identity and have been used to generate phylogenetic descriptions of the tree of life [362]. Amongst different bacterial species the Ef-Tu sequences have less than 30 % sequence divergence [363]. Low G + C Gram positive bacteria carry only a single copy of the *tuf* gene encoding for Ef-Tu [364]. In contrast, many enteric bacteria have two copies (*tufA* and *tufB*) while three tuf-like genes have been identified in *Streptomyces ramocissimus* [365,366].

Despite its highly conserved function in protein synthesis, non-canonical (moonlighting) functions have been described for Ef-Tu in all kingdoms of life. Ef-Tu lacks a signal secretion motif yet the ability to execute moonlighting functions often requires the molecule to traffic to different cellular sites, across organelle membranes and also onto the extracellular surface of the host cell. Ef-Tu is a multifunctional protein in higher order eukaryotes [367-372], parasites [373-376], fungi [377] and it is has been identified on the surface of a wide range of Gram positive and Gram negative pathogenic and commensal bacteria that associate with metazoan species [52,183,279,355,378-382]. Bacterial Ef-Tu interacts with nucleolin [383,384], fibrinogen and factor H [379,380], plasminogen and several complement factors [275,380,381], laminin [385], CD21 [386], fibronectin [355,385,387,388], is immunogenic [389] and adheres to the surface of Hep-2 cells [385] underscoring the multifunctional adhesive characteristics that have been assigned to this molecule (Table 4.1). Ef-Tu binds sulfated carbohydrate moieties found on glycolipids and sulfomucin and promotes the binding of *Lactobacillus reuteri* to mucosal surfaces indicating that Ef-Tu can interact with carbohydrates [390]. Notably, antibodies against Ef-Tu are induced during infections caused by a range of pathogens including *S. aureus* [174,391], *Mycoplasma capricolum* [392], *Mycoplasma ovipneumoniae* [389], *Chlamydia trachomatis* [393], *Burkholderia pseudomallei* [394] and *M. hyopneumoniae* [395]. Ef-Tu has been identified in six of the major surface proteome studies (excludes cell membrane and envelope isolations) [124-127,173,177] performed on *S. aureus* and Ef-Tu is one of twelve proteins consistently identified in the exoproteome of *S. aureus* isolates from patients with bacteraemia [396]. The major staphylococcal autolysin *Alt* is implicated in playing a role in secreting cytosolic proteins including Ef-Tu into the extracellular milieu [183]. Moonlighting proteins, including Ef-Tu, are likely to be exported via several mechanisms, including within secreted extracellular vesicles [397], during cell lysis [179] and via association with proteins that are secreted by the Sec machinery [129].

Table 4.1 List of moonlighting functions published for Ef-Tu in prokaryotes.

Species	Moonlighting function	Year	References
M. pneumoniae	Binds fibronectin	2002	[355,398]
Mycobacterium avium subsp. paratuberculosis	Binds fibronectin	2014	[387]
A. baumannii	Binds fibronectin	2012	[397]
M. hyopneumoniae	Fragments bind HP and fibronectin	2016	[86]
A. baumannii	Binds plasminogen	2015	[399]
P. aeruginosa	Binds Factor H and plasminogen	2007	[379]
Leptospira spp.	Binds Factor H and plasminogen (and other ECM)	2013	[381]
S. pneumoniae	Binds Factor H, FHL-1, CFHR1 and plasminogen	2014	[380]
Helicobacter pylori	Adheres to THP-1 cells, novel potential adhesion factor	2016	[400]
Lactobacillus johnsonii	Attachment to human intestinal cells and mucins, and participates in host immunomodulation (IL-8 production)	2004	[378]
Streptococcus gordonii	Binds saliva mucin MUC7	2009	[401]
B. subtilis	Role in cell shape maintenance, colocalises and modulates MreB filament formation	2010	[402,403]
E. coli	Interacts and modulates MreB filament formation	2005	[403,404]
K. pneumonia	Virulence factor for Leukopenia caused by *K. pneumonia*	2014	[405]
Francisella tularensis	Interacts with THP-1 nucleolin	2008	[383]

Psudomonas spp.	Part of the TVISS	2015	[406]
Listeria monocytogenes	Induces dendritic cell maturation	2016	[407]
Bacillus cereus	Target for Substance P (SP)	2013	[408]
S. aureus	Target for Substance P (SP)	2015	[409]
S. epidermidis	Target for Substance P (SP)	2015	[409]
A. baumannii	Interacts with DsbA	2014	[410]
B. subtilis	Binds calcium ions	2009	[411]
P. aeruginosa	Trimethylation of the lysine^{5} allowing binding to platelet-activating receptor	2013	[412]
Mycoplasma fermentans	Interacts with the intracytoplasmic domain of CD21 (EBV/C3d receptor)	2005	[386]
E. coli	Cleaved in response to phage infection inducing phage exclusion induction	1994	[413-415]
Acidovorax avenae	Rice plants recognise the central amino acids (175-225aa) of Ef-Tu as a PAMP	2014	[416]
E. coli	*Arabidopsis thaliana* recognises the first 18 aa of Ef-Tu as a PAMP	2004	[3,417]

Table is arranged based on function, showing the different species that have evolved the same Ef-Tu moonlighting functions. The majority of these moonlighting functions have only been described in the last decade.

The ability of Ef-Tu to be secreted onto the cell surface occurred early in the evolutionary interplay between plant pathogenic bacteria and their eukaryote hosts. Plants have evolved pattern-recognition receptors (PRR) in their cell membranes that are designed specifically to recognise pathogen-associated molecular pattern (PAMP) molecules released by bacterial and fungal pathogens [418-424]. Ef-Tu is a well described PAMP [419,425]. An Ef-Tu receptor (EFR) found within Brassica lineages [3,426] recognises the highly conserved N-terminal 18 amino acids (elf18) in the native Ef-Tu molecule [3,419,426]. Binding triggers signal transduction events in plant roots that ensure that pathogenic bacteria are either contained within callose deposits, destroyed by cellular apoptosis, or succumb to an oxidative burst elicited by the production of hydrogen peroxide [426]. A region spanning surface exposed amino acids 176 - 225 in Ef-Tu from the Gram-negative bacterial pathogen *A. avenae* interacts with a different PRR in monocotyledonous plants [416]. EFR has been transferred from the Brassica species *A. thaliana* into the monocot species, rice and transgenic rice plants display enhanced innate immune responses when exposed to elf18 from *Xanthomonas oryza*, a major rice pathogen [427]. These studies show that plants have evolved sophisticated molecular machinery to identify Ef-Tu that is released onto the cell surface by diverse plant pathogenic bacteria.

Protein cleavage is emerging as an important post-translational modification that can expand protein function [86,259,428,429]. This is evident in the genome-reduced Mollicutes where species-specific Mycoplasmal adhesins and lipoproteins are targets of complex processing events [79,86,145,259,306,314,430-440]. Cleavage fragments are retained on the bacterial cell surface and function as adhesins that bind HP-like glycosaminoglycans [259,306,314,432,433,435,437], fibronectin [259,434,436,439] and circulatory molecules such as plasmin(ogen) that regulate the fibrinolytic system [259,434,436-438]. Cleavage motifs have been chemically defined in *M. hyopneumoniae* using mass spectrometry and occur at phenylalanine residues in the motif S/T-X-F↓-X-D/E, within stretches of hydrophobic amino acids and at trypsin-like sites in diverse molecules including adhesins, lipoproteins and in metabolic enzymes that traffic to the cell surface [79,86,145,435,437]. Cleavage fragments are known to be further processed by aminopeptidases [86,145] that also localise on the cell surface despite lacking signal sequences [441,442].

This chapter describes potential novel moonlighting functions for Ef-Tu, with a focus on the types of cleavage fragments that are produced and what their putative function may be. As this protein was identified on the surface of *S. aureus* (Chapter 2) it became a protein of particular interest due to its classically cytosolic location (Ef-Tu is bioinformatically [180] predicted to reside within the cytosol of *S. aureus*, with no predicted transmembrane domains [257]). It was also identified as a HP-binding protein (Chapter 3) suggesting a possible role for its surface localization. Here Ef-Tu is described to be the target of multiple processing events on the cell surface that generate a complex pattern of cleavage fragments, many of which may retain putative binding functions. Cleavage sites were mapped by characterising neo-N-terminal peptides using a systems-wide, N-terminomics pipeline (Joel Steele, unpublished data) coupled with other proteomic approaches. Bioinformatics and structural modelling studies indicate that accumulation of positively charged amino acids in short linear motifs (SLiMs) increases the number of binding sites of the molecule (analysis undertaken by V. Jarocki) without unduly influencing structural constraints needed to execute the canonical function in the cytosol. The accumulation of positively charged residues in SLiMs may be a by-product of codon bias engendered by an A + T genome. This chapter collates data on Ef-Tu from a number of global proteomic studies in *S. aureus* in order to better understand the functions and presentation of Ef-Tu in *S. aureus* ($\mathrm{Sa}_{\text{Ef-Tu}}$).

4.2 Methods

4.2.1 Bacterial growth

S. aureus (SH1000 strain) was cultured in TSB (Oxoid) at 37°C with shaking and harvested during early stationary phase. Protease inhibitors (Roche Diagnostics) solubilized in PBS were added to wash the cells during the harvesting protocol. For *S. aureus* lysis, cell pellets were freeze-dried overnight and added to pre-cooled metal milling canisters with 12 small metal beads. Each canister was cooled in liquid nitrogen and milled at a maximum frequency of 30 Hz for 1 min, 15 times. Liquid nitrogen was used to cool the canister between each mill. Proteins were than solubilised in 7 M urea, 2 M thiourea, 50 mM LiCl, 50 mM Tris-HCl (pH 8.8), 1 % (w/v) C7bZ0 with protease inhibitors followed by sonication at maximum intensity for 30 s for 20 rounds resting on ice in between.

4.2.2 Enrichment of *S. aureus* surface proteins

For full details of surface proteome experiments, see Chapter 2. A brief description of the methods are as follows:

4.2.2.1. Biotinylation

S. aureus cells were washed with PBS after centrifugation before the resuspending in EZ-link sulfo-NHS-biotin (Thermo Fisher Scientific) for 1 min on ice to minimise cell lysis. The reaction was quenched with a final concentration of 50 mM Tris-HCl and cells were lysed with 7 M urea, 2 M thiourea, 40 mM Tris-HCl (pH 8.8), 1 % (w/v) C7bZ0. Biotinylated surface proteins were purified by avidin column chromatography and confirmed to be biotinylated by western blotting using Extravidin- HRP (Sigma).

4.2.2.2. Trypsin shaving

S. aureus cells were washed in cold PBS and protease inhibitors, followed by washing with cold PBS to remove excess protease inhibitors. Cell pellet was resuspended in warm PBS and then trypsin was added. Cells were incubated for 1 min to minimise cell lysis. The reaction was stopped by placing the reaction vessel in an ice bath prior to centrifugation using a pre-cooled centrifuge.

4.2.3 Preparation and separation of whole cell lysates for one- and two-dimensional gel electrophoresis

4.2.3.1. Whole cell lysis preparation

Lysis for *S. aureus* cells is described above in Section 2.2.7. Proteins were reduced and alkylated with 5 mM tributylphosphine and 20 mM acrylamide monomers for 90 min at room temperature. Insoluble material was removed by centrifugation and five volumes of acetone added to precipitate protein. After centrifugation, the protein pellet was solubilized in 7 M urea, 2 M thiourea, 1 % (w/v) C7BzO for one- and two-dimensional gel electrophoresis.

4.2.3.2. 1D -SDS-PAGE protein separation

Protein separation was performed as described in [79,437]. Approximately 100 µg of protein was separated on 4-20 % Criterion™ TGX™ Gels (Bio-Rad) in Tris-Glycine-SDS buffer (Bio-Rad), fixed and visualized by staining with either Flamingo fluorescent gel stain (Bio-Rad) or Coomassie Blue G-250 (Sigma).

4.2.3.3. 2D-PAGE protein separation

Approximately 300 µg of protein was cup-loaded onto 11 cm pH 4-7 IPG strips (BioRad) or 6-11 Immobiline drystrips (GE Healthcare) rehydrated with 7 M urea, 2 M thiourea, 1 % (w/v) C7BzO. Focusing was performed in a Bio-Rad Protean IEF cell unit. Following IEF, the strips were equilibrated for 20 min with equilibration (2 % SDS, 6 M urea, 250 mM Tris-HCl pH 8.5, 0.0025 % (w/v) bromophenol blue) solution before running in the second-dimension SDS-PAGE. Second-dimension SDS-PAGE was run as described for 1D SDS-PAGE (Section 4.2.3.2).

4.2.4 Heparin affinity chromatography

Affinity purification of HP-binding proteins for *S. aureus* was performed as described in Section 3.2.3. Briefly, *S. aureus* cells were and lysed in 10 mM sodium phosphate, pH 7 and protease inhibitors After centrifugation of cell debris and insoluble material, ~300 µg of soluble protein was loaded onto the Waters 2690 Alliance LC separations module attached to a 1 mL HiTrap Heparin HP column (GE healthcare). Proteins were washed and then eluted off the column with an increasing gradient of NaCl.

4.2.5 Liquid chromatography tandem mass spectrometry (LC-MS/MS) and MS/MS data analysis

LC-MS/MS was performed on samples as previously described in Section 2.2.14.

4.2.6 Dimethyl labelling and LC-MS/MS analysis of *S. aureus* proteins

4.2.6.1. Dimethyl labelling of proteins

Dimethyl labelling approach was undertaken by J. Steele as described previously [86,259]. Dimethyl labelled proteins were analysed using two mass spectrometers; the Sciex 5600 and the Thermo Scientific Q Exactive™.

4.2.6.2. LC-MS/MS (Sciex 5600) of dimethyl labelled proteins

Peptides from dimethyl labelled proteins described in section 2.16.1 were separated by nanoLC using an Ultimate nanoRSLC UPLC and autosampler system (Dionex, Amsterdam, Netherlands). Samples (2.5 µl) were concentrated and desalted onto a micro C18 precolumn (300 µm x 5 mm, Dionex) with H_2O:CH_3CN (98:2, 0.1 % TFA) at 15 µl/min. After a 4 min wash the pre-column was switched (Valco 10 port UPLC valve, Valco, Houston, TX) into line with a fritless nano column (75 µ x ~15 cm) containing C18AQ media (1.9 µ, 120 Å Dr Maisch, Ammerbuch-Entringen Germany). Peptides were eluted using a linear gradient of H_2O:CH_3CN (98:2, 0.1 % formic acid) to H_2O:CH_3CN (64:36, 0.1 % formic acid) at 200 nl/min over 240 min. High voltage 2000 V was applied to low volume Titanium union (Valco) with the tip positioned ~ 0.5 cm from the curtain plate (T=150 °C) of a 5600+ mass spectrometer (Sciex, Toronto, Canada). Positive ions were generated by electrospray and the 5600+ operated in information dependent acquisition mode (IDA).

A survey scan m/z 350-1750 was acquired (PWHH resolution ~30,000, 0.25 s acquisition time) with autocalibration enabled (at ~6 h intervals). Up to the 10 most abundant ions (>300 counts) with charge states > +2 and <+5 were sequentially isolated (width m/z ~3) and fragmented by CID with an optimal CE chosen based on m/z (product ion spectra were acquired at a resolution ~20,000 PWHH in 0.15 s). M/z ratios selected for MS/MS were dynamically excluded for 30 or 45 s.

Peak lists were generated using Mascot Daemon/Mascot Distiller (Matrix Science, London, England) or ProteinPilot (Sciex, v4.5) using default parameters, and submitted to the database search program Mascot (version 2.5.1, Matrix Science). Search parameters were: Precursor tolerance 10 ppm and product ion tolerances ± 0.05 Da; oxidation (M), deamidation (NQ), propionamide (C), Dimethyl (K), Dimethyl (N-term) specified as variable modifications; enzyme specificity was semi-ArgC; 1 missed cleavage was possible and the non-redundant protein database from NCBI (Jan 2015) searched.

4.2.6.3. LC-MS/MS (Thermo Scientific Q Exactive™) of dimethyl labelled proteins

Peptides from dimethyl labelled proteins described in section 2.18.1 were separated by nanoLC using an Ultimate nanoRSLC UPLC and autosampler system (Dionex, Amsterdam, Netherlands). Samples (2.5 µl) were concentrated and desalted onto a micro C18 precolumn (300 µm x 5 mm, Dionex) with H_2O:CH_3CN (98:2, 0.1 % TFA) at 15 µl/min. After a 4 min wash the pre-column was switched (Valco 10 port UPLC valve, Valco, Houston, TX) into line with a fritless nano column (75 µ x ~35 cm) containing C18AQ media (1.9 µ, 120 Å Dr Maisch, Ammerbuch-Entringen Germany). Peptides were eluted using a linear gradient of H_2O:CH_3CN (98:2, 0.1 % formic acid) to H_2O:CH_3CN (64:36, 0.1 % formic acid) at 200 nl/min over 30 or 240 min. High voltage 2000 V was applied to low volume Titanium union (Valco) with the column oven heated to 45 °C (Sonation, Biberach, Germany) and the tip positioned ~ 0.5 cm from the heated capillary (T=300 °C) of a QExactive Plus mass spectrometer (Thermo Fisher Scientific, Bremen, Germany). Positive ions were generated by electrospray and the QExactive operated in data dependent acquisition mode (DDA).

A survey scan m/z 350-1750 was acquired (resolution = 70,000 at m/z 200, with an AGC target value of 106 ions) and lockmass was enabled (m/z 445.12003) Up to the 10 most abundant ions (>80,000 counts, underfill ratio 10 %) with charge states > +2 and <+7 were sequentially isolated (width m/z 2.5) and fragmented by HCD (NCE = 30) with a AGC target of 105 ions (resolution = 17,500 at m/z 200). M/z ratios selected for MS/MS were dynamically excluded for 30 or 45 s.

Peak lists were generated using Mascot Daemon/Mascot Distiller (Matrix Science, London, England) or Proteome Discoverer (Thermo, v1.4) using default parameters, and submitted to the database search program Mascot (version 2.5.1, Matrix Science). Search parameters were: Precursor tolerance 4 ppm and product ion tolerances ± 0.05 Da; oxidation (M), deamidation (NQ), propionamide (C), Dimethyl (K), Dimethyl (N-term) specified as variable modifications; enzyme specificity was semi-ArgC; 1 missed cleavage was possible and the non-redundant protein database from NCBI (Jan 2015) searched.

4.2.7 Bioinformatic analysis of Ef-Tu

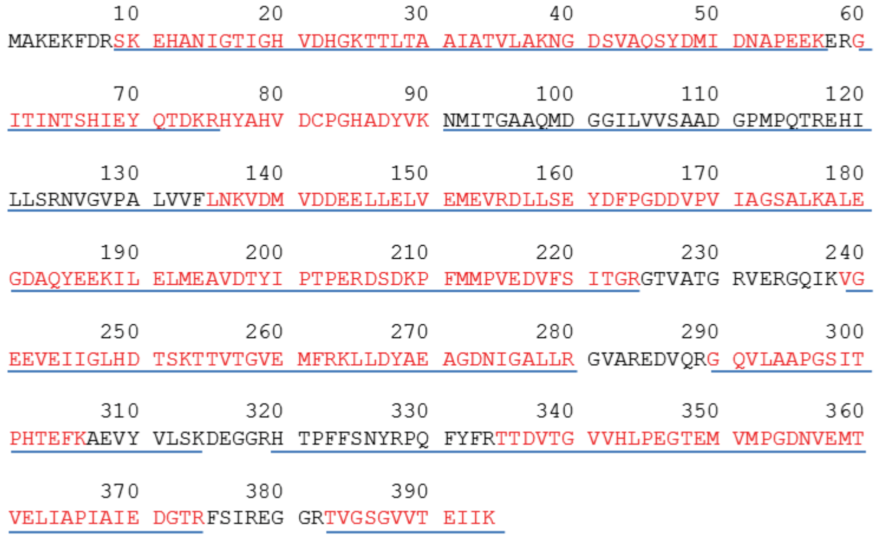
The amino acid sequence of Ef-Tu$_{\mathrm{Sau}}$ (Uniprot #: Q2G0N0) was analysed using a variety of bioinformatics tools. Bioinformatic analysis of Ef-Tu used the online resources: ProtParam [254], Clustal Omega [443,444], SignalP 4.1 Server (SignalP 4.0: discriminating signal peptides from transmembrane regions), SecretomeP 2.0 Server (Feature based prediction of non-classical and leaderless protein secretion), TMpred [257], Clustal Omega [443,444], and COILS (Addition of ‘yes’ to 2.5 fold weighting of positions a,d) [445].

Conservation of amino acid positions in each protein were detected (by V. Jarocki) using The ConSurf server [446]. Putative HP-binding sites were identified using the search patterns x-[HKR]-x(0,2)-[HKR]-x(0,2)-[HKR]-x and x-[HKR]-x(1,4)-[HKR]-x(1,4)-[HKR]-x via ScanProsite [311]. Putative protein-protein and protein-nucleic acid interaction sites were identified (by V. Jarocki) using ISIS [447]. Intrinsically disordered regions were predicted by Meta-Disorder (by V. Jarocki) [448,449], which combines the outputs from original prediction methods NORSnet, DISOPRED2, PROFbval and Ucon. Solvent accessibility of each amino acid position was ascertained using evolutionary information from multiple sequence alignments and a multi-level system in PredictProtein [450].

4.3 Results

4.3.1 *Staphylococcus aureus* Ef-Tu ($Sa_{Ef\text{-}Tu}$) is accessible on the bacterial surface.

LC-MS/MS analysis of tryptic peptides released from the cell surface of *S. aureus* were mapped to $Sa_{Ef\text{-}Tu}$. Tryptic peptides generated by digesting biotinylated cell surface proteins that were captured by streptavidin agarose chromatography also mapped to $Sa_{Ef\text{-}Tu}$. Peptides identified by mass spectrometry from both techniques spanned the entire length of $Sa_{Ef\text{-}Tu}$, (Figure 4.1 and Figure 4.2) consistent with the hypothesis that a sub-population of $Sa_{Ef\text{-}Tu}$ molecules are exposed on the cell surface while the remainder perform an essential function in the cytosol. Biotinylation data indicates that cleaved fragments of $Sa_{Ef\text{-}Tu}$ are also retained on the surface of *S. aureus* (Figure 4.2).



```
         10         20         30         40         50         60
MAKEKFDRSK EHANIGTIGH VDHGKTTLTA AIATVLAKNG DSVAQSYDMI DNAPEEKERG

         70         80         90        100        110        120
ITINTSHIEY QTDKRHYAHV DCPGHADYVK NMITGAAQMD GGILVVSAAD GPMPQTREHI

        130        140        150        160        170        180
LLSRNVGVPA LVVFLNKVDM VDDEELLELV EMEVRDLLSE YDFPGDDVPV IAGSALKALE

        190        200        210        220        230        240
GDAQYEEKIL ELMEAVDTYI PTPERDSDKP FMMPVEDVFS ITGRGTVATG RVERGQIKVG

        250        260        270        280        290        300
EEVEIIGLHD TSKTTVTGVE MFRKLLDYAE AGDNIGALLR GVAREDVQRG QVLAAPGSIT

        310        320        330        340        350        360
PHTEFKAEVY VLSKDEGGRH TPFFSNYRPQ FYFRTTDVTG VVHLPEGTEM VMPGDNVEMT

        370        380        390
VELIAPIAIE DGTRFSIREG GRTVGSGVVT EIIK
```

Figure 4.1 Sa$_{\text{Ef-Tu}}$ strain NCTC 8325 sequence showing regions identified in surface proteome analysis.

Peptides identified in surface trypsin shaving experiments are shown in red, and peptides identified from surface biotinylation are underlined in blue. Numbers indicate amino acid number. There is coverage to the majority of the protein from both analyses.

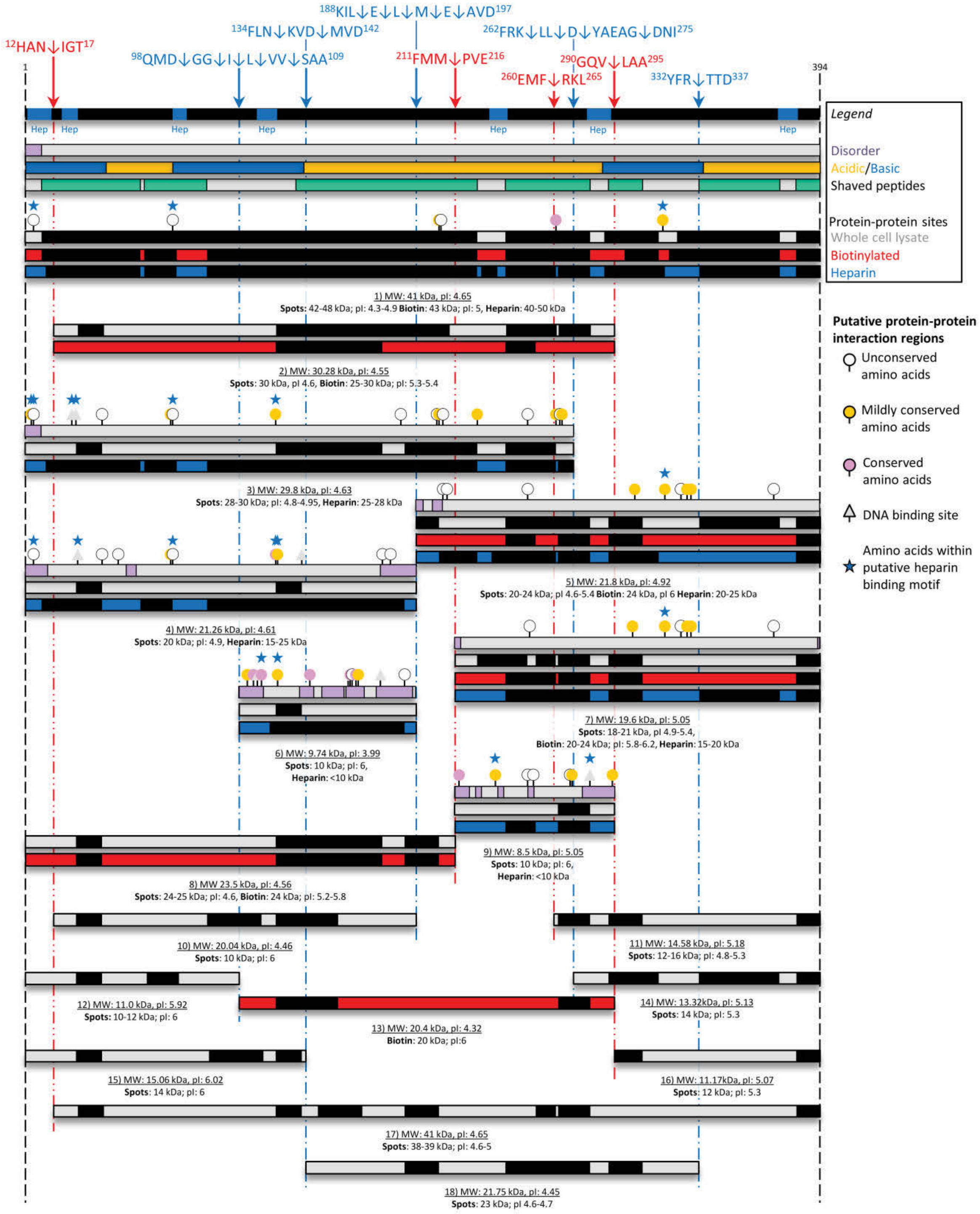


Figure 4.2 Cleavage map of $Sa_{Ef\text{-}Tu}$.

Peptides identified (black boxes within coloured bars) by mass spectrometry within $Sa_{Ef\text{-}Tu}$ fragments were obtained from 2D SDS PAGE of bacterial whole cell lysates (grey bars), avidin affinity chromatography of biotinylated surface proteins (red bars), and HP-agarose affinity chromatography (blue bars). Full length $Sa_{Ef\text{-}Tu}$ molecules are represented as black bars. Peptides released from trypsin shaving of cells are shown as the green boxes within the grey bar. Cleavage products of $Sa_{Ef\text{-}Tu}$ are also shown. Exact cleavage sites are shown in the amino acid sequences above the black bar. Cleavage sites were identified by dimethyl labelled peptides (blue arrows and broken lines) and by characterising semi-tryptic peptides generated after trypsin digestion (red arrows and broken lines). Bioinformatic tools such as ScanProsite [311], TMpred [257], COILS [445] and Meta-Disorder [448] were used to predict putative HP-binding motifs (Hep, blue boxes), transmembrane domains (none identified in $Sa_{Ef\text{-}Tu}$), coiled-coils (none identified in $Sa_{Ef\text{-}Tu}$), and disordered regions (purple boxes in grey bar), respectively. Circles just above fragments denote amino acid positions that are predicted to be surface exposed and represent putative protein:protein interaction regions. Those marked with an additional star denote amino acid residues that fall within predicted putative HP-binding domains. White circles mark evolutionary unconserved binding regions, whilst yellow circles are mildly conserved and pink are highly conserved. Amino acid positions marked by grey triangles depict predicted nucleic acid interaction regions.

4.3.2 $\text{Sa}_{\text{Ef-Tu}}$ is one of the most highly processed proteins in *S. aureus*

$\text{Sa}_{\text{Ef-Tu}}$ was identified in over 50 spots from the WCL 2D-PAGE analysis, as part of a global analysis of *S. aureus* proteins. These spots ranged in molecular weight on the gel from 10-100 kDa (Ef-Tu has a molecular weight of 43 kDa). Further cleavage evidence was identified using in-gel proteomic techniques including LC-MS/MS analysis of i) surface biotinylated proteins separated by 2D-PAGE, ii) 1D-SDS-PAGE gel slices loaded with biotinylated *S. aureus* surface proteins captured by avidin chromatography, and iii) 1D-SDS-PAGE gel slices loaded with proteins eluted from HP agarose columns. A combination of this data (Figure 4.2) showed that $\text{Sa}_{\text{Ef-Tu}}$ is one of the most highly proteolytically processed proteins in *S. aureus*.

As part of a larger study that sought to identify the repertoire of proteins in *S. aureus* that are targets of proteolytic processing events, a dimethyl labelling protocol was employed to tag N-terminal peptides and identify precise endoproteolytic cleavage sites (Table 4.2, data obtained by J. Steele and compiled by author). The sites are listed in Table 4.2 and were consistent with many of the cleaved peptide products identified in the gel-based proteomic techniques (Figure 4.2).

Table 4.2 Dimethyl-labelled and semi-tryptic N-terminal peptides identified in Sa$_{\text{Ef-Tu}}$.

No.	ID	Peptide Sequence	Score	E-value
		Dimethyl Labelled peptides		
2	N1	D.^{101} **G**GILVVSAADGPMPQTR^{117}.E	98	2.90E^{-05}
	N2	G.^{103} **I**LVVSAADGPMPQTR^{117}.E	81	1.30E^{-03}
	N3	I.^{104} **L**VVSAADGPMPQTR^{117}.E	104	5.90E^{-06}
	N4	L.^{105} **V**VSAADGPMPQTR^{117}.E	91	1.10E^{-04}
	N5	V.^{107} **S**AADGPMPQTR^{117}.E	69	9.90E^{-03}
3	N6	N.^{137} **K**VDMVDDEELLELVEMEVR^{155}.D	80	3.10E^{-03}
	N7	D.^{140} **M**VDDEELLELVEMEVR^{155}.D	78	3.40E^{-03}
4	N8	L.^{191} **E**LMEAVDTYIPTPER^{205}.D	78	3.60E^{-03}
	N9	E.^{192} **L**MEAVDTYIPTPER^{205}.D	78	3.20E^{-03}
	N10	L.^{193} **M**EAVDTYIPTPER^{205}.D	72	2.80E^{-03}
	N11	M.^{194}**E**AVDTYIPTPER^{205}.D	103	8.40E^{-06}
	N12	E.^{195} **A**VDTYIPTPER^{205}.D	77	9.60E^{-04}
7	N13	K.^{265} **L**LDYAEAGDNIGALLR^{280}.G	98	4.10E^{-05}
	N14	L.^{267} **D**YAEAGDNIGALLR^{280}.G	88	1.80E^{-04}
	N15	D.^{268} **Y**AEAGDNIGALLR^{280}.G	89	2.40E^{-04}
	N16	G.^{273} **D**NIGALLR^{280}.G	67	1.80E^{-02}
9	N17	R.^{335} **T**TDVTGVVHLPEGTEMVMPGDNVEMTVELIAPIAIEDGTR^{374}.F	86	7.7E^{-07}
		Semi-tryptic N-terminal Peptides		
8	S1	V.^{293} **L**AAPGSITPHTEFK^{306}.A	106	3.2E^{-05}
5	S2	M.^{214}**P**VEDVFSITGR^{224}.G	80	0.01
1	S3	N.^{15} **I**GTIGHVDHGK^{28}.T	80	0.011

6	S4	F.^{263} **R**KLLDYAEAGDNIGALLR^{280}.G	91	0.0012

Identified peptides have a Mascot score > 33 and an E-value < 0.05. “No.” listed in the first column is the number of the cleavage site. The exact site of cleavage is to the left of the amino acid that is bold and underlined for N-terminal cleavage fragments. Amino acid numbers are written at the start and end of each peptide identified by LC-MS/MS. Dimethyl-labelled N-termini analysis was performed by J. Steele.

4.3.3 $Sa_{Ef\text{-}Tu}$ and $Sa_{Ef\text{-}Tu}$ fragments are retained by heparin affinity chromatography.

Peptides spanning the length of the $Sa_{Ef\text{-}Tu}$ molecule were identified when LC-MS/MS analysis was performed on tryptic digests of high salt (> 500 mM) eluents of proteins from HP-agarose (Figure 4.2). Notably, two of six fragments that were enriched during HP affinity chromatography were also identified in surface biotinylation experiments (Figure 4.2). Six cleavage fragments that span different regions of $Sa_{Ef\text{-}Tu}$, were recovered during HP-agarose chromatography using salt concentrations well above the physiological concentration of 150 mM. All the fragments recovered from HP affinity chromatography contained clusters of positively charged amino acids that are predicted to form putative HP-binding sites (Table 4.3). These data suggests that the processing events that generate $Sa_{Ef\text{-}Tu}$ cleavage fragments occur on the surface of *S. aureus* and that the fragments retain an ability to interact with high sulfated glycosaminoglycans such as HP. Cleavage sites appear to avoid disrupting interaction sites such as the HP motifs identified.

4.3.4 Bioinformatic analysis of $Sa_{Ef\text{-}Tu}$.

4.3.4.1. Bioinformatic analysis of heparin-binding site in $Sa_{Ef\text{-}Tu}$

Putative HP-binding motifs (including clusters of basic amino acids) were computationally searched using ScanProsite [311] resulting in the identification of seven putative HP-binding regions in Ef-Tu (Table 4.3). These were included on the cleavage maps of $Sa_{Ef\text{-}Tu}$ (Figure 4.2) and were mapped onto 3-D models of $Sa_{Ef\text{-}Tu}$ (Figure 4.3 and Figure 4.4).

Table 4.3 Seven putative heparin-binding motifs identified in Sa$_{\text{Ef-Tu}}$.

Amino acid range	Sequence
	Ef-Tu (Uniprot #: Q2G0N0)
2 - 13:	`aKeKfdRsKeHa`
19 - 26:	`gHvdHgKt`
73 - 80:	`dKRHyaHv`
116 - 125:	`tReHillsRn`
230 - 239:	`gRveRgqiKv`
279 - 290	`lRgvaRedvqRg`
373 - 383:	`tRfsiReggRt`

The Ef-Tu protein sequence from *S. aureus* NCTC 8325 (Q2G0N0) was searched for patterns x-[HKR]-x(0,2)-[HKR]-x(0,2)-[HKR]-x and x-[HKR]-x(1,4)-[HKR]-x(1,4)-[HKR]-x using ScanProsite [311]. Putative HP-binding motifs are listed below with their amino acid location shown on the left column. Capitalised letters show amino acids that matched a specific residue in the pattern (positive residues). Lower case letters are amino acids that matched to an "x" in the patterns (x denotes any amino acid).

4.3.4.2. Molecular modelling of Sa$_{\text{Ef-Tu}}$.

The prediction tool MODELLER [451] was used to predict the structure of Sa$_{\text{Ef-Tu}}$ based off Ef-Tu from *E. coli*. For *S. aureus* NCTC 8325, the *E. coli* Ef-Tu (PDB: 1DG1_H) had a sequence ID percentage of 75.06 % and a zDOPE score of -0.88. All nine distinct cleavage sites for *S. aureus* have been mapped in the ribbon structures (Figure 4.3). Cleavage sites located in regions that are predicted to release the three domains are mostly surface accessible within the molecule. The space filler model is also shown to illustrate the location and accessibility of cleavage sites and putative HP-binding domains (Figure 4.4).

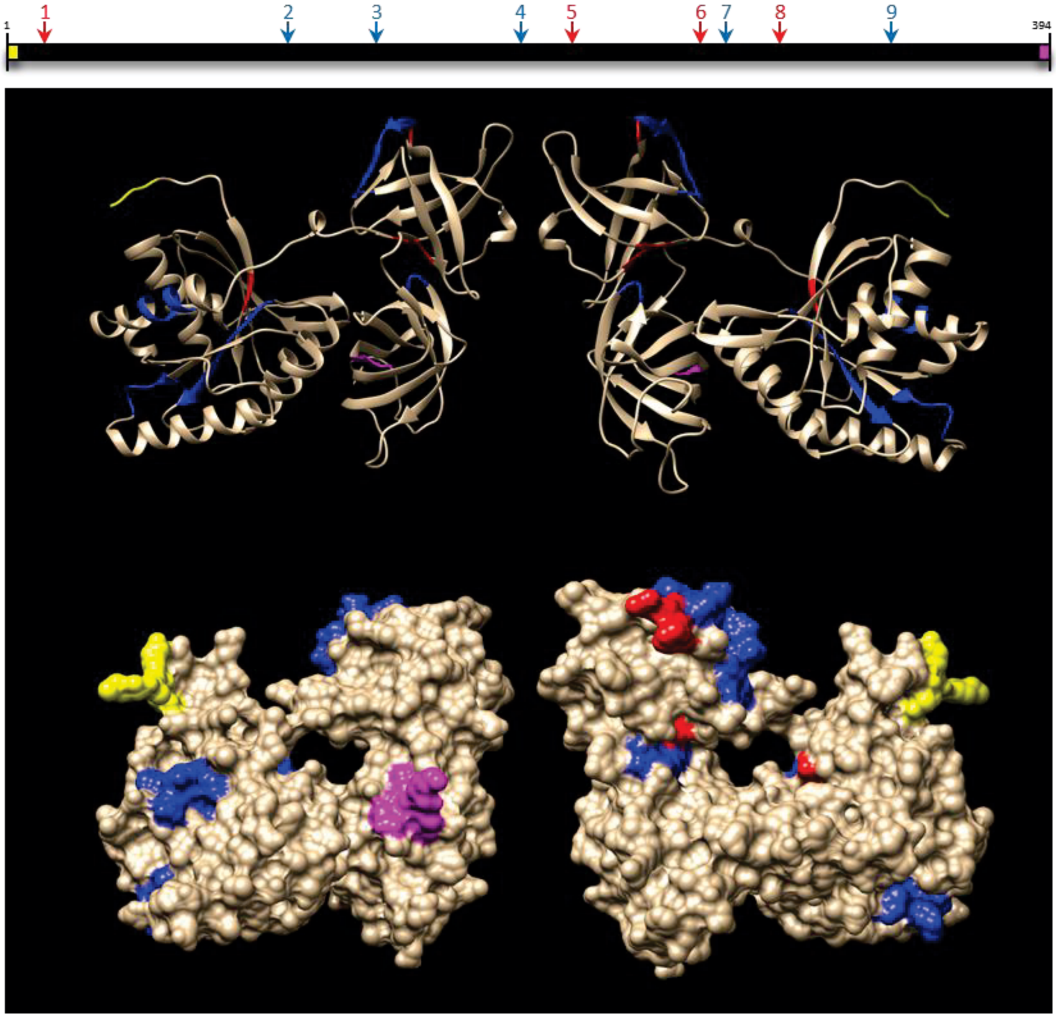


Figure 4.3 Predicted 3-D ribbon and space-filling structures of Sa$_{\text{Ef-Tu}}$ showing cleavage sites. Sa$_{\text{Ef-Tu}}$ molecules are represented as black bars with identified cleavage sites displayed as arrows (with blue denoting dimethyl labelling and red denoting semi-tryptic) with numbers to indicate which distinct cleavage site (as listed in Table 4.2). Cleavage sites can also be seen in the 3-D structures as blue and red sections for dimethyl labelling and semi-tryptic sites, respectively. For context, the N-terminus of the protein has been coloured in yellow, and the C-terminus in pink. Images are reversed sides of the each structure. Structure was predicted by MODELLER [451] and based on *E. coli* Ef-Tu homologue, PDB: 1DG1_H.

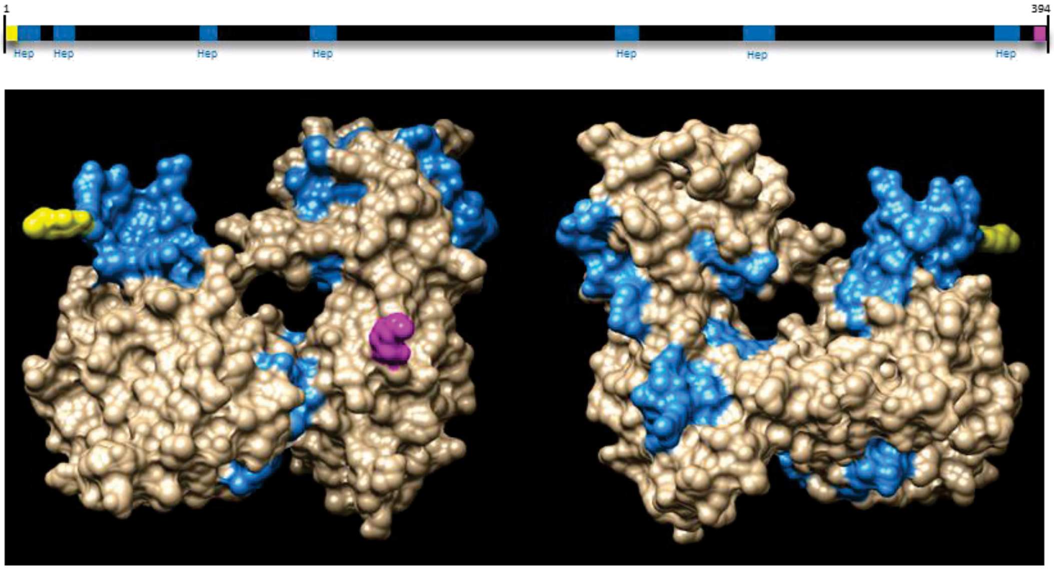
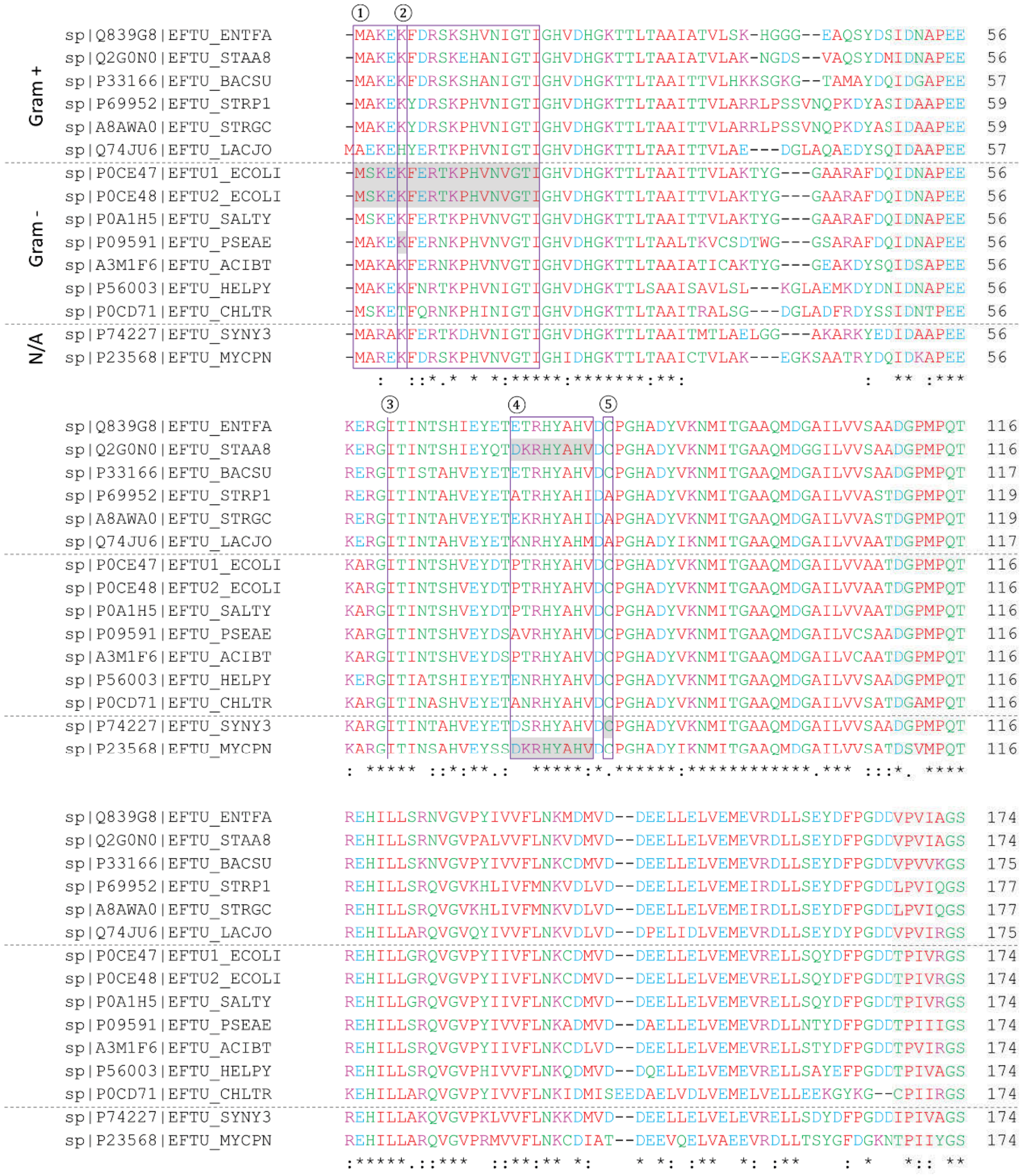


Figure 4.4 Predicted 3-D space-filling structures of $\text{Sa}_{\text{Ef-Tu}}$ with putative heparin-binding motifs.

Full length $\text{Sa}_{\text{Ef-Tu}}$ is represented as a black bar with predicted HP-binding sites shown as blue boxes and regions in the structures. For context, the N-terminus of the protein has been coloured in yellow, and the C-terminus in pink. Structures were predicted by MODELLER [451] and were based on *E. coli* Ef-Tu homologues, PDB: 1DG1_H.

4.3.4.3. Protein alignment of Ef-Tu from bacterial species.

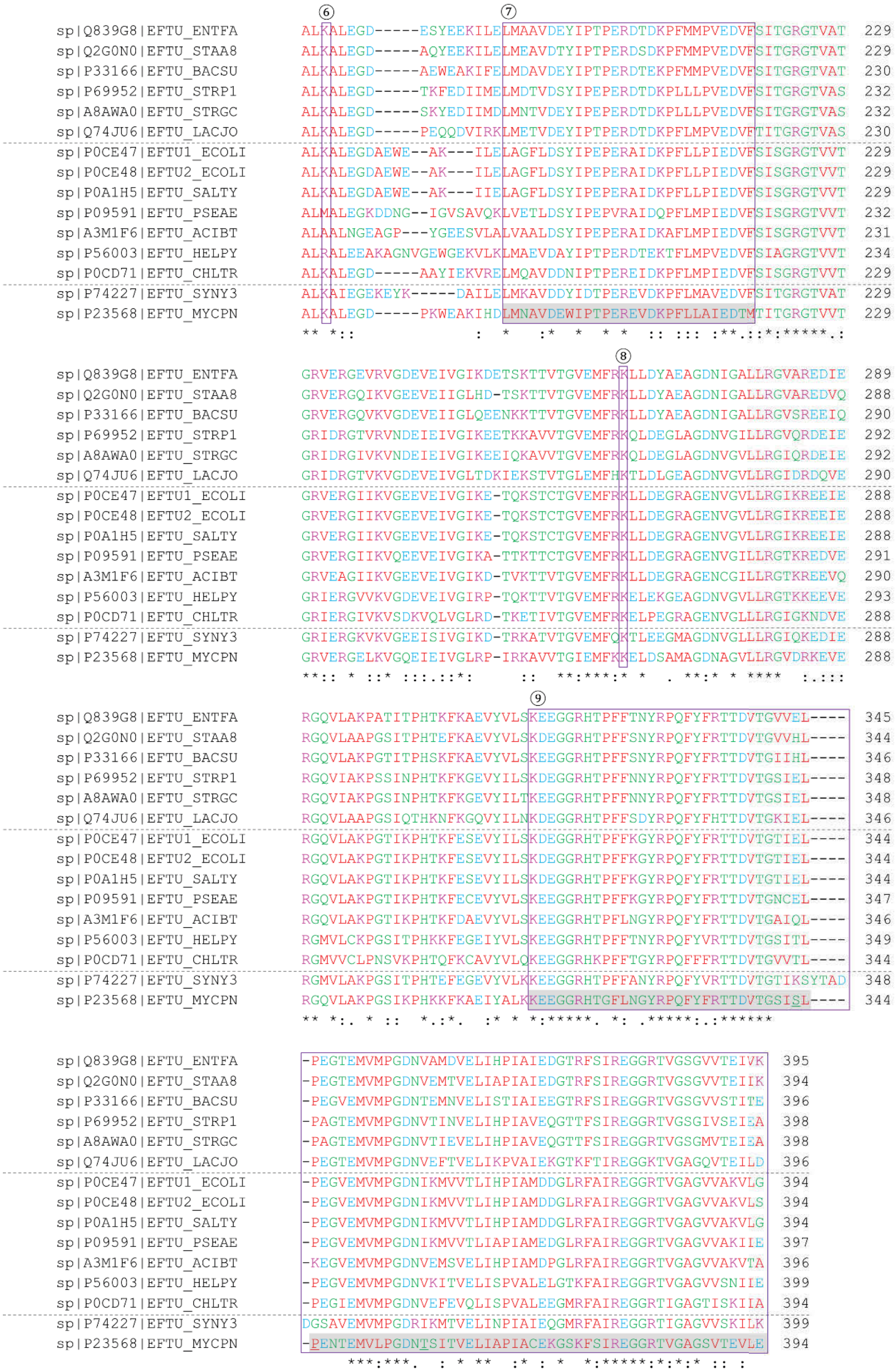
Ef-Tu from a wide range of bacterial species was aligned using Clustal Omega (for phylogeny output see Appendix C Figure C.1) [443,444] to identify conserved and non-conserved regions (Figure 4.5). Multiple known functional domains and modification sites were mapped to the alignment. As already established, Ef-Tu (overall) is a highly conserved molecule, with less than 30 % sequence divergence [363] across prokaryotes. Low G + C Gram positive bacteria carry only a single copy of the *tuf* gene [364]. In contrast, many enteric bacteria have two copies (*tufA* and *tufB*) [365,366], hence two Ef-Tu homologues in *E. coli* have been included in Figure 4.5 for comparison. In species with two copies of the gene, the two genes differ by less than 1.4 % (based on nucleotide comparison) [363]. In this example, there is only one amino acid difference and it is the final amino acid (G/S). Many of the sites/regions highlighted are conserved amongst species indicating that putative moonlighting domains may be shared across species. The putative HP-binding regions identified in the study (number 4 in Figure 4.5) generally have most of their positive residues (HKR) conserved across some other strains, implying that Ef-Tu from other bacterial strains may also bind HP.



```
                                    ①   ②
        sp|Q839G8|EFTU_ENTFA       -MAKEKFDRSKSHVNIGTIGHVDHGKTTLTAAIATVLSK-HGGG--EAQSYDSIDNAPEE   56
        sp|Q2G0N0|EFTU_STAA8       -MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAK-NGDS--VAQSYDMIDNAPEE   56
        sp|P33166|EFTU_BACSU       -MAKEKFDRSKSHANIGTIGHVDHGKTTLTAAITTVLHKKSGKG--TAMAYDQIDGAPEE   57
Gram +  sp|P69952|EFTU_STRP1       -MAKEKYDRSKPHVNIGTIGHVDHGKTTLTAAITTVLARRLPSSVNQPKDYASIDAAPEE   59
        sp|A8AWA0|EFTU_STRGC       -MAKEKYDRSKPHVNIGTIGHVDHGKTTLTAAITTVLARRLPSSVNQPKDYASIDAAPEE   59
        sp|Q74JU6|EFTU_LACJO       MAEKEHYERTKPHVNIGTIGHVDHGKTTLTAAITTVLAE---DGLAQAEDYSQIDAAPEE   57
--------------------------------------------------------------------------------------------
        sp|P0CE47|EFTU1_ECOLI      -MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYG---GAARAFDQIDNAPEE   56
        sp|P0CE48|EFTU2_ECOLI      -MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYG---GAARAFDQIDNAPEE   56
        sp|P0A1H5|EFTU_SALTY       -MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYG---GAARAFDQIDNAPEE   56
Gram -  sp|P09591|EFTU_PSEAE       -MAKEKFERNKPHVNVGTIGHVDHGKTTLTAALTKVCSDTWG---GSARAFDQIDNAPEE   56
        sp|A3M1F6|EFTU_ACIBT       -MAKAKFERNKPHVNVGTIGHVDHGKTTLTAAIATICAKTYG---GEAKDYSQIDSAPEE   56
        sp|P56003|EFTU_HELPY       -MAKEKFNRTKPHVNIGTIGHVDHGKTTLSAAISAVLSL---KGLAEMKDYDNIDNAPEE   56
        sp|P0CD71|EFTU_CHLTR       -MSKETFQRNKPHINIGTIGHVDHGKTTLTAAITRALSG---DGLADFRDYSSIDNTPEE   56
--------------------------------------------------------------------------------------------
N/A     sp|P74227|EFTU_SYNY3       -MARAKFERTKDHVNIGTIGHVDHGKTTLTAAITMTLAELGG---AKARKYEDIDAAPEE   56
        sp|P23568|EFTU_MYCPN       -MAREKFDRSKPHVNVGTIGHIDHGKTTLTAAICTVLAK---EGKSAATRYDQIDKAPEE   56
                                      :  ::*.* * *:*****:*******:**:                 :  ** :***

                                       ③           ④        ⑤
        sp|Q839G8|EFTU_ENTFA       KERGITINTSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQT   116
        sp|Q2G0N0|EFTU_STAA8       KERGITINTSHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQT   116
        sp|P33166|EFTU_BACSU       RERGITISTAHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQT   117
        sp|P69952|EFTU_STRP1       RERGITINTAHVEYETATRHYAHIDAPGHADYVKNMITGAAQMDGAILVVASTDGPMPQT   119
        sp|A8AWA0|EFTU_STRGC       RERGITINTAHVEYETEKRHYAHIDAPGHADYVKNMITGAAQMDGAILVVASTDGPMPQT   119
        sp|Q74JU6|EFTU_LACJO       KERGITINTAHVEYETKNRHYAHMDAPGHADYIKNMITGAAQMDGAILVVAATDGPMPQT   117
--------------------------------------------------------------------------------------------
        sp|P0CE47|EFTU1_ECOLI      KARGITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQT   116
        sp|P0CE48|EFTU2_ECOLI      KARGITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQT   116
        sp|P0A1H5|EFTU_SALTY       KARGITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQT   116
        sp|P09591|EFTU_PSEAE       KARGITINTSHVEYDSAVRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGPMPQT   116
        sp|A3M1F6|EFTU_ACIBT       KARGITINTSHVEYDSPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVCAATDGPMPQT   116
        sp|P56003|EFTU_HELPY       KERGITIATSHIEYETENRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQT   116
        sp|P0CD71|EFTU_CHLTR       KARGITINASHVEYETANRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSATDGAMPQT   116
--------------------------------------------------------------------------------------------
        sp|P74227|EFTU_SYNY3       KARGITINTAHVEYETDSRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQT   116
        sp|P23568|EFTU_MYCPN       KARGITINSAHVEYSSDKRHYAHVDCPGHADYIKNMITGAAQMDGAILVVSATDSVMPQT   116
                                   : ***** ::*:**.:  *****:*.******:************.*** :::*. ****

        sp|Q839G8|EFTU_ENTFA       REHILLSRNVGVPYIVVFLNKMDMVD--DEELLELVEMEVRDLLSEYDFPGDDVPVIAGS   174
        sp|Q2G0N0|EFTU_STAA8       REHILLSRNVGVPALVVFLNKVDMVD--DEELLELVEMEVRDLLSEYDFPGDDVPVIAGS   174
        sp|P33166|EFTU_BACSU       REHILLSKNVGVPYIVVFLNKCDMVD--DEELLELVEMEVRDLLSEYDFPGDDVPVVKGS   175
        sp|P69952|EFTU_STRP1       REHILLSRQVGVKHLIVFMNKVDLVD--DEELLELVEMEIRDLLSEYDFPGDDLPVIQGS   177
        sp|A8AWA0|EFTU_STRGC       REHILLSRQVGVKHLIVFMNKVDLVD--DEELLELVEMEIRDLLSEYDFPGDDLPVIQGS   177
        sp|Q74JU6|EFTU_LACJO       REHILLARQVGVQYIVVFLNKVDLVD--DPELIDLVEMEVRDLLSEYDYPGDDVPVIRGS   175
--------------------------------------------------------------------------------------------
        sp|P0CE47|EFTU1_ECOLI      REHILLGRQVGVPYIIVFLNKCDMVD--DEELLELVEMEVRELLSQYDFPGDDTPIVRGS   174
        sp|P0CE48|EFTU2_ECOLI      REHILLGRQVGVPYIIVFLNKCDMVD--DEELLELVEMEVRELLSQYDFPGDDTPIVRGS   174
        sp|P0A1H5|EFTU_SALTY       REHILLGRQVGVPYIIVFLNKCDMVD--DEELLELVEMEVRELLSQYDFPGDDTPIVRGS   174
        sp|P09591|EFTU_PSEAE       REHILLSRQVGVPYIVVFLNKADMVD--DAELLELVEMEVRDLLNTYDFPGDDTPIIIGS   174
        sp|A3M1F6|EFTU_ACIBT       REHILLSRQVGVPYIIVFLNKCDLVD--DEELLELVEMEVRELLSTYDFPGDDTPVIRGS   174
        sp|P56003|EFTU_HELPY       REHILLSRQVGVPHIVVFLNKQDMVD--DQELLELVEMEVRELLSAYEFPGDDTPIVAGS   174
        sp|P0CD71|EFTU_CHLTR       KEHILLARQVGVPYIVVFLNKIDMISEEDAELVDLVEMELVELLEEKGYKG--CPIIRGS   174
--------------------------------------------------------------------------------------------
        sp|P74227|EFTU_SYNY3       REHILLAKQVGVPKLVVFLNKKDMVD--DEELLELVELEVRELLSDYDFPGDDIPIVAGS   174
        sp|P23568|EFTU_MYCPN       REHILLARQVGVPRMVVFLNKCDIAT--DEEVQELVAEEVRDLLTSYGFDGKNTPIIYGS   174
                                   :*****.::***  ::**:** *:    * *: :**  *: :**    : *   *:: **
```



```
                              ⑥                   ⑦
sp|Q839G8|EFTU_ENTFA        ALKALEGD-----ESYEEKILELMAAVDEYIPTPERDTDKPFMMPVEDVFSITGRGTVAT  229
sp|Q2G0N0|EFTU_STAA8        ALKALEGD-----AQYEEKILELMEAVDTYIPTPERDSDKPFMMPVEDVFSITGRGTVAT  229
sp|P33166|EFTU_BACSU        ALKALEGD-----AEWEAKIFELMDAVDEYIPTPERDTEKPFMMPVEDVFSITGRGTVAT  230
sp|P69952|EFTU_STRP1        ALKALEGD-----TKFEDIIMELMDTVDSYIPEPERDTDKPLLLPVEDVFSITGRGTVAS  232
sp|A8AWA0|EFTU_STRGC        ALKALEGD-----SKYEDIIMDLMNTVDEYIPEPERDTDKPLLLPVEDVFSITGRGTVAS  232
sp|Q74JU6|EFTU_LACJO        ALKALEGD-----PEQQDVIRKLMETVDEYIPTPERDTDKPFLMPVEDVFTITGRGTVAS  230
sp|P0CE47|EFTU1_ECOLI       ALKALEGDAEWE--AK---ILELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGTVVT  229
sp|P0CE48|EFTU2_ECOLI       ALKALEGDAEWE--AK---ILELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGTVVT  229
sp|P0A1H5|EFTU_SALTY        ALKALEGDAEWE--AK---IIELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGTVVT  229
sp|P09591|EFTU_PSEAE        ALMALEGKDDNG--IGVSAVQKLVETLDSYIPEPVRAIDQPFLMPIEDVFSISGRGTVVT  232
sp|A3M1F6|EFTU_ACIBT        ALAALNGEAGP---YGEESVLALVAALDSYIPEPERAIDKAFLMPIEDVFSISGRGTVVT  231
sp|P56003|EFTU_HELPY        ALRALEEAKAGNVGEWGEKVLKLMAEVDAYIPTPERDTEKTFLMPVEDVFSIAGRGTVVT  234
sp|P0CD71|EFTU_CHLTR        ALKALEGD-----AAYIEKVRELMQAVDDNIPTPEREIDKPFLMPIEDVFSISGRGTVVT  229
sp|P74227|EFTU_SYNY3        ALKAIEGEKEYK-----DAILELMKAVDDYIDTPEREVDKPFLMAVEDVFSITGRGTVAT  229
sp|P23568|EFTU_MYCPN        ALKALEGD-----PKWEAKIHDLMNAVDEWIPTPEREVDKPFLLAIEDTMTITGRGTVVT  229
                            ** *::             :  *   :*  *  * *  :: ::: :**.::*:*****.:

                                                               ⑧
sp|Q839G8|EFTU_ENTFA        GRVERGEVRVGDEVEIVGIKDETSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIE  289
sp|Q2G0N0|EFTU_STAA8        GRVERGQIKVGEEVEIIGLHD-TSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQ  288
sp|P33166|EFTU_BACSU        GRVERGQVKVGDEVEIIGLQEENKKTTVTGVEMFRKLLDYAEAGDNIGALLRGVSREEIQ  290
sp|P69952|EFTU_STRP1        GRIDRGTVRVNDEIEIVGIKEETKKAVVTGVEMFRKQLDEGLAGDNVGILLRGVQRDEIE  292
sp|A8AWA0|EFTU_STRGC        GRIDRGIVKVNDEIEIVGIKEEIQKAVVTGVEMFRKQLDEGLAGDNVGVLLRGIQRDEIE  292
sp|Q74JU6|EFTU_LACJO        GRIDRGTVKVGDEVEIVGLTDKIEKSTVTGLEMFHKTLDLGEAGDNVGVLLRGIDRDQVE  290
sp|P0CE47|EFTU1_ECOLI       GRVERGIIKVGEEVEIVGIKE-TQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIE  288
sp|P0CE48|EFTU2_ECOLI       GRVERGIIKVGEEVEIVGIKE-TQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIE  288
sp|P0A1H5|EFTU_SALTY        GRVERGIIKVGEEVEIVGIKE-TQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIE  288
sp|P09591|EFTU_PSEAE        GRVERGIIKVQEEVEIVGIKA-TTKTTCTGVEMFRKLLDEGRAGENVGILLRGTKREDVE  291
sp|A3M1F6|EFTU_ACIBT        GRVEAGIIKVGEEVEIVGIKD-TVKTTVTGVEMFRKLLDEGRAGENCGILLRGTKREEVQ  290
sp|P56003|EFTU_HELPY        GRIERGVVKVGDEVEIVGIRP-TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVE  293
sp|P0CD71|EFTU_CHLTR        GRIERGIVKVSDKVQLVGLRD-TKETIVTGVEMFRKELPEGRAGENVGLLLRGIGKNDVE  288
sp|P74227|EFTU_SYNY3        GRIERGKVKVGEEISIVGIKD-TRKATVTGVEMFQKTLEEGMAGDNVGLLLRGIQKEDIE  288
sp|P23568|EFTU_MYCPN        GRVERGELKVGQEIEIVGLRP-IRKAVVTGIEMFKKELDSAMAGDNAGVLLRGVDRKEVE  288
                            **:: * ::* :::.::*:     ::  **:***:* *  . **:* * ****  :.:::

                                                     ⑨
sp|Q839G8|EFTU_ENTFA        RGQVLAKPATITPHTKFKAEVYVLSKEEGGRHTPFFTNYRPQFYFRTTDVTGVVEL----  345
sp|Q2G0N0|EFTU_STAA8        RGQVLAAPGSITPHTEFKAEVYVLSKDEGGRHTPFFSNYRPQFYFRTTDVTGVVHL----  344
sp|P33166|EFTU_BACSU        RGQVLAKPGTITPHSKFKAEVYVLSKEEGGRHTPFFSNYRPQFYFRTTDVTGIIHL----  346
sp|P69952|EFTU_STRP1        RGQVIAKPSSINPHTKFKGEVYILSKDEGGRHTPFFNNYRPQFYFRTTDVTGSIEL----  348
sp|A8AWA0|EFTU_STRGC        RGQVIAKPGSINPHTKFKGEVYILTKEEGGRHTPFFNNYRPQFYFRTTDVTGSIEL----  348
sp|Q74JU6|EFTU_LACJO        RGQVLAAPGSIQTHKNFKGQVYILNKDEGGRHTPFFSDYRPQFYFHTTDVTGKIEL----  346
sp|P0CE47|EFTU1_ECOLI       RGQVLAKPGTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDVTGTIEL----  344
sp|P0CE48|EFTU2_ECOLI       RGQVLAKPGTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDVTGTIEL----  344
sp|P0A1H5|EFTU_SALTY        RGQVLAKPGTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDVTGTIEL----  344
sp|P09591|EFTU_PSEAE        RGQVLAKPGTIKPHTKFECEVYVLSKEEGGRHTPFFKGYRPQFYFRTTDVTGNCEL----  347
sp|A3M1F6|EFTU_ACIBT        RGQVLAKPGTIKPHTKFDAEVYVLSKEEGGRHTPFLNGYRPQFYFRTTDVTGAIQL----  346
sp|P56003|EFTU_HELPY        RGMVLCKPGSITPHKKFEGEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITL----  349
sp|P0CD71|EFTU_CHLTR        RGMVVCLPNSVKPHTQFKCAVYVLQKEEGGRHKPFFTGYRPQFFFRTTDVTGVVTL----  344
sp|P74227|EFTU_SYNY3        RGMVLAKPGSITPHTEFEGEVYVLKKEEGGRHTPFFANYRPQFYVRTTDVTGTIKSYTAD  348
sp|P23568|EFTU_MYCPN        RGQVLAKPGSIKPHKKFKAEIYALKKEEGGRHTGFLNGYRPQFYFRTTDVTGSISL----  344
                            ** *:. * ::  *.:*.  :* * *:*****. *: .*****:.:******

sp|Q839G8|EFTU_ENTFA        -PEGTEMVMPGDNVAMDVELIHPIAIEDGTRFSIREGGRTVGSGVVTEIVK  395
sp|Q2G0N0|EFTU_STAA8        -PEGTEMVMPGDNVEMTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK  394
sp|P33166|EFTU_BACSU        -PEGVEMVMPGDNTEMNVELISTIAIEEGTRFSIREGGRTVGSGVVSTITE  396
sp|P69952|EFTU_STRP1        -PAGTEMVMPGDNVTINVELIHPIAVEQGTTFSIREGGRTVGSGIVSEIEA  398
sp|A8AWA0|EFTU_STRGC        -PAGTEMVMPGDNVTIEVELIHPIAVEQGTTFSIREGGRTVGSGMVTEIEA  398
sp|Q74JU6|EFTU_LACJO        -PEGTEMVMPGDNVEFTVELIKPVAIEKGTKFTIREGGKTVGAGQVTEILD  396
sp|P0CE47|EFTU1_ECOLI       -PEGVEMVMPGDNIKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVLG  394
sp|P0CE48|EFTU2_ECOLI       -PEGVEMVMPGDNIKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVLS  394
sp|P0A1H5|EFTU_SALTY        -PEGVEMVMPGDNIKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVLG  394
sp|P09591|EFTU_PSEAE        -PEGVEMVMPGDNIKMVVTLIAPIAMEDGLRFAIREGGRTVGAGVVAKIIE  397
sp|A3M1F6|EFTU_ACIBT        -KEGVEMVMPGDNVEMSVELIHPIAMDPGLRFAIREGGRTVGAGVVAKVTA  396
sp|P56003|EFTU_HELPY        -PEGVEMVMPGDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE  399
sp|P0CD71|EFTU_CHLTR        -PEGIEMVMPGDNVEFEVQLISPVALEEGMRFAIREGGRTIGAGTISKIIA  394
sp|P74227|EFTU_SYNY3        DGSAVEMVMPGDRIKMTVELINPIAIEQGMRFAIREGGRTIGAGVVSKILK  399
sp|P23568|EFTU_MYCPN        -PENTEMVLPGDNTSITVELIAPIACEKGSKFSIREGGRTVGAGSVTEVLE  394
                                 ***:***.  : * **  :* : *  *:*****:*:*:* :: :
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Figure 4.5 Alignments of Ef-Tu functional sites.

Ef-Tu from a number of bacterial species was aligned using Clustal Omega [443,444]. The species represented are, in order, *Enterococcus faecalis* (strain ATCC 700802 / V583), *S. aureus* (strain NCTC 8325)- $Sa_{Ef\text{-}Tu}$, *B. subtilis* (strain 168), *S. pyogenes* serotype M1, *S. gordon*ii (strain Challis / ATCC 35105 / BCRC 15272 / CH1 / DL1 / V288), *L. johnsonii* (strain CNCM I-12250 / La1 / NCC 533), *E. coli* (strain K12) with two Ef-Tu genes, *Salmonella enterica* serovar Typhimurium (strain LT2 / SGSC1412 / ATCC 700720), *P. aeruginosa* (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1), *A. baumannii* (strain ATCC 17978 / CIP 53.77 / LMG 1025 / NCDC KC755 / 5377), *H. pylori* (strain ATCC 700392 / 26695), *C. trachomatis* (strain D/UW-3/Cx), Synechocystis sp. (strain PCC 6803 / Kazusa), and *M. pneumoniae* (strain ATCC 29342 / M129). All protein sequences selected were reviewed according to Uniprot [101] and were from the strain the function was first assigned in (where possible). Symbols under each amino acid are given by Clustal Omega with * denoting a fully conserved amino acid, : denoting amino acids with strongly similar properties, and . denoting amino acids with weakly similar properties. The colour of the amino acids represents the residue physiochemical properties; red for small and hydrophobic, blue for acidic, pink for basic, and green is for hydroxyl, sulfhydryl, amine, and glycine residues. Where applicable, species in which the site was found in is shaded in grey. **1** efl18 a PAMP in *E. coli* [3]. **2** Trimethylation of the lysine at residue 5 in *P. aeruginosa* [412]. **3** Cleavage of Ef-Tu as a result of bacteriophage infection in *E. coli*. The cleavage occurs between Gly-59 and Ile-60 [413,414]. **4** HP motif (amino acids 73-80) predicted by the consensus sequence XBBBXXBX [312] that is shared between *S. aureus*, *M. pneumoniae*, and *M. hyopneumoniae*. **5** Oxidation of the cysteine residue (amino acid 82) of *Cyanobacterium Synechocystis* [452]. **6** Lysine glutarylation at residue 178 of Ef-Tu in *Mycobacterium tuberculosis* [453]. **7** Fibronectin-binding region in *M. pneumoniae* amino acids 192 to 219 [398,454]. **8** Lysine glutarylation of residue 266 Ef-Tu in *M. tuberculosis* [453]. **9** Fibronectin-binding region in *M. pneumoniae* positioned at amino acids 314 to 394, with amino acids crucial to this interaction underlined (serine 343, proline 345, and threonine 357) [398,454].

4.3.4.4. Processing events expose new predicted surface macromolecule interaction sites.

A single HP-binding consensus motif (XBBBXXBX, where B is a basic residue) [312] with the sequence dKRHyaHv is found within the amino acid sequence of Sa$_{\text{Ef-Tu}}$, yet several Sa$_{\text{Ef-Tu}}$ fragments were retained during HP-agarose chromatography that did not span this motif. Therefore sequences were examined for additional motifs enriched with clustered basic residues. In addition to the consensus HP-binding motif, six additional putative HP-binding motifs were found (Table 4.3), not all of these motifs possessed predicted protein-protein or protein-nucleic acid interactions sites within the parent protein; however they were exposed in the fragments produced by extracellular processing (Figure 4.2). Using ISIS [447], which predicts protein-protein interaction (PPI) sites from sequence information (bioinformatics analysis performed by Veronica Jarocki), Sa$_{\text{Ef-Tu}}$ is predicted to have ten surface-exposed PPI regions that are capable of binding macromolecules such as PGs (Table 4.4). This includes two that reside within putative HP-binding motifs ^{2}a**Ke**KfdRsKeHa^{13} and ^{73}**d**KRHyaHv^{80} . Notably, two of the three PPI residues (underlined and in bold) in the three binding sites were non-conserved residues as determined by ConSurf [446]. Putative HP-binding fragments typically displayed more putative PPI sites and were more intrinsically disordered than the parent molecule and some fragments displayed putative DNA and RNA interaction sites (Appendix C Item C.2, Table 4.4), which are absent in the unprocessed, parent molecule. Additionally, short linear motifs located in unconserved regions of Sa$_{\text{Ef-Tu}}$ that were not predicted binding sites in the parent molecule were predicted to be exposed in various fragments (Appendix C Item C.2).

Table 4.4 Number of binding sites in full length Sa$_{\mathrm{Ef\text{-}Tu}}$ and fragments of Sa$_{\mathrm{Ef\text{-}Tu}}$.

	Fragment number						
	Full length	**3**	**4**	**5**	**6**	**7**	**9**
Range (amino acid)	**1-394**	**1-266**	**1-192**	**193-394**	**104-192**	**214-394**	**214-292**
Exposed P:P	10	13	10	7	12	5	10
Buried P:P	6	12	6	5	2	5	1
DNA-binding	0	3	4	0	2	0	1

Analysis of Sa$_{\mathrm{Ef\text{-}Tu}}$ for putative protein-protein (P:P) and protein-nucleic acid interaction sites using ISIS [447]. Analysis was run and compiled by V. Jarocki. Number of sites states how many interacting amino acids are found in that fragment.

4.4 Discussion

These data show that $Sa_{Ef\text{-}Tu}$ moonlights on the cell surface of *S. aureus*, a pathogenic bacterium that belongs to the low G + C Firmicutes. These findings are also extended in the publication (see Appendix C Item C.1) to two other pathogenic low G + C firmicutes, *M. hyopneumoniae* and *M. pneumoniae*. Further, $Sa_{Ef\text{-}Tu}$ is the target of processing events on the bacterial cell surface, but the biological significance of this warrants further investigation. This data lends considerable weight to the growing perception that cellular localisation algorithms are limited in their ability to predict cellular location. Molecules are not strictly confined to compartments in the bacterial cell and can perform novel functions at different cellular locations [52,107,113,123,129,183,455]. Much remains to be learnt about how proteins, especially those lacking signal motifs, traffic across membranes.

This data sought to gain a better understanding of how Ef-Tu has evolved to be a surface exposed, processed, potential adhesin. $Sa_{Ef\text{-}Tu}$ and fragments of this protein were retained on HP-agarose. The amino acid sequence of $Sa_{Ef\text{-}Tu}$ contains the HP-binding motif XBBBXXBX (dKRHyaHv) as well as a number of other putative HP-binding motifs (Table 4.3). It is notable that while this motif is conserved in Ef-Tu from *M. pneumoniae*, *M. hyopneumoniae,* and *S. aureus* only part of the motif, with the sequence RHyaHv, is conserved in Ef-Tu from other bacterial sources (Figure 4.5). The addition of DK residues is predicted to impart a putative PPI site as predicted by ISIS [447]. Some organisms have an extra positive residue (K or R) in the middle of this region, but otherwise this region is highly conserved among species (Figure 4.5). This indicates that Ef-Tu may moonlight as a HP adhesin in other bacterial species and should be investigated for this role. Short linear motifs (SLiMs) typically ranging from three to ten amino acids play crucial roles in mediating PPIs [110,111,456]. In eukaryotes, these motifs are typically located in intrinsically unstructured, disordered regions of proteins that impart plasticity and are reported to favour transient, low affinity and reversible interactions [110,457].

Positively charged amino acids in SLiMs play a crucial role in interactions between proteins and highly sulphated glycosaminoglycans such as HP [312], actin [458], plasminogen [459], DNA [460,461] and fibronectin [428,439,462]. The analysis presented here identified SLiMs enriched in positively charged amino acids (putative HP-binding motifs listed in Table 4.3) in different regions of $\text{Sa}_{\text{Ef-Tu}}$. Further, ten surface-exposed PPI regions were identified, including two that reside within putative HP-binding motifs ^{2}a**Ke**KfdRsKeHa^{13} and ^{73}**d**KRHyaHv^{80} in the full length molecule. Overlapping SLiMs are frequently identified in multifunctional proteins [110,463]. In *M. hyopneumoniae*, the C-terminal sequence ^{1070}KKsslKvKitvK^{1081} in the multifunctional cilium adhesin, P97 binds both HP and fibronectin [439] and overlapping peptides from a region within phosphoglycerate kinase from group B streptococcus strain NCS13 with sequence ^{203}sKvsdKigvienlleKadKv^{222} and ^{213}enlleKadKvligggmtytf^{232} bind both actin and plasminogen [459]. Similarly, this data identified SLiMs enriched in positively charged amino acids from $\text{Sa}_{\text{Ef-Tu}}$. The accumulation of positively charged residues in SLiMs, possibly as a consequence of an A+T rich genome, facilitates binding to a wide range of host molecules in the low G + C Firmicutes. This data is consistent with the proposition that the accumulation of surface-exposed SLiMs represents a mechanism to generate protein multifunctionality.

S. aureus [87] and *M. hyopneumoniae* [79,314,432,433,439,441,442] display cell surface, HP-binding proteins that are important to the pathogenic potential of these species. Interactions between HP-binding proteins and target receptors in host cell membranes allow microbes to colonise different niche sites, traverse tissue barriers and disseminate from their initial point of contact and form biofilms [307]. *S. aureus* [291,293], *M. pneumoniae* [464,465] and *M.*

hyopneumoniae (our unpublished data) are all capable of forming biofilms. The extracellular matrix of *S. aureus* biofilms is derived from a mixture of eDNA and cytoplasmic proteins [239,240,293,337-340], and electrostatic interactions between cytoplasmic proteins and eDNA is thought to tether cells together in *S. aureus* and mixed-species biofilms [239]. In *S. aureus*, the addition of HP increases biofilm production in a protein-dependent manner which implies that HP-binding proteins are important for biofilm development [87]. Notably, Ef-Tu has been identified on the surface of *S. aureus* under biofilm inducing conditions [240]. These observations lend weight to the hypothesis that the accumulation of positively charged amino acids in SLiMs represents a powerful mechanism to promote PPIs that underpin essential biological processes such as the formation and maintenance of biofilms.

Bacterial pathogens including *Campylobacter jejuni* [428], *Mycoplasma gallisepticum* [440], and *C. trachomatis* [466] process molecules that are secreted to the cell surface. In *M. hyopneumoniae*, processing of cilium adhesin families has been extensively reported and cleavage motifs have been mapped [145,306,314,435]. Recently it was shown that lactate dehydrogenase is cleaved on the surface of *M. hyopneumoniae* generating fragments with multifunctional binding capabilities [86]. In *M. pneumoniae*, cleavage fragments of the major adhesin P1 and DnaK have been shown to comprise part of the cytoskeletal attachment organelle complex [467] and Mycoplasma derived lipoproteins are targets of processing events that release powerful immunomodulatory peptides [430,468-470]. These observations prompted the use of a protein dimethyl labelling strategy to investigate protein processing and from this, numerous processing sites in Ef-Tu were identified and characterised. Furthermore, surface biotinylation studies indicate that Ef-Tu is a target of multiple processing events on the surface of *S. aureus* and affinity chromatography enrichment protocols suggest that fragments derived from Ef-Tu can bind host molecules. This work indicates that the accumulation of positively charged residues in the SLiMs found in Ef-Tu facilitates binding to a wide range of host molecules and to negatively charged eDNA and that protein cleavage events expand the functional complexity of proteins that moonlight on the cell surface. This is a possible mechanism that has evolved to promote multifunctional behaviour more broadly and is well suited to the creation of novel binding sites in moonlighting proteins that must retain a strict conformational structure.

Cleavage fragments of cytosolic proteins that moonlight on the cell surface add another layer of complexity to the concept of multifunctional proteins. Processing exposes SLiMs that would otherwise be inaccessible for interactions with potential binding partners (Table 4.4). Recently, a peptidome study of a protease deficient strain of *L. lactis* identified 1800 distinct peptides fragments in spent growth medium that were derived from proteolytic activity targeting both surface accessible and cytosolically derived proteins [326]. Similar studies by the same group indicated that surface accessible proteins in other Firmicute species including *L. monocytogenes*, *E. faecalis* and *Streptococcus thermophilus* were also targeted by complex processing events [326]. It has previously been shown that processing events play an important role in the maturation of key adhesin families in pathogenic mycoplasma species [79,86,145,259,306,314,428,431-440]. This data extends these findings to show that surface proteolysis is critical in shaping the surface proteome and that processing represents a novel and under-recognised mechanism to expand protein function.

4.5 Conclusion

The phenomena of moonlighting proteins, is rapidly gaining traction in the literature, yet very few moonlighting proteins have been identified in *S. aureus*. As $\mathrm{Sa}_{\text{Ef-Tu}}$ was identified in the surface proteome analysis of *S. aureus* (outlined in Chapter 2), the aim of this chapter was to further characterize this protein. This data identified, for the first time, that $\mathrm{Sa}_{\mathrm{Ef\text{-}Tu}}$ is a surface moonlighting protein in *S. aureus*. Described in this chapter is an extensive repertoire of processed cleavage fragments of $\mathrm{Sa}_{\mathrm{Ef\text{-}Tu}}$, some of which reside on the surface of *S. aureus*. These surface exposed cleavage fragments were shown to display putative PPI sites that are inaccessible in the parent molecule, generating unprecedented functional diversity on the cell surface. HP-binding was also investigated, which indicated that $\mathrm{Sa}_{\mathrm{Ef\text{-}Tu}}$ and some of its cleavage products have the ability to bind to the host glycosaminoglycan, HP; describing a possible function for this protein in its surface location. Protein cleavage events were mapped using a systems-wide dimethyl labelling protocol that allows for the identification of modified N-terminal peptides (neo-N-termini) by liquid chromatography-tandem mass spectrometry (LC-MS/MS) and enabled us to determine how $\mathrm{Sa}_{\mathrm{Ef\text{-}Tu}}$ is processed and presented on the cell surface of *S. aureus*. Presented is a summary of novel findings of $\mathrm{Sa}_{\mathrm{Ef\text{-}Tu}}$ including; $\mathrm{Sa}_{\mathrm{Ef\text{-}Tu}}$ is displayed on the surface of *S. aureus* as both an intact molecule and as cleavage fragments, $\mathrm{Sa}_{\mathrm{Ef\text{-}Tu}}$ is highly processed into a variety of cleavage fragments that are present in the cytosol and on the surface, these cleavage fragments expose PPI sites that are buried in the parent molecule, and that $\mathrm{Sa}_{\mathrm{Ef\text{-}Tu}}$ binds to the host glycosaminoglycan, HP.

Chapter 5. General Discussion

S. aureus is a pathogenic bacterium of great public health concern. With resistant strains prevalent across the globe, there is huge financial strain caused from treating (or attempting to treat) these infections. The treatment cost more than doubles when the bacteria is resistant to antimicrobials [12]. HA-MRSA costs the European Union an extra € 380 million annually [13]. The development of an efficacious vaccine to prevent the onset of infections caused by *S. aureus* is a globally important aim because it would reduce antibiotic consumption and be a preventative measure to alleviate disease caused by this life threatening pathogen. Vaccine failure is a result of a limited understanding of the functions of approximately 50 % of the proteins encoded in the genome [165,471], a poor understanding of protein multifunctionality and an even poorer understanding of the role of post-translational modifications in altering protein function. This lack of success is, in part, not due to lack of effort though, as many vaccine targets have been identified, characterised, and trialled, although there is yet to be an efficacious vaccine on the market for *S. aureus* [195,196,210-212]. As there is still much to learn in regards to protein function, taking an ‘omics based approach should help highlight specific candidates for further functional investigations.

Alarmingly, there have even been cases of human *S. aureus* vaccine trials resulting in an increased mortality rate [472]. This occurred with the iron surface determinant B (IsaB) vaccine, which was identified for its antigenic properties in an *E. coli* surface displayed *S. aureus* peptide library [473]. This library was constructed using random fragments of *S. aureus* genomic data (up to 300bp in size) that was cloned into an expression vector with an inbuilt display platform [473]. As this method does not guarantee the expression of biologically-relevant proteins or peptides it is possible this could lead towards biologically irrelevant findings. Without the expression of intact proteins, or proteoforms native to *S. aureus*, this method was ultimately merely a genome-based expression prediction tool. Genome-centric methods are often used for vaccine development as they allow for high-throughput, in silico analysis [213]. This approach, known as reverse vaccinology, was made possible in the post-genomic era with the plethora of genomic data available for bioinformatics analysis [213]. Vaccines for a number of pathogenic bacteria have been developed this way, starting with the successful development of a Group B meningococcus (MenB) vaccine [474]. Although such approaches have been successful, they are not always fruitful. The lack of natural proteome expression and, therefore, lack of native proteoform diversity in such genomic-based models are potentially problematic. Further, bioinformatic analysis of the genome may assign proteins to their incorrect subcellular location and miss crucial surface moonlighting proteins [455]. There has also been research stating that protein antigenicity does not equate to vaccine immunogenicity (and protection), specifically in viral infections [475], however this may extend to bacterial studies as well. Genomic based prediction data also doesn’t account for antigen variability [475]. A successful vaccine must include antigens that stimulate a protective immune response and that are expressed on the surface of all the *S. aureus* variant strains circulating globally. Reverse vaccinology relies heavily on bioinformatics approaches to antigen selection, and target proteins that have canonical signal secretion motifs in their N-terminus. For these reasons, a comprehensive proteomic approach is needed to complement genomic-centric vaccine discovery. The combination of using multiple strategies (genomics and proteomics) has been suggested [476].

The **overarching aim** of this thesis was to provide further knowledge to guide the selection of novel therapeutic targets by building a better catalogue of *S. aureus* surface proteins using an empirical approach, rather than any prediction tools. This aim was accomplished by more deeply characterising the surface proteome of the bacteria (**Aim 1, Chapter 2**), which highlighted a number of novel putative therapeutic targets, proteins that were previously discarded from surface analysis due to the aforementioned issue of the protein not being found in their documented place. These global data highlight the current underestimation of cytosolic proteins that are potentially moonlighting on the surface of *S. aureus* (**Aim 1, Chapter 2**), and the potential high redundancy rate in adhesive capabilities of proteins in *S. aureus* (**Aim 2, Chapter 3**). This has resulted in the identification of a number of new potential therapeutic targets that are surface exposed, essential to *S. aureus*, and identified as putative adhesins. This includes the ancient GTPase, Ef-Tu (**Aim 3, Chapter 4**), that can and should be explored as a therapeutic target to combat this multi-drug resistant pathogen.

To determine the repertoire of surface-exposed proteins in *S. aureus*, two complementary methods were used. These involved the enzymatic shaving (trypsin shaving) of surface exposed peptides and the tagging of surface exposed primary amines with biotin (Figure 1.4). These two methods were chosen as they can each uncover different aspects regarding protein exposure and structure on the surface of *S. aureus*. Trypsin shaving was chosen as it can determine what portion of the protein is surface exposed, this is useful in therapeutic development as it is ideal to have accessible targets for the host immune system. Rather than predict exposed epitopes using genomic information, as in reverse vaccinology strategies, this resulted in experimental data indicating exposed regions. Secondly, cell surface biotinylation was used allowing intact biotinylated surface proteins to be purified using avidin chromatography. The power of this approach lies in its ability to recover proteoforms that cannot be detected reliably by enzymatic shaving (shotgun) protocols. This biotinylation data highlighted the presence of cleavage fragments on the cell surface of *S. aureus*. Given this novel finding, extensive analysis of these proteoforms was undertaken with whole cell lysates using gel-based approaches. By analysing these proteins by gel electrophoresis, not only is sample complexity reduced, but mass context is also maintained. Therefore there is a greater chance of identifying lower abundance proteins, and mass of the mature proteoforms can be estimated, allowing for the visualisation of native proteolytic processing.

The ability to maintain mass context allowed the precise mapping of cleavage events within various proteins of interest. This is the first investigation into global cleavage events in *S. aureus*, although for this thesis and in the interest of brevity, only data from proteins of interest were shown. These datasets prompted our laboratory group (S. Djordjevic, M. Padula, I. Berry, J. Steele, and N. Strange) to develop more comprehensive, systems-wide methods to map neo-N-termini in order to identify the scale of protein processing in *S. aureus*. These data suggest that protein processing is a wide-reaching phenomenon first studied in detail in the porcine pathogen *M. hyopneumoniae* [86,477]. Here we have extended these studies to investigate the *S. aureus* proteome. The hypothesis presented from the Djordjevic laboratory is that processing is a novel mechanism by which to increase proteome complexity [86]. Novel data presented here extends this concept to other members of the low G + C Firmicutes, specifically the globally important pathogen *S. aureus*. Previous publications have reported abnormal *S. aureus* protein migration in gels (below predicted MW), but this has never been further investigated [151]. Importantly, studies in our laboratory have shown that a little over 10 % of the predicted proteome was found to have neo-N-termini present in this analysis (excluding N-termini labelled after N-term methionine removal or any known removal of signal peptides). Improving knowledge of the mature proteoforms is important as these cleavage events are not predicted by the ORFs and would otherwise remain unrecognised. Consequently the number of functional polypeptide chains generated from a single ORF in biological systems may be significantly underestimated. This concept is further expanded when one considers that different proteoforms may fold revealing different regions of the molecule, exposing previously buried SLiMs. SLiMs represent a novel mechanism to increase or modify protein function without significantly affecting the canonical 3-D structure of the protein. Post-translational modifications via the addition or subtraction of chemical modifications (acetylation, phosphorylation, methylation, etc) add another dimension to the functional proteome that is yet to be fully explored [140]. As such, we have only a limited understanding of protein function and this knowledge gap plays a large part in our failure to develop efficacious vaccines for many clinically-important pathogens. There are multiple functionally-important regions within molecules. Some of these are critical for adherence while others may be deleterious for inclusion in vaccine formulations because they simulate an inappropriate immune response. By understanding how proteins are processed we are likely to garner important clues pertaining to novel protein function and include only the regions of molecules that are critical to evoking a protective and serologically diverse immune response in vaccine formulations. Furthermore, this leads to a better understanding of the complexity of *S. aureus* proteoforms and the potential in the proteome, which cannot be predicted by the genome.

The surface proteome analysis by these complementary methods resulted in the reproducible identification of 787 proteins (Table 2.1). This is, by far, the largest number of proteins identified to be on the surface of *S. aureus* compared to previously published research in this field (Table 1.1). This increase in identification is due to the inclusion of complementary methodologies, and importantly, confidence in the inclusion of annotated cytosolic proteins. However, it is likely that there is potential to identify many more proteins on the surface given the dynamic properties of any proteome. Future surface proteome research should include time-course experiments, growth media variations (including host cells or host mimicking environments), and the inclusion of other strains including of clinical isolates. As the proteome is highly variable in *S. aureus* [173,181], it would be extremely beneficial to determine the core set of surface proteins for this pathogen.

Of the total proteins identified, 536 (68 %) lacked leader sequences and were predicted bioinformatically to reside in the cytosol [180]. Bioinformatic prediction tools would not select these antigens as candidates for vaccine or therapeutic development and these are likely to be removed from a reverse vaccinology pipeline based on the premise that they are predicted to be inaccessible to antibodies and to the host immune response. Therefore, most surface proteome studies remove these proteins from their criteria of targets for further analysis, potentially ruling out a major subset of potentially important targets. However, predicted cytosolic proteins such as GAPDH have been used as therapeutic targets, and this protein has become a suggested target for a wide range of organisms [133]. This trend could follow with proteins highlighted in this thesis, such as the ribosomal proteins which were identified to be processed and bound to HP with high affinity (1+ M NaCl). This novel role for ribosomal proteins in *S. aureus* should be further investigated as their extraribosomal function may relate to pathogenesis. These proteins may be relevant to study for therapeutic target and ribosomal proteins have shown efficacy in other organisms [478].

The execution of cell surface analysis in *S. aureus* shown in this dissertation has identified areas of improvement to the current methodologies, namely the reduction of incubation times needed to conduct surface proteome analyses. Upon the initial experiment of incubating the cells in trypsin for 30 min, it was realised that this incubation period is rather long in the context of the bacterial lifecycle and metabolism. Moreover, these incubations are usually carried out in a mild buffer that lacks any nutrients for the cell, leading to cell stress. With the added concern of minimalizing cell lysis during trypsin incubation, a stringent trypsin shaving protocol was employed of only 1 min. Quicker incubation periods have previously been used to characterise the surface proteome of genome-reduced, delicate, cell wall-less pathogens belonging to the class *Mollicutes* [259]. However, *S. aureus* is known to have a robust cell and is therefore, usually exposed to longer incubation periods. Reduced incubation periods were also tested on the cell surface biotinylation procedure which was eventually reduced to 1 min. Using this abbreviated incubation time; a record number of proteins were identified. Therefore, these results recommend a reduction in incubation periods for all bacterial cell surface proteomics in the future.

As this data identified a number of putative surface moonlighting proteins, these proteins can now be investigated experimentally in a more rigorous manner. Many of these proteins have been identified in earlier studies, however they were relegated to supplementary files and were not discussed as potential therapeutic targets [124-127]. It is possible that a bias towards cytosolic protein identification in this study is due to the growth time-point used (early stationary phase). Cytosolic proteins being secreted to extracellular space has been observed during this growth phase in previous studies [479]. Although many cytosolic proteins were found reproducibly across two orthogonal methodological approaches, the identification relied on the samples being loaded onto the LC-MS/MS system being perfectly prepared. LC-MS/MS in itself does not hold any discriminatory power to delegate proteins to locations, therefore the preparation methods (biotinylation and enzymatic shaving) are relied on for this localisation information. For this reason, labelled microscopy approaches such as fluorescence microscopy and immunogold electron microscopy are suitable future steps for validating the cell surface location of these proteins. It would also be advantageous to assess protein localisation using live-cell imaging, with the potential to track protein localisation throughout the growth phases. This however requires each protein to be expressed as a recombinant antigen and the development of antigen-specific antiserum, or each protein to be expressed as a fluorescent protein, which is time consuming and costly. Although, as these are necessary steps for vaccine target validation, they warrant future experimental work. Further, antisera can be used to examine bactericidal properties or effects of the antibodies as shown in Chapter 2 with DnaK antiserum. These antibodies were able to promote the aggregation of *S. aureus* cells presumably by cross-linking DnaK molecules on the cell surface of different *S. aureus* cells. With high-resolution microscopy, physical expression patterns of these proteins on the surface could be monitored. Such techniques have shown that other (potential and proven) surface moonlighting proteins of *S. aureus* (aldolase and enolase, respectively) locate to the septal cleft and cross wall of dividing cells (see Figure 5.1) [129]. This location may also allow for their release into the surrounding areas once the cell has divided [129]. Hence such techniques may further our understanding of non-classical protein secretion.

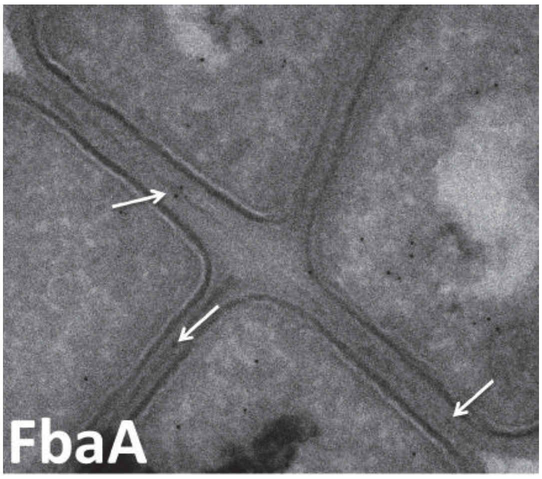

Figure 5.1 Immunogold labelling of *S. aureus* FbaA (aldolase) and detection by transmission electron microscopy (TEM).

Figure taken from Ebner, et al. 2015 [129] showing the localisation of Immunogold labelled aldolase (FbaA) with detection by transmission electron microscopy (TEM). Thin sections showing the centre of cross wall sections of tetrad cells with white arrows showing aldolase in the septal cleft location.

A large number (177) of these annotated cytosolic proteins were identified to be products of genes deemed as essential in *S. aureus* SH1000 (Table 2.1) [223], providing further evidence for them to be studied as potential therapeutic targets. The function of each of these proteins needs to be further investigated as their role on the surface of the bacteria remains unknown, and the proteins may not hold this essential role on the surface. However, this indicates that different strains of *S. aureus* are most likely to express these proteins but we can only assume, at this time, that these different stains also promote the same geographical moonlighting function on the cell surface. While this is not an unreasonable assumption, experimental evidence would be needed to confirm that vaccine candidates discovered in one strain of *S. aureus* are also found to moonlight on the cell surface of phylogenetically and serologically diverse strains of *S. aureus*. One protein of interest identified in this study, DnaK (also referred to as Chaperone protein DnaK, or HSP70), has been identified as a moonlighting protein that can traffic to the cell surface in other bacterial species [275-284]. Many moonlighting proteins are highly conserved, ancient proteins [44,116], a number of which have been shown to be chaperone proteins [113]. DnaK shares significant homology with human heat shock protein 70 (HSP70) and this homology should be taken into account in therapeutic development. As a vaccine antigen used to protect against *S. aureus*, it would be necessary to eliminate immunogenic motifs that are shared with the human DnaK molecule (HSP70) otherwise there may be an issue with stimulating an autoimmune response. The way certain proteins are presented on the bacterial cell surface (partly exposed or cleaved) also needs to be taken into account for therapeutic development. Herein lies another advantage of using the two complementary methods for surface analyses, trypsin shaving is able to deduce (to a certain extent) what portion of the protein is exposed, while biotinylation reveals exposed cleavage products. As DnaK appears to be presented on the surface as both the full length molecule, and as fragments, it may be more beneficial to elicit an immune response against only one part of the target protein that is exposed. As polyclonal antibodies were used in the experiments that disrupted normal cellular phenotypes, further work is needed to determine regions of DnaK that can be targeted effectively. A better understanding of how proteins are processed may lead to the development of monoclonal antibody therapies against selected antigens, a procedure that is considered safe and with great potential as a last resort therapy.

DnaK was also identified as a putative HP-binding protein (Chapter 3). This interaction was disrupted using NaCl at more than three times the natural physiological concentration (DnaK was eluted from the column by 0.5-1 M NaCl). The data presented in Chapter 3 represents a pool of *S. aureus* proteins with potential adhesin properties that are now candidates for further study. *S. aureus* is already known to interact with HP in the host, and the addition of HP, or removal of HP from host cells, has been shown to reduce infection levels [80,90]. The data shown here presents a number of proteins that may be responsible for this interaction. Quantitative binding between DnaK and HP (and other host GAGs) should be further investigated using microscale thermophoresis, surface plasmon resonance or thermal calorimetry. The impact of these findings on pathogenesis should also be studied in the future, determining whether blocking these proteins of interest can inhibit *S. aureus* cellular attachment and invasion of host cells. Undertaking further experiments in environments that better mimic the host will help narrow down the potential adhesin list shown here to the true adhesins. Determining the extent of surface protein's roles in host invasion and analysing the pathways involved are critical next steps to guide this data towards the suitable selection of therapeutic targets. The direct interaction needs to be analysed, as these experiments were run under native conditions, therefore DnaK may have been bound as part of a protein complex (and other members of the complex may have a strong interaction with HP). Other classically cytosolic, essential proteins identified on the surface also bound HP, including a number of ribosomal proteins found binding with high affinity (Table 3.1). Such proteins may have been identified due to their ancient DNA-binding properties [351], as HP columns are also used to mimic DNA (due to common negative charge) [89,309,480]. Multiple ribosomal proteins were retained on HP-agarose under high salt conditions (only eluted in 1+ M NaCl) indicating their potential as GAG, or DNA interactors. Interactions between moonlighting proteins that have a positive charge (or a region of positively charged amino acids), and negatively charged GAGs may be biologically significant as bacteria colonise the host by first attaching to cells via their surface displayed GAGs (among other receptors) [80,81,481], and cellular interaction with eDNA (also negatively charged) is crucial in biofilm development [239,342,343]. This is the first global approach to studying adhesins in *S. aureus*. As previous studies focused on specific adhesins, the functional redundancy *S. aureus* harbours was not fully appreciated. If these proteins are truly surface exposed, and have the ability to bind HP directly, this means that *S. aureus* has an extensive arsenal of adhesive proteins that were not previously identified. Such functional redundancy has previously been shown in *S. aureus* in regards to a protein's adhesive functions [58,64,315-317]. These data presented indicate that this functional redundancy may extend to *S. aureus's* GAG-binding ability. This knowledge is vital in the future development of anti-adhesive strategies as redundancy appears to have been underestimated, as it is still poorly understood. These data further support the recommendation for a multivalent vaccine strategy against this pathogen as simply blocking one adhesive protein may not confer protection.

Classically cytosolic moonlighting proteins have been targeted for vaccine strategies in bacteria [133], and this data presents a number of novel potential surface moonlighters that should be further explored in *S. aureus*. One protein of particular interest was Ef-Tu. Targeting Ef-Tu, or blocking its host targets has been shown to effectively reduce binding in other pathogens. The canonical function of Ef-Tu (in the cytosol) is not responsible for binding, therefore these studies show that blocking the surface moonlighting function can be advantageous to therapeutic development. Anti-Ef-Tu antibodies are able to prevent the binding of *M. pneumoniae* to immobilized Fn [355]. *F. tularensis* is an intracellular pathogen that displays Ef-Tu on its surface which it employs to bind to cell-surface accessible nucleolin on THP-1 cells [383]. The overall binding potential of *F. tularensis* was reduced when nucleolin was modified, interfering with the interaction between nucleolin and Ef-Tu [383]. In mice challenged with *B. thailandensis*, mucosal immunisation with Ef-Tu effectively reduced the lung bacterial burden [394]. However, as Ef-Tu has a known homologue in humans, (e)EF-1α (of which two isoforms exist: eEF-1α1 eEF-1α2) [367,370], it is important to target regions of the protein that are not shared with the human homologue.

Ef-Tu was found in 50 protein spots from 2D-PAGE analysis of *S. aureus* WCL (Appendix C Figure C.2). This extreme example of processing was unusual and has not previously been investigated in *S. aureus*. It is possible that the extent of this processing identified in Ef-Tu compared to the rest of the expressed proteins was biased due to the high expression level of Ef-Tu [354,355] allowing for easier identification of its cleavage fragments. However, this finding, and the evidence of processing in other molecules presented here should encourage future research into the processing of all molecules in *S. aureus*. On further investigation Ef-Tu was also found to be surface exposed (as the full-length protein, and cleaved fragments), and this protein (the full-length, and cleaved fragments) were retained in the HP affinity chromatography columns. This protein was one of only 66 that were retained on the column above 1 M NaCl concentrations (Table B.1 in Appendix B), indicating a potentially high affinity for HP. The specific cleavage events that occurred were shown to unveil potential protein binding sites that are hidden in the full length molecule (Table 4.4). These data suggest, for the first time, that Ef-Tu is the most processed protein in broth cultured *S. aureus,* and may moonlight on the surface of the bacteria as a novel adhesin. The review that forms part of Chapter 4 (to be submitted) discovered that this protein has a plethora of moonlighting functions across a range of genetically diverse prokaryotes. Hence, it appears that functional plasticity is a trend in Ef-Tu from many organisms.

The common theme throughout this dissertation is an underestimation of protein geographical promiscuity and functional redundancy in the prediction databases. Often, these proteins documented in databases as cytosolic are excluded from the published or analysed surface proteome results because many researchers believe these proteins to be an experimental artefact. With the increasing number of surface proteome (and secretome) analyses published, the emerging trend of geographically promiscuous 'cytosolic' proteins [113] has expanded the number of studies investigating this phenomenon. The presence of classically cytosolic proteins on the surface raises major questions; without a known signal secretion motif, how do moonlighting proteins locate extracellularly and how do moonlighting functions evolve?

A number of potential mechanisms and hypotheses have now been put forward regarding the presence of classically cytosolic proteins on the surface of bacteria. These include explosive cell lysis [179], membrane vesicle production [267], involvement of autolysin [183], and protein translocation via known pathways such as the Tat [153] or Sec pathways [129], or unknown pathways (Figure 2.15). As discussed in Chapter 2, cell lysis during the experimental procedure was often blamed for classically cytosolic proteins locating to the bacterial surface (or in the growth media). These possibilities were recently reviewed for *S. aureus* [182]. Ebner concluded that cell lysis was not the contributing factor to the excretion of cytoplasmic proteins (ECP). Further, this research claimed that the variation in proteins presented on the surface and in the secretome indicate that selectivity is an inherent feature of the protein export process

[129], a theory that has also been supported by Pasztor et al. [183]. The lack of variation within replicates in the data shown in the previous chapters also indicates this is unlikely a random event. Selectivity is implied as the protein fragments identified on the surface differ to those found in the cytosol, and this was found to be true for Ef-Tu (see Figure 4.2). This specified selectivity of exported cytosolic proteins, as well as the data presented here for the moonlighting capabilities of classically cytosolic proteins such as Ef-Tu implies that this export system selects proteins for their functionality to utilise the moonlighting function on the surface of the bacterium.

How does multifunctionality in proteins evolve? One common evolutionary pattern that has been observed is the duplication of genes to establish moonlighting roles [482]. Many enteric bacteria have two copies of the *tuf* gene encoding Ef-Tu (*tufA* and *tufB*), while three *tuf*-like genes have been identified in *S. ramocissimus* [365,366]. The ability of Ef-Tu to interact with *mreB* and impact cytoskeletal integrity [402,403], may have evolved due to gene duplication. This hypothesis is raised as only *tufB* has been shown to interact with *MreB* (not *tufA*) [404]. However, low G + C Gram positive bacteria carry only a single copy of the *tuf* gene [364], so for this group of bacteria including *S. aureus*, other factors must be responsible for moonlighting roles. As *S. aureus* has a small genome, limiting the genetic space available [164], is it more feasible that specific evolutionary mutations have occurred in the ORF, allowing the protein product multifunctional properties without sacrificing its canonical function. As many moonlighting proteins are metabolic enzymes [44,107,112,113], their 3D structure is vital to their function, as such, many mutations could render such proteins non-functional. Over millions of years, bacteria have acquired mutations in non-essential (usually non-conserved) regions of proteins allowing for the accumulation of SLiMs (as demonstrated in Chapter 4 with Ef-Tu) [52,110] . By simply changing a small number of amino acids, proteins may acquire the ability to interact with new molecules [111]. Specifically, in Ef-Tu (as shown in Chapter 4), positive amino acids are clustered in non-conserved regions of the protein allowing for HP-binding (and potentially other adhesive properties).

Further complexity can be added to a small genome via PTMs. The role of PTMs in bacterial host-pathogen interactions has previously been reviewed [186]. Although PTMs in *S. aureus* have been identified, their role in pathogenesis remains largely unclear [143]. However, some PTMs have now been linked to pathogenesis. For example, the phosphorylation of cysteine residues in staphylococcal accessary regulator A (SarA) and MarR family global transcriptional regulator A (MgrA) family of proteins has been shown to be crucial in regulating virulence factors and resistance to vancomycin [141]. The PTM this thesis focused on was proteolysis, which has also been noted to add complexity to the expressed proteome [477]. Some single gene products undergo proteolysis in order to become multiple mature, functional proteins (present as subunits) [483]. Many potential moonlighting proteins have been identified in these chapters to undergo proteolysis. However, the current definition of moonlighting does not include proteins that have undergone proteolysis to obtain their secondary function [484]. Any protein that undergoes proteolysis to gain another function is simply "multifunctional" (Figure 1.1). As it now appears that functional promiscuity and proteolysis go hand in hand and is widespread in the *S. aureus* proteome, there may need to be a shift in the definition of moonlighting to include proteins having undergone proteolysis. As shown in this thesis, *S. aureus* processes a wide variety of proteins. By cleaving the polypeptide chain, multiple SLiMs with bias for positive residues, or containing specific motifs may be released and this may contribute to mechanisms of pathogenesis. These smaller fragments may have "sticky" properties based on their amino acid constituents (positive residues having electrostatic interactions with negatively charged molecules such as HP and eDNA), rather than any tertiary structure (which may now be lost). Further, these cleavage events can expose putative PPI residues that were previously buried in the tertiary structure of the protein (see Table 4.4). As the tertiary structure is important to a protein's role, it is also tempting to hypothesise that proteins may refold in response to cleavage (Figure 1.1). Indeed, if flexible regions of the protein such as disordered regions and loops are isolated by cleavage, this can allow for structural adaptation and ultimately, functional variety [482,485-488]. With the extent of protein cleavage identified in *S. aureus* throughout the data presented, it is likely that *S. aureus* utilises this to expand proteome complexity within the restrictions of a small genome.

Taken together, these data show the overwhelming underestimation in the complexity of the *S. aureus* functional proteome. This dissertation indicates that proteins in *S. aureus* have been underestimated in regards to their geographical promiscuity and functional redundancy, and as Hernandez et al. (2014) states, our current knowledge of moonlighting proteins is only the "tip of the iceberg" [489].

5.1 Concluding remarks

This thesis presents data covering an extensive, global investigation into the surface proteome of *S. aureus*. This data is the first to support a dramatic reduction in incubation time for surface analyses in *S. aureus* (and other prokaryotes). The large number of cytosolic proteins that have repetitively been found on the surface of *S. aureus* should be further investigated as they may play a biological role as a moonlighting protein in that location. Such roles could include adhesion to host cells, as many classically cytosolic proteins were identified in this first global study of putative HP-binding proteins in *S. aureus*. As this pathogen is of high concern in both the nosocomial and greater community, this study is the first step towards better understanding the adhesion strategies of this pathogen on a global scale. This global approach allows for the recognition of the functional redundancy *S. aureus* holds in its adhesive proteins, a feature that is still underappreciated, especially in regards to therapeutic development. Further, this thesis presents data regarding a potential novel moonlighting protein, Ef-Tu. This protein is highly conserved in prokaryotes and has a plethora of moonlighting functions in other species. Most interestingly though, was the identified extensive cleavage that this protein undergoes in *S. aureus*. The data gathered is part of the first global study into cleavage in *S. aureus*, and shows that Ef-Tu is the most highly processed protein in *S. aureus*.

The data presented shows that the functional proteome of *S. aureus* is much more complex than originally thought. It now appears that *S. aureus* may possess a large number of surface moonlighting proteins and redundant surface adhesins, many of which are cleaved. This complexity is a primary reason as to why previous vaccine strategies may have failed. All these data will help guide future therapeutic attempts and aid in designing more effective vaccines against this problematic pathogen

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Appendix A

Extra information relating to Chapter 2

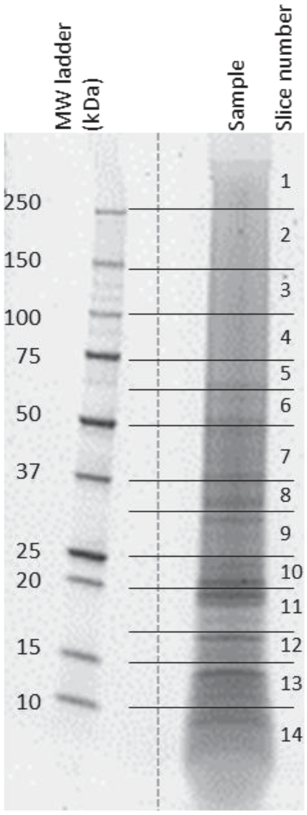

Figure A.1 Image of 1D-SDS-PAGE gel showing slice ranges for biotinylated samples analysed. Gel has been cropped to remove empty lanes and has been re-joined along the dotted line.

Table A.1 Live-Dead staining counts (including pre incubation and 2hr biotin incubation counts).

Experiment	Number of images counted	Number of replicates included	Total cells Live	Total cells Dead	% dead	Total cells counted
30min shave	10	3	1995	5	0.251	2000
1min shave	5	2	1160	5	0.431	1165
1min Biotin	9	2	3262	31	0.950	3293
2hr Biotin	3	1	1145	9	0.786	1154
Pre-incubation	15	4	2081	10	0.481	2091

Table A.2 List of proteins identified in 1D-SDS-PAGE gels from biotinylation experiments with slice number shown.

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195952	acetolactate synthase large subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	34	64450	13	0	11	0	27.5	1	2
88195952	acetolactate synthase large subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	36	64450	12	1	9	1	11.5	1	3
88195057	catalase [Staphylococcus aureus subsp. aureus NCTC 8325]	284	54908	16	8	14	7	23.9	1	3
88196503	cation transporter E1-E2 family ATPase [Staphylococcus aureus subsp. aureus NCTC 8325]	56	86690	16	1	15	1	14.1	1	2
88195392	coproporphyrinogen III oxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	37	42814	7	1	7	1	24.1	1	2
88194305	DNA-directed RNA polymerase subunit beta~ [Staphylococcus aureus subsp. aureus NCTC 8325]	355	134190	62	13	58	13	36.1	1	3
88196012	F0F1 ATP synthase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	65	6975	5	1	4	1	44.3	1	2
88196012	F0F1 ATP synthase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	42	6975	2	1	2	1	11.4	1	3
88196443	gluconate operon transcriptional repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	38	26578	6	2	5	1	11.9	1	1
88196443	gluconate operon transcriptional repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	36	26578	12	1	8	1	23.5	1	3
88193973	HsdR family type I site-specific deoxyribonuclease [Staphylococcus aureus subsp. aureus NCTC 8325]	30	109159	15	0	15	0	12.2	1	3
88193846	hypothetical protein SAOUHSC_00025 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	83373	23	1	21	1	26	1	3
88194064	hypothetical protein SAOUHSC_00258 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	114754	27	1	26	1	25	1	3
88194356	hypothetical protein SAOUHSC_00582 [Staphylococcus aureus subsp. aureus NCTC 8325]	60	15788	5	1	4	1	26.1	1	3
88194632	hypothetical protein SAOUHSC_00875 [Staphylococcus aureus subsp. aureus NCTC 8325]	45	39374	6	1	6	1	16.4	1	3
88194635	hypothetical protein SAOUHSC_00878 [Staphylococcus aureus subsp. aureus NCTC 8325]	129	44077	13	5	11	4	19.4	1	3
88196096	hypothetical protein SAOUHSC_02443 [Staphylococcus aureus subsp. aureus NCTC 8325]	41	20787	3	1	3	1	14	1	2
88196497	hypothetical protein SAOUHSC_02866 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	90352	21	1	18	1	13.3	1	3
88196108	lactose phosphotransferase system repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	39	29869	3	1	2	1	5.3	1	3
88196053	lytic regulatory protein [Staphylococcus aureus subsp. aureus NCTC 8325]	19	40640	7	0	7	0	18.7	1	2
88196193	molybdenum ABC transporter permease [Staphylococcus aureus subsp. aureus NCTC 8325]	47	24847	3	1	3	1	13.9	1	1
88196193	molybdenum ABC transporter permease [Staphylococcus aureus subsp. aureus NCTC 8325]	53	24847	4	2	3	1	10.3	1	2

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88196193	molybdenum ABC transporter permease [Staphylococcus aureus subsp. aureus NCTC 8325]	48	24847	7	1	7	1	22	1	3
88195871	phage terminase large subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	37	65249	15	1	15	1	23.6	1	2
88195922	phage terminase small subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	37	22208	4	1	2	1	4.6	1	1
88195112	phosphate transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	43	32134	2	1	2	1	7.8	1	1
88195112	phosphate transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	47	32134	7	1	7	1	17.7	1	3
88193970	PTS system transporter [Staphylococcus aureus subsp. aureus NCTC 8325]	45	50632	4	1	4	1	9.5	1	2
88194851	succinate dehydrogenase iron-sulfur subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	76	30563	12	1	11	1	31	1	3
88194954	succinyl-CoA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	180	31522	14	4	11	3	30.5	1	3
88194557	triosephosphate isomerase [Staphylococcus aureus subsp. aureus NCTC 8325]	112	27275	12	3	9	3	33.6	1	3
88194889	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	24	49813	5	0	4	0	11.6	1	1
88194889	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	38	49813	4	1	2	1	3.8	1	2
88194889	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	39	49813	9	1	7	1	12.2	1	3
88196249	urocanate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	61	60595	11	1	9	1	11.8	1	3
88195507	6-phosphofructokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	120	33376	15	3	14	3	40.7	2	3
88195682	ABC transporter permease [Staphylococcus aureus subsp. aureus NCTC 8325]	40	53089	19	1	16	1	24.1	2	3
88195952	acetolactate synthase large subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	34	64450	3	1	3	1	4.1	2	1
88195509	acetyl-CoA carboxylase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	49	31851	6	1	6	1	24.2	2	3
88195075	aconitate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	373	98908	33	14	29	14	28.3	2	3
88194939	acyl carrier protein [Staphylococcus aureus subsp. aureus NCTC 8325]	136	8544	10	5	9	4	50.6	2	3
88195971	alanine racemase [Staphylococcus aureus subsp. aureus NCTC 8325]	44	42796	13	1	13	1	24.6	2	3
88195799	aspartyl/glutamyl-tRNA amidotransferase subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	145	52788	15	3	15	3	33.4	2	3
88195441	aspartyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	64	66587	14	1	13	1	16.8	2	3
88195804	ATP-dependent DNA helicase PcrA [Staphylococcus aureus subsp. aureus NCTC 8325]	30	84021	10	0	10	0	11.8	2	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88194139	bifunctional homocysteine S-methyltransferase/5,10-methylenetetrahydrofolate reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	31	68436	17	1	16	1	23.2	2	2
88194139	bifunctional homocysteine S-methyltransferase/5,10-methylenetetrahydrofolate reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	37	68436	25	2	23	1	26.1	2	3
88194909	carbamoyl phosphate synthase large subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	32	117112	12	0	9	0	10.2	2	1
88194909	carbamoyl phosphate synthase large subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	152	117112	30	6	28	6	22.1	2	3
88194907	dihydroorotase [Staphylococcus aureus subsp. aureus NCTC 8325]	113	46342	12	3	10	3	21.2	2	3
161353532	DNA-directed RNA polymerase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	263	133136	42	11	36	11	27.1	2	3
88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	865	76564	61	29	42	18	46.2	2	3
88194541	excinuclease ABC subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	33	105303	22	0	18	0	11.9	2	3
88194652	glutamate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	196	45731	20	4	16	4	33.6	2	3
88195373	glycyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	301	53586	29	16	20	12	34.6	2	3
88194145	GTP-dependent nucleic acid-binding protein EngD [Staphylococcus aureus subsp. aureus NCTC 8325]	60	40570	6	2	6	2	12.6	2	3
88194331	hypothetical protein SAOUHSC_00552 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	28449	7	1	7	1	24.6	2	2
88194787	hypothetical protein SAOUHSC_01035 [Staphylococcus aureus subsp. aureus NCTC 8325]	186	62630	20	5	20	5	22.8	2	3
88195092	hypothetical protein SAOUHSC_01365 [Staphylococcus aureus subsp. aureus NCTC 8325]	79	37832	13	1	13	1	31.8	2	3
88195339	hypothetical protein SAOUHSC_01629 [Staphylococcus aureus subsp. aureus NCTC 8325]	35	31861	5	1	5	1	12.3	2	3
88195542	hypothetical protein SAOUHSC_01843 [Staphylococcus aureus subsp. aureus NCTC 8325]	43	100886	22	2	18	2	13.9	2	3
88195586	hypothetical protein SAOUHSC_01890 [Staphylococcus aureus subsp. aureus NCTC 8325]	70	57541	9	2	8	1	12	2	3
88196250	hypothetical protein SAOUHSC_02608 [Staphylococcus aureus subsp. aureus NCTC 8325]	51	34996	5	1	5	1	12.2	2	2
88194742	naphthoate synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	67	30406	7	1	7	1	18.7	2	3
88194237	Orn/Lys/Arg decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	39	50989	6	1	6	1	9.2	2	2
88195922	phage terminase small subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	37	22208	5	1	5	1	14.8	2	2
88195605	phosphoenolpyruvate carboxykinase [Staphylococcus aureus subsp. aureus NCTC 8325]	195	59340	23	6	22	6	29.8	2	3
88194767	phosphoribosylformylglycinamidine synthase II [Staphylococcus aureus subsp. aureus NCTC 8325]	276	79486	26	10	23	9	25.4	2	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88194984	polynucleotide phosphorylase/polyadenylase [Staphylococcus aureus subsp. aureus NCTC 8325]	70	77314	23	2	18	2	23.4	2	3
88195336	proline dipeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	80	39313	13	3	11	3	26.6	2	3
88194813	pyruvate carboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	118	128467	19	2	18	1	12.5	2	2
88194259	ribose-phosphate pyrophosphokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	94	35262	10	5	10	5	22.7	2	3
88195604	S-adenosylmethionine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	58	43614	11	1	10	1	19.4	2	3
88194516	UDP-N-acetylenolpyruvoylglucosamine reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	51	33776	7	1	6	1	14.7	2	3
88196016	uracil phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	69	23035	4	2	4	2	22.5	2	3
88195143	2-oxoglutarate dehydrogenase E1 component [Staphylococcus aureus subsp. aureus NCTC 8325]	363	105277	45	17	38	15	29.8	3	2
88194678	3-oxoacyl- synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	29	43712	2	0	2	0	5.6	3	1
88195359	50S ribosomal protein L33 [Staphylococcus aureus subsp. aureus NCTC 8325]	35	5869	3	1	2	1	28.6	3	3
88195682	ABC transporter permease [Staphylococcus aureus subsp. aureus NCTC 8325]	40	53089	17	1	15	1	24.3	3	2
88195935	accessory gene regulator protein A [Staphylococcus aureus subsp. aureus NCTC 8325]	104	24238	7	3	5	3	20.7	3	3
88195075	aconitate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	1044	98908	73	36	57	29	42.2	3	2
88193840	adenylosuccinate synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	105	47549	16	5	16	5	27.6	3	3
88195427	alanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74	98459	33	3	32	3	24.9	3	2
88195822	aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	59	51709	9	1	7	1	16.3	3	2
88194909	carbamoyl phosphate synthase large subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	280	117112	40	12	36	11	28	3	2
88194908	carbamoyl phosphate synthase small subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	39	40369	10	1	8	1	16.1	3	3
88194891	cell division protein [Staphylococcus aureus subsp. aureus NCTC 8325]	89	52902	11	3	11	3	19.4	3	3
88194626	D-alanine--poly(phosphoribitol) ligase subunit 1 [Staphylococcus aureus subsp. aureus NCTC 8325]	41	54636	16	1	15	1	24.1	3	3
88195984	D-alanyl-alanine synthetase A [Staphylococcus aureus subsp. aureus NCTC 8325]	42	40205	7	1	7	1	13.8	3	3
88194274	dihydropteroate synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	44	29504	3	1	3	1	9.4	3	3
88195565	dipeptidase PepV [Staphylococcus aureus subsp. aureus NCTC 8325]	79	52791	11	2	9	2	17.3	3	2

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88193829	DNA gyrase subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	327	99290	45	15	39	13	30.2	3	2
88193829	DNA gyrase subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	207	99290	33	12	30	10	25.1	3	3
88194305	DNA-directed RNA polymerase subunit beta~ [Staphylococcus aureus subsp. aureus NCTC 8325]	195	134190	19	8	19	8	14.4	3	1
88194305	DNA-directed RNA polymerase subunit beta~ [Staphylococcus aureus subsp. aureus NCTC 8325]	673	134190	76	28	61	26	39.6	3	2
88194541	excinuclease ABC subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	44	105303	25	0	25	0	20.8	3	2
88194226	glutamate synthase large subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	36	166244	33	1	33	1	20.5	3	2
88193869	hypothetical protein SAOUHSC_00049 [Staphylococcus aureus subsp. aureus NCTC 8325]	32	121654	19	1	18	1	16.2	3	2
88193895	hypothetical protein SAOUHSC_00080 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	71906	10	1	9	1	11.4	3	2
88194007	hypothetical protein SAOUHSC_00197 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	44701	6	1	6	1	16.6	3	2
88194609	hypothetical protein SAOUHSC_00851 [Staphylococcus aureus subsp. aureus NCTC 8325]	241	52498	16	6	15	5	23.7	3	3
88194746	hypothetical protein SAOUHSC_00989 [Staphylococcus aureus subsp. aureus NCTC 8325]	32	43163	4	1	3	1	9.9	3	2
88194926	hypothetical protein SAOUHSC_01187 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	74317	12	1	12	1	11.6	3	2
88195215	hypothetical protein SAOUHSC_01499 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	36713	12	0	12	0	25	3	3
88195555	hypothetical protein SAOUHSC_01857 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	144568	29	1	28	1	19.2	3	2
88195559	hypothetical protein SAOUHSC_01861 [Staphylococcus aureus subsp. aureus NCTC 8325]	55	39758	7	1	7	1	18.7	3	3
88195586	hypothetical protein SAOUHSC_01890 [Staphylococcus aureus subsp. aureus NCTC 8325]	63	57541	18	2	16	1	20.4	3	2
88195592	hypothetical protein SAOUHSC_01897 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	19141	6	1	6	1	25	3	3
88195666	hypothetical protein SAOUHSC_01975 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	46196	8	1	8	1	14.3	3	3
88196246	hypothetical protein SAOUHSC_02604 [Staphylococcus aureus subsp. aureus NCTC 8325]	74	31715	6	2	6	2	15.4	3	3
88196391	hypothetical protein SAOUHSC_02755 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	39168	6	0	6	0	12.3	3	3
88196609	hypothetical protein SAOUHSC_02990 [Staphylococcus aureus subsp. aureus NCTC 8325]	124	227909	16	1	16	1	8.3	3	2
542123273	hypothetical protein SAOUHSC_1307a [Staphylococcus aureus subsp. aureus NCTC 8325]	32	7495	2	1	2	1	24.6	3	1
88196248	imidazolonepropionase [Staphylococcus aureus subsp. aureus NCTC 8325]	24	45011	8	0	6	0	13.3	3	2

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88194899	isoleucyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	102	104820	30	3	26	3	21.7	3	2
88194899	isoleucyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	90	104820	35	4	31	4	24.1	3	3
88195572	leucyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	135	91728	31	6	25	5	23.5	3	2
88195572	leucyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	55	91728	25	2	24	2	17.1	3	3
88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	598	55964	38	17	28	13	40.4	3	3
88196287	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	68	54779	6	1	6	1	7.3	3	3
88195510	NADP-dependent malic enzyme [Staphylococcus aureus subsp. aureus NCTC 8325]	60	44206	11	2	11	2	15.4	3	3
88195360	penicillin-binding protein 3 [Staphylococcus aureus subsp. aureus NCTC 8325]	32	77190	6	1	6	1	7.8	3	1
88196282	permease domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	36	39456	12	1	10	1	20.2	3	2
88194772	phosphoribosylamine--glycine ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	219	45820	22	6	20	5	29.9	3	3
88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	435	63063	43	12	34	10	45.6	3	3
88196017	serine hydroxymethyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	226	45144	22	11	17	8	29.6	3	3
88193832	seryl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	32	48609	11	0	11	0	19.4	3	3
88194953	succinyl-CoA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	248	42030	20	7	16	7	30.9	3	3
88195938	sucrose-6-phosphate hydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	82	57892	11	2	11	2	17.6	3	3
88194979	translation initiation factor IF-2 [Staphylococcus aureus subsp. aureus NCTC 8325]	160	77823	30	4	29	3	31.9	3	3
88194968	uridylate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	133	26128	13	6	10	6	34.2	3	3
88195468	valyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	154	101660	22	8	20	7	19.1	3	2
88195468	valyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	45	101660	15	1	13	1	9.4	3	3
88194678	3-oxoacyl- synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	123	43712	13	2	12	2	22	4	3
88194299	50S ribosomal protein L11 [Staphylococcus aureus subsp. aureus NCTC 8325]	120	14865	9	2	8	2	38.6	4	3
88194138	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	43	85023	16	1	13	1	13.7	4	2
88194138	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	39	85023	17	1	15	1	15.6	4	3

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88195509	acetyl-CoA carboxylase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	52	31851	7	1	7	1	23.2	4	2
88196355	adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	45	51372	12	1	12	1	21.9	4	3
88195807	adenylosuccinate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	266	49572	22	10	20	9	34.8	4	3
88195427	alanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	58	98459	20	2	20	2	19.1	4	3
88195822	aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	61	51709	16	1	15	1	22.4	4	3
88194768	amidophosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	71	54363	12	2	12	2	16.2	4	3
88196493	ATP-dependent Clp protease ATP-binding subunit ClpC [Staphylococcus aureus subsp. aureus NCTC 8325]	486	77789	33	14	30	14	34.8	4	2
88196493	ATP-dependent Clp protease ATP-binding subunit ClpC [Staphylococcus aureus subsp. aureus NCTC 8325]	70	77789	12	1	12	1	16.8	4	3
88195804	ATP-dependent DNA helicase PcrA [Staphylococcus aureus subsp. aureus NCTC 8325]	36	84021	27	0	26	0	23.4	4	2
88194761	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	57	30824	6	2	6	2	21.7	4	3
88196559	choline dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	33	63570	7	1	7	1	9	4	3
88195397	DNA internalization-related competence protein ComEC/Rec2 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	82812	15	1	14	1	13.1	4	2
88195497	DNA polymerase I [Staphylococcus aureus subsp. aureus NCTC 8325]	44	99133	24	1	22	1	18	4	3
88194958	DNA topoisomerase I [Staphylococcus aureus subsp. aureus NCTC 8325]	97	79277	36	5	33	5	34	4	2
88196165	DNA topoisomerase III [Staphylococcus aureus subsp. aureus NCTC 8325]	53	81500	33	2	28	2	24.8	4	2
88195079	DNA topoisomerase IV subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	134	74318	33	6	28	5	27.5	4	2
161353532	DNA-directed RNA polymerase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	373	133136	48	15	42	14	25.6	4	2
88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	260	53190	30	9	21	8	35.2	4	2
88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	499	76564	30	15	27	14	32.5	4	1
88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	893	76564	53	25	39	21	45.3	4	2
88194286	endopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	371	90981	36	13	32	12	31.9	4	1
88194286	endopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	378	90981	51	14	45	13	37.5	4	2
88193997	formate acetyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	38	84808	9	1	9	1	15.4	4	1

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88193997	formate acetyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	154	84808	23	5	21	5	25.6	4	2
88195445	GTP pyrophosphokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	51	83642	28	3	26	3	31.1	4	2
88195445	GTP pyrophosphokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	35	83642	33	0	31	0	30.2	4	3
88194808	GTP-binding protein TypA [Staphylococcus aureus subsp. aureus NCTC 8325]	253	69152	25	7	22	7	31.4	4	2
88193995	hypothetical protein SAOUHSC_00185 [Staphylococcus aureus subsp. aureus NCTC 8325]	32	61009	12	0	12	0	15.4	4	2
88194064	hypothetical protein SAOUHSC_00258 [Staphylococcus aureus subsp. aureus NCTC 8325]	49	114754	26	1	25	1	20.9	4	2
88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	361	32955	17	10	12	6	35.5	4	3
88194331	hypothetical protein SAOUHSC_00552 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	28449	5	1	4	1	20.6	4	3
88194609	hypothetical protein SAOUHSC_00851 [Staphylococcus aureus subsp. aureus NCTC 8325]	123	52498	15	3	14	3	19.8	4	2
88194932	hypothetical protein SAOUHSC_01193 [Staphylococcus aureus subsp. aureus NCTC 8325]	119	60477	14	4	11	4	14.8	4	3
88195321	hypothetical protein SAOUHSC_01610 [Staphylococcus aureus subsp. aureus NCTC 8325]	59	16211	4	1	3	1	11	4	3
88195586	hypothetical protein SAOUHSC_01890 [Staphylococcus aureus subsp. aureus NCTC 8325]	53	57541	6	1	6	1	12	4	1
88195626	hypothetical protein SAOUHSC_01931 [Staphylococcus aureus subsp. aureus NCTC 8325]	49	163164	34	1	34	1	18.9	4	2
88195680	hypothetical protein SAOUHSC_01989 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	42406	10	1	9	1	16.1	4	2
88194748	MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	32	16440	6	1	6	1	37.4	4	3
88194828	neurofilament protein [Staphylococcus aureus subsp. aureus NCTC 8325]	47	72148	17	1	15	1	16.3	4	3
88194840	phenylalanyl-tRNA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	81	88866	16	2	15	2	15.1	4	2
88194341	phosphomethylpyrimidine kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	47	29838	10	1	10	1	26.1	4	3
88194772	phosphoribosylamine--glycine ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	174	45820	16	5	16	5	29.6	4	2
88194767	phosphoribosylformylglycinamidine synthase II [Staphylococcus aureus subsp. aureus NCTC 8325]	438	79486	30	14	27	13	25.5	4	2
88194984	polynucleotide phosphorylase/polyadenylase [Staphylococcus aureus subsp. aureus NCTC 8325]	134	77314	21	4	19	4	26.2	4	1
88194984	polynucleotide phosphorylase/polyadenylase [Staphylococcus aureus subsp. aureus NCTC 8325]	367	77314	43	14	39	13	42.3	4	2
88194531	preprotein translocase subunit SecA [Staphylococcus aureus subsp. aureus NCTC 8325]	106	95900	23	4	23	4	25.1	4	1

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88194531	preprotein translocase subunit SecA [Staphylococcus aureus subsp. aureus NCTC 8325]	326	95900	56	13	53	12	40.8	4	2
88194531	preprotein translocase subunit SecA [Staphylococcus aureus subsp. aureus NCTC 8325]	107	95900	40	4	37	4	31.3	4	3
88196480	PTS system glucose-specific transporter subunit IIABC [Staphylococcus aureus subsp. aureus NCTC 8325]	37	74368	15	1	14	1	19.6	4	2
88194845	recombination and DNA strand exchange inhibitor protein [Staphylococcus aureus subsp. aureus NCTC 8325]	44	88606	28	1	26	1	21.4	4	2
88193839	replicative DNA helicase [Staphylococcus aureus subsp. aureus NCTC 8325]	38	52538	5	1	5	1	7.7	4	3
88194507	ribonucleotide-diphosphate reductase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	156	82552	19	4	18	4	24.4	4	1
88194507	ribonucleotide-diphosphate reductase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	153	82552	25	5	24	5	25.9	4	2
88194941	SMC domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	44	136665	42	1	40	1	24.4	4	2
88194979	translation initiation factor IF-2 [Staphylococcus aureus subsp. aureus NCTC 8325]	202	77823	25	6	20	5	26.1	4	1
88194979	translation initiation factor IF-2 [Staphylococcus aureus subsp. aureus NCTC 8325]	349	77823	47	13	39	10	36.5	4	2
161353516	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA [Staphylococcus aureus subsp. aureus NCTC 8325]	42	70072	20	1	17	1	21.6	4	3
88194170	xanthine phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	90	20871	13	3	9	2	36.5	4	3
88195058	50S ribosomal protein L33 [Staphylococcus aureus subsp. aureus NCTC 8325]	30	5928	4	0	4	0	46.9	5	3
88195582	6,7-dimethyl-8-ribityllumazine synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	41	16386	4	1	4	1	19.5	5	3
88196059	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	41	28987	6	0	6	0	26.5	5	1
88196556	acetyl-CoA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	45	59711	14	1	13	1	19	5	2
88195010	aerobic glycerol-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	38	62349	17	0	17	0	22.8	5	3
88195441	aspartyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	170	66587	23	8	22	8	26.9	5	2
88196493	ATP-dependent Clp protease ATP-binding subunit ClpC [Staphylococcus aureus subsp. aureus NCTC 8325]	225	77789	19	5	17	4	22.4	5	1
88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	289	46326	25	11	22	11	33.5	5	1
88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	1566	46326	68	44	36	22	52.8	5	2
88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	502	46326	32	17	27	13	40	5	3
88194891	cell division protein [Staphylococcus aureus subsp. aureus NCTC 8325]	262	52902	17	8	15	8	28.9	5	2

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195925	chaperonin GroEL [Staphylococcus aureus subsp. aureus NCTC 8325]	396	57629	26	14	20	13	31	5	1
88195925	chaperonin GroEL [Staphylococcus aureus subsp. aureus NCTC 8325]	821	57629	53	27	34	17	47.8	5	2
88196559	choline dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	23	63570	4	0	4	0	7.9	5	1
88196559	choline dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	173	63570	19	9	18	9	31.3	5	2
88196031	CTP synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	63	59945	9	1	7	1	9.5	5	1
88196031	CTP synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	205	59945	18	9	17	9	24.6	5	2
88196042	deoxyribose-phosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	64	23313	11	1	11	1	36.4	5	3
88194274	dihydropteroate synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	68	29504	8	2	7	1	23.6	5	2
88193828	DNA gyrase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	371	72495	41	15	32	12	36.6	5	2
88193828	DNA gyrase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	121	72495	23	4	17	4	20	5	3
88196165	DNA topoisomerase III [Staphylococcus aureus subsp. aureus NCTC 8325]	40	81500	18	1	17	1	26.7	5	1
88196165	DNA topoisomerase III [Staphylococcus aureus subsp. aureus NCTC 8325]	44	81500	38	2	29	2	27.7	5	3
88195079	DNA topoisomerase IV subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	54	74318	8	1	8	1	10.1	5	3
88196060	glucosamine--fructose-6-phosphate aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	67	65809	5	1	5	1	12	5	1
88196060	glucosamine--fructose-6-phosphate aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	184	65809	12	5	12	5	18.6	5	2
88194226	glutamate synthase large subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	36	166244	34	1	31	1	16.5	5	3
88195472	glutamate-1-semialdehyde aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46	46359	12	1	12	1	23.1	5	3
88195394	GTP-binding protein LepA [Staphylococcus aureus subsp. aureus NCTC 8325]	115	68132	27	6	26	5	32.8	5	2
88195394	GTP-binding protein LepA [Staphylococcus aureus subsp. aureus NCTC 8325]	32	68132	14	1	14	1	19.4	5	3
88195060	guanosine 5~-monophosphate oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	67	36093	3	2	3	2	7.4	5	3
88193956	hypothetical protein SAOUHSC_00144 [Staphylococcus aureus subsp. aureus NCTC 8325]	43	273308	45	1	42	1	12	5	2
88194009	hypothetical protein SAOUHSC_00199 [Staphylococcus aureus subsp. aureus NCTC 8325]	33	58840	14	1	14	1	19.4	5	2
88194034	hypothetical protein SAOUHSC_00227 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	66034	14	1	14	1	15.3	5	2

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88194073	hypothetical protein SAOUHSC_00268 [Staphylococcus aureus subsp. aureus NCTC 8325]	41	68275	27	0	23	0	23	5	2
88194271	hypothetical protein SAOUHSC_00486 [Staphylococcus aureus subsp. aureus NCTC 8325]	103	77764	33	5	33	5	38	5	2
88194271	hypothetical protein SAOUHSC_00486 [Staphylococcus aureus subsp. aureus NCTC 8325]	79	77764	32	3	29	3	29.7	5	3
88194315	hypothetical protein SAOUHSC_00535 [Staphylococcus aureus subsp. aureus NCTC 8325]	35	36030	3	1	3	1	5.9	5	3
88194404	hypothetical protein SAOUHSC_00637 [Staphylococcus aureus subsp. aureus NCTC 8325]	76	28007	5	1	5	1	23.1	5	3
88194470	hypothetical protein SAOUHSC_00705 [Staphylococcus aureus subsp. aureus NCTC 8325]	31	17739	5	1	4	1	16.2	5	3
88194932	hypothetical protein SAOUHSC_01193 [Staphylococcus aureus subsp. aureus NCTC 8325]	201	60477	26	6	22	6	31.4	5	2
88194999	hypothetical protein SAOUHSC_01266 [Staphylococcus aureus subsp. aureus NCTC 8325]	53	64515	14	2	13	2	14.7	5	2
88194999	hypothetical protein SAOUHSC_01266 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	64515	14	1	14	1	15	5	3
88195110	hypothetical protein SAOUHSC_01383 [Staphylococcus aureus subsp. aureus NCTC 8325]	57	69241	11	2	11	2	18.2	5	1
88195110	hypothetical protein SAOUHSC_01383 [Staphylococcus aureus subsp. aureus NCTC 8325]	73	69241	16	5	13	4	16.1	5	2
88195110	hypothetical protein SAOUHSC_01383 [Staphylococcus aureus subsp. aureus NCTC 8325]	70	69241	22	3	20	3	28.6	5	3
88195552	hypothetical protein SAOUHSC_01854 [Staphylococcus aureus subsp. aureus NCTC 8325]	61	55058	16	2	15	2	35	5	1
88195552	hypothetical protein SAOUHSC_01854 [Staphylococcus aureus subsp. aureus NCTC 8325]	386	55058	41	15	34	11	48.1	5	2
88195552	hypothetical protein SAOUHSC_01854 [Staphylococcus aureus subsp. aureus NCTC 8325]	217	55058	40	7	36	6	39	5	3
88195779	hypothetical protein SAOUHSC_02097 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	45576	6	1	6	1	11.1	5	3
88196036	hypothetical protein SAOUHSC_02373 [Staphylococcus aureus subsp. aureus NCTC 8325]	32	45618	12	1	10	1	19.1	5	2
88196065	hypothetical protein SAOUHSC_02404 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	262863	78	1	69	1	23.2	5	3
88196250	hypothetical protein SAOUHSC_02608 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	34996	8	0	8	0	21.1	5	3
88196456	hypothetical protein SAOUHSC_02822 [Staphylococcus aureus subsp. aureus NCTC 8325]	75	76127	21	4	17	4	16.2	5	2
88196456	hypothetical protein SAOUHSC_02822 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	76127	20	0	15	0	19.9	5	3
88194248	methionyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	122	74838	23	5	23	5	27.7	5	2
88194248	methionyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	150	74838	16	6	15	6	19.9	5	3

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88195389	molecular chaperone DnaK [Staphylococcus aureus subsp. aureus NCTC 8325]	426	66321	47	13	38	11	55.7	5	1
88195389	molecular chaperone DnaK [Staphylococcus aureus subsp. aureus NCTC 8325]	1915	66321	108	66	71	42	70.2	5	2
88195389	molecular chaperone DnaK [Staphylococcus aureus subsp. aureus NCTC 8325]	1107	66321	78	38	56	27	60	5	3
88196188	molybdopterin biosynthesis protein MoeA [Staphylococcus aureus subsp. aureus NCTC 8325]	35	44988	4	0	4	0	9.8	5	1
88193969	N-acetylmuramic acid-6-phosphate etherase [Staphylococcus aureus subsp. aureus NCTC 8325]	34	32231	6	1	6	1	17.4	5	3
88194694	oligoendopeptidase F [Staphylococcus aureus subsp. aureus NCTC 8325]	90	69776	10	3	9	3	12	5	1
88194694	oligoendopeptidase F [Staphylococcus aureus subsp. aureus NCTC 8325]	147	69776	29	8	28	8	31.2	5	2
88194685	oligopeptide ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	37	64487	12	2	10	1	12.6	5	2
88194651	ornithine--oxo-acid transaminase [Staphylococcus aureus subsp. aureus NCTC 8325]	77	43390	11	1	10	1	26.8	5	3
88195360	penicillin-binding protein 3 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	77190	25	1	24	1	24.6	5	2
88194713	peptide chain release factor 3 [Staphylococcus aureus subsp. aureus NCTC 8325]	28	59564	5	0	5	0	7.9	5	1
88194713	peptide chain release factor 3 [Staphylococcus aureus subsp. aureus NCTC 8325]	70	59564	29	3	26	2	31.2	5	2
88195864	phage head-tail adaptor [Staphylococcus aureus subsp. aureus NCTC 8325]	41	13072	5	2	3	1	16.2	5	2
88195856	phage minor structural protein [Staphylococcus aureus subsp. aureus NCTC 8325]	52	143656	34	2	30	1	16.8	5	2
88195719	phage tape measure protein [Staphylococcus aureus subsp. aureus NCTC 8325]	45	125734	42	1	35	1	19.6	5	2
88195871	phage terminase large subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	40	65249	15	1	12	1	15.1	5	3
88194782	phosphoenolpyruvate-protein phosphotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	359	63179	31	12	23	9	26.6	5	1
88194782	phosphoenolpyruvate-protein phosphotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	771	63179	57	31	36	20	44.8	5	2
88194558	phosphoglyceromutase [Staphylococcus aureus subsp. aureus NCTC 8325]	219	56389	16	8	14	7	22	5	2
88194973	prolyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	97	63823	9	2	9	2	10.9	5	1
88194973	prolyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	285	63823	21	11	18	10	29.5	5	2
88194973	prolyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	113	63823	20	3	19	2	28	5	3
88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	327	63063	25	6	22	5	35	5	1

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	946	63063	71	26	49	18	55.2	5	2
88196481	pyruvate oxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	84	63717	20	4	19	4	21.6	5	1
88196481	pyruvate oxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	461	63717	34	18	30	15	33	5	2
88196481	pyruvate oxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	255	63717	24	10	22	9	35.8	5	3
88194507	ribonucleotide-diphosphate reductase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	136	82552	17	3	16	3	20.5	5	3
88195527	septation ring formation regulator EzrA [Staphylococcus aureus subsp. aureus NCTC 8325]	67	66206	8	1	8	1	8.7	5	1
88196104	tagatose 1,6-diphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	43	36573	15	1	13	1	27.3	5	3
88194030	teichoic acid biosynthesis protein TagB [Staphylococcus aureus subsp. aureus NCTC 8325]	65	60146	11	3	11	3	15	5	2
88195489	threonyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	92	74441	19	2	19	2	20	5	1
88195489	threonyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	216	74441	43	12	35	10	35.7	5	2
88195489	threonyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	122	74441	25	3	23	3	21.9	5	3
88195066	transketolase [Staphylococcus aureus subsp. aureus NCTC 8325]	220	68317	13	4	13	4	22.7	5	1
88195066	transketolase [Staphylococcus aureus subsp. aureus NCTC 8325]	986	68317	52	27	35	17	43.8	5	2
88195066	transketolase [Staphylococcus aureus subsp. aureus NCTC 8325]	778	68317	35	21	22	14	35.2	5	3
88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	181	48579	16	8	15	7	26.6	5	1
88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	130	48579	20	5	18	5	31.6	5	2
88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	182	48579	33	9	24	9	34.9	5	3
161353516	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA [Staphylococcus aureus subsp. aureus NCTC 8325]	190	70072	29	7	26	7	28.6	5	2
88196249	urocanate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	133	60595	22	5	20	5	23.5	5	2
88196500	1-pyrroline-5-carboxylate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	198	56832	22	8	22	8	35.2	6	1
88196500	1-pyrroline-5-carboxylate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	368	56832	35	12	31	11	44.7	6	2
88196500	1-pyrroline-5-carboxylate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	248	56832	27	7	24	7	39.1	6	3
88195664	3~-5~ exoribonuclease YhaM [Staphylococcus aureus subsp. aureus NCTC 8325]	40	35756	8	1	8	1	18.5	6	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195210	30S ribosomal protein S1 [Staphylococcus aureus subsp. aureus NCTC 8325]	210	43261	19	4	17	4	38.6	6	1
88195210	30S ribosomal protein S1 [Staphylococcus aureus subsp. aureus NCTC 8325]	287	43261	21	8	19	8	43.5	6	2
88196101	6-phospho-beta-galactosidase [Staphylococcus aureus subsp. aureus NCTC 8325]	21	54516	12	0	11	0	23	6	2
88196101	6-phospho-beta-galactosidase [Staphylococcus aureus subsp. aureus NCTC 8325]	36	54516	7	1	6	1	9.8	6	3
88195119	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	67	60219	25	1	23	1	29.1	6	1
88195119	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	90	60219	29	5	25	5	36.6	6	2
88195119	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	80	60219	23	4	20	4	27.8	6	3
88196556	acetyl-CoA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	45	59711	10	2	10	2	17.5	6	1
88195075	aconitate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	80	98908	20	3	18	3	17.5	6	1
88194939	acyl carrier protein [Staphylococcus aureus subsp. aureus NCTC 8325]	109	8544	5	4	4	3	31.2	6	2
88196355	adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	36	51372	7	1	7	1	14.8	6	1
88195010	aerobic glycerol-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	124	62349	18	3	17	3	24.2	6	1
88195010	aerobic glycerol-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	165	62349	23	4	22	4	25.7	6	2
88196026	aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	295	51937	14	6	13	5	24.2	6	1
88193945	aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	159	53626	21	7	19	7	35.8	6	1
88196026	aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	512	51937	25	15	21	12	36.4	6	2
88193945	aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	483	53626	47	19	36	17	58	6	2
88196026	aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	149	51937	15	3	14	3	21.1	6	3
88193945	aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	249	53626	24	9	20	9	30.5	6	3
88195500	alkaline phosphatase synthesis transcriptional regulatory protein [Staphylococcus aureus subsp. aureus NCTC 8325]	32	27105	6	1	6	1	21.8	6	1
88194162	alkyl hydroperoxide reductase subunit F [Staphylococcus aureus subsp. aureus NCTC 8325]	299	54687	27	11	20	9	31.4	6	1
88194162	alkyl hydroperoxide reductase subunit F [Staphylococcus aureus subsp. aureus NCTC 8325]	429	54687	33	15	26	12	40.4	6	2
88194162	alkyl hydroperoxide reductase subunit F [Staphylococcus aureus subsp. aureus NCTC 8325]	561	54687	34	15	27	13	39.1	6	3

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88194768	amidophosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	177	54363	15	4	14	4	29.8	6	2
88196037	aminobenzoyl-glutamate utilization protein B [Staphylococcus aureus subsp. aureus NCTC 8325]	32	42932	10	1	9	1	15.2	6	3
88194381	arginyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	157	62342	18	4	16	3	23.7	6	1
88194381	arginyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	104	62342	16	3	14	3	24.2	6	2
88194381	arginyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	138	62342	14	5	13	5	18.4	6	3
88195188	asparaginyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	130	49127	14	6	11	5	22.1	6	1
88195188	asparaginyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	264	49127	17	10	16	9	34.9	6	2
88195188	asparaginyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	163	49127	18	7	16	6	25.1	6	3
88195799	aspartyl/glutamyl-tRNA amidotransferase subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	56	52788	10	1	9	1	15.5	6	1
88195799	aspartyl/glutamyl-tRNA amidotransferase subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	126	52788	12	4	12	4	19.8	6	2
88195798	aspartyl/glutamyl-tRNA amidotransferase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	282	53623	23	12	23	12	32.6	6	1
88195798	aspartyl/glutamyl-tRNA amidotransferase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	549	53623	42	18	35	16	51.4	6	2
88195798	aspartyl/glutamyl-tRNA amidotransferase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	245	53623	29	10	28	10	47.2	6	3
88194962	ATP-dependent protease ATP-binding subunit HslU [Staphylococcus aureus subsp. aureus NCTC 8325]	83	52282	19	4	17	4	27.2	6	1
88194962	ATP-dependent protease ATP-binding subunit HslU [Staphylococcus aureus subsp. aureus NCTC 8325]	140	52282	32	7	29	6	40.5	6	2
88194962	ATP-dependent protease ATP-binding subunit HslU [Staphylococcus aureus subsp. aureus NCTC 8325]	61	52282	16	2	16	2	17.6	6	3
88196560	betaine aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	47	54589	13	1	12	1	19.2	6	1
88196560	betaine aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	97	54589	17	2	15	2	23.4	6	2
88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	334	54314	26	10	24	10	47	6	1
88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	1208	54314	49	32	30	21	55.3	6	2
88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	369	54314	37	13	32	10	50.6	6	3
88195057	catalase [Staphylococcus aureus subsp. aureus NCTC 8325]	276	54908	22	10	18	8	36.4	6	1

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88195057	catalase [Staphylococcus aureus subsp. aureus NCTC 8325]	799	54908	44	26	32	18	52	6	2
88194890	cell division protein [Staphylococcus aureus subsp. aureus NCTC 8325]	36	50182	9	1	9	1	16.2	6	2
88195925	chaperonin GroEL [Staphylococcus aureus subsp. aureus NCTC 8325]	627	57629	41	22	31	17	43.7	6	3
88194665	coenzyme A disulfide reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	30	49259	11	0	11	0	22.8	6	3
88194292	cysteinyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	88	53652	10	2	10	2	23.4	6	1
88194292	cysteinyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	36	53652	13	1	12	1	18.9	6	2
88195533	D-3-phosphoglycerate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	35	57583	15	0	13	0	19.5	6	2
88195533	D-3-phosphoglycerate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	50	57583	17	1	17	1	27.2	6	3
88194626	D-alanine--poly(phosphoribitol) ligase subunit 1 [Staphylococcus aureus subsp. aureus NCTC 8325]	26	54636	13	0	11	0	21.9	6	1
88194626	D-alanine--poly(phosphoribitol) ligase subunit 1 [Staphylococcus aureus subsp. aureus NCTC 8325]	58	54636	15	1	13	1	21.4	6	2
88195982	DEAD-box ATP dependent DNA helicase [Staphylococcus aureus subsp. aureus NCTC 8325]	112	56907	19	3	17	3	29.4	6	1
88195982	DEAD-box ATP dependent DNA helicase [Staphylococcus aureus subsp. aureus NCTC 8325]	425	56907	47	12	40	12	44.9	6	2
88195982	DEAD-box ATP dependent DNA helicase [Staphylococcus aureus subsp. aureus NCTC 8325]	198	56907	30	7	27	6	33.6	6	3
88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	193	49451	31	8	25	7	40.2	6	1
88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	1093	49451	68	47	37	25	49.4	6	2
88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	425	49451	47	20	36	15	50.2	6	3
88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	102	46644	14	4	13	4	28.9	6	1
88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	501	46644	33	18	25	13	30.1	6	2
88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	144	46644	23	4	22	4	42.9	6	3
88194907	dihydroorotase [Staphylococcus aureus subsp. aureus NCTC 8325]	88	46342	13	1	12	1	21.7	6	2
88195565	dipeptidase PepV [Staphylococcus aureus subsp. aureus NCTC 8325]	76	52791	11	2	10	2	15.6	6	1
88195565	dipeptidase PepV [Staphylococcus aureus subsp. aureus NCTC 8325]	124	52791	8	4	8	4	15.4	6	3
88194974	DNA polymerase III PolC [Staphylococcus aureus subsp. aureus NCTC 8325]	88	162357	27	2	21	1	10.9	6	2

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
161353534	DNA repair protein RadA [Staphylococcus aureus subsp. aureus NCTC 8325]	32	49832	15	1	12	1	20	6	2
161353534	DNA repair protein RadA [Staphylococcus aureus subsp. aureus NCTC 8325]	48	49832	18	1	17	1	24.9	6	3
88195080	DNA topoisomerase IV subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	34	90942	14	1	14	1	13.5	6	1
88195080	DNA topoisomerase IV subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	39	90942	22	1	20	1	18.6	6	2
88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	82	53190	18	2	18	2	29.2	6	3
88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	514	32474	28	13	23	12	58	6	3
88196009	F0F1 ATP synthase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	90	54550	16	6	14	6	23.5	6	1
88196009	F0F1 ATP synthase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	271	54550	32	9	23	8	35.1	6	2
88196009	F0F1 ATP synthase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	101	54550	14	6	12	6	17.5	6	3
88196007	F0F1 ATP synthase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	307	51368	28	9	24	9	43.6	6	2
88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	397	59819	35	13	27	9	37.8	6	1
88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	725	59819	45	28	25	14	37.5	6	2
88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	494	59819	38	18	30	14	35.7	6	3
88196060	glucosamine--fructose-6-phosphate aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	67	65809	9	2	8	1	10.5	6	3
88195310	glucose-6-phosphate 1-dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	278	56929	21	7	19	7	33.8	6	1
88195310	glucose-6-phosphate 1-dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	386	56929	32	11	26	9	34.8	6	2
88195310	glucose-6-phosphate 1-dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	358	56929	26	10	21	8	34	6	3
88195018	glutamine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	153	50808	14	6	12	5	19.3	6	1
88195018	glutamine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	480	50808	38	17	30	13	45.1	6	2
88194290	glutamyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	100	56253	12	2	11	2	14	6	1
88194290	glutamyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	319	56253	41	12	31	10	43	6	2
88194290	glutamyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	185	56253	16	5	14	4	22.9	6	3
88195342	glycine dehydrogenase subunit 1 [Staphylococcus aureus subsp. aureus NCTC 8325]	119	49685	12	2	11	2	23	6	2

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88195341	glycine dehydrogenase subunit 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	39	54748	11	0	10	0	12.4	6	1
88195341	glycine dehydrogenase subunit 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	51	54748	17	1	16	1	21.4	6	2
88195341	glycine dehydrogenase subunit 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	75	54748	14	1	13	1	18.8	6	3
88195373	glycyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	174	53586	15	7	14	6	24.6	6	1
88195373	glycyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	714	53586	42	26	32	19	43.8	6	2
88194173	GMP synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	243	58194	14	7	13	7	23	6	1
88194173	GMP synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	326	58194	31	10	25	9	39.4	6	2
88194173	GMP synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	176	58194	14	5	12	4	19.7	6	3
88193831	histidine ammonia-lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	58	56041	17	1	16	1	22.6	6	2
88195050	homoserine dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	46	46845	12	1	10	1	18.8	6	2
88195050	homoserine dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	119	46845	12	4	12	4	26.3	6	3
88193973	HsdR family type I site-specific deoxyribonuclease [Staphylococcus aureus subsp. aureus NCTC 8325]	62	109159	17	2	15	1	14.7	6	2
88194007	hypothetical protein SAOUHSC_00197 [Staphylococcus aureus subsp. aureus NCTC 8325]	33	44701	8	1	7	1	21.3	6	3
88194034	hypothetical protein SAOUHSC_00227 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	66034	8	1	8	1	11.2	6	3
88194035	hypothetical protein SAOUHSC_00228 [Staphylococcus aureus subsp. aureus NCTC 8325]	50	66272	18	1	15	1	18.8	6	2
88194035	hypothetical protein SAOUHSC_00228 [Staphylococcus aureus subsp. aureus NCTC 8325]	107	66272	26	4	24	4	30.1	6	3
88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	35591	8	1	8	1	23.3	6	1
88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	204	35591	16	6	16	6	42.5	6	2
88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	59	35591	14	2	14	2	32.7	6	3
88194224	hypothetical protein SAOUHSC_00433 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	41633	5	1	5	1	15.9	6	2
88194271	hypothetical protein SAOUHSC_00486 [Staphylococcus aureus subsp. aureus NCTC 8325]	58	77764	21	1	20	1	22.1	6	1
88194355	hypothetical protein SAOUHSC_00581 [Staphylococcus aureus subsp. aureus NCTC 8325]	114	48386	11	3	10	3	19.8	6	1
88194355	hypothetical protein SAOUHSC_00581 [Staphylococcus aureus subsp. aureus NCTC 8325]	227	48386	26	6	24	6	39.5	6	2

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88194470	hypothetical protein SAOUHSC_00705 [Staphylococcus aureus subsp. aureus NCTC 8325]	32	17739	6	1	5	1	20	6	2
88194477	hypothetical protein SAOUHSC_00712 [Staphylococcus aureus subsp. aureus NCTC 8325]	109	32339	12	4	11	4	27.6	6	3
88194596	hypothetical protein SAOUHSC_00838 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	33479	9	1	6	1	12.3	6	1
88194606	hypothetical protein SAOUHSC_00848 [Staphylococcus aureus subsp. aureus NCTC 8325]	76	48519	11	4	10	4	17.7	6	2
88194606	hypothetical protein SAOUHSC_00848 [Staphylococcus aureus subsp. aureus NCTC 8325]	254	48519	13	12	10	9	22.3	6	3
88194609	hypothetical protein SAOUHSC_00851 [Staphylococcus aureus subsp. aureus NCTC 8325]	138	52498	15	3	14	3	28.2	6	1
88194787	hypothetical protein SAOUHSC_01035 [Staphylococcus aureus subsp. aureus NCTC 8325]	149	62630	16	4	14	3	24.4	6	1
88194787	hypothetical protein SAOUHSC_01035 [Staphylococcus aureus subsp. aureus NCTC 8325]	269	62630	28	7	25	7	31.5	6	2
88194932	hypothetical protein SAOUHSC_01193 [Staphylococcus aureus subsp. aureus NCTC 8325]	128	60477	17	4	17	4	28.3	6	1
88194985	hypothetical protein SAOUHSC_01252 [Staphylococcus aureus subsp. aureus NCTC 8325]	140	58753	16	5	16	5	25	6	1
88194985	hypothetical protein SAOUHSC_01252 [Staphylococcus aureus subsp. aureus NCTC 8325]	254	58753	23	9	21	8	32.9	6	2
88194985	hypothetical protein SAOUHSC_01252 [Staphylococcus aureus subsp. aureus NCTC 8325]	172	58753	19	5	18	4	27	6	3
88195279	hypothetical protein SAOUHSC_01567 [Staphylococcus aureus subsp. aureus NCTC 8325]	31	13653	6	1	6	1	38.3	6	2
88195366	hypothetical protein SAOUHSC_01659 [Staphylococcus aureus subsp. aureus NCTC 8325]	247	51049	19	8	17	8	34.4	6	2
88195542	hypothetical protein SAOUHSC_01843 [Staphylococcus aureus subsp. aureus NCTC 8325]	46	100886	25	2	24	1	22.1	6	2
88195626	hypothetical protein SAOUHSC_01931 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	163164	35	1	34	1	18.5	6	3
88193965	indolepyruvate decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	122	60501	13	4	12	4	16.5	6	1
88193965	indolepyruvate decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	250	60501	19	7	17	6	24.5	6	2
88193965	indolepyruvate decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	231	60501	26	8	20	6	26.4	6	3
88194172	inosine-5~-monophosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	438	52818	38	13	32	12	50.6	6	1
88194172	inosine-5~-monophosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	1167	52818	57	35	38	22	52.7	6	2
88194172	inosine-5~-monophosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	352	52818	34	11	28	11	40	6	3
88194899	isoleucyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	66	104820	19	2	19	2	17.8	6	1

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88194278	lysyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	195	56684	30	7	28	7	40.8	6	1
88194278	lysyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	276	56684	30	11	25	11	34.7	6	2
88194278	lysyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	445	56684	33	17	28	14	43.6	6	3
88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	568	55964	41	17	30	13	52.8	6	1
88196287	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	69	54779	14	2	11	2	15.2	6	1
88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	1474	55964	95	40	56	24	65.3	6	2
88196287	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	125	54779	20	2	19	2	26.4	6	2
88196492	methylated-DNA--protein-cysteine methyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	40	18934	5	1	5	1	18.5	6	3
88194828	neurofilament protein [Staphylococcus aureus subsp. aureus NCTC 8325]	52	72148	20	2	18	1	21.9	6	2
88194694	oligoendopeptidase F [Staphylococcus aureus subsp. aureus NCTC 8325]	110	69776	23	2	23	2	24.8	6	3
88195864	phage head-tail adaptor [Staphylococcus aureus subsp. aureus NCTC 8325]	36	13072	4	1	4	1	26.1	6	1
88196598	phage infection protein [Staphylococcus aureus subsp. aureus NCTC 8325]	36	108649	36	1	35	1	24.4	6	3
88195856	phage minor structural protein [Staphylococcus aureus subsp. aureus NCTC 8325]	56	143656	36	1	31	1	18.2	6	3
88194996	phosphodiesterase [Staphylococcus aureus subsp. aureus NCTC 8325]	50	58477	23	2	22	2	26	6	2
88195605	phosphoenolpyruvate carboxykinase [Staphylococcus aureus subsp. aureus NCTC 8325]	251	59340	18	7	17	7	26.8	6	1
88195605	phosphoenolpyruvate carboxykinase [Staphylococcus aureus subsp. aureus NCTC 8325]	462	59340	31	18	28	16	33.2	6	2
88194782	phosphoenolpyruvate-protein phosphotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	332	63179	39	16	33	14	36.4	6	3
88196066	phosphoglucosamine mutase [Staphylococcus aureus subsp. aureus NCTC 8325]	248	49234	25	9	20	7	34.8	6	1
88196066	phosphoglucosamine mutase [Staphylococcus aureus subsp. aureus NCTC 8325]	194	49234	20	7	18	7	36.4	6	2
88196066	phosphoglucosamine mutase [Staphylococcus aureus subsp. aureus NCTC 8325]	398	49234	30	12	25	10	46.6	6	3
88194558	phosphoglyceromutase [Staphylococcus aureus subsp. aureus NCTC 8325]	51	56389	13	2	13	2	19.6	6	1
88194558	phosphoglyceromutase [Staphylococcus aureus subsp. aureus NCTC 8325]	107	56389	21	3	16	3	21.8	6	3
88193918	phosphonate ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	45	34978	13	2	12	1	30.2	6	2

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88193918	phosphonate ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	34	34978	15	1	14	1	29.9	6	3
88194769	phosphoribosylaminoimidazole synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	88	36994	8	2	7	2	21.9	6	3
88194766	phosphoribosylformylglycinamidine synthase I [Staphylococcus aureus subsp. aureus NCTC 8325]	54	24511	3	1	3	1	9.9	6	3
88194813	pyruvate carboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	113	128467	22	2	21	1	13.7	6	1
88195369	RNA polymerase sigma factor RpoD [Staphylococcus aureus subsp. aureus NCTC 8325]	86	42145	15	4	14	3	29.1	6	1
88193832	seryl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	136	48609	21	5	19	5	35.3	6	2
88194944	signal recognition particle protein [Staphylococcus aureus subsp. aureus NCTC 8325]	288	50672	33	11	27	11	48.4	6	1
88194944	signal recognition particle protein [Staphylococcus aureus subsp. aureus NCTC 8325]	458	50672	54	18	40	13	58.7	6	2
88194944	signal recognition particle protein [Staphylococcus aureus subsp. aureus NCTC 8325]	204	50672	50	8	41	7	57.6	6	3
88194942	signal recognition particle-docking protein FtsY [Staphylococcus aureus subsp. aureus NCTC 8325]	43	46561	8	1	8	1	15.9	6	1
88194942	signal recognition particle-docking protein FtsY [Staphylococcus aureus subsp. aureus NCTC 8325]	54	46561	17	1	17	1	30.8	6	2
88194850	succinate dehydrogenase flavoprotein subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	79	65462	14	2	13	2	17.5	6	1
88194850	succinate dehydrogenase flavoprotein subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	147	65462	23	6	19	5	29.8	6	2
88194850	succinate dehydrogenase flavoprotein subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	183	65462	21	9	19	8	25.7	6	3
88195938	sucrose-6-phosphate hydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	81	57892	13	2	11	1	19.6	6	2
88195858	tail length tape measure protein [Staphylococcus aureus subsp. aureus NCTC 8325]	41	169851	39	1	35	1	17.3	6	1
88195858	tail length tape measure protein [Staphylococcus aureus subsp. aureus NCTC 8325]	46	169851	54	2	45	1	22.3	6	2
88194030	teichoic acid biosynthesis protein TagB [Staphylococcus aureus subsp. aureus NCTC 8325]	41	60146	10	1	10	1	15.8	6	3
88196025	transcription termination factor Rho [Staphylococcus aureus subsp. aureus NCTC 8325]	84	49939	11	4	11	4	22.8	6	2
88196025	transcription termination factor Rho [Staphylococcus aureus subsp. aureus NCTC 8325]	51	49939	12	3	11	3	20.1	6	3
88194263	transcription-repair coupling factor [Staphylococcus aureus subsp. aureus NCTC 8325]	38	134135	26	2	23	2	14.3	6	2
88194263	transcription-repair coupling factor [Staphylococcus aureus subsp. aureus NCTC 8325]	34	134135	28	1	26	1	19.4	6	3
88194959	tRNA (uracil-5-)-methyltransferase Gid [Staphylococcus aureus subsp. aureus NCTC 8325]	53	48341	17	1	16	1	32.9	6	2

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88196003	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	78	44913	11	1	11	1	17.8	6	1
88196002	(3R)-hydroxymyristoyl-ACP dehydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	49	16071	4	2	4	2	19.2	7	3
88194312	2-amino-3-ketobutyrate coenzyme A ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	159	42864	21	4	19	4	37	7	1
88194312	2-amino-3-ketobutyrate coenzyme A ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	338	42864	25	12	22	11	41	7	2
88194312	2-amino-3-ketobutyrate coenzyme A ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	131	42864	20	4	19	4	39.2	7	3
88195143	2-oxoglutarate dehydrogenase E1 component [Staphylococcus aureus subsp. aureus NCTC 8325]	100	105277	29	4	27	4	18.9	7	1
88195143	2-oxoglutarate dehydrogenase E1 component [Staphylococcus aureus subsp. aureus NCTC 8325]	235	105277	36	8	34	7	25	7	3
88195664	3~-5~ exoribonuclease YhaM [Staphylococcus aureus subsp. aureus NCTC 8325]	32	35756	9	0	8	0	19.2	7	1
88195210	30S ribosomal protein S1 [Staphylococcus aureus subsp. aureus NCTC 8325]	405	43261	26	10	21	7	49.9	7	3
88194678	3-oxoacyl- synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	123	43712	8	2	7	2	19.8	7	2
88195316	6-phosphogluconate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	220	51770	23	8	20	8	29.3	7	1
88195316	6-phosphogluconate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	200	51770	25	8	23	7	29.3	7	2
88195316	6-phosphogluconate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	254	51770	30	7	29	7	35.7	7	3
88195934	accessory gene regulator protein C [Staphylococcus aureus subsp. aureus NCTC 8325]	34	47953	8	1	8	1	14	7	2
88195934	accessory gene regulator protein C [Staphylococcus aureus subsp. aureus NCTC 8325]	22	47953	8	0	8	0	17.6	7	3
88195520	acetate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	242	44015	17	7	17	7	37.8	7	1
88195520	acetate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	452	44015	29	14	26	12	49.5	7	2
88195520	acetate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	312	44015	23	8	21	6	40.2	7	3
88195333	acetyl-CoA carboxylase biotin carboxylase subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	122	50017	17	5	16	5	26.8	7	2
88195333	acetyl-CoA carboxylase biotin carboxylase subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	84	50017	18	2	14	2	24.8	7	3
88196355	adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	35	51372	16	1	13	1	23.5	7	2
88195807	adenylosuccinate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	241	49572	26	9	23	8	43.9	7	1
88195807	adenylosuccinate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	433	49572	30	17	27	14	47.6	7	2

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88193840	adenylosuccinate synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	166	47549	20	7	18	6	30	7	2
88195971	alanine racemase [Staphylococcus aureus subsp. aureus NCTC 8325]	61	42796	13	1	11	1	26.2	7	2
88195427	alanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	55	98459	21	1	20	1	21.7	7	1
88196382	amino acid ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	36	46145	20	1	18	1	34.8	7	1
88196382	amino acid ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	34	46145	10	0	9	0	18.9	7	2
88196037	aminobenzoyl-glutamate utilization protein B [Staphylococcus aureus subsp. aureus NCTC 8325]	37	42932	9	2	8	2	13.7	7	1
88195775	aminopeptidase PepS [Staphylococcus aureus subsp. aureus NCTC 8325]	101	47088	9	4	9	4	16	7	1
88195775	aminopeptidase PepS [Staphylococcus aureus subsp. aureus NCTC 8325]	114	47088	18	5	15	4	25.8	7	2
88195775	aminopeptidase PepS [Staphylococcus aureus subsp. aureus NCTC 8325]	140	47088	18	5	15	5	23.7	7	3
88194607	aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	91	46590	9	1	9	1	18.5	7	3
88195479	ATP-dependent protease ATP-binding subunit ClpX [Staphylococcus aureus subsp. aureus NCTC 8325]	106	46269	8	3	7	2	17.4	7	1
88195479	ATP-dependent protease ATP-binding subunit ClpX [Staphylococcus aureus subsp. aureus NCTC 8325]	112	46269	14	3	13	3	21.2	7	2
88195550	bifunctional 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase [Staphylococcus aureus subsp. aureus NCTC 8325]	121	40593	18	5	15	5	27.8	7	1
88195550	bifunctional 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase [Staphylococcus aureus subsp. aureus NCTC 8325]	101	40593	15	3	14	3	25.3	7	2
88195550	bifunctional 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase [Staphylococcus aureus subsp. aureus NCTC 8325]	85	40593	13	4	11	4	21.5	7	3
88194139	bifunctional homocysteine S-methyltransferase/5,10-methylenetetrahydrofolate reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	30	68436	12	1	11	1	12.7	7	1
88194316	branched-chain amino acid aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	526	40062	30	16	23	11	49.2	7	2
88194908	carbamoyl phosphate synthase small subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	45	40369	8	1	8	1	15.8	7	1
88194908	carbamoyl phosphate synthase small subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	151	40369	21	6	15	4	29.2	7	2
88194890	cell division protein [Staphylococcus aureus subsp. aureus NCTC 8325]	37	50182	14	1	14	1	30.8	7	3
88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	154	41012	13	6	10	5	22.1	7	1
88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	446	41012	27	10	17	7	28.2	7	2
88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	230	41012	23	6	19	6	34.9	7	3

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88193824	chromosomal replication initiation protein [Staphylococcus aureus subsp. aureus NCTC 8325]	37	51934	8	1	7	1	11	7	3
88194665	coenzyme A disulfide reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	47	49259	16	1	15	1	26.3	7	2
88194292	cysteinyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	139	53652	17	4	16	4	26.8	7	3
88194636	cytosol aminopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	46	54095	11	1	10	1	14.9	7	3
88195984	D-alanyl-alanine synthetase A [Staphylococcus aureus subsp. aureus NCTC 8325]	62	40205	13	1	12	1	23	7	1
88195984	D-alanyl-alanine synthetase A [Staphylococcus aureus subsp. aureus NCTC 8325]	110	40205	10	3	10	3	19.4	7	2
88194907	dihydroorotase [Staphylococcus aureus subsp. aureus NCTC 8325]	50	46342	5	1	4	1	7.1	7	1
88196221	D-isomer specific 2-hydroxyacid dehydrogenase NAD binding domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	165	34653	18	5	17	5	42.3	7	2
88193829	DNA gyrase subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	41	99290	23	2	21	2	17.6	7	1
88193825	DNA polymerase III subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	95	41888	13	3	12	3	18.3	7	1
88193825	DNA polymerase III subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	245	41888	19	11	18	10	37.7	7	2
88193825	DNA polymerase III subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	135	41888	20	6	18	5	39	7	3
88195079	DNA topoisomerase IV subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	58	74318	20	1	20	1	21.6	7	1
88196136	DNA-directed RNA polymerase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	474	34990	31	15	24	10	51	7	1
88196136	DNA-directed RNA polymerase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	578	34990	41	20	30	13	59.6	7	2
88196136	DNA-directed RNA polymerase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	637	34990	33	21	25	15	49.7	7	3
161353532	DNA-directed RNA polymerase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	176	133136	31	9	28	9	20.5	7	1
88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	1215	32474	43	27	28	18	68.6	7	2
88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	470	43077	19	10	17	8	39.1	7	1
88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	538	43077	26	13	23	10	47.7	7	2
88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	366	43077	20	10	16	8	37.8	7	3
88196007	F0F1 ATP synthase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	225	51368	17	7	15	7	24.5	7	1
88196007	F0F1 ATP synthase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	458	51368	26	12	24	10	39.6	7	3

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88196012	F0F1 ATP synthase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	49	6975	2	1	2	1	17.1	7	1
88194650	FMN oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	63	42083	12	1	10	1	23.5	7	2
88194650	FMN oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	43	42083	12	1	11	1	21.1	7	3
88193954	formate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	50	38094	11	1	10	1	18.5	7	2
88193954	formate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	52	38094	13	1	11	1	25.2	7	3
88195674	fumarate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	42	51075	11	1	11	1	19.3	7	1
88195674	fumarate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	75	51075	17	2	15	2	23.4	7	2
88194657	glucose-6-phosphate isomerase [Staphylococcus aureus subsp. aureus NCTC 8325]	177	49791	26	13	21	11	28.9	7	1
88194657	glucose-6-phosphate isomerase [Staphylococcus aureus subsp. aureus NCTC 8325]	328	49791	28	15	21	12	29.6	7	2
88194657	glucose-6-phosphate isomerase [Staphylococcus aureus subsp. aureus NCTC 8325]	277	49791	35	12	28	10	35.4	7	3
88194652	glutamate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	157	45731	19	4	16	4	30.7	7	1
88194652	glutamate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	228	45731	19	9	15	7	29	7	2
88194226	glutamate synthase large subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	43	166244	26	1	25	1	12.3	7	1
161353522	glutamate-1-semialdehyde aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	167	46727	20	6	16	5	31.5	7	1
161353522	glutamate-1-semialdehyde aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	103	46727	12	4	9	4	19.3	7	2
161353522	glutamate-1-semialdehyde aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	231	46727	21	9	17	7	29.8	7	3
88195018	glutamine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	209	50808	21	7	20	6	28.9	7	3
88195494	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	36956	17	0	17	0	29.9	7	1
88195494	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	306	36956	23	11	16	8	34	7	2
88195494	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	97	36956	22	6	18	5	24.6	7	3
88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	397	36258	32	16	23	10	35.4	7	1
88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	733	36258	49	29	28	15	52.1	7	2
88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	629	36258	45	22	27	13	47.3	7	3

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88194935	glycerol-3-phosphate acyltransferase PlsX [Staphylococcus aureus subsp. aureus NCTC 8325]	51	35408	8	1	8	1	14.6	7	1
88194935	glycerol-3-phosphate acyltransferase PlsX [Staphylococcus aureus subsp. aureus NCTC 8325]	87	35408	12	2	11	2	30.5	7	2
88195342	glycine dehydrogenase subunit 1 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	49685	7	1	6	1	8.3	7	1
88195209	GTP-binding protein EngA [Staphylococcus aureus subsp. aureus NCTC 8325]	149	48949	12	4	11	4	20.2	7	1
88195209	GTP-binding protein EngA [Staphylococcus aureus subsp. aureus NCTC 8325]	137	48949	15	5	14	5	25.5	7	2
88195209	GTP-binding protein EngA [Staphylococcus aureus subsp. aureus NCTC 8325]	107	48949	11	2	11	2	20.6	7	3
88194808	GTP-binding protein TypA [Staphylococcus aureus subsp. aureus NCTC 8325]	48	69152	18	1	17	1	19.5	7	1
88194808	GTP-binding protein TypA [Staphylococcus aureus subsp. aureus NCTC 8325]	80	69152	20	2	19	2	21	7	3
88194145	GTP-dependent nucleic acid-binding protein EngD [Staphylococcus aureus subsp. aureus NCTC 8325]	47	40570	9	1	8	1	16.7	7	1
88194145	GTP-dependent nucleic acid-binding protein EngD [Staphylococcus aureus subsp. aureus NCTC 8325]	119	40570	11	3	11	3	28.2	7	2
88194498	histidinol-phosphate aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	45	39763	5	1	5	1	11.9	7	1
88194498	histidinol-phosphate aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	107	39763	8	2	8	2	16.5	7	2
88194498	histidinol-phosphate aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	68	39763	7	2	7	2	18.8	7	3
88195442	histidyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	98	48252	12	2	12	2	22.6	7	2
88195250	HK97 family phage portal protein [Staphylococcus aureus subsp. aureus NCTC 8325]	37	47657	11	1	11	1	20.4	7	1
88195250	HK97 family phage portal protein [Staphylococcus aureus subsp. aureus NCTC 8325]	51	47657	11	1	10	1	21.8	7	2
88196491	HMG-CoA synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	71	43178	12	1	11	1	24	7	1
88196491	HMG-CoA synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	152	43178	16	4	15	4	28.1	7	2
88196491	HMG-CoA synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	109	43178	16	3	14	3	24.5	7	3
88193869	hypothetical protein SAOUHSC_00049 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	121654	27	1	25	1	21	7	3
88194009	hypothetical protein SAOUHSC_00199 [Staphylococcus aureus subsp. aureus NCTC 8325]	32	58840	11	0	10	0	16.8	7	1
88194355	hypothetical protein SAOUHSC_00581 [Staphylococcus aureus subsp. aureus NCTC 8325]	497	48386	33	15	25	14	42.5	7	3
88194520	hypothetical protein SAOUHSC_00756 [Staphylococcus aureus subsp. aureus NCTC 8325]	41	41771	6	0	6	0	16.6	7	1

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88194520	hypothetical protein SAOUHSC_00756 [Staphylococcus aureus subsp. aureus NCTC 8325]	51	41771	10	1	8	1	19.8	7	2
88194520	hypothetical protein SAOUHSC_00756 [Staphylococcus aureus subsp. aureus NCTC 8325]	51	41771	5	1	5	1	13.1	7	3
88194632	hypothetical protein SAOUHSC_00875 [Staphylococcus aureus subsp. aureus NCTC 8325]	54	39374	7	1	7	1	22.9	7	1
88194632	hypothetical protein SAOUHSC_00875 [Staphylococcus aureus subsp. aureus NCTC 8325]	59	39374	10	1	10	1	27.1	7	2
88194635	hypothetical protein SAOUHSC_00878 [Staphylococcus aureus subsp. aureus NCTC 8325]	118	44077	20	6	16	5	29.9	7	1
88194635	hypothetical protein SAOUHSC_00878 [Staphylococcus aureus subsp. aureus NCTC 8325]	168	44077	26	5	23	5	33.3	7	2
88194926	hypothetical protein SAOUHSC_01187 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	74317	13	1	12	1	12.7	7	1
88194988	hypothetical protein SAOUHSC_01255 [Staphylococcus aureus subsp. aureus NCTC 8325]	48	48588	4	1	4	1	5.7	7	1
88194988	hypothetical protein SAOUHSC_01255 [Staphylococcus aureus subsp. aureus NCTC 8325]	33	48588	11	0	10	0	17.3	7	2
88194988	hypothetical protein SAOUHSC_01255 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	48588	14	0	14	0	25.4	7	3
88195092	hypothetical protein SAOUHSC_01365 [Staphylococcus aureus subsp. aureus NCTC 8325]	63	37832	8	2	8	2	18.7	7	2
88195134	hypothetical protein SAOUHSC_01408 [Staphylococcus aureus subsp. aureus NCTC 8325]	89	43381	18	1	18	1	35.2	7	1
88195134	hypothetical protein SAOUHSC_01408 [Staphylococcus aureus subsp. aureus NCTC 8325]	155	43381	24	4	21	3	38.6	7	3
88195215	hypothetical protein SAOUHSC_01499 [Staphylococcus aureus subsp. aureus NCTC 8325]	61	36713	8	2	8	2	15.9	7	2
88195279	hypothetical protein SAOUHSC_01567 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	13653	8	1	8	1	45.8	7	1
88195433	hypothetical protein SAOUHSC_01728 [Staphylococcus aureus subsp. aureus NCTC 8325]	51	37960	13	1	13	1	29.7	7	1
88195502	hypothetical protein SAOUHSC_01802 [Staphylococcus aureus subsp. aureus NCTC 8325]	71	32371	12	3	10	3	21.4	7	1
88195502	hypothetical protein SAOUHSC_01802 [Staphylococcus aureus subsp. aureus NCTC 8325]	85	32371	14	3	11	3	24.6	7	2
88195502	hypothetical protein SAOUHSC_01802 [Staphylococcus aureus subsp. aureus NCTC 8325]	86	32371	12	4	8	3	22.5	7	3
88195516	hypothetical protein SAOUHSC_01816 [Staphylococcus aureus subsp. aureus NCTC 8325]	75	39529	10	3	9	3	19.4	7	2
88195516	hypothetical protein SAOUHSC_01816 [Staphylococcus aureus subsp. aureus NCTC 8325]	74	39529	10	2	10	2	21.9	7	3
88195532	hypothetical protein SAOUHSC_01832 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	42823	9	1	8	1	18.7	7	1
88195532	hypothetical protein SAOUHSC_01832 [Staphylococcus aureus subsp. aureus NCTC 8325]	24	42823	8	0	8	0	17.6	7	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195559	hypothetical protein SAOUHSC_01861 [Staphylococcus aureus subsp. aureus NCTC 8325]	92	39758	9	2	6	2	13.4	7	1
88195559	hypothetical protein SAOUHSC_01861 [Staphylococcus aureus subsp. aureus NCTC 8325]	120	39758	10	3	9	2	20.9	7	2
88195665	hypothetical protein SAOUHSC_01974 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	114351	26	1	25	1	17.8	7	3
88195666	hypothetical protein SAOUHSC_01975 [Staphylococcus aureus subsp. aureus NCTC 8325]	43	46196	10	1	9	1	18.3	7	2
88195838	hypothetical protein SAOUHSC_02158 [Staphylococcus aureus subsp. aureus NCTC 8325]	75	48089	7	1	7	1	12.9	7	1
88195838	hypothetical protein SAOUHSC_02158 [Staphylococcus aureus subsp. aureus NCTC 8325]	82	48089	10	2	10	2	18.9	7	2
88195838	hypothetical protein SAOUHSC_02158 [Staphylococcus aureus subsp. aureus NCTC 8325]	116	48089	10	3	9	3	18.2	7	3
88196065	hypothetical protein SAOUHSC_02404 [Staphylococcus aureus subsp. aureus NCTC 8325]	50	262863	75	1	74	1	23.9	7	1
88196065	hypothetical protein SAOUHSC_02404 [Staphylococcus aureus subsp. aureus NCTC 8325]	46	262863	89	1	84	1	25.7	7	2
88196123	hypothetical protein SAOUHSC_02471 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	56116	7	2	6	2	12.4	7	2
88196124	hypothetical protein SAOUHSC_02472 [Staphylococcus aureus subsp. aureus NCTC 8325]	52	44072	12	1	11	1	28	7	2
88196218	hypothetical protein SAOUHSC_02574 [Staphylococcus aureus subsp. aureus NCTC 8325]	76	40717	14	3	11	3	21.1	7	1
88196218	hypothetical protein SAOUHSC_02574 [Staphylococcus aureus subsp. aureus NCTC 8325]	48	40717	8	2	7	2	16.7	7	2
88196391	hypothetical protein SAOUHSC_02755 [Staphylococcus aureus subsp. aureus NCTC 8325]	80	39168	14	3	13	3	38.5	7	1
88196391	hypothetical protein SAOUHSC_02755 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	39168	9	1	9	1	21.2	7	2
88196426	hypothetical protein SAOUHSC_02790 [Staphylococcus aureus subsp. aureus NCTC 8325]	44	109832	23	2	21	2	19.3	7	3
88196609	hypothetical protein SAOUHSC_02990 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	227909	21	1	17	1	6.5	7	1
88196609	hypothetical protein SAOUHSC_02990 [Staphylococcus aureus subsp. aureus NCTC 8325]	231	227909	28	5	27	5	10	7	3
88196248	imidazolonepropionase [Staphylococcus aureus subsp. aureus NCTC 8325]	55	45011	10	1	10	1	23.1	7	1
88195501	isocitrate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	378	46394	34	15	28	12	42.2	7	1
88195501	isocitrate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	849	46394	47	28	34	19	53.8	7	2
88195501	isocitrate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	610	46394	33	21	24	14	41.9	7	3
88195645	lantibiotic epidermin biosynthesis protein EpiB [Staphylococcus aureus subsp. aureus NCTC 8325]	33	117561	23	1	23	1	15.1	7	3

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88194720	lipoyltransferase and lipoate-protein ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	69	37904	16	2	14	2	27.7	7	1
88194720	lipoyltransferase and lipoate-protein ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	108	37904	14	5	12	4	27.7	7	2
88194720	lipoyltransferase and lipoate-protein ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	64	37904	10	2	8	2	14.9	7	3
88196549	L-lactate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	176	34399	12	6	11	6	29.8	7	1
88196549	L-lactate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	219	34399	15	7	12	6	37	7	2
88196549	L-lactate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	162	34399	15	6	13	6	37.3	7	3
88196064	mannitol-1-phosphate 5-dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	50	40912	7	1	7	1	14.7	7	1
88195101	methicillin resistance factor [Staphylococcus aureus subsp. aureus NCTC 8325]	37	49645	12	1	10	1	17.2	7	1
88195101	methicillin resistance factor [Staphylococcus aureus subsp. aureus NCTC 8325]	51	49645	16	1	15	1	19.1	7	2
88195100	methicillin resistance factor FemA [Staphylococcus aureus subsp. aureus NCTC 8325]	103	49093	13	3	12	3	18.1	7	1
88195100	methicillin resistance factor FemA [Staphylococcus aureus subsp. aureus NCTC 8325]	162	49093	19	5	17	5	30.7	7	2
88195100	methicillin resistance factor FemA [Staphylococcus aureus subsp. aureus NCTC 8325]	145	49093	14	2	11	2	19	7	3
88196188	molybdopterin biosynthesis protein MoeA [Staphylococcus aureus subsp. aureus NCTC 8325]	65	44988	16	1	13	1	27.4	7	2
88194475	N-acetylglucosamine-6-phosphate deacetylase [Staphylococcus aureus subsp. aureus NCTC 8325]	58	43103	11	1	11	1	23.9	7	1
88194475	N-acetylglucosamine-6-phosphate deacetylase [Staphylococcus aureus subsp. aureus NCTC 8325]	62	43103	19	2	19	2	35.6	7	2
88193969	N-acetylmuramic acid-6-phosphate etherase [Staphylococcus aureus subsp. aureus NCTC 8325]	32	32231	12	1	12	1	29.9	7	1
88195812	NAD synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	40	30678	9	1	8	1	18.3	7	1
88195812	NAD synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	64	30678	12	1	10	1	25.3	7	2
88195812	NAD synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	45	30678	19	1	16	1	35.9	7	3
88195510	NADP-dependent malic enzyme [Staphylococcus aureus subsp. aureus NCTC 8325]	73	44206	6	3	6	3	11.7	7	1
88195510	NADP-dependent malic enzyme [Staphylococcus aureus subsp. aureus NCTC 8325]	109	44206	20	5	19	5	40.3	7	2
88194651	ornithine--oxo-acid transaminase [Staphylococcus aureus subsp. aureus NCTC 8325]	156	43390	14	4	14	4	31.3	7	1
88194651	ornithine--oxo-acid transaminase [Staphylococcus aureus subsp. aureus NCTC 8325]	399	43390	20	8	18	6	43.2	7	2

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88195317	peptidase T [Staphylococcus aureus subsp. aureus NCTC 8325]	78	40235	7	2	7	2	16.4	7	1
88195317	peptidase T [Staphylococcus aureus subsp. aureus NCTC 8325]	200	40235	25	8	22	7	43.2	7	2
88195317	peptidase T [Staphylococcus aureus subsp. aureus NCTC 8325]	87	40235	13	2	13	2	20.4	7	3
88196022	peptide chain release factor 1 [Staphylococcus aureus subsp. aureus NCTC 8325]	65	40325	4	3	4	3	9.5	7	2
88196022	peptide chain release factor 1 [Staphylococcus aureus subsp. aureus NCTC 8325]	109	40325	21	3	18	2	34.1	7	3
88194839	phenylalanyl-tRNA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	73	40081	13	3	13	3	27	7	1
88194839	phenylalanyl-tRNA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	146	40081	29	6	26	5	47.4	7	2
88194839	phenylalanyl-tRNA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	62	40081	16	2	15	2	28.1	7	3
88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	118	42575	20	6	19	6	36.4	7	1
88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	557	42575	48	24	40	23	58.8	7	2
88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	134	42575	31	8	26	8	46	7	3
88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	548	47088	32	17	26	15	42.2	7	1
88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	580	47088	44	18	35	14	46.5	7	2
88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	613	47088	35	18	25	14	41.7	7	3
88194772	phosphoribosylamine--glycine ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	220	45820	22	8	20	6	33.5	7	1
88194763	phosphoribosylaminoimidazole carboxylase ATPase subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	40	42466	11	1	11	1	26.7	7	1
88194763	phosphoribosylaminoimidazole carboxylase ATPase subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	114	42466	19	5	17	5	32.1	7	2
88194763	phosphoribosylaminoimidazole carboxylase ATPase subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	60	42466	11	1	9	1	18.2	7	3
88194767	phosphoribosylformylglycinamidine synthase II [Staphylococcus aureus subsp. aureus NCTC 8325]	63	79486	17	1	16	1	19.6	7	1
88195336	proline dipeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	101	39313	15	5	13	5	29.2	7	1
88195336	proline dipeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	127	39313	11	5	10	5	22.4	7	2
88196040	pyrimidine-nucleoside phosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	97	46279	21	4	19	4	34.9	7	1
88196040	pyrimidine-nucleoside phosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	646	46279	31	17	25	13	44.8	7	2

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88196040	pyrimidine-nucleoside phosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	130	46279	18	4	17	3	37.6	7	3
88194813	pyruvate carboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	160	128467	42	5	36	4	24.9	7	3
88194792	pyruvate dehydrogenase complex, E1 component subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	692	41357	39	20	27	13	51.1	7	2
88194792	pyruvate dehydrogenase complex, E1 component subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	558	41357	33	15	21	9	45.4	7	3
228937974	recombinase A [Staphylococcus aureus subsp. aureus NCTC 8325]	56	37633	16	2	16	2	36.6	7	1
228937974	recombinase A [Staphylococcus aureus subsp. aureus NCTC 8325]	318	37633	29	12	22	10	48.1	7	2
228937974	recombinase A [Staphylococcus aureus subsp. aureus NCTC 8325]	214	37633	21	8	18	7	43.8	7	3
161353524	recombination factor protein RarA [Staphylococcus aureus subsp. aureus NCTC 8325]	51	47221	12	1	11	1	18.6	7	1
161353524	recombination factor protein RarA [Staphylococcus aureus subsp. aureus NCTC 8325]	64	47221	19	2	18	2	29	7	2
88194259	ribose-phosphate pyrophosphokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	104	35262	3	2	3	2	9.3	7	1
88195673	ribosomal large subunit pseudouridine synthase D [Staphylococcus aureus subsp. aureus NCTC 8325]	28	31421	4	0	3	0	8.4	7	1
88195369	RNA polymerase sigma factor RpoD [Staphylococcus aureus subsp. aureus NCTC 8325]	181	42145	17	7	12	6	20.9	7	2
88195369	RNA polymerase sigma factor RpoD [Staphylococcus aureus subsp. aureus NCTC 8325]	109	42145	23	5	18	4	32.6	7	3
88195604	S-adenosylmethionine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	127	43614	10	3	10	3	19.6	7	2
88196017	serine hydroxymethyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	260	45144	22	11	19	9	29.6	7	1
88196017	serine hydroxymethyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	462	45144	34	21	27	17	46.1	7	2
88194953	succinyl-CoA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	351	42030	26	13	22	12	41.2	7	1
88194953	succinyl-CoA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	768	42030	44	24	33	17	48.2	7	2
88194215	trans-sulfuration enzyme family protein [Staphylococcus aureus subsp. aureus NCTC 8325]	109	41253	9	4	7	3	13.9	7	3
88195539	tyrosyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	67	47568	14	2	14	2	27.4	7	1
88195539	tyrosyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	76	47568	15	2	14	2	24.8	7	2
88195539	tyrosyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	92	47568	15	2	15	2	30	7	3
88196003	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	131	44913	21	4	20	4	27.6	7	2

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88196003	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	147	44913	14	3	13	3	26.4	7	3
88196079	UDP-N-acetylglucosamine pyrophosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	179	44866	19	8	18	7	37.5	7	1
88196079	UDP-N-acetylglucosamine pyrophosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	255	44866	24	11	22	11	40.3	7	2
88196079	UDP-N-acetylglucosamine pyrophosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	565	44866	43	17	28	14	41	7	3
88195554	UDP-N-acetylmuramate--L-alanine ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	62	49157	9	1	9	1	15.8	7	2
88195789	UDP-N-acetylmuramyl tripeptide synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74	49235	13	2	13	2	19.2	7	2
88195789	UDP-N-acetylmuramyl tripeptide synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	66	49235	14	1	12	1	19.7	7	3
88195149	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	73	39672	13	2	12	2	26.7	7	2
88195664	3~-5~ exoribonuclease YhaM [Staphylococcus aureus subsp. aureus NCTC 8325]	70	35756	24	3	20	3	39.6	8	2
88194677	3-oxoacyl-(acyl carrier protein) synthase III [Staphylococcus aureus subsp. aureus NCTC 8325]	60	33858	10	2	10	2	29.1	8	2
88194677	3-oxoacyl-(acyl carrier protein) synthase III [Staphylococcus aureus subsp. aureus NCTC 8325]	82	33858	15	3	13	2	33.5	8	3
88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	166	23773	14	5	11	4	36.4	8	1
88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	90	23773	13	2	11	2	39.2	8	2
88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	166	23773	8	5	7	4	28.1	8	3
88195507	6-phosphofructokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	62	33376	7	3	7	3	21.2	8	1
88195507	6-phosphofructokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	64	33376	13	2	11	2	30	8	2
88195832	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	167	32931	14	8	12	7	34.8	8	1
88195832	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	335	32931	37	14	30	13	64.1	8	2
88195508	acetyl-CoA carboxylase carboxyltransferase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	52	35048	6	2	6	2	16.9	8	1
88195508	acetyl-CoA carboxylase carboxyltransferase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	54	35048	13	2	13	2	34.4	8	2
88195509	acetyl-CoA carboxylase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	41	31851	8	1	8	1	25.6	8	1
88194607	aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	47	46590	9	1	9	1	20.4	8	1
88194906	aspartate carbamoyltransferase catalytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	43	33237	6	1	6	1	14.7	8	1

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88194906	aspartate carbamoyltransferase catalytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	212	33237	20	9	15	8	45.4	8	2
88194906	aspartate carbamoyltransferase catalytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	61	33237	6	1	5	1	16.7	8	3
88195441	aspartyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	69	66587	12	1	10	1	14.8	8	1
88194761	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	65	30824	7	2	6	1	19.2	8	1
88194761	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	273	30824	24	8	19	7	44.4	8	2
88194316	branched-chain amino acid aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	393	40062	25	12	18	9	35.8	8	1
88194316	branched-chain amino acid aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	590	40062	35	18	26	12	48.6	8	3
88195548	catabolite control protein A [Staphylococcus aureus subsp. aureus NCTC 8325]	318	36038	25	11	20	7	39.5	8	1
88195548	catabolite control protein A [Staphylococcus aureus subsp. aureus NCTC 8325]	468	36038	33	15	24	10	49.8	8	2
88195548	catabolite control protein A [Staphylococcus aureus subsp. aureus NCTC 8325]	153	36038	16	5	12	5	26.7	8	3
88196503	cation transporter E1-E2 family ATPase [Staphylococcus aureus subsp. aureus NCTC 8325]	47	86690	20	1	18	1	21.4	8	3
88194313	chaperone protein HchA [Staphylococcus aureus subsp. aureus NCTC 8325]	254	32156	23	9	17	7	37.3	8	1
88194313	chaperone protein HchA [Staphylococcus aureus subsp. aureus NCTC 8325]	460	32156	40	16	24	10	43.5	8	2
88196221	D-isomer specific 2-hydroxyacid dehydrogenase NAD binding domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	45	34653	9	2	8	2	20.2	8	3
88196464	D-lactate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	54	34782	7	2	6	2	16.5	8	1
88196464	D-lactate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	256	34782	13	8	11	8	33.3	8	2
88196464	D-lactate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	55	34782	5	2	5	2	11.4	8	3
88195497	DNA polymerase I [Staphylococcus aureus subsp. aureus NCTC 8325]	27	99133	18	0	17	0	12.1	8	2
88195326	DNA repair protein RecN [Staphylococcus aureus subsp. aureus NCTC 8325]	48	64282	24	1	23	1	32	8	2
88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	355	32474	27	12	25	12	73.4	8	1
88195365	endonuclease IV [Staphylococcus aureus subsp. aureus NCTC 8325]	55	33138	9	2	8	2	24.7	8	1
88195365	endonuclease IV [Staphylococcus aureus subsp. aureus NCTC 8325]	79	33138	15	4	13	4	36.8	8	2

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88196252	formimidoylglutamase [Staphylococcus aureus subsp. aureus NCTC 8325]	69	34491	7	3	6	3	14.5	8	1
88196252	formimidoylglutamase [Staphylococcus aureus subsp. aureus NCTC 8325]	79	34491	9	3	8	2	16.4	8	2
88196252	formimidoylglutamase [Staphylococcus aureus subsp. aureus NCTC 8325]	56	34491	7	2	7	2	21.2	8	3
88194472	fructose 1-phosphate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	56	32553	9	2	8	1	16.7	8	2
88194472	fructose 1-phosphate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	53	32553	5	1	5	1	29.4	8	3
88196553	fructose-1,6-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	459	33034	31	16	27	12	69.9	8	1
88196553	fructose-1,6-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	736	33034	47	28	35	19	72	8	2
88196553	fructose-1,6-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	461	33034	33	15	23	13	52.7	8	3
88194820	glycerophosphoryl diester phosphodiesterase [Staphylococcus aureus subsp. aureus NCTC 8325]	52	34712	10	2	9	2	27.9	8	2
161353525	GTP-binding protein Era [Staphylococcus aureus subsp. aureus NCTC 8325]	88	34249	12	5	11	4	24.4	8	1
161353525	GTP-binding protein Era [Staphylococcus aureus subsp. aureus NCTC 8325]	158	34249	17	8	13	6	26.8	8	2
161353525	GTP-binding protein Era [Staphylococcus aureus subsp. aureus NCTC 8325]	202	34249	15	10	11	7	29.1	8	3
88195060	guanosine 5~-monophosphate oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	36	36093	10	1	10	1	22.5	8	1
88195060	guanosine 5~-monophosphate oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	114	36093	17	5	13	4	27.1	8	2
88195390	heat shock protein GrpE [Staphylococcus aureus subsp. aureus NCTC 8325]	27	23994	10	0	10	0	37	8	1
88195390	heat shock protein GrpE [Staphylococcus aureus subsp. aureus NCTC 8325]	71	23994	15	2	14	2	45.2	8	2
88195203	heptaprenyl diphosphate syntase component II [Staphylococcus aureus subsp. aureus NCTC 8325]	43	35563	9	1	9	1	21	8	2
88195203	heptaprenyl diphosphate syntase component II [Staphylococcus aureus subsp. aureus NCTC 8325]	23	35563	6	0	5	0	11.5	8	3
88194542	HPr kinase/phosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	80	34461	16	4	12	4	29.7	8	1
88194542	HPr kinase/phosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	44	34461	10	1	10	1	31	8	2
88194542	HPr kinase/phosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	32	34461	9	1	9	1	24.2	8	3
88193837	hypothetical protein SAOUHSC_00015 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	73735	13	1	12	1	8.2	8	2
88193895	hypothetical protein SAOUHSC_00080 [Staphylococcus aureus subsp. aureus NCTC 8325]	41	71906	7	1	5	1	5.4	8	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88193995	hypothetical protein SAOUHSC_00185 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	61009	7	1	7	1	10.4	8	3
88194010	hypothetical protein SAOUHSC_00200 [Staphylococcus aureus subsp. aureus NCTC 8325]	49	42156	11	1	8	1	19.2	8	1
88194073	hypothetical protein SAOUHSC_00268 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	68275	14	1	14	1	18.4	8	1
88194073	hypothetical protein SAOUHSC_00268 [Staphylococcus aureus subsp. aureus NCTC 8325]	44	68275	19	2	17	2	20.5	8	3
88194110	hypothetical protein SAOUHSC_00309 [Staphylococcus aureus subsp. aureus NCTC 8325]	98	37753	18	1	18	1	32.8	8	1
88194110	hypothetical protein SAOUHSC_00309 [Staphylococcus aureus subsp. aureus NCTC 8325]	179	37753	18	4	15	4	35.5	8	2
88194110	hypothetical protein SAOUHSC_00309 [Staphylococcus aureus subsp. aureus NCTC 8325]	193	37753	12	5	12	5	31.1	8	3
88194120	hypothetical protein SAOUHSC_00319 [Staphylococcus aureus subsp. aureus NCTC 8325]	264	39147	21	6	18	5	37.1	8	1
88194120	hypothetical protein SAOUHSC_00319 [Staphylococcus aureus subsp. aureus NCTC 8325]	241	39147	18	7	14	6	29.7	8	2
88194120	hypothetical protein SAOUHSC_00319 [Staphylococcus aureus subsp. aureus NCTC 8325]	403	39147	19	12	14	8	36.3	8	3
88194265	hypothetical protein SAOUHSC_00480 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	45082	6	1	6	1	14.1	8	2
88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	211	32955	16	7	14	6	40.3	8	1
88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	910	32955	32	20	18	9	45.2	8	2
88194315	hypothetical protein SAOUHSC_00535 [Staphylococcus aureus subsp. aureus NCTC 8325]	54	36030	10	3	8	2	18.4	8	2
88194322	hypothetical protein SAOUHSC_00542 [Staphylococcus aureus subsp. aureus NCTC 8325]	280	31821	24	8	18	8	53.3	8	2
88194428	hypothetical protein SAOUHSC_00663 [Staphylococcus aureus subsp. aureus NCTC 8325]	35	19267	5	1	4	1	33.3	8	1
88194428	hypothetical protein SAOUHSC_00663 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	19267	5	2	4	1	23.2	8	2
88194549	hypothetical protein SAOUHSC_00788 [Staphylococcus aureus subsp. aureus NCTC 8325]	62	36238	9	2	8	1	21.1	8	1
88194549	hypothetical protein SAOUHSC_00788 [Staphylococcus aureus subsp. aureus NCTC 8325]	45	36238	9	1	9	1	17.8	8	3
88195118	hypothetical protein SAOUHSC_01391 [Staphylococcus aureus subsp. aureus NCTC 8325]	150	34177	26	7	20	6	40	8	2
88195134	hypothetical protein SAOUHSC_01408 [Staphylococcus aureus subsp. aureus NCTC 8325]	85	43381	16	2	16	2	32.5	8	2
88195141	hypothetical protein SAOUHSC_01415 [Staphylococcus aureus subsp. aureus NCTC 8325]	75	30066	4	2	3	1	10	8	1
88195141	hypothetical protein SAOUHSC_01415 [Staphylococcus aureus subsp. aureus NCTC 8325]	93	30066	4	3	3	2	12.6	8	2

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88195157	hypothetical protein SAOUHSC_01433 [Staphylococcus aureus subsp. aureus NCTC 8325]	78	30626	7	1	7	1	21.5	8	1
88195157	hypothetical protein SAOUHSC_01433 [Staphylococcus aureus subsp. aureus NCTC 8325]	109	30626	8	3	8	3	29	8	2
88195305	hypothetical protein SAOUHSC_01594 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	33485	10	1	10	1	21.9	8	1
88195305	hypothetical protein SAOUHSC_01594 [Staphylococcus aureus subsp. aureus NCTC 8325]	64	33485	13	2	11	1	23.8	8	2
88195371	hypothetical protein SAOUHSC_01664 [Staphylococcus aureus subsp. aureus NCTC 8325]	92	30765	8	4	8	4	18.8	8	2
88195380	hypothetical protein SAOUHSC_01673 [Staphylococcus aureus subsp. aureus NCTC 8325]	77	34892	13	4	10	4	25.7	8	1
88195380	hypothetical protein SAOUHSC_01673 [Staphylococcus aureus subsp. aureus NCTC 8325]	91	34892	10	4	10	4	31.1	8	2
88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	146	35160	19	4	17	4	42.6	8	1
88195433	hypothetical protein SAOUHSC_01728 [Staphylococcus aureus subsp. aureus NCTC 8325]	145	37960	16	4	15	4	30	8	2
88195433	hypothetical protein SAOUHSC_01728 [Staphylococcus aureus subsp. aureus NCTC 8325]	159	37960	15	5	14	5	30	8	3
88195557	hypothetical protein SAOUHSC_01859 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	33049	17	0	12	0	24.2	8	1
88195557	hypothetical protein SAOUHSC_01859 [Staphylococcus aureus subsp. aureus NCTC 8325]	94	33049	23	3	17	3	54.4	8	2
88195557	hypothetical protein SAOUHSC_01859 [Staphylococcus aureus subsp. aureus NCTC 8325]	50	33049	8	1	6	1	11.6	8	3
88195581	hypothetical protein SAOUHSC_01884 [Staphylococcus aureus subsp. aureus NCTC 8325]	66	38006	11	3	11	3	23.4	8	2
88195581	hypothetical protein SAOUHSC_01884 [Staphylococcus aureus subsp. aureus NCTC 8325]	72	38006	10	2	9	2	20.7	8	3
88195669	hypothetical protein SAOUHSC_01978 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	42669	16	1	14	1	24.1	8	3
88195779	hypothetical protein SAOUHSC_02097 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	45576	5	1	5	1	8.9	8	1
88196090	hypothetical protein SAOUHSC_02436 [Staphylococcus aureus subsp. aureus NCTC 8325]	55	76040	9	1	8	1	6.8	8	2
88196099	hypothetical protein SAOUHSC_02447 [Staphylococcus aureus subsp. aureus NCTC 8325]	35	36244	11	0	10	0	25.8	8	1
88196099	hypothetical protein SAOUHSC_02447 [Staphylococcus aureus subsp. aureus NCTC 8325]	90	36244	7	3	7	3	16.5	8	2
88196123	hypothetical protein SAOUHSC_02471 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	56116	5	1	5	1	9.4	8	3
88196124	hypothetical protein SAOUHSC_02472 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	44072	6	1	6	1	11.9	8	3
88196214	hypothetical protein SAOUHSC_02570 [Staphylococcus aureus subsp. aureus NCTC 8325]	49	75957	20	2	16	1	17.7	8	2

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88196218	hypothetical protein SAOUHSC_02574 [Staphylococcus aureus subsp. aureus NCTC 8325]	87	40717	11	3	10	3	19.4	8	3
88196246	hypothetical protein SAOUHSC_02604 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	31715	8	1	8	1	22.9	8	1
88196246	hypothetical protein SAOUHSC_02604 [Staphylococcus aureus subsp. aureus NCTC 8325]	89	31715	7	3	7	3	14.3	8	2
88196386	hypothetical protein SAOUHSC_02750 [Staphylococcus aureus subsp. aureus NCTC 8325]	29	60601	13	0	9	0	16.5	8	2
88196392	hypothetical protein SAOUHSC_02756 [Staphylococcus aureus subsp. aureus NCTC 8325]	33	10642	3	1	3	1	19.3	8	1
88196392	hypothetical protein SAOUHSC_02756 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	10642	2	1	2	1	14.8	8	2
88196392	hypothetical protein SAOUHSC_02756 [Staphylococcus aureus subsp. aureus NCTC 8325]	35	10642	3	1	3	1	19.3	8	3
88196462	hypothetical protein SAOUHSC_02828 [Staphylococcus aureus subsp. aureus NCTC 8325]	79	30041	3	2	3	2	10.4	8	1
88196477	hypothetical protein SAOUHSC_02844 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	36824	10	1	9	1	23.9	8	1
88196477	hypothetical protein SAOUHSC_02844 [Staphylococcus aureus subsp. aureus NCTC 8325]	100	36824	14	4	12	3	32.6	8	2
88196477	hypothetical protein SAOUHSC_02844 [Staphylococcus aureus subsp. aureus NCTC 8325]	80	36824	9	2	8	2	22	8	3
88196497	hypothetical protein SAOUHSC_02866 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	90352	24	1	22	1	21	8	2
88196527	hypothetical protein SAOUHSC_02899 [Staphylococcus aureus subsp. aureus NCTC 8325]	51	38170	8	1	8	1	17.9	8	1
88196527	hypothetical protein SAOUHSC_02899 [Staphylococcus aureus subsp. aureus NCTC 8325]	83	38170	9	2	8	2	20.8	8	2
88196528	hypothetical protein SAOUHSC_02900 [Staphylococcus aureus subsp. aureus NCTC 8325]	79	30986	10	2	9	2	23.9	8	2
88196528	hypothetical protein SAOUHSC_02900 [Staphylococcus aureus subsp. aureus NCTC 8325]	92	30986	14	3	12	3	35.5	8	3
88195796	lipid kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	90	34865	8	2	8	2	31.7	8	1
88195796	lipid kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	96	34865	9	2	8	2	17.8	8	2
88195796	lipid kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	97	34865	7	1	7	1	18.1	8	3
88194016	L-lactate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	97	29429	14	3	11	3	39.8	8	1
88194016	L-lactate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	255	29429	18	9	17	9	42	8	2
88195820	manganese-dependent inorganic pyrophosphatase [Staphylococcus aureus subsp. aureus NCTC 8325]	265	34047	24	8	22	7	46	8	1
88195820	manganese-dependent inorganic pyrophosphatase [Staphylococcus aureus subsp. aureus NCTC 8325]	424	34047	26	14	21	11	46	8	2

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195820	manganese-dependent inorganic pyrophosphatase [Staphylococcus aureus subsp. aureus NCTC 8325]	225	34047	19	7	18	7	45.3	8	3
88196064	mannitol-1-phosphate 5-dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	51	40912	9	1	8	1	20.4	8	3
88194922	methionyl-tRNA formyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	68	34190	19	3	19	3	42.8	8	1
88194922	methionyl-tRNA formyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	334	34190	24	11	16	9	36	8	2
88194922	methionyl-tRNA formyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	200	34190	21	9	19	8	49.2	8	3
88195946	MutS domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	45	61283	6	1	5	1	9.9	8	2
88193969	N-acetylmuramic acid-6-phosphate etherase [Staphylococcus aureus subsp. aureus NCTC 8325]	49	32231	9	1	9	1	24.8	8	2
88195208	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	61	36048	12	2	9	2	22.3	8	2
88195208	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	69	36048	12	2	11	2	30.1	8	3
88194742	naphthoate synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	170	30406	12	5	11	5	31.5	8	1
88194742	naphthoate synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	256	30406	20	9	17	7	41	8	2
88194142	ParB family chromosome partioning protein [Staphylococcus aureus subsp. aureus NCTC 8325]	47	32836	12	1	12	1	28.5	8	2
88193889	periplasmic binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	41	36721	13	1	13	1	26.7	8	1
88195239	phage tail tape meausure protein [Staphylococcus aureus subsp. aureus NCTC 8325]	49	225925	93	2	85	1	29.3	8	2
88194840	phenylalanyl-tRNA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	66	88866	11	1	11	1	10.9	8	3
88195861	phi PVL orf 13-like protein [Staphylococcus aureus subsp. aureus NCTC 8325]	151	34917	15	4	14	4	33.8	8	2
88195861	phi PVL orf 13-like protein [Staphylococcus aureus subsp. aureus NCTC 8325]	72	34917	16	1	16	1	42.3	8	3
88194769	phosphoribosylaminoimidazole synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	169	36994	10	6	8	5	24.9	8	1
88194769	phosphoribosylaminoimidazole synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	209	36994	17	8	14	6	33.9	8	2
88194349	phosphotransacetylase [Staphylococcus aureus subsp. aureus NCTC 8325]	160	34930	12	7	10	6	24.4	8	1
88194349	phosphotransacetylase [Staphylococcus aureus subsp. aureus NCTC 8325]	475	34930	21	14	15	9	39.6	8	2
88194349	phosphotransacetylase [Staphylococcus aureus subsp. aureus NCTC 8325]	139	34930	9	5	8	5	16.5	8	3
88195491	primosomal protein DnaI [Staphylococcus aureus subsp. aureus NCTC 8325]	42	35613	2	1	2	1	5.6	8	1

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88195491	primosomal protein DnaI [Staphylococcus aureus subsp. aureus NCTC 8325]	45	35613	10	1	9	1	26.8	8	2
88194280	pyridoxal biosynthesis lyase PdxS [Staphylococcus aureus subsp. aureus NCTC 8325]	189	31972	25	7	23	6	54.6	8	1
88194280	pyridoxal biosynthesis lyase PdxS [Staphylococcus aureus subsp. aureus NCTC 8325]	506	31972	25	13	23	11	54.6	8	2
88194280	pyridoxal biosynthesis lyase PdxS [Staphylococcus aureus subsp. aureus NCTC 8325]	148	31972	21	6	17	5	39	8	3
88194792	pyruvate dehydrogenase complex, E1 component subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	323	41357	14	9	11	7	24.3	8	1
88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	601	35224	37	19	26	12	56.6	8	1
88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	759	35224	39	24	26	15	51.4	8	2
88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	598	35224	33	18	24	13	59.1	8	3
88194758	quinol oxidase AA3 subunit II [Staphylococcus aureus subsp. aureus NCTC 8325]	40	41750	10	1	9	1	12.6	8	1
88194758	quinol oxidase AA3 subunit II [Staphylococcus aureus subsp. aureus NCTC 8325]	21	41750	11	0	10	0	13.7	8	2
88194480	response regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	29	26841	6	0	6	0	18.9	8	3
88194046	ribokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	59	32429	10	2	10	2	24.7	8	1
88194046	ribokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	395	32429	20	12	14	8	48.4	8	2
88194046	ribokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	139	32429	20	5	16	5	45.1	8	3
88194508	ribonucleotide-diphosphate reductase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	136	37489	12	6	11	6	22.3	8	1
88194508	ribonucleotide-diphosphate reductase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	72	37489	8	2	8	2	18.6	8	2
88194508	ribonucleotide-diphosphate reductase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	108	37489	12	4	10	4	25.4	8	3
88194259	ribose-phosphate pyrophosphokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	130	35262	10	4	10	4	23.4	8	2
88195673	ribosomal large subunit pseudouridine synthase D [Staphylococcus aureus subsp. aureus NCTC 8325]	66	31421	12	1	10	1	26.7	8	2
88194954	succinyl-CoA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	78	31522	9	2	9	2	32.8	8	1
88194954	succinyl-CoA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	247	31522	20	10	17	9	46.7	8	2
88196104	tagatose 1,6-diphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	83	36573	13	3	12	2	22.4	8	2
88195858	tail length tape measure protein [Staphylococcus aureus subsp. aureus NCTC 8325]	46	169851	34	2	30	1	16.2	8	3

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88194546	thioredoxin reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	221	33595	21	8	18	6	41.5	8	1
88194546	thioredoxin reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	660	33595	42	23	29	16	56.6	8	2
88194546	thioredoxin reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	422	33595	25	15	18	11	37.3	8	3
88195051	threonine synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	60	37846	10	1	10	1	25.2	8	1
88195051	threonine synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	51	37846	7	1	6	1	14.2	8	2
88194959	tRNA (uracil-5-)-methyltransferase Gid [Staphylococcus aureus subsp. aureus NCTC 8325]	46	48341	9	1	9	1	19.1	8	3
88195012	tRNA delta(2)-isopentenylpyrophosphate transferase [Staphylococcus aureus subsp. aureus NCTC 8325]	62	35845	7	3	6	2	18.3	8	3
88194690	tryptophanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	210	36886	17	8	13	7	28.3	8	1
88194690	tryptophanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	229	36886	17	9	16	8	31.3	8	2
88194690	tryptophanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	197	36886	15	7	14	7	35.9	8	3
88194516	UDP-N-acetylenolpyruvoylglucosamine reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	49	33776	13	2	13	2	25.4	8	2
88195149	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	87	39672	17	2	15	2	30.6	8	3
88195655	uroporphyrinogen decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	58	39327	13	2	11	2	20	8	1
88195655	uroporphyrinogen decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	88	39327	10	3	9	3	21.4	8	2
88195655	uroporphyrinogen decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	55	39327	6	2	5	2	13.6	8	3
88196436	UTP-glucose-1-phosphate uridylyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	83	29440	7	3	6	3	18.1	8	2
88194032	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	154	26640	9	6	8	5	30.3	9	1
88194028	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	101	25198	9	3	8	2	29.9	9	1
88194032	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	256	26640	22	10	17	8	57.1	9	2
88196546	3-methyl-2-oxobutanoate hydroxymethyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	59	28222	8	1	8	1	30.8	9	1
88196546	3-methyl-2-oxobutanoate hydroxymethyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	109	28222	8	2	8	2	26.6	9	3
88194677	3-oxoacyl-(acyl carrier protein) synthase III [Staphylococcus aureus subsp. aureus NCTC 8325]	58	33858	11	1	10	1	24.6	9	1
88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	278	24693	20	9	14	9	50	9	1

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	444	24693	28	18	17	11	43	9	2
88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	379	24693	29	17	20	12	49.1	9	3
88196159	50S ribosomal protein L2 [Staphylococcus aureus subsp. aureus NCTC 8325]	125	30136	14	3	13	2	43.3	9	1
88196159	50S ribosomal protein L2 [Staphylococcus aureus subsp. aureus NCTC 8325]	655	30136	42	20	28	12	65.7	9	2
88196159	50S ribosomal protein L2 [Staphylococcus aureus subsp. aureus NCTC 8325]	446	30136	33	14	20	10	54.2	9	3
88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	174	23703	13	6	11	5	41.8	9	2
88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	227	23703	17	6	16	5	41.4	9	3
88194605	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	148	28257	13	6	12	5	39.5	9	1
88194605	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	150	28257	17	7	16	7	55.7	9	2
88194089	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35	24967	11	1	11	1	39.6	9	2
88195832	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	177	32931	22	6	18	6	46.9	9	3
88195682	ABC transporter permease [Staphylococcus aureus subsp. aureus NCTC 8325]	41	53089	13	1	13	1	18.1	9	1
88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	94	35049	13	2	13	2	28.5	9	2
88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	134	35049	16	3	16	3	34.9	9	3
88195935	accessory gene regulator protein A [Staphylococcus aureus subsp. aureus NCTC 8325]	125	24238	9	4	8	4	30.3	9	1
88195935	accessory gene regulator protein A [Staphylococcus aureus subsp. aureus NCTC 8325]	148	24238	11	3	11	3	35.6	9	2
88193886	accessory regulator-like protein [Staphylococcus aureus subsp. aureus NCTC 8325]	92	29871	20	4	19	4	48.8	9	1
88193886	accessory regulator-like protein [Staphylococcus aureus subsp. aureus NCTC 8325]	145	29871	15	7	13	6	48.8	9	2
88193901	acetoin reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	85	27199	9	2	8	2	31	9	1
88193901	acetoin reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	288	27199	19	10	11	6	34.1	9	2
88193901	acetoin reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	218	27199	13	5	12	4	40.3	9	3
88196141	adenylate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	83	23959	6	2	5	2	15.8	9	1
88196141	adenylate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	222	23959	18	6	16	5	41.9	9	2

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195500	alkaline phosphatase synthesis transcriptional regulatory protein [Staphylococcus aureus subsp. aureus NCTC 8325]	102	27105	11	3	9	3	25.6	9	2
88196119	alpha-acetolactate decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	106	26207	7	2	7	2	23.9	9	2
88196119	alpha-acetolactate decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	157	26207	16	4	11	4	30.3	9	3
88196337	amino acid ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	82	27224	18	3	12	2	34.2	9	1
88196337	amino acid ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	70	27224	14	3	11	3	29.2	9	2
88194313	chaperone protein HchA [Staphylococcus aureus subsp. aureus NCTC 8325]	439	32156	24	14	15	10	37	9	3
88194636	cytosol aminopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	46	54095	12	1	12	1	18.1	9	1
88195564	D-alanine aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	69	31874	11	3	11	3	32.6	9	1
88195564	D-alanine aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	163	31874	9	6	7	5	24.1	9	2
88195564	D-alanine aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	185	31874	13	5	11	5	37.9	9	3
88193913	deoxyribose-phosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	40	23458	10	0	9	0	28.6	9	1
88196042	deoxyribose-phosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	249	23313	22	6	18	6	50	9	2
88193913	deoxyribose-phosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	272	23458	23	7	20	7	55.9	9	2
88195495	dephospho-CoA kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	68	23578	5	2	5	2	21.7	9	1
88195495	dephospho-CoA kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	114	23578	7	4	6	3	29.5	9	3
88194274	dihydropteroate synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	66	29504	8	3	8	3	25.1	9	1
88193828	DNA gyrase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	123	72495	19	3	16	3	18.8	9	1
88195297	DNA-binding response regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	107	28143	7	1	7	1	19.9	9	1
88195297	DNA-binding response regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	160	28143	9	2	8	2	25.7	9	2
88195297	DNA-binding response regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	111	28143	14	3	12	3	28.2	9	3
88194704	enoyl-(acyl carrier protein) reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	140	28005	18	8	14	6	32	9	1
88194704	enoyl-(acyl carrier protein) reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	107	28005	17	7	12	5	29.7	9	2
88194704	enoyl-(acyl carrier protein) reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	234	28005	24	13	17	9	38.3	9	3

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88196375	epimerase/dehydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	132	31173	16	5	15	5	30.4	9	2
88196375	epimerase/dehydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	129	31173	16	6	16	6	41.7	9	3
161353520	F0F1 ATP synthase subunit gamma [Staphylococcus aureus subsp. aureus NCTC 8325]	116	32086	14	4	13	3	31.2	9	1
161353520	F0F1 ATP synthase subunit gamma [Staphylococcus aureus subsp. aureus NCTC 8325]	324	32086	17	9	14	7	39.2	9	2
161353520	F0F1 ATP synthase subunit gamma [Staphylococcus aureus subsp. aureus NCTC 8325]	239	32086	17	8	12	4	38.5	9	3
88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	341	30817	29	14	21	10	51	9	1
88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	496	30817	34	19	21	12	45.5	9	2
88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	239	30817	23	9	20	8	50.3	9	3
88194852	glutamate racemase [Staphylococcus aureus subsp. aureus NCTC 8325]	51	29679	7	2	7	2	31.6	9	2
88194852	glutamate racemase [Staphylococcus aureus subsp. aureus NCTC 8325]	33	29679	8	0	8	0	25.9	9	3
88194820	glycerophosphoryl diester phosphodiesterase [Staphylococcus aureus subsp. aureus NCTC 8325]	101	34712	15	4	13	4	35.7	9	3
88195342	glycine dehydrogenase subunit 1 [Staphylococcus aureus subsp. aureus NCTC 8325]	39	49685	13	1	9	1	15.4	9	3
88194328	GTP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	126	33461	10	4	9	4	25.3	9	1
88194328	GTP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	110	33461	13	3	12	3	30.5	9	2
88194328	GTP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	92	33461	12	2	12	2	24.7	9	3
88194318	haloacid dehalogenase-like hydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	77	24977	6	1	5	1	21.1	9	1
88194318	haloacid dehalogenase-like hydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	35	24977	6	1	5	1	22.9	9	2
88195390	heat shock protein GrpE [Staphylococcus aureus subsp. aureus NCTC 8325]	112	23994	12	3	11	3	38.5	9	3
88194348	heme peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	140	29371	14	6	11	5	36	9	1
88194348	heme peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	106	29371	12	4	10	3	34	9	2
88194348	heme peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	99	29371	14	4	10	4	36.4	9	3
88195452	Holliday junction DNA helicase RuvB [Staphylococcus aureus subsp. aureus NCTC 8325]	39	37695	7	1	6	1	16.5	9	1
88194272	Hsp33-like chaperonin [Staphylococcus aureus subsp. aureus NCTC 8325]	88	31802	15	2	15	2	33.8	9	1

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88194272	Hsp33-like chaperonin [Staphylococcus aureus subsp. aureus NCTC 8325]	176	31802	8	4	8	4	21.5	9	2
88194272	Hsp33-like chaperonin [Staphylococcus aureus subsp. aureus NCTC 8325]	57	31802	8	1	8	1	19.8	9	3
88193837	hypothetical protein SAOUHSC_00015 [Staphylococcus aureus subsp. aureus NCTC 8325]	35	73735	9	1	9	1	10.4	9	3
88193846	hypothetical protein SAOUHSC_00025 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	83373	32	1	29	1	30.4	9	2
88194010	hypothetical protein SAOUHSC_00200 [Staphylococcus aureus subsp. aureus NCTC 8325]	35	42156	9	1	8	1	13.4	9	2
88194035	hypothetical protein SAOUHSC_00228 [Staphylococcus aureus subsp. aureus NCTC 8325]	48	66272	15	2	13	2	12.2	9	1
88194224	hypothetical protein SAOUHSC_00433 [Staphylococcus aureus subsp. aureus NCTC 8325]	39	41633	4	1	4	1	8.1	9	1
88194294	hypothetical protein SAOUHSC_00513 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	27190	8	1	8	1	28.2	9	1
88194294	hypothetical protein SAOUHSC_00513 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	27190	11	1	10	1	34.3	9	2
88194294	hypothetical protein SAOUHSC_00513 [Staphylococcus aureus subsp. aureus NCTC 8325]	72	27190	7	2	7	2	22.2	9	3
88194322	hypothetical protein SAOUHSC_00542 [Staphylococcus aureus subsp. aureus NCTC 8325]	100	31821	16	3	16	3	43.3	9	3
88194386	hypothetical protein SAOUHSC_00616 [Staphylococcus aureus subsp. aureus NCTC 8325]	72	30906	6	4	6	4	18	9	1
88194386	hypothetical protein SAOUHSC_00616 [Staphylococcus aureus subsp. aureus NCTC 8325]	78	30906	10	3	8	3	21.8	9	2
88194386	hypothetical protein SAOUHSC_00616 [Staphylococcus aureus subsp. aureus NCTC 8325]	51	30906	6	1	6	1	16.5	9	3
88194404	hypothetical protein SAOUHSC_00637 [Staphylococcus aureus subsp. aureus NCTC 8325]	103	28007	4	1	3	1	11.7	9	1
88194404	hypothetical protein SAOUHSC_00637 [Staphylococcus aureus subsp. aureus NCTC 8325]	156	28007	10	3	9	3	32.4	9	2
88194414	hypothetical protein SAOUHSC_00647 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	64010	11	0	11	0	16.5	9	1
88194440	hypothetical protein SAOUHSC_00675 [Staphylococcus aureus subsp. aureus NCTC 8325]	116	26304	8	2	7	2	26.5	9	1
88194440	hypothetical protein SAOUHSC_00675 [Staphylococcus aureus subsp. aureus NCTC 8325]	221	26304	15	5	12	3	37.4	9	2
88194440	hypothetical protein SAOUHSC_00675 [Staphylococcus aureus subsp. aureus NCTC 8325]	184	26304	11	4	9	4	32.4	9	3
88194455	hypothetical protein SAOUHSC_00690 [Staphylococcus aureus subsp. aureus NCTC 8325]	106	26671	20	2	19	2	40.1	9	3
88194471	hypothetical protein SAOUHSC_00706 [Staphylococcus aureus subsp. aureus NCTC 8325]	39	28455	14	1	13	1	28.7	9	1
88194471	hypothetical protein SAOUHSC_00706 [Staphylococcus aureus subsp. aureus NCTC 8325]	62	28455	10	2	9	2	18.9	9	2

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88194471	hypothetical protein SAOUHSC_00706 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	28455	13	1	12	1	37	9	3
88194477	hypothetical protein SAOUHSC_00712 [Staphylococcus aureus subsp. aureus NCTC 8325]	145	32339	13	4	11	4	31.5	9	1
88194477	hypothetical protein SAOUHSC_00712 [Staphylococcus aureus subsp. aureus NCTC 8325]	163	32339	10	4	10	4	24	9	2
88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	148	22199	15	5	14	5	46.3	9	1
88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	178	22199	16	6	13	5	42.1	9	2
88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	163	22199	15	5	13	4	44.2	9	3
88194596	hypothetical protein SAOUHSC_00838 [Staphylococcus aureus subsp. aureus NCTC 8325]	92	33479	11	3	11	3	27.7	9	2
88194596	hypothetical protein SAOUHSC_00838 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	33479	7	0	7	0	18.8	9	3
88194622	hypothetical protein SAOUHSC_00865 [Staphylococcus aureus subsp. aureus NCTC 8325]	91	27928	6	2	6	2	15.4	9	1
88194622	hypothetical protein SAOUHSC_00865 [Staphylococcus aureus subsp. aureus NCTC 8325]	97	27928	8	3	7	3	22.8	9	3
88194663	hypothetical protein SAOUHSC_00906 [Staphylococcus aureus subsp. aureus NCTC 8325]	173	33093	18	7	17	6	39.7	9	1
88194663	hypothetical protein SAOUHSC_00906 [Staphylococcus aureus subsp. aureus NCTC 8325]	509	33093	34	14	25	10	53	9	2
88194663	hypothetical protein SAOUHSC_00906 [Staphylococcus aureus subsp. aureus NCTC 8325]	507	33093	24	13	19	11	45.3	9	3
88194838	hypothetical protein SAOUHSC_01091 [Staphylococcus aureus subsp. aureus NCTC 8325]	61	26897	7	1	7	1	24.8	9	2
88194898	hypothetical protein SAOUHSC_01158 [Staphylococcus aureus subsp. aureus NCTC 8325]	159	23500	8	3	6	2	22.4	9	1
88194898	hypothetical protein SAOUHSC_01158 [Staphylococcus aureus subsp. aureus NCTC 8325]	565	23500	28	14	18	8	42.4	9	2
88194898	hypothetical protein SAOUHSC_01158 [Staphylococcus aureus subsp. aureus NCTC 8325]	302	23500	18	7	15	5	49.3	9	3
88194998	hypothetical protein SAOUHSC_01265 [Staphylococcus aureus subsp. aureus NCTC 8325]	73	29856	6	2	5	2	14.7	9	1
88194998	hypothetical protein SAOUHSC_01265 [Staphylococcus aureus subsp. aureus NCTC 8325]	71	29856	7	3	7	3	19.2	9	2
88194998	hypothetical protein SAOUHSC_01265 [Staphylococcus aureus subsp. aureus NCTC 8325]	75	29856	7	3	6	3	15.8	9	3
88195053	hypothetical protein SAOUHSC_01323 [Staphylococcus aureus subsp. aureus NCTC 8325]	72	29803	9	1	9	1	24	9	1
88195053	hypothetical protein SAOUHSC_01323 [Staphylococcus aureus subsp. aureus NCTC 8325]	185	29803	10	4	8	3	23.2	9	2
88195118	hypothetical protein SAOUHSC_01391 [Staphylococcus aureus subsp. aureus NCTC 8325]	58	34177	13	2	12	2	31.7	9	3

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88195157	hypothetical protein SAOUHSC_01433 [Staphylococcus aureus subsp. aureus NCTC 8325]	110	30626	10	4	10	4	26.2	9	3
88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	57	1029310	300	2	282	2	23.2	9	1
88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	65	1029310	362	3	337	2	29	9	2
88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	55	1029310	325	4	299	3	26	9	3
88195339	hypothetical protein SAOUHSC_01629 [Staphylococcus aureus subsp. aureus NCTC 8325]	50	31861	9	2	8	2	19.6	9	1
88195339	hypothetical protein SAOUHSC_01629 [Staphylococcus aureus subsp. aureus NCTC 8325]	90	31861	15	3	11	3	19.2	9	2
88195380	hypothetical protein SAOUHSC_01673 [Staphylococcus aureus subsp. aureus NCTC 8325]	72	34892	14	4	12	4	25.1	9	3
88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	309	35160	25	10	21	9	46.5	9	3
88195439	hypothetical protein SAOUHSC_01735 [Staphylococcus aureus subsp. aureus NCTC 8325]	109	28623	11	2	10	2	23.3	9	2
88195439	hypothetical protein SAOUHSC_01735 [Staphylococcus aureus subsp. aureus NCTC 8325]	76	28623	11	2	11	2	28.8	9	3
88195447	hypothetical protein SAOUHSC_01744 [Staphylococcus aureus subsp. aureus NCTC 8325]	14	85557	28	0	28	0	21.8	9	2
88195483	hypothetical protein SAOUHSC_01782 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	22932	4	1	4	1	13.9	9	1
88195483	hypothetical protein SAOUHSC_01782 [Staphylococcus aureus subsp. aureus NCTC 8325]	51	22932	10	2	10	2	35.1	9	2
88195483	hypothetical protein SAOUHSC_01782 [Staphylococcus aureus subsp. aureus NCTC 8325]	71	22932	13	3	10	2	27.2	9	3
88195521	hypothetical protein SAOUHSC_01821 [Staphylococcus aureus subsp. aureus NCTC 8325]	55	35924	10	1	7	1	17.1	9	1
88195521	hypothetical protein SAOUHSC_01821 [Staphylococcus aureus subsp. aureus NCTC 8325]	103	35924	10	3	9	3	20	9	2
88195521	hypothetical protein SAOUHSC_01821 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	35924	7	1	6	1	12.7	9	3
88195542	hypothetical protein SAOUHSC_01843 [Staphylococcus aureus subsp. aureus NCTC 8325]	44	100886	30	2	26	2	22.2	9	1
88195555	hypothetical protein SAOUHSC_01857 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	144568	35	1	31	1	18.1	9	3
88195570	hypothetical protein SAOUHSC_01873 [Staphylococcus aureus subsp. aureus NCTC 8325]	48	238046	70	1	61	1	22.1	9	3
88195579	hypothetical protein SAOUHSC_01882 [Staphylococcus aureus subsp. aureus NCTC 8325]	53	31845	7	1	7	1	21.1	9	1
88195579	hypothetical protein SAOUHSC_01882 [Staphylococcus aureus subsp. aureus NCTC 8325]	41	31845	6	0	6	0	14.5	9	3
88195602	hypothetical protein SAOUHSC_01907 [Staphylococcus aureus subsp. aureus NCTC 8325]	185	31452	15	5	13	5	33.6	9	1

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195602	hypothetical protein SAOUHSC_01907 [Staphylococcus aureus subsp. aureus NCTC 8325]	287	31452	18	6	18	6	39.4	9	2
88195602	hypothetical protein SAOUHSC_01907 [Staphylococcus aureus subsp. aureus NCTC 8325]	435	31452	27	11	18	8	55.6	9	3
88195669	hypothetical protein SAOUHSC_01978 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	42669	12	1	8	1	12.8	9	2
88195680	hypothetical protein SAOUHSC_01989 [Staphylococcus aureus subsp. aureus NCTC 8325]	46	42406	11	2	10	1	19.7	9	3
88195718	hypothetical protein SAOUHSC_02031 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	37017	7	1	7	1	18.1	9	1
88196035	hypothetical protein SAOUHSC_02372 [Staphylococcus aureus subsp. aureus NCTC 8325]	76	25839	6	1	6	1	20.2	9	1
88196035	hypothetical protein SAOUHSC_02372 [Staphylococcus aureus subsp. aureus NCTC 8325]	89	25839	6	1	6	1	26.5	9	2
88196096	hypothetical protein SAOUHSC_02443 [Staphylococcus aureus subsp. aureus NCTC 8325]	53	20787	3	1	3	1	11.2	9	1
88196100	hypothetical protein SAOUHSC_02448 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	33165	12	1	11	1	22.1	9	3
88196271	hypothetical protein SAOUHSC_02630 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	23010	24	1	19	1	54	9	2
88196339	hypothetical protein SAOUHSC_02699 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	28886	9	0	8	0	24.3	9	3
88196386	hypothetical protein SAOUHSC_02750 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	60601	8	1	8	1	18.9	9	1
88196406	hypothetical protein SAOUHSC_02770 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	30984	2	1	2	1	8.1	9	2
161353518	hypothetical protein SAOUHSC_02772 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	26173	6	1	5	1	15.1	9	1
161353518	hypothetical protein SAOUHSC_02772 [Staphylococcus aureus subsp. aureus NCTC 8325]	62	26173	7	4	5	3	15.9	9	2
161353518	hypothetical protein SAOUHSC_02772 [Staphylococcus aureus subsp. aureus NCTC 8325]	43	26173	8	2	7	2	19.7	9	3
88196454	hypothetical protein SAOUHSC_02820 [Staphylococcus aureus subsp. aureus NCTC 8325]	64	25788	13	2	12	2	37.2	9	1
88196454	hypothetical protein SAOUHSC_02820 [Staphylococcus aureus subsp. aureus NCTC 8325]	114	25788	13	4	13	4	38.1	9	2
88196454	hypothetical protein SAOUHSC_02820 [Staphylococcus aureus subsp. aureus NCTC 8325]	121	25788	18	4	15	4	38.5	9	3
88196456	hypothetical protein SAOUHSC_02822 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	76127	14	1	14	1	16.1	9	1
88196462	hypothetical protein SAOUHSC_02828 [Staphylococcus aureus subsp. aureus NCTC 8325]	45	30041	3	1	3	1	12.7	9	3
88196651	hypothetical protein SAOUHSC_03034 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	30419	2	1	2	1	8.3	9	2
88196651	hypothetical protein SAOUHSC_03034 [Staphylococcus aureus subsp. aureus NCTC 8325]	80	30419	7	1	7	1	19.7	9	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88194806	inositol monophosphatase family protein [Staphylococcus aureus subsp. aureus NCTC 8325]	61	30453	13	2	9	2	19.6	9	1
88194806	inositol monophosphatase family protein [Staphylococcus aureus subsp. aureus NCTC 8325]	40	30453	9	1	9	1	18.2	9	2
88194806	inositol monophosphatase family protein [Staphylococcus aureus subsp. aureus NCTC 8325]	99	30453	6	3	6	3	13.1	9	3
88195572	leucyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	75	91728	27	3	23	2	16.8	9	1
88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33	33022	7	0	7	0	17.4	9	1
88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	93	33022	11	5	8	5	21.8	9	2
88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	103	33022	12	3	12	3	30	9	3
88194685	oligopeptide ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	33	64487	12	1	12	1	14.5	9	3
88194237	Orn/Lys/Arg decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	47	50989	6	1	6	1	11.5	9	1
88194887	penicillin-binding protein 1 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	82657	26	1	23	1	21.4	9	2
88194887	penicillin-binding protein 1 [Staphylococcus aureus subsp. aureus NCTC 8325]	46	82657	14	1	13	1	13.7	9	3
88194996	phosphodiesterase [Staphylococcus aureus subsp. aureus NCTC 8325]	31	58477	13	0	13	0	21.2	9	1
88196343	phosphoglyceromutase [Staphylococcus aureus subsp. aureus NCTC 8325]	336	26663	19	11	16	10	39	9	1
88196343	phosphoglyceromutase [Staphylococcus aureus subsp. aureus NCTC 8325]	392	26663	20	11	16	10	50.9	9	2
88196343	phosphoglyceromutase [Staphylococcus aureus subsp. aureus NCTC 8325]	351	26663	20	13	15	10	41.7	9	3
88194341	phosphomethylpyrimidine kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	290	29838	15	9	14	9	42	9	2
88194764	phosphoribosylaminoimidazole-succinocarboxamide synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	118	26676	16	5	13	5	45.3	9	1
88194764	phosphoribosylaminoimidazole-succinocarboxamide synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	555	26676	34	16	26	14	67.1	9	2
88196480	PTS system glucose-specific transporter subunit IIABC [Staphylococcus aureus subsp. aureus NCTC 8325]	51	74368	11	1	9	1	8.4	9	1
88194254	pur operon repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	60	30376	8	1	8	1	25.5	9	1
88194254	pur operon repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	202	30376	9	5	9	5	32.5	9	3
88196043	purine nucleoside phosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	77	25892	9	3	8	3	25.8	9	1
88196043	purine nucleoside phosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	174	25892	11	6	9	5	29.2	9	2

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195596	putative translaldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	290	25689	19	11	17	9	51.1	9	1
88195596	putative translaldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	580	25689	34	22	22	15	61.2	9	2
88195308	pyrroline-5-carboxylate reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	75	28740	11	2	9	1	33.7	9	2
88194758	quinol oxidase AA3 subunit II [Staphylococcus aureus subsp. aureus NCTC 8325]	40	41750	13	1	11	1	15	9	3
88194480	response regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	45	26841	7	1	7	1	21.9	9	1
88194480	response regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	45	26841	4	1	4	1	15.8	9	2
88194940	ribonuclease III [Staphylococcus aureus subsp. aureus NCTC 8325]	41	27904	5	0	3	0	8.6	9	1
88194940	ribonuclease III [Staphylococcus aureus subsp. aureus NCTC 8325]	21	27904	6	0	5	0	16.5	9	2
88194479	sensor histidine kinase SaeS [Staphylococcus aureus subsp. aureus NCTC 8325]	41	39717	10	1	9	1	17.4	9	2
88195527	septation ring formation regulator EzrA [Staphylococcus aureus subsp. aureus NCTC 8325]	72	66206	27	1	25	1	29.1	9	2
88194291	serine acetyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	91	23740	10	3	8	2	29.3	9	1
88194291	serine acetyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	81	23740	8	1	7	1	25.1	9	2
88194942	signal recognition particle-docking protein FtsY [Staphylococcus aureus subsp. aureus NCTC 8325]	40	46561	19	1	15	1	26	9	3
88194851	succinate dehydrogenase iron-sulfur subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	39	30563	12	1	11	1	24	9	1
88194851	succinate dehydrogenase iron-sulfur subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	182	30563	20	7	19	7	51.3	9	2
88195419	transcription elongation factor GreA [Staphylococcus aureus subsp. aureus NCTC 8325]	38	17732	6	2	5	1	26.6	9	2
88194963	transcriptional repressor CodY [Staphylococcus aureus subsp. aureus NCTC 8325]	161	28737	17	7	16	7	33.9	9	1
88194963	transcriptional repressor CodY [Staphylococcus aureus subsp. aureus NCTC 8325]	208	28737	25	7	20	7	50.2	9	2
88194963	transcriptional repressor CodY [Staphylococcus aureus subsp. aureus NCTC 8325]	256	28737	22	10	18	10	43.2	9	3
88194215	trans-sulfuration enzyme family protein [Staphylococcus aureus subsp. aureus NCTC 8325]	55	41253	3	1	3	1	7.4	9	1
88194557	triosephosphate isomerase [Staphylococcus aureus subsp. aureus NCTC 8325]	71	27275	10	3	9	3	25.3	9	1
88194557	triosephosphate isomerase [Staphylococcus aureus subsp. aureus NCTC 8325]	234	27275	24	9	20	8	46.6	9	2
88195012	tRNA delta(2)-isopentenylpyrophosphate transferase [Staphylococcus aureus subsp. aureus NCTC 8325]	54	35845	11	1	10	1	24.1	9	1

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88193841	two-component response regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	51	27175	6	2	6	2	29.2	9	1
88193841	two-component response regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	77	27175	17	3	17	3	52.4	9	2
88193841	two-component response regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	40	27175	2	1	2	1	6.4	9	3
88194970	undecaprenyl pyrophosphate synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	93	29829	11	3	11	3	34.8	9	2
88194970	undecaprenyl pyrophosphate synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	45	29829	9	1	9	1	25.8	9	3
88194342	uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus NCTC 8325]	32	24922	10	0	8	0	34.4	9	2
88194968	uridylate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	213	26128	19	7	16	5	42.1	9	1
88194968	uridylate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	298	26128	17	10	13	8	38.3	9	2
88196436	UTP-glucose-1-phosphate uridylyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	50	29440	5	1	5	1	16.9	9	3
88195468	valyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	57	101660	25	1	22	1	19.3	9	1
88195537	1-acyl-sn-glycerol-3-phosphate acyltransferase domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	113	23059	12	5	8	4	32.7	10	1
88195537	1-acyl-sn-glycerol-3-phosphate acyltransferase domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	107	23059	14	5	10	5	36.1	10	2
88195537	1-acyl-sn-glycerol-3-phosphate acyltransferase domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	125	23059	11	4	9	4	35.1	10	3
88194032	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	74	26640	5	2	5	2	22.7	10	3
88196156	30S ribosomal protein S3 [Staphylococcus aureus subsp. aureus NCTC 8325]	493	24085	22	18	17	15	59.4	10	1
88196156	30S ribosomal protein S3 [Staphylococcus aureus subsp. aureus NCTC 8325]	974	24085	44	30	30	19	74.2	10	2
88196156	30S ribosomal protein S3 [Staphylococcus aureus subsp. aureus NCTC 8325]	831	24085	40	26	28	17	70.5	10	3
88195529	30S ribosomal protein S4 [Staphylococcus aureus subsp. aureus NCTC 8325]	250	22999	22	10	16	8	48	10	1
88195529	30S ribosomal protein S4 [Staphylococcus aureus subsp. aureus NCTC 8325]	588	22999	31	19	22	13	52	10	2
88195529	30S ribosomal protein S4 [Staphylococcus aureus subsp. aureus NCTC 8325]	358	22999	27	13	23	10	62.5	10	3
88194937	3-oxoacyl-(acyl-carrier-protein) reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	163	25870	11	6	9	5	32.8	10	1
88194937	3-oxoacyl-(acyl-carrier-protein) reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	240	25870	22	12	16	9	56.6	10	2
88194937	3-oxoacyl-(acyl-carrier-protein) reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	54	25870	9	1	9	1	25.4	10	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88196150	50S ribosomal protein L5 [Staphylococcus aureus subsp. aureus NCTC 8325]	648	20254	29	18	21	13	60.9	10	1
88196150	50S ribosomal protein L5 [Staphylococcus aureus subsp. aureus NCTC 8325]	1109	20254	54	34	29	19	72.1	10	2
88196150	50S ribosomal protein L5 [Staphylococcus aureus subsp. aureus NCTC 8325]	544	20254	26	16	19	14	82.1	10	3
88196147	50S ribosomal protein L6 [Staphylococcus aureus subsp. aureus NCTC 8325]	80	19774	15	4	12	4	39.9	10	1
88196147	50S ribosomal protein L6 [Staphylococcus aureus subsp. aureus NCTC 8325]	354	19774	18	11	13	8	60.1	10	2
88194605	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	125	28257	16	3	14	3	43.1	10	3
88195508	acetyl-CoA carboxylase carboxyltransferase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	42	35048	15	1	13	1	29.3	10	3
88196141	adenylate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	259	23959	13	8	11	6	40	10	3
88194163	alkyl hydroperoxide reductase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	428	20963	25	14	19	12	66.1	10	1
88194163	alkyl hydroperoxide reductase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	1356	20963	66	45	37	26	82.5	10	2
88194163	alkyl hydroperoxide reductase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	624	20963	38	22	25	14	84.1	10	3
88196337	amino acid ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	50	27224	15	3	13	2	33.3	10	3
88196590	arginine deiminase [Staphylococcus aureus subsp. aureus NCTC 8325]	37	46885	10	1	10	1	16.8	10	2
88194551	ATP-dependent Clp protease proteolytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	88	21500	6	3	4	2	15.4	10	1
88194551	ATP-dependent Clp protease proteolytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	148	21500	7	4	7	4	53.3	10	2
88193983	azoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	670	23338	21	13	14	8	56.2	10	1
88193983	azoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	1872	23338	45	34	15	10	48.6	10	2
88193983	azoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	1666	23338	45	32	19	14	80.3	10	3
88194904	bifunctional pyrimidine regulatory protein PyrR/uracil phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	58	19843	4	1	4	1	19.4	10	1
88194904	bifunctional pyrimidine regulatory protein PyrR/uracil phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	153	19843	8	4	7	4	35.4	10	2
88194891	cell division protein [Staphylococcus aureus subsp. aureus NCTC 8325]	88	52902	7	2	7	2	12.6	10	1
88194648	cyclophilin-type peptidyl-prolyl cis-trans isomerase [Staphylococcus aureus subsp. aureus NCTC 8325]	241	21605	20	10	12	7	36.5	10	1
88194648	cyclophilin-type peptidyl-prolyl cis-trans isomerase [Staphylococcus aureus subsp. aureus NCTC 8325]	455	21605	44	20	17	8	48.2	10	2

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88194648	cyclophilin-type peptidyl-prolyl cis-trans isomerase [Staphylococcus aureus subsp. aureus NCTC 8325]	332	21605	24	12	15	8	49.7	10	3
228937973	cytidylate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	58	24580	9	2	8	2	32.9	10	1
228937973	cytidylate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	230	24580	14	5	13	5	46.6	10	2
228937973	cytidylate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	276	24580	22	10	18	9	57.1	10	3
88193913	deoxyribose-phosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	117	23458	8	2	8	2	19.5	10	3
88194958	DNA topoisomerase I [Staphylococcus aureus subsp. aureus NCTC 8325]	34	79277	27	1	23	1	26.6	10	3
88196032	DNA-directed RNA polymerase subunit delta [Staphylococcus aureus subsp. aureus NCTC 8325]	49	20868	6	1	5	1	17.6	10	1
88196032	DNA-directed RNA polymerase subunit delta [Staphylococcus aureus subsp. aureus NCTC 8325]	38	20868	5	1	5	1	14.8	10	2
88196032	DNA-directed RNA polymerase subunit delta [Staphylococcus aureus subsp. aureus NCTC 8325]	112	20868	8	3	7	2	33.5	10	3
88196443	gluconate operon transcriptional repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	43	26578	5	1	5	1	19.9	10	2
88194281	glutamine amidotransferase subunit PdxT [Staphylococcus aureus subsp. aureus NCTC 8325]	101	20617	9	3	7	3	21	10	1
88194281	glutamine amidotransferase subunit PdxT [Staphylococcus aureus subsp. aureus NCTC 8325]	49	20617	5	1	5	1	22.6	10	2
88194281	glutamine amidotransferase subunit PdxT [Staphylococcus aureus subsp. aureus NCTC 8325]	64	20617	4	1	4	1	18.8	10	3
88194594	glycine cleavage system protein H [Staphylococcus aureus subsp. aureus NCTC 8325]	80	14084	4	2	4	2	45.2	10	3
88193831	histidine ammonia-lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	57	56041	13	1	13	1	22.2	10	3
88195442	histidyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	57	48252	10	1	10	1	20.5	10	1
88195442	histidyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	54	48252	8	1	8	1	15.2	10	3
88196115	hyaluronate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	37	91928	26	1	23	1	23	10	3
88194195	hypothetical protein SAOUHSC_00400 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	56512	11	1	9	1	12.7	10	2
88194195	hypothetical protein SAOUHSC_00400 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	56512	11	1	10	1	15.5	10	3
88194332	hypothetical protein SAOUHSC_00553 [Staphylococcus aureus subsp. aureus NCTC 8325]	230	22422	13	6	10	4	38.1	10	1
88194332	hypothetical protein SAOUHSC_00553 [Staphylococcus aureus subsp. aureus NCTC 8325]	428	22422	24	10	14	5	38.6	10	2
88194332	hypothetical protein SAOUHSC_00553 [Staphylococcus aureus subsp. aureus NCTC 8325]	249	22422	19	6	16	5	52.4	10	3

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88194414	hypothetical protein SAOUHSC_00647 [Staphylococcus aureus subsp. aureus NCTC 8325]	53	64010	11	1	11	1	15.7	10	3
88194422	hypothetical protein SAOUHSC_00656 [Staphylococcus aureus subsp. aureus NCTC 8325]	50	21247	9	1	9	1	35.1	10	1
88194549	hypothetical protein SAOUHSC_00788 [Staphylococcus aureus subsp. aureus NCTC 8325]	63	36238	10	1	10	1	31.4	10	2
88194674	hypothetical protein SAOUHSC_00917 [Staphylococcus aureus subsp. aureus NCTC 8325]	120	19138	3	3	3	3	15.2	10	1
88194674	hypothetical protein SAOUHSC_00917 [Staphylococcus aureus subsp. aureus NCTC 8325]	74	19138	6	2	6	2	26.3	10	2
88194674	hypothetical protein SAOUHSC_00917 [Staphylococcus aureus subsp. aureus NCTC 8325]	183	19138	9	3	9	3	40.9	10	3
88194805	hypothetical protein SAOUHSC_01054 [Staphylococcus aureus subsp. aureus NCTC 8325]	159	24004	15	5	14	5	31.4	10	1
88194805	hypothetical protein SAOUHSC_01054 [Staphylococcus aureus subsp. aureus NCTC 8325]	325	24004	23	14	15	8	43.1	10	2
88194805	hypothetical protein SAOUHSC_01054 [Staphylococcus aureus subsp. aureus NCTC 8325]	132	24004	14	6	12	4	28.4	10	3
88194838	hypothetical protein SAOUHSC_01091 [Staphylococcus aureus subsp. aureus NCTC 8325]	132	26897	9	2	8	2	23.6	10	3
88194879	hypothetical protein SAOUHSC_01137 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	27189	4	0	4	0	10.4	10	1
88194879	hypothetical protein SAOUHSC_01137 [Staphylococcus aureus subsp. aureus NCTC 8325]	35	27189	1	1	1	1	3	10	3
88195053	hypothetical protein SAOUHSC_01323 [Staphylococcus aureus subsp. aureus NCTC 8325]	80	29803	4	1	3	1	12.4	10	3
88195141	hypothetical protein SAOUHSC_01415 [Staphylococcus aureus subsp. aureus NCTC 8325]	62	30066	4	1	4	1	13.4	10	3
88195150	hypothetical protein SAOUHSC_01425 [Staphylococcus aureus subsp. aureus NCTC 8325]	66	19834	9	1	6	1	24.9	10	2
88195150	hypothetical protein SAOUHSC_01425 [Staphylococcus aureus subsp. aureus NCTC 8325]	109	19834	5	2	4	2	20.1	10	3
88195358	hypothetical protein SAOUHSC_01650 [Staphylococcus aureus subsp. aureus NCTC 8325]	45	20987	5	1	4	1	20.7	10	1
88195371	hypothetical protein SAOUHSC_01664 [Staphylococcus aureus subsp. aureus NCTC 8325]	26	30765	5	0	5	0	19.1	10	1
88195402	hypothetical protein SAOUHSC_01696 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	22449	9	1	8	1	29.9	10	1
88195402	hypothetical protein SAOUHSC_01696 [Staphylococcus aureus subsp. aureus NCTC 8325]	95	22449	11	4	11	4	44.8	10	2
88195469	hypothetical protein SAOUHSC_01768 [Staphylococcus aureus subsp. aureus NCTC 8325]	138	21403	9	4	8	4	33.3	10	1
88195469	hypothetical protein SAOUHSC_01768 [Staphylococcus aureus subsp. aureus NCTC 8325]	44	21403	6	1	6	1	23.7	10	2
88195469	hypothetical protein SAOUHSC_01768 [Staphylococcus aureus subsp. aureus NCTC 8325]	60	21403	2	1	2	1	12.4	10	3

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88195516	hypothetical protein SAOUHSC_01816 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	39529	4	1	4	1	12.5	10	1
88195556	hypothetical protein SAOUHSC_01858 [Staphylococcus aureus subsp. aureus NCTC 8325]	176	21676	15	7	11	5	41.4	10	2
88195556	hypothetical protein SAOUHSC_01858 [Staphylococcus aureus subsp. aureus NCTC 8325]	88	21676	10	3	10	3	41.4	10	3
88195603	hypothetical protein SAOUHSC_01908 [Staphylococcus aureus subsp. aureus NCTC 8325]	22	35031	7	0	6	0	15.6	10	1
88195670	hypothetical protein SAOUHSC_01979 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	17787	5	1	5	1	20.1	10	1
88195670	hypothetical protein SAOUHSC_01979 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	17787	1	1	1	1	3.9	10	3
88195678	hypothetical protein SAOUHSC_01987 [Staphylococcus aureus subsp. aureus NCTC 8325]	311	22330	19	12	14	9	46.7	10	1
88195678	hypothetical protein SAOUHSC_01987 [Staphylococcus aureus subsp. aureus NCTC 8325]	534	22330	33	21	23	14	57.3	10	2
88195701	hypothetical protein SAOUHSC_02013 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	18620	7	1	5	1	25.1	10	2
88195701	hypothetical protein SAOUHSC_02013 [Staphylococcus aureus subsp. aureus NCTC 8325]	87	18620	5	2	5	2	41.5	10	3
88195830	hypothetical protein SAOUHSC_02150 [Staphylococcus aureus subsp. aureus NCTC 8325]	234	21902	19	10	14	7	48.1	10	1
88195830	hypothetical protein SAOUHSC_02150 [Staphylococcus aureus subsp. aureus NCTC 8325]	410	21902	24	16	17	12	61	10	2
88195929	hypothetical protein SAOUHSC_02258 [Staphylococcus aureus subsp. aureus NCTC 8325]	242	23989	17	7	15	5	44.2	10	1
88195929	hypothetical protein SAOUHSC_02258 [Staphylococcus aureus subsp. aureus NCTC 8325]	227	23989	16	7	14	6	40.9	10	2
88195929	hypothetical protein SAOUHSC_02258 [Staphylococcus aureus subsp. aureus NCTC 8325]	129	23989	11	4	9	3	29.3	10	3
88196050	hypothetical protein SAOUHSC_02387 [Staphylococcus aureus subsp. aureus NCTC 8325]	98	24017	9	1	8	1	38	10	1
88196050	hypothetical protein SAOUHSC_02387 [Staphylococcus aureus subsp. aureus NCTC 8325]	403	24017	30	14	16	10	65.6	10	2
88196050	hypothetical protein SAOUHSC_02387 [Staphylococcus aureus subsp. aureus NCTC 8325]	231	24017	16	8	12	7	46.2	10	3
88196100	hypothetical protein SAOUHSC_02448 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	33165	13	1	12	1	33.3	10	2
88196214	hypothetical protein SAOUHSC_02570 [Staphylococcus aureus subsp. aureus NCTC 8325]	25	75957	22	0	19	0	20.9	10	3
88196339	hypothetical protein SAOUHSC_02699 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	28886	11	0	11	0	32.8	10	1
88196385	hypothetical protein SAOUHSC_02747 [Staphylococcus aureus subsp. aureus NCTC 8325]	56	23785	9	1	8	1	34.2	10	1
88196385	hypothetical protein SAOUHSC_02747 [Staphylococcus aureus subsp. aureus NCTC 8325]	89	23785	8	3	8	3	23.6	10	2

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88196385	hypothetical protein SAOUHSC_02747 [Staphylococcus aureus subsp. aureus NCTC 8325]	82	23785	8	3	8	3	34.7	10	3
88196414	hypothetical protein SAOUHSC_02778 [Staphylococcus aureus subsp. aureus NCTC 8325]	133	24589	6	3	5	2	23.8	10	1
88196414	hypothetical protein SAOUHSC_02778 [Staphylococcus aureus subsp. aureus NCTC 8325]	170	24589	15	3	13	2	32.5	10	2
88196414	hypothetical protein SAOUHSC_02778 [Staphylococcus aureus subsp. aureus NCTC 8325]	128	24589	4	3	4	3	16.9	10	3
88196600	hypothetical protein SAOUHSC_02980 [Staphylococcus aureus subsp. aureus NCTC 8325]	76	20717	4	1	4	1	19.9	10	1
88196600	hypothetical protein SAOUHSC_02980 [Staphylococcus aureus subsp. aureus NCTC 8325]	105	20717	4	1	3	1	21	10	2
88194270	hypoxanthine phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	55	20142	5	2	5	2	21.2	10	1
88194270	hypoxanthine phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	50	20142	8	1	8	1	36.9	10	2
88194101	lipase [Staphylococcus aureus subsp. aureus NCTC 8325]	38	76341	17	1	17	1	13.5	10	1
88195515	metal-dependent hydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	49	25234	2	1	2	1	9.6	10	2
88195515	metal-dependent hydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	35	25234	4	0	3	0	5.2	10	3
88195803	NAD-dependent DNA ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	29	75035	21	0	19	0	22.2	10	2
88194853	nucleoside-triphosphatase [Staphylococcus aureus subsp. aureus NCTC 8325]	42	21390	6	1	6	1	24.6	10	1
88194853	nucleoside-triphosphatase [Staphylococcus aureus subsp. aureus NCTC 8325]	84	21390	11	2	9	2	28.7	10	2
88194853	nucleoside-triphosphatase [Staphylococcus aureus subsp. aureus NCTC 8325]	82	21390	15	2	12	2	34.4	10	3
88194911	orotate phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	70	22029	9	2	7	2	17.7	10	1
88194911	orotate phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	111	22029	9	3	9	3	30.5	10	2
88194910	orotidine 5~-phosphate decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	40	25580	11	1	9	1	26.1	10	1
88194910	orotidine 5~-phosphate decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	74	25580	16	4	13	4	37.4	10	2
88194910	orotidine 5~-phosphate decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	33	25580	11	1	9	1	24.8	10	3
88194262	peptidyl-tRNA hydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	138	21689	15	7	13	6	40.5	10	1
88194262	peptidyl-tRNA hydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	149	21689	17	6	14	5	45.8	10	2
88194262	peptidyl-tRNA hydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	44	21689	12	1	10	1	31.6	10	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88194840	phenylalanyl-tRNA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	37	88866	12	1	11	1	13.4	10	1
88194764	phosphoribosylaminoimidazole-succinocarboxamide synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	109	26676	20	4	17	4	47.9	10	3
88194766	phosphoribosylformylglycinamidine synthase I [Staphylococcus aureus subsp. aureus NCTC 8325]	99	24511	7	4	5	4	21.1	10	1
88194766	phosphoribosylformylglycinamidine synthase I [Staphylococcus aureus subsp. aureus NCTC 8325]	358	24511	13	11	9	7	40.4	10	2
88196043	purine nucleoside phosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	65	25892	9	2	9	2	30.5	10	3
88195596	putative translaldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	446	25689	27	16	19	11	51.5	10	3
88195699	recombination regulator RecX [Staphylococcus aureus subsp. aureus NCTC 8325]	49	32221	10	1	10	1	31.6	10	1
88195943	redox-sensing transcriptional repressor Rex [Staphylococcus aureus subsp. aureus NCTC 8325]	85	23584	11	3	9	3	30.3	10	1
88195943	redox-sensing transcriptional repressor Rex [Staphylococcus aureus subsp. aureus NCTC 8325]	91	23584	15	3	13	3	45.5	10	2
88195943	redox-sensing transcriptional repressor Rex [Staphylococcus aureus subsp. aureus NCTC 8325]	55	23584	8	2	8	2	27	10	3
88193839	replicative DNA helicase [Staphylococcus aureus subsp. aureus NCTC 8325]	53	52538	6	1	6	1	13.3	10	2
88194940	ribonuclease III [Staphylococcus aureus subsp. aureus NCTC 8325]	35	27904	8	1	7	1	18.9	10	3
88195478	ribosome biogenesis GTP-binding protein YsxC [Staphylococcus aureus subsp. aureus NCTC 8325]	55	22671	7	1	7	1	16.8	10	1
88195478	ribosome biogenesis GTP-binding protein YsxC [Staphylococcus aureus subsp. aureus NCTC 8325]	91	22671	13	2	10	2	23.5	10	2
88194969	ribosome recycling factor [Staphylococcus aureus subsp. aureus NCTC 8325]	102	20341	11	3	10	3	37.5	10	2
88194969	ribosome recycling factor [Staphylococcus aureus subsp. aureus NCTC 8325]	94	20341	5	3	5	3	22.3	10	3
88194928	ribulose-phosphate 3-epimerase [Staphylococcus aureus subsp. aureus NCTC 8325]	38	23557	10	2	8	2	25.2	10	1
88194928	ribulose-phosphate 3-epimerase [Staphylococcus aureus subsp. aureus NCTC 8325]	43	23557	10	2	8	1	20.1	10	2
88194479	sensor histidine kinase SaeS [Staphylococcus aureus subsp. aureus NCTC 8325]	39	39717	14	1	10	1	20.5	10	3
88194291	serine acetyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	173	23740	10	5	8	3	28.8	10	3
88195361	superoxide dismutase [Staphylococcus aureus subsp. aureus NCTC 8325]	209	22697	12	6	8	4	25.1	10	1
88193908	superoxide dismutase [Staphylococcus aureus subsp. aureus NCTC 8325]	157	23026	14	5	12	5	37.7	10	1
88195361	superoxide dismutase [Staphylococcus aureus subsp. aureus NCTC 8325]	256	22697	21	9	13	5	46.7	10	2

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88193908	superoxide dismutase [Staphylococcus aureus subsp. aureus NCTC 8325]	177	23026	16	6	12	6	35.7	10	2
88195361	superoxide dismutase [Staphylococcus aureus subsp. aureus NCTC 8325]	594	22697	32	19	23	14	68.3	10	3
88193908	superoxide dismutase [Staphylococcus aureus subsp. aureus NCTC 8325]	465	23026	28	14	15	10	54.3	10	3
88194298	transcription antitermination protein [Staphylococcus aureus subsp. aureus NCTC 8325]	147	20651	7	5	7	5	26.4	10	2
88194263	transcription-repair coupling factor [Staphylococcus aureus subsp. aureus NCTC 8325]	38	134135	22	1	22	1	21.1	10	1
88194215	trans-sulfuration enzyme family protein [Staphylococcus aureus subsp. aureus NCTC 8325]	37	41253	6	1	6	1	13.7	10	2
88195149	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	65	39672	9	2	8	1	19.9	10	1
88196016	uracil phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	75	23035	6	1	6	1	24.4	10	1
88196016	uracil phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	299	23035	19	9	16	9	52.6	10	2
88194342	uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus NCTC 8325]	28	24922	2	0	2	0	8.3	10	1
88196205	urease subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	36	61741	8	1	7	1	6.8	10	1
88194170	xanthine phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	206	20871	17	7	15	6	41.7	10	1
88194170	xanthine phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	218	20871	22	10	15	6	51	10	2
88195058	50S ribosomal protein L33 [Staphylococcus aureus subsp. aureus NCTC 8325]	32	5928	5	0	4	0	44.9	11	1
88195359	50S ribosomal protein L33 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	5869	6	1	5	1	77.6	11	2
88196161	50S ribosomal protein L4 [Staphylococcus aureus subsp. aureus NCTC 8325]	176	22451	14	8	10	4	42.5	11	2
88196161	50S ribosomal protein L4 [Staphylococcus aureus subsp. aureus NCTC 8325]	221	22451	13	7	12	6	44.9	11	3
88196147	50S ribosomal protein L6 [Staphylococcus aureus subsp. aureus NCTC 8325]	161	19774	14	8	10	5	53.9	11	3
88196059	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	34	28987	8	1	7	1	22.7	11	2
88194939	acyl carrier protein [Staphylococcus aureus subsp. aureus NCTC 8325]	61	8544	7	2	6	1	50.6	11	1
88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	600	19180	31	14	18	9	75.7	11	1
88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	2419	19180	112	68	46	26	85.8	11	2
88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	454	19180	22	12	14	6	51.5	11	3

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88196590	arginine deiminase [Staphylococcus aureus subsp. aureus NCTC 8325]	44	46885	10	1	10	1	20.2	11	1
88194551	ATP-dependent Clp protease proteolytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	82	21500	10	2	9	2	38.5	11	3
88194961	ATP-dependent protease peptidase subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	70	19560	11	2	11	2	40.9	11	1
88194961	ATP-dependent protease peptidase subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	169	19560	15	5	12	4	41.4	11	2
88194961	ATP-dependent protease peptidase subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	61	19560	8	1	8	1	24.3	11	3
88195293	bacteriophage integrase [Staphylococcus aureus subsp. aureus NCTC 8325]	42	47452	14	1	13	1	29.4	11	1
88194148	bacteriophage L54a single-stranded DNA binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	157	18528	11	6	7	4	27.5	11	2
88194148	bacteriophage L54a single-stranded DNA binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	90	18528	8	3	6	2	31.1	11	3
161353523	bifunctional preprotein translocase subunit SecD/SecF [Staphylococcus aureus subsp. aureus NCTC 8325]	30	84201	22	1	20	1	15.9	11	2
161353523	bifunctional preprotein translocase subunit SecD/SecF [Staphylococcus aureus subsp. aureus NCTC 8325]	40	84201	32	1	27	1	22.1	11	3
88194904	bifunctional pyrimidine regulatory protein PyrR/uracil phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	172	19843	10	5	10	5	46.9	11	3
88193938	cap5L protein/glycosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	40	46547	11	1	10	1	21.7	11	2
88193938	cap5L protein/glycosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	35	46547	15	1	12	1	27.9	11	3
88193824	chromosomal replication initiation protein [Staphylococcus aureus subsp. aureus NCTC 8325]	50	51934	9	1	8	1	12.6	11	1
88195511	DNA polymerase III subunit alpha superfamily protein [Staphylococcus aureus subsp. aureus NCTC 8325]	37	122888	20	1	20	1	14.5	11	1
88195511	DNA polymerase III subunit alpha superfamily protein [Staphylococcus aureus subsp. aureus NCTC 8325]	51	122888	22	2	21	1	16.7	11	2
88195511	DNA polymerase III subunit alpha superfamily protein [Staphylococcus aureus subsp. aureus NCTC 8325]	46	122888	21	1	20	1	16.8	11	3
88195189	DnaQ family exonuclease/DinG family helicase [Staphylococcus aureus subsp. aureus NCTC 8325]	35	104152	19	1	17	1	14.9	11	3
88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	116	53190	8	1	8	1	15.4	11	1
88194661	exonuclease RexB [Staphylococcus aureus subsp. aureus NCTC 8325]	34	134420	15	1	13	1	8.9	11	1
88196010	F0F1 ATP synthase subunit delta [Staphylococcus aureus subsp. aureus NCTC 8325]	291	20486	15	7	11	5	47.5	11	1
88196010	F0F1 ATP synthase subunit delta [Staphylococcus aureus subsp. aureus NCTC 8325]	313	20486	20	8	15	6	59.8	11	2
88196010	F0F1 ATP synthase subunit delta [Staphylococcus aureus subsp. aureus NCTC 8325]	236	20486	17	7	15	6	53.1	11	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88196106	galactose-6-phosphate isomerase subunit LacB [Staphylococcus aureus subsp. aureus NCTC 8325]	62	18939	7	2	6	2	28.7	11	2
88195014	glutathione peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	127	18106	10	5	7	4	33.5	11	1
88195014	glutathione peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	42	18106	6	1	5	1	25.3	11	2
88195007	glycerol uptake operon antiterminator regulatory protein [Staphylococcus aureus subsp. aureus NCTC 8325]	38	20437	3	1	3	1	12.8	11	1
88195007	glycerol uptake operon antiterminator regulatory protein [Staphylococcus aureus subsp. aureus NCTC 8325]	51	20437	5	1	5	1	25.6	11	2
88194820	glycerophosphoryl diester phosphodiesterase [Staphylococcus aureus subsp. aureus NCTC 8325]	41	34712	7	1	7	1	15.3	11	1
88194594	glycine cleavage system protein H [Staphylococcus aureus subsp. aureus NCTC 8325]	54	14084	3	2	2	2	10.3	11	1
88194554	glycolytic operon regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	44	37187	6	1	5	1	10.4	11	1
88194554	glycolytic operon regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	39	37187	11	1	9	1	16.9	11	3
88196115	hyaluronate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	37	91928	25	1	22	1	21.9	11	2
88194007	hypothetical protein SAOUHSC_00197 [Staphylococcus aureus subsp. aureus NCTC 8325]	33	44701	7	1	6	1	12.7	11	1
88194155	hypothetical protein SAOUHSC_00356 [Staphylococcus aureus subsp. aureus NCTC 8325]	106	21293	8	1	8	1	38.4	11	3
88194323	hypothetical protein SAOUHSC_00543 [Staphylococcus aureus subsp. aureus NCTC 8325]	31	20899	7	0	6	0	20.7	11	2
88194323	hypothetical protein SAOUHSC_00543 [Staphylococcus aureus subsp. aureus NCTC 8325]	103	20899	7	1	7	1	33.5	11	3
88194422	hypothetical protein SAOUHSC_00656 [Staphylococcus aureus subsp. aureus NCTC 8325]	103	21247	17	4	16	4	52.1	11	2
88194422	hypothetical protein SAOUHSC_00656 [Staphylococcus aureus subsp. aureus NCTC 8325]	128	21247	14	5	10	4	45.4	11	3
88194453	hypothetical protein SAOUHSC_00688 [Staphylococcus aureus subsp. aureus NCTC 8325]	68	20875	8	2	7	2	21.8	11	2
88194453	hypothetical protein SAOUHSC_00688 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	20875	8	1	7	1	27.7	11	3
88194591	hypothetical protein SAOUHSC_00833 [Staphylococcus aureus subsp. aureus NCTC 8325]	56	20736	5	1	5	1	19	11	1
88194591	hypothetical protein SAOUHSC_00833 [Staphylococcus aureus subsp. aureus NCTC 8325]	55	20736	4	2	4	2	15.1	11	2
88194708	hypothetical protein SAOUHSC_00951 [Staphylococcus aureus subsp. aureus NCTC 8325]	174	19314	10	6	6	4	35.5	11	1
88194708	hypothetical protein SAOUHSC_00951 [Staphylococcus aureus subsp. aureus NCTC 8325]	206	19314	16	7	10	6	45.6	11	2
88194708	hypothetical protein SAOUHSC_00951 [Staphylococcus aureus subsp. aureus NCTC 8325]	60	19314	4	2	4	2	19.5	11	3

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88194746	hypothetical protein SAOUHSC_00989 [Staphylococcus aureus subsp. aureus NCTC 8325]	33	43163	9	1	5	1	9.6	11	1
88194780	hypothetical protein SAOUHSC_01027 [Staphylococcus aureus subsp. aureus NCTC 8325]	232	20077	22	8	17	6	57.8	11	1
88194780	hypothetical protein SAOUHSC_01027 [Staphylococcus aureus subsp. aureus NCTC 8325]	353	20077	31	13	24	10	65.6	11	2
88195077	hypothetical protein SAOUHSC_01349 [Staphylococcus aureus subsp. aureus NCTC 8325]	115	11489	8	4	5	4	37.8	11	1
88195077	hypothetical protein SAOUHSC_01349 [Staphylococcus aureus subsp. aureus NCTC 8325]	51	11489	4	1	4	1	33.7	11	2
88195077	hypothetical protein SAOUHSC_01349 [Staphylococcus aureus subsp. aureus NCTC 8325]	95	11489	5	3	4	3	37.8	11	3
88195150	hypothetical protein SAOUHSC_01425 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	19834	6	0	6	0	25.4	11	1
88195174	hypothetical protein SAOUHSC_01455 [Staphylococcus aureus subsp. aureus NCTC 8325]	51	133025	17	2	15	1	10.6	11	2
88195174	hypothetical protein SAOUHSC_01455 [Staphylococcus aureus subsp. aureus NCTC 8325]	46	133025	23	1	21	1	15	11	3
88195358	hypothetical protein SAOUHSC_01650 [Staphylococcus aureus subsp. aureus NCTC 8325]	75	20987	8	2	7	2	40.8	11	3
88195366	hypothetical protein SAOUHSC_01659 [Staphylococcus aureus subsp. aureus NCTC 8325]	50	51049	16	2	15	2	23.7	11	1
88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	328	35160	24	10	18	8	44.1	11	2
88195407	hypothetical protein SAOUHSC_01701 [Staphylococcus aureus subsp. aureus NCTC 8325]	53	20207	3	1	3	1	15.4	11	2
88195421	hypothetical protein SAOUHSC_01716 [Staphylococcus aureus subsp. aureus NCTC 8325]	41	47625	5	1	5	1	9.7	11	1
88195421	hypothetical protein SAOUHSC_01716 [Staphylococcus aureus subsp. aureus NCTC 8325]	44	47625	11	1	10	1	15.9	11	2
88195519	hypothetical protein SAOUHSC_01819 [Staphylococcus aureus subsp. aureus NCTC 8325]	108	18464	9	3	8	3	45.8	11	1
88195519	hypothetical protein SAOUHSC_01819 [Staphylococcus aureus subsp. aureus NCTC 8325]	150	18464	19	5	16	5	65.1	11	2
88195519	hypothetical protein SAOUHSC_01819 [Staphylococcus aureus subsp. aureus NCTC 8325]	109	18464	12	3	9	2	48.8	11	3
88195525	hypothetical protein SAOUHSC_01825 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	42339	8	1	7	1	23	11	2
88195525	hypothetical protein SAOUHSC_01825 [Staphylococcus aureus subsp. aureus NCTC 8325]	35	42339	14	1	14	1	24.1	11	3
88195538	hypothetical protein SAOUHSC_01838 [Staphylococcus aureus subsp. aureus NCTC 8325]	44	45775	12	2	11	2	18.2	11	1
88195555	hypothetical protein SAOUHSC_01857 [Staphylococcus aureus subsp. aureus NCTC 8325]	35	144568	22	1	20	1	12.4	11	1
88195570	hypothetical protein SAOUHSC_01873 [Staphylococcus aureus subsp. aureus NCTC 8325]	45	238046	41	1	39	1	15.4	11	1

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88195570	hypothetical protein SAOUHSC_01873 [Staphylococcus aureus subsp. aureus NCTC 8325]	54	238046	63	3	56	1	22.9	11	2
88195657	hypothetical protein SAOUHSC_01964 [Staphylococcus aureus subsp. aureus NCTC 8325]	91	19536	7	4	5	2	23.4	11	2
88195678	hypothetical protein SAOUHSC_01987 [Staphylococcus aureus subsp. aureus NCTC 8325]	791	22330	37	25	22	15	66.3	11	3
88195718	hypothetical protein SAOUHSC_02031 [Staphylococcus aureus subsp. aureus NCTC 8325]	25	37017	17	0	14	0	26.3	11	2
88195830	hypothetical protein SAOUHSC_02150 [Staphylococcus aureus subsp. aureus NCTC 8325]	451	21902	34	16	21	12	65.2	11	3
88195902	hypothetical protein SAOUHSC_02228 [Staphylococcus aureus subsp. aureus NCTC 8325]	23	7899	2	0	1	0	9.2	11	1
88195902	hypothetical protein SAOUHSC_02228 [Staphylococcus aureus subsp. aureus NCTC 8325]	26	7899	2	0	1	0	9.2	11	2
88196242	hypothetical protein SAOUHSC_02600 [Staphylococcus aureus subsp. aureus NCTC 8325]	106	20070	9	5	7	4	28.6	11	1
88196242	hypothetical protein SAOUHSC_02600 [Staphylococcus aureus subsp. aureus NCTC 8325]	93	20070	7	3	7	3	29.2	11	2
88196242	hypothetical protein SAOUHSC_02600 [Staphylococcus aureus subsp. aureus NCTC 8325]	140	20070	11	7	8	6	35.7	11	3
88196426	hypothetical protein SAOUHSC_02790 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	109832	27	2	23	2	20	11	2
88196446	hypothetical protein SAOUHSC_02812 [Staphylococcus aureus subsp. aureus NCTC 8325]	35	15982	1	0	1	0	7.2	11	1
88196446	hypothetical protein SAOUHSC_02812 [Staphylococcus aureus subsp. aureus NCTC 8325]	33	15982	6	0	6	0	21	11	3
88196497	hypothetical protein SAOUHSC_02866 [Staphylococcus aureus subsp. aureus NCTC 8325]	45	90352	13	1	13	1	12.5	11	1
88196640	hypothetical protein SAOUHSC_03022 [Staphylococcus aureus subsp. aureus NCTC 8325]	198	18643	19	8	13	5	66.1	11	2
88194270	hypoxanthine phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	37	20142	3	1	3	1	17.3	11	3
88195645	lantibiotic epidermin biosynthesis protein EpiB [Staphylococcus aureus subsp. aureus NCTC 8325]	33	117561	18	1	16	1	12.6	11	1
88194101	lipase [Staphylococcus aureus subsp. aureus NCTC 8325]	37	76341	19	1	17	1	22.5	11	3
88196053	lytic regulatory protein [Staphylococcus aureus subsp. aureus NCTC 8325]	38	40640	6	0	6	0	17.9	11	1
88194748	MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	41	16440	5	1	4	1	20.9	11	1
88195087	methionine sulfoxide reductase A [Staphylococcus aureus subsp. aureus NCTC 8325]	53	19598	8	2	8	2	46.2	11	1
88195087	methionine sulfoxide reductase A [Staphylococcus aureus subsp. aureus NCTC 8325]	71	19598	8	3	8	3	37.3	11	2
88195087	methionine sulfoxide reductase A [Staphylococcus aureus subsp. aureus NCTC 8325]	138	19598	8	4	6	3	33.7	11	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88196492	methylated-DNA--protein-cysteine methyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	58	18934	3	1	2	1	14.5	11	1
88196190	molybdopterin precursor biosynthesis MoaB [Staphylococcus aureus subsp. aureus NCTC 8325]	85	18489	6	2	6	2	30.4	11	1
88196190	molybdopterin precursor biosynthesis MoaB [Staphylococcus aureus subsp. aureus NCTC 8325]	241	18489	10	7	6	4	31.5	11	2
88196187	molybdopterin-guanine dinucleotide biosynthesis protein MobB [Staphylococcus aureus subsp. aureus NCTC 8325]	43	18557	4	1	3	1	14.3	11	1
88196187	molybdopterin-guanine dinucleotide biosynthesis protein MobB [Staphylococcus aureus subsp. aureus NCTC 8325]	41	18557	5	1	5	1	24.2	11	2
88195803	NAD-dependent DNA ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	28	75035	16	0	15	0	16.8	11	3
88194121	NADPH-dependent FMN reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	152	21301	11	4	8	4	33.5	11	1
88194121	NADPH-dependent FMN reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	124	21301	9	5	7	3	26.1	11	2
88194121	NADPH-dependent FMN reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	159	21301	11	6	7	4	30.9	11	3
88196598	phage infection protein [Staphylococcus aureus subsp. aureus NCTC 8325]	44	108649	35	1	31	1	24.3	11	2
88195856	phage minor structural protein [Staphylococcus aureus subsp. aureus NCTC 8325]	22	143656	26	0	25	0	17.3	11	1
88196596	PTS system fructose-specific transporter subunit IIABC [Staphylococcus aureus subsp. aureus NCTC 8325]	45	69838	16	1	13	1	14	11	2
88195154	PTS system transporter subunit IIA [Staphylococcus aureus subsp. aureus NCTC 8325]	78	17949	3	2	1	1	4.8	11	1
88195154	PTS system transporter subunit IIA [Staphylococcus aureus subsp. aureus NCTC 8325]	118	17949	6	3	5	2	36.1	11	2
88195154	PTS system transporter subunit IIA [Staphylococcus aureus subsp. aureus NCTC 8325]	76	17949	6	1	6	1	39.8	11	3
88195699	recombination regulator RecX [Staphylococcus aureus subsp. aureus NCTC 8325]	38	32221	4	1	4	1	15.1	11	2
88194660	signal peptidase IB [Staphylococcus aureus subsp. aureus NCTC 8325]	35	17587	5	0	5	0	29.7	11	1
88194660	signal peptidase IB [Staphylococcus aureus subsp. aureus NCTC 8325]	30	17587	9	0	7	0	33.5	11	2
161353531	SIS domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	120	19546	5	3	5	3	36.8	11	2
161353531	SIS domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	49	19546	3	1	3	1	18.1	11	3
88196104	tagatose 1,6-diphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	39	36573	6	1	5	1	12.6	11	1
88194298	transcription antitermination protein [Staphylococcus aureus subsp. aureus NCTC 8325]	54	20651	3	1	3	1	19.2	11	1
88194298	transcription antitermination protein [Staphylococcus aureus subsp. aureus NCTC 8325]	60	20651	8	2	7	1	34.1	11	3

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88195487	translation initiation factor IF-3 [Staphylococcus aureus subsp. aureus NCTC 8325]	131	20200	11	4	10	4	42.9	11	2
88195487	translation initiation factor IF-3 [Staphylococcus aureus subsp. aureus NCTC 8325]	43	20200	7	1	7	1	28	11	3
88195554	UDP-N-acetylmuramate--L-alanine ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	39	49157	4	1	4	1	7.3	11	1
88196205	urease subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	34	61741	16	1	13	1	17.9	11	2
88196205	urease subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	34	61741	17	1	15	1	16.3	11	3
88196002	(3R)-hydroxymyristoyl-ACP dehydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	29	16071	7	1	6	1	28.1	12	1
88196002	(3R)-hydroxymyristoyl-ACP dehydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	64	16071	8	3	6	2	39	12	2
88195002	(dimethylallyl)adenosine tRNA methylthiotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	53	58894	11	2	10	1	15	12	1
88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	237	13873	8	3	6	3	51.9	12	1
88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	1070	13873	29	22	16	12	54.3	12	2
88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	219	15277	16	9	11	8	48.9	12	1
88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	596	15277	45	26	19	13	52.6	12	2
88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	387	15277	27	14	15	9	49.6	12	3
88196138	30S ribosomal protein S13 [Staphylococcus aureus subsp. aureus NCTC 8325]	217	13711	15	7	12	7	59.5	12	1
88196145	30S ribosomal protein S5 [Staphylococcus aureus subsp. aureus NCTC 8325]	608	17732	28	18	24	15	72.9	12	1
88196145	30S ribosomal protein S5 [Staphylococcus aureus subsp. aureus NCTC 8325]	1079	17732	40	34	27	22	78.3	12	2
88196145	30S ribosomal protein S5 [Staphylococcus aureus subsp. aureus NCTC 8325]	716	17732	40	24	28	19	86.7	12	3
88194308	30S ribosomal protein S7 [Staphylococcus aureus subsp. aureus NCTC 8325]	369	17783	21	14	12	8	55.8	12	1
88194308	30S ribosomal protein S7 [Staphylococcus aureus subsp. aureus NCTC 8325]	526	17783	42	22	21	10	69.9	12	2
88194308	30S ribosomal protein S7 [Staphylococcus aureus subsp. aureus NCTC 8325]	265	17783	23	7	15	6	54.5	12	3
88194301	50S ribosomal protein L10 [Staphylococcus aureus subsp. aureus NCTC 8325]	229	17699	13	9	9	7	41.6	12	1
88194301	50S ribosomal protein L10 [Staphylococcus aureus subsp. aureus NCTC 8325]	420	17699	18	13	11	8	47	12	2
88194301	50S ribosomal protein L10 [Staphylococcus aureus subsp. aureus NCTC 8325]	398	17699	17	11	11	7	50.6	12	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88194299	50S ribosomal protein L11 [Staphylococcus aureus subsp. aureus NCTC 8325]	109	14865	10	2	7	2	39.3	12	2
88196130	50S ribosomal protein L13 [Staphylococcus aureus subsp. aureus NCTC 8325]	109	16323	16	5	10	5	40.7	12	1
88196130	50S ribosomal protein L13 [Staphylococcus aureus subsp. aureus NCTC 8325]	379	16323	27	17	18	12	57.9	12	2
88196130	50S ribosomal protein L13 [Staphylococcus aureus subsp. aureus NCTC 8325]	220	16323	16	9	11	8	44.8	12	3
88196143	50S ribosomal protein L15 [Staphylococcus aureus subsp. aureus NCTC 8325]	261	15587	19	9	13	8	47.9	12	2
88196143	50S ribosomal protein L15 [Staphylococcus aureus subsp. aureus NCTC 8325]	239	15587	20	8	15	6	61	12	3
88196155	50S ribosomal protein L16 [Staphylococcus aureus subsp. aureus NCTC 8325]	156	16232	12	6	8	4	36.8	12	1
88196155	50S ribosomal protein L16 [Staphylococcus aureus subsp. aureus NCTC 8325]	330	16232	16	11	9	7	46.5	12	2
88196155	50S ribosomal protein L16 [Staphylococcus aureus subsp. aureus NCTC 8325]	179	16232	17	9	12	7	49.3	12	3
88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	58	13739	9	3	9	3	71.3	12	1
88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	208	13739	11	5	9	4	48.4	12	2
88194948	50S ribosomal protein L19 [Staphylococcus aureus subsp. aureus NCTC 8325]	338	13354	18	11	14	7	72.4	12	1
88195485	50S ribosomal protein L20 [Staphylococcus aureus subsp. aureus NCTC 8325]	150	13678	8	4	8	4	48.3	12	1
88195485	50S ribosomal protein L20 [Staphylococcus aureus subsp. aureus NCTC 8325]	451	13678	30	15	21	10	63.6	12	2
88195485	50S ribosomal protein L20 [Staphylococcus aureus subsp. aureus NCTC 8325]	307	13678	21	11	17	7	65.3	12	3
88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	148	11326	8	2	8	2	57.8	12	1
88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	278	11326	9	6	7	6	67.6	12	2
88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	229	12827	12	6	11	5	68.4	12	1
88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	464	12827	23	12	15	8	81.2	12	2
88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	234	12827	10	7	8	5	53	12	3
88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	49	23703	10	1	10	1	33.6	12	1
88195058	50S ribosomal protein L33 [Staphylococcus aureus subsp. aureus NCTC 8325]	32	5928	3	0	3	0	51	12	2
88194302	50S ribosomal protein L7/L12 [Staphylococcus aureus subsp. aureus NCTC 8325]	279	12704	14	9	10	6	59.8	12	1

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88193838	50S ribosomal protein L9 [Staphylococcus aureus subsp. aureus NCTC 8325]	59	16629	7	1	7	1	29.3	12	1
88193838	50S ribosomal protein L9 [Staphylococcus aureus subsp. aureus NCTC 8325]	44	16629	9	1	9	1	32.7	12	2
88193838	50S ribosomal protein L9 [Staphylococcus aureus subsp. aureus NCTC 8325]	77	16629	13	3	12	3	50.7	12	3
88195582	6,7-dimethyl-8-ribityllumazine synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	77	16386	10	2	7	1	34.4	12	2
88194089	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	29	24967	11	0	11	0	50.2	12	3
88194390	accessory regulator A [Staphylococcus aureus subsp. aureus NCTC 8325]	232	14709	20	8	18	8	55.6	12	1
88195327	arginine repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	63	17087	9	1	8	1	28	12	1
88195327	arginine repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	51	17087	6	1	6	1	31.3	12	2
88195049	aspartate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	37	51971	18	1	16	1	22.6	12	1
88196503	cation transporter E1-E2 family ATPase [Staphylococcus aureus subsp. aureus NCTC 8325]	33	86690	26	1	25	1	25.2	12	1
88194884	cell division protein MraZ [Staphylococcus aureus subsp. aureus NCTC 8325]	32	17226	7	1	6	1	25.9	12	1
88194884	cell division protein MraZ [Staphylococcus aureus subsp. aureus NCTC 8325]	38	17226	9	2	9	2	37.1	12	2
88196031	CTP synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	56	59945	14	1	11	1	16	12	3
88195158	dihydrofolate reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	36	18239	6	0	6	0	25.2	12	2
88195158	dihydrofolate reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	84	18239	2	2	2	2	16.4	12	3
88196221	D-isomer specific 2-hydroxyacid dehydrogenase NAD binding domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	46	34653	5	1	5	1	12	12	1
88195397	DNA internalization-related competence protein ComEC/Rec2 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	82812	16	1	15	1	16.9	12	3
88194974	DNA polymerase III PolC [Staphylococcus aureus subsp. aureus NCTC 8325]	41	162357	23	1	23	1	14	12	1
88194241	DNA polymerase III subunit delta~ [Staphylococcus aureus subsp. aureus NCTC 8325]	36	32158	8	1	8	1	14	12	1
88194241	DNA polymerase III subunit delta~ [Staphylococcus aureus subsp. aureus NCTC 8325]	36	32158	11	1	9	1	24.4	12	2
88195080	DNA topoisomerase IV subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	40	90942	17	1	16	1	15.8	12	3
88194047	D-ribose pyranase [Staphylococcus aureus subsp. aureus NCTC 8325]	36	15156	3	1	2	1	16.4	12	1
88194047	D-ribose pyranase [Staphylococcus aureus subsp. aureus NCTC 8325]	43	15156	5	2	5	2	14.2	12	2

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88196270	EmrB/QacA family drug resistance transporter [Staphylococcus aureus subsp. aureus NCTC 8325]	38	70932	8	1	7	1	10.7	12	1
88196270	EmrB/QacA family drug resistance transporter [Staphylococcus aureus subsp. aureus NCTC 8325]	46	70932	5	2	4	1	4.5	12	2
88196011	F0F1 ATP synthase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	50	19527	14	2	11	2	37.6	12	1
88196011	F0F1 ATP synthase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	202	19527	25	8	18	7	53.2	12	2
88196011	F0F1 ATP synthase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	70	19527	8	3	7	3	29.5	12	3
88195790	ferritin [Staphylococcus aureus subsp. aureus NCTC 8325]	253	19576	12	8	10	7	35.5	12	1
88195790	ferritin [Staphylococcus aureus subsp. aureus NCTC 8325]	263	19576	12	8	9	5	40.4	12	2
88195790	ferritin [Staphylococcus aureus subsp. aureus NCTC 8325]	373	19576	18	10	11	6	39.2	12	3
88194473	fructose specific permease [Staphylococcus aureus subsp. aureus NCTC 8325]	26	68670	8	0	8	0	9.7	12	2
88195528	GAF domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	79	17100	3	2	3	2	14.3	12	1
88195014	glutathione peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	108	18106	4	3	4	3	22.8	12	3
88194594	glycine cleavage system protein H [Staphylococcus aureus subsp. aureus NCTC 8325]	44	14084	2	1	2	1	11.1	12	2
88196115	hyaluronate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	34	91928	24	1	21	1	22.8	12	1
88193956	hypothetical protein SAOUHSC_00144 [Staphylococcus aureus subsp. aureus NCTC 8325]	45	273308	33	2	32	2	11.8	12	1
88193956	hypothetical protein SAOUHSC_00144 [Staphylococcus aureus subsp. aureus NCTC 8325]	57	273308	35	1	35	1	12.6	12	3
88194010	hypothetical protein SAOUHSC_00200 [Staphylococcus aureus subsp. aureus NCTC 8325]	53	42156	7	1	7	1	14.2	12	3
88194169	hypothetical protein SAOUHSC_00371 [Staphylococcus aureus subsp. aureus NCTC 8325]	86	15113	4	1	4	1	32.6	12	1
88194169	hypothetical protein SAOUHSC_00371 [Staphylococcus aureus subsp. aureus NCTC 8325]	126	15113	5	4	4	3	23	12	2
88194169	hypothetical protein SAOUHSC_00371 [Staphylococcus aureus subsp. aureus NCTC 8325]	154	15113	11	4	10	3	51.9	12	3
88194220	hypothetical protein SAOUHSC_00428 [Staphylococcus aureus subsp. aureus NCTC 8325]	21	9993	1	0	1	0	14.6	12	1
88194283	hypothetical protein SAOUHSC_00502 [Staphylococcus aureus subsp. aureus NCTC 8325]	48	17830	9	1	9	1	39.2	12	1
88194283	hypothetical protein SAOUHSC_00502 [Staphylococcus aureus subsp. aureus NCTC 8325]	55	17830	11	2	11	2	34.6	12	2
88194293	hypothetical protein SAOUHSC_00512 [Staphylococcus aureus subsp. aureus NCTC 8325]	46	15711	3	1	3	1	17.2	12	1

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88194356	hypothetical protein SAOUHSC_00582 [Staphylococcus aureus subsp. aureus NCTC 8325]	67	15788	10	3	9	3	42.8	12	1
88194375	hypothetical protein SAOUHSC_00605 [Staphylococcus aureus subsp. aureus NCTC 8325]	44	18403	5	2	5	2	25.3	12	1
88194375	hypothetical protein SAOUHSC_00605 [Staphylococcus aureus subsp. aureus NCTC 8325]	54	18403	3	1	3	1	12.7	12	3
88194450	hypothetical protein SAOUHSC_00685 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	15179	8	1	6	1	32.1	12	2
88194450	hypothetical protein SAOUHSC_00685 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	15179	9	1	8	1	32.8	12	3
88194455	hypothetical protein SAOUHSC_00690 [Staphylococcus aureus subsp. aureus NCTC 8325]	80	26671	17	2	16	2	51.5	12	2
88194459	hypothetical protein SAOUHSC_00694 [Staphylococcus aureus subsp. aureus NCTC 8325]	278	17079	19	8	17	8	59.9	12	1
88194459	hypothetical protein SAOUHSC_00694 [Staphylococcus aureus subsp. aureus NCTC 8325]	345	17079	21	11	16	9	76.9	12	2
88194459	hypothetical protein SAOUHSC_00694 [Staphylococcus aureus subsp. aureus NCTC 8325]	177	17079	8	5	7	4	42.9	12	3
88194482	hypothetical protein SAOUHSC_00717 [Staphylococcus aureus subsp. aureus NCTC 8325]	60	16035	8	1	8	1	37	12	1
88194482	hypothetical protein SAOUHSC_00717 [Staphylococcus aureus subsp. aureus NCTC 8325]	51	16035	5	1	4	1	26	12	2
88194482	hypothetical protein SAOUHSC_00717 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	16035	11	1	11	1	54.1	12	3
88194780	hypothetical protein SAOUHSC_01027 [Staphylococcus aureus subsp. aureus NCTC 8325]	220	20077	19	7	17	6	57.8	12	3
88194810	hypothetical protein SAOUHSC_01061 [Staphylococcus aureus subsp. aureus NCTC 8325]	258	18569	9	5	7	4	43.8	12	2
88194810	hypothetical protein SAOUHSC_01061 [Staphylococcus aureus subsp. aureus NCTC 8325]	128	18569	5	2	5	2	26.2	12	3
88194880	hypothetical protein SAOUHSC_01138 [Staphylococcus aureus subsp. aureus NCTC 8325]	77	16991	7	3	5	2	19.9	12	1
88194880	hypothetical protein SAOUHSC_01138 [Staphylococcus aureus subsp. aureus NCTC 8325]	83	16991	9	4	7	3	32.2	12	2
88194989	hypothetical protein SAOUHSC_01256 [Staphylococcus aureus subsp. aureus NCTC 8325]	45	49878	11	2	10	1	18.2	12	2
88194989	hypothetical protein SAOUHSC_01256 [Staphylococcus aureus subsp. aureus NCTC 8325]	43	49878	9	1	8	1	17.5	12	3
88195161	hypothetical protein SAOUHSC_01437 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	42896	9	1	8	1	16.6	12	1
88195161	hypothetical protein SAOUHSC_01437 [Staphylococcus aureus subsp. aureus NCTC 8325]	41	42896	4	2	3	2	8.3	12	2
88195321	hypothetical protein SAOUHSC_01610 [Staphylococcus aureus subsp. aureus NCTC 8325]	93	16211	11	3	9	3	35.9	12	2
88195340	hypothetical protein SAOUHSC_01630 [Staphylococcus aureus subsp. aureus NCTC 8325]	69	14794	9	3	7	3	27.3	12	1

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195340	hypothetical protein SAOUHSC_01630 [Staphylococcus aureus subsp. aureus NCTC 8325]	121	14794	11	5	7	4	43	12	2
88195340	hypothetical protein SAOUHSC_01630 [Staphylococcus aureus subsp. aureus NCTC 8325]	78	14794	10	2	9	2	52.3	12	3
88195366	hypothetical protein SAOUHSC_01659 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	51049	24	1	22	1	35.3	12	3
88195407	hypothetical protein SAOUHSC_01701 [Staphylococcus aureus subsp. aureus NCTC 8325]	45	20207	6	1	6	1	29.1	12	3
88195432	hypothetical protein SAOUHSC_01727 [Staphylococcus aureus subsp. aureus NCTC 8325]	35	42458	9	1	9	1	11.8	12	1
88195514	hypothetical protein SAOUHSC_01814 [Staphylococcus aureus subsp. aureus NCTC 8325]	142	15216	11	6	9	6	38	12	2
88195538	hypothetical protein SAOUHSC_01838 [Staphylococcus aureus subsp. aureus NCTC 8325]	78	45775	17	4	14	4	20.3	12	2
88195553	hypothetical protein SAOUHSC_01855 [Staphylococcus aureus subsp. aureus NCTC 8325]	351	17991	20	9	14	7	63.2	12	1
88195553	hypothetical protein SAOUHSC_01855 [Staphylococcus aureus subsp. aureus NCTC 8325]	702	17991	37	19	23	11	83.4	12	2
88195553	hypothetical protein SAOUHSC_01855 [Staphylococcus aureus subsp. aureus NCTC 8325]	487	17991	21	13	13	9	62.6	12	3
88195566	hypothetical protein SAOUHSC_01869 [Staphylococcus aureus subsp. aureus NCTC 8325]	120	15724	15	5	12	5	54.3	12	1
88195566	hypothetical protein SAOUHSC_01869 [Staphylococcus aureus subsp. aureus NCTC 8325]	268	15724	15	8	12	7	57.9	12	2
88195566	hypothetical protein SAOUHSC_01869 [Staphylococcus aureus subsp. aureus NCTC 8325]	66	15724	13	2	10	2	47.9	12	3
88195581	hypothetical protein SAOUHSC_01884 [Staphylococcus aureus subsp. aureus NCTC 8325]	41	38006	16	1	14	1	29.1	12	1
88195657	hypothetical protein SAOUHSC_01964 [Staphylococcus aureus subsp. aureus NCTC 8325]	115	19536	6	5	5	4	21.6	12	1
88195657	hypothetical protein SAOUHSC_01964 [Staphylococcus aureus subsp. aureus NCTC 8325]	141	19536	9	6	8	5	37.1	12	3
88195660	hypothetical protein SAOUHSC_01968 [Staphylococcus aureus subsp. aureus NCTC 8325]	88	15935	5	4	5	4	34.3	12	1
88195668	hypothetical protein SAOUHSC_01977 [Staphylococcus aureus subsp. aureus NCTC 8325]	618	13302	29	16	16	10	66.7	12	1
88195668	hypothetical protein SAOUHSC_01977 [Staphylococcus aureus subsp. aureus NCTC 8325]	649	13302	22	16	13	10	64	12	2
88195687	hypothetical protein SAOUHSC_01999 [Staphylococcus aureus subsp. aureus NCTC 8325]	105	17249	14	2	12	2	54.3	12	1
88195687	hypothetical protein SAOUHSC_01999 [Staphylococcus aureus subsp. aureus NCTC 8325]	198	17249	17	9	13	9	54.3	12	2
88195687	hypothetical protein SAOUHSC_01999 [Staphylococcus aureus subsp. aureus NCTC 8325]	99	17249	14	6	11	5	45.7	12	3
88195895	hypothetical protein SAOUHSC_02221 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	29420	9	1	9	1	21.6	12	2

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88196036	hypothetical protein SAOUHSC_02373 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	45618	10	1	10	1	17.9	12	3
88196044	hypothetical protein SAOUHSC_02381 [Staphylococcus aureus subsp. aureus NCTC 8325]	176	16681	15	7	9	4	39.5	12	1
88196044	hypothetical protein SAOUHSC_02381 [Staphylococcus aureus subsp. aureus NCTC 8325]	117	16681	15	6	7	3	26.5	12	2
88196096	hypothetical protein SAOUHSC_02443 [Staphylococcus aureus subsp. aureus NCTC 8325]	71	20787	11	2	9	2	36	12	3
88196123	hypothetical protein SAOUHSC_02471 [Staphylococcus aureus subsp. aureus NCTC 8325]	31	56116	12	1	12	1	18.8	12	1
88196271	hypothetical protein SAOUHSC_02630 [Staphylococcus aureus subsp. aureus NCTC 8325]	55	23010	12	1	12	1	34	12	1
88196305	hypothetical protein SAOUHSC_02665 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	15904	4	1	4	1	20	12	1
88196305	hypothetical protein SAOUHSC_02665 [Staphylococcus aureus subsp. aureus NCTC 8325]	137	15904	11	5	9	4	44.3	12	2
88196306	hypothetical protein SAOUHSC_02666 [Staphylococcus aureus subsp. aureus NCTC 8325]	54	13331	6	1	4	1	30.5	12	1
88196306	hypothetical protein SAOUHSC_02666 [Staphylococcus aureus subsp. aureus NCTC 8325]	85	13331	9	2	8	2	44.9	12	2
88196310	hypothetical protein SAOUHSC_02670 [Staphylococcus aureus subsp. aureus NCTC 8325]	96	16295	7	2	5	2	28.2	12	1
88196329	hypothetical protein SAOUHSC_02689 [Staphylococcus aureus subsp. aureus NCTC 8325]	135	17408	5	2	5	2	31.6	12	1
88196329	hypothetical protein SAOUHSC_02689 [Staphylococcus aureus subsp. aureus NCTC 8325]	97	17408	9	2	9	2	49.7	12	3
88196514	hypothetical protein SAOUHSC_02886 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	19129	7	2	7	2	27.8	12	2
88196514	hypothetical protein SAOUHSC_02886 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	19129	7	1	7	1	29	12	3
88196540	hypothetical protein SAOUHSC_02912 [Staphylococcus aureus subsp. aureus NCTC 8325]	54	16928	6	1	5	1	32.9	12	2
88196540	hypothetical protein SAOUHSC_02912 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	16928	4	1	4	1	16.8	12	3
88196562	hypothetical protein SAOUHSC_02935 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	21729	6	1	6	1	27.8	12	1
88196562	hypothetical protein SAOUHSC_02935 [Staphylococcus aureus subsp. aureus NCTC 8325]	35	21729	10	1	9	1	31	12	2
88196613	hypothetical protein SAOUHSC_02994 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	13013	4	1	4	1	27.7	12	1
88196640	hypothetical protein SAOUHSC_03022 [Staphylococcus aureus subsp. aureus NCTC 8325]	152	18643	13	8	8	4	42.1	12	1
88196640	hypothetical protein SAOUHSC_03022 [Staphylococcus aureus subsp. aureus NCTC 8325]	253	18643	22	8	16	6	73.7	12	3
88196190	molybdopterin precursor biosynthesis MoaB [Staphylococcus aureus subsp. aureus NCTC 8325]	84	18489	10	4	10	4	47.6	12	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195202	nucleoside diphosphate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	100	15787	4	2	3	2	24.5	12	2
88195202	nucleoside diphosphate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	30	15787	4	0	4	0	26.6	12	3
88194685	oligopeptide ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	32	64487	9	1	9	1	13.8	12	1
88196282	permease domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	36	39456	20	1	16	1	24.2	12	1
88196282	permease domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	38	39456	12	1	11	1	24.2	12	3
88195239	phage tail tape meausure protein [Staphylococcus aureus subsp. aureus NCTC 8325]	43	225925	75	1	72	1	25.8	12	1
88195719	phage tape measure protein [Staphylococcus aureus subsp. aureus NCTC 8325]	45	125734	33	1	32	1	20.3	12	1
88195719	phage tape measure protein [Staphylococcus aureus subsp. aureus NCTC 8325]	57	125734	30	1	29	1	22.7	12	3
88194762	phosphoribosylaminoimidazole carboxylase catalytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	61	14733	9	1	8	1	48.9	12	1
88194762	phosphoribosylaminoimidazole carboxylase catalytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	130	14733	9	6	8	5	51.8	12	2
88193970	PTS system transporter [Staphylococcus aureus subsp. aureus NCTC 8325]	21	50632	5	0	4	0	11.8	12	3
88193839	replicative DNA helicase [Staphylococcus aureus subsp. aureus NCTC 8325]	54	52538	6	1	6	1	13.9	12	1
88195635	serine protease SplB [Staphylococcus aureus subsp. aureus NCTC 8325]	40	26081	10	1	9	1	32.1	12	3
88195965	serine-protein kinase RsbW [Staphylococcus aureus subsp. aureus NCTC 8325]	203	19170	12	6	10	5	40.8	12	1
88195965	serine-protein kinase RsbW [Staphylococcus aureus subsp. aureus NCTC 8325]	181	19170	8	5	7	5	34.9	12	2
88195965	serine-protein kinase RsbW [Staphylococcus aureus subsp. aureus NCTC 8325]	286	19170	16	7	14	5	56.2	12	3
88194660	signal peptidase IB [Staphylococcus aureus subsp. aureus NCTC 8325]	25	17587	9	0	8	0	35.5	12	3
88194941	SMC domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	34	136665	37	1	36	1	22.6	12	3
88196038	S-ribosylhomocysteinase [Staphylococcus aureus subsp. aureus NCTC 8325]	41	17502	2	1	2	1	8.3	12	1
88196038	S-ribosylhomocysteinase [Staphylococcus aureus subsp. aureus NCTC 8325]	199	17502	8	4	6	4	37.8	12	2
88194564	SsrA-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	141	17745	10	4	9	3	28.6	12	2
88194564	SsrA-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	83	17745	6	1	6	1	31.2	12	3
88195522	thiol peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	154	17994	11	5	9	4	45.7	12	1

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195522	thiol peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	195	17994	15	9	10	7	42.1	12	2
88195522	thiol peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	366	17994	17	12	13	9	58.5	12	3
88195419	transcription elongation factor GreA [Staphylococcus aureus subsp. aureus NCTC 8325]	72	17732	11	4	11	4	55.7	12	3
88195789	UDP-N-acetylmuramyl tripeptide synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	32	49235	9	0	9	0	21.3	12	1
88195002	(dimethylallyl)adenosine tRNA methylthiotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	60	58894	12	2	10	1	17.7	13	2
542123276	30S ribosomal protein S10 [Staphylococcus aureus subsp. aureus NCTC 8325]	145	11569	10	4	9	4	61.8	13	1
542123276	30S ribosomal protein S10 [Staphylococcus aureus subsp. aureus NCTC 8325]	257	11569	19	11	13	8	68.6	13	2
542123276	30S ribosomal protein S10 [Staphylococcus aureus subsp. aureus NCTC 8325]	152	11569	15	6	12	6	52.9	13	3
88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	629	13873	18	12	12	8	54.3	13	3
88196138	30S ribosomal protein S13 [Staphylococcus aureus subsp. aureus NCTC 8325]	542	13711	27	18	17	12	58.7	13	2
88196138	30S ribosomal protein S13 [Staphylococcus aureus subsp. aureus NCTC 8325]	329	13711	17	10	14	7	55.4	13	3
161353519	30S ribosomal protein S14 [Staphylococcus aureus subsp. aureus NCTC 8325]	28	7295	4	1	4	1	36.1	13	1
161353519	30S ribosomal protein S14 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	7295	5	1	5	1	39.3	13	2
161353519	30S ribosomal protein S14 [Staphylococcus aureus subsp. aureus NCTC 8325]	27	7295	6	1	5	1	42.6	13	3
88194983	30S ribosomal protein S15 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	10602	3	1	3	1	21.3	13	1
88194983	30S ribosomal protein S15 [Staphylococcus aureus subsp. aureus NCTC 8325]	101	10602	9	6	7	6	43.8	13	2
88194983	30S ribosomal protein S15 [Staphylococcus aureus subsp. aureus NCTC 8325]	68	10602	9	3	7	3	38.2	13	3
88194945	30S ribosomal protein S16 [Staphylococcus aureus subsp. aureus NCTC 8325]	46	10229	5	1	5	1	34.1	13	1
88194945	30S ribosomal protein S16 [Staphylococcus aureus subsp. aureus NCTC 8325]	84	10229	8	5	6	4	28.6	13	2
88196153	30S ribosomal protein S17 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	10169	6	0	5	0	37.9	13	1
88196153	30S ribosomal protein S17 [Staphylococcus aureus subsp. aureus NCTC 8325]	219	10169	14	9	11	6	67.8	13	2
88196153	30S ribosomal protein S17 [Staphylococcus aureus subsp. aureus NCTC 8325]	107	10169	10	3	9	3	65.5	13	3
88194149	30S ribosomal protein S18 [Staphylococcus aureus subsp. aureus NCTC 8325]	81	9304	8	4	7	4	46.2	13	1

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88194149	30S ribosomal protein S18 [Staphylococcus aureus subsp. aureus NCTC 8325]	240	9304	18	11	12	7	66.2	13	2
88194149	30S ribosomal protein S18 [Staphylococcus aureus subsp. aureus NCTC 8325]	102	9304	11	4	8	3	43.8	13	3
88196158	30S ribosomal protein S19 [Staphylococcus aureus subsp. aureus NCTC 8325]	36	10609	5	1	4	1	23.9	13	1
88196158	30S ribosomal protein S19 [Staphylococcus aureus subsp. aureus NCTC 8325]	156	10609	7	4	6	3	35.9	13	2
88196158	30S ribosomal protein S19 [Staphylococcus aureus subsp. aureus NCTC 8325]	155	10609	14	5	8	3	59.8	13	3
88195384	30S ribosomal protein S21 [Staphylococcus aureus subsp. aureus NCTC 8325]	50	6968	6	1	5	1	55.2	13	1
88195384	30S ribosomal protein S21 [Staphylococcus aureus subsp. aureus NCTC 8325]	110	6968	6	3	6	3	56.9	13	2
88195384	30S ribosomal protein S21 [Staphylococcus aureus subsp. aureus NCTC 8325]	119	6968	6	3	5	2	55.2	13	3
88194147	30S ribosomal protein S6 [Staphylococcus aureus subsp. aureus NCTC 8325]	83	11588	8	4	5	3	34.7	13	1
88194147	30S ribosomal protein S6 [Staphylococcus aureus subsp. aureus NCTC 8325]	94	11588	12	5	10	5	72.4	13	2
88194147	30S ribosomal protein S6 [Staphylococcus aureus subsp. aureus NCTC 8325]	193	11588	10	7	8	6	65.3	13	3
88196148	30S ribosomal protein S8 [Staphylococcus aureus subsp. aureus NCTC 8325]	191	14822	14	9	10	8	60.6	13	1
88196148	30S ribosomal protein S8 [Staphylococcus aureus subsp. aureus NCTC 8325]	570	14822	37	25	19	13	69.7	13	2
88196148	30S ribosomal protein S8 [Staphylococcus aureus subsp. aureus NCTC 8325]	283	14822	25	12	17	8	81.8	13	3
88196129	30S ribosomal protein S9 [Staphylococcus aureus subsp. aureus NCTC 8325]	65	14821	4	1	4	1	22.7	13	1
88196129	30S ribosomal protein S9 [Staphylococcus aureus subsp. aureus NCTC 8325]	325	14821	16	7	9	4	37.1	13	2
88196129	30S ribosomal protein S9 [Staphylococcus aureus subsp. aureus NCTC 8325]	164	14821	12	3	10	2	37.9	13	3
88196152	50S ribosomal protein L14 [Staphylococcus aureus subsp. aureus NCTC 8325]	80	13127	12	3	9	3	41	13	1
88196152	50S ribosomal protein L14 [Staphylococcus aureus subsp. aureus NCTC 8325]	171	13127	25	11	15	7	68.9	13	2
88196152	50S ribosomal protein L14 [Staphylococcus aureus subsp. aureus NCTC 8325]	103	13127	15	5	13	5	62.3	13	3
88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	85	13739	7	3	6	3	41	13	3
88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	126	13089	9	5	7	4	52.1	13	1
88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	357	13089	21	13	16	9	68.1	13	2

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88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	214	13089	14	8	12	7	67.2	13	3
88194948	50S ribosomal protein L19 [Staphylococcus aureus subsp. aureus NCTC 8325]	389	13354	19	12	15	9	65.5	13	2
88194948	50S ribosomal protein L19 [Staphylococcus aureus subsp. aureus NCTC 8325]	327	13354	18	11	14	8	63.8	13	3
88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	247	11326	11	6	10	6	80.4	13	3
88196160	50S ribosomal protein L23 [Staphylococcus aureus subsp. aureus NCTC 8325]	107	10599	10	2	7	2	63.7	13	1
88196160	50S ribosomal protein L23 [Staphylococcus aureus subsp. aureus NCTC 8325]	406	10599	13	12	9	8	79.1	13	2
88196160	50S ribosomal protein L23 [Staphylococcus aureus subsp. aureus NCTC 8325]	221	10599	13	5	10	4	75.8	13	3
88195456	50S ribosomal protein L27 [Staphylococcus aureus subsp. aureus NCTC 8325]	63	10308	6	2	5	2	25.5	13	1
88195456	50S ribosomal protein L27 [Staphylococcus aureus subsp. aureus NCTC 8325]	90	10308	6	2	5	2	47.9	13	2
88195456	50S ribosomal protein L27 [Staphylococcus aureus subsp. aureus NCTC 8325]	71	10308	3	2	3	2	19.1	13	3
88194930	50S ribosomal protein L28 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	6973	8	2	8	2	85.5	13	1
88194930	50S ribosomal protein L28 [Staphylococcus aureus subsp. aureus NCTC 8325]	121	6973	7	5	4	2	37.1	13	3
88196024	50S ribosomal protein L31 type B [Staphylococcus aureus subsp. aureus NCTC 8325]	46	9717	6	1	5	1	31	13	1
88196024	50S ribosomal protein L31 type B [Staphylococcus aureus subsp. aureus NCTC 8325]	32	9717	7	1	6	1	38.1	13	3
88195486	50S ribosomal protein L35 [Staphylococcus aureus subsp. aureus NCTC 8325]	26	7692	5	0	4	0	34.8	13	1
88195486	50S ribosomal protein L35 [Staphylococcus aureus subsp. aureus NCTC 8325]	72	7692	9	1	7	1	43.9	13	2
88195486	50S ribosomal protein L35 [Staphylococcus aureus subsp. aureus NCTC 8325]	150	7692	8	5	7	4	47	13	3
88194302	50S ribosomal protein L7/L12 [Staphylococcus aureus subsp. aureus NCTC 8325]	442	12704	22	13	14	7	71.3	13	2
88194302	50S ribosomal protein L7/L12 [Staphylococcus aureus subsp. aureus NCTC 8325]	491	12704	24	15	15	8	94.3	13	3
88194138	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	24	85023	14	0	14	0	13.3	13	1
88195582	6,7-dimethyl-8-ribityllumazine synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	56	16386	4	2	4	2	19.5	13	1
88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	72	35049	12	2	11	2	25	13	1
88194390	accessory regulator A [Staphylococcus aureus subsp. aureus NCTC 8325]	156	14709	15	5	13	4	38.7	13	2

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88194390	accessory regulator A [Staphylococcus aureus subsp. aureus NCTC 8325]	180	14709	16	8	14	8	46	13	3
88193886	accessory regulator-like protein [Staphylococcus aureus subsp. aureus NCTC 8325]	41	29871	17	2	13	2	28.8	13	3
88195822	aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	46	51709	7	1	7	1	12.6	13	1
88196590	arginine deiminase [Staphylococcus aureus subsp. aureus NCTC 8325]	41	46885	11	1	8	1	14.6	13	3
88195049	aspartate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	42	51971	13	1	13	1	23.9	13	2
88194148	bacteriophage L54a single-stranded DNA binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	62	18528	3	1	2	1	10.8	13	1
88195129	cold shock protein [Staphylococcus aureus subsp. aureus NCTC 8325]	45	7317	6	1	5	1	54.5	13	1
88195129	cold shock protein [Staphylococcus aureus subsp. aureus NCTC 8325]	61	7317	6	1	6	1	48.5	13	2
88195129	cold shock protein [Staphylococcus aureus subsp. aureus NCTC 8325]	58	7317	7	1	6	1	36.4	13	3
88194636	cytosol aminopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	44	54095	9	1	7	1	10.2	13	2
88194241	DNA polymerase III subunit delta~ [Staphylococcus aureus subsp. aureus NCTC 8325]	43	32158	9	1	8	1	19.7	13	3
88195326	DNA repair protein RecN [Staphylococcus aureus subsp. aureus NCTC 8325]	40	64282	14	1	13	1	15.4	13	1
88195326	DNA repair protein RecN [Staphylococcus aureus subsp. aureus NCTC 8325]	47	64282	23	1	22	1	25.2	13	3
88195189	DnaQ family exonuclease/DinG family helicase [Staphylococcus aureus subsp. aureus NCTC 8325]	41	104152	32	2	30	2	24.5	13	2
88194053	drug transporter [Staphylococcus aureus subsp. aureus NCTC 8325]	32	49025	6	1	6	1	15.3	13	1
88194053	drug transporter [Staphylococcus aureus subsp. aureus NCTC 8325]	33	49025	3	2	2	1	5.2	13	3
88194286	endopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	31	90981	29	1	28	1	27.4	13	3
88194661	exonuclease RexB [Staphylococcus aureus subsp. aureus NCTC 8325]	40	134420	31	1	28	1	16.4	13	2
88194661	exonuclease RexB [Staphylococcus aureus subsp. aureus NCTC 8325]	45	134420	33	1	31	1	19.3	13	3
88194473	fructose specific permease [Staphylococcus aureus subsp. aureus NCTC 8325]	64	68670	7	1	7	1	8.9	13	1
88194473	fructose specific permease [Staphylococcus aureus subsp. aureus NCTC 8325]	45	68670	12	1	10	1	13.8	13	3
88195528	GAF domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	125	17100	5	4	4	3	23.4	13	2
88196106	galactose-6-phosphate isomerase subunit LacB [Staphylococcus aureus subsp. aureus NCTC 8325]	17	18939	2	0	2	0	11.7	13	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195472	glutamate-1-semialdehyde aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	68	46359	9	1	8	1	13.8	13	2
88194554	glycolytic operon regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	43	37187	6	1	6	1	13.9	13	2
88193943	heme-degrading monooxygenase IsdI [Staphylococcus aureus subsp. aureus NCTC 8325]	42	12783	4	1	4	1	33.3	13	1
88193943	heme-degrading monooxygenase IsdI [Staphylococcus aureus subsp. aureus NCTC 8325]	349	12783	12	8	9	5	65.7	13	2
88193943	heme-degrading monooxygenase IsdI [Staphylococcus aureus subsp. aureus NCTC 8325]	133	12783	9	3	7	3	52.8	13	3
88193953	hypothetical protein SAOUHSC_00141 [Staphylococcus aureus subsp. aureus NCTC 8325]	59	13971	5	1	5	1	31.9	13	1
88193953	hypothetical protein SAOUHSC_00141 [Staphylococcus aureus subsp. aureus NCTC 8325]	54	13971	6	1	6	1	31.9	13	2
88193953	hypothetical protein SAOUHSC_00141 [Staphylococcus aureus subsp. aureus NCTC 8325]	51	13971	5	2	5	2	32.8	13	3
88194063	hypothetical protein SAOUHSC_00257 [Staphylococcus aureus subsp. aureus NCTC 8325]	249	11029	14	10	6	4	64.9	13	1
88194063	hypothetical protein SAOUHSC_00257 [Staphylococcus aureus subsp. aureus NCTC 8325]	242	11029	19	11	11	6	76.3	13	2
88194063	hypothetical protein SAOUHSC_00257 [Staphylococcus aureus subsp. aureus NCTC 8325]	152	11029	10	6	8	5	67	13	3
88194113	hypothetical protein SAOUHSC_00312 [Staphylococcus aureus subsp. aureus NCTC 8325]	48	16289	4	1	4	1	16.3	13	1
88194113	hypothetical protein SAOUHSC_00312 [Staphylococcus aureus subsp. aureus NCTC 8325]	71	16289	5	2	5	2	23.1	13	2
88194115	hypothetical protein SAOUHSC_00314 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	16162	5	1	4	1	18.7	13	1
88194115	hypothetical protein SAOUHSC_00314 [Staphylococcus aureus subsp. aureus NCTC 8325]	64	16162	6	1	6	1	37.4	13	2
88194155	hypothetical protein SAOUHSC_00356 [Staphylococcus aureus subsp. aureus NCTC 8325]	71	21293	8	1	8	1	30.5	13	1
88194220	hypothetical protein SAOUHSC_00428 [Staphylococcus aureus subsp. aureus NCTC 8325]	32	9993	4	1	4	1	33.7	13	2
88194220	hypothetical protein SAOUHSC_00428 [Staphylococcus aureus subsp. aureus NCTC 8325]	130	9993	6	2	4	1	42.7	13	3
88194234	hypothetical protein SAOUHSC_00444 [Staphylococcus aureus subsp. aureus NCTC 8325]	171	11590	23	3	20	2	69.5	13	2
88194234	hypothetical protein SAOUHSC_00444 [Staphylococcus aureus subsp. aureus NCTC 8325]	98	11590	12	2	11	2	74.3	13	3
88194266	hypothetical protein SAOUHSC_00481 [Staphylococcus aureus subsp. aureus NCTC 8325]	57	9850	6	2	5	2	46	13	1
88194266	hypothetical protein SAOUHSC_00481 [Staphylococcus aureus subsp. aureus NCTC 8325]	65	9850	6	1	4	1	35.6	13	2
88194293	hypothetical protein SAOUHSC_00512 [Staphylococcus aureus subsp. aureus NCTC 8325]	48	15711	4	1	4	1	18.7	13	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88194439	hypothetical protein SAOUHSC_00674 [Staphylococcus aureus subsp. aureus NCTC 8325]	119	16707	7	3	6	3	31.2	13	1
88194439	hypothetical protein SAOUHSC_00674 [Staphylococcus aureus subsp. aureus NCTC 8325]	84	16707	6	3	6	3	29.8	13	2
88194589	hypothetical protein SAOUHSC_00831 [Staphylococcus aureus subsp. aureus NCTC 8325]	85	15330	9	1	7	1	41.4	13	1
88194589	hypothetical protein SAOUHSC_00831 [Staphylococcus aureus subsp. aureus NCTC 8325]	305	15330	16	8	11	6	52.1	13	2
88194589	hypothetical protein SAOUHSC_00831 [Staphylococcus aureus subsp. aureus NCTC 8325]	118	15330	10	3	9	3	53.6	13	3
88194593	hypothetical protein SAOUHSC_00835 [Staphylococcus aureus subsp. aureus NCTC 8325]	93	13591	7	2	7	2	49.2	13	1
88194593	hypothetical protein SAOUHSC_00835 [Staphylococcus aureus subsp. aureus NCTC 8325]	172	13591	8	3	6	2	39	13	2
88194593	hypothetical protein SAOUHSC_00835 [Staphylococcus aureus subsp. aureus NCTC 8325]	116	13591	8	4	6	3	38.1	13	3
88194620	hypothetical protein SAOUHSC_00863 [Staphylococcus aureus subsp. aureus NCTC 8325]	41	10175	5	1	4	1	22.7	13	1
88194620	hypothetical protein SAOUHSC_00863 [Staphylococcus aureus subsp. aureus NCTC 8325]	51	10175	2	1	2	1	11.4	13	2
88194620	hypothetical protein SAOUHSC_00863 [Staphylococcus aureus subsp. aureus NCTC 8325]	108	10175	6	2	5	2	27.3	13	3
88194621	hypothetical protein SAOUHSC_00864 [Staphylococcus aureus subsp. aureus NCTC 8325]	64	16781	2	1	2	1	11.1	13	1
88194621	hypothetical protein SAOUHSC_00864 [Staphylococcus aureus subsp. aureus NCTC 8325]	60	16781	2	1	1	1	5.6	13	2
88194621	hypothetical protein SAOUHSC_00864 [Staphylococcus aureus subsp. aureus NCTC 8325]	88	16781	8	3	6	1	21.5	13	3
88194622	hypothetical protein SAOUHSC_00865 [Staphylococcus aureus subsp. aureus NCTC 8325]	64	27928	2	1	2	1	8.1	13	2
88194788	hypothetical protein SAOUHSC_01036 [Staphylococcus aureus subsp. aureus NCTC 8325]	60	8746	5	2	5	2	69.4	13	1
88194880	hypothetical protein SAOUHSC_01138 [Staphylococcus aureus subsp. aureus NCTC 8325]	61	16991	8	2	7	1	36.3	13	3
88194913	hypothetical protein SAOUHSC_01174 [Staphylococcus aureus subsp. aureus NCTC 8325]	48	14849	6	1	6	1	30.1	13	1
88194913	hypothetical protein SAOUHSC_01174 [Staphylococcus aureus subsp. aureus NCTC 8325]	83	14849	10	5	7	3	52.6	13	2
88194913	hypothetical protein SAOUHSC_01174 [Staphylococcus aureus subsp. aureus NCTC 8325]	71	14849	11	4	7	3	45.1	13	3
88194931	hypothetical protein SAOUHSC_01192 [Staphylococcus aureus subsp. aureus NCTC 8325]	126	13377	7	2	6	2	58.1	13	1
88194931	hypothetical protein SAOUHSC_01192 [Staphylococcus aureus subsp. aureus NCTC 8325]	133	13377	8	2	7	2	59.7	13	2
88194931	hypothetical protein SAOUHSC_01192 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	13377	6	1	6	1	46	13	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88194977	hypothetical protein SAOUHSC_01244 [Staphylococcus aureus subsp. aureus NCTC 8325]	104	11033	17	4	16	4	85.1	13	2
88194977	hypothetical protein SAOUHSC_01244 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	11033	5	1	5	1	33	13	3
88194978	hypothetical protein SAOUHSC_01245 [Staphylococcus aureus subsp. aureus NCTC 8325]	50	11530	7	1	7	1	49.5	13	2
88194978	hypothetical protein SAOUHSC_01245 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	11530	5	1	5	1	41.9	13	3
88195067	hypothetical protein SAOUHSC_01338 [Staphylococcus aureus subsp. aureus NCTC 8325]	150	11016	12	4	7	3	42.1	13	1
88195067	hypothetical protein SAOUHSC_01338 [Staphylococcus aureus subsp. aureus NCTC 8325]	77	11016	9	3	9	3	55.8	13	2
88195067	hypothetical protein SAOUHSC_01338 [Staphylococcus aureus subsp. aureus NCTC 8325]	95	11016	11	3	10	3	63.2	13	3
88195173	hypothetical protein SAOUHSC_01454 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	33381	4	1	4	1	11	13	1
88195173	hypothetical protein SAOUHSC_01454 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	33381	7	1	6	1	13.7	13	3
88195179	hypothetical protein SAOUHSC_01462 [Staphylococcus aureus subsp. aureus NCTC 8325]	205	13143	26	6	17	4	74.6	13	2
88195179	hypothetical protein SAOUHSC_01462 [Staphylococcus aureus subsp. aureus NCTC 8325]	85	13143	6	1	5	1	32.5	13	3
88195193	hypothetical protein SAOUHSC_01476 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	12187	3	1	3	1	28.6	13	1
88195332	hypothetical protein SAOUHSC_01622 [Staphylococcus aureus subsp. aureus NCTC 8325]	37	13265	6	1	6	1	44.2	13	1
88195332	hypothetical protein SAOUHSC_01622 [Staphylococcus aureus subsp. aureus NCTC 8325]	97	13265	10	5	9	4	43.3	13	2
88195332	hypothetical protein SAOUHSC_01622 [Staphylococcus aureus subsp. aureus NCTC 8325]	57	13265	9	4	8	3	39.2	13	3
88195401	hypothetical protein SAOUHSC_01695 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	13474	5	1	5	1	21.4	13	1
88195401	hypothetical protein SAOUHSC_01695 [Staphylococcus aureus subsp. aureus NCTC 8325]	75	13474	7	2	6	2	42.7	13	2
88195401	hypothetical protein SAOUHSC_01695 [Staphylococcus aureus subsp. aureus NCTC 8325]	60	13474	7	2	7	2	41.9	13	3
88195432	hypothetical protein SAOUHSC_01727 [Staphylococcus aureus subsp. aureus NCTC 8325]	39	42458	6	1	6	1	17.9	13	2
88195447	hypothetical protein SAOUHSC_01744 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	85557	17	1	17	1	16.4	13	3
88195514	hypothetical protein SAOUHSC_01814 [Staphylococcus aureus subsp. aureus NCTC 8325]	29	15216	6	0	5	0	32.8	13	1
88195514	hypothetical protein SAOUHSC_01814 [Staphylococcus aureus subsp. aureus NCTC 8325]	55	15216	9	2	7	2	43.1	13	3
88195571	hypothetical protein SAOUHSC_01874 [Staphylococcus aureus subsp. aureus NCTC 8325]	45	11337	2	1	2	1	21.4	13	1

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195592	hypothetical protein SAOUHSC_01897 [Staphylococcus aureus subsp. aureus NCTC 8325]	33	19141	4	1	4	1	20.5	13	1
88195603	hypothetical protein SAOUHSC_01908 [Staphylococcus aureus subsp. aureus NCTC 8325]	28	35031	12	0	11	0	33.8	13	3
88195660	hypothetical protein SAOUHSC_01968 [Staphylococcus aureus subsp. aureus NCTC 8325]	225	15935	11	7	9	6	44.3	13	2
88195660	hypothetical protein SAOUHSC_01968 [Staphylococcus aureus subsp. aureus NCTC 8325]	260	15935	16	10	13	8	77.1	13	3
88195661	hypothetical protein SAOUHSC_01969 [Staphylococcus aureus subsp. aureus NCTC 8325]	58	13204	9	1	9	1	48.8	13	1
88195661	hypothetical protein SAOUHSC_01969 [Staphylococcus aureus subsp. aureus NCTC 8325]	90	13204	15	3	11	3	49.6	13	2
88195661	hypothetical protein SAOUHSC_01969 [Staphylococcus aureus subsp. aureus NCTC 8325]	79	13204	13	3	10	3	59.5	13	3
88195665	hypothetical protein SAOUHSC_01974 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	114351	34	2	30	2	20.8	13	1
88195665	hypothetical protein SAOUHSC_01974 [Staphylococcus aureus subsp. aureus NCTC 8325]	41	114351	23	1	18	1	11	13	2
88195668	hypothetical protein SAOUHSC_01977 [Staphylococcus aureus subsp. aureus NCTC 8325]	374	13302	20	9	14	7	66.7	13	3
88195778	hypothetical protein SAOUHSC_02096 [Staphylococcus aureus subsp. aureus NCTC 8325]	66	10316	9	1	8	1	47.3	13	1
88195895	hypothetical protein SAOUHSC_02221 [Staphylococcus aureus subsp. aureus NCTC 8325]	33	29420	11	1	11	1	30.5	13	3
88196044	hypothetical protein SAOUHSC_02381 [Staphylococcus aureus subsp. aureus NCTC 8325]	164	16681	17	6	11	4	40.1	13	3
88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	61	10000	9	2	7	2	65.1	13	1
88196090	hypothetical protein SAOUHSC_02436 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	76040	13	1	13	1	17.5	13	3
88196173	hypothetical protein SAOUHSC_02525 [Staphylococcus aureus subsp. aureus NCTC 8325]	31	114631	23	1	21	1	14.7	13	1
88196173	hypothetical protein SAOUHSC_02525 [Staphylococcus aureus subsp. aureus NCTC 8325]	32	114631	28	1	26	1	17.5	13	3
88196179	hypothetical protein SAOUHSC_02532 [Staphylococcus aureus subsp. aureus NCTC 8325]	32	13978	1	1	1	1	5.2	13	1
88196179	hypothetical protein SAOUHSC_02532 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	13978	5	1	4	1	25	13	2
88196179	hypothetical protein SAOUHSC_02532 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	13978	5	1	5	1	28.4	13	3
88196210	hypothetical protein SAOUHSC_02566 [Staphylococcus aureus subsp. aureus NCTC 8325]	224	13660	15	9	10	5	55.7	13	1
88196210	hypothetical protein SAOUHSC_02566 [Staphylococcus aureus subsp. aureus NCTC 8325]	191	13660	11	6	7	4	51.3	13	2
88196210	hypothetical protein SAOUHSC_02566 [Staphylococcus aureus subsp. aureus NCTC 8325]	149	13660	11	5	9	4	64.3	13	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88196212	hypothetical protein SAOUHSC_02568 [Staphylococcus aureus subsp. aureus NCTC 8325]	92	12526	5	2	4	2	41.7	13	1
88196227	hypothetical protein SAOUHSC_02584 [Staphylococcus aureus subsp. aureus NCTC 8325]	44	30365	9	2	9	2	26.4	13	2
88196305	hypothetical protein SAOUHSC_02665 [Staphylococcus aureus subsp. aureus NCTC 8325]	64	15904	9	2	6	1	45.7	13	3
88196310	hypothetical protein SAOUHSC_02670 [Staphylococcus aureus subsp. aureus NCTC 8325]	95	16295	9	4	6	3	31	13	2
88196310	hypothetical protein SAOUHSC_02670 [Staphylococcus aureus subsp. aureus NCTC 8325]	119	16295	8	5	8	5	37.3	13	3
88196461	hypothetical protein SAOUHSC_02827 [Staphylococcus aureus subsp. aureus NCTC 8325]	22	10541	8	0	6	0	39.4	13	1
88196461	hypothetical protein SAOUHSC_02827 [Staphylococcus aureus subsp. aureus NCTC 8325]	88	10541	5	3	3	2	13.8	13	2
88196461	hypothetical protein SAOUHSC_02827 [Staphylococcus aureus subsp. aureus NCTC 8325]	43	10541	4	1	4	1	33	13	3
88196601	hypothetical protein SAOUHSC_02982 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	70889	22	2	20	2	21.6	13	1
88196611	hypothetical protein SAOUHSC_02992 [Staphylococcus aureus subsp. aureus NCTC 8325]	44	16733	7	2	7	2	30.3	13	1
88196611	hypothetical protein SAOUHSC_02992 [Staphylococcus aureus subsp. aureus NCTC 8325]	44	16733	6	2	6	2	26.1	13	2
88196611	hypothetical protein SAOUHSC_02992 [Staphylococcus aureus subsp. aureus NCTC 8325]	43	16733	13	1	10	1	39.4	13	3
88196613	hypothetical protein SAOUHSC_02994 [Staphylococcus aureus subsp. aureus NCTC 8325]	46	13013	5	1	5	1	43.7	13	2
88196613	hypothetical protein SAOUHSC_02994 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	13013	9	1	7	1	41.2	13	3
88196288	L-lactate permease [Staphylococcus aureus subsp. aureus NCTC 8325]	34	56606	12	1	8	1	11.7	13	1
88194248	methionyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	53	74838	15	2	14	2	18.7	13	1
88196188	molybdopterin biosynthesis protein MoeA [Staphylococcus aureus subsp. aureus NCTC 8325]	37	44988	8	1	7	1	10.7	13	3
88195946	MutS domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	48	61283	9	1	9	1	14.2	13	1
88195946	MutS domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	48	61283	13	1	13	1	19.2	13	3
88194221	MutT/nudix family protein [Staphylococcus aureus subsp. aureus NCTC 8325]	26	15044	6	0	5	0	18.3	13	1
88194221	MutT/nudix family protein [Staphylococcus aureus subsp. aureus NCTC 8325]	68	15044	10	3	10	3	41.2	13	2
88194221	MutT/nudix family protein [Staphylococcus aureus subsp. aureus NCTC 8325]	34	15044	3	1	3	1	11.5	13	3
88194828	neurofilament protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35	72148	18	1	17	1	20.6	13	1

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88194142	ParB family chromosome partioning protein [Staphylococcus aureus subsp. aureus NCTC 8325]	23	32836	9	0	8	0	18.5	13	3
88195239	phage tail tape meausure protein [Staphylococcus aureus subsp. aureus NCTC 8325]	38	225925	76	1	72	1	27.7	13	3
88194781	phosphocarrier protein HPr [Staphylococcus aureus subsp. aureus NCTC 8325]	236	9490	4	4	2	2	26.1	13	1
88194781	phosphocarrier protein HPr [Staphylococcus aureus subsp. aureus NCTC 8325]	217	9490	4	4	2	2	26.1	13	3
88194762	phosphoribosylaminoimidazole carboxylase catalytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	99	14733	6	3	6	3	37.4	13	3
88194765	phosphoribosylformylglycinamidine synthase PurS [Staphylococcus aureus subsp. aureus NCTC 8325]	150	9915	8	3	5	3	58.6	13	1
88195449	preprotein translocase subunit YajC [Staphylococcus aureus subsp. aureus NCTC 8325]	86	9665	3	2	3	2	22.1	13	1
88195449	preprotein translocase subunit YajC [Staphylococcus aureus subsp. aureus NCTC 8325]	65	9665	2	2	2	2	22.1	13	2
88195449	preprotein translocase subunit YajC [Staphylococcus aureus subsp. aureus NCTC 8325]	71	9665	5	1	4	1	34.9	13	3
88196596	PTS system fructose-specific transporter subunit IIABC [Staphylococcus aureus subsp. aureus NCTC 8325]	36	69838	18	0	17	0	23.8	13	1
88196063	PTS system mannitol-specific transporter subunit IIA [Staphylococcus aureus subsp. aureus NCTC 8325]	64	15533	4	2	4	2	24.3	13	2
88196063	PTS system mannitol-specific transporter subunit IIA [Staphylococcus aureus subsp. aureus NCTC 8325]	100	15533	7	3	6	2	22.9	13	3
88195308	pyrroline-5-carboxylate reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	70	28740	12	1	10	1	34.5	13	1
88194256	regulatory protein SpoVG [Staphylococcus aureus subsp. aureus NCTC 8325]	129	11271	8	5	8	5	68	13	1
88194256	regulatory protein SpoVG [Staphylococcus aureus subsp. aureus NCTC 8325]	457	11271	22	13	14	8	81	13	2
88194256	regulatory protein SpoVG [Staphylococcus aureus subsp. aureus NCTC 8325]	271	11271	17	7	13	6	83	13	3
88195635	serine protease SplB [Staphylococcus aureus subsp. aureus NCTC 8325]	36	26081	5	1	5	1	14.2	13	2
88195966	STAS domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	124	12197	4	2	4	2	29.6	13	1
88195966	STAS domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	287	12197	6	4	4	3	40.7	13	2
88194846	thioredoxin [Staphylococcus aureus subsp. aureus NCTC 8325]	278	11433	12	8	9	5	56.7	13	1
88194592	thioredoxin [Staphylococcus aureus subsp. aureus NCTC 8325]	72	12133	4	1	4	1	28.3	13	1
88194592	thioredoxin [Staphylococcus aureus subsp. aureus NCTC 8325]	81	12133	4	2	3	2	19.8	13	2
88194592	thioredoxin [Staphylococcus aureus subsp. aureus NCTC 8325]	86	12133	4	3	4	3	30.2	13	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195331	transcription antitermination protein NusB [Staphylococcus aureus subsp. aureus NCTC 8325]	164	15052	8	3	5	3	37.2	13	1
88195331	transcription antitermination protein NusB [Staphylococcus aureus subsp. aureus NCTC 8325]	231	15052	10	6	8	4	43.4	13	2
88195331	transcription antitermination protein NusB [Staphylococcus aureus subsp. aureus NCTC 8325]	241	15052	5	4	4	3	36.4	13	3
88194028	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	56	25198	9	2	7	1	23.7	14	3
88194945	30S ribosomal protein S16 [Staphylococcus aureus subsp. aureus NCTC 8325]	48	10229	3	1	3	1	35.2	14	3
88195395	30S ribosomal protein S20 [Staphylococcus aureus subsp. aureus NCTC 8325]	31	9016	7	1	6	1	65.1	14	1
88195395	30S ribosomal protein S20 [Staphylococcus aureus subsp. aureus NCTC 8325]	65	9016	12	1	11	1	67.5	14	2
88195395	30S ribosomal protein S20 [Staphylococcus aureus subsp. aureus NCTC 8325]	97	9016	9	3	7	2	59	14	3
88194930	50S ribosomal protein L28 [Staphylococcus aureus subsp. aureus NCTC 8325]	39	6973	8	1	7	1	66.1	14	2
88196154	50S ribosomal protein L29 [Staphylococcus aureus subsp. aureus NCTC 8325]	50	8085	6	1	4	1	50.7	14	1
88196154	50S ribosomal protein L29 [Staphylococcus aureus subsp. aureus NCTC 8325]	103	8085	3	2	3	2	42	14	2
88196154	50S ribosomal protein L29 [Staphylococcus aureus subsp. aureus NCTC 8325]	108	8085	5	2	5	2	53.6	14	3
88196144	50S ribosomal protein L30 [Staphylococcus aureus subsp. aureus NCTC 8325]	52	6550	3	1	3	1	40.7	14	1
88196144	50S ribosomal protein L30 [Staphylococcus aureus subsp. aureus NCTC 8325]	54	6550	2	1	1	1	13.6	14	2
88196144	50S ribosomal protein L30 [Staphylococcus aureus subsp. aureus NCTC 8325]	58	6550	4	1	4	1	55.9	14	3
88196024	50S ribosomal protein L31 type B [Staphylococcus aureus subsp. aureus NCTC 8325]	55	9717	5	3	4	2	36.9	14	2
88196059	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	34	28987	8	1	6	1	16.5	14	3
88195132	acylphosphatase [Staphylococcus aureus subsp. aureus NCTC 8325]	47	10154	5	1	4	1	31.5	14	1
88195132	acylphosphatase [Staphylococcus aureus subsp. aureus NCTC 8325]	56	10154	5	2	4	2	31.5	14	2
88195132	acylphosphatase [Staphylococcus aureus subsp. aureus NCTC 8325]	47	10154	5	1	4	1	31.5	14	3
88195293	bacteriophage integrase [Staphylococcus aureus subsp. aureus NCTC 8325]	42	47452	8	1	8	1	15.2	14	3
88195392	coproporphyrinogen III oxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	39	42814	6	1	6	1	11.8	14	1
88195392	coproporphyrinogen III oxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	42	42814	9	1	8	1	19.3	14	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195397	DNA internalization-related competence protein ComEC/Rec2 [Staphylococcus aureus subsp. aureus NCTC 8325]	33	82812	13	0	11	0	10.9	14	1
88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	115	9620	5	4	4	3	47.8	14	1
88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	243	9620	17	10	12	6	85.6	14	2
88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	325	9620	23	9	17	7	91.1	14	3
88195452	Holliday junction DNA helicase RuvB [Staphylococcus aureus subsp. aureus NCTC 8325]	36	37695	11	1	8	1	17.1	14	2
88194112	hypothetical protein SAOUHSC_00311 [Staphylococcus aureus subsp. aureus NCTC 8325]	70	10391	5	2	4	1	35.1	14	2
88194112	hypothetical protein SAOUHSC_00311 [Staphylococcus aureus subsp. aureus NCTC 8325]	44	10391	2	1	2	1	17	14	3
88194265	hypothetical protein SAOUHSC_00480 [Staphylococcus aureus subsp. aureus NCTC 8325]	42	45082	7	1	5	1	9.8	14	3
88194451	hypothetical protein SAOUHSC_00686 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	11317	3	1	3	1	41.4	14	2
88194451	hypothetical protein SAOUHSC_00686 [Staphylococcus aureus subsp. aureus NCTC 8325]	34	11317	2	0	2	0	13.1	14	3
88194603	hypothetical protein SAOUHSC_00845 [Staphylococcus aureus subsp. aureus NCTC 8325]	151	7014	11	7	8	6	75	14	1
88194603	hypothetical protein SAOUHSC_00845 [Staphylococcus aureus subsp. aureus NCTC 8325]	159	7014	12	7	7	6	62.5	14	2
88194603	hypothetical protein SAOUHSC_00845 [Staphylococcus aureus subsp. aureus NCTC 8325]	163	7014	15	6	12	6	84.4	14	3
88194729	hypothetical protein SAOUHSC_00972 [Staphylococcus aureus subsp. aureus NCTC 8325]	105	11187	5	1	5	1	48.4	14	2
88194729	hypothetical protein SAOUHSC_00972 [Staphylococcus aureus subsp. aureus NCTC 8325]	111	11187	3	2	3	2	24.2	14	3
88194746	hypothetical protein SAOUHSC_00989 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	43163	7	1	7	1	15.4	14	3
88194788	hypothetical protein SAOUHSC_01036 [Staphylococcus aureus subsp. aureus NCTC 8325]	152	8746	10	5	8	5	86.1	14	2
88194788	hypothetical protein SAOUHSC_01036 [Staphylococcus aureus subsp. aureus NCTC 8325]	147	8746	10	4	8	3	72.2	14	3
88194867	hypothetical protein SAOUHSC_01123 [Staphylococcus aureus subsp. aureus NCTC 8325]	81	8625	2	1	2	1	17.6	14	1
88194867	hypothetical protein SAOUHSC_01123 [Staphylococcus aureus subsp. aureus NCTC 8325]	56	8625	5	1	4	1	36.5	14	2
88194997	hypothetical protein SAOUHSC_01264 [Staphylococcus aureus subsp. aureus NCTC 8325]	40	8156	6	0	5	0	36.6	14	1
88194997	hypothetical protein SAOUHSC_01264 [Staphylococcus aureus subsp. aureus NCTC 8325]	126	8156	17	5	13	5	83.1	14	2
88194997	hypothetical protein SAOUHSC_01264 [Staphylococcus aureus subsp. aureus NCTC 8325]	62	8156	9	2	7	2	52.1	14	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88195162	hypothetical protein SAOUHSC_01438 [Staphylococcus aureus subsp. aureus NCTC 8325]	120	9401	4	3	3	3	37.3	14	2
88195162	hypothetical protein SAOUHSC_01438 [Staphylococcus aureus subsp. aureus NCTC 8325]	55	9401	4	2	4	2	54.2	14	3
88195193	hypothetical protein SAOUHSC_01476 [Staphylococcus aureus subsp. aureus NCTC 8325]	65	12187	5	1	5	1	36.2	14	2
88195193	hypothetical protein SAOUHSC_01476 [Staphylococcus aureus subsp. aureus NCTC 8325]	26	12187	1	0	1	0	9.5	14	3
88195321	hypothetical protein SAOUHSC_01610 [Staphylococcus aureus subsp. aureus NCTC 8325]	45	16211	8	1	6	1	35.2	14	1
88195426	hypothetical protein SAOUHSC_01721 [Staphylococcus aureus subsp. aureus NCTC 8325]	47	10297	4	2	4	2	30.2	14	1
88195426	hypothetical protein SAOUHSC_01721 [Staphylococcus aureus subsp. aureus NCTC 8325]	57	10297	7	2	5	2	33.7	14	2
88195426	hypothetical protein SAOUHSC_01721 [Staphylococcus aureus subsp. aureus NCTC 8325]	44	10297	4	2	3	2	26.7	14	3
88195435	hypothetical protein SAOUHSC_01730 [Staphylococcus aureus subsp. aureus NCTC 8325]	81	6678	7	1	6	1	61.7	14	1
88195435	hypothetical protein SAOUHSC_01730 [Staphylococcus aureus subsp. aureus NCTC 8325]	142	6678	9	6	8	5	70	14	3
88195558	hypothetical protein SAOUHSC_01860 [Staphylococcus aureus subsp. aureus NCTC 8325]	145	11848	6	3	6	3	42.7	14	2
88195558	hypothetical protein SAOUHSC_01860 [Staphylococcus aureus subsp. aureus NCTC 8325]	98	11848	5	1	5	1	45.6	14	3
88195571	hypothetical protein SAOUHSC_01874 [Staphylococcus aureus subsp. aureus NCTC 8325]	115	11337	8	3	7	2	45.6	14	2
88195571	hypothetical protein SAOUHSC_01874 [Staphylococcus aureus subsp. aureus NCTC 8325]	68	11337	2	1	2	1	24.3	14	3
88195702	hypothetical protein SAOUHSC_02014 [Staphylococcus aureus subsp. aureus NCTC 8325]	55	6301	1	1	1	1	20.8	14	1
88195702	hypothetical protein SAOUHSC_02014 [Staphylococcus aureus subsp. aureus NCTC 8325]	48	6301	1	1	1	1	20.8	14	2
88195778	hypothetical protein SAOUHSC_02096 [Staphylococcus aureus subsp. aureus NCTC 8325]	149	10316	13	4	10	3	53.8	14	2
88195778	hypothetical protein SAOUHSC_02096 [Staphylococcus aureus subsp. aureus NCTC 8325]	87	10316	6	3	5	2	33	14	3
88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	115	10000	12	5	9	4	86	14	2
88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	104	10000	9	4	7	4	67.4	14	3
88196212	hypothetical protein SAOUHSC_02568 [Staphylococcus aureus subsp. aureus NCTC 8325]	351	12526	10	7	9	6	95.4	14	2
88196212	hypothetical protein SAOUHSC_02568 [Staphylococcus aureus subsp. aureus NCTC 8325]	115	12526	7	2	7	2	70.4	14	3
88196227	hypothetical protein SAOUHSC_02584 [Staphylococcus aureus subsp. aureus NCTC 8325]	38	30365	5	1	5	1	23.4	14	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88196271	hypothetical protein SAOUHSC_02630 [Staphylococcus aureus subsp. aureus NCTC 8325]	43	23010	7	2	6	1	19.5	14	3
88196386	hypothetical protein SAOUHSC_02750 [Staphylococcus aureus subsp. aureus NCTC 8325]	26	60601	5	0	4	0	5.5	14	3
88196406	hypothetical protein SAOUHSC_02770 [Staphylococcus aureus subsp. aureus NCTC 8325]	30	30984	2	1	2	1	4	14	1
88196601	hypothetical protein SAOUHSC_02982 [Staphylococcus aureus subsp. aureus NCTC 8325]	51	70889	22	4	17	2	24.1	14	2
88196601	hypothetical protein SAOUHSC_02982 [Staphylococcus aureus subsp. aureus NCTC 8325]	50	70889	19	2	17	1	26.8	14	3
542123273	hypothetical protein SAOUHSC_1307a [Staphylococcus aureus subsp. aureus NCTC 8325]	43	7495	3	1	3	1	33.8	14	2
88196108	lactose phosphotransferase system repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	42	29869	6	1	6	1	15.2	14	2
88196288	L-lactate permease [Staphylococcus aureus subsp. aureus NCTC 8325]	26	56606	5	0	5	0	13.3	14	2
88193889	periplasmic binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	32	36721	4	1	4	1	10	14	3
88195922	phage terminase small subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	37	22208	5	1	4	1	11.7	14	3
88194781	phosphocarrier protein HPr [Staphylococcus aureus subsp. aureus NCTC 8325]	494	9490	18	9	8	4	70.5	14	2
88194765	phosphoribosylformylglycinamidine synthase PurS [Staphylococcus aureus subsp. aureus NCTC 8325]	358	9915	21	9	12	6	85.1	14	2
88194765	phosphoribosylformylglycinamidine synthase PurS [Staphylococcus aureus subsp. aureus NCTC 8325]	357	9915	14	6	8	5	81.6	14	3
88196103	PTS system lactose-specific transporter subunit IIA [Staphylococcus aureus subsp. aureus NCTC 8325]	27	11363	1	0	1	0	7.8	14	1
88196103	PTS system lactose-specific transporter subunit IIA [Staphylococcus aureus subsp. aureus NCTC 8325]	48	11363	2	1	2	1	22.3	14	2
88196061	PTS system mannitol-specific protein [Staphylococcus aureus subsp. aureus NCTC 8325]	45	55030	11	1	8	1	11.5	14	2
88196061	PTS system mannitol-specific protein [Staphylococcus aureus subsp. aureus NCTC 8325]	34	55030	9	1	8	1	17	14	3
88194845	recombination and DNA strand exchange inhibitor protein [Staphylococcus aureus subsp. aureus NCTC 8325]	30	88606	17	1	17	1	16.4	14	1
88194845	recombination and DNA strand exchange inhibitor protein [Staphylococcus aureus subsp. aureus NCTC 8325]	43	88606	24	2	23	1	21.1	14	3
88194941	SMC domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35	136665	25	1	25	1	16.7	14	1
88195966	STAS domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	160	12197	5	3	4	2	38.9	14	3
88194846	thioredoxin [Staphylococcus aureus subsp. aureus NCTC 8325]	447	11433	23	12	12	7	86.5	14	2
88194846	thioredoxin [Staphylococcus aureus subsp. aureus NCTC 8325]	464	11433	20	11	11	7	76.9	14	3

prot_acc2	Protein description	prot_score	prot_mass	prot_matches	prot_matches_sig	prot_sequences	prot_sequences_sig	prot_cover	Slice	Rep
88194959	tRNA (uracil-5-)-methyltransferase Gid [Staphylococcus aureus subsp. aureus NCTC 8325]	45	48341	5	1	5	1	11	14	1

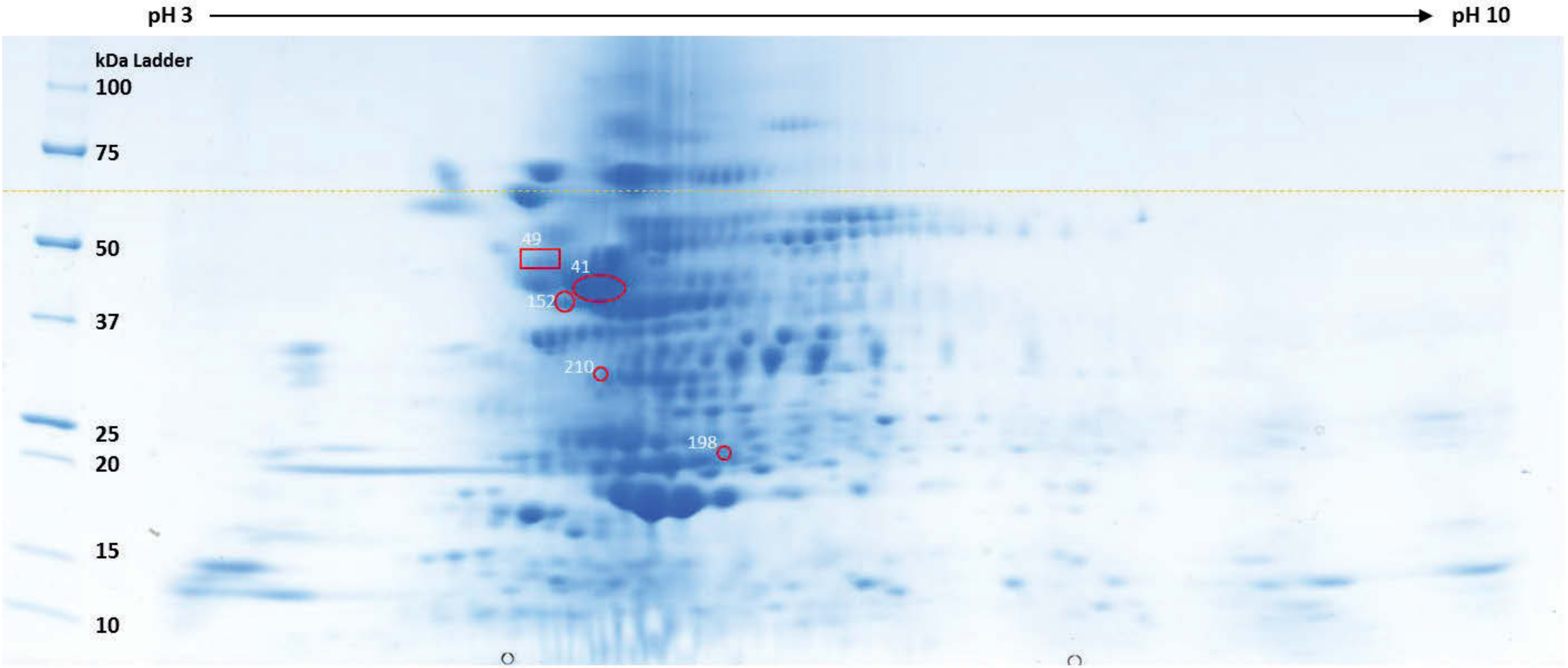

Figure A.2 2D-PAGE of surface biotinylated proteins showing where DnaK was found migrating below its predicted molecular weight of 66kDa. DnaK was identified at the following molecular weights: 48 kDa (spot 49), 43 kDa (spot 41), 40 kDa (spot 152), 30 kDa (spot 210), and 21 kDa (spot 198).

Appendix B

Extra information relating to Chapter 3

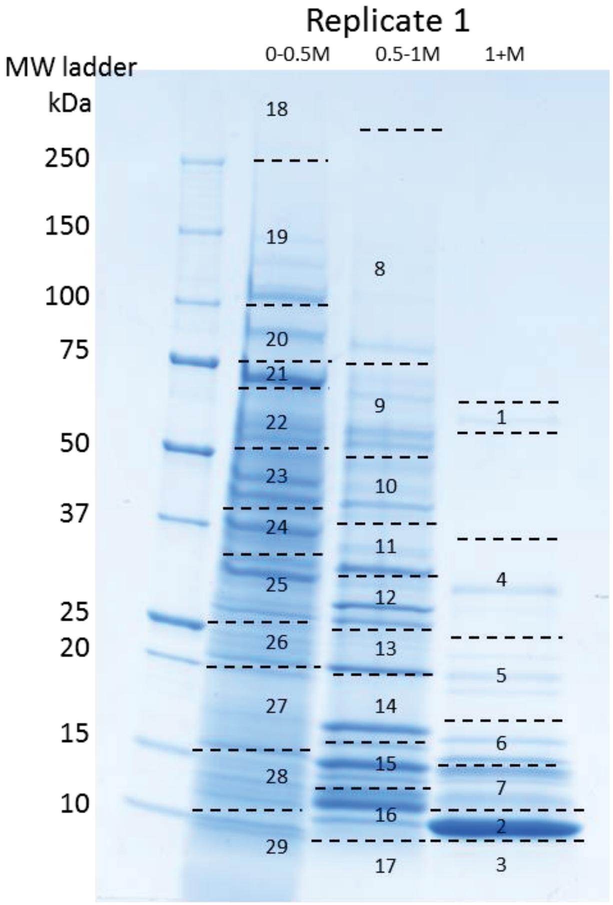

Figure B.1. Image of gel loaded with affinity chromatography elutions, showing where each “slice” was taken from (molecular weight range). These slices were the same across all three replicates.

Tables B.1-B.3 include proteins identified across the three elutions, with each elution in a separate table (B.1-B.3). The slice in which the protein was identified in is listed to indicate the MW range it was found in. Numbers listed under columns Rep1-Rep3 are the mascot scores given to that identification (MudPIT scoring). Surface exposure was noted if the protein was identified in the data from chapter 2. DNA binding was noted if there was any evidence of nucleic acid binding in domains, features, interactions, or DNA-binding in GO annotations according to the UniProt database for *S. aureus* NCTC 8325.

Table B.1. Summary of proteins identified in 1+M NaCl elution.

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	Dna Binding
Q2FW39	88196129	30S ribosomal protein S9 [Staphylococcus aureus subsp. aureus NCTC 8325]	14821		566	46	1	X	
Q2FW33	88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	13739		24	86	1	X	
Q2FXS8	88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	11326		205	80	1	X	X
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620		217	380	1	X	X
Q2FXJ2	88195542	hypothetical protein SAOUHSC_01843 [Staphylococcus aureus subsp. aureus NCTC 8325]	100886		36	38	1	X	
Q2FVG4	88196386	hypothetical protein SAOUHSC_02750 [Staphylococcus aureus subsp. aureus NCTC 8325]	60601	22		31	1	X	
Q2FWW1	88195840	MHC class II analog protein [Staphylococcus aureus subsp. aureus NCTC 8325]	65534	243	471	91	1	X	
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022		57	51	1	X	
Q2FW31	88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	13873	152	221	225	2	X	X
Q2G111	88194149	30S ribosomal protein S18 [Staphylococcus aureus subsp. aureus NCTC 8325]	9304	31	89	41	2	X	X
Q2FXY6	88195395	30S ribosomal protein S20 [Staphylococcus aureus subsp. aureus NCTC 8325]	9016	738	654	1162	2	X	X
Q2G113	88194147	30S ribosomal protein S6 [Staphylococcus aureus subsp. aureus NCTC 8325]	11588	35		27	2	X	X
Q2FW39	88196129	30S ribosomal protein S9 [Staphylococcus aureus subsp. aureus NCTC 8325]	14821	130	287	156	2	X	
Q2FW22	88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	13089	128	264	182	2	X	X
Q2FXQ1	88195485	50S ribosomal protein L20 [Staphylococcus aureus subsp. aureus NCTC 8325]	13678	64	114	109	2	X	X
Q2FXS8	88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	11326	268	303	280	2	X	X
Q2FW11	88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	12827		75	37	2	X	X
Q2FZ60	88194930	50S ribosomal protein L28 [Staphylococcus aureus subsp. aureus NCTC 8325]	6973	31	58	86	2	X	
Q2FW14	88196154	50S ribosomal protein L29 [Staphylococcus aureus subsp. aureus NCTC 8325]	8085	114	171	196	2	X	
Q2FXQ0	88195486	50S ribosomal protein L35 [Staphylococcus aureus subsp. aureus NCTC 8325]	7692	59	66	85	2	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	Dna Binding
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	4244	6212	5358	2	X	X
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310	36	43		2	X	
Q2FY01	88195380	hypothetical protein SAOUHSC_01673 [Staphylococcus aureus subsp. aureus NCTC 8325]	34892		42	39	2	X	
Q2FVQ4	88196288	L-lactate permease [Staphylococcus aureus subsp. aureus NCTC 8325]	56606	43		40	2	X	
Q2FZH6	88194781	phosphocarrier protein HPr [Staphylococcus aureus subsp. aureus NCTC 8325]	9490	48		63	2	X	
Q2FW31	88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	13873	81	180	179	3	X	X
Q2G111	88194149	30S ribosomal protein S18 [Staphylococcus aureus subsp. aureus NCTC 8325]	9304		30	30	3	X	X
Q2FXY6	88195395	30S ribosomal protein S20 [Staphylococcus aureus subsp. aureus NCTC 8325]	9016	183	204	591	3	X	X
P48940	88194308	30S ribosomal protein S7 [Staphylococcus aureus subsp. aureus NCTC 8325]	17783	77	167	62	3	X	X
Q2FW39	88196129	30S ribosomal protein S9 [Staphylococcus aureus subsp. aureus NCTC 8325]	14821	55	276	53	3	X	
Q2FW22	88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	13089		130	190	3	X	X
P60430	88196159	50S ribosomal protein L2 [Staphylococcus aureus subsp. aureus NCTC 8325]	30136		29	81	3	X	X
Q2FXS8	88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	11326	259	200	427	3	X	X
Q2FW11	88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	12827	67	158	61	3	X	X
Q2FZ60	88194930	50S ribosomal protein L28 [Staphylococcus aureus subsp. aureus NCTC 8325]	6973	47	73	76	3	X	
Q2FXQ0	88195486	50S ribosomal protein L35 [Staphylococcus aureus subsp. aureus NCTC 8325]	7692	54	32	111	3	X	
Q2FW29	88196139	50S ribosomal protein L36 [Staphylococcus aureus subsp. aureus NCTC 8325]	4302	63	44		3		
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	695	1326	837	3	X	X
Q2FVG4	88196386	hypothetical protein SAOUHSC_02750 [Staphylococcus aureus subsp. aureus NCTC 8325]	60601	28		17	3	X	
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022	52	50	47	3	X	
Q2FW31	88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	13873	137	100	40	4	X	X
Q2FXK6	88195529	30S ribosomal protein S4 [Staphylococcus aureus subsp. aureus NCTC 8325]	22999	87	101	88	4	X	X
P48940	88194308	30S ribosomal protein S7 [Staphylococcus aureus subsp. aureus NCTC 8325]	17783	149	153	136	4	X	X
Q2FW39	88196129	30S ribosomal protein S9 [Staphylococcus aureus subsp. aureus NCTC 8325]	14821	49	42		4	X	
Q2G170	88194087	5~-nucleotidase [Staphylococcus aureus subsp. aureus NCTC 8325]	33331	682	928	470	4	X	
Q2FW33	88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	13739	117	42	111	4	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	Dna Binding
P60430	88196159	50S ribosomal protein L2 [Staphylococcus aureus subsp. aureus NCTC 8325]	30136	875	983	596	4	X	X
Q2FXS8	88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	11326	132	95		4	X	X
Q2FW11	88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	12827	72	115		4	X	X
Q2FW17	88196151	50S ribosomal protein L24 [Staphylococcus aureus subsp. aureus NCTC 8325]	11529	63	81	51	4		X
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	76	68	103	4	X	X
Q2FW14	88196154	50S ribosomal protein L29 [Staphylococcus aureus subsp. aureus NCTC 8325]	8085		56	26	4	X	
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	239	347	422	4	X	X
Q2G1N7	88193886	accessory regulator-like protein [Staphylococcus aureus subsp. aureus NCTC 8325]	29871	92	94		4	X	X
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	308	181	200	4	X	X
Q2G0B5	88194455	hypothetical protein SAOUHSC_00690 [Staphylococcus aureus subsp. aureus NCTC 8325]	26671	106	100	86	4	X	
Q2FXM1	88195514	hypothetical protein SAOUHSC_01814 [Staphylococcus aureus subsp. aureus NCTC 8325]	15216	88	135	156	4	X	
Q2FWW1	88195840	MHC class II analog protein [Staphylococcus aureus subsp. aureus NCTC 8325]	65534	81	34		4	X	
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022	48	54	51	4	X	
Q2FZD3	88194845	recombination and DNA strand exchange inhibitor protein [Staphylococcus aureus subsp. aureus NCTC 8325]	88606		36	37	4	X	X
Q2FXP9	88195487	translation initiation factor IF-3 [Staphylococcus aureus subsp. aureus NCTC 8325]	20200	192	157	57	4	X	
Q2FW31	88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	13873	249	180		5	X	X
P0A0H0	88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	15277	53	119	51	5	X	X
Q2G111	88194149	30S ribosomal protein S18 [Staphylococcus aureus subsp. aureus NCTC 8325]	9304	36	31		5	X	X
Q2FXY6	88195395	30S ribosomal protein S20 [Staphylococcus aureus subsp. aureus NCTC 8325]	9016	44		45	5	X	X
Q2FXK6	88195529	30S ribosomal protein S4 [Staphylococcus aureus subsp. aureus NCTC 8325]	22999	466	327	307	5	X	X
P48940	88194308	30S ribosomal protein S7 [Staphylococcus aureus subsp. aureus NCTC 8325]	17783	247	218	89	5	X	X
Q2FW39	88196129	30S ribosomal protein S9 [Staphylococcus aureus subsp. aureus NCTC 8325]	14821	161	225	70	5	X	
Q2G170	88194087	5~-nucleotidase [Staphylococcus aureus subsp. aureus NCTC 8325]	33331	138	54		5	X	
P0A0F8	88196143	50S ribosomal protein L15 [Staphylococcus aureus subsp. aureus NCTC 8325]	15587	208	201	65	5	X	X
Q2FW13	88196155	50S ribosomal protein L16 [Staphylococcus aureus subsp. aureus NCTC 8325]	16232	77	66		5	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	Dna Binding
Q2FW33	88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	13739	108	32	38	5	X	
Q2FW22	88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	13089	64	105	84	5	X	X
P60430	88196159	50S ribosomal protein L2 [Staphylococcus aureus subsp. aureus NCTC 8325]	30136	331	395	122	5	X	X
Q2FXS8	88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	11326	247	264	65	5	X	X
Q2FW11	88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	12827	188	187	122	5	X	X
Q2FW17	88196151	50S ribosomal protein L24 [Staphylococcus aureus subsp. aureus NCTC 8325]	11529	66	51		5		X
Q2FZ60	88194930	50S ribosomal protein L28 [Staphylococcus aureus subsp. aureus NCTC 8325]	6973	42	31		5	X	
Q2FW14	88196154	50S ribosomal protein L29 [Staphylococcus aureus subsp. aureus NCTC 8325]	8085	34		71	5	X	
Q2FXQ0	88195486	50S ribosomal protein L35 [Staphylococcus aureus subsp. aureus NCTC 8325]	7692	51		29	5	X	
Q2FW07	88196161	50S ribosomal protein L4 [Staphylococcus aureus subsp. aureus NCTC 8325]	22451	249	222		5	X	X
Q2FW21	88196147	50S ribosomal protein L6 [Staphylococcus aureus subsp. aureus NCTC 8325]	19774	231	215	57	5	X	X
Q2FW66	88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	19180	40	32	89	5	X	
P0A0B7	88194163	alkyl hydroperoxide reductase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	20963	81	187		5	X	
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	404	426	163	5	X	X
Q2G001	88194591	hypothetical protein SAOUHSC_00833 [Staphylococcus aureus subsp. aureus NCTC 8325]	20736	82	92		5	X	
Q2FYS0	88195092	hypothetical protein SAOUHSC_01365 [Staphylococcus aureus subsp. aureus NCTC 8325]	37832	54	47	41	5	X	
Q2FY37	88195339	hypothetical protein SAOUHSC_01629 [Staphylococcus aureus subsp. aureus NCTC 8325]	31861	35	42		5	X	
Q2FXM1	88195514	hypothetical protein SAOUHSC_01814 [Staphylococcus aureus subsp. aureus NCTC 8325]	15216	95	94		5	X	
Q2FXJ2	88195542	hypothetical protein SAOUHSC_01843 [Staphylococcus aureus subsp. aureus NCTC 8325]	100886	37	32	41	5	X	
Q2FW79	88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	10000	70	98	91	5	X	
Q2FVX5	88196193	molybdenum ABC transporter permease [Staphylococcus aureus subsp. aureus NCTC 8325]	24847	39		39	5	X	
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022	51	62	49	5	X	
Q2G023	88194564	SsrA-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	17745	49	48		5	X	X
Q2FXP9	88195487	translation initiation factor IF-3 [Staphylococcus aureus subsp. aureus NCTC 8325]	20200	391	461	235	5	X	
Q2FW31	88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	13873	928	583	274	6	X	X
P0A0H0	88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	15277	222	164	112	6	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	Dna Binding
Q2FW30	88196138	30S ribosomal protein S13 [Staphylococcus aureus subsp. aureus NCTC 8325]	13711	128	138	55	6	X	X
Q2G111	88194149	30S ribosomal protein S18 [Staphylococcus aureus subsp. aureus NCTC 8325]	9304	34	32		6	X	X
Q2FW23	88196145	30S ribosomal protein S5 [Staphylococcus aureus subsp. aureus NCTC 8325]	17732	249	157		6	X	X
P48940	88194308	30S ribosomal protein S7 [Staphylococcus aureus subsp. aureus NCTC 8325]	17783	866	1017	733	6	X	X
Q2FW39	88196129	30S ribosomal protein S9 [Staphylococcus aureus subsp. aureus NCTC 8325]	14821	617	533	323	6	X	
Q2FW38	88196130	50S ribosomal protein L13 [Staphylococcus aureus subsp. aureus NCTC 8325]	16323		62	31	6	X	
P0A0F8	88196143	50S ribosomal protein L15 [Staphylococcus aureus subsp. aureus NCTC 8325]	15587	218	200	135	6	X	X
Q2FW13	88196155	50S ribosomal protein L16 [Staphylococcus aureus subsp. aureus NCTC 8325]	16232	155	188	100	6	X	X
Q2FW33	88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	13739	128	166	154	6	X	
Q2FW22	88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	13089	216	252	192	6	X	X
Q2FZ42	88194948	50S ribosomal protein L19 [Staphylococcus aureus subsp. aureus NCTC 8325]	13354	119	144	101	6	X	
Q2FXQ1	88195485	50S ribosomal protein L20 [Staphylococcus aureus subsp. aureus NCTC 8325]	13678		119	101	6	X	X
Q2FXS8	88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	11326	495	414	226	6	X	X
Q2FW11	88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	12827	1258	836	498	6	X	X
Q2FW17	88196151	50S ribosomal protein L24 [Staphylococcus aureus subsp. aureus NCTC 8325]	11529	94	89	94	6		X
Q2FZ60	88194930	50S ribosomal protein L28 [Staphylococcus aureus subsp. aureus NCTC 8325]	6973	41	42		6	X	
Q2FXQ0	88195486	50S ribosomal protein L35 [Staphylococcus aureus subsp. aureus NCTC 8325]	7692	43	59	39	6	X	
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	285	242	273	6	X	X
Q2G2M4	88194293	hypothetical protein SAOUHSC_00512 [Staphylococcus aureus subsp. aureus NCTC 8325]	15711	64	62	72	6	X	X
Q2G0F2	88194387	hypothetical protein SAOUHSC_00617 [Staphylococcus aureus subsp. aureus NCTC 8325]	18582	116	154	39	6	X	
Q2FY37	88195339	hypothetical protein SAOUHSC_01629 [Staphylococcus aureus subsp. aureus NCTC 8325]	31861	38		37	6	X	
Q2FXM1	88195514	hypothetical protein SAOUHSC_01814 [Staphylococcus aureus subsp. aureus NCTC 8325]	15216	639	635	411	6	X	
Q2FXJ2	88195542	hypothetical protein SAOUHSC_01843 [Staphylococcus aureus subsp. aureus NCTC 8325]	100886	40	32	33	6	X	
Q2FW79	88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	10000	60	73		6	X	
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022	50	61	48	6	X	
Q2FXP9	88195487	translation initiation factor IF-3 [Staphylococcus aureus subsp. aureus NCTC 8325]	20200	102	170	86	6	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	Dna Binding
Q2FW31	88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	13873	182	528	226	7	X	X
P0A0H0	88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	15277	54	116	60	7	X	X
Q2FW30	88196138	30S ribosomal protein S13 [Staphylococcus aureus subsp. aureus NCTC 8325]	13711	75	36	83	7	X	X
Q2FW19	161353519	30S ribosomal protein S14 [Staphylococcus aureus subsp. aureus NCTC 8325]	7295	29	52	37	7	X	X
Q2G2Q1	88194983	30S ribosomal protein S15 [Staphylococcus aureus subsp. aureus NCTC 8325]	10602	28	87	96	7	X	X
Q2FZ45	88194945	30S ribosomal protein S16 [Staphylococcus aureus subsp. aureus NCTC 8325]	10229	118	170	87	7	X	
Q2FW15	88196153	30S ribosomal protein S17 [Staphylococcus aureus subsp. aureus NCTC 8325]	10169	81	123	105	7	X	X
Q2G111	88194149	30S ribosomal protein S18 [Staphylococcus aureus subsp. aureus NCTC 8325]	9304	111	266	103	7	X	X
Q2FXY6	88195395	30S ribosomal protein S20 [Staphylococcus aureus subsp. aureus NCTC 8325]	9016	245	223	167	7	X	X
Q2FXZ7	88195384	30S ribosomal protein S21 [Staphylococcus aureus subsp. aureus NCTC 8325]	6968	91	110	79	7	X	
Q2G113	88194147	30S ribosomal protein S6 [Staphylococcus aureus subsp. aureus NCTC 8325]	11588	190	301	129	7	X	X
P48940	88194308	30S ribosomal protein S7 [Staphylococcus aureus subsp. aureus NCTC 8325]	17783	77	96	71	7	X	X
Q2FW39	88196129	30S ribosomal protein S9 [Staphylococcus aureus subsp. aureus NCTC 8325]	14821	213	304	262	7	X	
Q2FW22	88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	13089	772	1459	716	7	X	X
Q2FZ42	88194948	50S ribosomal protein L19 [Staphylococcus aureus subsp. aureus NCTC 8325]	13354		58	38	7	X	
Q2FXQ1	88195485	50S ribosomal protein L20 [Staphylococcus aureus subsp. aureus NCTC 8325]	13678		154	44	7	X	X
Q2FXS8	88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	11326	547	424	414	7	X	X
Q2FW11	88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	12827	179	284	104	7	X	X
Q2FW08	88196160	50S ribosomal protein L23 [Staphylococcus aureus subsp. aureus NCTC 8325]	10599	70	136	46	7	X	X
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	241		65	7	X	X
Q2FXT0	88195456	50S ribosomal protein L27 [Staphylococcus aureus subsp. aureus NCTC 8325]	10308	53	105		7	X	
Q2FZ60	88194930	50S ribosomal protein L28 [Staphylococcus aureus subsp. aureus NCTC 8325]	6973	101	199	84	7	X	
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	87		127	7	X	X
Q2FXQ0	88195486	50S ribosomal protein L35 [Staphylococcus aureus subsp. aureus NCTC 8325]	7692	81	107	77	7	X	
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	737	964	708	7	X	X
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077		75	28	7	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	Dna Binding
Q2G0R5	88194266	hypothetical protein SAOUHSC_00481 [Staphylococcus aureus subsp. aureus NCTC 8325]	9850		78	58	7	X	X
Q2FZZ9	88194593	hypothetical protein SAOUHSC_00835 [Staphylococcus aureus subsp. aureus NCTC 8325]	13591	77	136	76	7	X	
Q2G2D1	88194977	hypothetical protein SAOUHSC_01244 [Staphylococcus aureus subsp. aureus NCTC 8325]	11033	67	57	65	7	X	
Q2FXM1	88195514	hypothetical protein SAOUHSC_01814 [Staphylococcus aureus subsp. aureus NCTC 8325]	15216	179	286	269	7	X	
Q2FW79	88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	10000	80	108	66	7	X	
Q2FVY0	88196188	molybdopterin biosynthesis protein MoeA [Staphylococcus aureus subsp. aureus NCTC 8325]	44988	50	37	46	7	X	
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022		62	50	7	X	

Table B.2. Proteins identified in 0.5-1M NaCl elution.

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FYM1	88195143	2-oxoglutarate dehydrogenase E1 component [Staphylococcus aureus subsp. aureus NCTC 8325]	105277	99	75	40	8	X	
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	93	92	75	8	X	X
Q2G122	88194138	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	85023	132	83		8	X	
Q2FYS9	88195075	aconitate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	98908	398	423	470	8	X	
Q2FV74	88196493	ATP-dependent Clp protease ATP-binding subunit ClpC [Staphylococcus aureus subsp. aureus NCTC 8325]	77789		77	38	8	X	X
Q2FZI6	88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	54314		102	68	8	X	
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	214	510	434	8	X	
Q2FZ72	88194909	carbamoyl phosphate synthase large subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	117112		95	96	8	X	X
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012		140	96	8	X	X
O52582	88194665	coenzyme A disulfide reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	49259	76	71		8	X	X
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451	66	92	168	8	X	
Q2FYM2	88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46644	144	150	133	8	X	
Q2G2Q0	88193829	DNA gyrase subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	99290	167	280	175	8	X	X
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	101	115	94	8	X	X
P47768	161353532	DNA-directed RNA polymerase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	133136	259	200	266	8	X	X
Q2G0N5	88194305	DNA-directed RNA polymerase subunit beta~ [Staphylococcus aureus subsp. aureus NCTC 8325]	134190	384	321	276	8	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190	284	239	206	8	X	
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564	551	803	905	8	X	X
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	254	250	392	8	X	X
Q2G0P5	88194286	endopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	90981	153	93	113	8	X	X
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819	238	231	241	8	X	X
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	85	170	208	8	X	
Q2FY08	88195373	glycyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	53586	70	60	85	8	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G0R0	88194271	hypothetical protein SAOUHSC_00486 [Staphylococcus aureus subsp. aureus NCTC 8325]	77764		48	52	8	X	X
Q2G0Q8	88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	32955		81	66	8	X	
Q2FXZ9	88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	35160		34	74	8	X	
Q2G245	88195552	hypothetical protein SAOUHSC_01854 [Staphylococcus aureus subsp. aureus NCTC 8325]	55058	91	193	198	8	X	
Q2FXI9	88195555	hypothetical protein SAOUHSC_01857 [Staphylococcus aureus subsp. aureus NCTC 8325]	144568	29	110	54	8	X	X
Q2FVG4	88196386	hypothetical protein SAOUHSC_02750 [Staphylococcus aureus subsp. aureus NCTC 8325]	60601	25		22	8	X	
Q2FUW1	88196609	hypothetical protein SAOUHSC_02990 [Staphylococcus aureus subsp. aureus NCTC 8325]	227909	92	194	172	8	X	
Q2G0Y7	88194172	inosine-5~-monophosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	52818		50	51	8	X	X
Q2FV16	88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	55964		169	180	8	X	
Q2FXZ2	88195389	molecular chaperone DnaK [Staphylococcus aureus subsp. aureus NCTC 8325]	66321		124	73	8	X	
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022	54	61		8	X	
Q2G1Y0	88195803	NAD-dependent DNA ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	75035	66	172	196	8	X	X
Q2FZD8	88194840	phenylalanyl-tRNA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	88866	338		91	8	X	X
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088		199	186	8	X	
Q2FZJ0	88194767	phosphoribosylformylglycinamidine synthase II [Staphylococcus aureus subsp. aureus NCTC 8325]	79486	155	389	335	8	X	X
Q2FZ20	88194984	polynucleotide phosphorylase/polyadenylase [Staphylococcus aureus subsp. aureus NCTC 8325]	77314		155	79	8	X	X
O06446	88194531	preprotein translocase subunit SecA [Staphylococcus aureus subsp. aureus NCTC 8325]	95900	62	189	83	8	X	X
Q2G2C1	88194813	pyruvate carboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	128467		64	27	8	X	X
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224		69	95	8	X	
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	264	708	377	8	X	
Q2FXP7	88195489	threonyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74441	173	272	148	8	X	
Q2FYT8	88195066	transketolase [Staphylococcus aureus subsp. aureus NCTC 8325]	68317		338	225	8	X	
Q2G2D0	88194979	translation initiation factor IF-2 [Staphylococcus aureus subsp. aureus NCTC 8325]	77823	700	976	720	8	X	X
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579	322	282	103	8	X	
Q2FUQ3	161353516	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA [Staphylococcus aureus subsp. aureus NCTC 8325]	70072	53	109		8	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FV67	88196500	1-pyrroline-5-carboxylate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	56832		193	97	9	X	
Q2FYF9	88195210	30S ribosomal protein S1 [Staphylococcus aureus subsp. aureus NCTC 8325]	43261		145	74	9	X	X
P60430	88196159	50S ribosomal protein L2 [Staphylococcus aureus subsp. aureus NCTC 8325]	30136		36	36	9	X	X
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	133	249	146	9	X	X
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	71	66	101	9	X	X
Q2FY60	88195316	6-phosphogluconate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	51770		86	72	9	X	X
Q2FYZ4	88195010	aerobic glycerol-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	62349	116	308	94	9	X	X
Q2FWD6	88196026	aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	51937		113	80	9	X	X
Q2G1J0	88193945	aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	53626		226	243	9	X	X
O05204	88194162	alkyl hydroperoxide reductase subunit F [Staphylococcus aureus subsp. aureus NCTC 8325]	54687	67	230	138	9	X	X
Q2FZI9	88194768	amidophosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	54363		110	73	9	X	
Q2G0F8	88194381	arginyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	62342		91	69	9	X	
Q2FYH6	88195188	asparaginyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	49127		133	104	9	X	
Q2FWY9	88195799	aspartyl/glutamyl-tRNA amidotransferase subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	52788		84	105	9	X	
Q2FWZ0	88195798	aspartyl/glutamyl-tRNA amidotransferase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	53623		235	186	9	X	
Q2FXU5	88195441	aspartyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	66587		48	47	9	X	
Q2FZI6	88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	54314	124	406	506	9	X	
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	1196	1581	1076	9	X	
Q2FYU7	88195057	catalase [Staphylococcus aureus subsp. aureus NCTC 8325]	54908		193	215	9	X	
O07325	88194891	cell division protein [Staphylococcus aureus subsp. aureus NCTC 8325]	52902		117	95	9	X	
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012		822	358	9	X	X
Q2FWN4	88195925	chaperonin GroEL [Staphylococcus aureus subsp. aureus NCTC 8325]	57629		269	97	9	X	
O52582	88194665	coenzyme A disulfide reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	49259	79	508	96	9	X	X
Q2FZV6	88194636	cytosol aminopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	54095	96	117		9	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FWH5	88195982	DEAD-box ATP dependent DNA helicase [Staphylococcus aureus subsp. aureus NCTC 8325]	56907		131	41	9	X	X
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451	216	417	391	9	X	
Q2FYM2	88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46644	217	424	526	9	X	
Q2FXH9	88195565	dipeptidase PepV [Staphylococcus aureus subsp. aureus NCTC 8325]	52791		68	70	9	X	
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190	217	629	384	9	X	
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564		282	424	9	X	X
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	50	442	295	9	X	X
Q2FWE8	88196009	F0F1 ATP synthase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	54550		146	243	9	X	X
Q2FWF0	88196007	F0F1 ATP synthase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	51368		393	268	9	X	X
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819	898	644	434	9	X	X
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817		68	121	9	X	
Q2FY66	88195310	glucose-6-phosphate 1-dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	56929		164	175	9	X	X
Q2FYY6	88195018	glutamine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	50808		62	145	9	X	
Q2G241	88194290	glutamyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	56253	990	1260	815	9	X	X
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258		152	206	9	X	
Q2FY08	88195373	glycyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	53586	178	157	225	9	X	X
Q2G0Y6	88194173	GMP synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	58194		157	140	9	X	X
Q2G193	88194059	hypothetical protein SAOUHSC_00253 [Staphylococcus aureus subsp. aureus NCTC 8325]	57887		157	90	9		
Q2G0Z2	88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	35591	44	442	259	9	X	
Q2G055	88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	22199		115	161	9	X	
Q2FZY6	88194606	hypothetical protein SAOUHSC_00848 [Staphylococcus aureus subsp. aureus NCTC 8325]	48519	179	174	77	9	X	
Q2FZY3	88194609	hypothetical protein SAOUHSC_00851 [Staphylococcus aureus subsp. aureus NCTC 8325]	52498	423	237	155	9	X	
Q2FZD4	88194844	hypothetical protein SAOUHSC_01098 [Staphylococcus aureus subsp. aureus NCTC 8325]	64830	69	55		9		X
Q2FZ19	88194985	hypothetical protein SAOUHSC_01252 [Staphylococcus aureus subsp. aureus NCTC 8325]	58753		109	118	9	X	X
Q2FYL3	88195151	hypothetical protein SAOUHSC_01427 [Staphylococcus aureus subsp. aureus NCTC 8325]	55227		232	216	9		
Q2FXZ9	88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	35160		84	90	9	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G245	88195552	hypothetical protein SAOUHSC_01854 [Staphylococcus aureus subsp. aureus NCTC 8325]	55058	256	709	248	9	X	
Q2G1H0	88193965	indolepyruvate decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	60501		81	147	9	X	
Q2G0Y7	88194172	inosine-5~-monophosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	52818		310	321	9	X	X
Q2G0Q3	88194278	lysyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	56684	609	425	341	9	X	
Q2FV16	88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	55964	110	467	422	9	X	
Q2FXZ2	88195389	molecular chaperone DnaK [Staphylococcus aureus subsp. aureus NCTC 8325]	66321		144	119	9	X	
Q2G1U3	88194694	oligoendopeptidase F [Staphylococcus aureus subsp. aureus NCTC 8325]	69776		68	57	9	X	
Q2FY21	88195360	penicillin-binding protein 3 [Staphylococcus aureus subsp. aureus NCTC 8325]	77190	45	69	76	9	X	
Q2G1W2	88195605	phosphoenolpyruvate carboxykinase [Staphylococcus aureus subsp. aureus NCTC 8325]	59340		109	144	9	X	X
Q2FZH5	88194782	phosphoenolpyruvate-protein phosphotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	63179		197	121	9	X	
Q2G031	88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	42575		146	42	9	X	X
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088		370	243	9	X	
Q2FZJ0	88194767	phosphoribosylformylglycinamidine synthase II [Staphylococcus aureus subsp. aureus NCTC 8325]	79486		101	57	9	X	X
Q2G1Z4	88194973	prolyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	63823		81	97	9	X	
Q2FZG4	88194792	pyruvate dehydrogenase complex, E1 component subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	41357		84	102	9	X	
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	488	577	625	9	X	
P0A0J0	88195369	RNA polymerase sigma factor RpoD [Staphylococcus aureus subsp. aureus NCTC 8325]	42145		266	315	9	X	X
Q2FZP2	88194715	serine protease HtrA [Staphylococcus aureus subsp. aureus NCTC 8325]	87036		225	165	9	X	
Q2FZ46	88194944	signal recognition particle protein [Staphylococcus aureus subsp. aureus NCTC 8325]	50672	41	57	255	9	X	X
Q2FZC8	88194850	succinate dehydrogenase flavoprotein subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	65462		114	122	9	X	
Q2FXP7	88195489	threonyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74441	284	80	73	9	X	
Q2G2D2	88194976	transcription elongation factor NusA [Staphylococcus aureus subsp. aureus NCTC 8325]	43714		139	85	9		X
Q2FYT8	88195066	transketolase [Staphylococcus aureus subsp. aureus NCTC 8325]	68317		58	233	9	X	
Q2G2D0	88194979	translation initiation factor IF-2 [Staphylococcus aureus subsp. aureus NCTC 8325]	77823	79	463	246	9	X	X
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579		114	98	9	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
P0A0H0	88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	15277		54	40	10	X	X
Q2FZR9	88194678	3-oxoacyl- synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	43712	84	111	123	10	X	
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	212	192	163	10	X	X
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	192	158	180	10	X	X
Q2FY60	88195316	6-phosphogluconate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	51770	126	233	161	10	X	X
Q2FXL5	88195520	acetate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	44015	45	329	197	10	X	X
Q2G2S0	88195807	adenylosuccinate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	49572		171	118	10	X	
Q2G1S3	88193840	adenylosuccinate synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	47549		99	59	10	X	X
Q2G248	88195550	bifunctional 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase [Staphylococcus aureus subsp. aureus NCTC 8325]	40593	45		52	10	X	
Q2FZJ6	88194761	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30824		121	35	10	X	X
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	197	396	326	10	X	
Q2FZ73	88194908	carbamoyl phosphate synthase small subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	40369	170	133	64	10	X	
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012	628	500	651	10	X	X
Q2FXZ3	88195388	chaperone protein DnaJ [Staphylococcus aureus subsp. aureus NCTC 8325]	41735		81	67	10		
O52582	88194665	coenzyme A disulfide reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	49259	481	106	61	10	X	X
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451		147	159	10	X	
Q2FYM2	88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46644	46	359	145	10	X	
Q2G2H4	88193825	DNA polymerase III subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	41888	78	97	85	10	X	X
Q2FW32	88196136	DNA-directed RNA polymerase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	34990	427	241	111	10	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190		254	166	10	X	
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564		174	210	10	X	X
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474	233	353	168	10	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	716	987	892	10	X	X
Q2FWF0	88196007	F0F1 ATP synthase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	51368	135	101	110	10	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819	319	198	203	10	X	X
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	67		84	10	X	
Q2FZU0	88194657	glucose-6-phosphate isomerase [Staphylococcus aureus subsp. aureus NCTC 8325]	49791	36	97	79	10	X	
Q2FZU5	88194652	glutamate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	45731		112	61	10	X	
Q2FYY6	88195018	glutamine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	50808	34	49	52	10	X	
Q2G241	88194290	glutamyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	56253	449	101		10	X	X
Q2FXP2	88195494	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	36956	168	166		10	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	373	356	396	10	X	
Q2FZ55	88194935	glycerol-3-phosphate acyltransferase PlsX [Staphylococcus aureus subsp. aureus NCTC 8325]	35408	188	302	124	10	X	
Q2FY33	88195343	glycine cleavage system aminomethyltransferase T [Staphylococcus aureus subsp. aureus NCTC 8325]	40433	276	140	136	10		
Q2FY08	88195373	glycyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	53586	408	71	58	10	X	X
Q2FXU4	88195442	histidyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	48252	241	75		10	X	
Q2FV76	88196491	HMG-CoA synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	43178		90	50	10	X	
Q2G0Z2	88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	35591		166	33	10	X	
Q2G055	88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	22199	86	92	151	10	X	
Q2FZY6	88194606	hypothetical protein SAOUHSC_00848 [Staphylococcus aureus subsp. aureus NCTC 8325]	48519	84	70		10	X	
Q2FZW0	88194632	hypothetical protein SAOUHSC_00875 [Staphylococcus aureus subsp. aureus NCTC 8325]	39374	104	153	127	10	X	
Q2FZV7	88194635	hypothetical protein SAOUHSC_00878 [Staphylococcus aureus subsp. aureus NCTC 8325]	44077	114	251	152	10	X	
P52078	88194753	hypothetical protein SAOUHSC_00997 [Staphylococcus aureus subsp. aureus NCTC 8325]	45657	49	59	51	10		
Q2FYL3	88195151	hypothetical protein SAOUHSC_01427 [Staphylococcus aureus subsp. aureus NCTC 8325]	55227		240	182	10		
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310	37		39	10	X	
Q2FXN3	88195502	hypothetical protein SAOUHSC_01802 [Staphylococcus aureus subsp. aureus NCTC 8325]	32371	118	71	96	10	X	
Q2FXJ6	88195538	hypothetical protein SAOUHSC_01838 [Staphylococcus aureus subsp. aureus NCTC 8325]	45775	294	355	410	10	X	
Q2G245	88195552	hypothetical protein SAOUHSC_01854 [Staphylococcus aureus subsp. aureus NCTC 8325]	55058	115	122	154	10	X	
Q2FWW3	88195838	hypothetical protein SAOUHSC_02158 [Staphylococcus aureus subsp. aureus NCTC 8325]	48089		142	92	10	X	
Q2FXN4	88195501	isocitrate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	46394	149	299	259	10	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FV16	88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	55964		124	88	10	X	
Q2FYR2	88195100	methicillin resistance factor FemA [Staphylococcus aureus subsp. aureus NCTC 8325]	49093	235	52	154	10	X	
Q2FVY0	88196188	molybdopterin biosynthesis protein MoeA [Staphylococcus aureus subsp. aureus NCTC 8325]	44988	564	562	124	10	X	
Q2FZU6	88194651	ornithine--oxo-acid transaminase [Staphylococcus aureus subsp. aureus NCTC 8325]	43390		77	29	10	X	
Q2FVZ4	88196174	peptidoglycan pentaglycine interpeptide biosynthesis protein FmhB [Staphylococcus aureus subsp. aureus NCTC 8325]	48491	98	39		10		
Q2G031	88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	42575	778	634	867	10	X	X
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088	472	678	454	10	X	
Q2FZI5	88194772	phosphoribosylamine--glycine ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	45820	87	220	187	10	X	X
Q2FZJ4	88194763	phosphoribosylaminoimidazole carboxylase ATPase subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	42466		45	39	10	X	
Q2FZG4	88194792	pyruvate dehydrogenase complex, E1 component subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	41357	379	299	340	10	X	
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224		137	49	10	X	
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	124	168	165	10	X	
Q2FXT6	88195450	queuine tRNA-ribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	43281	42	34		10		
Q2FZ09	228937974	recombinase A [Staphylococcus aureus subsp. aureus NCTC 8325]	37633	65	73	121	10	X	X
P0A0J0	88195369	RNA polymerase sigma factor RpoD [Staphylococcus aureus subsp. aureus NCTC 8325]	42145	171		122	10	X	X
Q2FWE5	88196017	serine hydroxymethyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	45144	97	103	111	10	X	
Q2FZP2	88194715	serine protease HtrA [Staphylococcus aureus subsp. aureus NCTC 8325]	87036		95	110	10	X	
Q2FZ37	88194953	succinyl-CoA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	42030	237	320	200	10	X	X
Q2G2D0	88194979	translation initiation factor IF-2 [Staphylococcus aureus subsp. aureus NCTC 8325]	77823		101	164	10	X	X
Q2FZQ7	88194690	tryptophanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	36886	36	43		10	X	
Q2FXJ5	88195539	tyrosyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	47568	49		62	10	X	X
Q2FWF4	88196003	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	44913	62	95	96	10	X	
Q2FW81	88196079	UDP-N-acetylglucosamine pyrophosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	44866	30	35		10	X	
P0A0H0	88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	15277	50	57	91	11	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FW12	88196156	30S ribosomal protein S3 [Staphylococcus aureus subsp. aureus NCTC 8325]	24085	43	63	71	11	X	X
Q2G170	88194087	5~-nucleotidase [Staphylococcus aureus subsp. aureus NCTC 8325]	33331	54	119	92	11	X	
Q2G0P0	88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	24693	73	55	68	11	X	X
Q2FW38	88196130	50S ribosomal protein L13 [Staphylococcus aureus subsp. aureus NCTC 8325]	16323	59	68	63	11	X	
Q2FW33	88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	13739		83	94	11	X	
P60430	88196159	50S ribosomal protein L2 [Staphylococcus aureus subsp. aureus NCTC 8325]	30136	115	139	105	11	X	X
Q2FW17	88196151	50S ribosomal protein L24 [Staphylococcus aureus subsp. aureus NCTC 8325]	11529	34		78	11		X
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	1774	2265	1445	11	X	X
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	354	388	337	11	X	X
Q2FW21	88196147	50S ribosomal protein L6 [Staphylococcus aureus subsp. aureus NCTC 8325]	19774	56	72	114	11	X	X
Q2FXM8	88195507	6-phosphofructokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	33376		72	168	11	X	X
Q2FW75	88196085	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	36569	193	232	170	11		
Q2G2D8	88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35049	249	468	554	11	X	
Q2FZ75	88194906	aspartate carbamoyltransferase catalytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	33237		117	133	11	X	
Q2FZJ6	88194761	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30824	486	611	968	11	X	X
Q2FZI6	88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	54314		60	113	11	X	
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	186	376	359	11	X	
Q2G295	88195548	catabolite control protein A [Staphylococcus aureus subsp. aureus NCTC 8325]	36038	123	201	148	11	X	X
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012	49	505	415	11	X	X
Q2G0M7	88194313	chaperone protein HchA [Staphylococcus aureus subsp. aureus NCTC 8325]	32156	101	196	401	11	X	
Q2FYM2	88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46644	33	261	148	11	X	
Q2FW32	88196136	DNA-directed RNA polymerase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	34990	72	92		11	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190		82	161	11	X	
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564		91	120	11	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FY41	88195335	elongation factor P [Staphylococcus aureus subsp. aureus NCTC 8325]	20541	75	74	55	11		
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474	196	322	486	11	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	232	342	393	11	X	X
Q2FY16	88195365	endonuclease IV [Staphylococcus aureus subsp. aureus NCTC 8325]	33138	93	75		11	X	X
Q2FWE9	161353520	F0F1 ATP synthase subunit gamma [Staphylococcus aureus subsp. aureus NCTC 8325]	32086	264	134	291	11	X	
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819	144	178	173	11	X	X
Q2FV17	88196553	fructose-1,6-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	33034	64	262	154	11	X	
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	130	235	322	11	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	182	261	351	11	X	
Q2FZ55	88194935	glycerol-3-phosphate acyltransferase PlsX [Staphylococcus aureus subsp. aureus NCTC 8325]	35408	178	206		11	X	
Q2FYU4	88195060	guanosine 5~-monophosphate oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	36093	77	134		11	X	X
Q2G1C5	88194010	hypothetical protein SAOUHSC_00200 [Staphylococcus aureus subsp. aureus NCTC 8325]	42156	50		47	11	X	
Q2G0X1	88194197	hypothetical protein SAOUHSC_00402 [Staphylococcus aureus subsp. aureus NCTC 8325]	31468		100	170	11		
Q2G0Q8	88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	32955	347	503	379	11	X	
Q2G0F3	88194386	hypothetical protein SAOUHSC_00616 [Staphylococcus aureus subsp. aureus NCTC 8325]	30906	79	95	132	11	X	
Q2G0D0	88194440	hypothetical protein SAOUHSC_00675 [Staphylococcus aureus subsp. aureus NCTC 8325]	26304		136	126	11	X	X
Q2G055	88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	22199	132	184	179	11	X	
Q2FZT4	88194663	hypothetical protein SAOUHSC_00906 [Staphylococcus aureus subsp. aureus NCTC 8325]	33093	43	229	212	11	X	
Q2G2G6	88194802	hypothetical protein SAOUHSC_01050 [Staphylococcus aureus subsp. aureus NCTC 8325]	40034	55	56	45	11		
Q2FZE9	88194829	hypothetical protein SAOUHSC_01081 [Staphylococcus aureus subsp. aureus NCTC 8325]	38722		56	77	11	X	
Q2FYK7	88195157	hypothetical protein SAOUHSC_01433 [Staphylococcus aureus subsp. aureus NCTC 8325]	30626	103	162	233	11	X	
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310		37	38	11	X	
Q2FYJ0	88195174	hypothetical protein SAOUHSC_01455 [Staphylococcus aureus subsp. aureus NCTC 8325]	133025		38	36	11	X	
Q2FY01	88195380	hypothetical protein SAOUHSC_01673 [Staphylococcus aureus subsp. aureus NCTC 8325]	34892	137	49	113	11	X	
Q2FXZ9	88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	35160	95	465	505	11	X	
Q2G245	88195552	hypothetical protein SAOUHSC_01854 [Staphylococcus aureus subsp. aureus NCTC 8325]	55058	103	210	145	11	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FXI7	88195557	hypothetical protein SAOUHSC_01859 [Staphylococcus aureus subsp. aureus NCTC 8325]	33049	205	191	50	11	X	
Q2FVW9	88196199	hypothetical protein SAOUHSC_02554 [Staphylococcus aureus subsp. aureus NCTC 8325]	33990	70	64	78	11		
Q2FUQ5	88196664	hypothetical protein SAOUHSC_03049 [Staphylococcus aureus subsp. aureus NCTC 8325]	32177	106	64	186	11		X
Q2FXN4	88195501	isocitrate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	46394		53	44	11	X	
Q2FZX4	88194618	lipoyl synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	34863	46	72	78	11		
Q2FZ54	88194936	malonyl CoA-acyl carrier protein transacylase [Staphylococcus aureus subsp. aureus NCTC 8325]	33614	94		91	11		
Q2FWY1	88195820	manganese-dependent inorganic pyrophosphatase [Staphylococcus aureus subsp. aureus NCTC 8325]	34047	76	176	240	11	X	
Q2FZ68	88194922	methionyl-tRNA formyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	34190	452	193	443	11	X	
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022	23	24		11	X	
Q2FWU0	88195861	phi PVL orf 13-like protein [Staphylococcus aureus subsp. aureus NCTC 8325]	34917	45	103		11	X	
Q2G031	88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	42575	108	94	186	11	X	X
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088		40	146	11	X	
Q2FZI8	88194769	phosphoribosylaminoimidazole synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	36994		65	166	11	X	
Q2G0J0	88194349	phosphotransacetylase [Staphylococcus aureus subsp. aureus NCTC 8325]	34930	30	183	434	11	X	
Q2FXP5	88195491	primosomal protein DnaI [Staphylococcus aureus subsp. aureus NCTC 8325]	35613		27	48	11	X	
Q2G2S6	88195663	protein export protein PrsA [Staphylococcus aureus subsp. aureus NCTC 8325]	35616	396	541	522	11		
Q2G0Q1	88194280	pyridoxal biosynthesis lyase PdxS [Staphylococcus aureus subsp. aureus NCTC 8325]	31972	77	323	338	11	X	
Q2FZG4	88194792	pyruvate dehydrogenase complex, E1 component subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	41357	49	150	99	11	X	
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224	460	624	585	11	X	
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	100	157	247	11	X	
Q2FZJ9	88194758	quinol oxidase AA3 subunit II [Staphylococcus aureus subsp. aureus NCTC 8325]	41750		65	84	11	X	
Q2FWP6	88195908	repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	29046	51	46	138	11		
Q2G2Q2	88194982	riboflavin biosynthesis protein RibF [Staphylococcus aureus subsp. aureus NCTC 8325]	36669		57	37	11		
Q2G077	88194508	ribonucleotide-diphosphate reductase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	37489		68	73	11	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G0S2	88194259	ribose-phosphate pyrophosphokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	35262		44	109	11	X	
Q2FZ39	88194951	ribosomal biogenesis GTPase [Staphylococcus aureus subsp. aureus NCTC 8325]	33360	141	103	77	11		X
Q2FX95	88195673	ribosomal large subunit pseudouridine synthase D [Staphylococcus aureus subsp. aureus NCTC 8325]	31421	68	37	71	11	X	X
Q2FWJ4	88195964	RNA polymerase sigma factor SigB [Staphylococcus aureus subsp. aureus NCTC 8325]	29425		93	82	11		X
P60393	88194885	S-adenosyl-methyltransferase MraW [Staphylococcus aureus subsp. aureus NCTC 8325]	34808	247	184	140	11		
Q2FZP2	88194715	serine protease HtrA [Staphylococcus aureus subsp. aureus NCTC 8325]	87036		121	72	11	X	
Q2FZ36	88194954	succinyl-CoA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	31522	122	218	191	11	X	
Q2G041	88194546	thioredoxin reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	33595	109	212	255	11	X	
Q2G2D0	88194979	translation initiation factor IF-2 [Staphylococcus aureus subsp. aureus NCTC 8325]	77823		81	69	11	X	X
Q2G2Q3	88194981	tRNA pseudouridine synthase B [Staphylococcus aureus subsp. aureus NCTC 8325]	34571	238	117	102	11		X
Q2FZQ7	88194690	tryptophanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	36886	362	429	189	11	X	
Q2FXZ5	88195386	16S ribosomal RNA methyltransferase RsmE [Staphylococcus aureus subsp. aureus NCTC 8325]	28452	151		76	12		
Q2FUQ4	88196665	16S rRNA methyltransferase GidB [Staphylococcus aureus subsp. aureus NCTC 8325]	27342	192	127	70	12		
Q2G1C0	88194032	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	26640	64	82	125	12	X	
P0A0H0	88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	15277	68	69	101	12	X	X
Q2FW15	88196153	30S ribosomal protein S17 [Staphylococcus aureus subsp. aureus NCTC 8325]	10169	56		74	12	X	X
Q2FW12	88196156	30S ribosomal protein S3 [Staphylococcus aureus subsp. aureus NCTC 8325]	24085	305	118	286	12	X	X
Q2FV21	88196546	3-methyl-2-oxobutanoate hydroxymethyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	28222	571	274	394	12	X	
Q2G170	88194087	5~-nucleotidase [Staphylococcus aureus subsp. aureus NCTC 8325]	33331	98		101	12	X	
Q2G0P0	88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	24693	469	369	551	12	X	X
Q2FW38	88196130	50S ribosomal protein L13 [Staphylococcus aureus subsp. aureus NCTC 8325]	16323	107	108	82	12	X	
Q2FW33	88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	13739	132	100	108	12	X	
Q2FW22	88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	13089	86		98	12	X	X
P60430	88196159	50S ribosomal protein L2 [Staphylococcus aureus subsp. aureus NCTC 8325]	30136	56	98	177	12	X	X
Q2FW17	88196151	50S ribosomal protein L24 [Staphylococcus aureus subsp. aureus NCTC 8325]	11529	86	83	62	12		X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	401	505	326	12	X	X
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	3983	2237	3539	12	X	X
Q2FW07	88196161	50S ribosomal protein L4 [Staphylococcus aureus subsp. aureus NCTC 8325]	22451	37		174	12	X	X
Q2FW18	88196150	50S ribosomal protein L5 [Staphylococcus aureus subsp. aureus NCTC 8325]	20254	168	83	335	12	X	X
Q2FW21	88196147	50S ribosomal protein L6 [Staphylococcus aureus subsp. aureus NCTC 8325]	19774	293	134	224	12	X	X
Q2FZY7	88194605	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	28257	97	43	214	12	X	
Q2FX86	88195682	ABC transporter permease [Staphylococcus aureus subsp. aureus NCTC 8325]	53089	39		53	12	X	
Q2FW75	88196085	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	36569	51		64	12		
Q2G0V0	88194218	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	30437	118	106	191	12		
Q2G2D8	88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35049	292	153	312	12	X	
Q2FWM4	88195935	accessory gene regulator protein A [Staphylococcus aureus subsp. aureus NCTC 8325]	24238	74	38	65	12	X	X
Q2G1N7	88193886	accessory regulator-like protein [Staphylococcus aureus subsp. aureus NCTC 8325]	29871	130	83	165	12	X	X
Q2G1M1	88193901	acetoin reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	27199	59	115	160	12	X	
Q2FXM6	88195509	acetyl-CoA carboxylase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	31851	76		87	12	X	
Q2FZJ6	88194761	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30824	142	137	145	12	X	X
Q2FZI6	88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	54314		59	250	12	X	
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	190	191	266	12	X	
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012	84	199	322	12	X	X
Q2FXI0	88195564	D-alanine aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	31874	68	69	126	12	X	
Q2G224	88193913	deoxyribose-phosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	23458	157	90	64	12	X	
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451		40	265	12	X	
Q2FYM2	88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46644	99	60	168	12	X	
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190	143	152	173	12	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	212	230	488	12	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FZQ3	88194704	enoyl-(acyl carrier protein) reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	28005	108	60	167	12	X	X
Q2FWE8	88196009	F0F1 ATP synthase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	54550	40		40	12	X	X
Q2FWE9	161353520	F0F1 ATP synthase subunit gamma [Staphylococcus aureus subsp. aureus NCTC 8325]	32086	168		156	12	X	
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819	349	63	226	12	X	X
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	131	196	266	12	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	36	184	277	12	X	
Q2G0J1	88194348	heme peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	29371	151	38	167	12	X	
Q2G1Q1	88193872	hypothetical protein SAOUHSC_00052 [Staphylococcus aureus subsp. aureus NCTC 8325]	29768	120	46	125	12		
Q2G1P9	88193874	hypothetical protein SAOUHSC_00054 [Staphylococcus aureus subsp. aureus NCTC 8325]	29689	92	46	98	12		
Q2G1P8	88193875	hypothetical protein SAOUHSC_00055 [Staphylococcus aureus subsp. aureus NCTC 8325]	29381	74	46		12		
Q2G1C5	88194010	hypothetical protein SAOUHSC_00200 [Staphylococcus aureus subsp. aureus NCTC 8325]	42156	42	49	51	12	X	
Q2G0Q8	88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	32955	48	89	204	12	X	
Q2G2M3	88194294	hypothetical protein SAOUHSC_00513 [Staphylococcus aureus subsp. aureus NCTC 8325]	27190	210	129	203	12	X	X
Q2G0N7	88194303	hypothetical protein SAOUHSC_00523 [Staphylococcus aureus subsp. aureus NCTC 8325]	22666	233		191	12		
Q2G0I3	88194356	hypothetical protein SAOUHSC_00582 [Staphylococcus aureus subsp. aureus NCTC 8325]	15788	102	97	74	12	X	
Q2G0B5	88194455	hypothetical protein SAOUHSC_00690 [Staphylococcus aureus subsp. aureus NCTC 8325]	26671	80	100	127	12	X	
Q2G240	88194471	hypothetical protein SAOUHSC_00706 [Staphylococcus aureus subsp. aureus NCTC 8325]	28455	141	131	72	12	X	X
Q2G2T8	88194477	hypothetical protein SAOUHSC_00712 [Staphylococcus aureus subsp. aureus NCTC 8325]	32339	218	72	94	12	X	
Q2G058	88194527	hypothetical protein SAOUHSC_00764 [Staphylococcus aureus subsp. aureus NCTC 8325]	14132	37		38	12		
Q2G055	88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	22199	784	577	526	12	X	
Q2FZZ0	88194602	hypothetical protein SAOUHSC_00844 [Staphylococcus aureus subsp. aureus NCTC 8325]	30332	162	138	260	12		
Q2FZV7	88194635	hypothetical protein SAOUHSC_00878 [Staphylococcus aureus subsp. aureus NCTC 8325]	44077		54	71	12	X	
Q2FZG5	88194791	hypothetical protein SAOUHSC_01039 [Staphylococcus aureus subsp. aureus NCTC 8325]	23861	113	132	173	12	X	
Q2FZE0	88194838	hypothetical protein SAOUHSC_01091 [Staphylococcus aureus subsp. aureus NCTC 8325]	26897	234	179	54	12	X	X
Q2FZ87	88194894	hypothetical protein SAOUHSC_01153 [Staphylococcus aureus subsp. aureus NCTC 8325]	25331	181	48	78	12		
Q2FZ83	88194898	hypothetical protein SAOUHSC_01158 [Staphylococcus aureus subsp. aureus NCTC 8325]	23500	196	133	44	12	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FZ06	88194998	hypothetical protein SAOUHSC_01265 [Staphylococcus aureus subsp. aureus NCTC 8325]	29856	361	89		12	X	
Q2FYH7	88195187	hypothetical protein SAOUHSC_01470 [Staphylococcus aureus subsp. aureus NCTC 8325]	26938	179		203	12		
Q2FY37	88195339	hypothetical protein SAOUHSC_01629 [Staphylococcus aureus subsp. aureus NCTC 8325]	31861	192		144	12	X	
Q2FXZ9	88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	35160	114	105	374	12	X	
Q2FXU7	88195439	hypothetical protein SAOUHSC_01735 [Staphylococcus aureus subsp. aureus NCTC 8325]	28623	184		116	12	X	
Q2G245	88195552	hypothetical protein SAOUHSC_01854 [Staphylococcus aureus subsp. aureus NCTC 8325]	55058	146	98	131	12	X	
Q2FXE2	88195602	hypothetical protein SAOUHSC_01907 [Staphylococcus aureus subsp. aureus NCTC 8325]	31452		33	168	12	X	
Q2FW79	88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	10000	103	97	98	12	X	
Q2FVL2	88196339	hypothetical protein SAOUHSC_02699 [Staphylococcus aureus subsp. aureus NCTC 8325]	28886	353	224	617	12	X	
Q2FVG5	88196385	hypothetical protein SAOUHSC_02747 [Staphylococcus aureus subsp. aureus NCTC 8325]	23785	169	35	90	12	X	
Q2FUQ5	88196664	hypothetical protein SAOUHSC_03049 [Staphylococcus aureus subsp. aureus NCTC 8325]	32177	102		102	12		X
Q2FV52	88196515	immunodominant antigen A [Staphylococcus aureus subsp. aureus NCTC 8325]	24188	113	120		12	X	
Q2FXN4	88195501	isocitrate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	46394		48	73	12	X	
Q2FYU1	88195063	LexA repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	23287	67	33		12		X
Q2FX05	88195784	methionine aminopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	27485	541	378	301	12		
Q2FWW1	88195840	MHC class II analog protein [Staphylococcus aureus subsp. aureus NCTC 8325]	65534		90	61	12	X	
Q2FVX4	88196194	molybdenum ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	29033	159	145	247	12		
Q2FZL5	88194742	naphthoate synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	30406	40	42	117	12	X	
Q2FX22	88195767	phage repressor protein [Staphylococcus aureus subsp. aureus NCTC 8325]	27139	354	47	361	12		
Q2G031	88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	42575	74	61	242	12	X	X
Q2FVK8	88196343	phosphoglyceromutase [Staphylococcus aureus subsp. aureus NCTC 8325]	26663	115	238	444	12	X	
Q2G0J8	88194341	phosphomethylpyrimidine kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	29838		48	58	12	X	
Q2FZJ3	88194764	phosphoribosylaminoimidazole-succinocarboxamide synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	26676	205	302	446	12	X	
Q2G0J0	88194349	phosphotransacetylase [Staphylococcus aureus subsp. aureus NCTC 8325]	34930		38	59	12	X	
Q2G2S6	88195663	protein export protein PrsA [Staphylococcus aureus subsp. aureus NCTC 8325]	35616		54	79	12		

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FXE8	88195596	putative translaldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	25689	177	101	175	12	X	
Q2G0Q1	88194280	pyridoxal biosynthesis lyase PdxS [Staphylococcus aureus subsp. aureus NCTC 8325]	31972		88	221	12	X	
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224	61	123	207	12	X	
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	55	102	212	12	X	
Q2G2G9	88195699	recombination regulator RecX [Staphylococcus aureus subsp. aureus NCTC 8325]	32221	54		190	12	X	
Q2FWP6	88195908	repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	29046	183		148	12		
Q2FZ50	88194940	ribonuclease III [Staphylococcus aureus subsp. aureus NCTC 8325]	27904	303	61	140	12	X	X
Q2FY78	88195298	ribosomal large subunit pseudouridine synthase B [Staphylococcus aureus subsp. aureus NCTC 8325]	27952	144	48	199	12		X
Q2FXS6	88195460	rod shape-determining protein MreC [Staphylococcus aureus subsp. aureus NCTC 8325]	30991	67		314	12		
Q2G2C7	88194025	sorbitol dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	38432	50	55	55	12		
Q2FZ37	88194953	succinyl-CoA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	42030		82	69	12	X	X
Q2FZ27	88194963	transcriptional repressor CodY [Staphylococcus aureus subsp. aureus NCTC 8325]	28737	383	233	382	12	X	X
Q2G2D0	88194979	translation initiation factor IF-2 [Staphylococcus aureus subsp. aureus NCTC 8325]	77823	114	42	96	12	X	X
Q2FXP9	88195487	translation initiation factor IF-3 [Staphylococcus aureus subsp. aureus NCTC 8325]	20200	40		92	12	X	
Q2G030	88194557	triosephosphate isomerase [Staphylococcus aureus subsp. aureus NCTC 8325]	27275	94	81	162	12	X	
Q2FZ22	88194968	uridylate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	26128		40	131	12	X	X
Q2FZ44	88194946	16S rRNA-processing protein RimM [Staphylococcus aureus subsp. aureus NCTC 8325]	19030	238	220	236	13		
Q2FW30	88196138	30S ribosomal protein S13 [Staphylococcus aureus subsp. aureus NCTC 8325]	13711		60	86	13	X	X
Q2FW15	88196153	30S ribosomal protein S17 [Staphylococcus aureus subsp. aureus NCTC 8325]	10169	38	48	57	13	X	X
Q2FW12	88196156	30S ribosomal protein S3 [Staphylococcus aureus subsp. aureus NCTC 8325]	24085	244	290	412	13	X	X
Q2FXK6	88195529	30S ribosomal protein S4 [Staphylococcus aureus subsp. aureus NCTC 8325]	22999	75	228	441	13	X	X
Q2FZ53	88194937	3-oxoacyl-(acyl-carrier-protein) reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	25870	149	131	247	13	X	X
Q2G0P0	88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	24693	127	93	222	13	X	X
Q2FW38	88196130	50S ribosomal protein L13 [Staphylococcus aureus subsp. aureus NCTC 8325]	16323	92	111	133	13	X	
P0A0F8	88196143	50S ribosomal protein L15 [Staphylococcus aureus subsp. aureus NCTC 8325]	15587	80	57	128	13	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FW33	88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	13739	37	151	102	13	X	
Q2FW08	88196160	50S ribosomal protein L23 [Staphylococcus aureus subsp. aureus NCTC 8325]	10599		35	59	13	X	X
Q2FW17	88196151	50S ribosomal protein L24 [Staphylococcus aureus subsp. aureus NCTC 8325]	11529	82	75	72	13		X
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	159	274	236	13	X	X
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	337	402	487	13	X	X
Q2FW07	88196161	50S ribosomal protein L4 [Staphylococcus aureus subsp. aureus NCTC 8325]	22451	532	1041	1753	13	X	X
Q2FW18	88196150	50S ribosomal protein L5 [Staphylococcus aureus subsp. aureus NCTC 8325]	20254	837	696	961	13	X	X
Q2FW21	88196147	50S ribosomal protein L6 [Staphylococcus aureus subsp. aureus NCTC 8325]	19774	951	468	1282	13	X	X
Q2G2T3	88193838	50S ribosomal protein L9 [Staphylococcus aureus subsp. aureus NCTC 8325]	16629	72	93	95	13	X	X
Q2G0V0	88194218	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	30437		55	90	13		
Q2G2D8	88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35049		27	84	13	X	
Q2FY42	88195334	acetyl-CoA carboxylase biotin carboxyl carrier protein [Staphylococcus aureus subsp. aureus NCTC 8325]	17111		66	99	13		
Q2FW66	88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	19180	108	194	145	13	X	
P0A0B7	88194163	alkyl hydroperoxide reductase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	20963	344	359	362	13	X	
Q2FZI9	88194768	amidophosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	54363	33		34	13	X	
Q2G036	88194551	ATP-dependent Clp protease proteolytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	21500	87	132	93	13	X	
Q2G1F2	88193983	azoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	23338		142	305	13	X	
Q2FZJ6	88194761	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30824		46	70	13	X	X
Q2FXT8	161353523	bifunctional preprotein translocase subunit SecD/SecF [Staphylococcus aureus subsp. aureus NCTC 8325]	84201		51	53	13	X	
Q2FZ77	88194904	bifunctional pyrimidine regulatory protein PyrR/uracil phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	19843	78	56	255	13	X	X
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	95	174	404	13	X	
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012		92	280	13	X	X
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451		49	157	13	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	94	77	94	13	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190	83	94	227	13	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	64	159	358	13	X	X
Q2FWE7	88196010	F0F1 ATP synthase subunit delta [Staphylococcus aureus subsp. aureus NCTC 8325]	20486	71	74	227	13	X	
Q2G0Q0	88194281	glutamine amidotransferase subunit PdxT [Staphylococcus aureus subsp. aureus NCTC 8325]	20617		41	123	13	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258		85	258	13	X	
Q2FZZ8	88194594	glycine cleavage system protein H [Staphylococcus aureus subsp. aureus NCTC 8325]	14084		67	99	13	X	
Q2G179	88194073	hypothetical protein SAOUHSC_00268 [Staphylococcus aureus subsp. aureus NCTC 8325]	68275		62	78	13	X	
Q2G105	88194155	hypothetical protein SAOUHSC_00356 [Staphylococcus aureus subsp. aureus NCTC 8325]	21293	84	136	247	13	X	
Q2G0Z9	88194160	hypothetical protein SAOUHSC_00362 [Staphylococcus aureus subsp. aureus NCTC 8325]	23649		30	47	13		
Q2G0Z2	88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	35591		45	55	13	X	
Q2G0Q8	88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	32955		75	113	13	X	
Q2G0K7	88194332	hypothetical protein SAOUHSC_00553 [Staphylococcus aureus subsp. aureus NCTC 8325]	22422	76	84	117	13	X	
Q2G055	88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	22199	179	173	148	13	X	
Q2G038	88194549	hypothetical protein SAOUHSC_00788 [Staphylococcus aureus subsp. aureus NCTC 8325]	36238	41		14	13	X	
Q2G2G7	88194805	hypothetical protein SAOUHSC_01054 [Staphylococcus aureus subsp. aureus NCTC 8325]	24004	64	46	82	13	X	
Q2FZE0	88194838	hypothetical protein SAOUHSC_01091 [Staphylococcus aureus subsp. aureus NCTC 8325]	26897	125	68		13	X	X
Q2FZ87	88194894	hypothetical protein SAOUHSC_01153 [Staphylococcus aureus subsp. aureus NCTC 8325]	25331	169	117	126	13		
Q2G2D3	88194975	hypothetical protein SAOUHSC_01242 [Staphylococcus aureus subsp. aureus NCTC 8325]	17616	34	84	86	13		
Q2FYS0	88195092	hypothetical protein SAOUHSC_01365 [Staphylococcus aureus subsp. aureus NCTC 8325]	37832	47	55	41	13	X	
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310	24		42	13	X	
Q2FXR7	88195469	hypothetical protein SAOUHSC_01768 [Staphylococcus aureus subsp. aureus NCTC 8325]	21403	202	247	174	13	X	
Q2G245	88195552	hypothetical protein SAOUHSC_01854 [Staphylococcus aureus subsp. aureus NCTC 8325]	55058	45	111	84	13	X	
Q2FX90	88195678	hypothetical protein SAOUHSC_01987 [Staphylococcus aureus subsp. aureus NCTC 8325]	22330	193	180	205	13	X	
Q2FWX1	88195830	hypothetical protein SAOUHSC_02150 [Staphylococcus aureus subsp. aureus NCTC 8325]	21902	59	82	141	13	X	
Q2FWN0	88195929	hypothetical protein SAOUHSC_02258 [Staphylococcus aureus subsp. aureus NCTC 8325]	23989	60		58	13	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FW79	88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	10000	91	87	123	13	X	
Q2FVG5	88196385	hypothetical protein SAOUHSC_02747 [Staphylococcus aureus subsp. aureus NCTC 8325]	23785	209	142	263	13	X	
Q2FVG4	88196386	hypothetical protein SAOUHSC_02750 [Staphylococcus aureus subsp. aureus NCTC 8325]	60601	25	22	24	13	X	
Q2FVD5	88196414	hypothetical protein SAOUHSC_02778 [Staphylococcus aureus subsp. aureus NCTC 8325]	24589		33	125	13	X	X
Q2FUX3	88196593	immunodominant antigen B [Staphylococcus aureus subsp. aureus NCTC 8325]	19358	58	62	89	13	X	
Q2FX05	88195784	methionine aminopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	27485	101	51		13		
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022	28		62	13	X	
Q2FZG6	88194790	peptide deformylase [Staphylococcus aureus subsp. aureus NCTC 8325]	20547	221	246	314	13		
Q2G031	88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	42575	120	98	401	13	X	X
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088		51	86	13	X	
Q2FZJ1	88194766	phosphoribosylformylglycinamidine synthase I [Staphylococcus aureus subsp. aureus NCTC 8325]	24511		137	226	13	X	
Q2FZI7	88194770	phosphoribosylglycinamide formyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	21138	72	47	71	13		
Q2FXE8	88195596	putative translaldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	25689	157	276	340	13	X	
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224		68	174	13	X	
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063		71	49	13	X	
P0A0J3	88195361	superoxide dismutase [Staphylococcus aureus subsp. aureus NCTC 8325]	22697	56	107	160	13	X	
Q2G0P2	88194298	transcription antitermination protein [Staphylococcus aureus subsp. aureus NCTC 8325]	20651		49	56	13	X	
Q2G2D0	88194979	translation initiation factor IF-2 [Staphylococcus aureus subsp. aureus NCTC 8325]	77823		116	154	13	X	X
Q2FXP9	88195487	translation initiation factor IF-3 [Staphylococcus aureus subsp. aureus NCTC 8325]	20200	120	135	213	13	X	
Q2FWE6	88196016	uracil phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	23035	185	221	271	13	X	
Q2G0J7	88194342	uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus NCTC 8325]	24922	81	77	86	13	X	
Q2G0Y9	88194170	xanthine phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	20871		92	107	13	X	
Q2FWF5	88196002	(3R)-hydroxymyristoyl-ACP dehydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	16071	137	186	90	14	X	
Q2FW31	88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	13873	181	156	260	14	X	X
P0A0H0	88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	15277	199	249	262	14	X	X
Q2FW30	88196138	30S ribosomal protein S13 [Staphylococcus aureus subsp. aureus NCTC 8325]	13711	87	93	55	14	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FZ45	88194945	30S ribosomal protein S16 [Staphylococcus aureus subsp. aureus NCTC 8325]	10229	64		103	14	X	
Q2FW15	88196153	30S ribosomal protein S17 [Staphylococcus aureus subsp. aureus NCTC 8325]	10169	61	77	102	14	X	X
Q2FW10	88196158	30S ribosomal protein S19 [Staphylococcus aureus subsp. aureus NCTC 8325]	10609	37	84	96	14	X	X
Q2FXZ7	88195384	30S ribosomal protein S21 [Staphylococcus aureus subsp. aureus NCTC 8325]	6968		62	64	14	X	
Q2FW12	88196156	30S ribosomal protein S3 [Staphylococcus aureus subsp. aureus NCTC 8325]	24085	154	73	287	14	X	X
Q2FW23	88196145	30S ribosomal protein S5 [Staphylococcus aureus subsp. aureus NCTC 8325]	17732	541	354	738	14	X	X
P48940	88194308	30S ribosomal protein S7 [Staphylococcus aureus subsp. aureus NCTC 8325]	17783	301	125	414	14	X	X
Q2G170	88194087	5~-nucleotidase [Staphylococcus aureus subsp. aureus NCTC 8325]	33331		35	85	14	X	
Q2G0P0	88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	24693	36		130	14	X	X
Q2G0N9	88194301	50S ribosomal protein L10 [Staphylococcus aureus subsp. aureus NCTC 8325]	17699	363	200	294	14	X	X
P0A0F4	88194299	50S ribosomal protein L11 [Staphylococcus aureus subsp. aureus NCTC 8325]	14865		107	160	14	X	X
Q2FW38	88196130	50S ribosomal protein L13 [Staphylococcus aureus subsp. aureus NCTC 8325]	16323	853	654	1027	14	X	
P0A0F8	88196143	50S ribosomal protein L15 [Staphylococcus aureus subsp. aureus NCTC 8325]	15587	797	629	964	14	X	X
Q2FW13	88196155	50S ribosomal protein L16 [Staphylococcus aureus subsp. aureus NCTC 8325]	16232	205	162	168	14	X	X
Q2FW33	88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	13739	176	190	260	14	X	
Q2FW22	88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	13089	209	148	158	14	X	X
P60430	88196159	50S ribosomal protein L2 [Staphylococcus aureus subsp. aureus NCTC 8325]	30136	167	179	354	14	X	X
Q2FXS8	88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	11326	203	135	267	14	X	X
Q2FW11	88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	12827	280	209	288	14	X	X
Q2FW08	88196160	50S ribosomal protein L23 [Staphylococcus aureus subsp. aureus NCTC 8325]	10599	64	44	96	14	X	X
Q2FW17	88196151	50S ribosomal protein L24 [Staphylococcus aureus subsp. aureus NCTC 8325]	11529	148	172	173	14		X
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	219	334	280	14	X	X
Q2FXT0	88195456	50S ribosomal protein L27 [Staphylococcus aureus subsp. aureus NCTC 8325]	10308	37	31	53	14	X	
Q2FW14	88196154	50S ribosomal protein L29 [Staphylococcus aureus subsp. aureus NCTC 8325]	8085	100		151	14	X	
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	516	634	820	14	X	X
Q2FW07	88196161	50S ribosomal protein L4 [Staphylococcus aureus subsp. aureus NCTC 8325]	22451	93	155	245	14	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FW18	88196150	50S ribosomal protein L5 [Staphylococcus aureus subsp. aureus NCTC 8325]	20254	242	129	388	14	X	X
Q2FW21	88196147	50S ribosomal protein L6 [Staphylococcus aureus subsp. aureus NCTC 8325]	19774	247	191	287	14	X	X
Q2G2T3	88193838	50S ribosomal protein L9 [Staphylococcus aureus subsp. aureus NCTC 8325]	16629	502	538	693	14	X	X
Q2FXG2	88195582	6,7-dimethyl-8-ribityllumazine synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	16386	76		113	14	X	
Q2G2D8	88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35049	71	60	183	14	X	
Q2FW66	88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	19180	123	183	141	14	X	
P0A0B7	88194163	alkyl hydroperoxide reductase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	20963	165	159	196	14	X	
Q2FZ29	88194961	ATP-dependent protease peptidase subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	19560	119		89	14	X	
Q2FXT8	161353523	bifunctional preprotein translocase subunit SecD/SecF [Staphylococcus aureus subsp. aureus NCTC 8325]	84201		49	79	14	X	
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326		85	53	14	X	
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012	92	371	252	14	X	X
Q2FYM2	88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46644		132	146	14	X	
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	122	111	151	14	X	X
Q2FXU2	88195444	D-tyrosyl-tRNA(Tyr) deacylase [Staphylococcus aureus subsp. aureus NCTC 8325]	16686	173	124		14		
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190	86	160	132	14	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	126	164	291	14	X	X
Q2G2F8	88196011	F0F1 ATP synthase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	19527		56	133	14	X	
Q2FWE7	88196010	F0F1 ATP synthase subunit delta [Staphylococcus aureus subsp. aureus NCTC 8325]	20486		158	353	14	X	
Q2FWZ8	88195790	ferritin [Staphylococcus aureus subsp. aureus NCTC 8325]	19576	206	205	333	14	X	
Q2FYZ0	88195014	glutathione peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	18106	206	122	210	14	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	77	132	312	14	X	
Q2G105	88194155	hypothetical protein SAOUHSC_00356 [Staphylococcus aureus subsp. aureus NCTC 8325]	21293		37	38	14	X	
Q2G0Z2	88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	35591		78	48	14	X	
Q2G0T1	88194250	hypothetical protein SAOUHSC_00463 [Staphylococcus aureus subsp. aureus NCTC 8325]	20080	141	57	212	14		X
Q2G0R3	88194268	hypothetical protein SAOUHSC_00483 [Staphylococcus aureus subsp. aureus NCTC 8325]	14803	406	529	388	14		X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G0I3	88194356	hypothetical protein SAOUHSC_00582 [Staphylococcus aureus subsp. aureus NCTC 8325]	15788	105	69	100	14	X	
Q2G0G2	88194377	hypothetical protein SAOUHSC_00607 [Staphylococcus aureus subsp. aureus NCTC 8325]	19567	106	129	172	14		
Q2G0B5	88194455	hypothetical protein SAOUHSC_00690 [Staphylococcus aureus subsp. aureus NCTC 8325]	26671		61	135	14	X	
Q2G0B1	88194459	hypothetical protein SAOUHSC_00694 [Staphylococcus aureus subsp. aureus NCTC 8325]	17079	326	249	266	14	X	X
Q2G2G0	88194482	hypothetical protein SAOUHSC_00717 [Staphylococcus aureus subsp. aureus NCTC 8325]	16035	69	90	100	14	X	
Q2G055	88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	22199	134	127	231	14	X	
Q2FZZ9	88194593	hypothetical protein SAOUHSC_00835 [Staphylococcus aureus subsp. aureus NCTC 8325]	13591	74	88	64	14	X	
Q2FZP9	88194708	hypothetical protein SAOUHSC_00951 [Staphylococcus aureus subsp. aureus NCTC 8325]	19314		58	86	14	X	
Q2FZH7	88194780	hypothetical protein SAOUHSC_01027 [Staphylococcus aureus subsp. aureus NCTC 8325]	20077	115	36	127	14	X	
Q2FZG5	88194791	hypothetical protein SAOUHSC_01039 [Staphylococcus aureus subsp. aureus NCTC 8325]	23861		83	115	14	X	
Q2FYS0	88195092	hypothetical protein SAOUHSC_01365 [Staphylococcus aureus subsp. aureus NCTC 8325]	37832	42		37	14	X	
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310		37	42	14	X	
Q2FXZ9	88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	35160		56	192	14	X	
Q2FXR7	88195469	hypothetical protein SAOUHSC_01768 [Staphylococcus aureus subsp. aureus NCTC 8325]	21403	72	56	73	14	X	
Q2FXM1	88195514	hypothetical protein SAOUHSC_01814 [Staphylococcus aureus subsp. aureus NCTC 8325]	15216		34	149	14	X	
Q2FXL6	88195519	hypothetical protein SAOUHSC_01819 [Staphylococcus aureus subsp. aureus NCTC 8325]	18464	274	104	248	14	X	
Q2FXK3	88195531	hypothetical protein SAOUHSC_01831 [Staphylococcus aureus subsp. aureus NCTC 8325]	16060	54	49	59	14		
Q2G245	88195552	hypothetical protein SAOUHSC_01854 [Staphylococcus aureus subsp. aureus NCTC 8325]	55058		105	93	14	X	
Q2G247	88195553	hypothetical protein SAOUHSC_01855 [Staphylococcus aureus subsp. aureus NCTC 8325]	17991	350	255	576	14	X	
Q2FXH8	88195566	hypothetical protein SAOUHSC_01869 [Staphylococcus aureus subsp. aureus NCTC 8325]	15724	368	444	687	14	X	
Q2FX98	88195670	hypothetical protein SAOUHSC_01979 [Staphylococcus aureus subsp. aureus NCTC 8325]	17787	152		78	14	X	
Q2G280	88195687	hypothetical protein SAOUHSC_01999 [Staphylococcus aureus subsp. aureus NCTC 8325]	17249	435	192	414	14	X	
Q2FW79	88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	10000	168	107	119	14	X	
Q2FW65	88196095	hypothetical protein SAOUHSC_02442 [Staphylococcus aureus subsp. aureus NCTC 8325]	9217	74	46	63	14		
Q2FW64	88196096	hypothetical protein SAOUHSC_02443 [Staphylococcus aureus subsp. aureus NCTC 8325]	20787	112	72	137	14	X	
Q2FVW0	88196224	hypothetical protein SAOUHSC_02581 [Staphylococcus aureus subsp. aureus NCTC 8325]	17467		90	109	14		

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FVL2	88196339	hypothetical protein SAOUHSC_02699 [Staphylococcus aureus subsp. aureus NCTC 8325]	28886	80	63	198	14	X	
Q2FVF5	88196395	hypothetical protein SAOUHSC_02759 [Staphylococcus aureus subsp. aureus NCTC 8325]	17300		72	218	14		
Q2FV88	88196479	hypothetical protein SAOUHSC_02846 [Staphylococcus aureus subsp. aureus NCTC 8325]	15435	85	86	55	14		
Q2FUS9	88196640	hypothetical protein SAOUHSC_03022 [Staphylococcus aureus subsp. aureus NCTC 8325]	18643	41	103	77	14	X	
Q2FUX3	88196593	immunodominant antigen B [Staphylococcus aureus subsp. aureus NCTC 8325]	19358	342	251	361	14	X	
Q2G0Q3	88194278	lysyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	56684	125	202	177	14	X	
Q2FWA8	88196053	lytic regulatory protein [Staphylococcus aureus subsp. aureus NCTC 8325]	40640		107	119	14	X	
Q2FV75	88196492	methylated-DNA--protein-cysteine methyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	18934	71		55	14	X	
Q2FWW1	88195840	MHC class II analog protein [Staphylococcus aureus subsp. aureus NCTC 8325]	65534	45	34	53	14	X	
Q2FVX8	88196190	molybdopterin precursor biosynthesis MoaB [Staphylococcus aureus subsp. aureus NCTC 8325]	18489	77		66	14	X	
Q2FVY1	88196187	molybdopterin-guanine dinucleotide biosynthesis protein MobB [Staphylococcus aureus subsp. aureus NCTC 8325]	18557	154		91	14	X	
Q2FZJ5	88194762	phosphoribosylaminoimidazole carboxylase catalytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	14733	146	119	133	14	X	
Q2FYL0	88195154	PTS system transporter subunit IIA [Staphylococcus aureus subsp. aureus NCTC 8325]	17949	39		57	14	X	
Q2G252	88193848	rRNA large subunit methyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	18295	276		225	14		
Q2FWJ3	88195965	serine-protein kinase RsbW [Staphylococcus aureus subsp. aureus NCTC 8325]	19170	47	59		14	X	
Q2FZT7	88194660	signal peptidase IB [Staphylococcus aureus subsp. aureus NCTC 8325]	17587	79		106	14	X	
Q2FXL3	88195522	thiol peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	17994	111	115	187	14	X	
Q2FY73	88195303	transcriptional regulator Fur [Staphylococcus aureus subsp. aureus NCTC 8325]	17233	147	80	110	14		X
Q2G2D0	88194979	translation initiation factor IF-2 [Staphylococcus aureus subsp. aureus NCTC 8325]	77823	58	140	120	14	X	X
Q2FXP9	88195487	translation initiation factor IF-3 [Staphylococcus aureus subsp. aureus NCTC 8325]	20200	185	161	183	14	X	
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579	101	59	142	14	X	
Q2FWF5	88196002	(3R)-hydroxymyristoyl-ACP dehydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	16071	199	127	60	15	X	
#N/A	542123276	30S ribosomal protein S10 [Staphylococcus aureus subsp. aureus NCTC 8325]	11569	92	91	66	15	X	X^
Q2FW31	88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	13873	325	337	265	15	X	X
P0A0H0	88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	15277	55	92	66	15	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FW30	88196138	30S ribosomal protein S13 [Staphylococcus aureus subsp. aureus NCTC 8325]	13711	276	245	185	15	X	X
Q2G2Q1	88194983	30S ribosomal protein S15 [Staphylococcus aureus subsp. aureus NCTC 8325]	10602		82	73	15	X	X
Q2FZ45	88194945	30S ribosomal protein S16 [Staphylococcus aureus subsp. aureus NCTC 8325]	10229	92	144	54	15	X	
Q2FW15	88196153	30S ribosomal protein S17 [Staphylococcus aureus subsp. aureus NCTC 8325]	10169	235	101	486	15	X	X
Q2G111	88194149	30S ribosomal protein S18 [Staphylococcus aureus subsp. aureus NCTC 8325]	9304		33	33	15	X	X
Q2FW10	88196158	30S ribosomal protein S19 [Staphylococcus aureus subsp. aureus NCTC 8325]	10609	109	281	106	15	X	X
Q2FXZ7	88195384	30S ribosomal protein S21 [Staphylococcus aureus subsp. aureus NCTC 8325]	6968		60	96	15	X	
Q2FW12	88196156	30S ribosomal protein S3 [Staphylococcus aureus subsp. aureus NCTC 8325]	24085	41	113	113	15	X	X
Q2FW23	88196145	30S ribosomal protein S5 [Staphylococcus aureus subsp. aureus NCTC 8325]	17732	99	132	118	15	X	X
Q2FW20	88196148	30S ribosomal protein S8 [Staphylococcus aureus subsp. aureus NCTC 8325]	14822	275	296	285	15	X	X
Q2FW39	88196129	30S ribosomal protein S9 [Staphylococcus aureus subsp. aureus NCTC 8325]	14821	110	129	61	15	X	
Q2G0P0	88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	24693		49	85	15	X	X
P0A0F4	88194299	50S ribosomal protein L11 [Staphylococcus aureus subsp. aureus NCTC 8325]	14865	124	138	166	15	X	X
Q2FW38	88196130	50S ribosomal protein L13 [Staphylococcus aureus subsp. aureus NCTC 8325]	16323		66	55	15	X	
Q2FW16	88196152	50S ribosomal protein L14 [Staphylococcus aureus subsp. aureus NCTC 8325]	13127	147	35	40	15	X	X
P0A0F8	88196143	50S ribosomal protein L15 [Staphylococcus aureus subsp. aureus NCTC 8325]	15587	191	272	207	15	X	X
Q2FW13	88196155	50S ribosomal protein L16 [Staphylococcus aureus subsp. aureus NCTC 8325]	16232	85	74	100	15	X	X
Q2FW33	88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	13739	1476	1080	1686	15	X	
Q2FW22	88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	13089	844	512	434	15	X	X
Q2FZ42	88194948	50S ribosomal protein L19 [Staphylococcus aureus subsp. aureus NCTC 8325]	13354	151	132	127	15	X	
P60430	88196159	50S ribosomal protein L2 [Staphylococcus aureus subsp. aureus NCTC 8325]	30136	117	128	169	15	X	X
Q2FXS8	88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	11326	287	217	210	15	X	X
Q2FW11	88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	12827	196	144	174	15	X	X
Q2FW08	88196160	50S ribosomal protein L23 [Staphylococcus aureus subsp. aureus NCTC 8325]	10599	368	406	220	15	X	X
Q2FW17	88196151	50S ribosomal protein L24 [Staphylococcus aureus subsp. aureus NCTC 8325]	11529	513	516	454	15		X
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	254	344	238	15	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FXT0	88195456	50S ribosomal protein L27 [Staphylococcus aureus subsp. aureus NCTC 8325]	10308	237	480	452	15	X	
Q2FZ60	88194930	50S ribosomal protein L28 [Staphylococcus aureus subsp. aureus NCTC 8325]	6973		37	36	15	X	
Q2FW14	88196154	50S ribosomal protein L29 [Staphylococcus aureus subsp. aureus NCTC 8325]	8085	154	147	106	15	X	
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	289	546	333	15	X	X
Q2FW07	88196161	50S ribosomal protein L4 [Staphylococcus aureus subsp. aureus NCTC 8325]	22451	93	110	171	15	X	X
Q2FW21	88196147	50S ribosomal protein L6 [Staphylococcus aureus subsp. aureus NCTC 8325]	19774	67	68	212	15	X	X
P48860	88194302	50S ribosomal protein L7/L12 [Staphylococcus aureus subsp. aureus NCTC 8325]	12704	408	423	127	15	X	
Q2G2T3	88193838	50S ribosomal protein L9 [Staphylococcus aureus subsp. aureus NCTC 8325]	16629	169	315	163	15	X	X
Q2G2D8	88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35049		51	46	15	X	
Q2G2U9	88194390	accessory regulator A [Staphylococcus aureus subsp. aureus NCTC 8325]	14709	217	193	180	15	X	X
Q2FW66	88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	19180	33	74	68	15	X	
Q2FY49	88195327	arginine repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	17087	257	219	155	15	X	X
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012	294	487	340	15	X	X
Q2FYM2	88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46644		138	136	15	X	
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	68	144	90	15	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190		63	61	15	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077		143	142	15	X	X
Q2FWF1	88196006	F0F1 ATP synthase subunit epsilon [Staphylococcus aureus subsp. aureus NCTC 8325]	14835	199	158	85	15		
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	79	91		15	X	
Q2FYY7	88195017	glutamine synthetase repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	14268	34	21	20	15		X
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258		163	83	15	X	
Q2G141	88194115	hypothetical protein SAOUHSC_00314 [Staphylococcus aureus subsp. aureus NCTC 8325]	16162	99	29		15	X	X
Q2G0Z2	88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	35591		84	47	15	X	
Q2G0T4	88194234	hypothetical protein SAOUHSC_00444 [Staphylococcus aureus subsp. aureus NCTC 8325]	11590	263	420	232	15	X	X
Q2G0R3	88194268	hypothetical protein SAOUHSC_00483 [Staphylococcus aureus subsp. aureus NCTC 8325]	14803	122	138	121	15		X
Q2G0I3	88194356	hypothetical protein SAOUHSC_00582 [Staphylococcus aureus subsp. aureus NCTC 8325]	15788	117	119	89	15	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G0F2	88194387	hypothetical protein SAOUHSC_00617 [Staphylococcus aureus subsp. aureus NCTC 8325]	18582	252	85	170	15	X	
Q2G0D0	88194440	hypothetical protein SAOUHSC_00675 [Staphylococcus aureus subsp. aureus NCTC 8325]	26304		71	146	15	X	X
Q2G0B5	88194455	hypothetical protein SAOUHSC_00690 [Staphylococcus aureus subsp. aureus NCTC 8325]	26671	82	99	106	15	X	
Q2G0B1	88194459	hypothetical protein SAOUHSC_00694 [Staphylococcus aureus subsp. aureus NCTC 8325]	17079	54	189	119	15	X	X
Q2G065	88194520	hypothetical protein SAOUHSC_00756 [Staphylococcus aureus subsp. aureus NCTC 8325]	41771	39	39	44	15	X	
Q2G055	88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	22199	222	221	202	15	X	
Q2G1T3	88194589	hypothetical protein SAOUHSC_00831 [Staphylococcus aureus subsp. aureus NCTC 8325]	15330		56	40	15	X	
Q2FZZ9	88194593	hypothetical protein SAOUHSC_00835 [Staphylococcus aureus subsp. aureus NCTC 8325]	13591	270	358	158	15	X	
Q2FZV0	88194647	hypothetical protein SAOUHSC_00890 [Staphylococcus aureus subsp. aureus NCTC 8325]	14896	228	161	192	15		
Q2FZU8	88194649	hypothetical protein SAOUHSC_00892 [Staphylococcus aureus subsp. aureus NCTC 8325]	13419	47	44	71	15		X
Q2FZG5	88194791	hypothetical protein SAOUHSC_01039 [Staphylococcus aureus subsp. aureus NCTC 8325]	23861		99	100	15	X	
Q2G2D1	88194977	hypothetical protein SAOUHSC_01244 [Staphylococcus aureus subsp. aureus NCTC 8325]	11033	84	93	45	15	X	
Q2FYT7	88195067	hypothetical protein SAOUHSC_01338 [Staphylococcus aureus subsp. aureus NCTC 8325]	11016		36	48	15	X	
Q2FYS0	88195092	hypothetical protein SAOUHSC_01365 [Staphylococcus aureus subsp. aureus NCTC 8325]	37832		41	36	15	X	
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310		36	45	15	X	
Q2FXZ9	88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	35160		114	68	15	X	
Q2FXM1	88195514	hypothetical protein SAOUHSC_01814 [Staphylococcus aureus subsp. aureus NCTC 8325]	15216	280	318	281	15	X	
Q2FXK3	88195531	hypothetical protein SAOUHSC_01831 [Staphylococcus aureus subsp. aureus NCTC 8325]	16060	83	56	29	15		
Q2G245	88195552	hypothetical protein SAOUHSC_01854 [Staphylococcus aureus subsp. aureus NCTC 8325]	55058	55	50		15	X	
Q2G247	88195553	hypothetical protein SAOUHSC_01855 [Staphylococcus aureus subsp. aureus NCTC 8325]	17991	30	187	105	15	X	
Q2G2T0	88195661	hypothetical protein SAOUHSC_01969 [Staphylococcus aureus subsp. aureus NCTC 8325]	13204	112	119		15	X	
Q2FWW6	88195835	hypothetical protein SAOUHSC_02155 [Staphylococcus aureus subsp. aureus NCTC 8325]	14524	34		35	15		X
Q2FWI8	88195969	hypothetical protein SAOUHSC_02303 [Staphylococcus aureus subsp. aureus NCTC 8325]	13433	69	83	94	15		X
Q2FW79	88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	10000	214	254	222	15	X	
Q2FW65	88196095	hypothetical protein SAOUHSC_02442 [Staphylococcus aureus subsp. aureus NCTC 8325]	9217		72	43	15		
Q2FW64	88196096	hypothetical protein SAOUHSC_02443 [Staphylococcus aureus subsp. aureus NCTC 8325]	20787	126	111	155	15	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FVY9	88196179	hypothetical protein SAOUHSC_02532 [Staphylococcus aureus subsp. aureus NCTC 8325]	13978	67		68	15	X	X
Q9F0R1	88196210	hypothetical protein SAOUHSC_02566 [Staphylococcus aureus subsp. aureus NCTC 8325]	13660	143	226	181	15	X	X
Q2FVW0	88196224	hypothetical protein SAOUHSC_02581 [Staphylococcus aureus subsp. aureus NCTC 8325]	17467	251	123	84	15		
Q2FVN6	88196306	hypothetical protein SAOUHSC_02666 [Staphylococcus aureus subsp. aureus NCTC 8325]	13331	43	57	48	15	X	
Q2FVL2	88196339	hypothetical protein SAOUHSC_02699 [Staphylococcus aureus subsp. aureus NCTC 8325]	28886	88	146	119	15	X	
Q2FVF5	88196395	hypothetical protein SAOUHSC_02759 [Staphylococcus aureus subsp. aureus NCTC 8325]	17300		70	103	15		
Q2FVA7	88196460	hypothetical protein SAOUHSC_02826 [Staphylococcus aureus subsp. aureus NCTC 8325]	16506	160	59	89	15		X
Q2FV88	88196479	hypothetical protein SAOUHSC_02846 [Staphylococcus aureus subsp. aureus NCTC 8325]	15435	66	45		15		
Q2FUX3	88196593	immunodominant antigen B [Staphylococcus aureus subsp. aureus NCTC 8325]	19358	82	87	43	15	X	
Q2G0Q3	88194278	lysyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	56684		63	56	15	X	
Q2FX05	88195784	methionine aminopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	27485	31	56	66	15		
P0A088	88195155	methionine sulfoxide reductase B [Staphylococcus aureus subsp. aureus NCTC 8325]	16267		84	51	15	X	
Q2FWW1	88195840	MHC class II analog protein [Staphylococcus aureus subsp. aureus NCTC 8325]	65534	73	56	63	15	X	
Q2FVY0	88196188	molybdopterin biosynthesis protein MoeA [Staphylococcus aureus subsp. aureus NCTC 8325]	44988		47	45	15	X	
Q2FWL3	88195946	MutS domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	61283		46	47	15	X	
Q2FZJ5	88194762	phosphoribosylaminoimidazole carboxylase catalytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	14733	135	183	40	15	X	
Q2FXT7	88195449	preprotein translocase subunit YajC [Staphylococcus aureus subsp. aureus NCTC 8325]	9665		51	88	15	X	
Q2G1G5	88193970	PTS system transporter [Staphylococcus aureus subsp. aureus NCTC 8325]	50632	84	189	139	15	X	
Q2G2Q4	88194980	ribosome-binding factor A [Staphylococcus aureus subsp. aureus NCTC 8325]	13506	62	66	55	15		
Q2G2C7	88194025	sorbitol dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	38432	54	50		15		
Q2G1U6	88194691	transcriptional regulator Spx [Staphylococcus aureus subsp. aureus NCTC 8325]	15431	111	90	55	15		
Q2G2D0	88194979	translation initiation factor IF-2 [Staphylococcus aureus subsp. aureus NCTC 8325]	77823	68	65	62	15	X	X
Q2FXP9	88195487	translation initiation factor IF-3 [Staphylococcus aureus subsp. aureus NCTC 8325]	20200	92	120	129	15	X	
Q9RFJ6	88195576	virulence factor regulator protein [Staphylococcus aureus subsp. aureus NCTC 8325]	15590		50	90	15		X
#N/A	542123276	30S ribosomal protein S10 [Staphylococcus aureus subsp. aureus NCTC 8325]	11569	288	192	172	16	X	X^
Q2FW31	88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	13873	169	284	274	16	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
P0A0H0	88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	15277	180	151	158	16	X	X
Q2FW30	88196138	30S ribosomal protein S13 [Staphylococcus aureus subsp. aureus NCTC 8325]	13711	115	112	97	16	X	X
Q2FW19	161353519	30S ribosomal protein S14 [Staphylococcus aureus subsp. aureus NCTC 8325]	7295		21	24	16	X	X
Q2G2Q1	88194983	30S ribosomal protein S15 [Staphylococcus aureus subsp. aureus NCTC 8325]	10602	235	93	144	16	X	X
Q2FZ45	88194945	30S ribosomal protein S16 [Staphylococcus aureus subsp. aureus NCTC 8325]	10229	535	461	368	16	X	
Q2FW15	88196153	30S ribosomal protein S17 [Staphylococcus aureus subsp. aureus NCTC 8325]	10169	143	123	193	16	X	X
Q2G111	88194149	30S ribosomal protein S18 [Staphylococcus aureus subsp. aureus NCTC 8325]	9304	63	89	80	16	X	X
Q2FW10	88196158	30S ribosomal protein S19 [Staphylococcus aureus subsp. aureus NCTC 8325]	10609	606	618	475	16	X	X
Q2FXY6	88195395	30S ribosomal protein S20 [Staphylococcus aureus subsp. aureus NCTC 8325]	9016	231	377	197	16	X	X
Q2FXZ7	88195384	30S ribosomal protein S21 [Staphylococcus aureus subsp. aureus NCTC 8325]	6968	97	112	145	16	X	
Q2FW12	88196156	30S ribosomal protein S3 [Staphylococcus aureus subsp. aureus NCTC 8325]	24085		66	87	16	X	X
Q2FXK6	88195529	30S ribosomal protein S4 [Staphylococcus aureus subsp. aureus NCTC 8325]	22999	48	117	95	16	X	X
Q2FW23	88196145	30S ribosomal protein S5 [Staphylococcus aureus subsp. aureus NCTC 8325]	17732	31	197	125	16	X	X
Q2G113	88194147	30S ribosomal protein S6 [Staphylococcus aureus subsp. aureus NCTC 8325]	11588	78	106		16	X	X
Q2FW39	88196129	30S ribosomal protein S9 [Staphylococcus aureus subsp. aureus NCTC 8325]	14821	89	116	93	16	X	
Q2G0P0	88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	24693	52	80	74	16	X	X
Q2FW38	88196130	50S ribosomal protein L13 [Staphylococcus aureus subsp. aureus NCTC 8325]	16323	66	74	80	16	X	
P0A0F8	88196143	50S ribosomal protein L15 [Staphylococcus aureus subsp. aureus NCTC 8325]	15587	212	313	275	16	X	X
Q2FW33	88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	13739	154	116	92	16	X	
Q2FW22	88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	13089	137	330	259	16	X	X
Q2FZ42	88194948	50S ribosomal protein L19 [Staphylococcus aureus subsp. aureus NCTC 8325]	13354	63	76	93	16	X	
P60430	88196159	50S ribosomal protein L2 [Staphylococcus aureus subsp. aureus NCTC 8325]	30136	120	199	138	16	X	X
Q2FXS8	88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	11326	177	152	78	16	X	X
Q2FW11	88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	12827		83	81	16	X	X
Q2FW08	88196160	50S ribosomal protein L23 [Staphylococcus aureus subsp. aureus NCTC 8325]	10599	401	345	331	16	X	X
Q2FW17	88196151	50S ribosomal protein L24 [Staphylococcus aureus subsp. aureus NCTC 8325]	11529	123	208	82	16		X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	259	227	176	16	X	X
Q2FXT0	88195456	50S ribosomal protein L27 [Staphylococcus aureus subsp. aureus NCTC 8325]	10308	261	207	318	16	X	
Q2FZ60	88194930	50S ribosomal protein L28 [Staphylococcus aureus subsp. aureus NCTC 8325]	6973	36	50	34	16	X	
Q2FW14	88196154	50S ribosomal protein L29 [Staphylococcus aureus subsp. aureus NCTC 8325]	8085	678	608	715	16	X	
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	333	589	310	16	X	X
P0A0G2	88196144	50S ribosomal protein L30 [Staphylococcus aureus subsp. aureus NCTC 8325]	6550	127	177	165	16	X	
Q2FWD8	88196024	50S ribosomal protein L31 type B [Staphylococcus aureus subsp. aureus NCTC 8325]	9717	95	136	85	16	X	
Q2FW29	88196139	50S ribosomal protein L36 [Staphylococcus aureus subsp. aureus NCTC 8325]	4302	28	49	44	16		
Q2FW07	88196161	50S ribosomal protein L4 [Staphylococcus aureus subsp. aureus NCTC 8325]	22451	101	88	167	16	X	X
Q2FW18	88196150	50S ribosomal protein L5 [Staphylococcus aureus subsp. aureus NCTC 8325]	20254		44	127	16	X	X
Q2FW21	88196147	50S ribosomal protein L6 [Staphylococcus aureus subsp. aureus NCTC 8325]	19774	185	231	175	16	X	X
Q2G2T3	88193838	50S ribosomal protein L9 [Staphylococcus aureus subsp. aureus NCTC 8325]	16629	133	180	81	16	X	X
Q2G2D8	88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35049	79	59		16	X	
Q2G2U9	88194390	accessory regulator A [Staphylococcus aureus subsp. aureus NCTC 8325]	14709		49	44	16	X	X
Q2G2S0	88195807	adenylosuccinate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	49572	32	33		16	X	
Q2FW66	88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	19180		69	62	16	X	
Q2G0S3	88194258	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	48473		66	47	16		
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012	118	185	104	16	X	X
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	393	637	255	16	X	X
Q2FW32	88196136	DNA-directed RNA polymerase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	34990	32	192	82	16	X	X
Q2FY41	88195335	elongation factor P [Staphylococcus aureus subsp. aureus NCTC 8325]	20541	54	108	70	16		
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474		132	119	16	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	73	114	144	16	X	X
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	65	62		16	X	
Q2G241	88194290	glutamyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	56253	48	51		16	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	26	208	99	16	X	
Q2FY08	88195373	glycyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	53586	96	138	65	16	X	X
Q2FXY7	88195394	GTP-binding protein LepA [Staphylococcus aureus subsp. aureus NCTC 8325]	68132	31	38	43	16	X	X
Q2G276	88193826	hypothetical protein SAOUHSC_00003 [Staphylococcus aureus subsp. aureus NCTC 8325]	9132	203	198	96	16		X
Q2G1R1	88193862	hypothetical protein SAOUHSC_00041 [Staphylococcus aureus subsp. aureus NCTC 8325]	11132	86	167		16		
Q2G1V7	88194131	hypothetical protein SAOUHSC_00331 [Staphylococcus aureus subsp. aureus NCTC 8325]	7684	66	95	109	16		
Q2G116	88194144	hypothetical protein SAOUHSC_00345 [Staphylococcus aureus subsp. aureus NCTC 8325]	7877	203	278	85	16		
Q2G0Z2	88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	35591	122	181	173	16	X	
Q2G0T4	88194234	hypothetical protein SAOUHSC_00444 [Staphylococcus aureus subsp. aureus NCTC 8325]	11590	316	263	150	16	X	X
Q2G0R5	88194266	hypothetical protein SAOUHSC_00481 [Staphylococcus aureus subsp. aureus NCTC 8325]	9850	222	191	218	16	X	X
Q2G0R3	88194268	hypothetical protein SAOUHSC_00483 [Staphylococcus aureus subsp. aureus NCTC 8325]	14803	39	72	122	16		X
Q2G2E5	88194414	hypothetical protein SAOUHSC_00647 [Staphylococcus aureus subsp. aureus NCTC 8325]	64010		37	44	16	X	
Q2G2E4	88194415	hypothetical protein SAOUHSC_00648 [Staphylococcus aureus subsp. aureus NCTC 8325]	44986	36	37		16		
Q2G0D0	88194440	hypothetical protein SAOUHSC_00675 [Staphylococcus aureus subsp. aureus NCTC 8325]	26304	81	79	149	16	X	X
Q2G0B5	88194455	hypothetical protein SAOUHSC_00690 [Staphylococcus aureus subsp. aureus NCTC 8325]	26671	101	98	154	16	X	
Q2G2G0	88194482	hypothetical protein SAOUHSC_00717 [Staphylococcus aureus subsp. aureus NCTC 8325]	16035	37		51	16	X	
Q2G055	88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	22199	176	82	144	16	X	
Q2FZZ9	88194593	hypothetical protein SAOUHSC_00835 [Staphylococcus aureus subsp. aureus NCTC 8325]	13591	261	318	247	16	X	
Q2FZQ1	88194706	hypothetical protein SAOUHSC_00949 [Staphylococcus aureus subsp. aureus NCTC 8325]	56622		37	36	16		
Q2FZG5	88194791	hypothetical protein SAOUHSC_01039 [Staphylococcus aureus subsp. aureus NCTC 8325]	23861		87	78	16	X	
Q2G2C3	88194811	hypothetical protein SAOUHSC_01062 [Staphylococcus aureus subsp. aureus NCTC 8325]	10349	53	86	67	16		
Q2FZ59	88194931	hypothetical protein SAOUHSC_01192 [Staphylococcus aureus subsp. aureus NCTC 8325]	13377	201	213	102	16	X	
Q2G2D1	88194977	hypothetical protein SAOUHSC_01244 [Staphylococcus aureus subsp. aureus NCTC 8325]	11033	115	95	84	16	X	
Q2G2C9	88194978	hypothetical protein SAOUHSC_01245 [Staphylococcus aureus subsp. aureus NCTC 8325]	11530	152	144	109	16	X	
Q2FYY3	88195021	hypothetical protein SAOUHSC_01290 [Staphylococcus aureus subsp. aureus NCTC 8325]	7859	79	80	69	16		
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310	43	43		16	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FY44	88195332	hypothetical protein SAOUHSC_01622 [Staphylococcus aureus subsp. aureus NCTC 8325]	13265	56	51		16	X	
Q2FXW0	88195426	hypothetical protein SAOUHSC_01721 [Staphylococcus aureus subsp. aureus NCTC 8325]	10297		157	38	16	X	
Q2FXS4	88195462	hypothetical protein SAOUHSC_01761 [Staphylococcus aureus subsp. aureus NCTC 8325]	18373	35		54	16		
Q2FXM1	88195514	hypothetical protein SAOUHSC_01814 [Staphylococcus aureus subsp. aureus NCTC 8325]	15216	26	91	142	16	X	
Q2FXL6	88195519	hypothetical protein SAOUHSC_01819 [Staphylococcus aureus subsp. aureus NCTC 8325]	18464		79	79	16	X	
Q2FXJ6	88195538	hypothetical protein SAOUHSC_01838 [Staphylococcus aureus subsp. aureus NCTC 8325]	45775		96	47	16	X	
Q2G247	88195553	hypothetical protein SAOUHSC_01855 [Staphylococcus aureus subsp. aureus NCTC 8325]	17991	67	179	206	16	X	
Q2FX11	88195778	hypothetical protein SAOUHSC_02096 [Staphylococcus aureus subsp. aureus NCTC 8325]	10316	111	117	79	16	X	
Q2FX10	88195779	hypothetical protein SAOUHSC_02097 [Staphylococcus aureus subsp. aureus NCTC 8325]	45576		50	100	16	X	
Q2FWD5	88196027	hypothetical protein SAOUHSC_02364 [Staphylococcus aureus subsp. aureus NCTC 8325]	12678	61	55	82	16		
Q2FWB0	88196051	hypothetical protein SAOUHSC_02388 [Staphylococcus aureus subsp. aureus NCTC 8325]	11981	138	122	103	16		X
Q2FW79	88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	10000	338	448	294	16	X	
Q2FW64	88196096	hypothetical protein SAOUHSC_02443 [Staphylococcus aureus subsp. aureus NCTC 8325]	20787	100	90	148	16	X	
Q9F0R1	88196210	hypothetical protein SAOUHSC_02566 [Staphylococcus aureus subsp. aureus NCTC 8325]	13660	92	51	129	16	X	X
Q2FVL2	88196339	hypothetical protein SAOUHSC_02699 [Staphylococcus aureus subsp. aureus NCTC 8325]	28886		158	124	16	X	
Q2FVG5	88196385	hypothetical protein SAOUHSC_02747 [Staphylococcus aureus subsp. aureus NCTC 8325]	23785	47	38		16	X	
Q2FVD4	88196415	hypothetical protein SAOUHSC_02779 [Staphylococcus aureus subsp. aureus NCTC 8325]	11166	73	85	59	16		
Q2FX05	88195784	methionine aminopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	27485	93	76		16		
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022		47	54	16	X	
Q2FX22	88195767	phage repressor protein [Staphylococcus aureus subsp. aureus NCTC 8325]	27139		49	48	16		
Q2FXT7	88195449	preprotein translocase subunit YajC [Staphylococcus aureus subsp. aureus NCTC 8325]	9665	49		68	16	X	
Q2G1G5	88193970	PTS system transporter [Staphylococcus aureus subsp. aureus NCTC 8325]	50632	53	87	51	16	X	
Q2G0S7	88194254	pur operon repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	30376	37	68		16	X	X
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224	50		24	16	X	
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063		45	64	16	X	
Q2G2Q4	88194980	ribosome-binding factor A [Staphylococcus aureus subsp. aureus NCTC 8325]	13506	135	103	118	16		

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FZ37	88194953	succinyl-CoA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	42030		55	64	16	X	X
Q2FZD2	88194846	thioredoxin [Staphylococcus aureus subsp. aureus NCTC 8325]	11433	68	242	128	16	X	
Q2FXP9	88195487	translation initiation factor IF-3 [Staphylococcus aureus subsp. aureus NCTC 8325]	20200	112	219	162	16	X	
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579		46	43	16	X	
#N/A	542123276	30S ribosomal protein S10 [Staphylococcus aureus subsp. aureus NCTC 8325]	11569	101	104	178	17	X	X^
Q2FW31	88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	13873	100	88	343	17	X	X
P0A0H0	88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	15277	117	74	194	17	X	X
Q2FW30	88196138	30S ribosomal protein S13 [Staphylococcus aureus subsp. aureus NCTC 8325]	13711	205	45	134	17	X	X
Q2FZ45	88194945	30S ribosomal protein S16 [Staphylococcus aureus subsp. aureus NCTC 8325]	10229	102	108	101	17	X	
Q2FW15	88196153	30S ribosomal protein S17 [Staphylococcus aureus subsp. aureus NCTC 8325]	10169	95		98	17	X	X
Q2FW10	88196158	30S ribosomal protein S19 [Staphylococcus aureus subsp. aureus NCTC 8325]	10609	34		107	17	X	X
Q2FXY6	88195395	30S ribosomal protein S20 [Staphylococcus aureus subsp. aureus NCTC 8325]	9016	103	166	209	17	X	X
Q2FXZ7	88195384	30S ribosomal protein S21 [Staphylococcus aureus subsp. aureus NCTC 8325]	6968	101	142	150	17	X	
Q2G0P0	88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	24693	22	114	118	17	X	X
Q2G0N9	88194301	50S ribosomal protein L10 [Staphylococcus aureus subsp. aureus NCTC 8325]	17699		78	79	17	X	X
P0A0F8	88196143	50S ribosomal protein L15 [Staphylococcus aureus subsp. aureus NCTC 8325]	15587		42	146	17	X	X
Q2FW33	88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	13739	32	241	117	17	X	
Q2FW22	88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	13089	170	78	237	17	X	X
P60430	88196159	50S ribosomal protein L2 [Staphylococcus aureus subsp. aureus NCTC 8325]	30136	84	71	97	17	X	X
Q2FXQ1	88195485	50S ribosomal protein L20 [Staphylococcus aureus subsp. aureus NCTC 8325]	13678	62	132	114	17	X	X
Q2FXS8	88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	11326	86	72	201	17	X	X
Q2FW11	88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	12827		31	81	17	X	X
Q2FW08	88196160	50S ribosomal protein L23 [Staphylococcus aureus subsp. aureus NCTC 8325]	10599	41	116	203	17	X	X
Q2FW17	88196151	50S ribosomal protein L24 [Staphylococcus aureus subsp. aureus NCTC 8325]	11529	91	73	125	17		X
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773		52	147	17	X	X
Q2FXT0	88195456	50S ribosomal protein L27 [Staphylococcus aureus subsp. aureus NCTC 8325]	10308	35	74	85	17	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FZ60	88194930	50S ribosomal protein L28 [Staphylococcus aureus subsp. aureus NCTC 8325]	6973	31		46	17	X	
Q2FW14	88196154	50S ribosomal protein L29 [Staphylococcus aureus subsp. aureus NCTC 8325]	8085	197	136	233	17	X	
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	101	240	407	17	X	X
P0A0G2	88196144	50S ribosomal protein L30 [Staphylococcus aureus subsp. aureus NCTC 8325]	6550	363		256	17	X	
Q2FW07	88196161	50S ribosomal protein L4 [Staphylococcus aureus subsp. aureus NCTC 8325]	22451		218	239	17	X	X
Q2FW18	88196150	50S ribosomal protein L5 [Staphylococcus aureus subsp. aureus NCTC 8325]	20254	93		277	17	X	X
Q2FW21	88196147	50S ribosomal protein L6 [Staphylococcus aureus subsp. aureus NCTC 8325]	19774	46	36	104	17	X	X
P48860	88194302	50S ribosomal protein L7/L12 [Staphylococcus aureus subsp. aureus NCTC 8325]	12704		118	118	17	X	
Q2G2T3	88193838	50S ribosomal protein L9 [Staphylococcus aureus subsp. aureus NCTC 8325]	16629	47	34	83	17	X	X
P0A0B7	88194163	alkyl hydroperoxide reductase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	20963		39	93	17	X	
Q2FY49	88195327	arginine repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	17087		107	125	17	X	X
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012		39	112	17	X	X
Q2FZW4	88194628	D-alanine--poly(phosphoribitol) ligase subunit 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	9058		71	152	17		
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	170	180	307	17	X	X
Q2FW32	88196136	DNA-directed RNA polymerase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	34990	53	66	180	17	X	X
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474	55	110	231	17	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	36	33	255	17	X	X
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258		30	115	17	X	
Q2G0R3	88194268	hypothetical protein SAOUHSC_00483 [Staphylococcus aureus subsp. aureus NCTC 8325]	14803		39	78	17		X
Q2G055	88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	22199		42	133	17	X	
Q2FZZ9	88194593	hypothetical protein SAOUHSC_00835 [Staphylococcus aureus subsp. aureus NCTC 8325]	13591		58	58	17	X	
Q2G1X1	88194864	hypothetical protein SAOUHSC_01120 [Staphylococcus aureus subsp. aureus NCTC 8325]	8893		33	136	17		
Q2FZB4	88194867	hypothetical protein SAOUHSC_01123 [Staphylococcus aureus subsp. aureus NCTC 8325]	8625		63	128	17	X	
Q2FZA5	88194876	hypothetical protein SAOUHSC_01134 [Staphylococcus aureus subsp. aureus NCTC 8325]	7188	139	53	143	17		
Q2FZA4	88194877	hypothetical protein SAOUHSC_01135 [Staphylococcus aureus subsp. aureus NCTC 8325]	4493	64	196	103	17	X	
Q2FZA3	88194878	hypothetical protein SAOUHSC_01136 [Staphylococcus aureus subsp. aureus NCTC 8325]	4453	85	137	84	17	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FZ07	88194997	hypothetical protein SAOUHSC_01264 [Staphylococcus aureus subsp. aureus NCTC 8325]	8156	44	60	67	17	X	
Q2FXW0	88195426	hypothetical protein SAOUHSC_01721 [Staphylococcus aureus subsp. aureus NCTC 8325]	10297	107		178	17	X	
Q2FXM1	88195514	hypothetical protein SAOUHSC_01814 [Staphylococcus aureus subsp. aureus NCTC 8325]	15216		36	115	17	X	
Q2FXJ2	88195542	hypothetical protein SAOUHSC_01843 [Staphylococcus aureus subsp. aureus NCTC 8325]	100886	28	32		17	X	
Q2FXH8	88195566	hypothetical protein SAOUHSC_01869 [Staphylococcus aureus subsp. aureus NCTC 8325]	15724	37	28	58	17	X	
Q2FW79	88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	10000	175	136	129	17	X	
Q2FVC3	88196426	hypothetical protein SAOUHSC_02790 [Staphylococcus aureus subsp. aureus NCTC 8325]	109832		15	27	17	X	X
Q2FVX5	88196193	molybdenum ABC transporter permease [Staphylococcus aureus subsp. aureus NCTC 8325]	24847		38	39	17	X	
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022	61	53	61	17	X	
Q2FW28	88196140	translation initiation factor IF-1 [Staphylococcus aureus subsp. aureus NCTC 8325]	8274	157	106	548	17	X	
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579	60		137	17	X	

Table B.3. Proteins identified in 0-0.5M NaCl elution.

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	65		58	18	X	X
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	63	35	404	18	X	X
Q2FYS9	88195075	aconitate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	98908	75	91	122	18	X	
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326		21	91	18	X	
Q2G2Q0	88193829	DNA gyrase subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	99290	27	45		18	X	X
P47768	161353532	DNA-directed RNA polymerase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	133136	50		60	18	X	X
Q2G0N5	88194305	DNA-directed RNA polymerase subunit beta~ [Staphylococcus aureus subsp. aureus NCTC 8325]	134190		80	101	18	X	X
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564	67	125	49	18	X	X
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	119	108	263	18	X	X
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	79		86	18	X	
Q2G1H9	88193956	hypothetical protein SAOUHSC_00144 [Staphylococcus aureus subsp. aureus NCTC 8325]	273308	219	58		18	X	
Q2FXJ2	88195542	hypothetical protein SAOUHSC_01843 [Staphylococcus aureus subsp. aureus NCTC 8325]	100886	32	31	38	18	X	
Q2FUW1	88196609	hypothetical protein SAOUHSC_02990 [Staphylococcus aureus subsp. aureus NCTC 8325]	227909	437	332	487	18	X	
Q2FV16	88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	55964		117	110	18	X	
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022	68	61	47	18	X	
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579		216	41	18	X	
Q2FV67	88196500	1-pyrroline-5-carboxylate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	56832	38	159	115	19	X	
Q2FYM1	88195143	2-oxoglutarate dehydrogenase E1 component [Staphylococcus aureus subsp. aureus NCTC 8325]	105277	1480	978	511	19	X	
Q2FY60	88195316	6-phosphogluconate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	51770	81	103	132	19	X	X
Q2FYS9	88195075	aconitate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	98908	971	1036	688	19	X	
Q2G2S0	88195807	adenylosuccinate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	49572	61	63		19	X	
Q2FXV9	88195427	alanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	98459	230	194	69	19	X	X
Q2FZS8	88194669	ATP-dependent Clp protease ATP-binding subunit ClpB [Staphylococcus aureus subsp. aureus NCTC 8325]	98271	247	119	52	19		
Q2FZI6	88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	54314	325	305	225	19	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
		[Staphylococcus aureus subsp. aureus NCTC 8325]							
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	295	412	309	19	X	
Q2FZ72	88194909	carbamoyl phosphate synthase large subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	117112	614	515	227	19	X	X
Q2FYU7	88195057	catalase [Staphylococcus aureus subsp. aureus NCTC 8325]	54908	165	160	172	19	X	
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012		127	90	19	X	X
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451	276	275	237	19	X	
Q2FYM2	88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46644	161	160	106	19	X	
Q2G2Q0	88193829	DNA gyrase subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	99290	713	406	313	19	X	X
Q2FXN9	88195497	DNA polymerase I [Staphylococcus aureus subsp. aureus NCTC 8325]	99133	83	131		19	X	X
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	40		68	19	X	X
P47768	161353532	DNA-directed RNA polymerase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	133136	917	725	557	19	X	X
Q2G0N5	88194305	DNA-directed RNA polymerase subunit beta~ [Staphylococcus aureus subsp. aureus NCTC 8325]	134190	1112	955	652	19	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190		49	62	19	X	
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564	565	870	672	19	X	X
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474	67	52	79	19	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	551	594	590	19	X	X
Q2G0P5	88194286	endopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	90981	403	432	370	19	X	X
Q2FVV9	88196225	formate dehydrogenase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	111173	165	169		19		
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819	304	296	287	19	X	X
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	24	120	75	19	X	
Q2FWA0	88196060	glucosamine--fructose-6-phosphate aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	65809	69	78		19	X	
Q2FY66	88195310	glucose-6-phosphate 1-dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	56929	48		88	19	X	X
Q2FYY6	88195018	glutamine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	50808	62	59	71	19	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	131	242	257	19	X	
Q2FY08	88195373	glycyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	53586		69	97	19	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G0Q8	88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	32955	47	88	98	19	X	
Q2FZV7	88194635	hypothetical protein SAOUHSC_00878 [Staphylococcus aureus subsp. aureus NCTC 8325]	44077		108	149	19	X	
Q2FXI9	88195555	hypothetical protein SAOUHSC_01857 [Staphylococcus aureus subsp. aureus NCTC 8325]	144568	30	25		19	X	X
Q2G2B2	88196433	hypothetical protein SAOUHSC_02798 [Staphylococcus aureus subsp. aureus NCTC 8325]	178419	170	152	155	19	X	
Q2FUW1	88196609	hypothetical protein SAOUHSC_02990 [Staphylococcus aureus subsp. aureus NCTC 8325]	227909	347	354	391	19	X	
Q2G0Y7	88194172	inosine-5~-monophosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	52818		223	184	19	X	X
Q2FXN4	88195501	isocitrate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	46394	29	67	32	19	X	
Q2FZ82	88194899	isoleucyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	104820	1095	877	513	19	X	
Q2FXH2	88195572	leucyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	91728	223	251	227	19	X	
Q2FV16	88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	55964	238	305	243	19	X	
Q2FXZ2	88195389	molecular chaperone DnaK [Staphylococcus aureus subsp. aureus NCTC 8325]	66321		71	46	19	X	
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022	47		59	19	X	
Q2G1W2	88195605	phosphoenolpyruvate carboxykinase [Staphylococcus aureus subsp. aureus NCTC 8325]	59340	40	70	35	19	X	X
Q2G031	88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	42575	30	44	41	19	X	X
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088	216	267	463	19	X	
Q2FZJ0	88194767	phosphoribosylformylglycinamidine synthase II [Staphylococcus aureus subsp. aureus NCTC 8325]	79486	317	397	238	19	X	X
O06446	88194531	preprotein translocase subunit SecA [Staphylococcus aureus subsp. aureus NCTC 8325]	95900	195	168	195	19	X	X
Q2FXE8	88195596	putative translaldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	25689	44	77	64	19	X	
Q2G0Q1	88194280	pyridoxal biosynthesis lyase PdxS [Staphylococcus aureus subsp. aureus NCTC 8325]	31972		77	86	19	X	
Q2G2C1	88194813	pyruvate carboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	128467	1203	669	459	19	X	X
Q2FZG4	88194792	pyruvate dehydrogenase complex, E1 component subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	41357	81	146	153	19	X	
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224	65	190	102	19	X	
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	561	675	549	19	X	
Q2FZ37	88194953	succinyl-CoA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	42030		93	54	19	X	X
Q2FXP7	88195489	threonyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74441	76	88	65	19	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FYT8	88195066	transketolase [Staphylococcus aureus subsp. aureus NCTC 8325]	68317	76	145	81	19	X	
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579	238	230	396	19	X	
Q2FXR8	88195468	valyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	101660	131	197	240	19	X	
Q2FYM1	88195143	2-oxoglutarate dehydrogenase E1 component [Staphylococcus aureus subsp. aureus NCTC 8325]	105277	576	336	101	20	X	
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	81	71		20	X	X
Q2FY60	88195316	6-phosphogluconate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	51770	79	135		20	X	X
Q2FYS9	88195075	aconitate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	98908	585	747	378	20	X	
Q2FXV9	88195427	alanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	98459	257	203		20	X	X
Q2FW66	88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	19180		52	24	20	X	
Q2FZS8	88194669	ATP-dependent Clp protease ATP-binding subunit ClpB [Staphylococcus aureus subsp. aureus NCTC 8325]	98271	784	520	267	20		
Q2FV74	88196493	ATP-dependent Clp protease ATP-binding subunit ClpC [Staphylococcus aureus subsp. aureus NCTC 8325]	77789	137	498	99	20	X	X
Q2FZI6	88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	54314	143	390	46	20	X	
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	261	323	208	20	X	
Q2FZ72	88194909	carbamoyl phosphate synthase large subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	117112	120	135		20	X	X
Q2FYU7	88195057	catalase [Staphylococcus aureus subsp. aureus NCTC 8325]	54908		159	72	20	X	
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451	275	327	237	20	X	
Q2FYM2	88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46644	94	167	145	20	X	
Q2G2Q0	88193829	DNA gyrase subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	99290	229	224	54	20	X	X
Q2FXN9	88195497	DNA polymerase I [Staphylococcus aureus subsp. aureus NCTC 8325]	99133	182	126		20	X	X
P47768	161353532	DNA-directed RNA polymerase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	133136	265	277		20	X	X
Q2G0N5	88194305	DNA-directed RNA polymerase subunit beta~ [Staphylococcus aureus subsp. aureus NCTC 8325]	134190	212	292	102	20	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190	90	116	85	20	X	
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564	1749	1751	1112	20	X	X
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474	173	228		20	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	567	626	526	20	X	X
Q2G0P5	88194286	endopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	90981	1925	1745	1489	20	X	X
Q2FVV9	88196225	formate dehydrogenase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	111173	100	158		20		
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819	91	418	257	20	X	X
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	82	121		20	X	
Q2FWA0	88196060	glucosamine--fructose-6-phosphate aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	65809	76	74	46	20	X	
Q2FYY6	88195018	glutamine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	50808		67	19	20	X	
Q2FXP2	88195494	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	36956	16	96	52	20	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	136	323	206	20	X	
Q2G1Y6	88194808	GTP-binding protein TypA [Staphylococcus aureus subsp. aureus NCTC 8325]	69152	593	490	333	20	X	
Q2G253	88193846	hypothetical protein SAOUHSC_00025 [Staphylococcus aureus subsp. aureus NCTC 8325]	83373	76	300	85	20	X	
Q2G0Q8	88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	32955	87	199	103	20	X	
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310	35	38		20	X	
Q2FXL6	88195519	hypothetical protein SAOUHSC_01819 [Staphylococcus aureus subsp. aureus NCTC 8325]	18464		79	78	20	X	
Q2G2B2	88196433	hypothetical protein SAOUHSC_02798 [Staphylococcus aureus subsp. aureus NCTC 8325]	178419	221	184	199	20	X	
Q2FUW1	88196609	hypothetical protein SAOUHSC_02990 [Staphylococcus aureus subsp. aureus NCTC 8325]	227909	291	307	237	20	X	
Q2G0Y7	88194172	inosine-5~-monophosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	52818		125	78	20	X	X
Q2FZ82	88194899	isoleucyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	104820	391	101	39	20	X	
Q2FXH2	88195572	leucyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	91728	150	150		20	X	
Q2FV16	88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	55964	120	386	266	20	X	
Q2G1R9	88194248	methionyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74838	444	746	256	20	X	X
Q2FXZ2	88195389	molecular chaperone DnaK [Staphylococcus aureus subsp. aureus NCTC 8325]	66321		256	63	20	X	
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022	47	50	42	20	X	
Q2FZD8	88194840	phenylalanyl-tRNA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	88866	390	336		20	X	X
Q2G1W2	88195605	phosphoenolpyruvate carboxykinase [Staphylococcus aureus subsp. aureus NCTC 8325]	59340		58	40	20	X	X
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088	57	467	375	20	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FZJ0	88194767	phosphoribosylformylglycinamidine synthase II [Staphylococcus aureus subsp. aureus NCTC 8325]	79486	981	1275	745	20	X	X
Q2FZ20	88194984	polynucleotide phosphorylase/polyadenylase [Staphylococcus aureus subsp. aureus NCTC 8325]	77314	486	581	290	20	X	X
O06446	88194531	preprotein translocase subunit SecA [Staphylococcus aureus subsp. aureus NCTC 8325]	95900	1163	1058	553	20	X	X
Q2FXE8	88195596	putative translaldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	25689	73	106	64	20	X	
Q2G2C1	88194813	pyruvate carboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	128467	209	139		20	X	X
Q2FZG4	88194792	pyruvate dehydrogenase complex, E1 component subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	41357		147	102	20	X	
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224	81	325	94	20	X	
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	799	743	775	20	X	
Q2G078	88194507	ribonucleotide-diphosphate reductase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	82552	341	453	180	20	X	
Q2FWJ5	88195963	S1 RNA-binding domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	80885	138	96		20		X
Q2FZC8	88194850	succinate dehydrogenase flavoprotein subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	65462		84	72	20	X	
Q2FXP7	88195489	threonyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74441	631	649	216	20	X	
Q2FYT8	88195066	transketolase [Staphylococcus aureus subsp. aureus NCTC 8325]	68317	211	439	108	20	X	
Q2G2D0	88194979	translation initiation factor IF-2 [Staphylococcus aureus subsp. aureus NCTC 8325]	77823	106	526		20	X	X
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579	730	711	870	20	X	
Q2G256	161353526	tRNA CCA-pyrophosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	46407	45	50		20		X
Q2FYM1	88195143	2-oxoglutarate dehydrogenase E1 component [Staphylococcus aureus subsp. aureus NCTC 8325]	105277	80	76		21	X	
Q2FYS9	88195075	aconitate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	98908	181	355	139	21	X	
Q2FXV9	88195427	alanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	98459	23	31		21	X	X
Q2FXU5	88195441	aspartyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	66587	415	432	65	21	X	
Q2FV74	88196493	ATP-dependent Clp protease ATP-binding subunit ClpC [Staphylococcus aureus subsp. aureus NCTC 8325]	77789	200	190		21	X	X
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	497	822	697	21	X	
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451	149	251	147	21	X	
Q2G274	88193828	DNA gyrase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	72495	391	209	56	21	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
P47768	161353532	DNA-directed RNA polymerase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	133136	47	119		21	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190	102	94		21	X	
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564	300	453	121	21	X	X
Q2FY41	88195335	elongation factor P [Staphylococcus aureus subsp. aureus NCTC 8325]	20541	69	103	103	21		
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474	149	231		21	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	269	431	265	21	X	X
Q2G0P5	88194286	endopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	90981	652	531	165	21	X	X
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819	53	109		21	X	X
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817		109	85	21	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	90	208	53	21	X	
Q2FXY7	88195394	GTP-binding protein LepA [Staphylococcus aureus subsp. aureus NCTC 8325]	68132	157	293		21	X	X
Q2G1Y6	88194808	GTP-binding protein TypA [Staphylococcus aureus subsp. aureus NCTC 8325]	69152	93	49		21	X	
Q2G253	88193846	hypothetical protein SAOUHSC_00025 [Staphylococcus aureus subsp. aureus NCTC 8325]	83373	112	200		21	X	
Q2FYQ2	88195110	hypothetical protein SAOUHSC_01383 [Staphylococcus aureus subsp. aureus NCTC 8325]	69241	137	323	124	21	X	
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310	39	40	44	21	X	
Q2G2B2	88196433	hypothetical protein SAOUHSC_02798 [Staphylococcus aureus subsp. aureus NCTC 8325]	178419	144	181	79	21	X	
Q2FVB2	88196456	hypothetical protein SAOUHSC_02822 [Staphylococcus aureus subsp. aureus NCTC 8325]	76127	317	167		21	X	
Q2FZ82	88194899	isoleucyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	104820	75	81	34	21	X	
Q2FV16	88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	55964		169	68	21	X	
Q2G1R9	88194248	methionyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74838	1204	1110	849	21	X	X
Q2FXZ2	88195389	molecular chaperone DnaK [Staphylococcus aureus subsp. aureus NCTC 8325]	66321	727	741	518	21	X	
Q2G1U3	88194694	oligoendopeptidase F [Staphylococcus aureus subsp. aureus NCTC 8325]	69776	83	282	63	21	X	
Q2FZH5	88194782	phosphoenolpyruvate-protein phosphotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	63179	43	222		21	X	
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088	75	299	63	21	X	
Q2FZJ0	88194767	phosphoribosylformylglycinamidine synthase II [Staphylococcus aureus subsp. aureus NCTC 8325]	79486	347	332	52	21	X	X
O06446	88194531	preprotein translocase subunit SecA [Staphylococcus aureus subsp. aureus NCTC 8325]	95900	72	138		21	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G1Z4	88194973	prolyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	63823	142	75		21	X	
Q2G1G8	88193967	PTS system glucose-specific protein [Staphylococcus aureus subsp. aureus NCTC 8325]	72010	38		39	21		
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	1583	1413	1791	21	X	
Q2G078	88194507	ribonucleotide-diphosphate reductase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	82552	283	171		21	X	
Q2FXK8	88195527	septation ring formation regulator EzrA [Staphylococcus aureus subsp. aureus NCTC 8325]	66206	311	377	194	21	X	
Q2FXP7	88195489	threonyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74441	937	568	265	21	X	
Q2FYT8	88195066	transketolase [Staphylococcus aureus subsp. aureus NCTC 8325]	68317	772	906	688	21	X	
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579	2253	1619	2004	21	X	
Q2FUQ3	161353516	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA [Staphylococcus aureus subsp. aureus NCTC 8325]	70072	468	295		21	X	X
Q2FV67	88196500	1-pyrroline-5-carboxylate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	56832	401	293	315	22	X	
Q2FYF9	88195210	30S ribosomal protein S1 [Staphylococcus aureus subsp. aureus NCTC 8325]	43261	82	258	201	22	X	X
Q2FY60	88195316	6-phosphogluconate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	51770	162	112	225	22	X	X
Q2FYP2	88195119	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	60219	361	216	159	22	X	
Q2FV14	88196556	acetyl-CoA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	59711	227	102	36	22	X	
Q2FYS9	88195075	aconitate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	98908	243	494	377	22	X	
Q2G2S0	88195807	adenylosuccinate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	49572	71		91	22	X	
Q2FWD6	88196026	aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	51937	261	249	128	22	X	X
Q2G1J0	88193945	aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	53626	437	267	279	22	X	X
Q2FW66	88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	19180	57	81	75	22	X	
O05204	88194162	alkyl hydroperoxide reductase subunit F [Staphylococcus aureus subsp. aureus NCTC 8325]	54687	308	256	175	22	X	X
Q2FZI9	88194768	amidophosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	54363	519	265	354	22	X	
Q2G0F8	88194381	arginyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	62342	350	391	87	22	X	
Q2FYH6	88195188	asparaginyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	49127	257	198	253	22	X	
Q2FWY9	88195799	aspartyl/glutamyl-tRNA amidotransferase subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	52788	348	219	314	22	X	
Q2FWZ0	88195798	aspartyl/glutamyl-tRNA amidotransferase subunit B [Staphylococcus aureus subsp. aureus NCTC	53623	642	379	543	22	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
		8325]							
Q2FXU5	88195441	aspartyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	66587	475	78	91	22	X	
Q2FV74	88196493	ATP-dependent Clp protease ATP-binding subunit ClpC [Staphylococcus aureus subsp. aureus NCTC 8325]	77789		156	85	22	X	X
Q2FZ28	88194962	ATP-dependent protease ATP-binding subunit HslU [Staphylococcus aureus subsp. aureus NCTC 8325]	52282	314	74	111	22	X	X
Q2G0S3	88194258	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	48473	108	87	163	22		
Q2FZI6	88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	54314	812	508	562	22	X	
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	643	432	537	22	X	
Q2FYU7	88195057	catalase [Staphylococcus aureus subsp. aureus NCTC 8325]	54908	370	384	355	22	X	
O07325	88194891	cell division protein [Staphylococcus aureus subsp. aureus NCTC 8325]	52902	165	218	103	22	X	
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012	237	374	614	22	X	X
Q2FWN4	88195925	chaperonin GroEL [Staphylococcus aureus subsp. aureus NCTC 8325]	57629	687	669	786	22	X	
Q2G2H5	88193824	chromosomal replication initiation protein [Staphylococcus aureus subsp. aureus NCTC 8325]	51934	63		63	22	X	X
O52582	88194665	coenzyme A disulfide reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	49259		36	49	22	X	X
Q2FWD1	88196031	CTP synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	59945	159	133	100	22	X	
Q2G2M6	88194292	cysteinyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	53652	106	77	78	22	X	
Q2FZV6	88194636	cytosol aminopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	54095	143	66	90	22	X	
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451	712	566	485	22	X	
Q2FYM2	88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46644	557	552	426	22	X	
Q2FXH9	88195565	dipeptidase PepV [Staphylococcus aureus subsp. aureus NCTC 8325]	52791		126	94	22	X	
P47768	161353532	DNA-directed RNA polymerase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	133136		104	112	22	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190	140	146	121	22	X	
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564	634	435	479	22	X	X
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474	250	345	458	22	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	338	674	610	22	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G0P5	88194286	endopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	90981	476	164	476	22	X	X
Q2FWE8	88196009	F0F1 ATP synthase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	54550	340	416	254	22	X	X
Q2FWF0	88196007	F0F1 ATP synthase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	51368	437	628	686	22	X	X
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819	813	582	616	22	X	X
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	92	88	129	22	X	
Q2FWA0	88196060	glucosamine--fructose-6-phosphate aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	65809	389	201	237	22	X	
Q2FY66	88195310	glucose-6-phosphate 1-dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	56929	515	224	285	22	X	X
Q2FYY6	88195018	glutamine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	50808	184	244	286	22	X	
Q2G241	88194290	glutamyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	56253	250	204	94	22	X	X
Q2FXP2	88195494	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	36956		180	150	22	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	147	222	257	22	X	
Q2FY34	88195342	glycine dehydrogenase subunit 1 [Staphylococcus aureus subsp. aureus NCTC 8325]	49685	131	78		22	X	
Q2FY35	88195341	glycine dehydrogenase subunit 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	54748	91	71		22	X	
Q2FY08	88195373	glycyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	53586	286	391	201	22	X	X
Q2G0Y6	88194173	GMP synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	58194	299	410	226	22	X	X
Q2G1Y6	88194808	GTP-binding protein TypA [Staphylococcus aureus subsp. aureus NCTC 8325]	69152	104		112	22	X	
Q2FYV4	88195050	homoserine dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	46845	118	44		22	X	X
Q2G253	88193846	hypothetical protein SAOUHSC_00025 [Staphylococcus aureus subsp. aureus NCTC 8325]	83373	327	158	366	22	X	
Q2G0Z2	88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	35591	483	567	590	22	X	
Q2G0R0	88194271	hypothetical protein SAOUHSC_00486 [Staphylococcus aureus subsp. aureus NCTC 8325]	77764	148	89	60	22	X	X
Q2G0Q8	88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	32955	40	98	145	22	X	
Q2G0I4	88194355	hypothetical protein SAOUHSC_00581 [Staphylococcus aureus subsp. aureus NCTC 8325]	48386		79	74	22	X	
Q2FZY6	88194606	hypothetical protein SAOUHSC_00848 [Staphylococcus aureus subsp. aureus NCTC 8325]	48519	194	136	123	22	X	
Q2FZY3	88194609	hypothetical protein SAOUHSC_00851 [Staphylococcus aureus subsp. aureus NCTC 8325]	52498	339	179	142	22	X	
Q2FZG9	88194787	hypothetical protein SAOUHSC_01035 [Staphylococcus aureus subsp. aureus NCTC 8325]	62630	67	60		22	X	X
Q2FZ58	88194932	hypothetical protein SAOUHSC_01193 [Staphylococcus aureus subsp. aureus NCTC 8325]	60477	296	106	91	22	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FZ19	88194985	hypothetical protein SAOUHSC_01252 [Staphylococcus aureus subsp. aureus NCTC 8325]	58753	372	199	173	22	X	X
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310	40	43	44	22	X	
Q2FWB5	88196046	hypothetical protein SAOUHSC_02383 [Staphylococcus aureus subsp. aureus NCTC 8325]	52914	36		86	22		
Q2G1U8	88196330	hypothetical protein SAOUHSC_02690 [Staphylococcus aureus subsp. aureus NCTC 8325]	59150	41	82		22		
Q2G2B2	88196433	hypothetical protein SAOUHSC_02798 [Staphylococcus aureus subsp. aureus NCTC 8325]	178419	99	76	141	22	X	
Q2G1H0	88193965	indolepyruvate decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	60501	206	221	165	22	X	
Q2G0Y7	88194172	inosine-5~-monophosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	52818	632	616	632	22	X	X
Q2FXN4	88195501	isocitrate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	46394		101	42	22	X	
Q2FZ82	88194899	isoleucyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	104820	74		59	22	X	
Q2G0Q3	88194278	lysyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	56684	475	362	217	22	X	
Q2FV16	88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	55964	715	569	783	22	X	
Q2G1R9	88194248	methionyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74838	236	76		22	X	X
Q2FXZ2	88195389	molecular chaperone DnaK [Staphylococcus aureus subsp. aureus NCTC 8325]	66321	147	117	225	22	X	
Q2G235	161353521	nicotinate phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	55857	346	196		22		
Q2G1U3	88194694	oligoendopeptidase F [Staphylococcus aureus subsp. aureus NCTC 8325]	69776	140		101	22	X	
Q2G1W2	88195605	phosphoenolpyruvate carboxykinase [Staphylococcus aureus subsp. aureus NCTC 8325]	59340	985	371	454	22	X	X
Q2FZH5	88194782	phosphoenolpyruvate-protein phosphotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	63179	388	430	378	22	X	
P0C0V7	88196066	phosphoglucosamine mutase [Staphylococcus aureus subsp. aureus NCTC 8325]	49234	153	125	190	22	X	
Q2G031	88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	42575	104	111	126	22	X	X
Q2G029	88194558	phosphoglyceromutase [Staphylococcus aureus subsp. aureus NCTC 8325]	56389		94	89	22	X	
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088	220	453	540	22	X	
Q2FZJ0	88194767	phosphoribosylformylglycinamidine synthase II [Staphylococcus aureus subsp. aureus NCTC 8325]	79486	324	182	231	22	X	X
O06446	88194531	preprotein translocase subunit SecA [Staphylococcus aureus subsp. aureus NCTC 8325]	95900	120	132	134	22	X	X
Q2G1Z4	88194973	prolyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	63823	659	180	76	22	X	
P02976	88193885	protein A [Staphylococcus aureus subsp. aureus NCTC 8325]	56403	309	265	198	22	X	
Q2FZG4	88194792	pyruvate dehydrogenase complex, E1 component subunit alpha [Staphylococcus aureus subsp.	41357	76	121	114	22	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
		aureus NCTC 8325]							
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	721	608	623	22	X	
P0A0J0	88195369	RNA polymerase sigma factor RpoD [Staphylococcus aureus subsp. aureus NCTC 8325]	42145	263	243	581	22	X	X
Q2FXK8	88195527	septation ring formation regulator EzrA [Staphylococcus aureus subsp. aureus NCTC 8325]	66206	70	38	81	22	X	
P95689	88193832	seryl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	48609	398	106	186	22	X	X
Q2FZ48	88194942	signal recognition particle-docking protein FtsY [Staphylococcus aureus subsp. aureus NCTC 8325]	46561	76	78	77	22	X	X
Q2FZC8	88194850	succinate dehydrogenase flavoprotein subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	65462	187	153	105	22	X	
Q2FZ37	88194953	succinyl-CoA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	42030		69	105	22	X	X
Q2FXP7	88195489	threonyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74441	183	145		22	X	
Q2G2D2	88194976	transcription elongation factor NusA [Staphylococcus aureus subsp. aureus NCTC 8325]	43714	359	178	241	22		X
Q2FYT8	88195066	transketolase [Staphylococcus aureus subsp. aureus NCTC 8325]	68317	250	294	268	22	X	
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579	780	756	845	22	X	
Q2FUQ3	161353516	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA [Staphylococcus aureus subsp. aureus NCTC 8325]	70072	73	28		22	X	X
Q2FWF4	88196003	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	44913		82	136	22	X	
Q2FVT5	88196249	urocanate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	60595	275	226	77	22	X	
Q2FV67	88196500	1-pyrroline-5-carboxylate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	56832	82		141	23	X	
Q2G0M8	88194312	2-amino-3-ketobutyrate coenzyme A ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	42864	174	136	178	23	X	
Q2FYM1	88195143	2-oxoglutarate dehydrogenase E1 component [Staphylococcus aureus subsp. aureus NCTC 8325]	105277		31	59	23	X	
Q2FYF9	88195210	30S ribosomal protein S1 [Staphylococcus aureus subsp. aureus NCTC 8325]	43261	127	64		23	X	X
Q2FZR9	88194678	3-oxoacyl- synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	43712	312	160	271	23	X	
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	77	65	117	23	X	X
Q2FY60	88195316	6-phosphogluconate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	51770	762	534	626	23	X	X
Q2FXL5	88195520	acetate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	44015	498	403	669	23	X	X
Q2G124	88194136	acetyl-CoA acetyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	41677	80		70	23		
Q2FV14	88196556	acetyl-CoA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	59711	54	28		23	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FYS9	88195075	aconitate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	98908		184	195	23	X	
Q2G2S0	88195807	adenylosuccinate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	49572	467	441	336	23	X	
Q2G1S3	88193840	adenylosuccinate synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	47549	159	295	297	23	X	X
Q2G1J0	88193945	aldehyde dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	53626	59	28		23	X	X
Q2FW66	88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	19180	54		66	23	X	
Q2FZI9	88194768	amidophosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	54363	536	46		23	X	
Q2FYH6	88195188	asparaginyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	49127	154	75	98	23	X	
Q2FWY9	88195799	aspartyl/glutamyl-tRNA amidotransferase subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	52788	49		96	23	X	
Q2FWZ0	88195798	aspartyl/glutamyl-tRNA amidotransferase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	53623	124	40	185	23	X	
Q2FXQ7	88195479	ATP-dependent protease ATP-binding subunit ClpX [Staphylococcus aureus subsp. aureus NCTC 8325]	46269	233	65	125	23	X	X
Q2G248	88195550	bifunctional 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase [Staphylococcus aureus subsp. aureus NCTC 8325]	40593	153	141	219	23	X	
Q2FZJ6	88194761	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30824	62	124	310	23	X	X
Q2G0S3	88194258	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	48473	188	94	154	23		
Q2FZI6	88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	54314	491	197	406	23	X	
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	145	236	449	23	X	
Q2FZ73	88194908	carbamoyl phosphate synthase small subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	40369		75	81	23	X	
Q2FWG8	88195989	cardiolipin synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	56483	57		53	23		
Q2FYU7	88195057	catalase [Staphylococcus aureus subsp. aureus NCTC 8325]	54908	107	60	97	23	X	
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012	1015	672	658	23	X	X
Q2FWN4	88195925	chaperonin GroEL [Staphylococcus aureus subsp. aureus NCTC 8325]	57629	94	170	451	23	X	
Q2FZ10	88194994	competence-damage inducible protein cinA [Staphylococcus aureus subsp. aureus NCTC 8325]	43241	74		61	23		
Q2FWH3	88195984	D-alanyl-alanine synthetase A [Staphylococcus aureus subsp. aureus NCTC 8325]	40205	84	64		23	X	X
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451	464	467	486	23	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FYM2	88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46644	155	168	105	23	X	
Q2FZ74	88194907	dihydroorotase [Staphylococcus aureus subsp. aureus NCTC 8325]	46342	78	62	88	23	X	
Q2G2H4	88193825	DNA polymerase III subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	41888	312	297	338	23	X	X
Q2FW32	88196136	DNA-directed RNA polymerase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	34990	331	344	438	23	X	X
Q2G0N5	88194305	DNA-directed RNA polymerase subunit beta~ [Staphylococcus aureus subsp. aureus NCTC 8325]	134190	124	32	186	23	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190	171	126	185	23	X	
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564	539	296	621	23	X	X
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474	772	564	806	23	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	1612	1605	1678	23	X	X
Q2G0P5	88194286	endopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	90981	308	113	300	23	X	X
Q2FWE8	88196009	F0F1 ATP synthase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	54550	191	98	183	23	X	X
Q2FWF0	88196007	F0F1 ATP synthase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	51368	591	363	422	23	X	X
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819	329	302	477	23	X	X
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	74	109	159	23	X	
Q2FX94	88195674	fumarate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	51075	191	45		23	X	
Q2FY66	88195310	glucose-6-phosphate 1-dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	56929	98	42	105	23	X	X
Q2FZU0	88194657	glucose-6-phosphate isomerase [Staphylococcus aureus subsp. aureus NCTC 8325]	49791	181	232	372	23	X	
Q2FZU5	88194652	glutamate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	45731	214	116	310	23	X	
Q2FXR4	88195472	glutamate-1-semialdehyde aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46359	310		146	23	X	
Q2FYY6	88195018	glutamine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	50808	337	201	132	23	X	
Q2FXP2	88195494	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	36956	149	78	240	23	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	641	555	874	23	X	
Q2FY08	88195373	glycyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	53586	178	100	91	23	X	X
Q2FYG0	88195209	GTP-binding protein EngA [Staphylococcus aureus subsp. aureus NCTC 8325]	48949	187	150	187	23	X	X
Q2G115	88194145	GTP-dependent nucleic acid-binding protein EngD [Staphylococcus aureus subsp. aureus NCTC 8325]	40570	265	143	38	23	X	X
Q2FV76	88196491	HMG-CoA synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	43178	154	180	191	23	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FV77	88196490	hydroxymethylglutaryl-CoA reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	46208	193	122	220	23		
Q2G253	88193846	hypothetical protein SAOUHSC_00025 [Staphylococcus aureus subsp. aureus NCTC 8325]	83373	39	68	188	23	X	
Q2G0Z2	88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	35591	128	218	243	23	X	
Q2G0Q8	88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	32955	62	60	165	23	X	
Q2G0G6	88194373	hypothetical protein SAOUHSC_00603 [Staphylococcus aureus subsp. aureus NCTC 8325]	35438	67		129	23		
Q2FZY3	88194609	hypothetical protein SAOUHSC_00851 [Staphylococcus aureus subsp. aureus NCTC 8325]	52498	49	45		23	X	
Q2FZW0	88194632	hypothetical protein SAOUHSC_00875 [Staphylococcus aureus subsp. aureus NCTC 8325]	39374	126		97	23	X	
Q2FZV7	88194635	hypothetical protein SAOUHSC_00878 [Staphylococcus aureus subsp. aureus NCTC 8325]	44077	535	666	581	23	X	
Q2FYM7	88195134	hypothetical protein SAOUHSC_01408 [Staphylococcus aureus subsp. aureus NCTC 8325]	43381	571	298	828	23	X	
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310	41	36	38	23	X	
Q2FXN3	88195502	hypothetical protein SAOUHSC_01802 [Staphylococcus aureus subsp. aureus NCTC 8325]	32371	216	85	271	23	X	
Q2G245	88195552	hypothetical protein SAOUHSC_01854 [Staphylococcus aureus subsp. aureus NCTC 8325]	55058		27	50	23	X	
Q2FXI5	88195559	hypothetical protein SAOUHSC_01861 [Staphylococcus aureus subsp. aureus NCTC 8325]	39758	45	45	59	23	X	
Q2FWY6	88195802	hypothetical protein SAOUHSC_02121 [Staphylococcus aureus subsp. aureus NCTC 8325]	45353	56	42	115	23		
Q2FWW3	88195838	hypothetical protein SAOUHSC_02158 [Staphylococcus aureus subsp. aureus NCTC 8325]	48089	117	137	116	23	X	
Q2G1W0	88196218	hypothetical protein SAOUHSC_02574 [Staphylococcus aureus subsp. aureus NCTC 8325]	40717	86		78	23	X	
Q2FVT6	88196248	imidazolonepropionase [Staphylococcus aureus subsp. aureus NCTC 8325]	45011	95	60	117	23	X	
Q2G0Y7	88194172	inosine-5~-monophosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	52818	188	205	266	23	X	X
Q2FXN4	88195501	isocitrate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	46394	577	434	633	23	X	
Q2FZN7	88194720	lipoyltransferase and lipoate-protein ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	37904		45	217	23	X	
Q2G1Y5	88196549	L-lactate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	34399	71		35	23	X	X
Q2G0Q3	88194278	lysyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	56684	107	79		23	X	
Q2FV16	88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	55964	263	147	392	23	X	
Q2FYR1	88195101	methicillin resistance factor [Staphylococcus aureus subsp. aureus NCTC 8325]	49645	53	119	69	23	X	
Q2FXZ2	88195389	molecular chaperone DnaK [Staphylococcus aureus subsp. aureus NCTC 8325]	66321		69	77	23	X	
Q2FVY0	88196188	molybdopterin biosynthesis protein MoeA [Staphylococcus aureus subsp. aureus NCTC 8325]	44988	234		128	23	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FXM5	88195510	NADP-dependent malic enzyme [Staphylococcus aureus subsp. aureus NCTC 8325]	44206	68	35	155	23	X	
Q2FZU6	88194651	ornithine--oxo-acid transaminase [Staphylococcus aureus subsp. aureus NCTC 8325]	43390	147	72	172	23	X	
Q2FY59	88195317	peptidase T [Staphylococcus aureus subsp. aureus NCTC 8325]	40235		112	134	23	X	
Q2FWE0	88196022	peptide chain release factor 1 [Staphylococcus aureus subsp. aureus NCTC 8325]	40325	55	81	166	23	X	
Q2G052	88194533	peptide chain release factor 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	33191	90	63	77	23		
Q2FZD9	88194839	phenylalanyl-tRNA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	40081	176	152	236	23	X	X
Q2G1W2	88195605	phosphoenolpyruvate carboxykinase [Staphylococcus aureus subsp. aureus NCTC 8325]	59340	351	22	144	23	X	X
Q2G031	88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	42575	961	479	669	23	X	X
Q2G029	88194558	phosphoglyceromutase [Staphylococcus aureus subsp. aureus NCTC 8325]	56389		45	220	23	X	
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088	651	762		23	X	
Q2FZI5	88194772	phosphoribosylamine--glycine ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	45820	304	299	310	23	X	X
Q2FZJ4	88194763	phosphoribosylaminoimidazole carboxylase ATPase subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	42466	80	91	58	23	X	
Q2FZJ0	88194767	phosphoribosylformylglycinamidine synthase II [Staphylococcus aureus subsp. aureus NCTC 8325]	79486		54	134	23	X	X
O06446	88194531	preprotein translocase subunit SecA [Staphylococcus aureus subsp. aureus NCTC 8325]	95900		39	91	23	X	X
Q2FY40	88195336	proline dipeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	39313	70		123	23	X	
Q2FWC1	88196040	pyrimidine-nucleoside phosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	46279	224	104	142	23	X	
Q2FZG4	88194792	pyruvate dehydrogenase complex, E1 component subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	41357	480	359	506	23	X	
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224		43	292	23	X	
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	549	322	725	23	X	
Q2FZ09	228937974	recombinase A [Staphylococcus aureus subsp. aureus NCTC 8325]	37633	277	165	313	23	X	X
P0A0J0	88195369	RNA polymerase sigma factor RpoD [Staphylococcus aureus subsp. aureus NCTC 8325]	42145	418	187	228	23	X	X
Q2G1W4	88195604	S-adenosylmethionine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	43614	294	170	332	23	X	X
Q2FWE5	88196017	serine hydroxymethyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	45144	389	158	249	23	X	
P95689	88193832	seryl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	48609	102		84	23	X	X
Q2FZ36	88194954	succinyl-CoA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	31522	89	84	41	23	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FZ37	88194953	succinyl-CoA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	42030	475	546	564	23	X	X
Q2FXP7	88195489	threonyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74441	102	66		23	X	
Q2G2D2	88194976	transcription elongation factor NusA [Staphylococcus aureus subsp. aureus NCTC 8325]	43714	123	87	146	23		X
Q2FYT8	88195066	transketolase [Staphylococcus aureus subsp. aureus NCTC 8325]	68317	53	145	244	23	X	
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579	347	260	689	23	X	
Q2FXJ5	88195539	tyrosyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	47568	386	89	242	23	X	X
Q2FWD4	88196028	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	45046	80	48	63	23		
Q2FWF4	88196003	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	44913	281	129	201	23	X	
Q2FW81	88196079	UDP-N-acetylglucosamine pyrophosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	44866	82	151	62	23	X	
Q2FXJ0	88195554	UDP-N-acetylmuramate--L-alanine ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	49157	106	56		23	X	X
Q2FZR9	88194678	3-oxoacyl- synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	43712	52	89		24	X	
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	361	354	234	24	X	X
Q2FXM8	88195507	6-phosphofructokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	33376	379	246	118	24	X	X
Q2FY60	88195316	6-phosphogluconate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	51770	68	92		24	X	X
Q2FW75	88196085	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	36569	143	178	164	24		
Q2G2D8	88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35049	280	240	283	24	X	
Q2FZ75	88194906	aspartate carbamoyltransferase catalytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	33237	382	197	119	24	X	
Q2G1K9	88193926	bifunctional acetaldehyde-CoA/alcohol dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	94885	31		31	24		
Q2FZI6	88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	54314	108		97	24	X	
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	200	253	229	24	X	
Q2G0M4	88194316	branched-chain amino acid aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	40062	170	95	78	24	X	
Q2G295	88195548	catabolite control protein A [Staphylococcus aureus subsp. aureus NCTC 8325]	36038	561	310	320	24	X	X
Q2FYU7	88195057	catalase [Staphylococcus aureus subsp. aureus NCTC 8325]	54908		43	44	24	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012	418	249	537	24	X	X
Q2G0M7	88194313	chaperone protein HchA [Staphylococcus aureus subsp. aureus NCTC 8325]	32156	107	151	130	24	X	
Q2FWN4	88195925	chaperonin GroEL [Staphylococcus aureus subsp. aureus NCTC 8325]	57629	89	206	209	24	X	
Q2FXR3	88195473	delta-aminolevulinic acid dehydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	36559	43	64		24		
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451	180	182	175	24	X	
Q2FYM2	88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46644	135	291	164	24	X	
Q2FVW4	88196221	D-isomer specific 2-hydroxyacid dehydrogenase NAD binding domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	34653	623	164	283	24	X	X
Q2FW32	88196136	DNA-directed RNA polymerase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	34990	166	109	96	24	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190	137	119	77	24	X	
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564	208	99	158	24	X	X
Q2FY41	88195335	elongation factor P [Staphylococcus aureus subsp. aureus NCTC 8325]	20541	247	138	237	24		
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474	3695	2628	2345	24	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	546	574	412	24	X	X
Q2G0P5	88194286	endopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	90981	74	21	136	24	X	X
Q2FWF0	88196007	F0F1 ATP synthase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	51368	83		77	24	X	X
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819	185	151	283	24	X	X
Q2FV17	88196553	fructose-1,6-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	33034	260	274	190	24	X	
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	138	172	279	24	X	
Q2FYY6	88195018	glutamine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	50808	45	106		24	X	
Q2FXP2	88195494	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	36956	144	103	113	24	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	376	295	228	24	X	
Q2FZ55	88194935	glycerol-3-phosphate acyltransferase PlsX [Staphylococcus aureus subsp. aureus NCTC 8325]	35408	118	73	53	24	X	
Q2FY08	88195373	glycyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	53586	56	66		24	X	X
Q2FY06	161353525	GTP-binding protein Era [Staphylococcus aureus subsp. aureus NCTC 8325]	34249		47	29	24	X	X
Q2FYU4	88195060	guanosine 5~-monophosphate oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	36093	67	57	47	24	X	X
Q2G045	88194542	HPr kinase/phosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	34461	550	341	109	24	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G253	88193846	hypothetical protein SAOUHSC_00025 [Staphylococcus aureus subsp. aureus NCTC 8325]	83373	127	49	39	24	X	
Q2G1I3	88193952	hypothetical protein SAOUHSC_00139 [Staphylococcus aureus subsp. aureus NCTC 8325]	38454	56	57		24		
Q2G136	88194120	hypothetical protein SAOUHSC_00319 [Staphylococcus aureus subsp. aureus NCTC 8325]	39147	289	151	177	24	X	
Q2G105	88194155	hypothetical protein SAOUHSC_00356 [Staphylococcus aureus subsp. aureus NCTC 8325]	21293		86	65	24	X	
Q2G0Z2	88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	35591		218	204	24	X	
Q2G0Q8	88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	32955	555	665	444	24	X	
Q2G0G6	88194373	hypothetical protein SAOUHSC_00603 [Staphylococcus aureus subsp. aureus NCTC 8325]	35438	253	151	166	24		
Q2G0D0	88194440	hypothetical protein SAOUHSC_00675 [Staphylococcus aureus subsp. aureus NCTC 8325]	26304		114	105	24	X	X
Q2FZV7	88194635	hypothetical protein SAOUHSC_00878 [Staphylococcus aureus subsp. aureus NCTC 8325]	44077	149	48	33	24	X	
Q2FZE9	88194829	hypothetical protein SAOUHSC_01081 [Staphylococcus aureus subsp. aureus NCTC 8325]	38722	265	270	125	24	X	
Q2FYS0	88195092	hypothetical protein SAOUHSC_01365 [Staphylococcus aureus subsp. aureus NCTC 8325]	37832	87	80		24	X	
Q2FYP3	88195118	hypothetical protein SAOUHSC_01391 [Staphylococcus aureus subsp. aureus NCTC 8325]	34177		88	56	24	X	
Q2FYM7	88195134	hypothetical protein SAOUHSC_01408 [Staphylococcus aureus subsp. aureus NCTC 8325]	43381		82	154	24	X	
Q2FYK7	88195157	hypothetical protein SAOUHSC_01433 [Staphylococcus aureus subsp. aureus NCTC 8325]	30626	220	50	54	24	X	
Q2FY01	88195380	hypothetical protein SAOUHSC_01673 [Staphylococcus aureus subsp. aureus NCTC 8325]	34892	102	47	36	24	X	
Q2FXZ9	88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	35160	285	177	129	24	X	
Q2FXN3	88195502	hypothetical protein SAOUHSC_01802 [Staphylococcus aureus subsp. aureus NCTC 8325]	32371	173	87	41	24	X	
Q2FWX8	88195823	hypothetical protein SAOUHSC_02143 [Staphylococcus aureus subsp. aureus NCTC 8325]	38523	81	53	20	24		
Q2FW93	88196067	hypothetical protein SAOUHSC_02406 [Staphylococcus aureus subsp. aureus NCTC 8325]	34603	116		67	24		
Q2FVW9	88196199	hypothetical protein SAOUHSC_02554 [Staphylococcus aureus subsp. aureus NCTC 8325]	33990	163	154	114	24		
Q2FVT8	88196246	hypothetical protein SAOUHSC_02604 [Staphylococcus aureus subsp. aureus NCTC 8325]	31715	68	58	59	24	X	
Q2G1U8	88196330	hypothetical protein SAOUHSC_02690 [Staphylococcus aureus subsp. aureus NCTC 8325]	59150	34	87	36	24		
Q2FV40	88196527	hypothetical protein SAOUHSC_02899 [Staphylococcus aureus subsp. aureus NCTC 8325]	38170		67	42	24	X	
Q2FV39	88196528	hypothetical protein SAOUHSC_02900 [Staphylococcus aureus subsp. aureus NCTC 8325]	30986	68		53	24	X	
Q2G0Y7	88194172	inosine-5~-monophosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	52818	79	145	154	24	X	X
Q2FXN4	88195501	isocitrate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	46394	57	100	50	24	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FZX4	88194618	lipoyl synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	34863	127	109	40	24		
Q2FZN7	88194720	lipoyltransferase and lipoate-protein ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	37904	315	75	135	24	X	
Q2G1Y5	88196549	L-lactate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	34399	124	128	54	24	X	X
Q2FV16	88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	55964	256	129	217	24	X	
Q2FWY1	88195820	manganese-dependent inorganic pyrophosphatase [Staphylococcus aureus subsp. aureus NCTC 8325]	34047	257	375	195	24	X	
Q2G0I7	88194352	mevalonate diphosphate decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	36799	77		56	24		
Q2FXZ2	88195389	molecular chaperone DnaK [Staphylococcus aureus subsp. aureus NCTC 8325]	66321	80		31	24	X	
Q2G236	88195812	NAD synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	30678	290	33	255	24	X	X
Q2G1N4	88193889	periplasmic binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	36721	167	60	76	24	X	
Q2G1W2	88195605	phosphoenolpyruvate carboxykinase [Staphylococcus aureus subsp. aureus NCTC 8325]	59340	47		75	24	X	X
Q2FZH5	88194782	phosphoenolpyruvate-protein phosphotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	63179		41	48	24	X	
Q2G031	88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	42575	262	204	126	24	X	X
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088	82	247	270	24	X	
Q2FZI5	88194772	phosphoribosylamine--glycine ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	45820		61	69	24	X	X
Q2FZI8	88194769	phosphoribosylaminoimidazole synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	36994	140	183	132	24	X	
Q2FZJ0	88194767	phosphoribosylformylglycinamidine synthase II [Staphylococcus aureus subsp. aureus NCTC 8325]	79486	56	52		24	X	X
Q2G0J0	88194349	phosphotransacetylase [Staphylococcus aureus subsp. aureus NCTC 8325]	34930	338	363	337	24	X	
O34090	88195475	porphobilinogen deaminase [Staphylococcus aureus subsp. aureus NCTC 8325]	34333	264	191	52	24		
Q2FXP5	88195491	primosomal protein DnaI [Staphylococcus aureus subsp. aureus NCTC 8325]	35613	63		49	24	X	
Q2FY40	88195336	proline dipeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	39313	80	50	35	24	X	
Q2G2S6	88195663	protein export protein PrsA [Staphylococcus aureus subsp. aureus NCTC 8325]	35616	748	640	462	24		
Q2G0Q1	88194280	pyridoxal biosynthesis lyase PdxS [Staphylococcus aureus subsp. aureus NCTC 8325]	31972	424	330	421	24	X	
Q2FZG4	88194792	pyruvate dehydrogenase complex, E1 component subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	41357	195	240	138	24	X	
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224	853	827	519	24	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	347	318	390	24	X	
Q2FZJ9	88194758	quinol oxidase AA3 subunit II [Staphylococcus aureus subsp. aureus NCTC 8325]	41750		37	50	24	X	
Q2G2Q2	88194982	riboflavin biosynthesis protein RibF [Staphylococcus aureus subsp. aureus NCTC 8325]	36669	102		75	24		
Q2G1A6	88194046	ribokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	32429	88	112		24	X	
Q2G077	88194508	ribonucleotide-diphosphate reductase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	37489	128	101	61	24	X	
Q2G0S2	88194259	ribose-phosphate pyrophosphokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	35262	144	179	79	24	X	
Q2FZ39	88194951	ribosomal biogenesis GTPase [Staphylococcus aureus subsp. aureus NCTC 8325]	33360		42	46	24		X
Q2FWJ4	88195964	RNA polymerase sigma factor SigB [Staphylococcus aureus subsp. aureus NCTC 8325]	29425	200	98	81	24		X
Q2FZ36	88194954	succinyl-CoA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	31522	410	285	471	24	X	
Q2FZ37	88194953	succinyl-CoA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	42030	62		68	24	X	X
P0A011	88196104	tagatose 1,6-diphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	36573	89	53		24	X	
Q2G041	88194546	thioredoxin reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	33595	385	260	239	24	X	
Q2FYK5	88195159	thymidylate synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	36816	164	70	44	24		
Q2FYT8	88195066	transketolase [Staphylococcus aureus subsp. aureus NCTC 8325]	68317		137	77	24	X	
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579	518	222	301	24	X	
Q2FZQ7	88194690	tryptophanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	36886	131	49	52	24	X	
Q2G069	88194516	UDP-N-acetylenolpyruvoylglucosamine reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	33776		65	31	24	X	
Q2FYL5	88195149	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	39672	100	97	77	24	X	
Q2FV67	88196500	1-pyrroline-5-carboxylate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	56832		128	65	25	X	
Q2FYN7	88195124	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	25242	38	55		25		
Q2G1C0	88194032	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	26640	344	273	238	25	X	
Q2FW12	88196156	30S ribosomal protein S3 [Staphylococcus aureus subsp. aureus NCTC 8325]	24085	87	137	242	25	X	X
Q2FV21	88196546	3-methyl-2-oxobutanoate hydroxymethyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	28222	352	299	144	25	X	
Q2G0P0	88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	24693	235	463	364	25	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
P60430	88196159	50S ribosomal protein L2 [Staphylococcus aureus subsp. aureus NCTC 8325]	30136	146	145	123	25	X	X
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	263	256	222	25	X	X
Q2FY60	88195316	6-phosphogluconate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	51770	174	178	154	25	X	X
Q2FZY7	88194605	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	28257	349	341	282	25	X	
Q2FX86	88195682	ABC transporter permease [Staphylococcus aureus subsp. aureus NCTC 8325]	53089		53	36	25	X	
Q2G0V0	88194218	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	30437	328	328	313	25		
Q2G2D8	88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35049	1043	1194	954	25	X	
Q2FWM4	88195935	accessory gene regulator protein A [Staphylococcus aureus subsp. aureus NCTC 8325]	24238	46	144	69	25	X	X
Q2G1N7	88193886	accessory regulator-like protein [Staphylococcus aureus subsp. aureus NCTC 8325]	29871	100	109	81	25	X	X
Q2FXL5	88195520	acetate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	44015	69	130	62	25	X	X
Q2G1M1	88193901	acetoin reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	27199	301	263	189	25	X	
Q2G124	88194136	acetyl-CoA acetyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	41677	67	33	13	25		
Q2FXM7	88195508	acetyl-CoA carboxylase carboxyltransferase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	35048	90	48		25	X	
Q2FYS9	88195075	aconitate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	98908	52	163	153	25	X	
Q2FW27	88196141	adenylate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	23959		41	48	25	X	X
Q2FXV9	88195427	alanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	98459	78	70		25	X	X
Q2FXN6	88195500	alkaline phosphatase synthesis transcriptional regulatory protein [Staphylococcus aureus subsp. aureus NCTC 8325]	27105	306	249	138	25	X	X
Q2FW66	88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	19180	70	94	124	25	X	
P0A0B7	88194163	alkyl hydroperoxide reductase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	20963	46	171	163	25	X	
Q2FVL4	88196337	amino acid ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	27224	29		45	25	X	
Q2FWZ0	88195798	aspartyl/glutamyl-tRNA amidotransferase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	53623	180	300	223	25	X	
Q2G1F2	88193983	azoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	23338		124	136	25	X	
Q2FZJ6	88194761	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30824	565	520	601	25	X	X
Q2FZK7	88194750	bifunctional autolysin [Staphylococcus aureus subsp. aureus NCTC 8325]	137300	40		52	25	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G0S3	88194258	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	48473	60	76	68	25		
Q2FZI6	88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	54314	523	484	540	25	X	
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	168	339	297	25	X	
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012	492	482	675	25	X	X
Q2G0M7	88194313	chaperone protein HchA [Staphylococcus aureus subsp. aureus NCTC 8325]	32156	268	287	241	25	X	
Q2FWN4	88195925	chaperonin GroEL [Staphylococcus aureus subsp. aureus NCTC 8325]	57629	248	380	192	25	X	
Q2FYF5	228937973	cytidylate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	24580	164	155	214	25	X	
Q2FXI0	88195564	D-alanine aminotransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	31874	205	241	257	25	X	
Q2G224	88193913	deoxyribose-phosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	23458	136	117	45	25	X	
Q2FXP1	88195495	dephospho-CoA kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	23578	136	106		25	X	X
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451	288	427	305	25	X	
Q2FYM2	88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46644	98	54	105	25	X	
Q2G0Q7	88194274	dihydropteroate synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	29504	144	89	84	25	X	
Q2G2H4	88193825	DNA polymerase III subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	41888		60	69	25	X	X
Q2FY79	88195297	DNA-binding response regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	28143	448	390	266	25	X	X
Q2FW32	88196136	DNA-directed RNA polymerase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	34990	77	113	125	25	X	X
P47768	161353532	DNA-directed RNA polymerase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	133136		59	62	25	X	X
Q2G0N5	88194305	DNA-directed RNA polymerase subunit beta~ [Staphylococcus aureus subsp. aureus NCTC 8325]	134190	113	127	178	25	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190	212	183	261	25	X	
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564	287	446	339	25	X	X
Q2FY41	88195335	elongation factor P [Staphylococcus aureus subsp. aureus NCTC 8325]	20541	976	1058	943	25		
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474	658	715	804	25	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	702	979	723	25	X	X
Q2G0P5	88194286	endopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	90981	183	187	372	25	X	X
Q2FZQ3	88194704	enoyl-(acyl carrier protein) reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	28005	234	170	160	25	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FWF0	88196007	F0F1 ATP synthase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	51368		127	107	25	X	X
Q2FWE9	161353520	F0F1 ATP synthase subunit gamma [Staphylococcus aureus subsp. aureus NCTC 8325]	32086		88	24	25	X	
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819	287	396	356	25	X	X
Q2FV17	88196553	fructose-1,6-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	33034	61	113	80	25	X	
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	565	635	523	25	X	
Q2FY27	88195354	glucokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	35056	98	84		25	X	
Q2FYY6	88195018	glutamine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	50808	63	99	83	25	X	
Q2FXP2	88195494	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	36956	70	127	131	25	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	306	334	386	25	X	
Q2G0Y6	88194173	GMP synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	58194		72	57	25	X	X
Q2G0L1	88194328	GTP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	33461	77	169	24	25	X	
Q2G0J1	88194348	heme peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	29371	154	195	177	25	X	
Q2G045	88194542	HPr kinase/phosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	34461	184	59		25	X	X
Q2G253	88193846	hypothetical protein SAOUHSC_00025 [Staphylococcus aureus subsp. aureus NCTC 8325]	83373	119	139	146	25	X	
Q2G2E9	88193851	hypothetical protein SAOUHSC_00030 [Staphylococcus aureus subsp. aureus NCTC 8325]	67739	39	36	44	25		
Q2G105	88194155	hypothetical protein SAOUHSC_00356 [Staphylococcus aureus subsp. aureus NCTC 8325]	21293	50	41	74	25	X	
Q2G0Z2	88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	35591		34	145	25	X	
Q2G1S2	88194249	hypothetical protein SAOUHSC_00462 [Staphylococcus aureus subsp. aureus NCTC 8325]	29263	123	124		25		
Q2G0Q8	88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	32955	419	226	337	25	X	
Q2G2L2	88194404	hypothetical protein SAOUHSC_00637 [Staphylococcus aureus subsp. aureus NCTC 8325]	28007		64	71	25	X	
Q2G0D6	88194434	hypothetical protein SAOUHSC_00669 [Staphylococcus aureus subsp. aureus NCTC 8325]	23723	45		58	25		
Q2G0D0	88194440	hypothetical protein SAOUHSC_00675 [Staphylococcus aureus subsp. aureus NCTC 8325]	26304	180	234	249	25	X	X
Q2G0B5	88194455	hypothetical protein SAOUHSC_00690 [Staphylococcus aureus subsp. aureus NCTC 8325]	26671	71	72		25	X	
Q2G2T8	88194477	hypothetical protein SAOUHSC_00712 [Staphylococcus aureus subsp. aureus NCTC 8325]	32339	128	109	74	25	X	
Q2G059	88194526	hypothetical protein SAOUHSC_00763 [Staphylococcus aureus subsp. aureus NCTC 8325]	23853	97		30	25		
Q2G055	88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	22199	149	126	120	25	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G039	161353530	hypothetical protein SAOUHSC_00787 [Staphylococcus aureus subsp. aureus NCTC 8325]	34790	107	64		25		X
Q2G019	88194568	hypothetical protein SAOUHSC_00808 [Staphylococcus aureus subsp. aureus NCTC 8325]	28401	123	174	199	25		
Q2FZZ0	88194602	hypothetical protein SAOUHSC_00844 [Staphylococcus aureus subsp. aureus NCTC 8325]	30332	289	331	375	25		
Q2FZV7	88194635	hypothetical protein SAOUHSC_00878 [Staphylococcus aureus subsp. aureus NCTC 8325]	44077	136	148	74	25	X	
Q2FZT4	88194663	hypothetical protein SAOUHSC_00906 [Staphylococcus aureus subsp. aureus NCTC 8325]	33093	326	473	340	25	X	
Q2FZG5	88194791	hypothetical protein SAOUHSC_01039 [Staphylococcus aureus subsp. aureus NCTC 8325]	23861	101	116	192	25	X	
Q2FZE9	88194829	hypothetical protein SAOUHSC_01081 [Staphylococcus aureus subsp. aureus NCTC 8325]	38722	189	260	189	25	X	
Q2FZ83	88194898	hypothetical protein SAOUHSC_01158 [Staphylococcus aureus subsp. aureus NCTC 8325]	23500	268	289	141	25	X	
Q2FYV1	88195053	hypothetical protein SAOUHSC_01323 [Staphylococcus aureus subsp. aureus NCTC 8325]	29803	86	139		25	X	
Q2FYM3	88195141	hypothetical protein SAOUHSC_01415 [Staphylococcus aureus subsp. aureus NCTC 8325]	30066	162	181	122	25	X	
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310	34	44	45	25	X	
Q2FY71	88195305	hypothetical protein SAOUHSC_01594 [Staphylococcus aureus subsp. aureus NCTC 8325]	33485	112	91		25	X	
Q2FY10	88195371	hypothetical protein SAOUHSC_01664 [Staphylococcus aureus subsp. aureus NCTC 8325]	30765	84		61	25	X	X
Q2FY00	88195381	hypothetical protein SAOUHSC_01675 [Staphylococcus aureus subsp. aureus NCTC 8325]	27239	89	44	38	25		
Q2FXZ9	88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	35160	481	517	447	25	X	
Q2FXN3	88195502	hypothetical protein SAOUHSC_01802 [Staphylococcus aureus subsp. aureus NCTC 8325]	32371	84	76	68	25	X	
Q2FXJ8	88195536	hypothetical protein SAOUHSC_01836 [Staphylococcus aureus subsp. aureus NCTC 8325]	53080	35	43		25		
Q2FXJ6	88195538	hypothetical protein SAOUHSC_01838 [Staphylococcus aureus subsp. aureus NCTC 8325]	45775		119	196	25	X	
Q2G247	88195553	hypothetical protein SAOUHSC_01855 [Staphylococcus aureus subsp. aureus NCTC 8325]	17991		182	205	25	X	
Q2FXE2	88195602	hypothetical protein SAOUHSC_01907 [Staphylococcus aureus subsp. aureus NCTC 8325]	31452	105	182	201	25	X	
Q2FWX1	88195830	hypothetical protein SAOUHSC_02150 [Staphylococcus aureus subsp. aureus NCTC 8325]	21902	102	31	58	25	X	
Q2FWN0	88195929	hypothetical protein SAOUHSC_02258 [Staphylococcus aureus subsp. aureus NCTC 8325]	23989	118	88	90	25	X	
Q2FW01	88196167	hypothetical protein SAOUHSC_02519 [Staphylococcus aureus subsp. aureus NCTC 8325]	34742	218	133	55	25		
Q2FVW9	88196199	hypothetical protein SAOUHSC_02554 [Staphylococcus aureus subsp. aureus NCTC 8325]	33990	122	114	89	25		
Q2G2W5	88196271	hypothetical protein SAOUHSC_02630 [Staphylococcus aureus subsp. aureus NCTC 8325]	23010	48	56	52	25	X	
Q2FVQ2	88196290	hypothetical protein SAOUHSC_02650 [Staphylococcus aureus subsp. aureus NCTC 8325]	23348	117	133	128	25		

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FVL2	88196339	hypothetical protein SAOUHSC_02699 [Staphylococcus aureus subsp. aureus NCTC 8325]	28886	803	839	682	25	X	
Q2FVB4	88196454	hypothetical protein SAOUHSC_02820 [Staphylococcus aureus subsp. aureus NCTC 8325]	25788	254	244	132	25	X	
Q2FVB2	88196456	hypothetical protein SAOUHSC_02822 [Staphylococcus aureus subsp. aureus NCTC 8325]	76127	34		38	25	X	
Q2FV52	88196515	immunodominant antigen A [Staphylococcus aureus subsp. aureus NCTC 8325]	24188	154	142	124	25	X	
Q2G0Y7	88194172	inosine-5~-monophosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	52818		132	170	25	X	X
Q2G0F6	88194383	iron compound ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	31069	161	129	176	25		
Q2FXN4	88195501	isocitrate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	46394	182	337	101	25	X	
Q2FV16	88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	55964	233	294	269	25	X	
Q2FZ54	88194936	malonyl CoA-acyl carrier protein transacylase [Staphylococcus aureus subsp. aureus NCTC 8325]	33614	230	253	236	25		
Q2FWY1	88195820	manganese-dependent inorganic pyrophosphatase [Staphylococcus aureus subsp. aureus NCTC 8325]	34047	127	99	55	25	X	
Q2FX05	88195784	methionine aminopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	27485	264	299	152	25		
Q2FVX4	88196194	molybdenum ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	29033	248	361	347	25		
Q2FZL5	88194742	naphthoate synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	30406	327	308	211	25	X	
Q2FZG6	88194790	peptide deformylase [Staphylococcus aureus subsp. aureus NCTC 8325]	20547	78		71	25		
Q2G1N4	88193889	periplasmic binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	36721	95		115	25	X	
Q2G1W2	88195605	phosphoenolpyruvate carboxykinase [Staphylococcus aureus subsp. aureus NCTC 8325]	59340	125	58	67	25	X	X
Q2G031	88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	42575	178	211	191	25	X	X
Q2FVK8	88196343	phosphoglyceromutase [Staphylococcus aureus subsp. aureus NCTC 8325]	26663	322	517	512	25	X	
Q2G0J8	88194341	phosphomethylpyrimidine kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	29838	126	141	84	25	X	
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088	323	525	473	25	X	
Q2FZI5	88194772	phosphoribosylamine--glycine ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	45820		131	92	25	X	X
Q2FZJ3	88194764	phosphoribosylaminoimidazole-succinocarboxamide synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	26676	464	707	398	25	X	
Q2FZJ0	88194767	phosphoribosylformylglycinamidine synthase II [Staphylococcus aureus subsp. aureus NCTC 8325]	79486	113	67		25	X	X
Q2G0J0	88194349	phosphotransacetylase [Staphylococcus aureus subsp. aureus NCTC 8325]	34930	121	106	131	25	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G2S6	88195663	protein export protein PrsA [Staphylococcus aureus subsp. aureus NCTC 8325]	35616	340	403	458	25		
Q2FWB8	88196043	purine nucleoside phosphorylase [Staphylococcus aureus subsp. aureus NCTC 8325]	25892	33	71	65	25	X	
Q2FXE8	88195596	putative translaldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	25689	283	379	202	25	X	
Q2G0Q1	88194280	pyridoxal biosynthesis lyase PdxS [Staphylococcus aureus subsp. aureus NCTC 8325]	31972	344	437	533	25	X	
Q2FZG4	88194792	pyruvate dehydrogenase complex, E1 component subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	41357	173	193	241	25	X	
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224	452	537	441	25	X	
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	401	759	753	25	X	
Q2FZJ9	88194758	quinol oxidase AA3 subunit II [Staphylococcus aureus subsp. aureus NCTC 8325]	41750		49	54	25	X	
Q2FZ09	228937974	recombinase A [Staphylococcus aureus subsp. aureus NCTC 8325]	37633	169	175	157	25	X	X
Q2G0S2	88194259	ribose-phosphate pyrophosphokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	35262	267	144	145	25	X	
Q2FXS6	88195460	rod shape-determining protein MreC [Staphylococcus aureus subsp. aureus NCTC 8325]	30991	202	180	239	25		
Q2FXK8	88195527	septation ring formation regulator EzrA [Staphylococcus aureus subsp. aureus NCTC 8325]	66206		74	79	25	X	
Q2FZC8	88194850	succinate dehydrogenase flavoprotein subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	65462		53	80	25	X	
Q2FZC7	88194851	succinate dehydrogenase iron-sulfur subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	30563	146	160	90	25	X	
Q2FZ36	88194954	succinyl-CoA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	31522	152	150	376	25	X	
Q2FZ37	88194953	succinyl-CoA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	42030	169	226	184	25	X	X
Q2G041	88194546	thioredoxin reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	33595	127	177	261	25	X	
Q2FXP7	88195489	threonyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74441		83	133	25	X	
Q2FWD9	88196023	thymidine kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	22200	90	104	61	25		X
Q2G0P2	88194298	transcription antitermination protein [Staphylococcus aureus subsp. aureus NCTC 8325]	20651	38	22		25	X	
Q2G2D2	88194976	transcription elongation factor NusA [Staphylococcus aureus subsp. aureus NCTC 8325]	43714	104	209	129	25		X
Q2FVV8	88196226	transcriptional regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	33783	105	72	117	25		
Q2FZ27	88194963	transcriptional repressor CodY [Staphylococcus aureus subsp. aureus NCTC 8325]	28737	1050	767	728	25	X	X
Q2FYT8	88195066	transketolase [Staphylococcus aureus subsp. aureus NCTC 8325]	68317		50	68	25	X	
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579	411	449	447	25	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G030	88194557	triosephosphate isomerase [Staphylococcus aureus subsp. aureus NCTC 8325]	27275	101	256	185	25	X	
Q2G2U6	88193841	two-component response regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	27175	142	124	26	25	X	X
Q2FZ22	88194968	uridylate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	26128	183	184	166	25	X	X
Q2FXJ7	88195537	1-acyl-sn-glycerol-3-phosphate acyltransferase domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	23059	87	76	34	26	X	
Q2G1C0	88194032	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	26640		158	73	26	X	
Q2G2C4	88194028	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	25198	80	69		26	X	
Q2FW12	88196156	30S ribosomal protein S3 [Staphylococcus aureus subsp. aureus NCTC 8325]	24085	295	360	322	26	X	X
Q2FXK6	88195529	30S ribosomal protein S4 [Staphylococcus aureus subsp. aureus NCTC 8325]	22999	179	271	225	26	X	X
Q2FW23	88196145	30S ribosomal protein S5 [Staphylococcus aureus subsp. aureus NCTC 8325]	17732	52		74	26	X	X
Q2FZ53	88194937	3-oxoacyl-(acyl-carrier-protein) reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	25870	579	401	318	26	X	X
Q2G0P0	88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	24693		123	135	26	X	X
P0A0F4	88194299	50S ribosomal protein L11 [Staphylococcus aureus subsp. aureus NCTC 8325]	14865	72	86	114	26	X	X
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	131	130	156	26	X	X
Q2FW18	88196150	50S ribosomal protein L5 [Staphylococcus aureus subsp. aureus NCTC 8325]	20254	482	367	386	26	X	X
Q2FW21	88196147	50S ribosomal protein L6 [Staphylococcus aureus subsp. aureus NCTC 8325]	19774	274	286	191	26	X	X
Q2FZY7	88194605	ABC transporter ATP-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	28257	86	95	91	26	X	
Q2G0V0	88194218	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	30437	60	95	88	26		
Q2G2D8	88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35049	148	214	240	26	X	
Q2FXV9	88195427	alanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	98459	53	38		26	X	X
Q2FW66	88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	19180	495	207	282	26	X	
P0A0B7	88194163	alkyl hydroperoxide reductase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	20963	339	388	372	26	X	
Q2FWY9	88195799	aspartyl/glutamyl-tRNA amidotransferase subunit A [Staphylococcus aureus subsp. aureus NCTC 8325]	52788	54	64		26	X	
Q2FWZ0	88195798	aspartyl/glutamyl-tRNA amidotransferase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	53623	146	68	174	26	X	
Q2G036	88194551	ATP-dependent Clp protease proteolytic subunit [Staphylococcus aureus subsp. aureus NCTC	21500	205	150	100	26	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
		8325]							
Q2G1F2	88193983	azoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	23338	292	301	264	26	X	
Q2G112	88194148	bacteriophage L54a single-stranded DNA binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	18528	41	63	69	26	X	X
Q2FZJ6	88194761	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30824	184	254	407	26	X	X
Q2FZI6	88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	54314	221		183	26	X	
Q2FZ77	88194904	bifunctional pyrimidine regulatory protein PyrR/uracil phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	19843	196	213	155	26	X	X
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	95	271	345	26	X	
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012	355	337	625	26	X	X
Q2FWN4	88195925	chaperonin GroEL [Staphylococcus aureus subsp. aureus NCTC 8325]	57629	169	99	119	26	X	
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451	172	102	124	26	X	
Q2FYM2	88195142	dihydrolipoamide succinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	46644		79	113	26	X	
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	34	82	86	26	X	X
Q2FX97	88195671	DNA-binding response regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	23880	182	137	195	26		X
Q2FX09	88195780	DNA-binding response regulator VraR [Staphylococcus aureus subsp. aureus NCTC 8325]	23530	386	97	262	26		X
Q2FW32	88196136	DNA-directed RNA polymerase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	34990		110	55	26	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190	298	140	128	26	X	
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564	37	110	145	26	X	X
Q2FY41	88195335	elongation factor P [Staphylococcus aureus subsp. aureus NCTC 8325]	20541	50	34	87	26		
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474	436	530	437	26	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	496	391	395	26	X	X
Q2G0P5	88194286	endopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	90981	113	109	161	26	X	X
Q2FWE7	88196010	F0F1 ATP synthase subunit delta [Staphylococcus aureus subsp. aureus NCTC 8325]	20486	476	210	565	26	X	
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819	65	117	237	26	X	X
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	246	312	305	26	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G0Q0	88194281	glutamine amidotransferase subunit PdxT [Staphylococcus aureus subsp. aureus NCTC 8325]	20617	97	75	98	26	X	
Q2FXP2	88195494	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	36956		81	150	26	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	238	210	343	26	X	
Q2FZZ8	88194594	glycine cleavage system protein H [Staphylococcus aureus subsp. aureus NCTC 8325]	14084	90	73		26	X	
Q2G0Y6	88194173	GMP synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	58194		43	48	26	X	X
Q2G260	88193909	hypothetical protein SAOUHSC_00094 [Staphylococcus aureus subsp. aureus NCTC 8325]	21834	46	111	81	26	X	
Q2G105	88194155	hypothetical protein SAOUHSC_00356 [Staphylococcus aureus subsp. aureus NCTC 8325]	21293	320	252	312	26	X	
Q2G0Z9	88194160	hypothetical protein SAOUHSC_00362 [Staphylococcus aureus subsp. aureus NCTC 8325]	23649	151	67	103	26		
Q2G0Z2	88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	35591		41	55	26	X	
Q2G0Q8	88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	32955	190	123	302	26	X	
Q2G0K7	88194332	hypothetical protein SAOUHSC_00553 [Staphylococcus aureus subsp. aureus NCTC 8325]	22422	173	166	190	26	X	
Q2FZZ0	88194602	hypothetical protein SAOUHSC_00844 [Staphylococcus aureus subsp. aureus NCTC 8325]	30332		86	131	26		
Q2G2G7	88194805	hypothetical protein SAOUHSC_01054 [Staphylococcus aureus subsp. aureus NCTC 8325]	24004	87	66	52	26	X	
Q2FZE9	88194829	hypothetical protein SAOUHSC_01081 [Staphylococcus aureus subsp. aureus NCTC 8325]	38722	117	75	55	26	X	
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310	33	46	42	26	X	
Q2FY39	88195337	hypothetical protein SAOUHSC_01627 [Staphylococcus aureus subsp. aureus NCTC 8325]	21459	71	61	80	26		
Q2FXZ9	88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	35160	296	170	332	26	X	
Q2FXW5	88195421	hypothetical protein SAOUHSC_01716 [Staphylococcus aureus subsp. aureus NCTC 8325]	47625	56		45	26	X	
Q2FXR7	88195469	hypothetical protein SAOUHSC_01768 [Staphylococcus aureus subsp. aureus NCTC 8325]	21403	65	96		26	X	
Q2FXL6	88195519	hypothetical protein SAOUHSC_01819 [Staphylococcus aureus subsp. aureus NCTC 8325]	18464	79	79	67	26	X	
Q2FXJ6	88195538	hypothetical protein SAOUHSC_01838 [Staphylococcus aureus subsp. aureus NCTC 8325]	45775	72	64	115	26	X	
Q2FX90	88195678	hypothetical protein SAOUHSC_01987 [Staphylococcus aureus subsp. aureus NCTC 8325]	22330	250	318	204	26	X	
Q2FWX1	88195830	hypothetical protein SAOUHSC_02150 [Staphylococcus aureus subsp. aureus NCTC 8325]	21902	845	373	416	26	X	
Q2FWX0	88195831	hypothetical protein SAOUHSC_02151 [Staphylococcus aureus subsp. aureus NCTC 8325]	28121	54	44	66	26	X	
Q2FWN0	88195929	hypothetical protein SAOUHSC_02258 [Staphylococcus aureus subsp. aureus NCTC 8325]	23989	342	236	221	26	X	
Q2FWB1	88196050	hypothetical protein SAOUHSC_02387 [Staphylococcus aureus subsp. aureus NCTC 8325]	24017	122	178	98	26	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FVL2	88196339	hypothetical protein SAOUHSC_02699 [Staphylococcus aureus subsp. aureus NCTC 8325]	28886		66	123	26	X	
Q2FVD5	88196414	hypothetical protein SAOUHSC_02778 [Staphylococcus aureus subsp. aureus NCTC 8325]	24589	145	132	166	26	X	X
Q2G2L6	88196446	hypothetical protein SAOUHSC_02812 [Staphylococcus aureus subsp. aureus NCTC 8325]	15982	127	76	256	26	X	
Q2G220	88196600	hypothetical protein SAOUHSC_02980 [Staphylococcus aureus subsp. aureus NCTC 8325]	20717	106	53		26	X	
Q2G0R1	88194270	hypoxanthine phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	20142	119	97	116	26	X	
Q9RQQ0	88196620	ica operon transcriptional regulator IcaR [Staphylococcus aureus subsp. aureus NCTC 8325]	21973	91	87	42	26		X
Q2FV52	88196515	immunodominant antigen A [Staphylococcus aureus subsp. aureus NCTC 8325]	24188	81	69		26	X	
Q2G0Y7	88194172	inosine-5~-monophosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	52818		91	81	26	X	X
Q2FV16	88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	55964		133	105	26	X	
Q2FXM0	88195515	metal-dependent hydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	25234	70	81	51	26	X	
P0A086	88195156	methionine sulfoxide reductase A [Staphylococcus aureus subsp. aureus NCTC 8325]	20575	125	92	168	26		
Q2FVX4	88196194	molybdenum ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	29033		52	121	26		
Q2FZC5	88194853	nucleoside-triphosphatase [Staphylococcus aureus subsp. aureus NCTC 8325]	21390	65	121		26	X	
Q2FZ70	88194911	orotate phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	22029	368	347	320	26	X	
Q2FZ71	88194910	orotidine 5~-phosphate decarboxylase [Staphylococcus aureus subsp. aureus NCTC 8325]	25580	93	94		26	X	
Q2FZG6	88194790	peptide deformylase [Staphylococcus aureus subsp. aureus NCTC 8325]	20547	379	225	275	26		
Q2G1W2	88195605	phosphoenolpyruvate carboxykinase [Staphylococcus aureus subsp. aureus NCTC 8325]	59340		54	45	26	X	X
Q2G031	88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	42575	95		68	26	X	X
Q2FVK8	88196343	phosphoglyceromutase [Staphylococcus aureus subsp. aureus NCTC 8325]	26663		114	101	26	X	
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088	122	150	195	26	X	
Q2FZJ3	88194764	phosphoribosylaminoimidazole-succinocarboxamide synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	26676		136	29	26	X	
Q2FZJ1	88194766	phosphoribosylformylglycinamidine synthase I [Staphylococcus aureus subsp. aureus NCTC 8325]	24511	218	154	112	26	X	
Q2FZI7	88194770	phosphoribosylglycinamide formyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	21138	69	48		26		
Q2G0J0	88194349	phosphotransacetylase [Staphylococcus aureus subsp. aureus NCTC 8325]	34930	45	96	65	26	X	
Q2G2S6	88195663	protein export protein PrsA [Staphylococcus aureus subsp. aureus NCTC 8325]	35616	97	220	196	26		

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FXE8	88195596	putative translaldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	25689	251	438	218	26	X	
Q2G0Q1	88194280	pyridoxal biosynthesis lyase PdxS [Staphylococcus aureus subsp. aureus NCTC 8325]	31972	73	109	233	26	X	
Q2FZG4	88194792	pyruvate dehydrogenase complex, E1 component subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	41357		76	98	26	X	
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224	312	216	195	26	X	
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	314	93	399	26	X	
Q2FZJ9	88194758	quinol oxidase AA3 subunit II [Staphylococcus aureus subsp. aureus NCTC 8325]	41750	22	42	46	26	X	
Q2FWL6	88195943	redox-sensing transcriptional repressor Rex [Staphylococcus aureus subsp. aureus NCTC 8325]	23584	75	132		26	X	X
Q2FZ21	88194969	ribosome recycling factor [Staphylococcus aureus subsp. aureus NCTC 8325]	20341	205	220	187	26	X	
Q2FZ36	88194954	succinyl-CoA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	31522		41	116	26	X	
P0A0J3	88195361	superoxide dismutase [Staphylococcus aureus subsp. aureus NCTC 8325]	22697	122	126	149	26	X	
Q2G261	88193908	superoxide dismutase [Staphylococcus aureus subsp. aureus NCTC 8325]	23026	56	81	85	26	X	
Q2G041	88194546	thioredoxin reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	33595		35	90	26	X	
Q2G0P2	88194298	transcription antitermination protein [Staphylococcus aureus subsp. aureus NCTC 8325]	20651	607	355	500	26	X	
Q2FZ27	88194963	transcriptional repressor CodY [Staphylococcus aureus subsp. aureus NCTC 8325]	28737	297	127	219	26	X	X
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579	253	114	292	26	X	
Q2G030	88194557	triosephosphate isomerase [Staphylococcus aureus subsp. aureus NCTC 8325]	27275		123	99	26	X	
Q2FWE6	88196016	uracil phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	23035	509	502	485	26	X	
Q2G0J7	88194342	uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus NCTC 8325]	24922	247	151	86	26	X	
Q2G0P7	88194284	UvrB/UvrC motif-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	18698	43	78		26		X
Q2G0Y9	88194170	xanthine phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	20871	210	158	135	26	X	
Q2FWF5	88196002	(3R)-hydroxymyristoyl-ACP dehydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	16071	82	135	57	27	X	
Q2FW31	88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	13873	112	110		27	X	X
P0A0H0	88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	15277		129	91	27	X	X
Q2FW30	88196138	30S ribosomal protein S13 [Staphylococcus aureus subsp. aureus NCTC 8325]	13711	85	116	100	27	X	X
Q2FW12	88196156	30S ribosomal protein S3 [Staphylococcus aureus subsp. aureus NCTC 8325]	24085		64	140	27	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FW23	88196145	30S ribosomal protein S5 [Staphylococcus aureus subsp. aureus NCTC 8325]	17732	431	501	371	27	X	X
P48940	88194308	30S ribosomal protein S7 [Staphylococcus aureus subsp. aureus NCTC 8325]	17783	102	433		27	X	X
Q2FW20	88196148	30S ribosomal protein S8 [Staphylococcus aureus subsp. aureus NCTC 8325]	14822	300	216	568	27	X	X
Q2G0P0	88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	24693	65	120	104	27	X	X
Q2G0N9	88194301	50S ribosomal protein L10 [Staphylococcus aureus subsp. aureus NCTC 8325]	17699	679	412	203	27	X	X
P0A0F4	88194299	50S ribosomal protein L11 [Staphylococcus aureus subsp. aureus NCTC 8325]	14865	918	686	401	27	X	X
Q2FW38	88196130	50S ribosomal protein L13 [Staphylococcus aureus subsp. aureus NCTC 8325]	16323	254	246	148	27	X	
P0A0F8	88196143	50S ribosomal protein L15 [Staphylococcus aureus subsp. aureus NCTC 8325]	15587	205		42	27	X	X
Q2FW13	88196155	50S ribosomal protein L16 [Staphylococcus aureus subsp. aureus NCTC 8325]	16232	91	143	102	27	X	X
Q2FW33	88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	13739	162	172	55	27	X	
Q2FZ42	88194948	50S ribosomal protein L19 [Staphylococcus aureus subsp. aureus NCTC 8325]	13354	111	141	73	27	X	
Q2FXQ1	88195485	50S ribosomal protein L20 [Staphylococcus aureus subsp. aureus NCTC 8325]	13678	98	95		27	X	X
Q2FXS8	88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	11326	166	138	130	27	X	X
Q2FW11	88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	12827		146	62	27	X	X
Q2FW17	88196151	50S ribosomal protein L24 [Staphylococcus aureus subsp. aureus NCTC 8325]	11529	65	67	71	27		X
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	326	274	165	27	X	X
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	52	43	50	27	X	X
Q2FWD8	88196024	50S ribosomal protein L31 type B [Staphylococcus aureus subsp. aureus NCTC 8325]	9717	66	65	42	27	X	
Q2FW18	88196150	50S ribosomal protein L5 [Staphylococcus aureus subsp. aureus NCTC 8325]	20254	66	86	30	27	X	X
P48860	88194302	50S ribosomal protein L7/L12 [Staphylococcus aureus subsp. aureus NCTC 8325]	12704		122	70	27	X	
Q2FXG2	88195582	6,7-dimethyl-8-ribityllumazine synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	16386	140	287	128	27	X	
Q2FY60	88195316	6-phosphogluconate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	51770	35	148	46	27	X	X
Q2G0V0	88194218	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	30437	56	68	84	27		
Q2G2D8	88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35049	347	481	345	27	X	
Q2G2U9	88194390	accessory regulator A [Staphylococcus aureus subsp. aureus NCTC 8325]	14709	86	91	163	27	X	X
Q2FZ51	88194939	acyl carrier protein [Staphylococcus aureus subsp. aureus NCTC 8325]	8544	44	45		27	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FXV9	88195427	alanyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	98459	54	65		27	X	X
Q2FXN6	88195500	alkaline phosphatase synthesis transcriptional regulatory protein [Staphylococcus aureus subsp. aureus NCTC 8325]	27105	37	39		27	X	X
Q2FW66	88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	19180	406	554	281	27	X	
P0A0B7	88194163	alkyl hydroperoxide reductase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	20963	145	330	152	27	X	
Q2FZI9	88194768	amidophosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	54363	132	55		27	X	
Q2FY49	88195327	arginine repressor [Staphylococcus aureus subsp. aureus NCTC 8325]	17087	219	170		27	X	X
Q2FWZ0	88195798	aspartyl/glutamyl-tRNA amidotransferase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	53623		156	84	27	X	
Q2G036	88194551	ATP-dependent Clp protease proteolytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	21500	96	52		27	X	
Q2FZ29	88194961	ATP-dependent protease peptidase subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	19560	147	170		27	X	
Q2G1F2	88193983	azoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	23338		57	55	27	X	
Q2FZJ6	88194761	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30824	280	362	386	27	X	X
Q2FZI6	88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	54314		226	132	27	X	
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326	57	233	124	27	X	
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012	518	752	526	27	X	X
Q2FWN4	88195925	chaperonin GroEL [Staphylococcus aureus subsp. aureus NCTC 8325]	57629	333	397	115	27	X	
Q2FYK6	88195158	dihydrofolate reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	18239	203	118	146	27	X	
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451		324	67	27	X	
Q2FZ74	88194907	dihydroorotase [Staphylococcus aureus subsp. aureus NCTC 8325]	46342	71	208	72	27	X	
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	98	110	99	27	X	X
Q2FY79	88195297	DNA-binding response regulator [Staphylococcus aureus subsp. aureus NCTC 8325]	28143		46	74	27	X	X
Q2FW32	88196136	DNA-directed RNA polymerase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	34990		102	63	27	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190	94	111		27	X	
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564	62	344	211	27	X	X
Q2FY41	88195335	elongation factor P [Staphylococcus aureus subsp. aureus NCTC 8325]	20541	110	103	54	27		

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474	394	423	461	27	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	408	722	509	27	X	X
Q2G0P5	88194286	endopeptidase [Staphylococcus aureus subsp. aureus NCTC 8325]	90981	129	171	156	27	X	X
Q2G2F8	88196011	F0F1 ATP synthase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	19527	109	99	115	27	X	
Q2FWE7	88196010	F0F1 ATP synthase subunit delta [Staphylococcus aureus subsp. aureus NCTC 8325]	20486	471	423	218	27	X	
Q2G282	88195685	ferric uptake regulator-like protein [Staphylococcus aureus subsp. aureus NCTC 8325]	17172	110	156	79	27		X
Q2FWZ8	88195790	ferritin [Staphylococcus aureus subsp. aureus NCTC 8325]	19576	346	415	243	27	X	
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819		93	124	27	X	X
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	290	430	340	27	X	
Q2G2R0	88196106	galactose-6-phosphate isomerase subunit LacB [Staphylococcus aureus subsp. aureus NCTC 8325]	18939	126	121		27	X	
Q2FYY6	88195018	glutamine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	50808		21	26	27	X	
Q2FYZ0	88195014	glutathione peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	18106	126	124		27	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	373	423	416	27	X	
Q2G260	88193909	hypothetical protein SAOUHSC_00094 [Staphylococcus aureus subsp. aureus NCTC 8325]	21834	44	49	49	27	X	
Q2G193	88194059	hypothetical protein SAOUHSC_00253 [Staphylococcus aureus subsp. aureus NCTC 8325]	57887		61	41	27		
Q2G105	88194155	hypothetical protein SAOUHSC_00356 [Staphylococcus aureus subsp. aureus NCTC 8325]	21293	251	279	222	27	X	
Q2G0Z9	88194160	hypothetical protein SAOUHSC_00362 [Staphylococcus aureus subsp. aureus NCTC 8325]	23649	58	55		27		
Q2G0Z2	88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	35591	45	152	62	27	X	
Q2G0T4	88194234	hypothetical protein SAOUHSC_00444 [Staphylococcus aureus subsp. aureus NCTC 8325]	11590	181	140	103	27	X	X
Q2G0R0	88194271	hypothetical protein SAOUHSC_00486 [Staphylococcus aureus subsp. aureus NCTC 8325]	77764	76	106		27	X	X
Q2G0Q8	88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	32955	271	283	190	27	X	
Q2G0I3	88194356	hypothetical protein SAOUHSC_00582 [Staphylococcus aureus subsp. aureus NCTC 8325]	15788	104	70	57	27	X	
Q2G0G2	88194377	hypothetical protein SAOUHSC_00607 [Staphylococcus aureus subsp. aureus NCTC 8325]	19567	82	64		27		
Q2G0B1	88194459	hypothetical protein SAOUHSC_00694 [Staphylococcus aureus subsp. aureus NCTC 8325]	17079	247	197	179	27	X	X
Q2G2G0	88194482	hypothetical protein SAOUHSC_00717 [Staphylococcus aureus subsp. aureus NCTC 8325]	16035	238	199	197	27	X	
Q2G074	88194511	hypothetical protein SAOUHSC_00746 [Staphylococcus aureus subsp. aureus NCTC 8325]	35559	55		43	27		

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G055	88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	22199	97	178	98	27	X	
Q2G1T3	88194589	hypothetical protein SAOUHSC_00831 [Staphylococcus aureus subsp. aureus NCTC 8325]	15330		51	84	27	X	
Q2FZZ0	88194602	hypothetical protein SAOUHSC_00844 [Staphylococcus aureus subsp. aureus NCTC 8325]	30332	50		98	27		
Q2FZX3	88194619	hypothetical protein SAOUHSC_00862 [Staphylococcus aureus subsp. aureus NCTC 8325]	15392	97	54	53	27		
Q2FZV7	88194635	hypothetical protein SAOUHSC_00878 [Staphylococcus aureus subsp. aureus NCTC 8325]	44077	113	184		27	X	
Q2FZP9	88194708	hypothetical protein SAOUHSC_00951 [Staphylococcus aureus subsp. aureus NCTC 8325]	19314	24	142		27	X	
Q2FZH7	88194780	hypothetical protein SAOUHSC_01027 [Staphylococcus aureus subsp. aureus NCTC 8325]	20077	62	64		27	X	
Q2FZG5	88194791	hypothetical protein SAOUHSC_01039 [Staphylococcus aureus subsp. aureus NCTC 8325]	23861	107	80	102	27	X	
Q2FZE9	88194829	hypothetical protein SAOUHSC_01081 [Staphylococcus aureus subsp. aureus NCTC 8325]	38722	119	137	137	27	X	
Q2FZA1	88194880	hypothetical protein SAOUHSC_01138 [Staphylococcus aureus subsp. aureus NCTC 8325]	16991	95	137		27	X	
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310	44	38	42	27	X	
Q2FY55	88195321	hypothetical protein SAOUHSC_01610 [Staphylococcus aureus subsp. aureus NCTC 8325]	16211	35	122		27	X	
Q2FXZ9	88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	35160	213	460	200	27	X	
Q2G2A1	88195398	hypothetical protein SAOUHSC_01692 [Staphylococcus aureus subsp. aureus NCTC 8325]	15753	58	71		27		
Q2FXW5	88195421	hypothetical protein SAOUHSC_01716 [Staphylococcus aureus subsp. aureus NCTC 8325]	47625	45	42		27	X	
Q2FXM1	88195514	hypothetical protein SAOUHSC_01814 [Staphylococcus aureus subsp. aureus NCTC 8325]	15216	111	187	149	27	X	
Q2FXL6	88195519	hypothetical protein SAOUHSC_01819 [Staphylococcus aureus subsp. aureus NCTC 8325]	18464	638	840	198	27	X	
Q2FXJ6	88195538	hypothetical protein SAOUHSC_01838 [Staphylococcus aureus subsp. aureus NCTC 8325]	45775	249	224	273	27	X	
Q2G247	88195553	hypothetical protein SAOUHSC_01855 [Staphylococcus aureus subsp. aureus NCTC 8325]	17991	542	707	407	27	X	
Q2FXI9	88195555	hypothetical protein SAOUHSC_01857 [Staphylococcus aureus subsp. aureus NCTC 8325]	144568	43		42	27	X	X
Q2FXH8	88195566	hypothetical protein SAOUHSC_01869 [Staphylococcus aureus subsp. aureus NCTC 8325]	15724	533	545	332	27	X	
Q2G2Y3	88195614	hypothetical protein SAOUHSC_01919 [Staphylococcus aureus subsp. aureus NCTC 8325]	35842	38	87		27		
Q2G2F3	88195657	hypothetical protein SAOUHSC_01964 [Staphylococcus aureus subsp. aureus NCTC 8325]	19536		136	86	27	X	
Q2G2T0	88195661	hypothetical protein SAOUHSC_01969 [Staphylococcus aureus subsp. aureus NCTC 8325]	13204	58	31	75	27	X	
Q2FX89	88195679	hypothetical protein SAOUHSC_01988 [Staphylococcus aureus subsp. aureus NCTC 8325]	18099	177	163		27		X
Q2G280	88195687	hypothetical protein SAOUHSC_01999 [Staphylococcus aureus subsp. aureus NCTC 8325]	17249	342	266	135	27	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FWX1	88195830	hypothetical protein SAOUHSC_02150 [Staphylococcus aureus subsp. aureus NCTC 8325]	21902	206	227	42	27	X	
Q2FWB7	88196044	hypothetical protein SAOUHSC_02381 [Staphylococcus aureus subsp. aureus NCTC 8325]	16681	191	192	147	27	X	
Q2FW79	88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	10000	98	103	100	27	X	
Q2FW65	88196095	hypothetical protein SAOUHSC_02442 [Staphylococcus aureus subsp. aureus NCTC 8325]	9217	96	93	108	27		
Q2FW64	88196096	hypothetical protein SAOUHSC_02443 [Staphylococcus aureus subsp. aureus NCTC 8325]	20787	94	116	72	27	X	
Q2FVW9	88196199	hypothetical protein SAOUHSC_02554 [Staphylococcus aureus subsp. aureus NCTC 8325]	33990		100	32	27		
Q2FVW0	88196224	hypothetical protein SAOUHSC_02581 [Staphylococcus aureus subsp. aureus NCTC 8325]	17467	120	188	61	27		
Q2FVU2	88196242	hypothetical protein SAOUHSC_02600 [Staphylococcus aureus subsp. aureus NCTC 8325]	20070	150	103		27	X	
Q2FVN6	88196306	hypothetical protein SAOUHSC_02666 [Staphylococcus aureus subsp. aureus NCTC 8325]	13331	39	65	69	27	X	
Q2FVN3	88196309	hypothetical protein SAOUHSC_02669 [Staphylococcus aureus subsp. aureus NCTC 8325]	17424	38	57		27		X
Q2G1U9	88196329	hypothetical protein SAOUHSC_02689 [Staphylococcus aureus subsp. aureus NCTC 8325]	17408	174	111		27	X	
Q2FVL2	88196339	hypothetical protein SAOUHSC_02699 [Staphylococcus aureus subsp. aureus NCTC 8325]	28886	92	164	171	27	X	
Q2FVF5	88196395	hypothetical protein SAOUHSC_02759 [Staphylococcus aureus subsp. aureus NCTC 8325]	17300	228	213	279	27		
Q2G2L6	88196446	hypothetical protein SAOUHSC_02812 [Staphylococcus aureus subsp. aureus NCTC 8325]	15982	255	253	79	27	X	
Q2FV88	88196479	hypothetical protein SAOUHSC_02846 [Staphylococcus aureus subsp. aureus NCTC 8325]	15435		37	53	27		
Q2FUS9	88196640	hypothetical protein SAOUHSC_03022 [Staphylococcus aureus subsp. aureus NCTC 8325]	18643	158	196	47	27	X	
Q2FUX3	88196593	immunodominant antigen B [Staphylococcus aureus subsp. aureus NCTC 8325]	19358	198	171		27	X	
Q2G0Y7	88194172	inosine-5~-monophosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	52818		37	92	27	X	X
Q2FXN4	88195501	isocitrate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	46394	29	54	40	27	X	
Q2FWA8	88196053	lytic regulatory protein [Staphylococcus aureus subsp. aureus NCTC 8325]	40640	94	94	150	27	X	
Q2FV16	88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	55964	151	193	122	27	X	
P0A086	88195156	methionine sulfoxide reductase A [Staphylococcus aureus subsp. aureus NCTC 8325]	20575	91	68	55	27		
Q2G1R9	88194248	methionyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74838	99	100	99	27	X	X
Q2FXZ2	88195389	molecular chaperone DnaK [Staphylococcus aureus subsp. aureus NCTC 8325]	66321	77	84	117	27	X	
Q2FVX4	88196194	molybdenum ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	29033		154	73	27		
Q2FVX9	88196189	molybdenum cofactor biosynthesis protein MoaC [Staphylococcus aureus subsp. aureus NCTC	17683	175	157		27		

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
		8325]							
Q2FVX8	88196190	molybdopterin precursor biosynthesis MoaB [Staphylococcus aureus subsp. aureus NCTC 8325]	18489	301	195	107	27	X	
Q2FWL3	88195946	MutS domain-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	61283	43		44	27	X	
Q2G135	88194121	NADPH-dependent FMN reductase [Staphylococcus aureus subsp. aureus NCTC 8325]	21301	81	122		27	X	
Q2FZG6	88194790	peptide deformylase [Staphylococcus aureus subsp. aureus NCTC 8325]	20547	132	84		27		
Q2FZD9	88194839	phenylalanyl-tRNA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	40081		110	73	27	X	X
Q2G031	88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	42575	201	154	157	27	X	X
Q2FVK8	88196343	phosphoglyceromutase [Staphylococcus aureus subsp. aureus NCTC 8325]	26663	60	98		27	X	
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088	137	368	100	27	X	
Q2FZI5	88194772	phosphoribosylamine--glycine ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	45820	35	170		27	X	X
Q2FZJ5	88194762	phosphoribosylaminoimidazole carboxylase catalytic subunit [Staphylococcus aureus subsp. aureus NCTC 8325]	14733	168	241	162	27	X	
Q2G2S6	88195663	protein export protein PrsA [Staphylococcus aureus subsp. aureus NCTC 8325]	35616	168	352	419	27		
Q2FYL0	88195154	PTS system transporter subunit IIA [Staphylococcus aureus subsp. aureus NCTC 8325]	17949	82	88	53	27	X	
Q2FXE8	88195596	putative translaldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	25689	110	249	103	27	X	
Q2G0Q1	88194280	pyridoxal biosynthesis lyase PdxS [Staphylococcus aureus subsp. aureus NCTC 8325]	31972	57	271	71	27	X	
Q2FZG4	88194792	pyruvate dehydrogenase complex, E1 component subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	41357	46	131	89	27	X	
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224	41	351	131	27	X	
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	126	381	231	27	X	
Q2FZJ9	88194758	quinol oxidase AA3 subunit II [Staphylococcus aureus subsp. aureus NCTC 8325]	41750	105	221	126	27	X	
Q2G0S2	88194259	ribose-phosphate pyrophosphokinase [Staphylococcus aureus subsp. aureus NCTC 8325]	35262	67	119		27	X	
Q2FZ21	88194969	ribosome recycling factor [Staphylococcus aureus subsp. aureus NCTC 8325]	20341	113	106	165	27	X	
Q2G2Q4	88194980	ribosome-binding factor A [Staphylococcus aureus subsp. aureus NCTC 8325]	13506	97	55	107	27		
Q2FXK8	88195527	septation ring formation regulator EzrA [Staphylococcus aureus subsp. aureus NCTC 8325]	66206		70	209	27	X	
Q2FWJ3	88195965	serine-protein kinase RsbW [Staphylococcus aureus subsp. aureus NCTC 8325]	19170	158	223	58	27	X	
Q2FZT7	88194660	signal peptidase IB [Staphylococcus aureus subsp. aureus NCTC 8325]	17587	112	72	84	27	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FWC3	88196038	S-ribosylhomocysteinase [Staphylococcus aureus subsp. aureus NCTC 8325]	17502		116	26	27	X	
Q2FZ36	88194954	succinyl-CoA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	31522	152	109	76	27	X	
Q2FZ37	88194953	succinyl-CoA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	42030	66	79	79	27	X	X
Q2FXL3	88195522	thiol peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	17994	166	309	240	27	X	
Q2G0P2	88194298	transcription antitermination protein [Staphylococcus aureus subsp. aureus NCTC 8325]	20651	445	532	148	27	X	
Q2G2D2	88194976	transcription elongation factor NusA [Staphylococcus aureus subsp. aureus NCTC 8325]	43714		28	91	27		X
Q2FY73	88195303	transcriptional regulator Fur [Staphylococcus aureus subsp. aureus NCTC 8325]	17233	463	447	323	27		X
Q2FZ27	88194963	transcriptional repressor CodY [Staphylococcus aureus subsp. aureus NCTC 8325]	28737	170	86	118	27	X	X
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579	259	432	204	27	X	
Q2FWE6	88196016	uracil phosphoribosyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	23035	53	182	185	27	X	
Q2G2K6	88196204	urease subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	15155	27	48		27		
Q2G0P7	88194284	UvrB/UvrC motif-containing protein [Staphylococcus aureus subsp. aureus NCTC 8325]	18698	150	105	51	27		X
#N/A	542123276	30S ribosomal protein S10 [Staphylococcus aureus subsp. aureus NCTC 8325]	11569	168	190	108	28	X	X^
Q2FW31	88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	13873		150	135	28	X	X
P0A0H0	88194307	30S ribosomal protein S12 [Staphylococcus aureus subsp. aureus NCTC 8325]	15277		45	50	28	X	X
Q2FW30	88196138	30S ribosomal protein S13 [Staphylococcus aureus subsp. aureus NCTC 8325]	13711		90	32	28	X	X
Q2FZ45	88194945	30S ribosomal protein S16 [Staphylococcus aureus subsp. aureus NCTC 8325]	10229	94	128	81	28	X	
Q2FW15	88196153	30S ribosomal protein S17 [Staphylococcus aureus subsp. aureus NCTC 8325]	10169	154	106	112	28	X	X
Q2G111	88194149	30S ribosomal protein S18 [Staphylococcus aureus subsp. aureus NCTC 8325]	9304	39	70	81	28	X	X
Q2FW10	88196158	30S ribosomal protein S19 [Staphylococcus aureus subsp. aureus NCTC 8325]	10609	58	47	83	28	X	X
Q2FXY6	88195395	30S ribosomal protein S20 [Staphylococcus aureus subsp. aureus NCTC 8325]	9016		68	75	28	X	X
Q2FW12	88196156	30S ribosomal protein S3 [Staphylococcus aureus subsp. aureus NCTC 8325]	24085	111	128	196	28	X	X
Q2FW23	88196145	30S ribosomal protein S5 [Staphylococcus aureus subsp. aureus NCTC 8325]	17732	145	190	216	28	X	X
Q2G113	88194147	30S ribosomal protein S6 [Staphylococcus aureus subsp. aureus NCTC 8325]	11588	149	151	113	28	X	X
P48940	88194308	30S ribosomal protein S7 [Staphylococcus aureus subsp. aureus NCTC 8325]	17783	65	109		28	X	X
Q2FW20	88196148	30S ribosomal protein S8 [Staphylococcus aureus subsp. aureus NCTC 8325]	14822	915	969	214	28	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FW39	88196129	30S ribosomal protein S9 [Staphylococcus aureus subsp. aureus NCTC 8325]	14821		101	89	28	X	
Q2G0P0	88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	24693	134	115	123	28	X	X
Q2G0N9	88194301	50S ribosomal protein L10 [Staphylococcus aureus subsp. aureus NCTC 8325]	17699	243	231	87	28	X	X
P0A0F4	88194299	50S ribosomal protein L11 [Staphylococcus aureus subsp. aureus NCTC 8325]	14865	189	259	181	28	X	X
Q2FW38	88196130	50S ribosomal protein L13 [Staphylococcus aureus subsp. aureus NCTC 8325]	16323	76	64	38	28	X	
Q2FW16	88196152	50S ribosomal protein L14 [Staphylococcus aureus subsp. aureus NCTC 8325]	13127	55	49	36	28	X	X
Q2FW33	88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	13739	179	182	87	28	X	
Q2FW22	88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	13089	96	115	57	28	X	X
Q2FXS8	88195458	50S ribosomal protein L21 [Staphylococcus aureus subsp. aureus NCTC 8325]	11326	173	155		28	X	X
Q2FW11	88196157	50S ribosomal protein L22 [Staphylococcus aureus subsp. aureus NCTC 8325]	12827	88	112	62	28	X	X
Q2FW08	88196160	50S ribosomal protein L23 [Staphylococcus aureus subsp. aureus NCTC 8325]	10599		143	39	28	X	X
Q2FW17	88196151	50S ribosomal protein L24 [Staphylococcus aureus subsp. aureus NCTC 8325]	11529	47	46	47	28		X
Q2G0S0	88194261	50S ribosomal protein L25/general stress protein Ctc [Staphylococcus aureus subsp. aureus NCTC 8325]	23773	109	204	98	28	X	X
Q2FXT0	88195456	50S ribosomal protein L27 [Staphylococcus aureus subsp. aureus NCTC 8325]	10308	85	68	85	28	X	
Q2FZ60	88194930	50S ribosomal protein L28 [Staphylococcus aureus subsp. aureus NCTC 8325]	6973	33		35	28	X	
Q2FW14	88196154	50S ribosomal protein L29 [Staphylococcus aureus subsp. aureus NCTC 8325]	8085	132	218	136	28	X	
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	91	111	104	28	X	X
P0A0G2	88196144	50S ribosomal protein L30 [Staphylococcus aureus subsp. aureus NCTC 8325]	6550	245	190	348	28	X	
Q2FWD8	88196024	50S ribosomal protein L31 type B [Staphylococcus aureus subsp. aureus NCTC 8325]	9717	738	526	307	28	X	
Q2FW18	88196150	50S ribosomal protein L5 [Staphylococcus aureus subsp. aureus NCTC 8325]	20254	57	163	156	28	X	X
Q2FW21	88196147	50S ribosomal protein L6 [Staphylococcus aureus subsp. aureus NCTC 8325]	19774	123	157	117	28	X	X
P48860	88194302	50S ribosomal protein L7/L12 [Staphylococcus aureus subsp. aureus NCTC 8325]	12704	486	418	113	28	X	
Q2G2T3	88193838	50S ribosomal protein L9 [Staphylococcus aureus subsp. aureus NCTC 8325]	16629	126	155	60	28	X	X
Q2FY60	88195316	6-phosphogluconate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	51770	42	88	74	28	X	X
Q2FW75	88196085	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	36569		29	41	28		
Q2G0V0	88194218	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	30437	66	151	124	28		

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G2D8	88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35049	401	454	314	28	X	
Q2G2U9	88194390	accessory regulator A [Staphylococcus aureus subsp. aureus NCTC 8325]	14709	190	216	108	28	X	X
Q2FXN6	88195500	alkaline phosphatase synthesis transcriptional regulatory protein [Staphylococcus aureus subsp. aureus NCTC 8325]	27105	50	50		28	X	X
Q2FW66	88196094	alkaline shock protein 23 [Staphylococcus aureus subsp. aureus NCTC 8325]	19180	140	171	79	28	X	
P0A0B7	88194163	alkyl hydroperoxide reductase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	20963	163	184	119	28	X	
Q2FWZ0	88195798	aspartyl/glutamyl-tRNA amidotransferase subunit B [Staphylococcus aureus subsp. aureus NCTC 8325]	53623	118	144	119	28	X	
Q2FZJ6	88194761	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30824	302	400	156	28	X	X
Q2FZI6	88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	54314	114	242	158	28	X	
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326		147	102	28	X	
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012	253	390	344	28	X	X
Q2FXZ3	88195388	chaperone protein DnaJ [Staphylococcus aureus subsp. aureus NCTC 8325]	41735	56	36		28		
Q2FWN4	88195925	chaperonin GroEL [Staphylococcus aureus subsp. aureus NCTC 8325]	57629	147	225	123	28	X	
Q2G2A3	88194795	dihydrolipoamide dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	49451	197	389	138	28	X	
Q2G1Z8	88194974	DNA polymerase III PolC [Staphylococcus aureus subsp. aureus NCTC 8325]	162357	35	32		28	X	X
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	166	477	367	28	X	X
Q2FW32	88196136	DNA-directed RNA polymerase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	34990	213	209		28	X	X
Q2FYF1	88195217	elastin binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	53190	68	95		28	X	
Q2G0N1	88194309	elongation factor G [Staphylococcus aureus subsp. aureus NCTC 8325]	76564	140	223	175	28	X	X
Q2FY41	88195335	elongation factor P [Staphylococcus aureus subsp. aureus NCTC 8325]	20541	105	136	104	28		
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474	258	571	323	28	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	373	475	390	28	X	X
Q2FWF1	88196006	F0F1 ATP synthase subunit epsilon [Staphylococcus aureus subsp. aureus NCTC 8325]	14835	126	179	51	28		
Q2FWZ8	88195790	ferritin [Staphylococcus aureus subsp. aureus NCTC 8325]	19576	97	172	80	28	X	
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819	123	145	188	28	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G239	88194473	fructose specific permease [Staphylococcus aureus subsp. aureus NCTC 8325]	68670	43	56		28	X	
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	399	475	339	28	X	
Q2FXP2	88195494	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	36956		143	111	28	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	207	406	287	28	X	
Q2FY08	88195373	glycyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	53586	93	96	83	28	X	X
Q2FXW1	88195425	Holliday junction resolvase-like protein [Staphylococcus aureus subsp. aureus NCTC 8325]	15855	153	155	119	28		
Q2G1I2	88193953	hypothetical protein SAOUHSC_00141 [Staphylococcus aureus subsp. aureus NCTC 8325]	13971	114	102		28	X	
Q2G105	88194155	hypothetical protein SAOUHSC_00356 [Staphylococcus aureus subsp. aureus NCTC 8325]	21293	49	75	70	28	X	
Q2G0Z2	88194167	hypothetical protein SAOUHSC_00369 [Staphylococcus aureus subsp. aureus NCTC 8325]	35591	110	188	123	28	X	
Q2G0T4	88194234	hypothetical protein SAOUHSC_00444 [Staphylococcus aureus subsp. aureus NCTC 8325]	11590	435	392	206	28	X	X
Q2G0R3	88194268	hypothetical protein SAOUHSC_00483 [Staphylococcus aureus subsp. aureus NCTC 8325]	14803	52	75		28		X
Q2G0R0	88194271	hypothetical protein SAOUHSC_00486 [Staphylococcus aureus subsp. aureus NCTC 8325]	77764	73	159	53	28	X	X
Q2G0Q8	88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	32955	212	253	203	28	X	
Q2G0K7	88194332	hypothetical protein SAOUHSC_00553 [Staphylococcus aureus subsp. aureus NCTC 8325]	22422		107	38	28	X	
Q2G0B5	88194455	hypothetical protein SAOUHSC_00690 [Staphylococcus aureus subsp. aureus NCTC 8325]	26671		97	82	28	X	
Q2G2G0	88194482	hypothetical protein SAOUHSC_00717 [Staphylococcus aureus subsp. aureus NCTC 8325]	16035	107	122	142	28	X	
Q2G055	88194530	hypothetical protein SAOUHSC_00767 [Staphylococcus aureus subsp. aureus NCTC 8325]	22199	114	78	49	28	X	
Q2FZZ9	88194593	hypothetical protein SAOUHSC_00835 [Staphylococcus aureus subsp. aureus NCTC 8325]	13591	76	90	66	28	X	
Q2FZZ3	88194599	hypothetical protein SAOUHSC_00841 [Staphylococcus aureus subsp. aureus NCTC 8325]	11447	94	81		28		
Q2FZV8	88194634	hypothetical protein SAOUHSC_00877 [Staphylococcus aureus subsp. aureus NCTC 8325]	12477	145	195	127	28		
Q2FZV7	88194635	hypothetical protein SAOUHSC_00878 [Staphylococcus aureus subsp. aureus NCTC 8325]	44077	152	168	83	28	X	
Q2FZG5	88194791	hypothetical protein SAOUHSC_01039 [Staphylococcus aureus subsp. aureus NCTC 8325]	23861	88	103	98	28	X	
Q2FZD6	88194842	hypothetical protein SAOUHSC_01096 [Staphylococcus aureus subsp. aureus NCTC 8325]	9639	113		74	28		
Q2FZ85	88194896	hypothetical protein SAOUHSC_01155 [Staphylococcus aureus subsp. aureus NCTC 8325]	11244		54	64	28		
Q2FZ69	88194912	hypothetical protein SAOUHSC_01173 [Staphylococcus aureus subsp. aureus NCTC 8325]	8102	54	52	53	28		
Q2FZ59	88194931	hypothetical protein SAOUHSC_01192 [Staphylococcus aureus subsp. aureus NCTC 8325]	13377	313	265	145	28	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G2C9	88194978	hypothetical protein SAOUHSC_01245 [Staphylococcus aureus subsp. aureus NCTC 8325]	11530	249	147	79	28	X	
Q2FYV0	88195054	hypothetical protein SAOUHSC_01324 [Staphylococcus aureus subsp. aureus NCTC 8325]	12276	70	60	62	28		
Q2FYT9	88195065	hypothetical protein SAOUHSC_01336 [Staphylococcus aureus subsp. aureus NCTC 8325]	9198	160	132	108	28		
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310	54	46	36	28	X	
Q2FYI5	88195179	hypothetical protein SAOUHSC_01462 [Staphylococcus aureus subsp. aureus NCTC 8325]	13143	258	347	237	28	X	
Q2FYH9	88195185	hypothetical protein SAOUHSC_01468 [Staphylococcus aureus subsp. aureus NCTC 8325]	13663	131	76	51	28		
Q2G257	88195194	hypothetical protein SAOUHSC_01477 [Staphylococcus aureus subsp. aureus NCTC 8325]	24566		170	41	28	X	
Q2FY44	88195332	hypothetical protein SAOUHSC_01622 [Staphylococcus aureus subsp. aureus NCTC 8325]	13265	157	110	76	28	X	
Q2FY28	88195353	hypothetical protein SAOUHSC_01645 [Staphylococcus aureus subsp. aureus NCTC 8325]	12274	58	68		28		
Q2FXZ9	88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	35160	405	418	157	28	X	
Q2FXZ8	88195383	hypothetical protein SAOUHSC_01677 [Staphylococcus aureus subsp. aureus NCTC 8325]	24987	90	116	83	28		
Q2FXM1	88195514	hypothetical protein SAOUHSC_01814 [Staphylococcus aureus subsp. aureus NCTC 8325]	15216	191	196	178	28	X	
Q2FXL6	88195519	hypothetical protein SAOUHSC_01819 [Staphylococcus aureus subsp. aureus NCTC 8325]	18464	127	234	79	28	X	
Q2FXJ6	88195538	hypothetical protein SAOUHSC_01838 [Staphylococcus aureus subsp. aureus NCTC 8325]	45775	71	110		28	X	
Q2G247	88195553	hypothetical protein SAOUHSC_01855 [Staphylococcus aureus subsp. aureus NCTC 8325]	17991	572	580	348	28	X	
Q2FXH8	88195566	hypothetical protein SAOUHSC_01869 [Staphylococcus aureus subsp. aureus NCTC 8325]	15724	59	141	72	28	X	
Q2G2T0	88195661	hypothetical protein SAOUHSC_01969 [Staphylococcus aureus subsp. aureus NCTC 8325]	13204	158	157		28	X	
Q2G2H0	88195698	hypothetical protein SAOUHSC_02010 [Staphylococcus aureus subsp. aureus NCTC 8325]	11324	109	97	148	28		
Q2FX11	88195778	hypothetical protein SAOUHSC_02096 [Staphylococcus aureus subsp. aureus NCTC 8325]	10316	62		49	28	X	
Q2FWX6	88195825	hypothetical protein SAOUHSC_02145 [Staphylococcus aureus subsp. aureus NCTC 8325]	6560	36	40	32	28		
Q2FWI8	88195969	hypothetical protein SAOUHSC_02303 [Staphylococcus aureus subsp. aureus NCTC 8325]	13433	42	58		28		X
Q2FWD5	88196027	hypothetical protein SAOUHSC_02364 [Staphylococcus aureus subsp. aureus NCTC 8325]	12678	44	49		28		
Q2FW79	88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	10000	284	215	168	28	X	
Q2FW64	88196096	hypothetical protein SAOUHSC_02443 [Staphylococcus aureus subsp. aureus NCTC 8325]	20787	99	166	153	28	X	
Q2FVY9	88196179	hypothetical protein SAOUHSC_02532 [Staphylococcus aureus subsp. aureus NCTC 8325]	13978	79	90	58	28	X	X
Q2FVW9	88196199	hypothetical protein SAOUHSC_02554 [Staphylococcus aureus subsp. aureus NCTC 8325]	33990	93	90	82	28		

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q9F0R1	88196210	hypothetical protein SAOUHSC_02566 [Staphylococcus aureus subsp. aureus NCTC 8325]	13660	70	68	78	28	X	X
Q2G2W6	88196267	hypothetical protein SAOUHSC_02626 [Staphylococcus aureus subsp. aureus NCTC 8325]	16296	94	88		28		
Q2FVN6	88196306	hypothetical protein SAOUHSC_02666 [Staphylococcus aureus subsp. aureus NCTC 8325]	13331		76	63	28	X	
Q2FVL2	88196339	hypothetical protein SAOUHSC_02699 [Staphylococcus aureus subsp. aureus NCTC 8325]	28886	251	318	139	28	X	
Q2FVF5	88196395	hypothetical protein SAOUHSC_02759 [Staphylococcus aureus subsp. aureus NCTC 8325]	17300	27	113	62	28		
Q2FVE0	88196410	hypothetical protein SAOUHSC_02774 [Staphylococcus aureus subsp. aureus NCTC 8325]	16474	43	29		28		
Q2FVD4	88196415	hypothetical protein SAOUHSC_02779 [Staphylococcus aureus subsp. aureus NCTC 8325]	11166	189	192	199	28		
Q2FVA6	88196461	hypothetical protein SAOUHSC_02827 [Staphylococcus aureus subsp. aureus NCTC 8325]	10541	91	61		28	X	
Q2FV89	88196478	hypothetical protein SAOUHSC_02845 [Staphylococcus aureus subsp. aureus NCTC 8325]	13206	85	90	37	28		
Q2FXN4	88195501	isocitrate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	46394	36	36		28	X	
P68805	542123274	large-conductance mechanosensitive channel [Staphylococcus aureus subsp. aureus NCTC 8325]	13607		113	55	28		
Q2FV16	88196554	malate:quinone oxidoreductase [Staphylococcus aureus subsp. aureus NCTC 8325]	55964	66	162	23	28	X	
Q2G1R9	88194248	methionyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	74838	54	60		28	X	X
Q2FXZ2	88195389	molecular chaperone DnaK [Staphylococcus aureus subsp. aureus NCTC 8325]	66321	84	96	93	28	X	
Q2FVX4	88196194	molybdenum ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	29033		98	141	28		
Q2G031	88194556	phosphoglycerate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	42575	182	153	123	28	X	X
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088	103	459	80	28	X	
Q2FZI5	88194772	phosphoribosylamine--glycine ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	45820		75	61	28	X	X
Q2FZJ3	88194764	phosphoribosylaminoimidazole-succinocarboxamide synthase [Staphylococcus aureus subsp. aureus NCTC 8325]	26676		130	92	28	X	
Q2G0J0	88194349	phosphotransacetylase [Staphylococcus aureus subsp. aureus NCTC 8325]	34930		91	52	28	X	
Q2FXT7	88195449	preprotein translocase subunit YajC [Staphylococcus aureus subsp. aureus NCTC 8325]	9665		32	68	28	X	
Q2G2S6	88195663	protein export protein PrsA [Staphylococcus aureus subsp. aureus NCTC 8325]	35616	221	272	269	28		
Q2G1G5	88193970	PTS system transporter [Staphylococcus aureus subsp. aureus NCTC 8325]	50632	144	131	77	28	X	
Q2FXE8	88195596	putative translaldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	25689		86	104	28	X	
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224	97	246	107	28	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063	297	292	202	28	X	
Q2FZJ9	88194758	quinol oxidase AA3 subunit II [Staphylococcus aureus subsp. aureus NCTC 8325]	41750	98	170	125	28	X	
Q2G0S5	88194256	regulatory protein SpoVG [Staphylococcus aureus subsp. aureus NCTC 8325]	11271	106	111		28	X	
Q2FZ21	88194969	ribosome recycling factor [Staphylococcus aureus subsp. aureus NCTC 8325]	20341	129	119	62	28	X	
Q2G2Q4	88194980	ribosome-binding factor A [Staphylococcus aureus subsp. aureus NCTC 8325]	13506	688	535	397	28		
Q2FZ36	88194954	succinyl-CoA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	31522	79	114	106	28	X	
Q2FZ37	88194953	succinyl-CoA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	42030	84	162	129	28	X	X
Q2FXL3	88195522	thiol peroxidase [Staphylococcus aureus subsp. aureus NCTC 8325]	17994	40	164		28	X	
Q2FZD2	88194846	thioredoxin [Staphylococcus aureus subsp. aureus NCTC 8325]	11433	113	157	128	28	X	
Q2FY45	88195331	transcription antitermination protein NusB [Staphylococcus aureus subsp. aureus NCTC 8325]	15052	130	247	65	28	X	X
Q2FY73	88195303	transcriptional regulator Fur [Staphylococcus aureus subsp. aureus NCTC 8325]	17233	84	95	43	28		X
Q2FZ27	88194963	transcriptional repressor CodY [Staphylococcus aureus subsp. aureus NCTC 8325]	28737	216	254	218	28	X	X
Q2FW28	88196140	translation initiation factor IF-1 [Staphylococcus aureus subsp. aureus NCTC 8325]	8274	94	60	191	28	X	
Q2G2D0	88194979	translation initiation factor IF-2 [Staphylococcus aureus subsp. aureus NCTC 8325]	77823	76	92	47	28	X	X
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579	130	179	85	28	X	
Q2FXR8	88195468	valyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	101660	69	77	107	28	X	
Q9RFJ6	88195576	virulence factor regulator protein [Staphylococcus aureus subsp. aureus NCTC 8325]	15590	94	134		28		X
#N/A	542123276	30S ribosomal protein S10 [Staphylococcus aureus subsp. aureus NCTC 8325]	11569		38	42	29	X	X^
Q2FW31	88196137	30S ribosomal protein S11 [Staphylococcus aureus subsp. aureus NCTC 8325]	13873	81	167	101	29	X	X
Q2FW30	88196138	30S ribosomal protein S13 [Staphylococcus aureus subsp. aureus NCTC 8325]	13711	155	139	123	29	X	X
Q2FW10	88196158	30S ribosomal protein S19 [Staphylococcus aureus subsp. aureus NCTC 8325]	10609		45	50	29	X	X
Q2FXY6	88195395	30S ribosomal protein S20 [Staphylococcus aureus subsp. aureus NCTC 8325]	9016	57	70	77	29	X	X
Q2FW12	88196156	30S ribosomal protein S3 [Staphylococcus aureus subsp. aureus NCTC 8325]	24085	42	55	43	29	X	X
Q2FW23	88196145	30S ribosomal protein S5 [Staphylococcus aureus subsp. aureus NCTC 8325]	17732		62	73	29	X	X
Q2FW20	88196148	30S ribosomal protein S8 [Staphylococcus aureus subsp. aureus NCTC 8325]	14822		65	27	29	X	X
Q2G0P0	88194300	50S ribosomal protein L1 [Staphylococcus aureus subsp. aureus NCTC 8325]	24693	68	132	197	29	X	X

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
P0A0F4	88194299	50S ribosomal protein L11 [Staphylococcus aureus subsp. aureus NCTC 8325]	14865	172	156	133	29	X	X
Q2FW38	88196130	50S ribosomal protein L13 [Staphylococcus aureus subsp. aureus NCTC 8325]	16323		35	41	29	X	
P0A0F8	88196143	50S ribosomal protein L15 [Staphylococcus aureus subsp. aureus NCTC 8325]	15587	58	61	55	29	X	X
Q2FW33	88196135	50S ribosomal protein L17 [Staphylococcus aureus subsp. aureus NCTC 8325]	13739		57	102	29	X	
Q2FW22	88196146	50S ribosomal protein L18 [Staphylococcus aureus subsp. aureus NCTC 8325]	13089		63	65	29	X	X
Q2FW06	88196162	50S ribosomal protein L3 [Staphylococcus aureus subsp. aureus NCTC 8325]	23703	43	46		29	X	X
P0A0G2	88196144	50S ribosomal protein L30 [Staphylococcus aureus subsp. aureus NCTC 8325]	6550	446	373	263	29	X	
Q2FW18	88196150	50S ribosomal protein L5 [Staphylococcus aureus subsp. aureus NCTC 8325]	20254	96	166	142	29	X	X
Q2FW21	88196147	50S ribosomal protein L6 [Staphylococcus aureus subsp. aureus NCTC 8325]	19774		55	37	29	X	X
P48860	88194302	50S ribosomal protein L7/L12 [Staphylococcus aureus subsp. aureus NCTC 8325]	12704	90	92	158	29	X	
Q2G2D8	88194402	ABC transporter substrate-binding protein [Staphylococcus aureus subsp. aureus NCTC 8325]	35049	172	327	203	29	X	
P0A0B7	88194163	alkyl hydroperoxide reductase subunit C [Staphylococcus aureus subsp. aureus NCTC 8325]	20963	73	52	52	29	X	
Q2FZI6	88194771	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Staphylococcus aureus subsp. aureus NCTC 8325]	54314	79	104	120	29	X	
Q2G2A4	88194794	branched-chain alpha-keto acid dehydrogenase subunit E2 [Staphylococcus aureus subsp. aureus NCTC 8325]	46326		42	79	29	X	
Q2FZ89	88194892	cell division protein FtsZ [Staphylococcus aureus subsp. aureus NCTC 8325]	41012	123	195	190	29	X	X
Q2FWN4	88195925	chaperonin GroEL [Staphylococcus aureus subsp. aureus NCTC 8325]	57629		50	83	29	X	
Q2FZW4	88194628	D-alanine--poly(phosphoribitol) ligase subunit 2 [Staphylococcus aureus subsp. aureus NCTC 8325]	9058		54	45	29		
Q2FYG2	88195207	DNA-binding protein HU [Staphylococcus aureus subsp. aureus NCTC 8325]	9620	148	152	124	29	X	X
Q2FZ23	88194967	elongation factor Ts [Staphylococcus aureus subsp. aureus NCTC 8325]	32474	131	174	182	29	X	
Q2G0N0	88194310	elongation factor Tu [Staphylococcus aureus subsp. aureus NCTC 8325]	43077	92	164	245	29	X	X
Q2G296	88195544	formate--tetrahydrofolate ligase [Staphylococcus aureus subsp. aureus NCTC 8325]	59819		75	135	29	X	X
Q2FWD3	88196029	fructose-bisphosphate aldolase [Staphylococcus aureus subsp. aureus NCTC 8325]	30817	180	285	373	29	X	
Q2FYY6	88195018	glutamine synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	50808	65	81	229	29	X	
Q2G032	88194555	glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus subsp. aureus NCTC 8325]	36258	74	60	90	29	X	
Q2FYT0	88195074	glycine betaine transporter [Staphylococcus aureus subsp. aureus NCTC 8325]	60433	39	40	37	29		

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2G0Q8	88194273	hypothetical protein SAOUHSC_00488 [Staphylococcus aureus subsp. aureus NCTC 8325]	32955	84	103	154	29	X	
Q2G0K7	88194332	hypothetical protein SAOUHSC_00553 [Staphylococcus aureus subsp. aureus NCTC 8325]	22422	71	86		29	X	
Q2G0B5	88194455	hypothetical protein SAOUHSC_00690 [Staphylococcus aureus subsp. aureus NCTC 8325]	26671		91	95	29	X	
Q2FZV7	88194635	hypothetical protein SAOUHSC_00878 [Staphylococcus aureus subsp. aureus NCTC 8325]	44077		49	86	29	X	
Q2FZA4	88194877	hypothetical protein SAOUHSC_01135 [Staphylococcus aureus subsp. aureus NCTC 8325]	4493	479	284	465	29	X	
Q2FZA3	88194878	hypothetical protein SAOUHSC_01136 [Staphylococcus aureus subsp. aureus NCTC 8325]	4453	193	272	287	29	X	
Q2FZ07	88194997	hypothetical protein SAOUHSC_01264 [Staphylococcus aureus subsp. aureus NCTC 8325]	8156	112	104	72	29	X	
Q2FYJ6	88195168	hypothetical protein SAOUHSC_01447 [Staphylococcus aureus subsp. aureus NCTC 8325]	1029310	40	40	38	29	X	
Q2FXZ9	88195382	hypothetical protein SAOUHSC_01676 [Staphylococcus aureus subsp. aureus NCTC 8325]	35160	77	115	93	29	X	
Q2FXW0	88195426	hypothetical protein SAOUHSC_01721 [Staphylococcus aureus subsp. aureus NCTC 8325]	10297	100	61		29	X	
Q2FXV1	88195435	hypothetical protein SAOUHSC_01730 [Staphylococcus aureus subsp. aureus NCTC 8325]	6678		61	107	29	X	
Q2FXM1	88195514	hypothetical protein SAOUHSC_01814 [Staphylococcus aureus subsp. aureus NCTC 8325]	15216	74	110	131	29	X	
Q2FXL6	88195519	hypothetical protein SAOUHSC_01819 [Staphylococcus aureus subsp. aureus NCTC 8325]	18464	80	81	77	29	X	
Q2FXJ2	88195542	hypothetical protein SAOUHSC_01843 [Staphylococcus aureus subsp. aureus NCTC 8325]	100886	33	31	32	29	X	
Q2G247	88195553	hypothetical protein SAOUHSC_01855 [Staphylococcus aureus subsp. aureus NCTC 8325]	17991	124	258	266	29	X	
Q2FXH8	88195566	hypothetical protein SAOUHSC_01869 [Staphylococcus aureus subsp. aureus NCTC 8325]	15724	64	72	67	29	X	
Q2FW79	88196081	hypothetical protein SAOUHSC_02425 [Staphylococcus aureus subsp. aureus NCTC 8325]	10000	95	93	139	29	X	
Q2FVL2	88196339	hypothetical protein SAOUHSC_02699 [Staphylococcus aureus subsp. aureus NCTC 8325]	28886	51	41	101	29	X	
Q2FXH2	88195572	leucyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	91728		28	42	29	X	
Q2FXZ2	88195389	molecular chaperone DnaK [Staphylococcus aureus subsp. aureus NCTC 8325]	66321	81	82	59	29	X	
Q2G160	88194096	N-acetylneuraminate lyase [Staphylococcus aureus subsp. aureus NCTC 8325]	33022		50	53	29	X	
Q2FXM5	88195510	NADP-dependent malic enzyme [Staphylococcus aureus subsp. aureus NCTC 8325]	44206	41	44	53	29	X	
Q2G028	88194559	phosphopyruvate hydratase [Staphylococcus aureus subsp. aureus NCTC 8325]	47088		56	114	29	X	
Q2G2S6	88195663	protein export protein PrsA [Staphylococcus aureus subsp. aureus NCTC 8325]	35616		106	114	29		
Q2G0Q1	88194280	pyridoxal biosynthesis lyase PdxS [Staphylococcus aureus subsp. aureus NCTC 8325]	31972	75	67	125	29	X	
Q2G2A5	88194793	pyruvate dehydrogenase complex, E1 component subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	35224		43	73	29	X	

Uniprot ID	GI number	Protein Description	Mass	Rep1	Rep2	Rep3	Slice	Surface exposure	DNA binding
Q2FXM9	88195506	pyruvate kinase [Staphylococcus aureus subsp. aureus NCTC 8325]	63063		55	72	29	X	
Q2FZ36	88194954	succinyl-CoA synthetase subunit alpha [Staphylococcus aureus subsp. aureus NCTC 8325]	31522	68	108	118	29	X	
Q2FZ37	88194953	succinyl-CoA synthetase subunit beta [Staphylococcus aureus subsp. aureus NCTC 8325]	42030		42	117	29	X	X
Q2FZ27	88194963	transcriptional repressor CodY [Staphylococcus aureus subsp. aureus NCTC 8325]	28737	103	102		29	X	X
Q2FW28	88196140	translation initiation factor IF-1 [Staphylococcus aureus subsp. aureus NCTC 8325]	8274	254	212	245	29	X	
Q2G2D0	88194979	translation initiation factor IF-2 [Staphylococcus aureus subsp. aureus NCTC 8325]	77823	24	26	64	29	X	X
Q2FXQ6	88195480	trigger factor [Staphylococcus aureus subsp. aureus NCTC 8325]	48579	69	63	138	29	X	
Q2FWF4	88196003	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Staphylococcus aureus subsp. aureus NCTC 8325]	44913	41		44	29	X	
Q2FXR8	88195468	valyl-tRNA synthetase [Staphylococcus aureus subsp. aureus NCTC 8325]	101660		51	54	29	X	

Table B.4 Panther GO output for identified proteins in heparin binding experiments.

Overall ontology - Molecular function	
Molecular function	**Number of proteins**
transporter activity	24
translation regulator activity	12
protein binding transcription factor activity	2
enzyme regulator activity	1
catalytic activity	238
receptor activity	3
nucleic acid binding transcription factor activity	10
antioxidant activity	7
structural molecule activity	35
Binding	93
Unknown (no output from Panther GO)	206

Data analysed via the Panther Classification System accessed from http://pantherdb.org/.

Item B.1 Motifs searched against all proteins identified in the 1+ M NaCl elution with all motif matches listed against individual proteins.

Motifs searched:

USERPAT1 {X-[HRK]-[HRK]-[HRK]-X-X-[HRK]-X}
USERPAT2 {X-[HRK]-[HRK]-X-[HRK]-X}
USERPAT3 {X-[HRK]-X-[HRK]-[HRK]-X}
USERPAT4 {X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X}
USERPAT5 {X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X}

Hits for:

Q2FW33, Q2FW39, Q2FXJ2, Q2FXS8, Q2G160, Q2FWW1, Q2FYG2, Q2FYJ6, Q2FZ60, Q2G111, Q2G113, Q2FVG4, Q2FY01, Q2FZH6, P48940, P60430, Q2FW11, Q2FW14, Q2FW22, Q2FW29, Q2FW31, Q2FXQ0, Q2FXQ1, Q2FXY6, Q2G1N7, Q2FVQ4, Q2G0B5, Q2G0S0, Q2G170, P0A0B7, P0A0F8, P0A0H0, Q2FW06, Q2FW07, Q2FW08, Q2FW13, Q2FW15, Q2FW17, Q2FW19, Q2FW21, Q2FW23, Q2FW30, Q2FW38, Q2FW66, Q2FW79, Q2FXK6, Q2FXP9, Q2FXT0, Q2FXZ7, Q2FY37, Q2FZ42, Q2FZ45, Q2FZD3, Q2G023, Q2G0N0, Q2G2M4, Q2G2Q1, Q2FVX5, Q2FVY0, Q2FXM1, Q2FYS0, Q2FZZ9, Q2G001, Q2G0F2, Q2G0R5, Q2G2D1

```
>sp|Q2G160|NANA_STAA8  (293 aa)
RecName: Full=N-acetylneuraminate lyase {ECO:0000255|HAMAP-Rule:MF_01237,
ECO:0000303|PubMed:23418011};        Short=NAL {ECO:0000255|HAMAP-Rule:MF_01237,
ECO:0000303|PubMed:23418011};        Short=Neu5Ac lyase {ECO:0000255|HAMAP-
Rule:MF_01237, ECO:0000303|PubMed:23418011};        EC=4.1.3.3 {ECO:0000255|HAMAP-
Rule:MF_01237, ECO:0000269|PubMed:23418011}; AltName: Full=N-acetylneuraminate
pyruvate-lyase {ECO:0000255|HAMAP-Rule:MF_01237}; AltName: Full=N-acetylneuraminic
acid aldolase {ECO:0000255|HAMAP-Rule:MF_01237}; AltName: Full=Sialate lyase
{ECO:0000255|HAMAP-Rule:MF_01237}; AltName: Full=Sialic acid aldolase
{ECO:0000255|HAMAP-Rule:MF_01237}; AltName: Full=Sialic acid lyase
{ECO:0000255|HAMAP-Rule:MF_01237};.  [Staphylococcus aureus (strain NCTC 8325)]
MNKDLKGLYAALLVPFDENGQVNEQGLKQIAQNAIETEELDGLYVNGSSGENFLLNTEQKKQVFKVAKEAV
GDKVKLIAQVGSLDLNEAIELGKYATELGYDALSAVTPFYYPFTFEEIRDYYFDIIEATQNNMIIYAIPDLTGVNI
SIEQFSELFNHEKIVGVKYTAPNFFLLERIRKAFPDKLILSGFDEMLVQATISGVDGAIGSTYNVNGRRARKIFD
LARQGQIQEAYQLQHDSNDIIETVLSMGIYPTLKEILRHRGIDAGLPKRPFKPFNEAHRQTLDQLIAKYDL

   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     59 - 69:       qKkqvfKva..Ke
     157 - 166:      nHe...KivgvKy
     175 - 185:      eRir..KafpdKl
     255 - 263:      lKeil.Rh...Rg

   >USERPAT3 (user pattern) :
```

```
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     175 - 180:     eRiRKa
     215 - 220:     rRaRKi

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     175 - 180:     eRi.R..Ka
     214 - 220:     gRraR..Ki
     259 - 263:     lR..H..Rg
     269 - 275:     pK..RpfKp

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     214 - 219:     gRRaRk


>tr|Q2FYG2|Q2FYG2_STAA8  (90 aa)
SubName: Full=DNA-binding protein HU, putative {ECO:0000313|EMBL:ABD30575.1};.
[Staphylococcus aureus (strain NCTC 8325)]
MNKTDLINAVAEQADLTKKEAGSAVDAVFESIQNSLAKGEKVQLIGFGNFEVRERAARKGRNPQTGKEIDIP
ASKVPAFKAGKALKDAVK

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     52 - 59:     vRe.RaaRk
     54 - 62:     eRaaRkgRn
     79 - 87:     fKagKalKd

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     52 - 62:     vReraaRkg..Rn
     74 - 84:     sKvpafKag..Ka
     79 - 87:     fKag..Kal..Kd

  >USERPAT2 (user pattern) :
```

```
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    57 - 62:      aRKgRn


>sp|Q2FXS8|RL21_STAA8  (102 aa)
RecName: Full=50S ribosomal protein L21 {ECO:0000255|HAMAP-Rule:MF_01363};.
[Staphylococcus aureus (strain NCTC 8325)]
MFAIIETGGKQIKVEEGQEIFVEKLDVNEGDTFTFDKVLFVGGDSVKVGAPTVEGATVTATVNKQGRGKKIT
VFTYKRRKNSKRKKGHRQPYTKLTIDKINA

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    63 - 71:      nKqgRgkKi
    76 - 84:      yKrrKnsKr
    79 - 87:      rKnsKrkKg
    82 - 90:      sKrkKghRq

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    63 - 71:      nKqg..Rgk..Ki
    76 - 86:      yKrr..KnskrKk
    77 - 89:      kRrknsKrkkgHr
    78 - 90:      rRknskRkkghRq
    83 - 95:      kRkkghRqpytKl
    88 - 100:      hRqpytKltidKi

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    66 - 71:      gRgKKi
    76 - 81:      yKrRKn
    82 - 87:      sKrKKg
    85 - 90:      kKgHRq

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792
```

```
    76 - 81:       yKRrKn
    82 - 87:       sKRkKg
    84 - 89:       rKKgHr

  >USERPAT1 (user pattern) :
  Pattern: X-[HRK]-[HRK]-[HRK]-X-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 14782

    77 - 84:       kRRKnsKr
    82 - 89:       sKRKkgHr
    83 - 90:       kRKKghRq


>sp|Q2FXJ2|ISDH_STAA8  (895 aa)
RecName: Full=Iron-regulated surface determinant protein H; AltName: Full=Haptoglobin
receptor A; AltName: Full=Staphylococcus aureus surface protein I; Flags: Precursor;.
[Staphylococcus aureus (strain NCTC 8325)]
MNKHHPKLRSFYSIRKSTLGVASVIVSTLFLITSQHQAQAAENTNTSDKISENQNNNATTTQPPKDTNQTQP
ATQPANTAKNYPAADESLKDAIKDPALENKEHDIGPREQVNFQLLDKNNETQYYHFFSIKDPADVYYTKKKA
EVELDINTASTWKKFEVYENNQKLPVRLVSYSPVPEDHAYIRFPVSDGTQELKIVSSTQIDDGEETNYDYTKLV
FAKPIYNDPSLVKSDTNDAVVTNDQSSSVASNQTNTNTSNQNISTINNANNQPQATTNMSQPAQPKSSTN
ADQASSQPAHETNSNGNTNDKTNESSNQSDVNQQYPPADESLQDAIKNPAIIDKEHTADNWRPIDFQMK
NDKGERQFYHYASTVEPATVIFTKTGPIIELGLKTASTWKKFEVYEGDKKLPVELVSYDSDKDYAYIRFPVSNG
TREVKIVSSIEYGENIHEDYDYTLMVFAQPITNNPDDYVDEETYNLQKLLAPYHKAKTLERQVYELEKLQEKLP
EKYKAEYKKKLDQTRVELADQVKSAVTEFENVTPTNDQLTDLQEAHFVVFESEENSESVMDGFVEHPFYTAT
LNGQKYVVMKTKDDSYWKDLIVEGKRVTTVSKDPKNNSRTLIFPYIPDKAVYNAIVKVVVANIGYEGQYHVR
IINQDINTKDDDTSQNNTSEPLNVQTGQEGKVADTDVAENSSTATNPKDASDKADVIEPESDVVKDADNNI
DKDVQHDVDHLSDMSDNNHFDKYDLKEMDTQIAKDTDRNVDKDADNSVGMSSNVDTDKDSNKNKDKV
IQLNHIADKNNHTGKAAKLDVVKQNYNNTDKVTDKKTTEHLPSDIHKTVDKTVKTKEKAGTPSKENKLSQSK
MLPKTGETTSSQSWWGLYALLGMLALFIPKFRKESK

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    2 - 8:         nKh.Hp.Kl
    3 - 10:         kHhpKl.Rs
    140 - 144:      tK..K..Ka
    356 - 364:      mKndKgeRq
    484 - 489:      yH..Ka.Kt
    512 - 516:      yK..K..Kl
    781 - 787:      nKn.Kd.Kv
    795 - 803:      dKnnHtgKa
    798 - 806:      nHtgKaaKl
    837 - 844:      dKtvKt.Ke
    840 - 846:      vKt.Ke.Ka
    888 - 893:      pKf.R..Ke
```

```
  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    2 - 10:       nKhhp.Kl...Rs
    101 - 110:    nKe...HdigpRe
    356 - 364:    mKnd..Kge..Rq
    359 - 368:    dKge..Rqfy.Hy
    484 - 493:    yHka..Ktle.Rq
    498 - 508:    eKlqe.Klpe.Ky
    502 - 510:    eKlpe.Ky...Ka
    506 - 515:    eKy...KaeykKk
    508 - 516:    yKaey.Kk...Kl
    512 - 521:    yKk...KldqtRv
    581 - 590:    qKyvvmKt...Kd
    608 - 617:    sKdp..Knns.Rt
    721 - 731:    dKdvq.Hdvd.Hl
    738 - 747:    nHfd..Kydl.Ke
    753 - 763:    aKdtd.Rnvd.Kd
    777 - 787:    dKdsn.Knkd.Kv
    791 - 800:    nHiad.Knn..Ht
    795 - 803:    dKnn..Htg..Ka
    798 - 806:    nHtg..Kaa..Kl
    801 - 811:    gKaa..KldvvKq
    817 - 828:    dKvtdkKtte.Hl
    832 - 844:    iHktvdKtvktKe
    837 - 846:    dKtvktKe...Ka
    850 - 860:    sKen..KlsqsKm
    853 - 864:    nKlsqsKmlp.Kt

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    3 - 8:        kHHpKl
    484 - 489:    yHKaKt

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    888 - 893:    pKfRKe


>tr|Q2FWW1|Q2FWW1_STAA8  (584 aa)
SubName: Full=MHC class II analog protein {ECO:0000313|EMBL:ABD31208.1};.
[Staphylococcus aureus (strain NCTC 8325)]
```

```
MKFKSLITTTLALGVLASTGANFNNNEASAAAKPLDKSSSSLHHGYSKVHVPYAITVNGTSQNILSSLTFNKN
QNISYKDLEDRVKSVLKSDRGISDIDLRLSKQAKYTVYFKNGTKKVIDLKAGIYTADLINTSEIKAININVDTKKQ
VEDKKKDKANYQVPYTITVNGTSQNILSNLTFNKNQNISYKDLEDKVKSVLESNRGITDVDLRLSKQAKYTVN
FKNGTKKVIDLKSGIYTANLINSSDIKSININVDTKKHIENKAKRNYQVPYSINLNGTSTNILSNLSFSNKPWTN
YKNLTSQIKSVLKHDRGISEQDLKYAKKAYYTVYFKNGGKRILQLNSKNYTANLVHAKDVKRIEITVKTGTKAK
ADRYVPYTIAVNGTSTPILSDLKFTGDPRVGYKDISKKVKSVLKHDRGIGERELKYAKKATYTVHFKNGTKKVI
NINSNISQLNLLYVQDIKKIDIDVKTGTKAKADSYVPYTIAVNGTSTPILSKLKISNKQLISYKYLNDKVKSVLKSE
RGISDLDLKFAKQAKYTVYFKNGKKQVVNLKSDIFTPNLFSAKDIKKIDIDVKQYTKSKKNK

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    42 - 51:      lHhgysKv...Hv
    78 - 87:      yKdledRv...Ks
    83 - 91:      dRv...Ksvl.Ks
    85 - 94:      vKsvl.Ksd..Rg
    100 - 108:    lRls..Kqa..Ky
    112 - 124:    fKngtkKvidlKa
    147 - 158:    kKqvedKkkd.Ka
    189 - 198:    yKdledKv...Ks
    211 - 219:    lRls..Kqa..Ky
    223 - 235:    fKngtkKvidlKs
    257 - 265:    tKk...Hien.Ka
    258 - 268:    kKhienKak..Rn
    305 - 314:    iKsvlkHd...Rg
    352 - 360:    vHa...Kdvk.Ri
    364 - 375:    vKtgt.KakadRy
    399 - 410:    pRvgy.KdiskKv
    403 - 412:    yKdiskKv...Ks
    407 - 417:    sKkv..KsvlkHd
    410 - 419:    vKsvlkHd...Rg
    414 - 424:    lKhd..RgigeRe
    417 - 427:    dRgigeRel..Ky
    422 - 431:    eRel..Kyak.Ka
    435 - 444:    vHf...KngtkKv
    469 - 477:    vKtgt.Ka...Ka
    496 - 504:    sKl...Kisn.Kq
    508 - 517:    yKylndKv...Ks
    513 - 521:    dKv...Ksvl.Ks
    515 - 524:    vKsvl.Kse..Rg
    530 - 538:    lKfa..Kqa..Ky
    574 - 583:    vKqyt.Ksk..Kn

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126
```

```
    100 - 108:    lRlsKqaKy
    152 - 158:    dKk.Kd.Ka
    211 - 219:    lRlsKqaKy
    257 - 261:    tK..K..Hi
    263 - 268:    nKa.K..Rn
    309 - 314:    lK..Hd.Rg
    320 - 326:    lKyaK..Ka
    352 - 359:    vHa.KdvKr
    354 - 360:    aKdvK..Ri
    368 - 375:    tKa.KadRy
    407 - 412:    sK..Kv.Ks
    414 - 419:    lK..Hd.Rg
    422 - 430:    eRelKyaKk
    425 - 431:    lKyaK..Ka
    530 - 538:    lKfaKqaKy
    542 - 548:    fKngK..Kq
    564 - 570:    aKdiK..Ki
    578 - 583:    tKs.K..Kn

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    153 - 158:    kKKdKa
    309 - 314:    lKHdRg
    407 - 412:    sKKvKs
    414 - 419:    lKHdRg

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    263 - 268:    nKaKRn
    578 - 583:    tKsKKn


>sp|Q2FW39|RS9_STAA8  (132 aa)
RecName: Full=30S ribosomal protein S9 {ECO:0000255|HAMAP-Rule:MF_00532};.
[Staphylococcus aureus (strain NCTC 8325)]
MTLAQVEYRGTGRRKNSVARVRLVPGEGNITVNNRDVREYLPFESLILDLNQPFDVTETKGNYDVLVNVHG
GGFTGQAQAIRHGIARALLEADPEYRGSLKRAGLLTRDPRMKERKKPGLKAARRSPQFSKR

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    8 - 16:       yRgtg.Rr...Kn
```

```
    12 - 21:       gRr...KnsvaRv
    14 - 23:       rKnsvaRv...Rl
    107 - 118:     tRdprmKerk.Kp
    110 - 122:     pRmkerKkpglKa
    115 - 126:     rKkpglKaar.Rs

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    12 - 16:       gR..R..Kn
    107 - 114:     tRdpRm.Ke
    110 - 117:     pRm.KerKk
    112 - 118:     mKerK..Kp
    120 - 126:     lKaaR..Rs

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    112 - 117:     mKeRKk


>sp|Q2FW33|RL17_STAA8  (122 aa)
RecName: Full=50S ribosomal protein L17 {ECO:0000255|HAMAP-Rule:MF_01368};.
[Staphylococcus aureus (strain NCTC 8325)]
MGYRKLGRTSDQRKAMLRDLATSLIISERIETTEARAKEVRSVVEKLITLGKKGDLASRRNAAKTLRNVEILNE
DETTQTALQKLFGEIAERYTERQGGYTRILKQGPRRGDGAESVIIELV

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    3 - 9:        yR..KlgRt
    35 - 42:       aRa.KevRs

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    3 - 14:       yRklg.RtsdqRk
    7 - 19:       gRtsdqRkamlRd
    35 - 47:       aRakevRsvveKl
    58 - 68:       sRrnaaKtl..Rn
    101 - 111:     tRil..KqgprRg
```

```
>tr|Q2FVG4|Q2FVG4_STAA8  (545 aa)
SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:ABD31754.1};.  [Staphylococcus
aureus (strain NCTC 8325)]
MNKDKQLHNDKINLSQLVLLGLGSLIGSGWLFGAWEASSIAGPAAIISWVLGFLVIGTIAYNYIEIGTMFPQS
GGMSNYAQYTHGSLLGFIAAWANWVSLVTIIPIEAVSAVQYMSSWPWHWAKPMRYLMENGSISTYGLLA
VYLIIVIFSLLNYWSVKLLTSFTSLISVFKLGVPMLTIIMLMLSGFDTSNYGHSASTFMPYGSAPIFAATTASGIIF
SFNSFQTIINMGSEIKNPEKNIARGIAISLSISAVLYIILQSTFITSMPQSMLQHSGWNGINFNSPFADLAILLGI
NWLAILLYIEAFVSPFGTGVSFVAVTGRVLRAMEKNGHIPKFLGKMNEKYHIPRVAIIFNAIISMIMVTLFRD
WGTLAAVISTATLVAYLTGPTTVIALRKMGPTMTRPFRAKILKVMAPLSFVLASLAIYWAMWPTTAEVILIIIL
GLPIYFFYEYRMNWRNTKKQIGGSLWIIVYLIVLSILSFIGSKEFKGLNMIHYPFDFIVIIIVALIFYYIGTTSSFESV
YFRRATRINTKMRESLNNESKSSH

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

      2 - 9:         nKd.KqlHn
      4 - 12:         dKqlHndKi
      120 - 128:     wHwaKpmRy
      329 - 337:     eKngHipKf
      343 - 350:     eKy.HipRv
      402 - 409:     tRpfRa.Ki
      405 - 412:     fRa.KilKv
      456 - 462:     wRntK..Kq
      523 - 529:     fR..RatRi

   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

      2 - 12:         nKdkqlHnd..Ki
      120 - 128:     wHwa..Kpm..Ry
      234 - 244:     iKnpe.Knia.Rg
      322 - 331:     gRvl..Rame.Kn
      325 - 334:     lRame.Kng..Hi
      329 - 337:     eKng..Hip..Kf
      332 - 341:     gHip..Kflg.Km
      335 - 345:     pKflg.Kmne.Ky
      339 - 350:     gKmne.KyhipRv
      402 - 412:     tRpfraKil..Kv
      452 - 462:     yRmnw.Rntk.Kq
      523 - 533:     fRrat.Rint.Km
      527 - 535:     tRint.Km...Re


>sp|Q2G113|RS6_STAA8  (98 aa)
```

```
RecName: Full=30S ribosomal protein S6 {ECO:0000255|HAMAP-Rule:MF_00360};.
[Staphylococcus aureus (strain NCTC 8325)]
MRTYEVMYIVRPNIEEDAKKALVERFNGILATEGAEVLEAKDWGKRRLAYEINDFKDGFYNIVRVKSDNNKA
TDEFQRLAKISDDIIRYMVIREDEDK

   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

      40 - 48:       aKdwg.Kr...Rl
      63 - 72:       vRv...KsdnnKa

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

      44 - 48:       gK..R..Rl


>sp|Q2G111|RS18_STAA8  (80 aa)
RecName: Full=30S ribosomal protein S18 {ECO:0000255|HAMAP-Rule:MF_00270};.
[Staphylococcus aureus (strain NCTC 8325)]
MAGGPRRGGRRRKKVCYFTANGITHIDYKDTELLKRFISERGKILPRRVTGTSAKYQRMLTTAIKRSRHMALL
PYVKEEQ

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

      5 - 11:        pR..RggRr
      6 - 14:        rRggRrrKk
      9 - 15:        gRrrK..Kv
      64 - 70:       iKrsR..Hm

   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

      5 - 15:        pRrggrRrk..Kv
      35 - 44:       kRfiseRg...Ki
      40 - 49:       eRg...KilprRv

   >USERPAT2 (user pattern) :
   Pattern: X-[HRK]-[HRK]-X-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792
```

```
     9 - 14:        gRRrKk
     10 - 15:       rRRkKv
     64 - 69:       iKRsRh

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     9 - 14:        gRrRKk
     10 - 15:       rRrKKv
     65 - 70:       kRsRHm


>sp|Q2FZ60|RL28_STAA8  (62 aa)
RecName: Full=50S ribosomal protein L28 {ECO:0000255|HAMAP-Rule:MF_00373};.
[Staphylococcus aureus (strain NCTC 8325)]
MGKQCFVTGRKASTGNRRSHALNSTKRRWNANLQKVRILVDGKPKKVWVSARALKSGKVTRV

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     16 - 21:       nRRsHa

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     16 - 21:       nR..Rs.Ha
     25 - 29:       tK..R..Rw
     42 - 47:       gKp.K..Kv
     51 - 59:       aRalKsgKv
     54 - 62:       lKsgKvtRv

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     42 - 47:       gKpKKv

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669
```

51 - 59: aRal..Ksg..Kv
54 - 62: lKsg..Kvt..Rv

```
>sp|Q2FYJ6|EBH_STAA8  (9535 aa)
RecName: Full=Extracellular matrix-binding protein ebh; AltName: Full=ECM-binding protein
homolog; Flags: Precursor;.  [Staphylococcus aureus (strain NCTC 8325)]
MNYRDKIQKFSIRKYTVGTFSTVIATLVFLGFNTSQAHAAETNQPASVVKQKQQSNNEQTENRESQVQNSQ
NSQNGQSLSATHENEQPNISQANLVDQKVAQSSTTNDEQPASQNVNTKKDSATAATTQPDKEQSKHKQN
ESQSANKNGNDNRAAHVENHEANVVTASDSSDNGNVQHDRNELQAFFDANYHDYRFIDRENADSGTFN
YVKGIFDKINTLLGSNDPINNKDLQLAYKELEQAVALIRTMPQRQQTSRRSNRIQTRSVESRAAEPRSVSDYQ
NANSSYYVENANDGSGYPVGTYINASSKGAPYNLPTTPWNTLKASDSKEIALMTAKQTGDGYQWVIKFNK
GHAPHQNMIFWFALPADQVPVGRTDFVTVNSDGTNVQWSHGAGAGANKPLQQMWEYGVNDPHRSH
DFKIRNRSGQVIYDWPTVHIYSLEDLSRASDYFSEAGATPATKAFGRQNFEYINGQKPAESPGVPKVYTFIGQ
GDASYTISFKTQGPTVNKLYYAAGGRALEYNQLFMYSQLYVESTQDHQQRLNGLRQVVNRTYRIGTTKRVE
VSQGNVQTKKVLESTNLNIDDFVDDPLSYVKTPSNKVLGFYSNNANTNAFRPGGAQQLNEYQLSQLFTDQK
LQEAARTRNPIRLMIGFDYPDAYGNSETLVPVNLTVLPEIQHNIKFFKNDDTQNIAEKPFSKQAGHPVFYVYA
GNQGNASVNLGGSVTSIQPLRINLTSNENFTDKDWQITGIPRTLHIENSTNRPNNARERNIELVGNLLPGDY
FGTIRFGRKEQLFEIRVKPHTPTITTTAEQLRGTALQKVPVNISGIPLDPSALVYLVAPTNQTTNGGSEADQIPS
GYTILATGTPDGVHNTITIRPQDYVVFIPPVGKQIRAVVYYNKVVASNMSNAVTILPDDIPPTINNPVGINAKY
YRGDEVNFTMGVSDRHSGIKNTTITTLPNGWTSNLTKADKNNGSLSITGRVSMNQAFNSDITFKVSATDNV
NNTTNDSQSKHVSIHVGKISEDAHPIVLGNTEKVVVVNPTAVSNDEKQSIITAFMNKNQNIRGYLASTDPVT
VDNNGNVTLHYRDGSSTTLDATNVMTYEPVVKPEYQTVNAAKTATVTIAKGQSFSIGDIKQYFTLSNGQPIP
SGTFTNITSDRTIPTAQEVSQMNAGTQLYHITATNAYHKDSEDFYISLKIIDVKQPEGDQRVYRTSTYDLTTDE
ISKVKQAFINANRDVITLAEGDISVTNTPNGANVSTITVNINKGRLTKSFASNLANMNFLRWVNFPQDYTVT
WTNAKIANRPTDGGLSWSDDHKSLIYRYDATLGTQITTNDILTMLKATTTVPGLRNNITGNEKSQAEAGGR
PNFRTTGYSQSNATTDGQRQFTLNGQVIQVLDIINPSNGYGGQPVTNSNTRANHSNSTVVNVNEPAANG
AGAFTIDHVVKSNSTHNASDAVYKAQLYLTPYGPKQYVEHLNQNTGNTTDAINIYFVPSDLVNPTISVGNYT
NHQVFSGETFTNTITANDNFGVQSVTVPNTSQITGTVDNNHQHVSATAPNVTSATNKTINLLATDTSGNTA
TTSFNVTVKPLRDKYRVGTSSTAANPVRIANISNNATVSQADQTTIINSLTFTETVPNRSYARASANEITSKTV
SNVSRTGNNANVTVTVTYQDGTTSTVTVPVKHVIPEIVAHSHYTVQGQDFPAGNGSSASDYFKLSNGSDIA
DATITWVSGQAPNKDNTRIGEDITVTAHILIDGETTPITKTATYKVVRTVPKHVFETARGVLYPGVSDMYDAK
QYVKPVNNSWSTNAQHMNFQFVGTYGPNKDVVGISTRLIRVTYDNRQTEDLTILSKVKPDPPRIDANSVTY
KAGLTNQEIKVNNVLNNSSVKLFKADNTPLNVTNITHGSGFSSVVTVSDALPNGGIKAKSSISMNNVTYTTQ
DEHGQVVTVTRNESVDSNDSATVTVTPQLQATTEGAVFIKGGDGFDFGHVERFIQNPPHGATVAWHDSP
DTWKNTVGNTHKTAVVTLPNGQGTRNVEVPVKVYPVANAKAPSRDVKGQNLTNGTDAMNYITFDPNTN
TNGITAAWANRQQPNNQQAGVQHLNVDVTYPGISAAKRVPVTVNVYQFEFPQTTYTTTVGGTLASGTQA
SGYAHMQNATGLPTDGFTYKWNRDTTGTNDANWSAMNKPNVAKVVNAKYDVIYNGHTFATSLPAKFVV
KDVQPAKPTVTETAAGAITIAPGANQTVNTHAGNVTTYADKLVIKRNGNVVTTFTRRNNTSPWVKEASAA
TVAGIAGTNNGITVAAGTFNPADTIQVVATQGSGETVSDEQRSDDFTVVAPQPNQATTKIWQNGHIDITP
NNPSGHLINPTQAMDIAYTEKVGNGAEHSKTINVVRGQNNQWTIANKPDYVTLDAQTGKVTFNANTIKPN
SSITITPKAGTGHSVSSNPSTLTAPAAHTVNTTEIVKDYGSNVTAAEINNAVQVANKRTATIKNGTAMPTNLA
GGSTTTIPVTVTYNDGSTEEVQESIFTKADKRELITAKNHLDDPVSTEGKKPGTITQYNNAMHNAQQQINTA
KTEAQQVINNERATPQQVSDALTKVRAAQTKIDQAKALLQNKEDNSQLVTSKNNLQSSVNQVPSTAGMT
QQSIDNYNAKKREAETEITAAQRVIDNGDATAQQISDEKHRVDNALTALNQAKHDLTADTHALEQAVQQL
NRTGTTTGKKPASITAYNNSIRALQSDLTSAKNSANAIIQKPIRTVQEVQSALTNVNRVNERLTQAINQLVPL
ADNSALKTAKTKLDEEINKSVTTDGMTQSSIQAYENAKRAGQTESTNAQNVINNGDATDQQIAAEKTKVEE
KYNSLKQAIAGLTPDLAPLQTAKTQLQNDIDQPTSTTGMTSASIAAFNEKLSAARTKIQEIDRVLASHPDVATI
RQNVTAANAAKSALDQARNGLTVDKAPLENAKNQLQHSIDTQTSTTGMTQDSINAYNAKLTAARNKIQQI
NQVLAGSPTVEQINTNTSTANQAKSDLDHARQALTPDKAPLQTAKTQLEQSINQPTDTTGMTTASLNAYN
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QKLQAARQKLTEINQVLNGNPTVQNINDKVTEANQAKDQLNTARQGLTLDRQPALTTLHGASNLNQAQQ
NNFTQQINAAQNHAALETIKSNITALNTAMTKLKDSVADNNTIKSDQNYTDATPANKQAYDNAVNAAKGV
IGETTNPTMDVNTVNQKAASVKSTKDALDGQQNLQRAKTEATNAITHASDLNQAQKNALTQQVNSAQN
VQAVNDIKQTTQSLNTAMTGLKRGVANHNQVVQSDNYVNADTNKKNDYNNAYNHANDIINGNAQHPVI
TPSDVNNALSNVTSKEHALNGEAKLNAAKQEANTALGHLNNLNNAQRQNLQSQINGAHQIDAVNTIKQN
ATNLNSAMGNLRQAVADKDQVKRTEDYADADTAKQNAYNSAVSSAETIINQTTNPTMSVDDVNRATSAV
TSNKNALNGYEKLAQSKTDAARAIDALPHLNNAQKADVKSKINAASNIAGVNTVKQQGTDLNTAMGNLQ
GAINDEQTTLNSQNYQDATPSKKTAYTNAVQAAKDILNKSNGQNKTKDQVTEAMNQVNSAKNNLDGTRL
LDQAKQTAKQQLNNMTHLTTAQKTNLTNQINSGTTVAGVQTVQSNANTLDQAMNTLRQSIANKDATKA
SEDYVDANNDKQTAYNNAVAAAETIINANSNPEMNPSTITQKAEQVNSSKTALNGDENLAAAKQNAKTYL
NTLTSITDAQKNNLISQITSATRVSGVDTVKQNAQHLDQAMASLQNGINNESQVKSSEKYRDADTNKQQE
YDNAITAAKAILNKSTGPNTAQNAVEAALQRVNNAKDALNGDAKLIAAQNAAKQHLGTLTHITTAQRNDLT
NQISQATNLAGVESVKQNANSLDGAMGNLQTAINDKSGTLASQNFLDADEQKRNAYNQAVSAAETILNK
QTGPNTAKTAVEQALNNVNNAKHALNGTQNLNNAKQAAITAINGASDLNQKQKDALKAQANGAQRVSN
AQDVQHNATELNTAMGTLKHAIADKTNTLASSKYVNADSTKQNAYTTKVTNAEHIISGTPTVVTTPSEVTA
AANQVNSAKQELNGDERLREAKQNANTAIDALTQLNTPQKAKLKEQVGQANRLEDVQTVQTNGQALNN
AMKGLRDSIANETTVKTSQNYTDASPNNQSTYNSAVSNAKGIINQTNNPTMDTSAITQATTQVNNAKNGL
NGAENLRNAQNTAKQNLNTLSHLTNNQKSAISSQIDRAGHVSEVTATKNAATELNTQMGNLEQAIHDQN
TVKQSVKFTDADKAKRDAYTNAVSRAEAILNKTQGANTSKQDVEAAIQNVSSAKNALNGDQNVTNAKNA
AKNALNNLTSINNAQKRDLTTKIDQATTVAGVEAVSNTSTQLNTAMANLQNGINDKTNTLASENYHDADS
DKKTAYTQAVTNAENILNKNSGSNLDKTAVENALSQVANAKGALNGNHNLEQAKSNANTTINGLQHLTTA
QKDKLKQQVQQAQNVAGVDTVKSSANTLNGAMGTLRNSIQDNTATKNGQNYLDATERNKTNYNNAVD
SANGVINATSNPNMDANAINQIATQVTSTKNALDGTHNLTQAKQTATNAIDGATNLNKAQKDALKAQVT
SAQRVANVTSIQQTANELNTAMGQLQHGIDDENATKQTQKYRDAEQSKKTAYDQAVAAAKAILNKQTGS
NSDKAAVDRALQQVTSTKDALNGDAKLAEAKAAAKQNLGTLNHITNAQRTDLEGQINQATTVDGVNTVK
TNANTLDGAMNSLQGSINDKDATLRNQNYLDADESKRNAYTQAVTAAEGILNKQTGGNTSKADVDNALN
AVTRAKAALNGADNLRNAKTSATNTIDGLPNLTQLQKDNLKHQVEQAQNVAGVNGVKDKGNTLNTAMG
ALRTSIQNDNTTKTSQNYLDASDSNKNNYNTAVNNANGVINATNNPNMDANAINGMANQVNTTKAALN
GAQNLAQAKTNATNTINNAHDLNQKQKDALKTQVNNAQRVSDANNVQHTATELNSAMTALKAAIADKE
RTKASGNYVNADQEKRQAYDSKVTNAENIISGTPNATLTVNDVNSAASQVNAAKTALNGDNNLRVAKEHA
NNTIDGLAQLNNAQKAKLKEQVQSATTLDGVQTVKNSSQTLNTAMKGLRDSIANEATIKAGQNYTDASPN
NRNEYDSAVTAAKAIINQTSNPTMEPNTITQVTSQVTTKEQALNGARNLAQAKTTAKNNLNNLTSINNAQK
DALTRSIDGATTVAGVNQETAKATELNNAMHSLQNGINDETQTKQTQKYLDAEPSKKSAYDQAVNAAKAI
LTKASGQNVDKAAVEQALQNVNSTKTALNGDAKLNEAKAAAKQTLGTLTHINNAQRTALDNEITQATNVE
GVNTVKAKAQQLDGAMGQLETSIRDKDTTLQSQNYQDADDAKRTAYSQAVNAAATILNKTAGGNTPKAD
VERAMQAVTQANTALNGIQNLDRAKQAANTAITNASDLNTKQKEALKAQVTSAGRVSAANGVEHTATEL
NTAMTALKRAIADKAETKASGNYVNADANKRQAYDEKVTAAENIVSGTPTPTLTPADVTNAATQVTNAKT
QLNGNHNLEVAKQNANTAIDGLTSLNGPQKAKLKEQVGQATTLPNVQTVRDNAQTLNTAMKGLRDSIAN
EATIKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQVTAKQQALNGQENLRTAQ
TNAKQHLNGLSDLTDAQKDAVKRQIEGATHVNEVTQAQNNADALNTAMTNLKNGIQDQNTIKQGVNFT
DADEAKRNAYTNAVTQAEQILNKAQGPNTSKDGVETALENVQRAKNELNGNQNVANAKTTAKNALNNLT
SINNAQKEALKSQIEGATTVAGVNQVSTTASELNTAMSNLQNGINDEAATKAALNGTQNLEKAKQHANTA
IDGLSHLTNAQKEALKQLVQQSTTVAEAQGNEQKANNVDAAMDKLRQSIADNATTKQNQNYTDASQNK
KDAYNNAVTTAQGIIDQTTSPTLDPTVINQAAGQVSTTKNALNGNENLEAAKQQASQSLGSLDNLNNAQK
QTVTDQINGAHTVDEANQIKQNAQNLNTAMGNLKQAIADKDATKATVNFTDADQAKQQAYNTAVTNAE
NIISKANGGNATQAEVEQAIKQVNAAKQALNGNANVQHAKDEATALINSSNDLNQAQKDALKQQVQNA
TTVAGVNNVKQTAQELNNAMTQLKQGIADKEQTKADGNFVNADPDKQNAYNQAVAKAEALISATPDVV
VTPSEITAALNKVTQAKNDLNGNTNLATAKQNVQHAIDQLPNLNQAQRDEYSKQITQATLVPNVNAIQQA
ATTLNDAMTQLKQGIANKAQIKGSENYHDADTDKQTAYDNAVTKAEELLKQTTNPTMDPNTIQQALTKVN
DTNQALNGNQKLADAKQDAKTTLGTLDHLNDAQKQALTTQVEQAPDIATVNNVKQNAQNLNNAMTNL

```
NNALQDKTETLNSINFTDADQAKKDAYTNAVSHAEGILSKANGSNASQTEVEQAMQRVNEAKQALNGND
NVQRAKDAAKQVITNANDLNQAMTQLKQGIADKDQTKANGNFVNADTDKQNAYNNAVAHAEQIISGTP
NANVDPQQVAQALQQVNQAKGDLNGNHNLQVAKDNANTAIDQLPNLNQPQKTALKDQVSHAELVTGV
NAIKQNADALNNAMGTLKQQIQANSQVPQSVDFTQADQDKQQAYNNAANQAQQIANGIPTPVLTPDTV
TQAVTTMNQAKDALNGDEKLAQAKQEALANLDTLRDLNQPQRDALRNQINQAQALATVEQTKQNAQN
VNTAMSNLKQGIANKDTVKASENYHDADADKQTAYTNAVSQAEGIINQTTNPTLNPDEITRALTQVTDAK
NGLNGEAKLATEKQNAKDAVSGMTHLNDAQKQALKGQIDQSPEIATVNQVKQTATSLDQAMDQLSQAI
NDKAQTLADGNYLNADPDKQNAYKQAVAKAEALLNKQSGTNEVQAQVESITNEVNAAKQALNGNDNLA
NAKQQAKQQLANLTHLNDAQKQSFESQITQAPLVTDVTTINQKAQTLDHAMELLRNSVADNQTTLASEDY
HDATAQRQNDYNQAVTAANNIINQTTSPTMNPDDVNGATTQVNNTKVALDGDENLAAAKQQANNRLD
QLDHLNNAQKQQLQSQITQSSDIAAVNGHKQTAESLNTAMGNLINAIADHQAVEQRGNFINADTDKQTA
YNTAVNEAAAMINKQTGQNANQTEVEQAITKVQTTLQALNGDHNLQVAKTNATQAIDALTSLNDPQKTA
LKDQVTAATLVTAVHQIEQNANTLNQAMHGLRQSIQDNAATKANSKYINEDQPEQQNYDQAVQAANNII
NEQTATLDNNAINQAATTVNTTKAALHGDVKLQNDKDHAKQTVSQLAHLNNAQKHMEDTLIDSETTRTA
VKQDLTEAQALDQLMDALQQSIADKDATRASSAYVNAEPNKKQSYDEAVQNAESIIAGLNNPTINKGNVSS
ATQAVISSKNALDGVERLAQDKQTAGNSLNHLDQLTPAQQQALENQINNATTRDKVAEIIAQAQALNEAM
KALKESIKDQPQTEASSKFINEDQAQKDAYTQAVQHAKDLINKTTDPTLAKSIIDQATQAVTDAKNNLHGD
QKLAQDKQRATETLNNLSNLNTPQRQALENQINNAATRGEVAQKLTEAQALNQAMEALRNSIQDQQQTE
AGSKFINEDKPQKDAYQAAVQNAKDLINQTNNPTLDKAQVEQLTQAVNQAKDNLHGDQKLADDKQHAV
TDLNQLNGLNNPQRQALESQINNAATRGEVAQKLAEAKALDQAMQALRNSIQDQQQTESGSKFINEDKP
QKDAYQAAVQNAKDLINQTGNPTLDKSQVEQLTQAVTTAKDNLHGDQKLARDQQQAVTTVNALPNLNH
AQQQALTDAINAAPTRTEVAQHVQTATELDHAMETLKNKVDQVNTDKAQPNYTEASTDKKEAVDQALQ
AAESITDPTNGSNANKDAVDQVLTKLQEKENELNGNERVAEAKTQAKQTIDQLTHLNADQIATAKQNIDQ
ATKLQPIAELVDQATQLNQSMDQLQQAVNEHANVEQTVDYTQADSDKQNAYKQAIADAENVLKQNANK
QQVDQALQNILNAKQALNGDERVALAKTNGKHDIDQLNALNNAQQDGFKGRIDQSNDLNQIQQIVDEAK
ALNRAMDQLSQEITDNEGRTKGSTNYVNADTQVKQVYDETVDKAKQALDKSTGQNLTAKQVIKLNDAVT
AAKKALNGEERLNNRKAEALQRLDQLTHLNNAQRQLAIQQINNAETLNKASRAINRATKLDNAMGSVQQY
IDEQHLGVISSTNYINADDNLKANYDNAIANAAHELDKVQGNAIAKAEAEQLKQNIIDAQNALNGDQNLAN
AKDKANAFVNSLNGLNQQQQDLAHKAINNADTVSDVTDIVNNQIDLNDAMETLKHLVDNEIPNAEQTVN
YQNADDNAKTNFDDAKRLANTLLNSDNTNVNDINGAIQAVNDAIHNLNGDQRLQDAKDKAIQSINQALA
NKLKEIEASNATDQDKLIAKNKAEELANSIINNINKATSNQAVSQVQTAGNHAIEQVHANEIPKAKIDANKD
VDKQVQALIDEIDRNPNLTDKEKQALKDRINQILQQGHNGINNAMTKEEIEQAKAQLAQALQDIKDLVKAK
EDAKQDVDKQVQALIDEIDQNPNLTDKEKQALKDRINQILQQGHNDINNAMTKEAIEQAKERLAQALQDIK
DLVKAKEDAKNDIDKRVQALIDEIDQNPNLTDKEKQALKDRINQILQQGHNDINNALTKEEIEQAKAQLAQA
LQDIKDLVKAKEDAKNAIKALANAKRDQINSNPDLTPEQKAKALKEIDEAEKRALQNVENAQTIDQLNRGLN
LGLDDIRNTHVWEVDEQPAVNEIFEATPEQILVNGELIVHRDDIITEQDILAHINLIDQLSAEVIDTPSTATISDS
LTAKVEVTLLDGSKVIVNVPVKVVEKELSVVKQQAIESIENAAQQKINEINNSVTLTLEQKEAAIAEVNKLKQQ
AIDHVNNAPDVHSVEEIQQQEQAHIEQFNPEQFTIEQAKSNAIKSIEDAIQHMIDEIKARTDLTDKEKQEAIA
KLNQLKEQAIQAIQRAQSIDEISEQLEQFKAQMKAANPTAKELAKRKQEAISRIKDFSNEKINSIRNSEIGTAD
EKQAAMNQINEIVLETIRDINNAHTLQQVEAALNNGIARISAVQIVTSDRAKQSSSTGNESNSHLTIGYGTAN
HPFNSSTIGHKKKLDEDDDIDPLHMRHFSNNFGNVIKNAIGVVGISGLLASFWFFIAKRRRKEDEEEELEIRD
NNKDSIKETLDDTKHLPLLFAKRRRKEDEEDVTVEEKDSLNNGESLDKVKHTPFFLPKRRRKEDEEDVEVTNE
NTDEKVLKDNEHSPLLFAKRRKDKEEDVETTTSIESKDEDVPLLLAKKKNQKDNQSKDKKSASKNTSKKVAAK
KKKKKAKKNKK

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126
```

```
    3 - 10:        yRd.KiqKf
    135 - 139:     sK..H..Kq
    256 - 262:     sR..RsnRi
    347 - 354:     iKfnKg.Ha
    350 - 357:     nKg.HapHq
    412 - 420:     pHrsHdfKi
    415 - 422:     sHdfKi.Rn
    418 - 424:     fKi.Rn.Rs
    672 - 680:     qHniKffKn
    780 - 786:     iRfgR..Ke
    791 - 797:     iRv.Kp.Ht
    1256 - 1263:   nKg.RltKs
    1577 - 1584:   vKplRd.Ky
    1580 - 1586:   lRd.Ky.Rv
    2514 - 2520:   tKadK..Re
    2637 - 2641:   aK..K..Re
    2666 - 2670:   eK..H..Rv
    2777 - 2784:   lKtaKt.Kl
    4110 - 4117:   eRl.ReaKq
    4133 - 4139:   qKa.Kl.Ke
    4313 - 4318:   dKa.K..Rd
    4511 - 4517:   qKd.Kl.Kq
    5055 - 5061:   dKe.Rt.Ka
    5120 - 5127:   lRvaKe.Ha
    5141 - 5147:   qKa.Kl.Ke
    5645 - 5651:   qKa.Kl.Ke
    5952 - 5958:   eKa.Kq.Ha
    7434 - 7440:   dKd.Ha.Kq
    8902 - 8909:   qKa.KalKe
    9202 - 9206:   aK..R..Kq
    9314 - 9319:   gHk.K..Kl
    9328 - 9333:   lHm.R..Hf
    9362 - 9368:   aKrrR..Ke
    9399 - 9405:   aKrrR..Ke
    9425 - 9430:   dKv.K..Ht
    9435 - 9441:   pKrrR..Ke
    9469 - 9476:   aKrrKd.Ke
    9497 - 9504:   aKk.KnqKd
    9507 - 9512:   sKd.K..Ks
    9523 - 9530:   aKkkKk.Ka
    9524 - 9532:   kKkkKkaKk
    9525 - 9533:   kKkkKakKn
    9527 - 9535:   kKkaKknKk

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    3 - 15:        yRdkiqKfsirKy
```

131 - 139: dKeqs.Kh...Kq
152 - 161: nRaa..Hven.He
191 - 200: yHdy..Rfid.Re
246 - 258: iRtmpqRqqtsRr
251 - 262: qRqqtsRrsn.Ri
256 - 266: sRrsn.Riqt.Rs
260 - 271: nRiqt.RsvesRa
264 - 276: tRsvesRaaepRs
347 - 357: iKfnkgHap..Hq
412 - 422: pHrs..HdfkiRn
413 - 424: hRshdfKirn.Rs
535 - 545: dHqq..RlnglRq
538 - 550: qRlnglRqvvnRt
543 - 553: lRqvvnRty..Ri
548 - 558: nRty..RigttKr
636 - 644: aRt...Rnpi.Rl
672 - 680: qHni..Kff..Kn
688 - 698: eKpfs.Kqag.Hp
755 - 764: nRpnnaRe...Rn
791 - 797: iRv...Kp...Ht
1005 - 1015: sKhvsiHvg..Ki
1256 - 1263: nKg...Rlt..Ks
1433 - 1443: dHvv..KsnstHn
1577 - 1586: vKplrdKy...Rv
1753 - 1763: tKtatyKvv..Rt
1758 - 1768: yKvv..RtvpkHv
1842 - 1851: sKv...KpdppRi
2038 - 2047: aKaps.Rdv..Kg
2173 - 2185: nKpnvaKvvnaKy
2582 - 2591: tKv...RaaqtKi
2584 - 2596: vRaaqtKidqaKa
2777 - 2784: lKta..Kt...Kl
2836 - 2844: eKt...Kvee.Ky
2838 - 2849: tKvee.KynslKq
2891 - 2900: eKlsaaRt...Ki
2974 - 2983: aKltaaRn...Ki
3009 - 3018: aKsdldHa...Rq
3057 - 3066: qKlqaaRq...Kl
3211 - 3221: qKaasvKst..Kd
3480 - 3492: eKlaqsKtdaaRa
3503 - 3511: qKadv.Ks...Ki
3799 - 3807: vKsse.Ky...Rd
4005 - 4013: qKq...Kdal.Ka
4110 - 4117: eRl...Rea..Kq
4133 - 4139: qKa...Kl...Ke
4511 - 4517: qKd...Kl...Kq
4634 - 4643: nKaq..Kdal.Ka
4681 - 4689: tKqtq.Ky...Rd
4740 - 4751: aKlaeaKaaa.Kq
5008 - 5017: aHdlnqKq...Kd

5013 - 5021: qKq...Kdal.Kt
5055 - 5061: dKe...Rt...Ka
5120 - 5127: lRva..Ke...Ha
5141 - 5147: qKa...Kl...Ke
5370 - 5381: aKlneaKaaa.Kq
5517 - 5525: tKq...Keal.Ka
5554 - 5565: kRaiadKaet.Ka
5645 - 5651: qKa...Kl...Ke
5952 - 5958: eKa...Kq...Ha
6453 - 6464: qKladaKqda.Kt
6582 - 6590: qRa...Kdaa.Kq
6697 - 6708: qKtal.KdqvsHa
6926 - 6937: aKlateKqna.Kd
7005 - 7017: dKqnayKqavaKa
7421 - 7431: tKaal.Hgdv.Kl
7425 - 7436: lHgdv.KlqndKd
7429 - 7440: vKlqndKdha.Kq
7609 - 7618: mKal..Kesi.Kd
7644 - 7653: qHa...KdlinKt
7673 - 7683: aKnnl.Hgdq.Kl
7677 - 7688: lHgdq.KlaqdKq
7681 - 7690: qKlaqdKq...Ra
7799 - 7809: aKdnl.Hgdq.Kl
7803 - 7814: lHgdq.KladdKq
7807 - 7816: qKladdKq...Ha
7925 - 7935: aKdnl.Hgdq.Kl
7929 - 7938: lHgdq.Kla..Rd
8059 - 8070: eRvaeaKtqa.Kq
8181 - 8193: eRvalaKtngkHd
8271 - 8280: dKa...KqaldKs
8346 - 8355: nKas..Rain.Ra
8349 - 8358: sRain.Rat..Kl
8559 - 8568: qRlqdaKd...Ka
8592 - 8600: dKlia.Kn...Ka
8640 - 8649: pKa...KidanKd
8642 - 8653: aKidanKdvd.Kq
8669 - 8677: dKe...Kqal.Kd
8671 - 8679: eKqal.Kd...Ri
8713 - 8721: iKdlv.Ka...Ke
8717 - 8725: vKa...Keda.Kq
8719 - 8730: aKeda.KqdvdKq
8746 - 8754: dKe...Kqal.Kd
8748 - 8756: eKqal.Kd...Ri
8790 - 8798: iKdlv.Ka...Ke
8794 - 8802: vKa...Keda.Kn
8796 - 8807: aKeda.KndidKr
8823 - 8831: dKe...Kqal.Kd
8825 - 8833: eKqal.Kd...Ri
8867 - 8875: iKdlv.Ka...Ke
8871 - 8879: vKa...Keda.Kn

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    8873 - 8883:    aKeda.Knai.Ka
    8902 - 8909:    qKa...Kal..Ke
    9198 - 9206:    aKela.Kr...Kq
    9362 - 9368:    aKr...Rr...Ke
    9376 - 9386:    iRdnn.Kdsi.Ke
    9399 - 9405:    aKr...Rr...Ke
    9435 - 9441:    pKr...Rr...Ke
    9455 - 9464:    eKvl..Kdne.Hs
    9469 - 9476:    aKrr..Kd...Ke
    9497 - 9509:    aKkknqKdnqsKd
    9502 - 9512:    qKdnqsKdk..Ks
    9507 - 9516:    sKdk..Ksas.Kn
    9509 - 9521:    dKksasKntskKv
    9514 - 9526:    sKntskKvaakKk
    9518 - 9530:    sKkvaaKkkkkKa
    9523 - 9535:    aKkkkkKakknKk

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    412 - 417:      pHRsHd
    9314 - 9319:    gHKkKl
    9362 - 9367:    aKRrRk
    9363 - 9368:    kRRrKe
    9399 - 9404:    aKRrRk
    9400 - 9405:    kRRrKe
    9435 - 9440:    pKRrRk
    9436 - 9441:    kRRrKe
    9469 - 9474:    aKRrKd
    9471 - 9476:    rRKdKe
    9523 - 9528:    aKKkKk
    9524 - 9529:    kKKkKk
    9525 - 9530:    kKKkKa
    9527 - 9532:    kKKaKk
    9530 - 9535:    aKKnKk

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    4313 - 4318:    dKaKRd
    9314 - 9319:    gHkKKl
    9328 - 9333:    lHmRHf
    9362 - 9367:    aKrRRk
    9363 - 9368:    kRrRKe
    9399 - 9404:    aKrRRk
    9400 - 9405:    kRrRKe
```

```
    9425 - 9430:    dKvKHt
    9435 - 9440:    pKrRRk
    9436 - 9441:    kRrRKe
    9469 - 9474:    aKrRKd
    9507 - 9512:    sKdKKs
    9523 - 9528:    aKkKKk
    9524 - 9529:    kKkKKk
    9525 - 9530:    kKkKKa
    9528 - 9533:    kKaKKn

  >USERPAT1 (user pattern) :
  Pattern: X-[HRK]-[HRK]-[HRK]-X-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 14782

    9469 - 9476:    aKRRkdKe
    9497 - 9504:    aKKKnqKd
    9523 - 9530:    aKKKkkKa
    9525 - 9532:    kKKKkaKk
    9526 - 9533:    kKKKakKn


>tr|Q2FY01|Q2FY01_STAA8  (315 aa)
SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:ABD30748.1};.  [Staphylococcus
aureus (strain NCTC 8325)]
MPGIIQIDDMNQSQALIGNNDEHLKAIEESFDVVIHARGQEVAVKGTKIENVEKAESVLINLLKVIDLGNNITI
KDVEAAIKMAHNNTIQHLLDLYDEEITKDAFGKTIRAKTMGQRIYVNAMKNNDLVFGIGPAGTGKTFLAVV
YAAKQLRKGAVKRIVLTRPAVEAGESLGFLPGDLKEKVDPYLRPLYDGLYTVLGREQTERFIERGIIEIAPLAYM
RGRTLEDAFVILDEAQNTTHAQMKMFLTRLGFGSKMVVTGDQTQIDLPKGVKSGLKEAVSRLHNVKGISIL
KLDQSDVVRHPLVSKIIEHYEGEN

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    101 - 113:     tKdafgKtiraKt
    106 - 118:     gKtiraKtmgqRi
    148 - 159:     aKqlr.KgavkRi
    152 - 164:     rKgavkRivltRp
    199 - 210:     gReqteRfie.Rg
    239 - 250:     tHaqm.KmfltRl
    268 - 277:     pKgv..Ksgl.Ke
    271 - 282:     vKsgl.KeavsRl
    275 - 287:     lKeavsRlhnvKg
    300 - 311:     rHplvsKiie.Hy

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
```

```
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     106 - 113:     gKtiRa.Kt
     148 - 154:     aKqlR..Kg
     280 - 287:     sRl.HnvKg


>sp|Q2FXY6|RS20_STAA8  (83 aa)
RecName: Full=30S ribosomal protein S20 {ECO:0000255|HAMAP-Rule:MF_00500};.
[Staphylococcus aureus (strain NCTC 8325)]
MANIKSAIKRVKTTEKAEARNISQKSAMRTAVKNAKTAVSNNADNKNELVSLAVKLVDKAAQSNLIHSNKA
DRIKSQLMTANK

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     4 - 13:       iKsaikRv...Kt
     8 - 17:       iKrv..Ktte.Ka
     11 - 21:       vKtte.Kaea.Rn
     15 - 26:       eKaea.RnisqKs
     19 - 30:       aRnisqKsam.Rt
     24 - 34:       qKsam.Rtav.Kn
     28 - 37:       mRtav.Kna..Kt
     66 - 76:       iHsn..KadriKs

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     8 - 13:       iKRvKt

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     8 - 13:       iK..Rv.Kt
     66 - 74:       iHsnKadRi
     69 - 76:       nKadRi.Ks


>sp|Q2FXQ1|RL20_STAA8  (118 aa)
RecName: Full=50S ribosomal protein L20 {ECO:0000255|HAMAP-Rule:MF_00382};.
[Staphylococcus aureus (strain NCTC 8325)]
MPRVKGGTVTRARRKKTIKLAKGYFGSKHTLYKVAKQQVMKSGQYAFRDRRQRKRDFRKLWITRINAAAR
QHEMSYSRLMNGLKKAGIDINRKMLSEIAISDEKAFAQLVTKAKDALK
```

```
  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     10 - 15:       tRaRRk
     12 - 17:       aRrKKt
     47 - 52:       fRdRRq
     50 - 55:       rRqRKr

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     10 - 17:       tRarRk.Kt
     12 - 20:       aRrkKtiKl
     15 - 23:       kKtiKlaKg
     47 - 55:       fRdrRqrKr
     49 - 56:       dRrqRk.Rd
     52 - 59:       qRk.RdfRk
     54 - 60:       kRdfR..Kl

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     10 - 20:       tRarrkKti..Kl
     13 - 23:       rRkktiKla..Kg
     27 - 37:       sKhtlyKva..Kq
     32 - 42:       yKva..KqqvmKs
     47 - 59:       fRdrrqRkrdfRk
     49 - 60:       dRrqrkRdfr.Kl
     53 - 65:       rKrdfrKlwitRi

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     12 - 17:       aRRkKt
     49 - 54:       dRRqRk

  >USERPAT1 (user pattern) :
  Pattern: X-[HRK]-[HRK]-[HRK]-X-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 14782
```

```
    13 - 20:      rRKKtiKl
    52 - 59:      qRKRdfRk


>sp|Q2FXQ0|RL35_STAA8  (66 aa)
RecName: Full=50S ribosomal protein L35 {ECO:0000255|HAMAP-Rule:MF_00514};.
[Staphylococcus aureus (strain NCTC 8325)]
MPKMKTHRGAAKRVKRTASGQLKRSRAFTSHLFANKSTKQKRQLRKARLVSKSDMKRVKQLLAYKK

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    2 - 9:       pKm.KthRg
    11 - 17:      aKrvK..Rt
    22 - 27:      lK..Rs.Ra
    35 - 43:      nKstKqkRq
    38 - 46:      tKqkRqlRk
    41 - 49:      kRqlRkaRl
    55 - 60:      mK..Rv.Kq

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    2 - 14:       pKmkthRgaakRv
    6 - 17:       tHrgaaKrvk.Rt
    22 - 32:      lKrs..RaftsHl
    25 - 37:      sRaftsHlfanKs
    30 - 42:      sHlfanKstkqKr
    35 - 47:      nKstkqKrqlrKa
    40 - 49:      qKrqlrKa...Rl
    44 - 53:      lRka..Rlvs.Ks
    47 - 58:      aRlvs.KsdmkRv
    51 - 60:      sKsdmkRv...Kq

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    4 - 9:       mKtHRg
    12 - 17:      kRvKRt
    38 - 43:      tKqKRq

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
```

```
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     11 - 16:       aKRvKr
     22 - 27:       lKRsRa
     44 - 49:       lRKaRl
     55 - 60:       mKRvKq


>sp|Q2FW31|RS11_STAA8  (129 aa)
RecName: Full=30S ribosomal protein S11 {ECO:0000255|HAMAP-Rule:MF_01310};.
[Staphylococcus aureus (strain NCTC 8325)]
MARKQVSRKRRVKKNIENGVAHIRSTFNNTIVTITDEFGNALSWSSAGALGFKGSKKSTPFAAQMASETASK
SAMEHGLKTVEVTVKGPGPGRESAIRALQSAGLEVTAIRDVTPVPHNGCRPPKRRRV

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     2 - 14:       aRkqvsRkrrvKk
     3 - 15:       rKqvsrKrrvkKn
     71 - 81:       sKsameHgl..Kt
     117 - 128:     pHngc.RppkrRr
     121 - 129:     cRppk.Rr...Rv

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     7 - 12:       sRKrRv
     9 - 14:       kRRvKk
     124 - 129:     pKRrRv

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     7 - 12:       sRkRRv
     10 - 15:       rRvKKn
     124 - 129:     pKrRRv

  >USERPAT1 (user pattern) :
  Pattern: X-[HRK]-[HRK]-[HRK]-X-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 14782

     7 - 14:       sRKRrvKk
```

```
    8 - 15:        rKRRvkKn

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    7 - 15:        sRkrRvkKn
    52 - 58:        fKgsK..Ks
    121 - 129:      cRppKrrRv


>sp|Q2FW22|RL18_STAA8  (119 aa)
RecName: Full=50S ribosomal protein L18 {ECO:0000255|HAMAP-Rule:MF_01337};.
[Staphylococcus aureus (strain NCTC 8325)]
MISKIDKNKVRLKRHARVRTNLSGTAEKPRLNVYRSNKHIYAQIIDDNKGVTLAQASSKDSDIATTATKVELA
TKVGEAIAKKAADKGIKEIVFDRGGYLYHGRVKALAEAARESGLEF

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    3 - 10:        sKidKn.Kv
    6 - 12:        dKn.Kv.Rl
    8 - 15:        nKv.RlkRh
    10 - 18:        vRlkRhaRv
    13 - 20:        kRhaRv.Rt
    34 - 40:        yRsnK..Hi
    101 - 107:      yHg.Rv.Ka

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    3 - 15:        sKidknKvrlkRh
    6 - 16:        dKnkv.Rlkr.Ha
    8 - 20:        nKvrlkRharvRt
    27 - 36:        eKp...RlnvyRs
    29 - 40:        pRlnvyRsnk.Hi
    81 - 91:        aKkaadKgi..Ke
    101 - 107:      yHg...Rv...Ka

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    10 - 15:        vRlKRh
```

```
  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     13 - 18:      kRHaRv


>sp|Q2FW14|RL29_STAA8  (69 aa)
RecName: Full=50S ribosomal protein L29 {ECO:0000255|HAMAP-Rule:MF_00374};.
[Staphylococcus aureus (strain NCTC 8325)]
MKAKEIRDLTTSEIEEQIKSSKEELFNLRFQLATGQLEETARIRTVRKTIARLKTVAREREIEQSKANQ

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     1 - 8:        mKa.KeiRd
     41 - 48:      aRi.RtvRk
     43 - 49:      iRtvR..Kt

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     1 - 8:        mKa...Kei..Rd
     41 - 53:      aRirtvRktiaRl
     46 - 55:      vRktiaRl...Kt
     51 - 59:      aRl...Ktva.Re
     53 - 61:      lKtva.Re...Re


>sp|Q2FW11|RL22_STAA8  (117 aa)
RecName: Full=50S ribosomal protein L22 {ECO:0000255|HAMAP-Rule:MF_01331};.
[Staphylococcus aureus (strain NCTC 8325)]
MEAKAVARTIRIAPRKVRLVLDLIRGKNAAEAIAILKLTNKASSPVIEKVLMSALANAEHNYDMNTDELVVKE
AYANEGPTLKRFRPRAQGRASAINKRTSHITIVVSDGKEEAKEA

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     3 - 12:       aKava.Rti..Ri
     7 - 17:       aRti..RiaprKv
     10 - 19:      iRiaprKv...Rl
     82 - 93:      lKrfrpRaqg.Ra
```

```
   >USERPAT2 (user pattern) :
   Pattern: X-[HRK]-[HRK]-X-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

      14 - 19:       pRKvRl
      82 - 87:       lKRfRp

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

      14 - 19:       pR..Kv.Rl
      82 - 89:       lKrfRp.Ra
      97 - 103:       nK..RtsHi


>tr|Q2FVQ4|Q2FVQ4_STAA8  (532 aa)
SubName: Full=L-lactate permease {ECO:0000313|EMBL:ABD31656.1};.  [Staphylococcus
aureus (strain NCTC 8325)]
MLVNTFNPFDNLLLSSLIAAIPIVLFLLCLTVFKMKGIYAAITTLVVTLLIAIPFFKLPVGIASGAVVEGFFQGIIPI
GYIVMMAVLLYKITVESGQFLTIQDSITNISQDQRIQVLLIGFAFNAFLEGAAGFGVPIAICALLLTQLGFNPLK
AAMLCLVANAASGAFGAIGIPVGVVETLKLPGDVSVLGVSQSATLTLAIINFIIPFLLIFIIDGFRGVKETLPAILV
VSITYTLTQGLLTVFSGPELADIIPPLLTMLALAVFSKKFQPKHIYRVNKDEEIEPAKAHSAKAVLHAWSPFIVLT
VIVMIWSAPFFKNLFLPNGALSSLVFKFNLPGTISEVTHKPLVLTLNIIGQTGTAILLTIIITILMSKKVNFKDAGR
LFGVTFKELWLPVLTICFILAISKITTYGGLSAAMGQGIAKAGNVFPVLSPILGWIGVFMTGSVVNNNSLFAPI
QASVAQQIGTSGSLLVSANTVGGVAAKLISPQSIAIATAAVKQVGKESELLKMTLKYSVCLLIFICIWTFILSLL

   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

      267 - 278:      sKkfqpKhiy.Rv
      272 - 281:      pKhiy.Rvn..Kd
      287 - 298:      aKahsaKavl.Ha
      373 - 384:      sKkvnfKdag.Rl

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

      272 - 278:      pK..HiyRv
      273 - 281:      kHiyRvnKd
      287 - 294:      aKa.HsaKa
```

```
>sp|P48940|RS7_STAA8  (156 aa)
RecName: Full=30S ribosomal protein S7 {ECO:0000255|HAMAP-Rule:MF_00480};.
[Staphylococcus aureus (strain NCTC 8325)]
MPRKGSVPKRDVLPDPIHNSKLVTKLINKIMLDGKRGTAQRILYSAFDLVEQRSGRDALEVFEEAINNIMPVL
EVKARRVGGSNYQVPVEVRPERRTTLGLRWLVNYARLRGEKTMEDRLANEILDAANNTGGAVKKREDTHK
MAEANKAFAHYRW

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    17 - 26:      iHns..Klvt.Kl
    20 - 30:      sKlvt.Klin.Ki
    108 - 120:      aRlrgeKtmedRl
    135 - 144:      vKk...RedthKm
    148 - 156:      nKafa.Hy...Rw

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    75 - 80:      vKaRRv

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    75 - 80:      vKa.R..Rv
    91 - 97:      vRpeR..Rt
    108 - 115:      aRl.RgeKt
    135 - 139:      vK..K..Re


>sp|Q2FW29|RL36_STAA8  (37 aa)
RecName: Full=50S ribosomal protein L36 {ECO:0000255|HAMAP-Rule:MF_00251};.
[Staphylococcus aureus (strain NCTC 8325)] MKVRPSVKPICEKCKVIKRKGKVMVICENPKHKQRQG

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    1 - 9:       mKv...Rpsv.Kp
    3 - 14:       vRpsv.KpiceKc
    7 - 19:       vKpiceKckviKr
    12 - 23:       eKckviKrkg.Kv
    30 - 36:       pKh...Kq...Rq
```

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  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    12 - 19:      eKc.KviKr
    14 - 21:      cKviKr.Kg
    17 - 23:      iKr.Kg.Kv
    30 - 36:      pKh.Kq.Rq

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    18 - 23:      kRKgKv
    31 - 36:      kHKqRq


>sp|Q2FZD3|MUTS2_STAA8  (782 aa)
RecName: Full=Endonuclease MutS2 {ECO:0000255|HAMAP-Rule:MF_00092};        EC=3.1.-.-
{ECO:0000255|HAMAP-Rule:MF_00092};.  [Staphylococcus aureus (strain NCTC 8325)]
MRQKTLDVLEFEKIKSLVANETISDLGLEKVNQMMPATNFETVVFQMEETDEIAQIYNKHRLPSLSGLSKVS
AFIHRADIGGVLNVSELNLIKRLIQVQNQFKTFYNQLVEEDEGVKYPILDDKMNQLPVLTDLFQQINETCDTY
DLYDNASYELQGIRSKISSTNQRIRQNLDRIVKSQANQKKLSDAIVTVRNERNVIPVKAEYRQDFNGIVHDQS
ASGQTLYIEPSSVVEMNNQISRLRHDEAIEKERILTQLTGYVAADKDALLVAEQVMGQLDFLIAKARYSRSIK
GTKPIFKEDRTVYLPKAYHPLLNRETVVANTIEFMEDIETVIITGPNTGGKTVTLKTLGLIIVMAQSGLLIPTLDG
SQLSVFKNVYCDIGDEQSIEQSLSTFSSHMTNIVEILKHADKHSLVLFDELGAGTDPSEGAALAMSILDHVRKI
GSLVMATTHYPELKAYSYNREGVMNASVEFDVDTLSPTYKLLMGVPGRSNAFDISKKLGLSLNIINKAKTMI
GTDEKEINEMIESLERNYKRVETQRLELDRLVKEAEQVHDDLSKQYQQFQNYEKSLIEEAKEKANQKIKAATK
EADDIIKDLRQLREQKGADVKEHELIDKKKRLDDHYEAKSIKQNVQKQKYDKIVAGDEVKVLSYGQKGEVLEI
VNDEEAIVQMGIIKMKLPIEDLEKKQKEKVKPTKMVTRQNRQTIKTELDLRGYRYEDALIELDQYLDQAVLSN
YEQVYIIHGKGTGALQKGVQQHLKKHKSVSDFRGGMPSEGGFGVTVATLK

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    58 - 62:      nK..H..Rl
    239 - 244:      sRl.R..Hd
    282 - 289:      aKa.RysRs
    284 - 292:      aRysRsiKg
    287 - 295:      sRsiKgtKp
    404 - 410:      lK..HadKh
    405 - 411:      kHadK..Hs
    436 - 441:      dHv.R..Ki
    528 - 534:      eRnyK..Rv
    592 - 600:      iKdlRqlRe
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    595 - 603:     lRqlReqKg
    613 - 618:     dKk.K..Rl
    632 - 639:     qKq.KydKi
    682 - 689:     eKkqKe.Kv
    685 - 691:     qKe.Kv.Kp
    687 - 694:     eKv.KptKm
    753 - 760:     qHlkKh.Ks

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    167 - 176:     qRi...RqnldRi
    169 - 179:     iRqnldRiv..Ks
    282 - 292:     aKarysRsi..Kg
    287 - 295:     sRsi..Kgt..Kp
    290 - 299:     iKgt..Kpif.Ke
    293 - 302:     tKpif.Ked..Rt
    306 - 316:     pKay..HpllnRe
    528 - 539:     eRnyk.RvetqRl
    532 - 544:     kRvetqRleldRl
    537 - 547:     qRleldRlv..Ke
    573 - 581:     aKe...Kanq.Ki
    575 - 583:     eKanq.Ki...Ka
    579 - 587:     qKi...Kaat.Ke
    592 - 600:     iKdl..Rql..Re
    595 - 603:     lRql..Req..Kg
    598 - 608:     lReq..KgadvKe
    601 - 610:     qKgadvKe...He
    606 - 615:     vKe...HelidKk
    608 - 618:     eHelidKkk..Rl
    613 - 622:     dKkk..Rldd.Hy
    615 - 626:     kKrlddHyea.Ks
    620 - 629:     dHyea.Ksi..Kq
    624 - 634:     aKsi..KqnvqKq
    627 - 639:     iKqnvqKqkydKi
    682 - 694:     eKkqkeKvkptKm
    687 - 698:     eKvkptKmvt.Rq
    692 - 701:     tKmvt.Rqn..Rq
    696 - 705:     tRqn..Rqti.Kt
    748 - 760:     qKgvqqHlkkhKs

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    239 - 244:     sRlRHd
    436 - 441:     dHvRKi
```

```
    613 - 618:     dKkKRl
    753 - 758:     qHlKKh
    755 - 760:     lKkHKs

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    613 - 618:     dKKkRl
    682 - 687:     eKKqKe
    755 - 760:     lKKhKs


>sp|Q2FXP9|IF3_STAA8  (175 aa)
RecName: Full=Translation initiation factor IF-3 {ECO:0000255|HAMAP-Rule:MF_00080};.
[Staphylococcus aureus (strain NCTC 8325)]
MSTIAKDQTQINDKIRAKELRLIGQDGEQIGVKSKREALKMAERVDLDLVVVAPNAKPPVARIMDYGKFKFE
QQKKEKEMKKKQKIINVKEIRLSPTIEEHDFQTKLKNGRKFLTKGDKCKVSIRFRGRAITHKEIGQRVLEKYAD
ECKDIATVEQKPKMDGRQMFIMLAPTAEK

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    13 - 19:      dKi.Ra.Ke
    15 - 22:      iRa.KelRl
    32 - 37:      vKs.K..Re
    74 - 82:      qKkeKemKk
    77 - 84:      eKemKk.Kq
    80 - 86:      mKk.Kq.Ki
    105 - 112:     tKl.KngRk
    107 - 113:     lKngR..Kf
    115 - 122:     tKgdKc.Kv
    124 - 130:     iRf.Rg.Ra

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    13 - 22:      dKira.Kel..Rl
    32 - 41:      vKsk..Real.Km
    34 - 45:      sKrealKmae.Rv
    67 - 76:      gKf...KfeqqKk
    69 - 79:      fKfeqqKke..Ke
    74 - 84:      qKke..KemkkKq
    75 - 86:      kKekemKkkq.Ki
    80 - 91:      mKkkq.KiinvKe
```

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    84 - 94:       qKiinvKei..Rl
    100 - 112:     eHdfqtKlkngRk
    105 - 117:     tKlkngRkfltKg
    110 - 122:     gRkfltKgdkcKv
    115 - 126:     tKgdkcKvsi.Rf
    120 - 130:     cKvsi.Rfrg.Ra
    124 - 135:     iRfrg.RaithKe
    128 - 140:     gRaithKeigqRv
    133 - 144:     hKeigqRvle.Ky
    156 - 164:     qKp...Kmdg.Rq

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    32 - 37:       vKsKRe

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    74 - 79:       qKKeKe
    81 - 86:       kKKqKi


>tr|Q2FXM1|Q2FXM1_STAA8  (137 aa)
SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:ABD30882.1};.  [Staphylococcus
aureus (strain NCTC 8325)]
MYKNILLGVDTQLKNEKALKEVSKLAGEGTVVTVLNAISEQDAQASIKAGVHLNKLTEERSKRLEKTRKALED
YGIDYDQIIVRGNAKEELLKHANSGKYEIVVLSNRKAEDKKKFVLGSVSHKVAKRATIPVLIVK

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    13 - 21:       lKneKalKe
    59 - 67:       eRskRleKt
    62 - 70:       kRleKtrKa
    112 - 116:     dK..K..Kf
    122 - 128:     sH..KvaKr
    123 - 129:     hKvaK..Ra

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669
```

```
   13 - 21:      lKne..Kal..Ke
   16 - 25:      eKal..Kevs.Kl
   47 - 56:      iKagv.Hln..Kl
   51 - 61:      vHln..KlteeRs
   54 - 64:      nKlteeRsk..Rl
   59 - 69:      eRsk..RlektRk
   61 - 70:      sKrle.Ktr..Ka
   83 - 94:      vRgna.KeellKh
   107 - 116:     nRkaedKk...Kf

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

   59 - 64:      eRsKRl
   65 - 70:      eKtRKa


>sp|Q2FXK6|RS4_STAA8  (200 aa)
RecName: Full=30S ribosomal protein S4 {ECO:0000255|HAMAP-Rule:MF_01306};.
[Staphylococcus aureus (strain NCTC 8325)]
MARFRGSNWKKSRRLGISLSGTGKELEKRPYAPGQHGPNQRKKLSEYGLQLREKQKLRYLYGMTERQFRNT
FDIAGKKFGVHGENFMILLASRLDAVVYSLGLARTRRQARQLVNHGHILVDGKRVDIPSYSVKPGQTISVREK
SQKLNIIVESVEINNFVPEYLNFDADSLTGTFVRLPERSELPAEINEQLIVEYYSR

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

   2 - 11:      aRf...RgsnwKk
   4 - 15:      fRgsnwKksr.Rl
   35 - 44:      qHgpnqRk...Kl
   51 - 59:      lRekq.Kl...Ry
   104 - 112:     aRtr..Rqa..Rq
   106 - 117:     tRrqa.RqlvnHg
   110 - 119:     aRqlvnHg...Hi
   141 - 148:     vRe...Ksq..Kl

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

   9 - 14:      wKKsRr

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
```

```
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

      9 - 15:         wKksR..Rl
      40 - 44:         qR..K..Kl
      51 - 57:         lRe.Kq.Kl
      53 - 59:         eKq.Kl.Ry
      104 - 112:       aRtrRqaRq
      141 - 148:       vRe.KsqKl

   >USERPAT3 (user pattern) :
   Pattern: X-[HRK]-X-[HRK]-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

      10 - 15:         kKsRRl
      104 - 109:       aRtRRq


>sp|Q2FW17|RL24_STAA8  (105 aa)
RecName: Full=50S ribosomal protein L24 {ECO:0000255|HAMAP-Rule:MF_01326};.
[Staphylococcus aureus (strain NCTC 8325)]
MHIKKGDNVKVIAGKDKGKEGKVIATLPKKDRVVVEGVNIMKKHQKPTQLNPEGGILETEAAIHVSNVQLL
DPKTNEPTRVGYKFVDGKKVRIAKKSGEEIKSNN

   >USERPAT3 (user pattern) :
   Pattern: X-[HRK]-X-[HRK]-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

      1 - 6:          mHiKKg

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

      1 - 6:          mHi.K..Kg
      14 - 20:         gKd.Kg.Ke
      16 - 23:         dKg.KegKv
      28 - 33:         pK..Kd.Rv
      41 - 47:         mKk.Hq.Kp
      88 - 96:         gKkvRiaKk
      91 - 97:         vRiaK..Ks

   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669
```

```
   1 - 11:       mHik..KgdnvKv
   4 - 16:       kKgdnvKviagKd
   9 - 20:       vKviagKdkg.Ke
   14 - 23:      gKdkg.Keg..Kv
   41 - 47:      mKk...Hq...Kp
   79 - 90:      tRvgy.KfvdgKk
   83 - 93:      yKfvdgKkv..Ri
   88 - 97:      gKkv..Riak.Ks

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

   28 - 33:      pKKdRv
   42 - 47:      kKHqKp
   88 - 93:      gKKvRi


>sp|Q2FW06|RL3_STAA8  (220 aa)
RecName: Full=50S ribosomal protein L3 {ECO:0000255|HAMAP-Rule:MF_01325};.
[Staphylococcus aureus (strain NCTC 8325)]
MTKGILGRKIGMTQVFGENGELIPVTVVEAKENVVLQKKTVEVDGYNAIQVGFEDKKAYKKDAKSNKYANK
PAEGHAKKADAAPKRFIREFRNVDVDAYEVGQEVSVDTFVAGDVIDVTGVSKGKGFQGAIKRHGQSRGPM
SHGSHFHRAPGSVGMASDASRVFKGQKMPGRMGGNTVTVQNLEVVQVDTENKVILVKGNVPGPKKGLV
EIRTSIKKGNK

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

   55 - 61:      dK..KayKk
   56 - 62:      kKayK..Kd
   59 - 65:      yK..KdaKs
   60 - 68:      kKdaKsnKy
   75 - 80:      gHa.K..Ka
   84 - 90:      pK..RfiRe
   85 - 93:      kRfiRefRn
   131 - 135:      iK..R..Hg
   142 - 150:      sHgsHfhRa
   161 - 169:      sRvfKgqKm

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

   55 - 65:      dKkaykKda..Ks
   59 - 68:      yKkda.Ksn..Ky
```

```
    63 - 72:      aKsn..Kyan.Kp
    66 - 77:      nKyan.KpaegHa
    70 - 80:      nKpaegHak..Ka
    84 - 93:      pKrfi.Ref..Rn
    131 - 139:      iKr...Hgqs.Rg
    132 - 144:      kRhgqsRgpmsHg
    137 - 149:      sRgpmsHgshfHr
    142 - 150:      sHgs..Hfh..Ra
    161 - 169:      sRvf..Kgq..Km
    164 - 173:      fKgq..Kmpg.Rm

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    75 - 80:      gHaKKa
    145 - 150:      sHfHRa


>sp|P0A0B7|AHPC_STAA8  (189 aa)
RecName: Full=Alkyl hydroperoxide reductase C;        EC=1.11.1.15; AltName:
Full=Peroxiredoxin; AltName: Full=Thioredoxin peroxidase;.  [Staphylococcus aureus (strain
NCTC 8325)]
MSLINKEILPFTAQAFDPKKDQFKEVTQEDLKGSWSVVCFYPADFSFVCPTELEDLQNQYEELQKLGVNVFS
VSTDTHFVHKAWHDHSDAISKITYTMIGDPSQTITRNFDVLDEATGLAQRGTFIIDPDGVVQASEINADGIG
RDASTLAHKIKAAQYVRKNPGEVCPAKWEEGAKTLQPGLDLVGKI

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    77 - 83:      tHfvH..Ka
    80 - 86:      vH..KawHd
    81 - 88:      hKawHd.Hs
    151 - 156:      aH..Ki.Ka

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    77 - 88:      tHfvh.KawhdHs

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792
```

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    151 - 156:     aHKiKa


>sp|P0A0H0|RS12_STAA8  (137 aa)
RecName: Full=30S ribosomal protein S12 {ECO:0000255|HAMAP-Rule:MF_00403};.
[Staphylococcus aureus (strain NCTC 8325)]
MPTINQLVRKPRQSKIKKSDSPALNKGFNSKKKKFTDLNSPQKRGVCTRVGTMTPKKPNSALRKYARVRLSN
NIEINAYIPGIGHNLQEHSVVLVRGGRVKDLPGVRYHIVRGALDTSGVDGRRQGRSLYGTKKPKN

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    8 - 13:       vRKpRq
    30 - 35:       sKKkKf
    132 - 137:     tKKpKn

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    8 - 16:       vRkpRqsKi
    11 - 19:       pRqsKikKs
    30 - 35:       sKk.K..Kf
    62 - 68:       lR..KyaRv
    63 - 70:       rKyaRv.Rl
    95 - 102:      vRggRv.Kd
    106 - 113:     vRy.HivRg
    122 - 128:     gR..RqgRs
    132 - 137:     tK..Kp.Kn

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    8 - 18:       vRkp..RqskiKk
    9 - 19:       rKprqsKik..Ks
    25 - 35:       nKgfnsKkk..Kf
    62 - 70:       lRkya.Rv...Rl
    95 - 102:      vRgg..Rv...Kd
    106 - 113:     vRy...Hiv..Rg

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792
```

```
    14 - 19:     sKiKKs
    30 - 35:     sKkKKf


>sp|Q2G023|SSRP_STAA8  (154 aa)
RecName: Full=SsrA-binding protein {ECO:0000255|HAMAP-Rule:MF_00023}; AltName:
Full=Small protein B {ECO:0000255|HAMAP-Rule:MF_00023};.  [Staphylococcus aureus (strain
NCTC 8325)]
MAKKKSPGTLAENRKARHDYNIEDTIEAGIVLQGTEIKSIRRGSANLKDSYAQVKNGEMYLNNMHIAPYEEG
NRFNHDPLRSRKLLLHKREIIKLGDQTREIGYSIVPLKLYLKHGHCKVLLGVARGKKKYDKRQALKEKAVKRDV
ARDMKARY

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    2 - 6:      aK..K..Ks
    13 - 19:     nRkaR..Hd
    37 - 43:     iKsiR..Rg
    80 - 85:     lRs.R..Kl
    87 - 91:     lH..K..Re
    113 - 120:    lKhgHc.Kv
    125 - 131:    aRgkK..Ky
    127 - 134:    gKk.KydKr
    129 - 135:    kKydK..Rq
    137 - 144:    lKe.KavKr
    139 - 145:    eKavK..Rd
    147 - 154:    aRdmKa.Ry

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    13 - 18:     nRKaRh
    113 - 118:    lKHgHc

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    14 - 19:     rKaRHd
    80 - 85:     lRsRKl
    125 - 130:    aRgKKk

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
```

```
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     73 - 82:       nRfn..Hdpl.Rs
     76 - 85:       nHdpl.Rsr..Kl
     80 - 90:       lRsr..KlllhKr
     82 - 91:       sRklllHk...Re
     83 - 95:       rKlllhKreiiKl
     109 - 120:     lKlylkHghc.Kv
     125 - 135:     aRgkk.Kydk.Rq
     127 - 139:     gKkkydKrqalKe
     132 - 144:     dKrqalKekavKr
     137 - 149:     lKekavKrdvaRd
     142 - 154:     vKrdvaRdmkaRy

   >USERPAT1 (user pattern) :
   Pattern: X-[HRK]-[HRK]-[HRK]-X-X-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 14782

     127 - 134:     gKKKydKr


>tr|Q2G001|Q2G001_STAA8  (179 aa)
SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:ABD29959.1};.  [Staphylococcus
aureus (strain NCTC 8325)]
MELQQAIANRRSVKKFKRDMHIDDALLYQAIEKAADAPNHGMREPWRVVHVPKDRLGDMSKDISKFAFP
NELDKQQCHYDAVTKLGGMLLLILKTDPRQRQNDENYFAFGAYAQNLMLLLYEAGIGTCWKSPLYIYDPKV
RKTLGIKKDEVLAGFLYLTDLEEDMPKAPRKNRNLITLY

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     9 - 15:       nR..RsvKk
     10 - 18:       rRsvKkfKr
     13 - 19:       vKkfK..Rd
     14 - 22:       kKfkRdmHi
     46 - 54:       wRvvHvpKd
     49 - 56:       vHvpKd.Rl
     138 - 143:     pKv.R..Kt
     166 - 174:     pKapRknRn

   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     9 - 19:       nRrsvkKfk..Rd
```

```
    13 - 22:       vKkfk.Rdm..Hi
    39 - 48:       nHgm..Repw.Rv
    42 - 51:       mRepw.Rvv..Hv
    46 - 56:       wRvv..HvpkdRl
    93 - 101:      lKtdp.Rq...Rq
    138 - 148:     pKvr..KtlgiKk
    166 - 174:     pKapr.Kn...Rn

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    13 - 18:       vKKfKr
    169 - 174:     pRKnRn

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    14 - 19:       kKfKRd
    138 - 143:     pKvRKt


>tr|Q2FYS0|Q2FYS0_STAA8  (343 aa)
SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:ABD30460.1};.  [Staphylococcus
aureus (strain NCTC 8325)]
MEPILEMIKTLTGINSPSGDTEEAIQFVEKYAKDLGYQTTLTNKGALLITVPGKNDEVQRCITAHVDTLGAMV
KEIKEDGRLAIELIGGFTYNAIEGEYCQIKTDAGQIYTGTICLHETSVHVYRNNHEIPRDQKHMEIRIDEVTTSE
EDTKSLGISVGDFVSFDPRTVITSSGFIKSRHLDDKASVAMILQLLKKLKEEQIILPHTTQFYISNNEEIGYGANA
SIDSKIKEYIALDMGALGDGQASDEYTVSICAKDASGPYHKQLKSHLVNLCKINNIPYKVDIYPYYGSDASAAL
HAGADIRHGLFGAGIESSHAMERTHIDSIKATEKLLYAYCLSPIE

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    73 - 82:       vKei..Kedg.Rl
    116 - 126:     lHetsvHvy..Rn
    121 - 129:     vHvy..Rnn..He
    124 - 133:     yRnn..Heip.Rd
    127 - 137:     nHeip.Rdqk.Hm
    131 - 141:     pRdqk.Hmei.Ri
    176 - 185:     iKsr..Hldd.Ka
    263 - 271:     yHkql.Ks...Hl
    316 - 324:     sHame.Rt...Hi
    320 - 329:     eRt...HidsiKa
    322 - 333:     tHidsiKate.Kl
```

```
   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

      121 - 129:      vHvyRnnHe
      131 - 137:      pRdqK..Hm
      176 - 181:      iKs.R..Hl
      194 - 199:      lK..Kl.Ke
      263 - 269:      yH..KqlKs
      264 - 271:      hKqlKs.Hl

   >USERPAT3 (user pattern) :
   Pattern: X-[HRK]-X-[HRK]-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

      176 - 181:      iKsRHl

   >USERPAT2 (user pattern) :
   Pattern: X-[HRK]-[HRK]-X-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

      194 - 199:      lKKlKe


>sp|Q2FY37|LIPM_STAA8  (276 aa)
RecName: Full=Octanoyltransferase LipM {ECO:0000255|HAMAP-Rule:MF_02118};
EC=2.3.1.181 {ECO:0000255|HAMAP-Rule:MF_02118}; AltName: Full=Octanoyl-[acyl-carrier-
protein]:[GcvH] N-octanoyltransferase {ECO:0000255|HAMAP-Rule:MF_02118};.
[Staphylococcus aureus (strain NCTC 8325)]
MTETWNFINTGSKDPYYNMAMDEALLNFVSRGEIDPVIRFYTWNPATLSIGYFQRLQKEIDIDKVKEKGFGL
VRRQTGGRGVLHDKELTYSVIVPESHPNMPSTVTEAYRVISQGLLEGFKNLGFDTYFAVPKTPEERQKLKQP
RSSVCFDAPSWYELVVEGRKIAGSAQTRQKGVILQHGSILQDIDIDELFDMFIYKNERLKLKMKEAFVEKAVA
INDISDEHITISQMEEAFEKGFKKGLNIELKPLELTEAQLAEVEELTEKYRSDEWMFRK

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

      63 - 69:       dKv.Ke.Kg
      137 - 143:      eRq.Kl.Kq
      139 - 146:      qKl.KqpRs
      198 - 205:      yKneRl.Kl
      201 - 207:      eRl.Kl.Km
      203 - 209:      lKl.Km.Ke
      236 - 242:      eKgfK..Kg
```

```
  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     63 - 69:       dKv...Ke...Kg
     74 - 85:       rRqtggRgvl.Hd
     79 - 87:       gRgvl.Hd...Ke
     132 - 143:      pKtpeeRqkl.Kq
     137 - 146:      eRqkl.Kqp..Rs
     198 - 209:      yKnerlKlkm.Ke


>sp|Q2FW79|Y2425_STAA8  (86 aa)
RecName: Full=UPF0457 protein SAOUHSC_02425;.  [Staphylococcus aureus (strain NCTC
8325)]
MAMTVKKDNNEVRIQWRVADIKIPTSEIKNITQDQDIHAVPKLDSKDVSRIGSTFGKTNRVIIDTEDHEYIIYT
QNDQKVYNELTK

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     12 - 23:       vRiqw.RvadiKi
     37 - 47:       iHavp.Klds.Kd
     41 - 51:       pKlds.Kdvs.Ri


>sp|Q2FW66|ASP23_STAA8  (169 aa)
RecName: Full=Alkaline shock protein 23;.  [Staphylococcus aureus (strain NCTC 8325)]
MTVDNNKAKQAYDNQTGVNEKEREERQKQQEQNQEPQFKNKLTFSDEVVEKIAGIAAREVKGILDMKGG
LTDTFTNAFSSGNNVTQGVSVEVGEKQAAVDLKVILEYGESAPKIFRKVTELVKEQVKYITGLDVVEVNMQV
DDVMTQKEWKQKHEKNNENNNQERQGLQ

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     20 - 27:       eKe.ReeRq
     22 - 29:       eReeRq.Kq
     112 - 118:      pKifR..Kv
     147 - 155:      qKewKqkHe
     150 - 157:      wKqkHe.Kn

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
```

```
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     20 - 29:       eKereeRq...Kq
     147 - 157:     qKewkqKhe..Kn

   >USERPAT3 (user pattern) :
   Pattern: X-[HRK]-X-[HRK]-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     150 - 155:     wKqKHe

   >USERPAT2 (user pattern) :
   Pattern: X-[HRK]-[HRK]-X-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     152 - 157:     qKHeKn


>sp|P0A0F8|RL15_STAA8  (146 aa)
RecName: Full=50S ribosomal protein L15 {ECO:0000255|HAMAP-Rule:MF_01341};.
[Staphylococcus aureus (strain NCTC 8325)]
MKLHELKPAEGSRKERNRVGRGVATGNGKTSGRGHKGQKARSGGGVRPGFEGGQLPLFRRLPKRGFTNIN
RKEYAIVNLDQLNKFEDGTEVTPALLVESGVVKNEKSGIKILGNGSLDKKLTVKAHKFSASAAEAIDAKGGAH
EVI

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     1 - 8:        mKl.HelKp
     12 - 19:       sRkeRn.Rv
     15 - 22:       eRn.RvgRg
     32 - 40:       gRghKgqKa
     35 - 42:       hKgqKa.Rs
     58 - 64:       fR..RlpKr
     59 - 65:       rRlpK..Rg
     123 - 128:     vKa.H..Kf

   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     1 - 8:        mKl...Hel..Kp
     12 - 22:       sRkernRvg..Rg
     28 - 37:       gKtsg.Rgh..Kg
```

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    32 - 42:      gRgh..KgqkaRs
    102 - 111:     vKne..Ksgi.Ki
    118 - 128:     dKkltvKah..Kf

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    12 - 17:      sRKeRn

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    32 - 37:      gRgHKg
    123 - 128:     vKaHKf


>sp|Q2FW21|RL6_STAA8  (178 aa)
RecName: Full=50S ribosomal protein L6 {ECO:0000255|HAMAP-Rule:MF_01365};.
[Staphylococcus aureus (strain NCTC 8325)]
MSRVGKKIIDIPSDVTVTFDGNHVTVKGPKGELSRTLNERMTFKQEENTIEVVRPSDSKEDRTNHGTTRALL
NNMVQGVSQGYVKVLELVGVGYRAQMQGKDLILNVGYSHPVEIKAEENITFSVEKNTVVKVEGISKEQVG
ALASNIRSVRPPEPYKGKGIRYQGEYVRRKEGKTGK

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    2 - 8:        sRvgK..Ki
    58 - 66:      sKedRtnHg
    157 - 164:     yKg.KgiRy
    169 - 176:     vRr.KegKt

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    22 - 31:      nHvtv.Kgp..Kg
    26 - 36:      vKgp..KgelsRt
    29 - 41:      pKgelsRtlneRm
    34 - 45:      sRtlneRmtf.Kq
    53 - 63:      vRpsdsKed..Rt
    58 - 66:      sKed..Rtn..Hg
    61 - 70:      dRtn..Hgtt.Ra
    157 - 164:     yKg...Kgi..Ry
```

```
    169 - 176:     vRr...Keg..Kt

  >USERPAT1 (user pattern) :
  Pattern: X-[HRK]-[HRK]-[HRK]-X-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 14782

    169 - 176:     vRRKegKt


>sp|Q2FW13|RL16_STAA8  (144 aa)
RecName: Full=50S ribosomal protein L16 {ECO:0000255|HAMAP-Rule:MF_01342};.
[Staphylococcus aureus (strain NCTC 8325)]
MLLPKRVKYRRQHRPKTTGRSKGGNYVTFGEFGLQATTTSWITSRQIESARIAMTRYMKRGGKVWIKIFPH
TPYTKKPLEVRMGAGKGAVEGWIAVVKPGRILFEVAGVSEEVAREALRLASHKLPVKTKFVKREELGGETNE
S

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    4 - 9:        pKRvKy
    9 - 14:        yRRqHr
    12 - 17:        qHRpKt

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    4 - 12:        pKrvKyrRq
    7 - 15:        vKyrRqhRp
    9 - 17:        yRrqHrpKt
    55 - 61:        tRymK..Rg
    58 - 64:        mK..RggKv
    127 - 134:     vKt.KfvKr
    129 - 135:     tKfvK..Re

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    4 - 15:        pKrvkyRrqh.Rp
    5 - 17:        kRvkyrRqhrpKt
    10 - 21:        rRqhrpKttg.Rs
    15 - 23:        pKttg.Rs...Kg
    50 - 61:        aRiamtRymk.Rg
    55 - 64:        tRymk.Rgg..Kv
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    58 - 68:      mKrgg.Kvwi.Ki
    62 - 72:      gKvwi.Kifp.Ht
    66 - 77:      iKifp.HtpytKk
    76 - 88:      kKplevRmgagKg
    114 - 125:     aReal.RlashKl
    118 - 129:     lRlashKlpv.Kt
    122 - 134:     sHklpvKtkfvKr
    127 - 135:     vKt...Kfvk.Re

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    7 - 12:      vKyRRq
    10 - 15:      rRqHRp


>sp|Q2FW07|RL4_STAA8  (207 aa)
RecName: Full=50S ribosomal protein L4 {ECO:0000255|HAMAP-Rule:MF_01328};.
[Staphylococcus aureus (strain NCTC 8325)]
MANYDVLKLDGTKSGSIELSDAVFGIEPNNSVLFEAINLQRASLRQGTHAVKNRSAVSGGGRKPWKQKGTG
RARQGTIRAPQWRGGGIVFGPTPRSYAYKMPKKMRRLALRSALSFKAQENGLTVVDAFNFEAPKTKEFKN
VLSTLEQPKKVLVVTENEDVNVELSARNIPGVQVTTAQGLNVLDITNADSLVITEAAAKKVEEVLG

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    40 - 50:      qRasl.Rqgt.Ha
    44 - 55:      lRqgt.HavknRs
    61 - 69:      gRkpw.Kq...Kg
    62 - 73:      rKpwkqKgtg.Ra
    67 - 75:      qKgtg.Ra...Rq
    71 - 80:      gRa...RqgtiRa
    73 - 85:      aRqgtiRapqwRg
    94 - 105:      pRsyayKmpk.Km
    99 - 108:      yKmpk.Kmr..Rl
    102 - 112:     pKkmr.Rlal.Rs
    134 - 141:     pKt...Kef..Kn

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    48 - 55:      tHavKn.Rs
    61 - 67:      gR..KpwKq
    62 - 69:      rKpwKq.Kg
```

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     99 - 107:      yKmpKkmRr
     102 - 108:      pKkmR..Rl
     134 - 141:      pKt.KefKn

   >USERPAT2 (user pattern) :
   Pattern: X-[HRK]-[HRK]-X-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     102 - 107:      pKKmRr

   >USERPAT3 (user pattern) :
   Pattern: X-[HRK]-X-[HRK]-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     103 - 108:      kKmRRl


>tr|Q2FVX5|Q2FVX5_STAA8  (223 aa)
SubName: Full=Molybdenum ABC transporter, permease protein, putative
{ECO:0000313|EMBL:ABD31561.1};.  [Staphylococcus aureus (strain NCTC 8325)]
MPDLTPFWISIRVAVISTIIVTVLGIFISKWLYRRKGSWVKVLESLLILPIVLPPTVLGFILLIIFSPRGPIGQFFANV
LHLPVVFTLTGAVIASVIVSFPLMYQHTVQGFRGIDTKMINTARTMGASETKIFLKLILPLAKRSILAGIMMSF
ARALGEFGATLMVAGYIPNKTNTLPLEIYFLVEQGRENEAWLWVLVLVAFSIVVISTINLLNKDKYKEVD

   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     29 - 37:      sKwly.Rr...Kg
     33 - 42:      yRr...KgswvKv
     215 - 221:      nKd...Ky...Ke

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     33 - 37:      yR..R..Kg
     215 - 221:      nKd.Ky.Ke


>sp|Q2G2M4|MRNC_STAA8  (134 aa)
RecName: Full=Mini-ribonuclease 3 {ECO:0000255|HAMAP-Rule:MF_01468};        Short=Mini-
3 {ECO:0000255|HAMAP-Rule:MF_01468};        Short=Mini-RNase 3 {ECO:0000255|HAMAP-
Rule:MF_01468};        EC=3.1.26.- {ECO:0000255|HAMAP-Rule:MF_01468}; AltName:
Full=Mini-RNase III {ECO:0000255|HAMAP-Rule:MF_01468};        Short=Mini-III
{ECO:0000255|HAMAP-Rule:MF_01468};.  [Staphylococcus aureus (strain NCTC 8325)]
```

```
MDNQQDNHIKLLNPLTLAYMGDAVLDQYVRTYIVLKLKSKPNKLHQMSKKYVSAKSQAQTLEYLMEQEWF
TDEEMDILKRGRNAKSHTKAKNTDVQTYRKSSAIEAVIGFLYLEKREERLEALLNKIITIVNER

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     35 - 41:       lKl.Ks.Kp
     37 - 44:       lKs.KpnKl
     39 - 46:       sKpnKl.Hq
     78 - 86:       lKrgRnaKs
     81 - 88:       gRnaKs.Ht
     84 - 90:       aKs.Ht.Ka
     86 - 92:       sHt.Ka.Kn
     114 - 120:     eK..ReeRl

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     35 - 46:       lKlks.KpnklHq
     39 - 51:       sKpnklHqmskKy
     44 - 56:       lHqmskKyvsaKs
     78 - 88:       lKrg..RnaksHt
     79 - 90:       kRgrnaKsht.Ka
     81 - 92:       gRnaksHtka.Kn

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     78 - 83:       lKRgRn


>tr|Q2G0F2|Q2G0F2_STAA8  (168 aa)
SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:ABD29755.1};.  [Staphylococcus
aureus (strain NCTC 8325)]
MKKLLTASIIACSVVMGVGLVNTSAEAASGNSIDTVKQLIKGDQSLENVKIGESIKDVLTKYKNPMYSYNEDG
TEHYYEFHTKKGMLLVTTDGKKNNGKVTHISMMYNDANGPTYQAVKNYVGKAVTHTEYSKVAGNFGYIEK
GKTTYQFASAPKDKNIKLYRIDLEK

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     55 - 64:       iKdvltKy...Kn
```

```
     75 - 85:       eHyyefHtk..Kg
     93 - 103:       gKknngKvt..Hi
     118 - 129:      vKnyvgKavt.Ht
     123 - 134:      gKavt.HteysKv
     154 - 164:      pKdkniKly..Ri

   >USERPAT3 (user pattern) :
   Pattern: X-[HRK]-X-[HRK]-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     80 - 85:       fHtKKg

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     80 - 85:       fHt.K..Kg
     154 - 161:      pKd.KniKl
     156 - 164:      dKniKlyRi


>sp|Q2FZ42|RL19_STAA8  (116 aa)
RecName: Full=50S ribosomal protein L19 {ECO:0000255|HAMAP-Rule:MF_00402};.
[Staphylococcus aureus (strain NCTC 8325)]
MTNHKLIEAVTKSQLRTDLPSFRPGDTLRVHVRIIEGTRERIQVFEGVVIKRRGGGVSETFTVRKISSGVGVER
TFPLHTPKIEKIEVKRRGKVRRAKLYYLRSLRGKAARIQEIR

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     28 - 34:       lRv.Hv.Ri
     50 - 54:       iK..R..Rg
     78 - 86:       lHtpKieKi
     88 - 94:       vKr.Rg.Kv
     89 - 97:       kRrgKvrRa
     92 - 99:       gKvrRa.Kl
     102 - 109:      lRslRg.Ka
     105 - 112:      lRg.KaaRi

   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     28 - 34:       lRv...Hv...Ri
     73 - 83:       eRtfplHtp..Ki
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     78 - 86:      lHtp..Kie..Ki
     81 - 91:      pKie..KievkRr
     84 - 96:      eKievkRrgkvRr
     88 - 99:      vKrrg.KvrraKl
     92 - 104:      gKvrraKlyylRs
     97 - 109:      aKlyylRslrgKa
     102 - 112:     lRslrgKaa..Ri

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     89 - 94:      kRRgKv
     94 - 99:      vRRaKl

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     92 - 97:      gKvRRa


>sp|Q2FW38|RL13_STAA8  (145 aa)
RecName: Full=50S ribosomal protein L13 {ECO:0000255|HAMAP-Rule:MF_01366};.
[Staphylococcus aureus (strain NCTC 8325)]
MRQTFMANESNIERKWYVIDAEGQTLGRLSSEVASILRGKNKVTYTPHVDTGDYVIVINASKIEFTGNKETD
KVYYRHSNHPGGIKSITAGELRRTNPERLIENSIKGMLPSTRLGEKQGKKLFVYGGAEHPHAAQQPENYELR
G

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     37 - 43:      lRg.Kn.Kv
     76 - 82:      yR..HsnHp
     117 - 123:     eKqgK..Kl

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     37 - 43:      lRg...Kn...Kv
     68 - 79:      nKetd.KvyyrHs
     72 - 82:      dKvyyrHsn..Hp
     76 - 87:      yRhsn.HpggiKs
     113 - 123:     tRlge.Kqgk.Kl
```

```
>sp|Q2FW30|RS13_STAA8  (121 aa)
RecName: Full=30S ribosomal protein S13 {ECO:0000255|HAMAP-Rule:MF_01315};.
[Staphylococcus aureus (strain NCTC 8325)]
MARIAGVDIPREKRVVISLTYIYGIGTSTAQKILEEANVSADTRVKDLTDDELGRIREVVDGYKVEGDLRRETN
LNIKRLMEISSYRGIRHRRGLPVRGQKTKNNARTRKGPVKTVANKKK

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     10 - 15:       pReKRv
     89 - 94:       iRhRRg
     106 - 111:      aRtRKg

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     10 - 15:       pRe.K..Rv
     86 - 94:       yRgiRhrRg
     97 - 104:       vRgqKt.Kn
     106 - 111:      aRt.R..Kg

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     86 - 94:       yRgir.Hr...Rg
     89 - 99:       iRhr..RglpvRg
     92 - 104:       rRglpvRgqktKn
     97 - 108:       vRgqktKnna.Rt
     102 - 111:      tKnna.Rtr..Kg
     106 - 115:      aRtr..Kgpv.Kt
     108 - 120:      tRkgpvKtvanKk

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     89 - 94:       iRHrRg


>sp|Q2FW23|RS5_STAA8  (166 aa)
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```
RecName: Full=30S ribosomal protein S5 {ECO:0000255|HAMAP-Rule:MF_01307};.
[Staphylococcus aureus (strain NCTC 8325)]
MARREEETKEFEERVVTINRVAKVVKGGRRFRFTALVVVGDKNGRVGFGTGKAQEVPEAIKKAVEAAKKDL
VVVPRVEGTTPHTITGRYGSGSVFMKPAAPGTGVIAGGPVRAVLELAGITDILSKSLGSNTPINMVRATIDGL
QNLKNAEDVAKLRGKTVEELYN

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    3 - 15:       rReeetKefeeRv
    19 - 27:      nRva..Kvv..Kg
    22 - 31:      aKvv..Kggr.Rf
    25 - 33:      vKggr.Rf...Rf
    154 - 160:    aKl...Rg...Kt

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    19 - 27:      nRvaKvvKg
    22 - 30:      aKvvKggRr
    25 - 33:      vKggRrfRf
    154 - 160:    aKl.Rg.Kt

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    28 - 33:      gRRfRf


>sp|Q2FW19|RS14Z_STAA8  (61 aa)
RecName: Full=30S ribosomal protein S14 type Z {ECO:0000255|HAMAP-Rule:MF_01364};.
[Staphylococcus aureus (strain NCTC 8325)]
MAKTSMVAKQQKKQKYAVREYTRCERCGRPHSVYRKFKLCRICFRELAYKGQIPGVRKASW

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    8 - 16:       aKqqKkqKy
    22 - 30:      tRceRcgRp
    25 - 32:      eRcgRp.Hs
    34 - 42:      yRkfKlcRi
```

```
   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     8 - 16:       aKqqk.Kq...Ky
     11 - 20:      qKkq..Kyav.Re
     14 - 24:      qKyav.Reyt.Rc
     18 - 27:      vReyt.Rce..Rc
     22 - 32:      tRce..RcgrpHs
     25 - 37:      eRcgrpHsvyrKf
     30 - 42:      pHsvyrKfklcRi
     35 - 46:      rKfklcRicf.Re
     40 - 51:      cRicf.RelayKg

   >USERPAT2 (user pattern) :
   Pattern: X-[HRK]-[HRK]-X-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     11 - 16:      qKKqKy
     34 - 39:      yRKfKl


>tr|Q2G0R5|Q2G0R5_STAA8  (87 aa)
SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:ABD29634.1};.  [Staphylococcus
aureus (strain NCTC 8325)]
MRLDKYLKVSRLIKRRTLAKEVSDQGRITINGNVAKAGSDVKVEDVLTIRFGQKLVTVKVTALNEHASKDNA
KGMYEIIEERRLEEA

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     1 - 9:       mRldKylKv
     4 - 12:       dKylKvsRl
     7 - 15:       lKvsRliKr
     10 - 17:      sRliKr.Rt

   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     1 - 9:       mRld..Kyl..Kv
     4 - 12:       dKyl..Kvs..Rl
     7 - 17:       lKvs..RlikrRt
     10 - 21:      sRlikrRtla.Ke
     49 - 60:      iRfgq.KlvtvKv
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     65 - 74:       eHas..Kdna.Kg


>sp|Q2G0N0|EFTU_STAA8  (394 aa)
RecName: Full=Elongation factor Tu {ECO:0000255|HAMAP-Rule:MF_00118};         Short=EF-
Tu {ECO:0000255|HAMAP-Rule:MF_00118};.  [Staphylococcus aureus (strain NCTC 8325)]
MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERGITINTSHIEYQT
DKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMPQTREHILLSRNVGVPALVVFLNKVDM
VDDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALEGDAQYEEKILELMEAVDTYIPTPERDSDKPFM
MPVEDVFSITGRGTVATGRVERGQIKVGEEVEIIGLHDTSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAR
EDVQRGQVLAAPGSITPHTEFKAEVYVLSKDEGGRHTPFFSNYRPQFYFRTTDVTGVVHLPEGTEMVMPG
DNVEMTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     2 - 9:         aKe.KfdRs
     4 - 11:        eKfdRs.Ke
     7 - 13:        dRs.Ke.Ha
     19 - 26:       gHvdHg.Kt
     73 - 80:       dKr.HyaHv

   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     2 - 13:        aKekfdRske.Ha
     19 - 26:       gHvd..Hg...Kt
     73 - 80:       dKr...Hya..Hv
     116 - 125:     tRe...HillsRn
     230 - 239:     gRve..Rgqi.Kv
     279 - 290:     lRgva.RedvqRg
     373 - 383:     tRfsi.Regg.Rt

   >USERPAT1 (user pattern) :
   Pattern: X-[HRK]-[HRK]-[HRK]-X-X-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 14782

     73 - 80:       dKRHyaHv


>tr|Q2FZZ9|Q2FZZ9_STAA8  (118 aa)
SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:ABD29961.1};.  [Staphylococcus
aureus (strain NCTC 8325)]
MIKFYQYKNCTTCKKAAKFLDEYGVSYEPIDIVQHTPTINEFKTIIANTGVEINKLFNTHGAKYRELDLKNKLQT
LSDDEKLELLSSDGMLVKRPLAVMGDKITLGFKEDQYKETWLA
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```
   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

      13 - 19:       cK..KaaKf
      59 - 66:       tHgaKy.Re

   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

      54 - 66:       nKlfntHgakyRe
      59 - 71:       tHgakyReldlKn
      64 - 73:       yReldlKn...Kl


>sp|Q2FZ45|RS16_STAA8  (91 aa)
RecName: Full=30S ribosomal protein S16 {ECO:0000255|HAMAP-Rule:MF_00385};.
[Staphylococcus aureus (strain NCTC 8325)]
MAVKIRLTRLGSKRNPFYRIVVADARSPRDGRIIEQIGTYNPTSANAPEIKVDEALALKWLNDGAKPTDTVHN
ILSKEGIMKKFDEQKKAK

   >USERPAT4 (user pattern) :
   Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

      3 - 10:        vKi.RltRl
      25 - 33:        aRspRdgRi

   >USERPAT5 (user pattern) :
   Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
   Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

      3 - 15:        vKirltRlgskRn
      8 - 20:        tRlgskRnpfyRi
      25 - 33:        aRsp..Rdg..Ri
      71 - 83:        vHnilsKegimKk


>tr|Q2G2D1|Q2G2D1_STAA8  (94 aa)
SubName: Full=Uncharacterized protein {ECO:0000313|EMBL:ABD30345.1};.  [Staphylococcus
aureus (strain NCTC 8325)]
MKKKKIPMRKCILSNEMHPKKDMIRVVVNKEGEIFADVTGKKQGRGAYVSKDVAMVEKAQQKEILEKYFK
ASKEQLDPVYKEIIRLIYREEIPK
```

```
  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     1 - 6:        mKKkKi

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

     1 - 6:        mKkKKi
     17 - 22:      mHpKKd

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     1 - 6:        mKk.K..Ki
     17 - 22:      mHp.K..Kd
     40 - 46:      gK..KqgRg
     66 - 74:      eKyfKasKe

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     1 - 11:       mKkk..KipmrKc
     17 - 26:      mHpk..Kdmi.Rv
     19 - 31:      pKkdmiRvvvnKe
     57 - 68:      eKaqq.KeileKy
     61 - 71:      qKeileKyf..Ka
     66 - 74:      eKyf..Kas..Ke
     80 - 90:      yKeii.Rliy.Re


>sp|Q2G2Q1|RS15_STAA8  (89 aa)
RecName: Full=30S ribosomal protein S15 {ECO:0000255|HAMAP-Rule:MF_01343};.
[Staphylococcus aureus (strain NCTC 8325)]
MAISQERKNEIIKEYRVHETDTGSPEVQIAVLTAEINAVNEHLRTHKKDHHSRRGLLKMVGRRRHLLNYLRSK
DIQRYRELIKSLGIRR

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669
```

```
    7 - 19:        rKneiiKeyrvHe
    41 - 52:       eHlrthKkdh.Hs
    43 - 54:       lRthk.KdhhsRr
    45 - 55:       tHkkdhHsr..Rg
    47 - 59:       kKdhhsRrgllKm
    52 - 64:       sRrgllKmvgrRr
    57 - 66:       lKmvgrRr...Hl
    70 - 78:       lRs...Kdiq.Ry
    72 - 80:       sKdiq.Ry...Re
    76 - 84:       qRy...Reli.Ks
    78 - 89:       yReli.KslgiRr

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    12 - 19:       iKeyRv.He
    41 - 48:       eHl.RthKk
    43 - 51:       lRthKkdHh
    45 - 52:       tHk.KdhHs
    46 - 54:       hKkdHhsRr
    47 - 55:       kKdhHsrRg
    61 - 66:       gRr.R..Hl

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    43 - 48:       lRtHKk
    47 - 52:       kKdHHs
    50 - 55:       hHsRRg
    61 - 66:       gRrRHl

  >USERPAT1 (user pattern) :
  Pattern: X-[HRK]-[HRK]-[HRK]-X-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 14782

    45 - 52:       tHKKdhHs

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    46 - 51:       hKKdHh
    49 - 54:       dHHsRr
    61 - 66:       gRRrHl
```

```
>sp|Q2FXZ7|RS21_STAA8  (58 aa)
RecName: Full=30S ribosomal protein S21 {ECO:0000255|HAMAP-Rule:MF_00358};.
[Staphylococcus aureus (strain NCTC 8325)]
MSKTVVRKNESLEDALRRFKRSVSKSGTIQEVRKREFYEKPSVKRKKKSEAARKRKFK

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    16 - 21:      lRRfKr
    43 - 48:      vKRkKk
    44 - 49:      kRKkKs
    52 - 57:      aRKrKf

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    16 - 22:      lRrfK..Rs
    32 - 36:      vR..K..Re
    43 - 49:      vKrkK..Ks
    52 - 57:      aRk.R..Kf

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    16 - 26:      lRrfk.Rsvs.Ks
    32 - 41:      vRk...RefyeKp
    34 - 46:      kRefyeKpsvkRk
    39 - 49:      eKpsvkRkk..Ks
    43 - 54:      vKrkk.KseaaRk
    47 - 57:      kKseaaRkr..Kf

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    17 - 22:      rRfKRs
    43 - 48:      vKrKKk
    44 - 49:      kRkKKs
    52 - 57:      aRkRKf
```

```
>sp|Q2FXT0|RL27_STAA8  (94 aa)
RecName: Full=50S ribosomal protein L27 {ECO:0000255|HAMAP-Rule:MF_00539};.
[Staphylococcus aureus (strain NCTC 8325)]
MLKLNLQFFASKKGVSSTKNGRDSESKRLGAKRADGQFVTGGSILYRQRGTKIYPGENVGRGGDDTLFAKID
GVVKFERKGRDKKQVSVYAVAE

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    18 - 28:      tKng..RdsesKr
    21 - 33:      gRdsesKrlgaKr
    46 - 53:      yRq...Rgt..Ki
    75 - 86:      vKfer.KgrdkKq

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    46 - 53:      yRq.RgtKi
    75 - 83:      vKfeRkgRd
    78 - 86:      eRkgRdkKq

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    78 - 83:      eRKgRd

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    81 - 86:      gRdKKq


>sp|Q2FW15|RS17_STAA8  (87 aa)
RecName: Full=30S ribosomal protein S17 {ECO:0000255|HAMAP-Rule:MF_01345};.
[Staphylococcus aureus (strain NCTC 8325)]
MSERNDRKVYVGKVVSDKMDKTITVLVETYKTHKLYGKRVKYSKKYKTHDENNSAKLGDIVKIQETRPLSAT
KRFRLVEIVEESVII

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126
```

```
    3 - 9:        eRndR..Kv
    30 - 35:      yKt.H..Kl
    37 - 45:      gKrvKysKk
    40 - 48:      vKysKkyKt
    43 - 50:      sKkyKt.Hd
    72 - 77:      tK..Rf.Rl

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

    3 - 14:       eRndr.KvyvgKv
    7 - 19:       rKvyvgKvvsdKm
    12 - 22:      gKvvsdKmd..Kt
    30 - 40:      yKth..KlygkRv
    32 - 42:      tHklygKrv..Ky
    33 - 45:      hKlygkRvkysKk
    37 - 46:      gKrv..Kysk.Ky
    38 - 50:      kRvkysKkyktHd

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    30 - 35:      yKtHKl

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    37 - 42:      gKRvKy
    43 - 48:      sKKyKt
    72 - 77:      tKRfRl


>sp|Q2FW08|RL23_STAA8  (91 aa)
RecName: Full=50S ribosomal protein L23 {ECO:0000255|HAMAP-Rule:MF_01369};.
[Staphylococcus aureus (strain NCTC 8325)]
MEARDILKRPVITEKSSEAMAEDKYTFDVDTRVNKTQVKMAVEEIFNVKVASVNIMNYKPKKKRMGRYQG
YTNKRRKAIVTLKEGSIDLFN

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669
```

```
    31 - 40:      tRvn..Ktqv.Km
    58 - 68:      yKpkkkRmg..Ry

  >USERPAT3 (user pattern) :
  Pattern: X-[HRK]-X-[HRK]-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    58 - 63:      yKpKKk
    60 - 65:      pKkKRm
    73 - 78:      nKrRKa

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

    58 - 65:      yKpkKk.Rm
    60 - 68:      pKkkRmgRy
    73 - 78:      nKr.R..Ka

  >USERPAT2 (user pattern) :
  Pattern: X-[HRK]-[HRK]-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 109792

    60 - 65:      pKKkRm
    73 - 78:      nKRrKa

  >USERPAT1 (user pattern) :
  Pattern: X-[HRK]-[HRK]-[HRK]-X-X-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 14782

    61 - 68:      kKKRmgRy


>tr|Q2FVY0|Q2FVY0_STAA8  (419 aa)
SubName: Full=Molybdopterin biosynthesis protein moeA, putative
{ECO:0000313|EMBL:ABD31556.1};.  [Staphylococcus aureus (strain NCTC 8325)]
MVVEKRNPIPVKEAIQRIVNQQSSMPAITVALEKSLNHILAEDIVATYDIPRFDKSPYDGFAIRSVDSQGASG
QNRIEFKVIDHIGAGSVSDKLVGDHEAVRIMTGAQIPNGADAVVMFEQTIELEDTFTIRKPFSKNENISLKGE
ETKTGDVVLKKGQVINPGAIAVLATYGYAEVKVIKQPSVAVIATGSELLDVNDVLEDGKIRNSNGPMIRALAE
KLGLEVGIYKTQKDDLDSGIQVVKEAMEKHDIVITTGGVSVGDFDYLPEIYKAVKAEVLFNKVAMRPGSVTT
VAFVDGKYLFGLSGNPSACFTGFELFVKPAVKHMCGALEVFPQIIKATLMEDFTKANPFTRFIRAKATLTSAG
ATVVPSGFNKSGAVVAIAHANCMVMLPGGSRGFKAGHTVDIILTESDAAEEELLL

  >USERPAT5 (user pattern) :
  Pattern: X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X
```

```
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 1756669

     75 - 85:       nRief.Kvid.Hi
     92 - 103:      dKlvgdHeav.Ri
     351 - 358:     tRfi..Ra...Ka
     394 - 402:     sRgf..Kag..Ht

  >USERPAT4 (user pattern) :
  Pattern: X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X
  Approximate number of expected random matches in ~ 100'000 sequences (50'000'000
residues): 988126

     351 - 358:     tRfiRa.Ka
     394 - 402:     sRgfKagHt
```

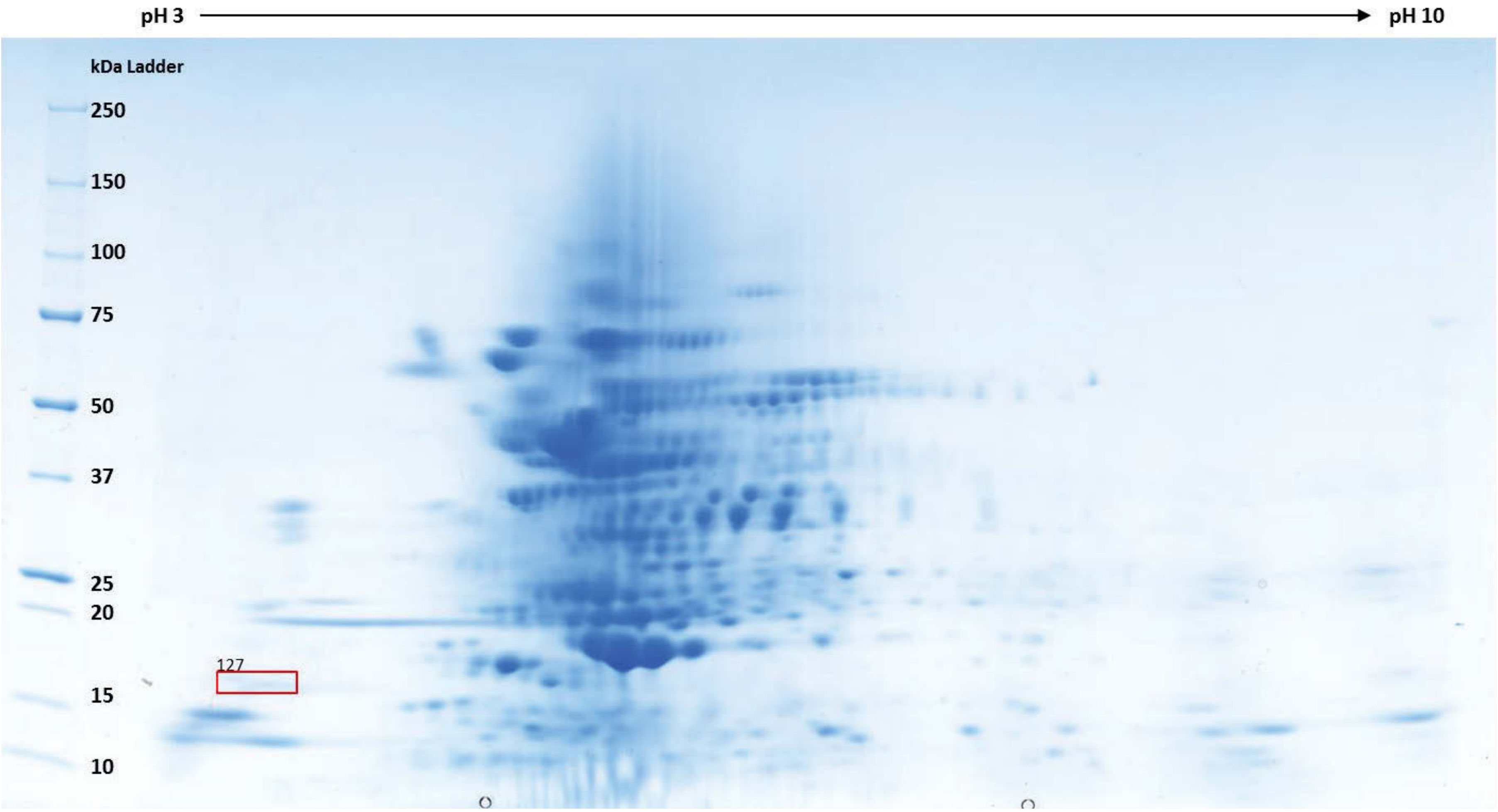

Figure B.2. 2D-PAGE gel of surface biotinylated proteins showing spot 127, where 30S Ribosomal protein S7 was identified.

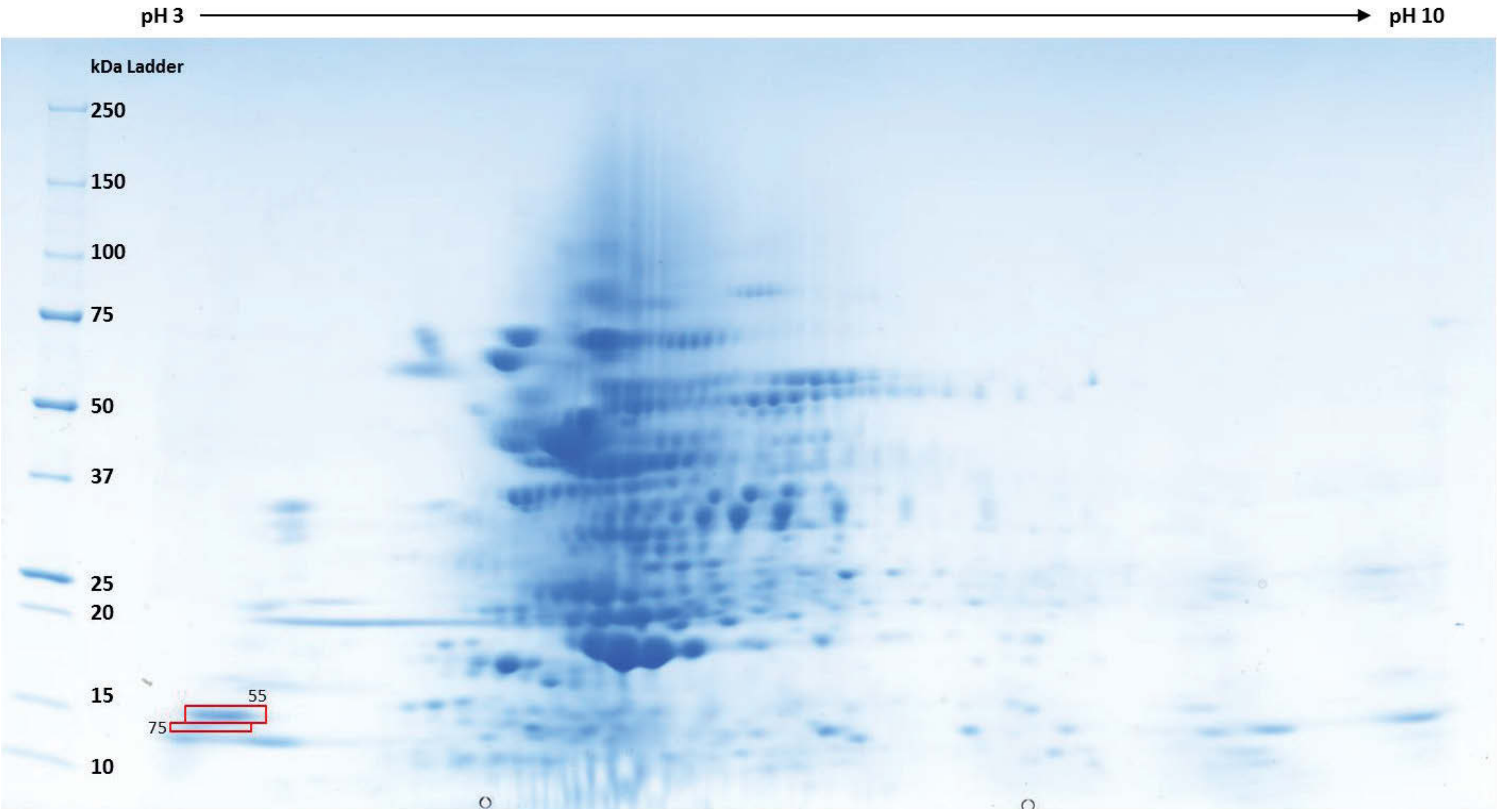

Figure B.3. 2D-PAGE gel of surface biotinylated proteins showing spot 55 and 75, where 30S Ribosomal protein S9 was identified.

Table B.5 List of proteins identified in the study by Mishra et al. [89]. Proteins also identified in the Chapter 3 heparin analysis are in yellow. BLASTp analysis [102] was used to compare each protein across the two strains. A total of ~75% of the proteins Mishra et al. identified were also identified in Chapter 3.

SAUSA300_0955	Autolysin
SAUSA300_0113	Immunoglobulin G-binding protein A
SAUSA300_0760	Enolase
SAUSA300_1150	Elongation factor Ts
SAUSA300_0756	Glyceraldehyde-3-phosphate dehydrogenase
SAUSA300_0533	Elongation factor Tu
SAUSA300_2436	Surface protein G (putative cell wall surface anchor family protein)
SAUSA300_1790	Foldase protein PrsA precursor
SAUSA300_0602	Uncharacterized protein
SAUSA300_0307	Lipoprotein family 5′-nucleotidase
SAUSA300_0993	Pyruvate dehydrogenase E1 component alpha subunit
SAUSA300_0536	Molecular chaperone Hsp31 and glyoxalase 3
SAUSA300_2079	Fructose bisphosphate aldolase
SAUSA300_1362	DNA-binding protein HU
SAUSA300_0994	Pyruvate dehydrogenase E1 component beta subunit
SAUSA300_0618	ABC transporter substrate-binding protein
SAUSA300_2573	IsaB
SAUSA300_2199	50S ribosomal protein L22
SAUSA300_2189	50S ribosomal protein L6
SAUSA300_2506	Probable transglycosylase IsaA
SAUSA300_1603	50S ribosomal protein L21
SAUSA300_2177	50S ribosomal protein L17
SAUSA300_2196	50S ribosomal protein L29
SAUSA300_2195	30S ribosomal protein S17
SAUSA300_0994	Putative pyruvate dehydrogenase E1 beta subunit
SAUSA300_2192	50S ribosomal protein L5
SAUSA300_2540	Fructose-bisphosphate aldolase class I
SAUSA300_1644	Pyruvate kinase
SAUSA300_0757	Phosphoglycerate kinase
SAUSA300_1540	Chaperone protein DnaK
SAUSA300_0235	l-Lactate dehydrogenase
SAUSA300_2198	30S ribosomal protein S3
SAUSA300_0532	Elongation factor G
SAUSA300_1201	Glutamine synthetase
SAUSA300_1640	Isocitrate dehydrogenase
SAUSA300_2362	2,3-Bisphosphoglycerate-dependent phosphoglycerate mutase
SAUSA300_0536	Molecular chaperone Hsp31
SAUSA300_1138	Succinyl-CoA synthetase, beta subunit

SAUSA300_1365	30S ribosomal protein S1
SAUSA300_1641	Citrate synthase II, GltA
SAUSA300_0523	50S ribosomal protein L1
SAUSA300_2078	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
SAUSA300_0973	Phosphoribosylformylglycinamide cycloligase
SAUSA300_2362	2,3-Bisphosphoglycerate-independent phosphoglycerate mutase
SAUSA300_0389	GMP synthase
SAUSA300_2178	DNA-directed RNA polymerase
SAUSA300_0129	2-Butanediol dehydrogenase
SAUSA300_1239	Transketolase
SAUSA300_0539	Branched-chain amino acid transferase
SAUSA300_0758	Triose phosphate isomerase
SAUSA300_1666	30S ribosomal protein S4
SAUSA300_0871	Fumarylacetoacetate hydrolase
SAUSA300_0886	3-Oxoacyl-synthase 2
SAUSA300_1491	Xaa-Pro dipeptidase
SAUSA300_1804	Glucosamine-6-phosphate isomerase
SAUSA300_1622	Trigger factor
SAUSA300_0966	N5-carboxyaminoimidazole ribonucleotide
SAUSA300_2092	DNA protection during starvation protein
SAUSA300_0976	Phosphoribosylamine-glycine ligase
SAUSA300_0491	Cysteine synthase
SAUSA300_0965	FolD
SAUSA300_1080	FtsZ
SAUSA300_1367	Cytidylate kinase
SAUSA300_1696	d-Alanine aminotransferase
SAUSA300_0860	Ornithine aminotransferase
SAUSA300_1880	Glutamyl-tRNA amidotransferase
SAUSA300_0135	Superoxide dismutase
SAUSA300_2067	Serine hydroxymethyltransferase
SAUSA300_0948	Naphthoate synthase
SAUSA300_1657	Acetate kinase
SAUSA300_2187	30S ribosomal protein S5
SAUSA300_1725	Transaldolase
SAUSA300_2091	Purine nucleoside phosphorylase Deo-D type
SAUSA300_0009	Serine-tRNA ligase
SAUSA300_1874	Ferritin
SAUSA300_2202	50S ribosomal protein L23
SAUSA300_2517	Amidohydrolase family protein
SAUSA300_1615	Delta-aminolevulinic acid dehydratase
SAUSA300_2190	30S ribosomal protein S8
SAUSA300_1139	Succinyl-CoA synthetase, alpha subunit
SAUSA300_0531	30S ribosomal protein S7

SAUSA300_0672	MarR family transcriptional regulator
SAUSA300_0688	Oxidoreductase/aldo-keto reductase family
SAUSA300_1109	Methionyl-tRNA formyl transferase
SAUSA300_0114	SarS
SAUSA300_1653	Metal-dependent hydrolase
SAUSA300_0916	Conserved hypothetical protein
SAUSA300_0605	SarA
SAUSA300_1442	SrrA
SAUSA300_0380	AhpC
SAUSA300_2097	Uncharacterized protein
SAUSA300_1494	LipM
SAUSA300_1900	Manganese-dependent inorganic pyrophosphatase
SAUSA300_1131	30S ribosomal protein S16
SAUSA300_1304	Glyoxylase family protein
SAUSA300_2245	SarR
SAUSA300_2315	Lipoprotein
SAUSA300_1659	Probable thiol peroxidase
SAUSA300_0015	50S ribosomal protein L9
SAUSA300_2132	Uncharacterized protein
SAUSA300_0032	Penicillin-binding protein 2’
SAUSA300_1058	Alpha-hemolysin
SAUSA300_0055	Zinc-dependent alcohol dehydrogenase
SAUSA300_2579	N-acetyl-muramoyl-l-alanine amidase
SAUSA300_1975	Aerolysin/leukocidin family protein
SAUSA300_1974	Leukocidin/hemolysin
SAUSA300_0099	1-Phosphatidylinositol phosphodiesterase
SAUSA300_1382	LukS
SAUSA300_1381	LukF
SAUSA300_1920	Chemotaxis inhibitory protein
SAUSA300_1052	Fibrinogen-binding protein
SAUSA300_0964	Chitinase
SAUSA300_0801	Enterotoxin, Seq
SAUSA300_0883	Putative surface protein
SAUSA300_2164	Surface protein
SAUSA300_0220	Formate acetyltransferase
SAUSA300_1149	30S ribosomal protein S2
SAUSA300_0186	Phosphate acetyltransferase
SAUSA300_1331	Alanine dehydrogenase
SAUSA300_0067	Universal stress protein
SAUSA300_1976	Succinyl diaminopimelate desuccinylase
SAUSA300_2462	NAD(P)H-flavin oxidoreductase
SAUSA300_0234	Putative flavohemoprotein
SAUSA300_0141	Phosphopentomutase

SAUSA300_2463	d-Lactate dehydrogenase
SAUSA300_1719	Arsenate reductase
SAUSA300_1541	GrpE
SAUSA300_1191	Complement inhibitor
SAUSA300_0540	HAD family hydrolase
SAUSA300_0173	Uncharacterized protein
SAUSA300_0969	PurS
SAUSA300_2529	PhnB
SAUSA300_1358	Nucleoside diphosphate kinase

Match	100
Homologous	3
Non-match	30
Total	**133**
% Match	0.75188

Appendix C

Extra information relating to Chapter 4

Item C.1 Copy of manuscript accepted for publication by Scientific Reports (starts on next page). All supplementary files are included at the end of the manuscript.

Elongation factor Tu is a multifunctional and processed moonlighting protein

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Many bacterial moonlighting proteins were originally described in medically, agriculturally, and commercially important members of the low G+C Firmicutes. We show Elongation factor Tu (Ef-Tu) moonlights on the surface of the human pathogens *Staphylococcus aureus* (Sa$_{\text{Ef-Tu}}$) and *Mycoplasma pneumoniae* (Mpn$_{\text{Ef-Tu}}$), and the porcine pathogen *Mycoplasma hyopneumoniae* (Mhp$_{\text{Ef-Tu}}$). Ef-Tu is also a target of multiple processing events on the cell surface and these were characterised using an N-terminomics pipeline. Recombinant Mpn$_{\text{Ef-Tu}}$ bound strongly to a diverse range of host molecules, and when bound to plasminogen, was able to convert plasminogen to plasmin in the presence of plasminogen activators. Fragments of Ef-Tu retain binding capabilities to host proteins. Bioinformatics and structural modelling studies indicate that the accumulation of positively charged amino acids in short linear motifs (SLiMs), and protein processing promote multifunctional behaviour. Codon bias engendered by an A+T rich genome may influence how positively-charged residues accumulate in SLiMs.

INTRODUCTION

Elongation factor Thermo unstable (Ef-Tu) is one the most abundant proteins in bacteria [1,2]. It functions as an essential and universally conserved GTPase that ensures translational accuracy by catalysing the reaction that adds the correct amino acid to a growing nascent polypeptide chain [3]. After the incoming aminoacyl-tRNA docks with the mRNA, GTPase activity induces a conformational change releasing Ef-Tu from the ribosome [3-5]. In *Escherichia coli*, Ef-Tu is comprised of three functional domains known as domain I (amino acids 1 – 200), domain II (amino acids 209 – 299) and domain III (amino acids 301 – 393) [6]. Domain I forms a helix structure with Rossmann fold topology, a structural motif found in proteins that bind nucleotides, while domains II and III are largely comprised of beta sheets [3,7]. The GTP/GDP binding domains are housed in domain I, while domains I and II are needed for nucleotide exchange. Domains II and III physically adjust to form an amino acid tRNA binding site [3,5]. Ef-Tu sequences derived from phylogenetically diverse species share considerable sequence identity and have been used to generate phylogenetic descriptions of the tree of life [8]. In eukaryotes, domain III also has a role in actin polymerisation via an actin-bundling domain [9,10].

Despite its highly conserved function in protein synthesis, non-canonical functions have been described for Ef-Tu in all kingdoms of life. Ef-Tu lacks a signal secretion motif yet the ability to execute moonlighting functions often requires the molecule to localise to the cell surface. Ef-Tu is a multifunctional protein in higher order eukaryotes [11-16], parasites [17-20], fungi [21] and it is has been identified on the surface of a wide range of Gram positive and Gram negative pathogenic and commensal bacteria that associate with metazoan species [2,22-29]. Bacterial Ef-Tu interacts with nucleolin [30,31], fibrinogen and factor H [23,26], plasminogen and several complement factors [26,27,32], laminin [33], CD21 [34], fibronectin [2,33,35,36], is immunogenic [37] and adheres to the surface of

Hep-2 cells [33] underscoring the multifunctional adhesive characteristics that have been assigned to this molecule. Ef-Tu binds sulfated carbohydrate moieties found on glycolipids and sulfomucin and promotes the binding of *Lactobacillus reuteri* to mucosal surfaces indicating that Ef-Tu can interact with carbohydrates [38]. Notably, antibodies against Ef-Tu are induced during infections caused by *Staphylococcus aureus* [39,40] *Mycoplasma capricolum* [41], *Mycoplasma ovipneumoniae* [37], *Chlamydia trachomatis* [42], *Burkholderia pseudomallei* [43] and *Mycoplasma hyopneumoniae* [44]. Ef-Tu has been identified in six surfacome studies (excludes cell membrane and envelope isolations) [45-50] performed on *S. aureus* and Ef-Tu is one of twelve proteins consistently identified in the exoproteome of *S. aureus* from patients with bacteraemia [51]. The major staphylococcal autolysin *Alt* is implicated in playing a role in secreting cytosolic proteins including Ef-Tu into the extracellular milieu [24]. Moonlighting proteins are likely to be exported via several mechanisms including within secreted extracellular vesicles [52], during cell lysis [53] and via association with proteins that are secreted by the Sec machinery [54].

The ability of Ef-Tu to be secreted onto the cell surface occurred early in the evolutionary interplay between plant pathogenic bacteria and their eukaryote hosts and is a well described pathogen associated molecular pattern (PAMP) molecule [55,56]. Plants have evolved pattern recognition receptors (PRR) in their cell membranes that are designed specifically to recognise PAMP molecules released by bacterial and fungal pathogens [56-62]. An Ef-Tu receptor (EFR) found within Brassica lineages [63,64] recognises the highly conserved N-terminal 18 amino acids (elf18) in the native Ef-Tu molecule [56,63,64]. Binding triggers signal transduction events in plant roots that ensure that pathogenic bacteria are either contained within callose deposits, destroyed by cellular apoptosis, or succumb to an oxidative burst elicited by the production of hydrogen peroxide [63]. A region spanning surface exposed amino acids 176 – 225, in Ef-Tu from the Gram-negative bacterial pathogen *Acidovorax avenae,* interacts with a different PRR in monocotyledonous plants (see Figure 1) [65]. EFR has been transferred from the Brassica species *Arabidopsis thaliana* into the monocot species, rice and transgenic rice plants display enhanced innate immune responses when exposed to elf18 from *Xanthomonas oryza*, a major rice pathogen [66]. These studies show that plants have evolved sophisticated molecular machinery to identify Ef-Tu that is released onto the cell surface by diverse plant pathogenic bacteria.

Protein cleavage is emerging as an important post-translational modification that can expand protein function [67-70]. This is evident in the genome reduced Mollicutes where species specific Mycoplasmal adhesins and lipoproteins are targets of complex processing events [67,71-86]. Cleavage fragments are retained on the bacterial cell surface and function as adhesins that bind heparin-like glycosaminoglycans [67,73-75,77,79,80], fibronectin [67,76,78,84] and circulatory molecules such a plasmin(ogen) that regulate the fibrinolytic system [67,76,78,79,81]. Cleavage motifs have been chemically defined in *M. hyopneumoniae* using mass spectrometry and occur at phenylalanine residues in the motif S/T-X-F↓-X-D/E, within stretches of hydrophobic amino acids, and at trypsin-like sites in diverse molecules including adhesins, lipoproteins and in metabolic enzymes that traffic to the cell surface [77,79,82,83,85]. Cleavage fragments are known to be further processed by aminopeptidases [83,85] that also localise on the cell surface [87,88]. We propose that protein processing represents another layer by which proteins can expand and modify protein function and is under recognised as a post-translational modification in prokaryotes.

In this study we identified Ef-Tu, and an extensive repertoire of processed cleavage fragments of Ef-Tu, on the surface of human pathogens *S. aureus* and *Mycoplasma pneumoniae,* and the porcine pathogen *M. hyopneumoniae*. Protein cleavage events were mapped using a systems wide dimethyl labelling protocol that allows for the identification of modified N-terminal peptides (neo-N-termini) by liquid chromatography tandem mass spectrometry (LC-MS/MS) and enabled us to determine how Ef-Tu is processed and presented on the cell surfaces of these pathogens. We further characterised the non-canonical functions of Ef-Tu from *M. pneumoniae* ($\mathrm{Mpn}_{\mathrm{Ef\text{-}Tu}}$) and show that it is a multifunctional protein that can not only bind to and activate plasminogen in the presence of host activators, but is also capable of binding to structurally and chemically diverse host molecules.

Results

Bioinformatic analysis of $\mathbf{Mhp}_{\mathbf{Ef\text{-}Tu}}$, $\mathbf{Sa}_{\mathbf{Ef\text{-}Tu}}$ and $\mathbf{Mpn}_{\mathbf{Ef\text{-}Tu}}$. The amino acid sequences of Ef-Tu from *M. pneumoniae* ($\mathrm{Mpn}_{\mathrm{Ef\text{-}Tu}}$), *M. hyopneumoniae* ($\mathrm{Mhp}_{\mathrm{Ef\text{-}Tu}}$), and *S. aureus* ($\mathrm{Sa}_{\mathrm{Ef\text{-}Tu}}$) share 60.7% sequence identity. $\mathrm{Mpn}_{\mathrm{Ef\text{-}Tu}}$ resides on the cell surface of *M. pneumoniae* and binds fibronectin [2]. The fibronectin-binding regions have been mapped and are located at the end of domain I and at the beginning of domain II [89,90] and most of domain III is also involved in binding fibronectin [89]. It is not known if sequence conservation in fibronectin-binding regions of $\mathrm{Mhp}_{\mathrm{Ef\text{-}Tu}}$ and $\mathrm{Sa}_{\mathrm{Ef\text{-}Tu}}$ is sufficient to afford these Ef-Tu homologs the ability to bind fibronectin. Several Mycoplasma species [73,91] and *S. aureus* [92-94] are known to interact with heparin. Putative heparin-binding domains were computationally predicted and mapped onto each of the Ef-Tu molecules (Figure 1). Several of these were conserved in all three Ef-Tu sequences in domains I, II and III.

$\mathbf{Mhp}_{\mathbf{Ef\text{-}Tu}}$, $\mathbf{Sa}_{\mathbf{Ef\text{-}Tu}}$ and $\mathbf{Mpn}_{\mathbf{Ef\text{-}Tu}}$ are accessible on the bacterial surface and are retained during heparin-agarose chromatography. LC-MS/MS analysis of tryptic peptides released from the cell surface of *S. aureus*, *M. pneumoniae* and *M. hyopneumoniae* were separately mapped to $\mathrm{Sa}_{\mathrm{Ef\text{-}Tu}}$, $\mathrm{Mpn}_{\mathrm{Ef\text{-}Tu}}$ and $\mathrm{Mhp}_{\mathrm{Ef\text{-}Tu}}$ respectively. In other experiments, tryptic peptides generated by digesting biotinylated cell surface proteins that were captured by avidin agarose chromatography were also separately mapped to $Sa_{Ef\text{-}Tu}$, $Mpn_{Ef\text{-}Tu}$ and $Mhp_{Ef\text{-}Tu}$. Peptides identified by mass spectrometry from both techniques spanned the entire length of Ef-Tu, (Figure S1) consistent with the hypothesis that a sub-population of Ef-Tu molecules are exposed on the cell surface of the three pathogens (Figure 2) while the remainder perform an essential function in the cytosol. Tryptic peptides spanning the length of $Sa_{Ef\text{-}Tu}$, $Mpn_{Ef\text{-}Tu}$ and $Mhp_{Ef\text{-}Tu}$ were also characterised when LC-MS/MS analysis was performed on tryptic digests of high salt (> 500 mM) eluents of proteins that were retained on heparin agarose (Figure 2).

$Mhp_{Ef\text{-}Tu}$, $Sa_{Ef\text{-}Tu}$ and $Mpn_{Ef\text{-}Tu}$ are cleaved on the bacterial cell surface. As part of a larger study that sought to identify the repertoire of proteins in *M. pneumoniae*, *M. hyopneumoniae* and *S. aureus* that are targets of proteolytic processing events, we employed a dimethyl labelling protocol to tag N-terminal peptides and identify precise endoproteolytic cleavage sites (Table 1). Further evidence that $Sa_{Ef\text{-}Tu}$, $Mpn_{Ef\text{-}Tu}$ and $Mhp_{Ef\text{-}Tu}$ are targets of protein cleavage events was obtained by LC-MS/MS analysis of i) SDS-PAGE gel slices separately loaded with biotinylated *M. pneumoniae*, *M. hyopneumoniae* and *S. aureus* surface proteins captured by avidin chromatography, ii) bacterial proteins that eluted from heparin agarose using high salt (> 500 mM NaCl), iii) protein spots representing bacterial whole cell lysates and surface biotinylated proteins separated by 2D-PAGE, and iv) size fractioned whole cell lysate proteins resolved by SDS-PAGE.

Of the 15 cleavage fragments of $Mpn_{Ef\text{-}Tu}$ identified in this study, 11 were identified in the biotinylated 1D and 2D SDS-PAGE. Notably, three of the four cleavage fragments derived from $Mhp_{Ef\text{-}Tu}$ and two of six fragments of $Sa_{Ef\text{-}Tu}$ that were enriched during heparin affinity chromatography were also identified in biotinylation experiments (Figure S4, S5 and S6). Ten, four and six cleavage fragments that span different regions of $\text{Mpn}_{\text{Ef-Tu}}$, $\text{Mhp}_{\text{Ef-Tu}}$ and $\text{Sa}_{\text{Ef-Tu}}$ respectively were recovered from a heparin agarose chromatography using salt concentrations well above the physiological concentration of 150 mM. All the fragments recovered from heparin affinity chromatography across all three pathogens contained at least one of the predicted heparin-binding domains that reside within $\text{Mpn}_{\text{Ef-Tu}}$, $\text{Mhp}_{\text{Ef-Tu}}$ and $\text{Sa}_{\text{Ef-Tu}}$. These data suggest that the processing events that generate Ef-Tu cleavage fragments, occur on the surface of each of these pathogens and that the fragments may retain an ability to interact with high sulfated glycosaminoglycans such as heparin. To ascertain the nature of the protease(s) responsible for Ef-Tu surface cleavage, the MEROPs database was used to search 56 cleavage events. However, no strong predictions could be made after searching both P4-P3-P2-P1↓P1’-P2’-P3’-P4’ and P2-P1↓P1’-P2’ cleavage motifs.

Processing events expose new predicted surface macromolecule interaction sites. A single heparin-binding consensus motif (XBBBXXBX, where B is a basic residue) with the sequence DKRHYAHV is found within the amino acid sequences of $\text{Sa}_{\text{Ef-Tu}}$, $\text{Mpn}_{\text{Ef-Tu}}$, and $\text{Mhp}_{\text{Ef-Tu}}$, yet we found several Ef-Tu fragments that were retained during heparin agarose chromatography that did not span this motif. $\text{Sa}_{\text{Ef-Tu}}$, $\text{Mpn}_{\text{Ef-Tu}}$, and $\text{Mhp}_{\text{Ef-Tu}}$ sequences were examined for additional motifs enriched with clustered basic residues. In $\text{Mpn}_{\text{Ef-Tu}}$ we identified 12 putative heparin-binding motifs dispersed throughout the protein (Table S1). Many of these putative heparin-binding motifs, particularly sequences ^{37}aKegKsaatRy^{47}, ^{183}pKweaKiHd^{191} and ^{248}lRpiRKa^{254} were localised to non-essential regions defined here as evolutionary unconserved regions (See S9 - Supplementary Materials: Bioinformatics and Table S1). Using ISIS [95], which predicts protein-protein interaction (PPI) sites from sequence information, $\text{Mpn}_{\text{Ef-Tu}}$ is predicted to have eight surface exposed PPI sites that are capable of binding macromolecules (**Table S2A)**

such as glycosaminoglycans including four that reside within putative heparin-binding motifs ^{2}a**Re**KfdRsKpHv^{13}, ^{73}**d**KRHyaHv^{80} and ^{370}e**K**gsKfsiReggRt^{383} (Table S1). Notably, the key residues (underlined and in bold) in the four binding sites were all unconserved residues as determined by ConSurf [96]. Putative heparin-binding fragments derived from Mpn$_{\text{Ef-Tu}}$ typically displayed more putative PPI sites and were more intrinsically disordered than the parent molecule and some fragments displayed putative nucleic acid interaction sites (Figure 2), which are absent in the unprocessed, parent molecule. Additionally, three short linear motifs located in unconserved regions of Ef-Tu that were not predicted binding sites in the parent molecule were predicted to be exposed in Mpn$_{\text{Ef-Tu}}$ fragment 3 (^{37}**aKegKs**aat**Ry**^{47}), fragment 4 (^{183}**p**KweaKiHd^{191}), fragment 5 (^{37}**aKegK**saatRy^{47}), fragment 6 (^{248}lR**p**i**R**Ka^{254}), fragment 7 (^{37}aK**e**gKsaatRy^{47} and ^{183}**pKwea**KiHd^{191}), fragment 10 (^{183}**p**K**w**e**a**Ki**H**d^{191}), fragment 12 (^{183}**pKweaK**i**H**d^{191}) and fragment 13 (^{248}**lRpiR**Ka^{254}) (**Table S1)**.

Molecular modelling of Ef-Tu. The prediction tool MODELLER [97] was used to predict the structures of Ef-Tu for all three pathogens based of Ef-Tu from *E. coli*. For the *M. pneumoniae* prediction, the *E. coli* Ef-Tu (PDB: 4G5G_A) had a structure ID percentage of 70.5% and a zDOPE score of -0.93. For *M. hyopneumoniae*, the *E. coli* Ef-Tu (PDB: 1DG1_H) had a structure ID percentage of 68.6% and a zDOPE score of -0.72. For *S. aureus*, the *E. coli* Ef-Tu (PDB: 1DG1_H) had a structure ID percentage of 75.1% and a zDOPE score of -0.88. All nine distinct cleavage sites for *M. pneumoniae* and *S. aureus* and four sites for *M. hyopneumoniae* have all been mapped in the ribbon structures (Figure S2). Cleavage sites located in regions that are predicted to release the three domains are mostly surface accessible within the molecule. The location and accessibility of the heparin-binding domains in Mpn$_{\text{Ef-Tu}}$, Mhp$_{\text{Ef-Tu}}$ and Sa$_{\text{Ef-Tu}}$ and the two published fibronectin-binding domains in Mpn$_{\text{Ef-Tu}}$ are depicted in Figure S3.

Mpn$_{\text{Ef-Tu}}$ and Mhp$_{\text{Ef-Tu}}$ are potential multifunctional binding proteins. It was notable that Mpn$_{\text{Ef-Tu}}$ was recovered from *M. pneumoniae* native cell lysates that were loaded onto affinity columns coupled with A549 epithelial cell surface proteins, fetuin, fibronectin, actin or plasminogen (Figure S4). Consistent with these data, rMpn$_{\text{Ef-Tu}}$ bound to immobilized A594 cells in microtitre plate binding assays (Figure 3A). Proteins that bind (recombinant pyruvate dehydrogenase subunit B) and that do not bind (P08 fragment of P1 adhesin) to A594 cells were used positive and negative controls respectively [98]. Binding of rMpn$_{\text{Ef-Tu}}$ to A594 cells was partially inhibited when anti-rMpn$_{\text{Ef-Tu}}$ antibodies, but not pre-immune antiserum, was present (Figure 3B). Mhp$_{\text{Ef-Tu}}$ was recovered from native cell lysates of *M. hyopneumoniae* that were loaded onto affinity columns coupled with PK15 epithelial cell surface proteins, fibronectin, actin, or plasminogen (Figure S4). Mpn$_{\text{Ef-Tu}}$ has previously been shown to bind fibronectin [2] and we independently confirmed this in microtitre plate binding assays. Furthermore, our binding assay suggests that *M. pneumoniae* encodes fibronectin-binding proteins other than Ef-Tu (Figure 4). Mpn$_{\text{Ef-Tu}}$, and nine of the fifteen cleavage fragments of Mpn$_{\text{Ef-Tu}}$, were recovered from affinity columns loaded with fibronectin (Figure S3). Of the nine cleavage fragments, seven spanned the known fibronectin-binding regions described previously (see Figure 1) [89,90]. We also identified fragments from columns coupled to fibronectin that spanned the N-terminus of Mpn$_{\text{Ef-Tu}}$ suggesting that other fibronectin-binding domains are yet to be identified in this molecule. Mhp$_{\text{Ef-Tu}}$ and six cleavage fragments of Mhp$_{\text{Ef-Tu}}$ were retained by columns coupled with fibronectin (Figure S5). The cleavage fragments spanned the N- and C-terminal ends, as well as the central region of Mhp$_{\text{Ef-Tu}}$ suggesting that it may contain fibronectin-binding domains.

Ten fragments spanning different regions of Mpn$_{\text{Ef-Tu}}$ (Figure S4) and one Mhp$_{\text{Ef-Tu}}$ fragment (Figure S5) were identified from affinity columns coupled with biotinylated surface proteins derived from A549 and PK-15 cells, respectively. $Mpn_{Ef\text{-}Tu}$ and $Mhp_{Ef\text{-}Tu}$, and fragments derived from them, were recovered from actin-coupled columns (Figures S4 and S5). Five fragments of $Mpn_{Ef\text{-}Tu}$ were recovered during affinity chromatography using fetuin as bait (Figure S4).

M. pneumoniae [99-101] and *M. hyopneumoniae* [78,81] have both been shown to bind plasminogen onto their cell surface and assist with its conversion to plasmin. In the current study, $Mpn_{Ef\text{-}Tu}$ and $Mhp_{Ef\text{-}Tu}$ were both recovered during plasminogen agarose chromatography. Fragments spanning different regions of $Mpn_{Ef\text{-}Tu}$ (Figure S4) and $Mhp_{Ef\text{-}Tu}$ (Figure S5) were recovered from plasminogen coupled agarose beads.

$Mpn_{Ef\text{-}Tu}$ is a multifunctional adhesin. Antibodies raised against $rMpn_{Ef\text{-}Tu}$ were used to show that $Mpn_{Ef\text{-}Tu}$ resides on the surface of colonies of *M. pneumoniae* (Figure S7). Our surfaceome studies (unpublished data) identified candidate proteins that could be used as a negative control for these studies and antibodies raised against recombinant 1-phosphofructokinase (FruK) from *M. pneumoniae* were used for this purpose (Figure S7). To further investigate the binding capabilities of $rMpn_{Ef\text{-}Tu}$, we examined the ability of the molecule to interact with a range of host molecules. $rMpn_{Ef\text{-}Tu}$ bound to fetuin ($K_D = 53 \pm 14$ nM), actin ($K_D = 19 \pm 3$ nM) and heparin ($K_D = 42.5 \pm 1.5$ nM) in the nanomolar range and to plasminogen ($K_D = 933 \pm 388$ nM) in the micromolar range, using microscale thermophoresis (Figure S8). We extended these studies using microtitre plate binding assays to confirm that $rMpn_{Ef\text{-}Tu}$ binds plasminogen and fibronectin, and also show that $rMpn_{Ef\text{-}Tu}$ binds fibrinogen, vitronectin, lactoferrin and laminin in a dose dependent manner (Figure 4). Binding of $rMpn_{Ef\text{-}Tu}$ to plasminogen was significantly reduced by the addition of an increasing concentration of NaCl and ε-aminocaproic acid (Figure 5A). Notably, ε-aminocaproic acid was effective at blocking interactions between *M. pneumoniae* and plasminogen while high concentrations of NaCl were less effective (Figure 5A).

These data suggest that lysine residues play a significant role in binding interactions between Ef-Tu and plasminogen, and *M. pneumoniae* cells and plasminogen.

In the presence of plasminogen activators tPA and uPA, plasminogen bound to rMpn$_{\text{Ef-Tu}}$ is converted to plasmin and can degrade fibrinogen and vitronectin (Figure 5B). Collectively these studies highlight the widespread multifunctional capabilities of Ef-Tu and the cleavage fragments derived from it.

Discussion

Ef-Tu moonlights on the cell surface of *S. aureus*, *M. pneumoniae* and *M. hyopneumoniae*, three phylogenetically diverse, pathogenic bacteria that belong to the low G + C Firmicutes. Using a combination of microscale thermophoresis and microtitre plate binding assays we show that rMpn$_{\text{Ef-Tu}}$ binds strongly to heparin ($K_D = 42.5 \pm 1.5$ nM), fetuin ($K_D = 53 \pm 14$ nM) and actin ($K_D = 19 \pm 3$ nM), as well as to laminin, plasminogen, vitronectin, lactoferrin, fibronectin, and fibrinogen. Plasminogen bound to rMpn$_{\text{Ef-Tu}}$ can be converted to plasmin in the presence of plasminogen activators tPA and uPA, (Figure 5). We also extend these finding by showing that Sa$_{\text{Ef-Tu}}$, Mpn$_{\text{Ef-Tu}}$ and Mhp$_{\text{Ef-Tu}}$ are targets of processing events on the cell surface of these bacterial pathogens but the biological significance of this warrants further investigation (see below). Molecules are not strictly confined to compartments in the bacterial cell and can perform novel functions at different cellular locations [24,25,54,102-105]. Much remains to be learnt about how proteins, especially those lacking signal motifs, localise on bacterial cell surfaces.

We sought to gain a better understanding of how Ef-Tu has evolved to be a multifunctional binding protein. Sa$_{\text{Ef-Tu}}$, Mpn$_{\text{Ef-Tu}}$ and Mhp$_{\text{Ef-Tu}}$ all putatively bind heparin, each sharing the consensus heparin-binding motif XBBBXXBX (sequence: dKRHyaHv) as well as a number of other heparin-binding motifs (see Figure 1 and Table S1). It is notable that while this motif (dKRHyaHv) is conserved in the Ef-Tu from *M. pneumoniae*, *M. hyopneumoniae* and *S. aureus* only part of the motif, with the sequence RHyaHv, is conserved in Ef-Tu from other bacterial sources. The addition of DK residues is predicted to impart a putative PPI site. Twelve putative heparin-binding motifs identified in Mpn$_{\text{Ef-Tu}}$ (Table S1) were predicted to predominantly localise to non-essential, unconserved regions of the molecule that do not unduly influence its ability to function as an elongation factor. Short linear motifs (SLiMs) typically ranging from three to ten amino acids play crucial roles in mediating PPIs [106-108]. In eukaryotes, these motifs are typically located in intrinsically unstructured, disordered regions of proteins that impart plasticity and are reported to favour transient, low affinity and reversible interactions [106,109]. Notably, Mpn$_{\text{Ef-Tu}}$ formed strong interactions with fetuin, heparin, and actin suggesting that the accumulation of SLiMs may be sufficient to form high affinity interactions.

Positively charged amino acids in SLiMs play a crucial role in interactions between proteins and highly sulphated glycosaminoglycans such as heparin [110], actin [111], plasminogen [112], DNA [113,114] and fibronectin [69,84,115]. Here we identified SLiMs enriched in positively charged amino acids in different regions of Mpn$_{\text{Ef-Tu}}$, including sequences ^{37}aKegKsaatRy^{47}, ^{183}pKweaKiHd^{191}, and ^{248}lRpiRKa^{254}, and identified eight surface exposed PPI sites, including three that reside within putative heparin-binding motifs ^{2}a**Re**KfdRsKpHv^{13}, ^{73}**d**KRHyaHv^{80}, and ^{370}e**K**gsKfsiReggRt^{383}. It is notable that the lysine analog, ε-amino caproic acid, was shown to be a potent inhibitor of interactions between Mpn$_{\text{Ef-Tu}}$ and plasminogen, and M129 whole cells and plasminogen, underscoring the important role played by positively charged amino acids in binding interactions with host molecules (Figure 5A). Overlapping SLiMs are frequently identified in multifunctional proteins [106,116]. In *M. hyopneumoniae*, the C-terminal sequence ^{1070}KKsslKvKitvK^{1081} in the multifunctional cilium adhesin, P97 binds both heparin and fibronectin [84] and overlapping peptides from a region within phosphoglycerate kinase from group B streptococcus strain NCS13 with sequence ^{203}sKvsdKigvienlleKadKv^{222} and ^{213}enlleKadKvligggmtytf^{232} bind both actin and plasminogen [112]. Similarly, we were able to identify SLiMs enriched in positively charged amino acids in $\mathrm{Sa}_{\mathrm{Ef\text{-}Tu}}$ and $\mathrm{Mhp}_{\mathrm{Ef\text{-}Tu}}$. The accumulation of positively charged residues in SLiMs, possibly as a consequence of an A+T rich genome, facilitates binding to a wide range of host molecules in the low G + C Firmicutes. Our data is consistent with the proposition that the accumulation of surface exposed SLiMs represents a mechanism to generate protein multifunctionality in bacterial proteins.

S. aureus [92] and *M. hyopneumoniae* [73-75,82,84,87,88], display cell surface, heparin-binding proteins that are important to the pathogenic potential of these species. Interactions between heparin-binding proteins and target receptors in host cell membrane allow microbes to colonise a wide range of niche sites, traverse tissue barriers and disseminate from their initial point of contact and form biofilms [117]. *S. aureus* [118,119], *M. pneumoniae* [120,121] and *M. hyopneumoniae* (our unpublished data) are all capable of forming biofilms. The extracellular matrix of *S. aureus* biofilms is derived from a mixture of eDNA and cytoplasmic proteins [118,122-127] and electrostatic interactions between cytoplasmic proteins and eDNA is thought to tether cells together in *S. aureus* and mixed species biofilms [127]. In *S. aureus*, the addition of heparin increases biofilm production in a protein dependant manner which implies that heparin-binding proteins are important for biofilm development [92]. Notably, Ef-Tu has been identified on the surface of *S. aureus* under biofilm inducing conditions [122]. These observations lend weight to the hypothesis that the accumulation of positively charged amino acids in SLiMS represents a powerful mechanism to promote PPIs that underpin essential biological processes such as the formation and maintenance of biofilms.

Bacterial pathogens including *Campylobacter jejuni* [69], *Mycoplasma gallisepticum* [86], and *Chlamydia trachomatis* [128] process molecules that are secreted to the cell surface. In *M. hyopneumoniae*, processing of cilium adhesin families has been reported extensively and cleavage motifs have been mapped [73,77,80,83]. Recently we showed that lactate dehydrogenase is cleaved on the surface of *M. hyopneumoniae* generating fragments with putative multifunctional binding capabilities [68]. In *M. pneumoniae*, cleavage fragments of the major adhesin P1 and DnaK have been shown to comprise part of the cytoskeletal attachment organelle complex [129] and Mycoplasma derived lipoproteins are targets of processing events that release powerful immunomodulatory peptides [71,130-132]. These observations prompted us to utilise a systems wide, protein dimethyl labelling strategy to investigate protein processing. Here we identified and characterised numerous processing sites in Ef-Tu derived from all three bacterial pathogens. Furthermore, our surface biotinylation studies indicate $\mathrm{Mpn}_{\text{Ef-Tu}}$, $\mathrm{Mhp}_{\text{Ef-Tu}}$ $\mathrm{Sa}_{\text{Ef-Tu}}$, were a target of multiple processing events of the surfaces of *M. pneumoniae*, *M. hyopneumoniae* and *S. aureus*, respectively. Our work strongly suggests that the accumulation of positively charged residues in the SLiMs found in Ef-Tu facilitates binding to a wide range of host molecules, and potentially to eDNA and that protein cleavage events expand the functional complexity of proteins that moonlight on the cell surface. We propose that processing is a mechanism that has evolved to promote multifunctional behaviour more broadly and lends itself to the creation of novel binding sites in moonlighting proteins that retain a strict conformational structure needed to execute their canonical function.

Fifteen cleavage fragments of $\mathrm{Mpn}_{\mathrm{Ef\text{-}Tu}}$ were identified in this study of which eleven reside on the cell surface. Unlike $\mathrm{Mpn}_{\mathrm{Ef\text{-}Tu}}$, none of the fragments were retained in all six affinity chromatography columns, but five were identified in at least five affinity columns (fragments 5, 6, 7, 8, and 10 in Figure S4). Fragments 5, 8, and 10 were retained in columns coupled with: A549 surface proteins, fetuin, fibronectin, actin, and heparin. Fragments 6 and 7 were retained in columns coupled with: A549 surface proteins, fibronectin, actin, heparin, and plasminogen. Fragment 4 was identified in eluents from columns coupled with A549 surface proteins and heparin while Fragment 9 was identified in eluents from columns coupled with fetuin and actin (see Figure S4). These data indicate that retention of the fragments during affinity chromatography is dependent on the host molecule that is coupled to the agarose beads and the sequence of the Ef-Tu fragment. Further studies are needed to quantify the binding characteristics of fragments of Ef-Tu with host molecules.

Cleavage fragments of cytosolic proteins that moonlight on the cell surface add another layer of complexity to the concept of multifunctional proteins. We show that processing exposes SLiMs that would otherwise be inaccessible for interactions with potential binding partners. Recently, a peptidome study of a protease deficient strain of *Lactococcus lactis* identified 1800 distinct peptides fragments in spent growth medium that were derived from proteolytic activity targeting both surface accessible and cytosolically derived proteins [133]. Similar studies by the same group indicated that surface accessible proteins in other Firmicute species including *Listeria monocytogenes*, *Enterococcus faecalis* and *Streptococcus thermophilus* were also targeted by complex processing events [133]. Previously we have shown that processing events play an important role in the maturation of key adhesin families in pathogenic mycoplasma species [67,72-86]. Here we extend these findings to show that surface proteolysis is critical in shaping the surface proteome more broadly and that processing represents a novel and under recognised mechanism to expand protein function.

In summary, Ef-Tu moonlights on the surface of bacteria where it is a target of proteolytic processing events. Computational analysis of fragments of $\mathrm{Mpn}_{\mathrm{Ef\text{-}Tu}}$ suggest they are inherently more disordered and display putative PPI sites that are inaccessible in the parent molecule, generating unprecedented functional diversity on the cell surface. Further studies, using systems wide methodologies, are needed to determine how processing generates biologically important effector molecules and if protein processing is fundamental to the expansion of protein function in bacteria belonging to different phylogenetic clades.

Experimental Section

A full description of the experimental section is listed in the S10 - Supplementary Materials 3.

1.1. Strains and cultures and reagents

M. pneumoniae (M129 strain; ATCC 29342) was cultured in modified Hayflick's medium at 37°C in tissue culture flasks as described previously [134].

M. hyopneumoniae (J strain) was cultured in modified Friis medium at 37°C with shaking as described previously [135,136].

S. aureus (SH 1000 strain) was cultured in TSB (Oxoid, Hampshire, UK) at 37°C with shaking and harvested during early stationary phase. Protease inhibitors (Roche Diagnostics®, North Ryde, Australia) in PBS were added to the cells during harvest and washes with PBS. For *S. aureus* lysis, cell pellets were freeze-dried overnight before added to pre-cooled metal milling canisters with 12 small metal beads. The canister was cooled in liquid nitrogen and milled at a maximum frequency of 30 Hz for 1 minute for 15 rounds; cooling in liquid nitrogen between rounds. Proteins were than solubilised in 7 M urea, 2 M thiourea, 50 mM LiCl, 50 mM Tris-HCl (pH 8.8), 1% (w/v) C7bZ0 with protease inhibitors followed by sonication at maximum intensity for 30 seconds for 20 rounds resting on ice in between.

Human lung carcinoma cells (A549; ATCC CCL-185) were cultured in RPMI 1640 medium (Invitrogen, Carlsbad, CA) supplemented with 10% heat inactivated fetal bovine serum at 37°C with 5% CO_2 in tissue culture flasks.

Porcine kidney epithelial (PK-15) cells were cultured in DMEM medium (Invitrogen) supplemented with 10% heat inactivated fetal bovine serum at 37°C with 5% CO_2 in tissue culture flasks.

Details about host proteins and human proteins used in this article are supplied in supplementary materials (S10.1).

1.2. Enrichment of M. pneumoniae, M. hyopneumoniae and *S. aureus surface proteins*

1.2.1. Biotinylation

Biotinylation of the *M. pneumoniae* cell surface was carried out as described in [67]. *M. hyopneumoniae* and *S. aureus* cells were washed with PBS after centrifugation before the resuspending in EZ-link sulfo-NHS-biotin (Thermo Fisher Scientific, North Ryde, Australia). *M. hyopneumoniae* and *S. aureus* cells were biotinylated for 30 seconds and 1 minute, respectively. Quenching, lysis (for *M. hyopneumoniae*), avidin purification and western blotting were the same as for *M. pneumoniae*. Lysis for *S. aureus* cells is described above in Section 1.1.

1.2.2. Triton X-114 phase extraction of biotinylated M. hyopneumoniae proteins

Triton X-114 phase extraction of proteins was carried as described in [77,83,137]and biotinylated surface proteins were purified by avidin column chromatography.

1.2.3. Trypsin shaving

Trypsin shaving of *M. pneumoniae* cells was carried out as described previously [75] with modifications. Trypsin was added to adherent *M. pneumoniae* cells within tissue culture flasks, and *M. hyopneumoniae* and *S. aureus* cells were resuspended in trypsin.

1.3. Preparation and separation of whole cell lysates for one- and two-dimensional gel electrophoresis

1.3.1. Whole cell lysis preparation

M. pneumoniae and *M. hyopneumoniae* whole cell lysates were prepared as previously described [75]. Lysis for *S. aureus* cells is described above in section 1.1. Proteins were reduced and alkylated with 5 mM tributylphosphine and 20 mM acrylamide monomers for 90 min at room temperature. Insoluble material was removed by centrifugation and five volumes of acetone added to precipitate protein. After centrifugation, the protein pellet was solubilized in 7 M urea, 2 M thiourea, 1% (w/v) C7BzO for one- and two-dimensional gel electrophoresis.

1.3.2. 1D and 2D SDS-PAGE protein separation

Protein separation was performed as described in [79,82]. 80 μg of protein was separated for 1D SDS-PAGE and 250 μg of protein was cup-loaded for 2D SDS-PAGE separation.

1.3.3. Trypsin Digest

In-gel trypsin digestion was performed as described in [77]. After digestion, tryptic peptides were stored at 4°C until needed for liquid chromatography tandem mass spectrometry.

1.4. Heparin affinity chromatography

Affinity purification of heparin-binding proteins for *M. pneumoniae* was performed as described in [67]. *M. hyopneumoniae* cells were and lysed in 10 mM sodium phosphate, pH 7 with three 30 second rounds of sonication. *S. aureus* cells were lysed as described in section 1.1 except that protein was solubilised in 10 mM sodium phosphate, pH 7 with protease inhibitors followed by sonication at maximum intensity for 30 seconds for 4 rounds resting on ice in between. After centrifugation, ~300 µg of soluble protein from both *M. hyopneumoniae* and *S. aureus* lysates were treated exactly the same as *M. pneumoniae*.

1.5. Avidin purification of host-binding M. pneumoniae proteins

Purified fibronectin (Merck Millipore, Darmstadt, Germany), plasminogen (Merck Millipore), actin (Sigma, St. Louis, MO) and fetuin (Sigma) used in this section are described in supplementary section S10.1. Avidin purification of these host-binding *M. pneumoniae* proteins was carried out as described in [67]. Avidin purification of *M. pneumoniae* proteins that bind A549 surface proteins was performed as described in [67].

1.6. Avidin purification of host-binding M. hyopneumoniae proteins

Purified fibronectin (Merck Millipore), plasminogen (Sigma) and actin (Sigma) used in this section are described in supplementary section S10.1. Avidin purification of these host-binding *M. hyopneumoniae* proteins was performed as described in [84]. Avidin purification of *M. hyopneumoniae* proteins that bind PK-15 surface proteins was performed as described in [82].

1.7. Liquid chromatography tandem mass spectrometry (LC-MS/MS) and MS/MS data analysis

LC-MS/MS was performed as described in [82]. Mascot (Version 6.1) was used to search MS/MS data files as previously described [82] with modifications (see supplementary section S10.2 for details).

1.8. Expression and purification of rMpn$_{Ef\text{-}Tu}$

Expression and purification of rMpn$_{\text{Ef-Tu}}$ was performed in one of two methods as described by [100] and [88]. Details and modifications to methods can be found in supplementary materials (section S10.3).

1.9. Binding of rMpn$_{Ef\text{-}Tu}$ to A549 cells

1.9.1. Binding assays

For this experiment and all subsequent experiments, animal experiments were approved by the ethical board of Landesdirektion Sachsen, Dresden, Germany with the permit no. (permit 24-9168.25-1/2011-1). ELISA experiments were carried out as described in [98]. Guinea pig rMpn$_{\text{Ef-Tu}}$ antiserum (1:750) followed by anti-guinea pig IgG (1:1,000; Dako) dilutions were used. Tetramethylbenzidine (Sigma) was added followed by 1 M HCl and absorbance was measured at 450 nm (620 nm as reference).

1.9.2. Influence of anti-rMpn$_{\text{Ef-Tu}}$ on binding

Freshly grown A549 cells were used to coat wells in 96-well microtitre plates for 2 h at 37°C as described in section 1.9.1. $rMpn_{Ef\text{-}Tu}$ (10 µg/ml) was incubated with guinea pig $rMpn_{Ef\text{-}Tu}$ antiserum or pre-immune serum (1:100) concentrations were used.

1.10. Binding of $rMpn_{Ef\text{-}Tu}$ to human proteins in ELISA

Purified human proteins used were supplied by Sigma and described in supplementary section S10.1. Binding of $rMpn_{Ef\text{-}Tu}$ (15 µg/ml) to extracellular matrix proteins was performed as described previously [98]. The dilutions for the appropriate antisera are: (Sigma) anti-plasminogen: 1:2,500; anti-lactoferrin 1:5,000; anti-laminin 1:750; anti-vitronectin 1:5,000; anti-fibrinogen 1:3,000; anti-fibronectin 1:1,000. Followed by anti-rabbit IgG (Dako, Glostrup, Denmark) or anti-goat IgG (both 1:2,000).

1.11. Microscale thermophoresis

Microscale thermophoresis to determine the binding affinities between Ef-Tu and a fluorescently labelled host protein was performed as described in [84]. Time for Microscale thermophoresis was set to 30 s with fluorescence set to 5 s before and 30 s after each run. Each sample was scanned with 40%, 60% and 80% MST Power. Dissociation curves were plotted with hot/cold, jump or thermophoresis settings to determine dissociation constant.

1.12. Binding affinity of $rMpn_{Ef\text{-}Tu}$ to plasminogen

1.12.1. Effect of NaCl on plasminogen-binding

Briefly, 96-well microtitre plates were coated with $rMpn_{Ef\text{-}Tu}$ as described. Plasminogen (2.5 µg) together with increasing concentrations of NaCl were added to the wells and incubated for 1.5 h at 37°C. Wells were incubated with rabbit anti-plasminogen (1:3,000) followed by anti-rabbit IgG (1:2,000). Detection was done as described in section 1.9.1.

1.12.2. Effect of ε-aminocaproic acid on plasminogen-binding

ELISA was carried out as reported in [98]. In brief, the wells of ELISA plates were coated with rMpn$_{\text{Ef-Tu}}$. 2.5 µg of plasminogen and increasing concentrations of ε-aminocaproic acid were added to the wells and incubated for 1.5 h at 37°C. Wells were incubated with rabbit anti-plasminogen (1:3,000) followed by anti-rabbit IgG (1:2,000) and OD$_{420nm}$ was measured.

1.13. Plasminogen activation and degradation of human fibrinogen and vitronectin

Degradation of human fibrinogen and vitronectin by activated plasminogen was carried out as described in [98].10 µg/ml of human plasminogen was added to the wells which were then incubated with fibrinogen or vitronectin (each 15 µg/ml) and urinary plasminogen activator (uPA; Sigma) or tissue plasminogen activator (tPA; each 75 ng/ml; Sigma).

1.14. Binding of anti- rMpn$_{\text{Ef-Tu}}$ *antibodies to M. pneumoniae whole cell lysate proteins*

Freshly grown *M. pneumoniae* cells were harvested and used to coat wells in 96-well microtitre plate for 2 h at 37°C as described previously [100]. Wells were blocked before adding guinea pig rMpn$_{\text{Ef-Tu}}$ antisera (1:500) followed by anti-guinea pig IgG (1:1,000). As a control wells were incubated with guinea pig antisera raised against total *M. pneumoniae* proteins.

1.15. Surface localisation of Ef-Tu on M. pneumoniae

1.15.1. Localisation of Ef-Tu on the surface of *M. pneumoniae* colonies

M. pneumoniae colonies were grown on PPLO agar plates and blotted onto nitrocellulose as described previously [100]. Antisera to PdhB and 1-phosphofructokinase (FruK) were used as positive and negative controls, respectively.

1.15.2. Surface localisation of Ef-Tu on *M. pneumoniae* cells

Immunofluorescence experiments were carried out as described in [100]. Again guinea pig antisera to PdhB and FruK were used as positive and negative controls, respectively.

1.16. Dimethyl labelling and LC-MS/MS analysis of M. pneumoniae, M. hyopneumoniae and *S. aureus proteins*

1.16.1. Dimethyl labelling of proteins

Dimethyl labelling of proteins was performed as described previously [67,68].

1.16.2. LC-MS/MS of dimethyl labelled proteins

Dimethyl labelled proteins were analysed by two mass spectrometers; the Sciex 5600 and the Thermo Scientific Q Exactive™. For full technical set up and method details see supplementary materials (section S10.4).

1.17. Bioinformatic analysis of Ef-Tu

Bioinformatic analysis of elongation factor tu used the online resources: ProtParam [138], Clustal Omega [139], SignalP 4.1 Server [140], SecretomeP 2.0 Server [141], TMpred [142] and COILS (Addition of 'yes' to 2.5 fold weighting of positions a,d) [143]. The amino acid sequences of $\mathrm{Mpn}_{\mathrm{Ef\text{-}Tu}}$(Uniprot #: P23568), $\mathrm{Mhp}_{\mathrm{Ef\text{-}Tu}}$ (Uniprot #: Q4A9G1) and $\mathrm{Sa}_{\mathrm{Ef\text{-}Tu}}$ (Uniprot #: Q2G0N0) were analysed using a variety of bioinformatics tools. Conservation of amino acid positions in each protein were detected using The ConSurf server [96]. Putative heparin-binding sites were identified using the search patterns x-[HKR]-x(0,2)-[HKR]-x(0,2)-[HKR]-x and x-[HKR]-x(1,4)-[HKR]-x(1,4)-[HKR]-x via ScanProsite [144]. Putative protein-protein and protein-nucleic acid interaction sites were identified using ISIS [95]. Intrinsically disordered regions were predicted by Meta-Disorder [145,146], which combines the outputs from original prediction methods NORSnet, DISOPRED2, PROFbval and Ucon. Solvent accessibility of each amino acid position was ascertained using evolutionary information from multiple sequence alignments and a multi-level system [147]. Nucleotide, DNA and RNA binding regions were predicted by SomeNA [148].

Data availability statement

The datasets generated during and/or analysed during the current study are available from the corresponding author on reasonable request.

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Competing financial interests

No competing interests.

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Author Contributions

M.W. acquired data and analysed it for *M. pneumoniae* except those listed for I.J.B. and L.H. K.L.H. acquired data and analysed it for *S. aureus* except data for the N-terminome that was acquired by J.R.S. M.W. and K.H. prepared all figures and tables except those listed for L.H. and A.G. M.W., K.L.H., R.D. and I.G.C. assisted with drafting the manuscript. A.G. produced the recombinant Ef-Tu of *M. pneumoniae* and the guinea pig antiserum. L.H. acquired binding data for A549 cells and most host proteins, performed plasminogen binding and activation studies, conducted experiments with recombinant antisera, and prepared figures with A.G. I.J.B. acquired N-terminome data for *M. pneumoniae* and *M. hyopneumoniae*, and I.J.B. and M.W. analysed it. I.J.B. assisted with the preparation of cleavage maps. VMJ performed the SLiM analysis and prepared figures. B.B.A.R. and J.L.T. acquired and analysed surfaceome data for *M. hyopneumoniae*. M.P.P. oversaw the acquisition of mass spectrometry data and assisted with data interpretation. S.P.D. initiated this study, wrote most of the manuscript, and secured funding. R.D. supervised the binding studies performed by L.H. and A.G. and secured funding. I.G.C. provided intellectual input and reviewed drafts of the manuscript. All authors reviewed and approved the manuscript.

Tables and Figures

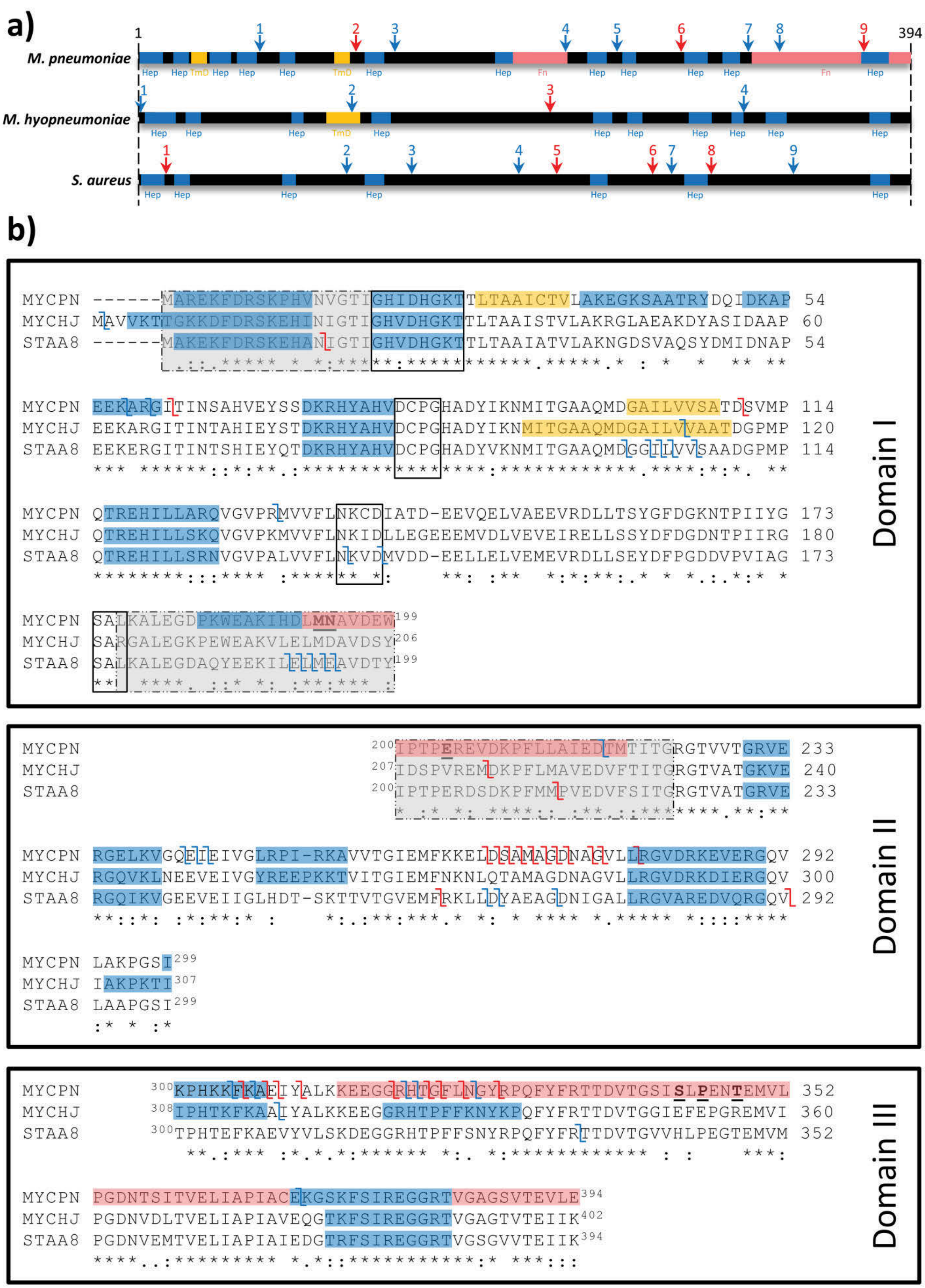
Table 1: Dimethyl labelled and semi-tryptic peptides identified in Mpn$_{\text{Ef-Tu}}$, Mhp$_{\text{Ef-Tu}}$ and Sa$_{\text{Ef-Tu}}$

No.	**ID**	**Peptide Sequence**	**Score**	**E-value**
		Dimethyl Labelled peptides from Mpn$_{\text{Ef-Tu}}$		
1	N1	K.^{58}**A**RGITINSAHVEYSSDKR^{75}.H	41	3.00E^{-03}
	N2	R.^{60}**G**ITINSAHVEYSSDKR^{75}.H	94	1.20E^{-08}
3	N3	R.^{131}**M**VVFLNK^{137}.C	57	1.30E^{-03}
5	N4	Q.^{242}**E**IEIVGLRPIR^{252}.K	48	3.30E^{-03}
	N5	E.^{243}**I**EIVGLRPIR^{252}.K	35	0.033
	N6	I.^{244}**E**IVGLRPIR^{252}.K	37	0.014
7	N7	K.^{305}**F**KAEIYALKKEEGGR^{319}.H	110	9.40E^{-09}
	N8	K.^{307}**A**EIYALKKEEGGR^{319}.H	69	2.60E^{-05}
8	N9	R.^{320}**H**TGFLNGYRPQFYFR^{334}.T	61	2.80E^{-05}
	N10	H.^{321}**T**GFLNGYRPQFYFR^{334}.T	39	2.90E^{-03}
	N11	N.^{326}**G**YRPQFYFR^{334}.T	43	1.70E^{-03}
		Semi-tryptic C-terminal Peptides from Mpn$_{\text{Ef-Tu}}$		
6	S1	R.^{253}KAVVTGIEMFKKEL**D**^{267}.S	47	4.50E^{-04}
	S2	R.^{253}KAVVTGIEMFKKELD**S**^{268}.A	56	4.50E^{-05}
	S3	R.^{253}KAVVTGIEMFKKELDSAM**A**^{273}.G	55	7.30E^{-05}
	S4	R.^{253}KAVVTGIEMFKKELDSAMA**G**^{272}.D	95	4.50E^{-09}
	S5	R.^{253}KAVVTGIEMFKKELDSAMAGDN**A**^{275}.G	96	3.30E^{-09}
	S6	R.^{253}KAVVTGIEMFKKELDSAMAGDNA**G**^{276}.V	113	2.90E^{-09}
	S7	R.^{253}KAVVTGIEMFKKELDSAMAGDNAGVL**L**^{279}.R	55	2.00E^{-05}
7	S8	R.^{290}GQVLAKPGSIKPHKK**F**^{305}.K	46	1.50E^{-04}
	S9	R.^{290}GQVLAKPGSIKPHKKFK**A**^{307}.E	61	2.10E^{-06}
	S10	R.^{290}GQVLAKPGSIKPHKKFKA**E**^{308}.I	27*	4.40E^{-03}
	S11	R.^{290}GQVLAKPGSIKPHKKFKAEI**Y**^{310}.A	38	2.40E^{-03}
8	S12	R.^{290}GQVLAKPGSIKPHKKFKAEIYALKKEEG**G**^{318}.R	85	7.00E^{-08}
	S13	R.^{290}GQVLAKPGSIKPHKKFKAEIYALKKEEGGR**H**^{320}.T	24	8.20E^{-03}
	S14	R.^{290}GQVLAKPGSIKPHKKFKAEIYALKKEEGGRH**T**^{321}.G	15*	0.048
	S15	R.^{290}GQVLAKPGSIKPHKKFKAEIYALKKEEGGRHT**G**^{322}.F	48	3.00E^{-04}

	S16	R.^{290}GQVLAKPGSIKPHKKFKAEIYALKKEEGGRHTGFL**N**^{325}.G	25*	9.50E^{-03}
	S17	R.^{320}HTGFLN**G**^{326}.Y	21*	0.058
		Semi-tryptic N-terminal Peptides from Mpn$_{\text{Ef-Tu}}$		
1	S18	I.^{62}**T**INSAHVEYSSDKR^{75}.H	37	4.60E^{-03}
2	S19	D.^{111}**S**VMPQTREHILLAR^{124}.Q	65	7.00E^{-05}
4	S20	D.^{218}**T**MTITGR^{224}.G	41	0.041
6	S21	L.^{267}**D**SAMAGDNAGVLLR^{280}.G	73	2.40E^{-06}
	S22	D.^{268}**S**AMAGDNAGVLLR^{280}.G	85	3.60E^{-06}
	S23	S.^{269}**A**MAGDNAGVLLR^{280}.G	58	1.30E^{-03}
	S24	A.^{270}**M**AGDNAGVLLR^{280}.G	53	7.20E^{-04}
	S25	M.^{271}**A**GDNAGVLLR^{280}.G	75	1.90E^{-05}
	S26	A.^{272}**G**DNAGVLLR^{280}.G	59	7.70E^{-04}
	S27	G.^{273}**D**NAGVLLR^{280}.G	57	1.30E^{-03}
	S28	D.^{274}**N**AGVLLR^{280}.G	42	0.031
8	S29	H.^{321}**T**GFLNGYRPQFYFR^{334}.T	76	6.00E^{-06}
	S30	T.^{322}**G**FLNGYRPQFYFR^{334}.T	47	3.00E^{-03}
	S31	G.^{323}**F**LNGYRPQFYFR^{334}.T	77	3.00E^{-05}
	S32	L.^{325}**N**GYRPQFYFR^{334}.T	62	5.30E^{-05}
	S33	N.^{326}**G**YRPQFYFR^{334}.T	47	2.90E^{-04}
	S34	G.^{327}**Y**RPQFYFR^{334}.T	59	1.40E^{-03}
9	S35	C.^{370}**E**KGSKFSIR^{378}.E	66	1.30E^{-03}
	S36	C.^{370}**E**KGSKFSIREGGR^{382}.T	35	6.60E^{-03}
		Dimethyl Labelled peptides from Mhp$_{\text{Ef-Tu}}$		
	N1	M.^{2}**A**VVKTTGKKDFR^{14}.S	84	5.70E^{-07}
1	N2	A.^{3}**V**VKTTGKKDFR^{14}.S	36	0.021
	N3	V.^{4}**V**KTTGKKDFR^{14}.S	34	0.019
2	N4	V.^{112}**V**AATDGPMPQTR^{123}.E	74	1.70E^{-05}
4	N5	A.^{316}**A**IYALKKEEGGR^{327}.H	50.1	3.00E^{-05}
		Semi-tryptic N-terminal Peptides from Mhp$_{\text{Ef-Tu}}$		
3	S1	M.^{215}**D**KPFLMAVEDVFTITGR^{231}.G	68	2.50E^{-05}
		Dimethyl Labelled peptides from Sa$_{\text{Ef-Tu}}$		
2	N1	D.^{101}**G**GILVVSAADGPMPQTR^{117}.E	98	2.90E^{-05}

	N2	G.^{103}**I**LVVSAADGPMPQTR^{117}.E	81	1.30E^{-03}
	N3	I.^{104}**L**VVSAADGPMPQTR^{117}.E	104	5.90E^{-06}
	N4	L.^{105}**V**VSAADGPMPQTR^{117}.E	91	1.10E^{-04}
	N5	V.^{107}**S**AADGPMPQTR^{117}.E	69	9.90E^{-03}
3	N6	N.^{137}**K**VDMVDDEELLELVEMEVR^{155}.D	80	3.10E^{-03}
	N7	D.^{140}**M**VDDEELLELVEMEVR^{155}.D	78	3.40E^{-03}
4	N8	L.^{191}**E**LMEAVDTYIPTPER^{205}.D	78	3.60E^{-03}
	N9	E.^{192}**L**MEAVDTYIPTPER^{205}.D	78	3.20E^{-03}
	N10	L.^{193}**M**EAVDTYIPTPER^{205}.D	72	2.80E^{-03}
	N11	M.^{194}**E**AVDTYIPTPER^{205}.D	103	8.40E^{-06}
	N12	E.^{195}**A**VDTYIPTPER^{205}.D	77	9.60E^{-04}
7	N13	K.^{265}**L**LDYAEAGDNIGALLR^{280}.G	98	4.10E^{-05}
	N14	L.^{267}**D**YAEAGDNIGALLR^{280}.G	88	1.80E^{-04}
	N15	D.^{268}**Y**AEAGDNIGALLR^{280}.G	89	2.40E^{-04}
	N16	G.^{273}**D**NIGALLR^{280}.G	67	1.80E^{-02}
9	N17	R.^{335}**T**TDVTGVVHLPEGTEMVMPGDNVEMTVELIAPIAIEDGTR^{374}.F	86	7.70E^{-07}
		Semi-tryptic N-terminal Peptides from Sa$_{\mathbf{Ef\text{-}Tu}}$		
8	S1	V.^{293}**L**AAPGSITPHTEFK^{306}.A	106	3.20E^{-05}
5	S2	M.^{214}**P**VEDVFSITGR^{224}.G	80	0.010
1	S3	N.^{15}**I**GTIGHVDHGK^{28}.T	80	1.10E^{-04}
6	S4	F.^{263}**R**KLLDYAEAGDNIGALLR^{280}.G	91	1.20E^{-03}

Identified peptides have a Mascot score > 33 and an E-value < 0.05 unless marked with a *. Peptides marked with a * implies the peptide score was < 33 but still lies within major cleavage site. The exact site of cleavage is to the left of the amino acid that is bold and underlined for N-terminal cleavage fragments and to the right of C-terminal cleavage fragments. Amino acid numbers are written at the start and end of each peptide identified by LC-MS/MS.



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MYCHJ MAVVKTTGKKDFDRSKEHINIGTIGHVDHGKTTLTAAISTVLAKRGLAEAKDYASIDAAP 60
STAA8 ------MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAP 54
               .::.***** * *:*****:***********.*****.* : *  *  ** **

MYCPN EEKARGITINSAHVEYSSDKRHYAHVDCPGHADYIKNMITGAAQMDGAILVVSATDSVMP 114
MYCHJ EEKARGITINTAHIEYSTDKRHYAHVDCPGHADYIKNMITGAAQMDGAILVVAATDGPMP 120
STAA8 EEKERGITINTSHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMP 114
      *** ******::*:**.:****************:************.****:*:*. **

MYCPN QTREHILLARQVGVPRMVVFLNKCDIATD-EEVQELVAEEVRDLLTSYGFDGKNTPIIYG 173
MYCHJ QTREHILLSKQVGVPKMVVFLNKIDLLEGEEEMVDLVEVEIRELLSSYDFDGDNTPIIRG 180
STAA8 QTREHILLSRNVGVPALVVFLNKVDMVDD-EELLELVEMEVRDLLSEYDFPGDDVPVIAG 173
      ********:::**** :****** *:    **: :**  *:*:**:.* * *.:.*:* *

MYCPN SALKALEGDPKWEAKIHDLMNAVDEW 199
MYCHJ SARGALEGKPEWEAKVLELMDAVDSY 206
STAA8 SALKALEGDAQYEEKILELMEAVDTY 199
      **  ****.  ::* *: :**:*** :

MYCPN                          200 IPTPEREVDKPFLLAIEDTMTITGRGTVVTGRVE 233
MYCHJ                          207 IDSPVREMDKPFLMAVEDVFTITGRGTVATGKVE 240
STAA8                          200 IPTPERDSDKPFMMPVEDVFSITGRGTVATGRVE 233
                                   * :* *: ****:: :** .:*******.**:**

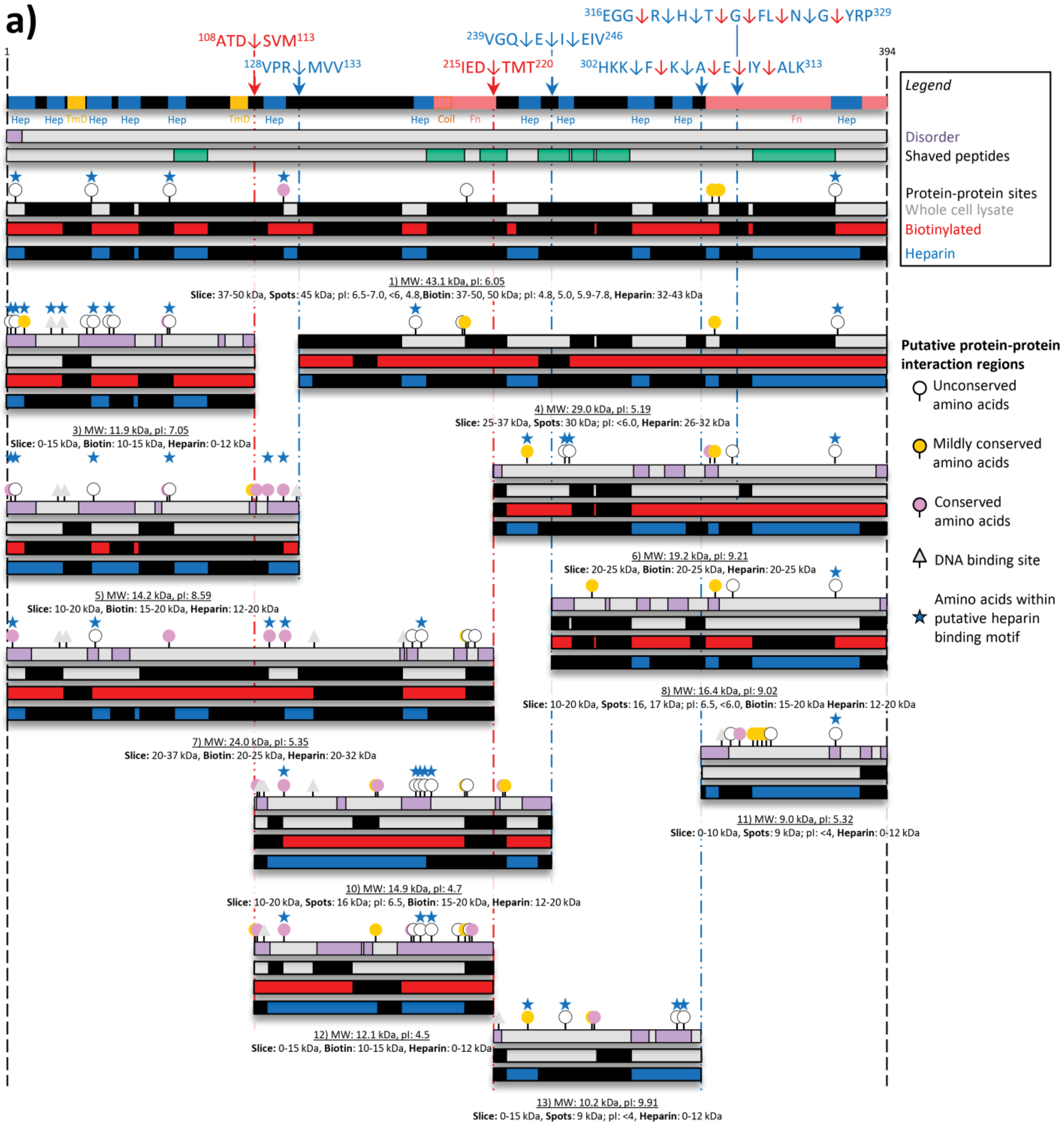
MYCPN RGELKVGQEIEIVGLRPI-RKAVVTGIEMFKKELDSAMAGDNAGVLLRGVDRKEVERGQV 292
MYCHJ RGQVKLNEEVEIVGYREEPKKTVITGIEMFNKNLQTAMAGDNAGVLLRGVDRKDIERGQV 300
STAA8 RGQIKVGEEVEIIGLHDT-SKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQV 292
      **::*: :*:**:* :    *:.:**:***.* *: * **** *.***** *::::****

MYCPN LAKPGSI 299
MYCHJ IAKPKTI 307
STAA8 LAAPGSI 299
      :* * :*

MYCPN           300 KPHKKFKAEIYALKKEEGGRHTGFLNGYRPQFYFRTTDVTGSISLPENTEMVL 352
MYCHJ           308 IPHTKFKAAIYALKKEEGGRHTPFFKNYKPQFYFRTTDVTGGIEFEPGREMVI 360
STAA8           300 TPHTEFKAEVYVLSKDEGGRHTPFFSNYRPQFYFRTTDVTGVVHLPEGTEMVM 352
                     **.:*** :*.*.*:****** *:. *:************ : :    ***:

MYCPN PGDNTSITVELIAPIACEKGSKFSIREGGRTVGAGSVTEVLE 394
MYCHJ PGDNVDLTVELIAPIAVEQGTKFSIREGGRTVGAGTVTEIIK 402
STAA8 PGDNVEMTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394
      ****..:********* *.*::***********:* ***:::
```

Figure 1. Bioinformatic analysis of Mpn$_{\text{Ef-Tu}}$, Mhp$_{\text{Ef-Tu}}$, and Sa$_{\text{Ef-Tu}}$. A) Schematic of Mpn$_{\text{Ef-Tu}}$, Mhp$_{\text{Ef-Tu}}$ and Sa$_{\text{Ef-Tu}}$ highlighting putative heparin and fibronectin-binding domains and cleavage sites. ScanProsite [144] was used to predict heparin-binding motifs (dark blue boxes) by searching clusters of basic residues with the "X-[HRK]-X(0,2)-[HRK]-X(0,2)-[HRK]-X" and "X-[HRK]-X(1,4)-[HRK]-X(1,4)-[HRK]-X" motifs. A putative transmembrane domain (Score 505) was predicted in Mhp$_{\text{Ef-Tu}}$ using TMpred [142] (yellow box). In Mpn$_{\text{Ef-Tu,}}$ two fibronectin-binding regions (salmon boxes) and two predicted transmembrane domains (scores) are depicted in Panels A and B [89,90]. Key amino acids in Mpn$_{\text{Ef-Tu}}$ involved in binding fibronectin [89,90] are underlined. Cleavage sites identified in this study are shown as arrows above the black bar (blue indicates cleavage sites identified by dimethyl labelling and red indicates cleavage sites identified by the characterisation of semi-tryptic peptides by LC-MS/MS). B) Amino acid sequence alignments of Mpn$_{\text{Ef-Tu}}$, Mhp$_{\text{Ef-Tu}}$ and Sa$_{\text{Ef-Tu}}$. For consistency, features described in Figure 1A are represented by the same colour scheme in Figure 1B. Cleavage sites identified in this study are depicted by the symbol ʅ. Sequence alignments have been separated into the three domains and the nucleotide-binding motifs (boxed regions) and the two pattern recognition receptors (broken black outline grey box from *Acidovorax avenae* [65] and *Brassica*-specific receptors [64]) are shown.


a)
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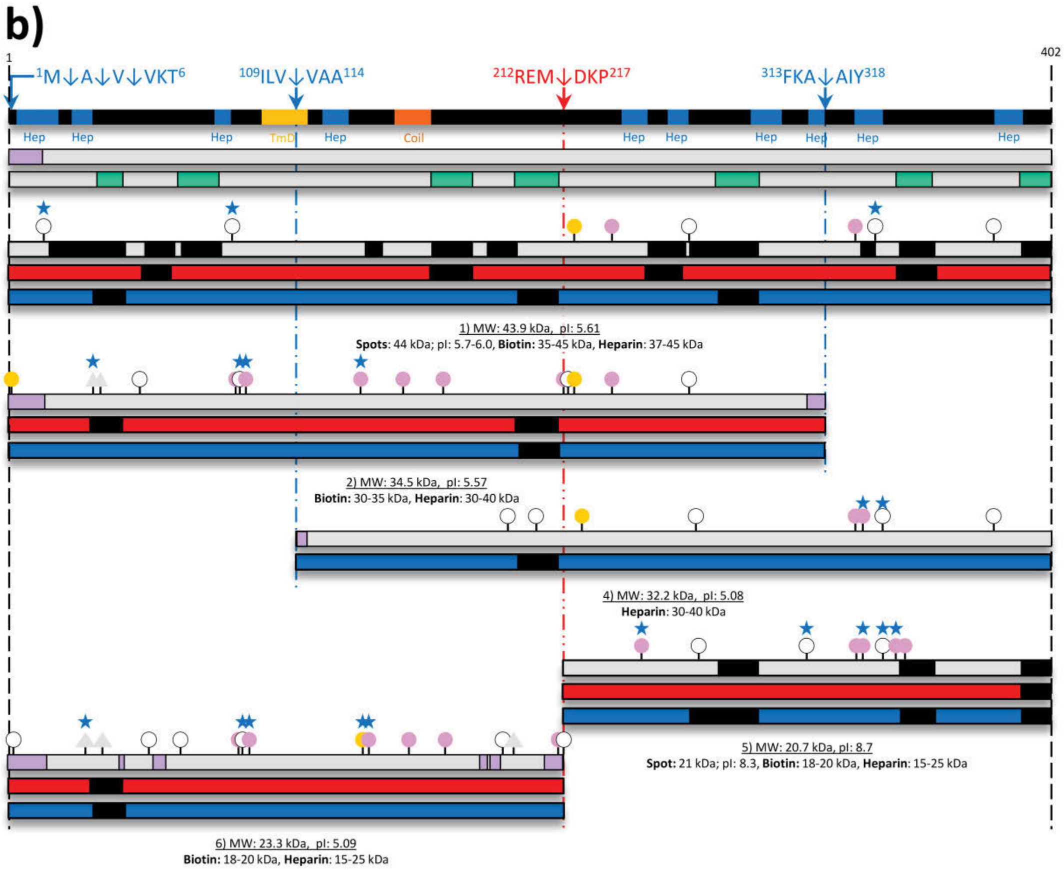
^{108}ATD↓SVM^{113}
^{239}VGQ↓E↓I↓EIV^{246}
1
394
^{128}VPR↓MVV^{133}
^{215}IED↓TMT^{220}
^{302}HKK↓F↓K↓A↓E↓IY↓ALK^{313}
Hep
Hep
TmD
Hep
Hep
Hep
TmD
Hep
Hep
Coil
Fn
Hep
Hep
Hep
Hep
Fn
Hep
Legend
Disorder
Shaved peptides
Protein-protein sites
Whole cell lysate
Biotinylated
Heparin
1) MW: 43.1 kDa, pI: 6.05
Slice: 37-50 kDa, Spots: 45 kDa; pI: 6.5-7.0, <6, 4.8, Biotin: 37-50, 50 kDa; pI: 4.8, 5.0, 5.9-7.8, Heparin: 32-43 kDa
Putative protein-protein interaction regions
Unconserved amino acids
Mildly conserved amino acids
Conserved amino acids
DNA binding site
Amino acids within putative heparin binding motif
4) MW: 29.0 kDa, pI: 5.19
Slice: 25-37 kDa, Spots: 30 kDa; pI: <6.0, Heparin: 26-32 kDa
3) MW: 11.9 kDa, pI: 7.05
Slice: 0-15 kDa, Biotin: 10-15 kDa, Heparin: 0-12 kDa
6) MW: 19.2 kDa, pI: 9.21
Slice: 20-25 kDa, Biotin: 20-25 kDa, Heparin: 20-25 kDa
5) MW: 14.2 kDa, pI: 8.59
Slice: 10-20 kDa, Biotin: 15-20 kDa, Heparin: 12-20 kDa
8) MW: 16.4 kDa, pI: 9.02
Slice: 10-20 kDa, Spots: 16, 17 kDa; pI: 6.5, <6.0, Biotin: 15-20 kDa Heparin: 12-20 kDa
7) MW: 24.0 kDa, pI: 5.35
Slice: 20-37 kDa, Biotin: 20-25 kDa, Heparin: 20-32 kDa
11) MW: 9.0 kDa, pI: 5.32
Slice: 0-10 kDa, Spots: 9 kDa; pI: <4, Heparin: 0-12 kDa
10) MW: 14.9 kDa, pI: 4.7
Slice: 10-20 kDa, Spots: 16 kDa; pI: 6.5, Biotin: 15-20 kDa, Heparin: 12-20 kDa
12) MW: 12.1 kDa, pI: 4.5
Slice: 0-15 kDa, Biotin: 10-15 kDa, Heparin: 0-12 kDa
13) MW: 10.2 kDa, pI: 9.91
Slice: 0-15 kDa, Spots: 9 kDa; pI: <4, Heparin: 0-12 kDa


b)
1
402
1M↓A↓V↓VKT6
109ILV↓VAA114
212REM↓DKP217
313FKA↓AIY318
Hep
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Hep
TmD
Hep
Coil
Hep
Hep
Hep
Hep
Hep
Hep
1) MW: 43.9 kDa, pI: 5.61
Spots: 44 kDa; pI: 5.7-6.0, Biotin: 35-45 kDa, Heparin: 37-45 kDa
2) MW: 34.5 kDa, pI: 5.57
Biotin: 30-35 kDa, Heparin: 30-40 kDa
4) MW: 32.2 kDa, pI: 5.08
Heparin: 30-40 kDa
5) MW: 20.7 kDa, pI: 8.7
Spot: 21 kDa; pI: 8.3, Biotin: 18-20 kDa, Heparin: 15-25 kDa
6) MW: 23.3 kDa, pI: 5.09
Biotin: 18-20 kDa, Heparin: 15-25 kDa

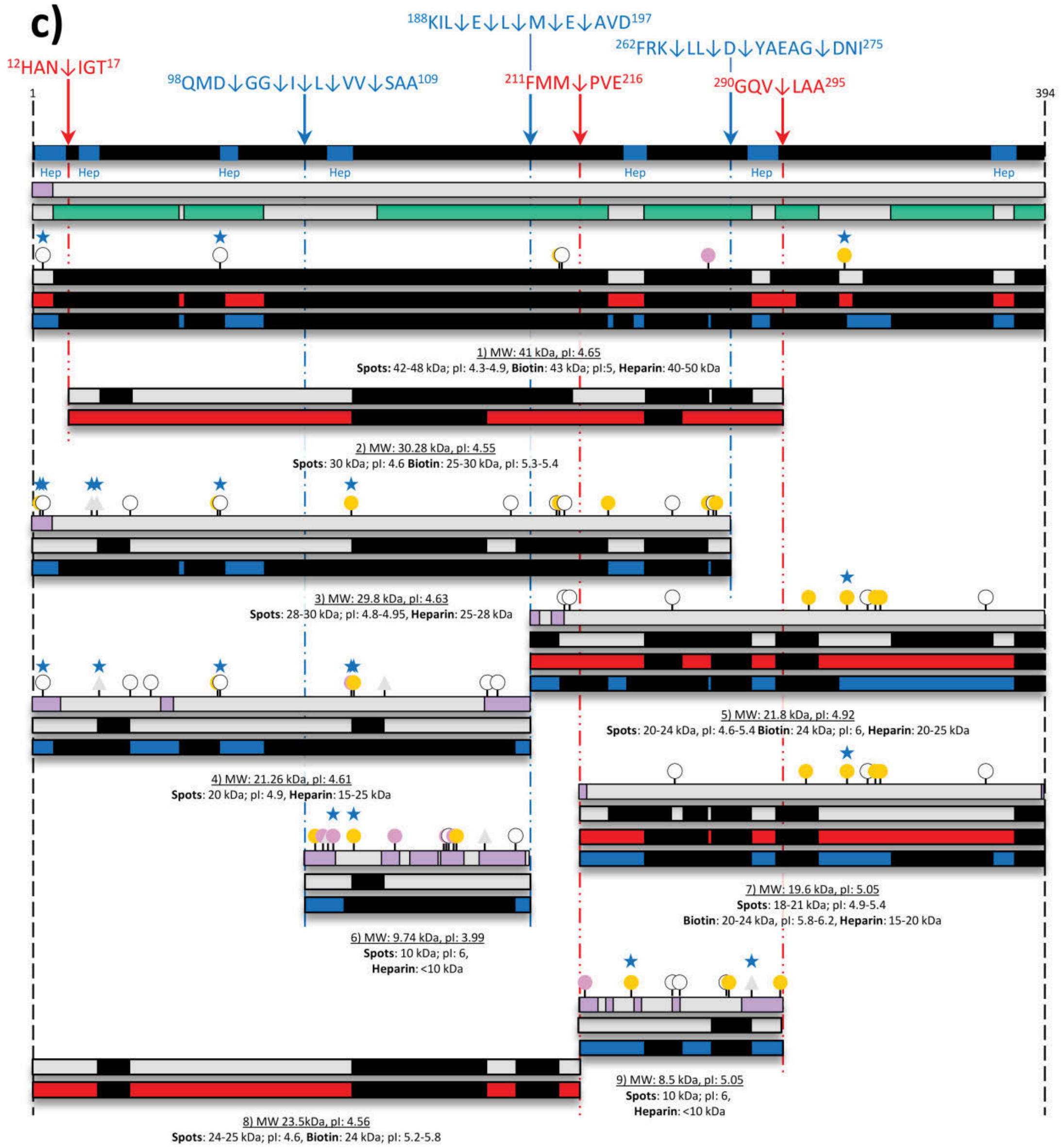

Figure 2. Binding to heparin by Ef-Tu and cleavage fragments of Ef-Tu. Panel A-C show Mpn$_{\text{Ef-Tu},}$ Mhp$_{\text{Ef-Tu},}$ and Sa$_{\text{Ef-Tu},}$ and surface accessible cleavage fragments of these molecules retained during heparin-agarose chromatography respectively. Peptides identified (black boxes within coloured bars) by mass spectrometry within Ef-Tu fragments were obtained from 1D and 2D SDS PAGE of bacterial whole cell lysates (grey bars), avidin affinity chromatography of biotinylated surface proteins (red bars), and heparin-agarose affinity chromatography (blue bars).

Full length Ef-Tu molecules are represented as black bars. Cleavage products of Ef-Tu are also shown. Cleavage sites were identified by identifying dimethyl labelled peptides (blue arrows and broken lines) and by characterising semi-tryptic peptides generated after trypsin digestion (red arrows and broken lines). Exact cleavage sites are shown in the amino acid sequences above the black bar. For *M. pneumoniae*, the two fibronectin-binding regions (salmon boxes, Fn) and two putative transmembrane domains described by [89,90] were included. Bioinformatic tools such as ScanProsite [144], TMpred [142], COILS [143] and Meta-Disorder [145] were used to predict putative heparin-binding motifs (Hep, blue boxes), transmembrane domains (TmD, yellow box for *M. hyopneumoniae*), coiled-coils (Coil, orange boxes), and disordered regions (purple boxes in grey bar), respectively. Peptides released from trypsin shaving of cells are shown as the green boxes in the grey bar. Circles just above fragments denote amino acid positions that are predicted to be surface exposed and represent putative protein-protein interaction regions (visual cues can be seen on the right of the cleavage map, sites listed in Tables S2A, S2B, and S2C). Those marked with an additional star denote amino acid residues that fall within predicted putative heparin-binding domains. White circles mark evolutionary unconserved binding regions, whilst yellow circles are mildly conserved and pink are highly conserved. Amino acid positions marked by grey triangles depict predicted nucleic acid interaction regions.

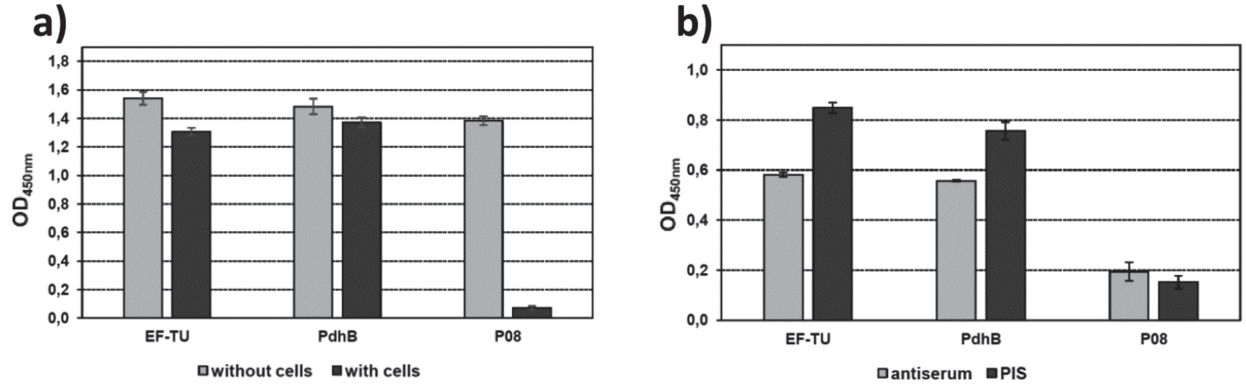

Figure 3: Binding of rMpn$_{Ef\text{-}Tu}$ to human A549 epithelial cells. A) A549 cells ('with cells') were bound to wells of a 96-well mictrotitre plate and incubated with rEf-Tu. Bound rMpn$_{Ef\text{-}Tu}$ was detected with antisera raised against rMpn$_{Ef\text{-}Tu}$. rPdhB and rP08 were used as a positive and negative control [98], respectively. Bars represent standard deviation of eight replicates. B) rMpn$_{Ef\text{-}Tu}$ was incubated with either antisera raised against rMpn$_{Ef\text{-}Tu}$ or pre-immune sera (PIS) and added to A549 cells in ELISA plates. rPdhB and rP08 and the corresponding antisera were used as a positive and negative control [98], respectively. Bars represent standard deviation of eight replicates.

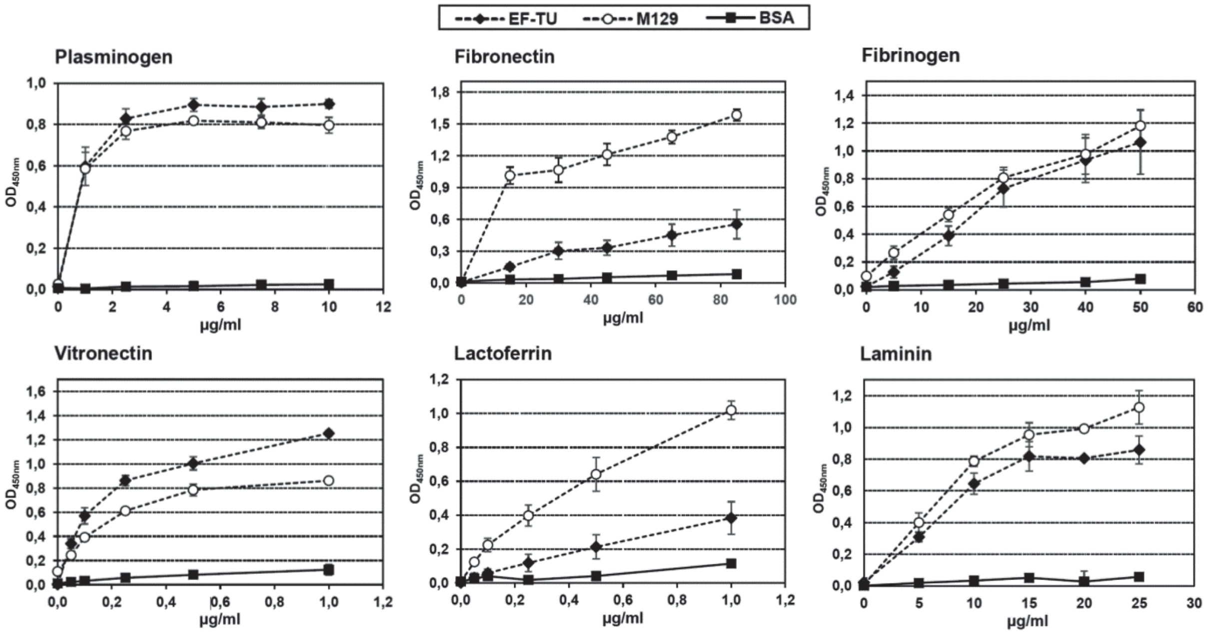

Figure 4: Microtitre plate binding assays depicting the interaction of rMpn$_{\text{Ef-Tu}}$ with human proteins. Wells of microtitre plates were coated with rMpn$_{\text{Ef-Tu}}$ and incubated with increasing concentrations of host proteins. Antisera against each of the host proteins was used to detect interaction with rMpn$_{\text{Ef-Tu}}$. *M. pneumoniae* cells and BSA were used as a positive and negative control, respectively. Bars represent standard deviation of eight replicates.

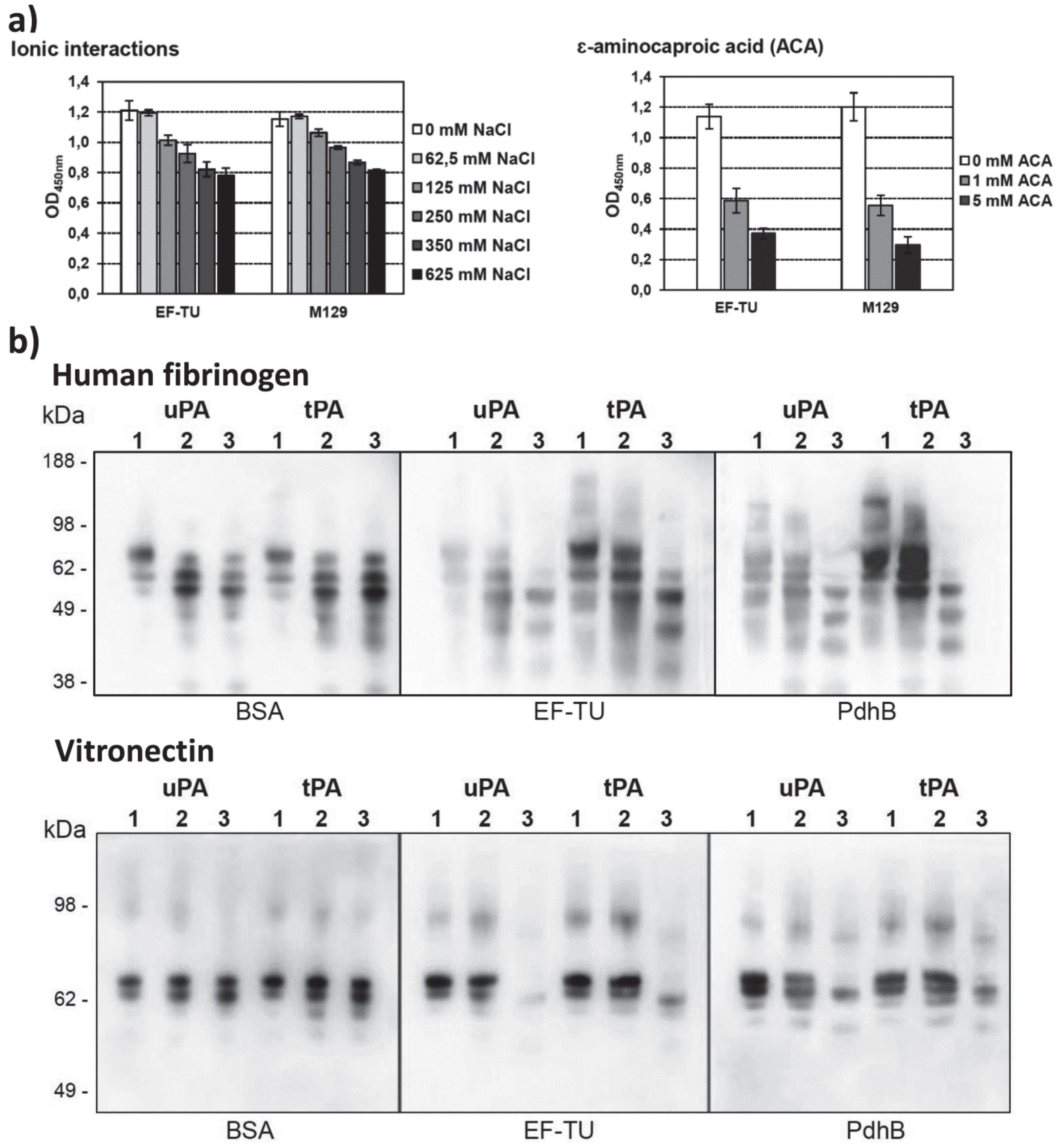

Figure 5: Influence of ions and lysine analog ACA on binding of rMpn$_{Ef\text{-}Tu}$ to plasminogen and degradation of human fibrinogen and vitronectin by activated plasminogen. A) Microtitre plate wells were coated with rMpn$_{Ef\text{-}Tu}$ and incubated with plasminogen and increasing concentrations of either NaCl (‘ionic interactions’) or ε-aminocaproic acid (‘ACA’).

Bound plasminogen was detected with anti-plasminogen antibodies. In control experiments *M. pneumoniae* cells were coated onto microtitre plates and incubated with plasminogen and increasing concentrations of either NaCl or ACA. Bars represent standard deviation of eight replicates. B) Fibrinogen or vitronectin was mixed with either urinary plasminogen activator (uPA) or tissue plasminogen activator (tPA) and added to microtitre plates previously coated with rMpn$_{\text{Ef-Tu}}$ and plasminogen. Samples were separated by SDS-PAGE, blotted onto nitrocellulose membrane and probed with anti-vitronectin and anti-fibrinogen antisera. Lane 1 is at 0 hours, lane 2 is after over-night incubation without plasminogen, and lane 3 is after over-night incubation with plasminogen. Full length blots can be seen in Figure S9.

Elongation factor Tu is a multifunctional and processed moonlighting protein

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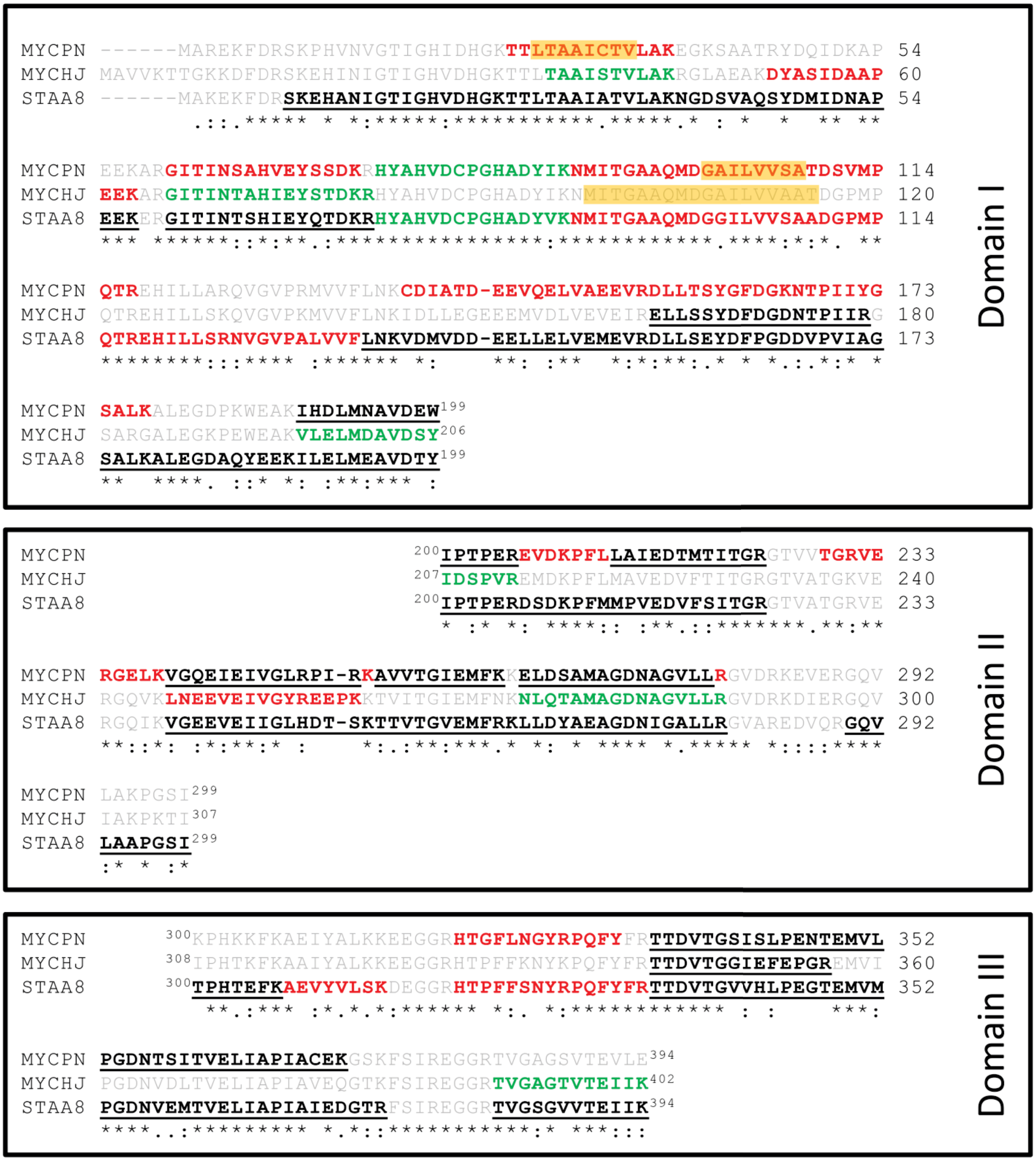
Supplementary Tables and Figures



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MYCHJ MAVVKTTGKKDFDRSKEHINIGTIGHVDHGKTTLTAAISTVLAKRGLAEAKDYASIDAAP 60
STAA8 ------MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAP 54
             .::.***** * *:*****:***********.*****.* : *  *  ** **

MYCPN EEKARGITINSAHVEYSSDKRHYAHVDCPGHADYIKNMITGAAQMDGAILVVSATDSVMP 114
MYCHJ EEKARGITINTAHIEYSTDKRHYAHVDCPGHADYIKNMITGAAQMDGAILVVAATDGPMP 120
STAA8 EEKERGITINTSHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGPMP 114
      *** ******::*:**.:****************:************.****:*:*. **

MYCPN QTREHILLARQVGVPRMVVFLNKCDIATD-EEVQELVAEEVRDLLTSYGFDGKNTPIIYG 173
MYCHJ QTREHILLSKQVGVPKMVVFLNKIDLLEGEEEMVDLVEVEIRELLSSYDFDGDNTPIIRG 180
STAA8 QTREHILLSRNVGVPALVVFLNKVDMVDD-EELLELVEMEVRDLLSEYDFPGDDVPVIAG 173
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MYCHJ SARGALEGKPEWEAKVLELMDAVDSY206
STAA8 SALKALEGDAQYEEKILELMEAVDTY199
      **  ****. ::* *: :**:*** :

MYCPN                        200IPTPEREVDKPFLLAIEDTMTITGRGTVVTGRVE 233
MYCHJ                        207IDSPVREMDKPFLMAVEDVFTITGRGTVATGKVE 240
STAA8                        200IPTPERDSDKPFMMPVEDVFSITGRGTVATGRVE 233
                                * :* *: ****:: :**.::*******.**:**

MYCPN RGELKVGQEIEIVGLRPI-RKAVVTGIEMFKKELDSAMAGDNAGVLLRGVDRKEVERGQV 292
MYCHJ RGQVKLNEEVEIVGYREEPKKTVITGIEMFNKNLQTAMAGDNAGVLLRGVDRKDIERGQV 300
STAA8 RGQIKVGEEVEIIGLHDT-SKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQV 292
      **::*: :*:**:* :    *:.:**:***.* *: * **** *.***** *::::****

MYCPN LAKPGSI299
MYCHJ IAKPKTI307
STAA8 LAAPGSI299
      :* * :*

MYCPN     300KPHKKFKAEIYALKKEEGGRHTGFLNGYRPQFYFRTTDVTGSISLPENTEMVL 352
MYCHJ     308IPHTKFKAAIYALKKEEGGRHTPFFKNYKPQFYFRTTDVTGGIEFEPGREMVI 360
STAA8     300TPHTEFKAEVYVLSKDEGGRHTPFFSNYRPQFYFRTTDVTGVVHLPEGTEMVM 352
              **.:*** :*.*.*:****** *:. *:************ : :    ***:

MYCPN PGDNTSITVELIAPIACEKGSKFSIREGGRTVGAGSVTEVLE394
MYCHJ PGDNVDLTVELIAPIAVEQGTKFSIREGGRTVGAGTVTEIIK402
STAA8 PGDNVEMTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK394
      ****..:********* *.*::***********:* ***:::
```

Figure S1. Peptides that map to Ef-Tu identified from surface biotinylation and shaving experiments. The sequence alignment for all three pathogens are shown separated into the three domains of Ef-Tu. Peptides identified from surface trypsin shaving of whole cells are coloured green where red text indicate peptides from biotinylated surface proteins. Peptides that were identified from both experiments are highlighted as black underlined text. Yellow boxes indicate transmembrane domains for: *M. pneumoniae* adapted from [89] and *M. hyopneumoniae* predicted by TMpred [142].

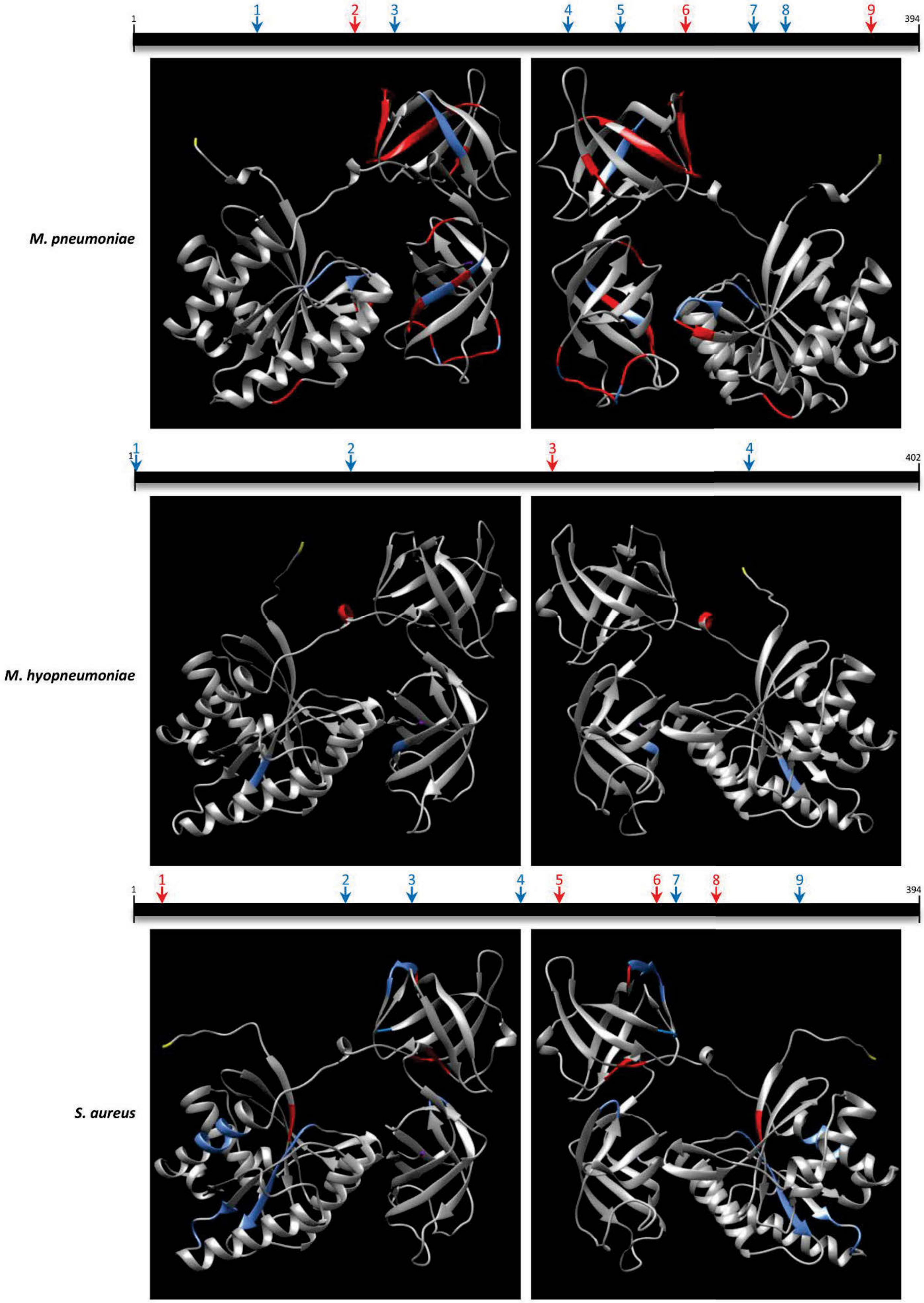

1
2
3
4
5
6
7
8
9
1
394
M. pneumoniae
1
2
3
4
1
402
M. hyopneumoniae
1
2
3
4
5
6
7
8
9
1
394
S. aureus

Figure S2. Predicted 3D ribbon structures of Mpn$_{\mathbf{Ef\text{-}Tu}}$, Mhp$_{\mathbf{Ef\text{-}Tu}}$ and Sa$_{\mathbf{Ef\text{-}Tu}}$. Ef-Tu molecules are represented as black bars with identified cleavage sites displayed as arrows (blue, dimethyl labelling and red, semi-tryptic) with numbers to indicate each distinct cleavage site. Cleavage sites can also be seen in the ribbon structures as blue and red sections for dimethyl labelling and semi-tryptic sites, respectively. Images are reversed sides of each structure. Structures were predicted by MODELLER [97] and were based on *E. coli* Ef-Tu homologues: PDB: 4G5G_A (*M. pneumoniae*), PDB: 1DG1_H (*M. hyopneumoniae*) and PDB: 1DG1_H (*S. aureus*). For context, the N-terminus of the protein is shown in yellow, and the C-terminus in purple.

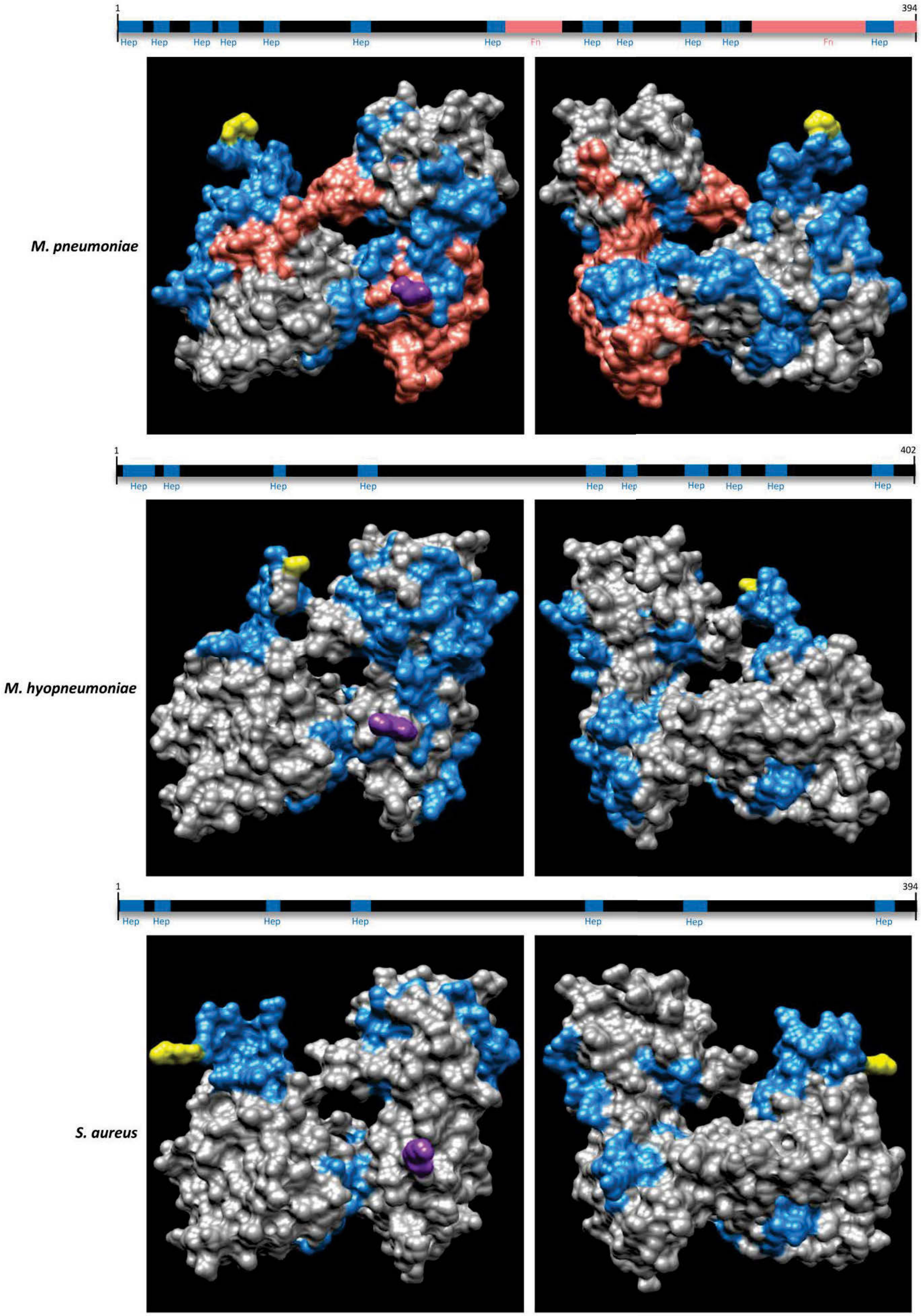

1
394
Hep Hep Hep Hep Hep Hep Hep Fn Hep Hep Hep Hep Fn Hep
M. pneumoniae
1
402
Hep Hep Hep Hep Hep Hep Hep Hep Hep Hep
M. hyopneumoniae
1
394
Hep Hep Hep Hep Hep Hep Hep
S. aureus

Figure S3. Predicted 3D space-filling structures for all three pathogens. Full length Ef-Tu are represented as black bars with predicted heparin-binding sites for each pathogen shown in blue boxes and regions in the structures. The two published fibronectin-binding domains for *M. pneumoniae* have also been mapped. Structures were predicted by MODELLER and were based on *E. coli* Ef-Tu homologues: PDB: 4G5G_A (*M. pneumoniae*), PDB: 1DG1_H (*M. hyopneumoniae*) and PDB: 1DG1_H (*S. aureus*). The N-terminus of the protein is shown in yellow, and the C-terminus in purple.

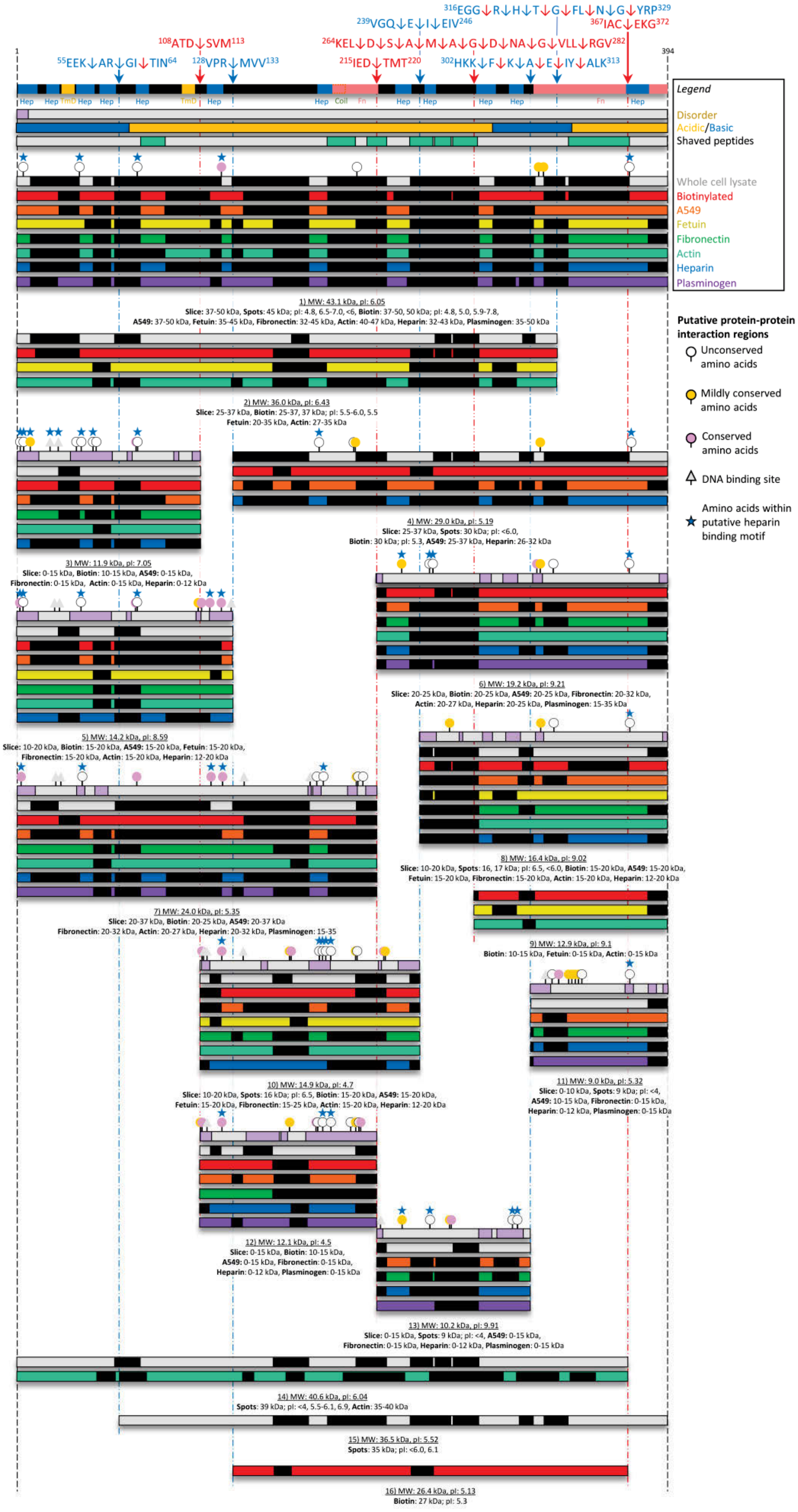

^{316}EGG↓R↓H↓T↓G↓FL↓N↓G↓YRP^{329}
^{239}VGQ↓E↓I↓EIV^{246}
^{367}IAC↓EKG^{372}
^{108}ATD↓SVM^{113}
^{264}KEL↓D↓S↓A↓M↓A↓G↓D↓NA↓G↓VLL↓RGV^{282}
1
^{55}EEK↓AR↓GI↓TIN^{64}
^{128}VPR↓MVV^{133}
^{215}IED↓TMT^{220}
^{302}HKK↓F↓K↓A↓E↓IY↓ALK^{313}
394
Hep
Hep
TmD
Hep
Hep
Hep
TmD
Hep
Hep
Coil
Fn
Hep
Hep
Hep
Hep
Fn
Hep
Legend
Disorder
Acidic/Basic
Shaved peptides
Whole cell lysate
Biotinylated
A549
Fetuin
Fibronectin
Actin
Heparin
Plasminogen
Putative protein-protein interaction regions
Unconserved amino acids
Mildly conserved amino acids
Conserved amino acids
DNA binding site
Amino acids within putative heparin binding motif
1) MW: 43.1 kDa, pI: 6.05
Slice: 37-50 kDa, Spots: 45 kDa; pI: 4.8, 6.5-7.0, <6, Biotin: 37-50, 50 kDa; pI: 4.8, 5.0, 5.9-7.8,
A549: 37-50 kDa, Fetuin: 35-45 kDa, Fibronectin: 32-45 kDa, Actin: 40-47 kDa, Heparin: 32-43 kDa, Plasminogen: 35-50 kDa
2) MW: 36.0 kDa, pI: 6.43
Slice: 25-37 kDa, Biotin: 25-37, 37 kDa; pI: 5.5-6.0, 5.5
Fetuin: 20-35 kDa, Actin: 27-35 kDa
3) MW: 11.9 kDa, pI: 7.05
Slice: 0-15 kDa, Biotin: 10-15 kDa, A549: 0-15 kDa,
Fibronectin: 0-15 kDa, Actin: 0-15 kDa, Heparin: 0-12 kDa
4) MW: 29.0 kDa, pI: 5.19
Slice: 25-37 kDa, Spots: 30 kDa; pI: <6.0,
Biotin: 30 kDa; pI: 5.3, A549: 25-37 kDa, Heparin: 26-32 kDa
5) MW: 14.2 kDa, pI: 8.59
Slice: 10-20 kDa, Biotin: 15-20 kDa, A549: 15-20 kDa, Fetuin: 15-20 kDa,
Fibronectin: 15-20 kDa, Actin: 15-20 kDa, Heparin: 12-20 kDa
6) MW: 19.2 kDa, pI: 9.21
Slice: 20-25 kDa, Biotin: 20-25 kDa, A549: 20-25 kDa, Fibronectin: 20-32 kDa,
Actin: 20-27 kDa, Heparin: 20-25 kDa, Plasminogen: 15-35 kDa
7) MW: 24.0 kDa, pI: 5.35
Slice: 20-37 kDa, Biotin: 20-25 kDa, A549: 20-37 kDa
Fibronectin: 20-32 kDa, Actin: 20-27 kDa, Heparin: 20-32 kDa, Plasminogen: 15-35
8) MW: 16.4 kDa, pI: 9.02
Slice: 10-20 kDa, Spots: 16, 17 kDa; pI: 6.5, <6.0, Biotin: 15-20 kDa, A549: 15-20 kDa,
Fetuin: 15-20 kDa, Fibronectin: 15-20 kDa, Actin: 15-20 kDa, Heparin: 12-20 kDa
9) MW: 12.9 kDa, pI: 9.1
Biotin: 10-15 kDa, Fetuin: 0-15 kDa, Actin: 0-15 kDa
10) MW: 14.9 kDa, pI: 4.7
Slice: 10-20 kDa, Spots: 16 kDa; pI: 6.5, Biotin: 15-20 kDa, A549: 15-20 kDa,
Fetuin: 15-20 kDa, Fibronectin: 15-25 kDa, Actin: 15-20 kDa, Heparin: 12-20 kDa
11) MW: 9.0 kDa, pI: 5.32
Slice: 0-10 kDa, Spots: 9 kDa; pI: <4,
A549: 10-15 kDa, Fibronectin: 0-15 kDa,
Heparin: 0-12 kDa, Plasminogen: 0-15 kDa
12) MW: 12.1 kDa, pI: 4.5
Slice: 0-15 kDa, Biotin: 10-15 kDa,
A549: 0-15 kDa, Fibronectin: 0-15 kDa,
Heparin: 0-12 kDa, Plasminogen: 0-15 kDa
13) MW: 10.2 kDa, pI: 9.91
Slice: 0-15 kDa, Spots: 9 kDa; pI: <4, A549: 0-15 kDa,
Fibronectin: 0-15 kDa, Heparin: 0-12 kDa, Plasminogen: 0-15 kDa
14) MW: 40.6 kDa, pI: 6.04
Spots: 39 kDa; pI: <4, 5.5-6.1, 6.9, Actin: 35-40 kDa
15) MW: 36.5 kDa, pI: 5.52
Spots: 35 kDa; pI: <6.0, 6.1
16) MW: 26.4 kDa, pI: 5.13
Biotin: 27 kDa; pI: 5.3

Figure S4. Cleavage map of Mpn$_{\mathbf{Ef\text{-}Tu}}$. Peptides (black boxes in coloured bars) identified by mass spectrometry of affinity chromatography of A549 surface proteins (orange bars), fetuin (yellow bars), fibronectin (green bars), actin (teal bars) and plasminogen (purple bars). Circles and triangles fragments indicate amino acid binding sites with either proteins or DNA, respectively. Purple boxes within grey bars are disordered regions within fragments. Red bars indicate peptides identified from surface biotinylation and peptides released from trypsin surface shaving can be seen as the green boxes in the grey bar above the full length protein.

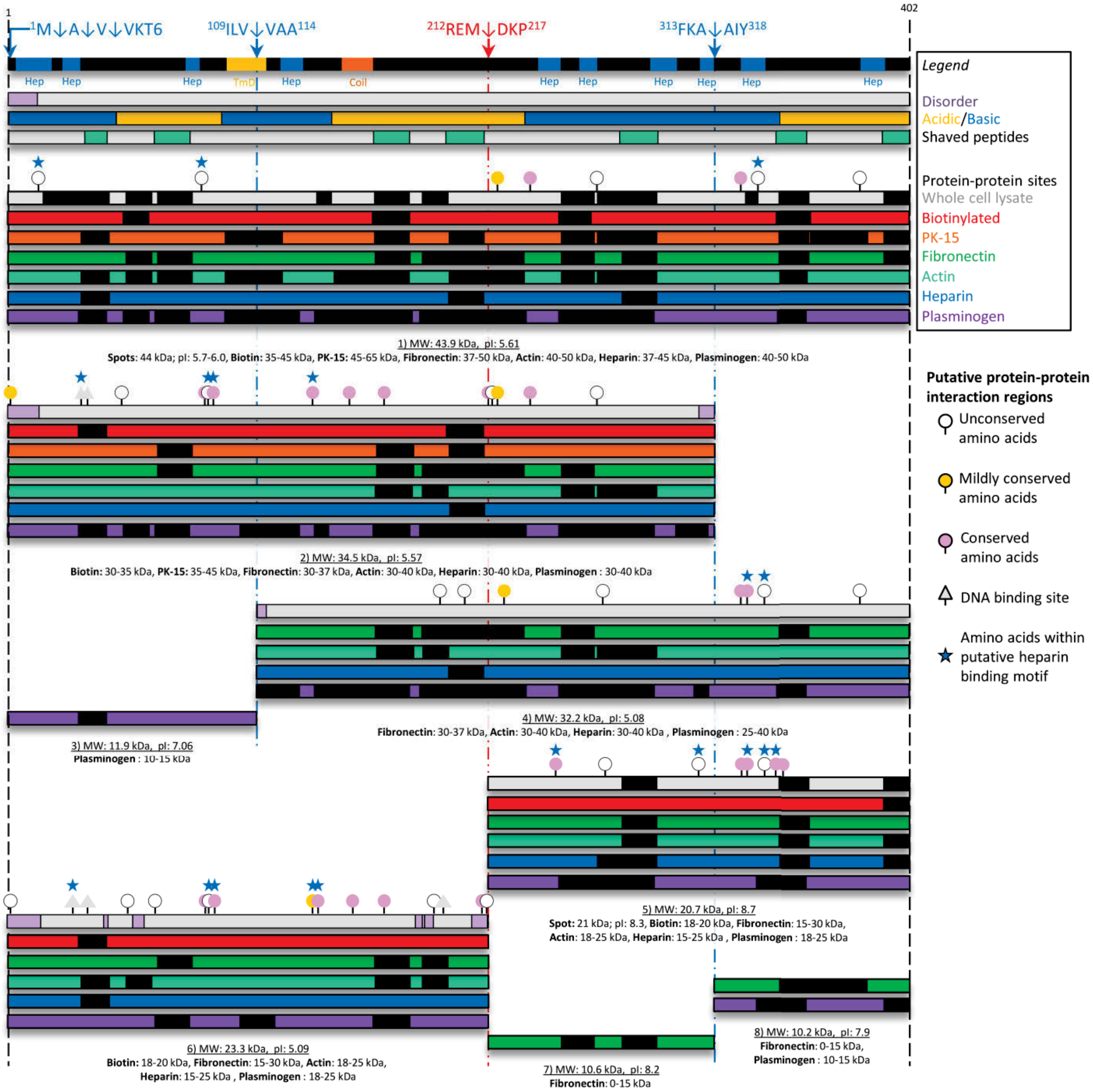


Figure S5. Cleavage map of Mhp$_{\text{Ef-Tu}}$. Peptides (black boxes in coloured bars) identified by mass spectrometry of affinity chromatography of PK-15 surface proteins (orange bars), fibronectin (green bars), actin (teal bars) and plasminogen (purple bars). Circles and triangles fragments indicate amino acid binding sites with either proteins or DNA, respectively. Purple boxes within grey bars are disordered regions within fragments. Red bars indicate peptides identified from surface biotinylation and peptides released from trypsin surface shaving can be seen as the green boxes in the grey bar above the full length protein.

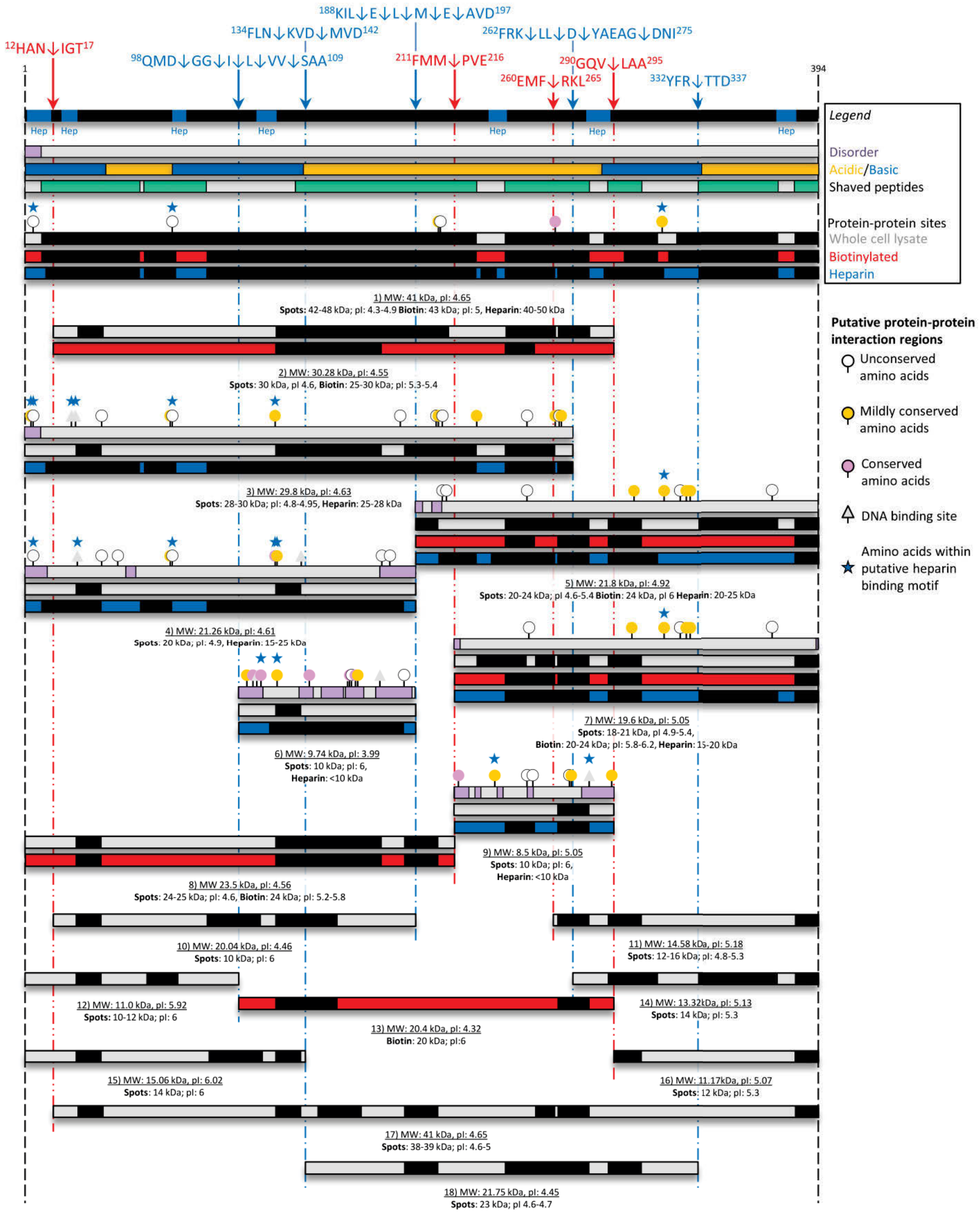


Figure S6. Cleavage map of Ef-Tu$_{\mathrm{Sa}}$. An expansion of the cleavage maps in Figure 2. Includes peptides (black boxes in coloured bars) identified by mass spectrometry of Ef-Tu fragments that don’t bind heparin or not on the surface (Fragments 10 – 18). Circles and triangles fragments indicate amino acid binding sites with either proteins or DNA, respectively. Purple boxes within grey bars are disordered regions within fragments. Red bars indicate peptides identified from surface biotinylation and peptides released from trypsin surface shaving can be seen as the green boxes in the grey bar above the full length protein.

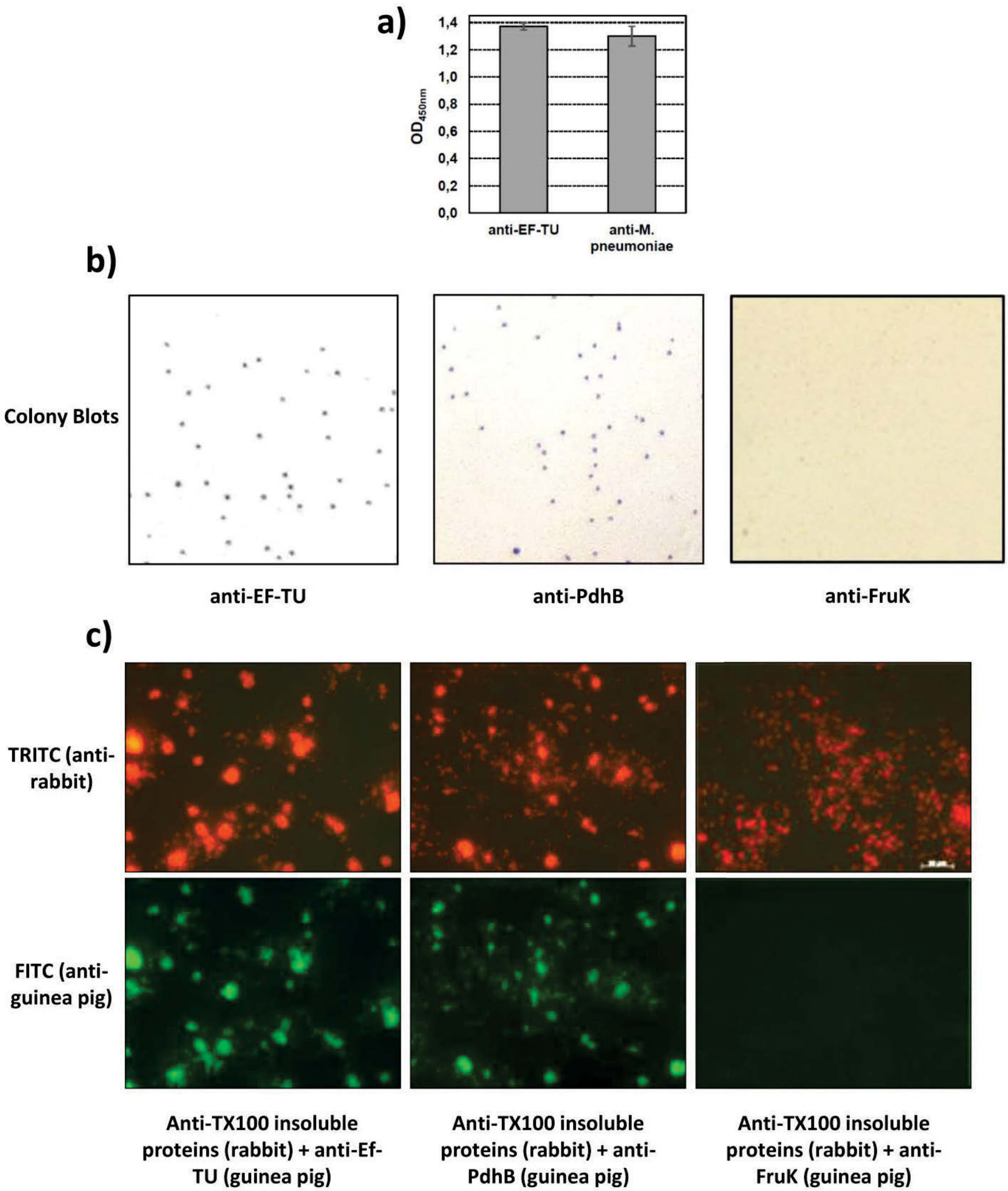


Figure S7: Mpn$_{\text{Ef-Tu}}$ resides on the surface of *M. pneumoniae*. A) Anti - rMpn$_{\text{Ef-Tu}}$ antibodies recognise *M. pneumoniae* cells in a whole cell ELISA assay; eight replicates. B) Colony blots of *M. pneumoniae* probed with anti - rMpn$_{\text{Ef-Tu}}$ antibodies, PdhB (positive control) and 1-

phosphofructokinase (negative control). C) Immunofluorescence microscopy of *M. pneumoniae* cells probed with antibodies against TX100 insoluble proteins (TRITC; cell control), Ef-Tu, PdhB (positive control) and 1-phosphofructokinase as the negative control (FITC).

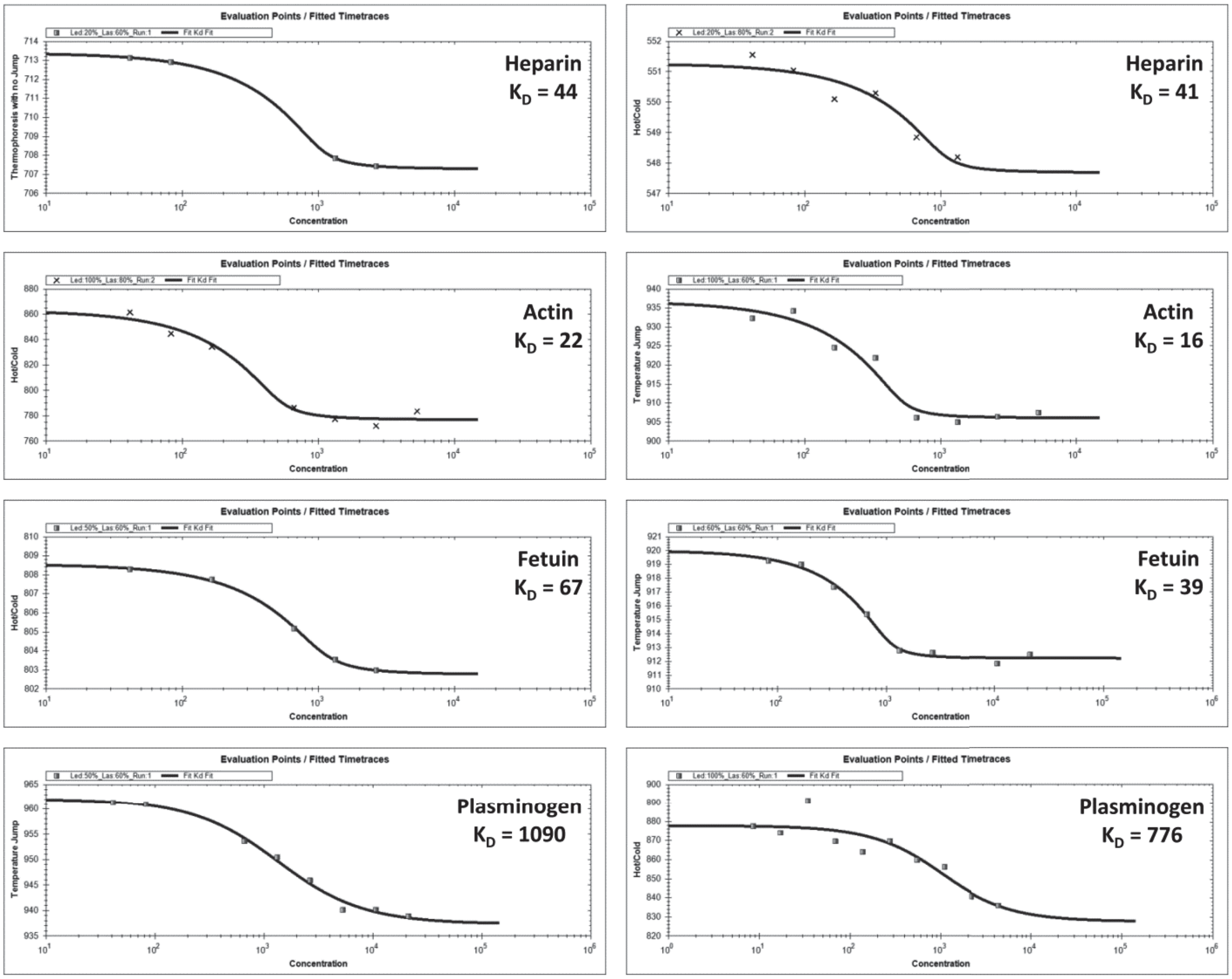


Figure S8: Microscale thermophoresis output depicting the interaction of rMpn$_{\text{Ef-Tu}}$ with human molecules. Concentration of rMpn$_{\text{Ef-Tu}}$ is plotted against thermophoretic movement of fluorescent human molecules. Experiments performed in duplicate, each panel representing one replicate.

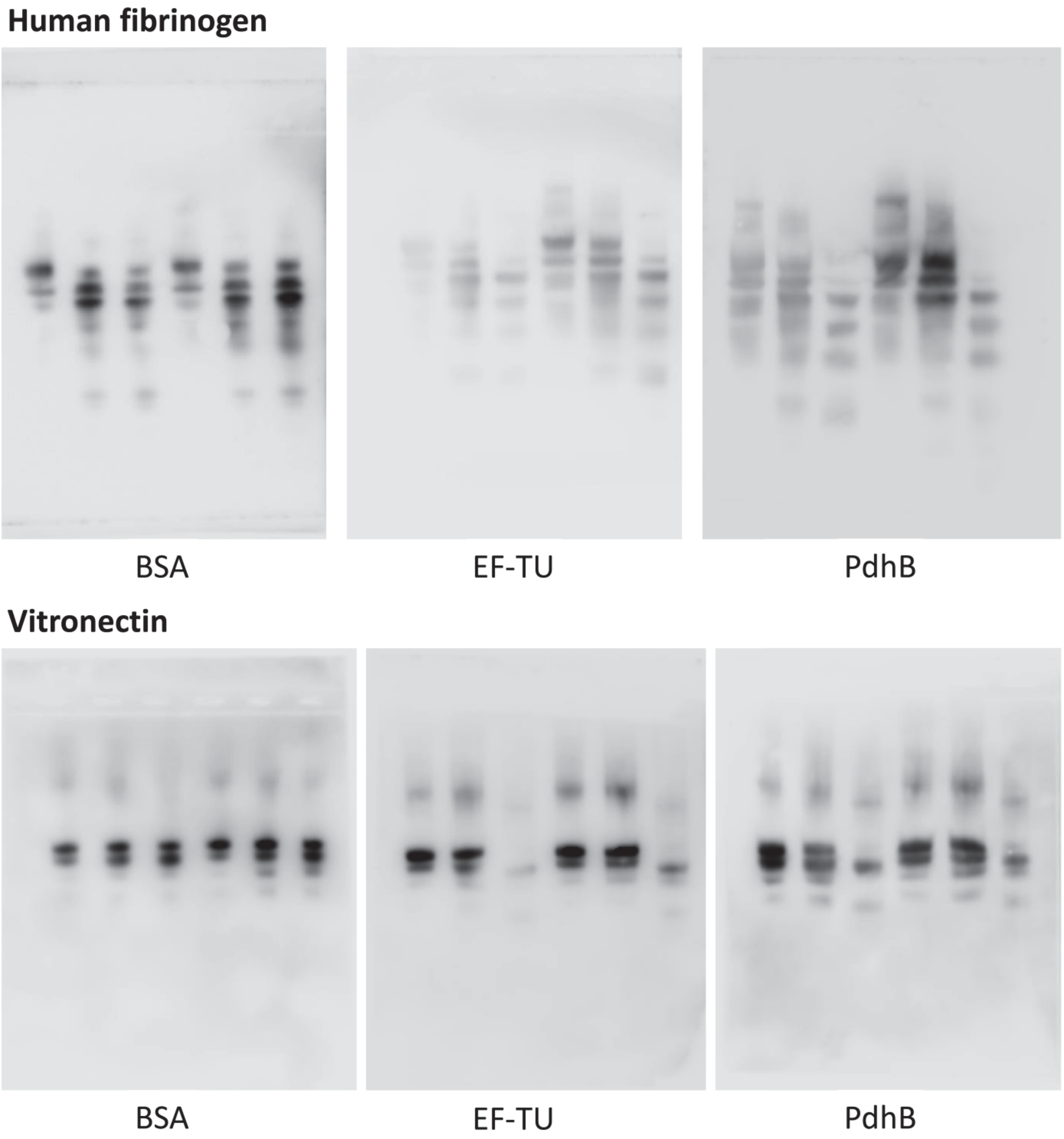


Figure S9: Full length blots showing degradation of human fibrinogen and vitronectin. Contrast adjusted (increased) to demonstrate no additional bands in full blots. Corresponding to Figure 5B, degradation with plasminogen activated by either urinary plasminogen activator or tissue plasminogen activator. Contrast and brightness editing are equal across the blots.

Will be presented as “Supplementary file S8- Tables”

Table S1. Putative heparin-binding motifs identified in Mpn$_{\text{Ef-Tu}}$, Mhp$_{\text{Ef-Tu}}$, and Sa$_{\text{Ef-Tu}}$.

Amino acid range	**Sequence**
	Mpn$_{\text{Ef-Tu}}$ (Uniprot #: P23568)
2 - 13:	aReKfdRsKpHv
19 - 26:	gHidHgKt$^{=}$
37 - 47:	aKegKsaatRy
51 - 60:	dKapeeKaRg
73 - 80:	dKRHyaHv*
116 - 125:	tReHillaRq$^{=}$
183 - 191:	pKweaKiHd
230 - 239:	gRveRgelKv$^{=}$
248 - 254:	lRpiRKa
279 - 290:	lRgvdRKeveRg
299 - 307:	iKpH*KKfK*a
370 - 383:	eKgsKfsiReggRt$^{=}$
	Mhp$_{\text{Ef-Tu}}$ (Uniprot #: Q4A9G1)
4 - 19:	vKttgKKdfdRsKeHi
25 - 32:	gHvdHgKt$^{=}$
79 - 86:	dKRHyaHv*
122 - 131:	tReHillsKq$^{=}$
237 - 246:	gKveRgqvKl$^{=}$
255 - 262:	yReepKKt
287 - 298:	lRgvdrKdieRg
302 - 315:	aKpKtiipHtKfKa
327 - 337:	gRHtpffKnyKp
381 - 391:	tKfsiReggRt$^{=}$
	Sa$_{\text{Ef-Tu}}$ (Uniprot #: Q2G0N0)
2 - 13:	aKeKfdRsKeHa
19 - 26:	gHvdHgKt$^{=}$
73 - 80:	dKRHyaHv*
116 - 125:	tReHillsRn$^{=}$
230 - 239:	gRveRgqiKv$^{=}$
279 - 290:	lRgvaRedvqRg
373 - 383:	tRfsiReggRt$^{=}$

Mpn$_{\text{Ef-Tu}}$, Mhp$_{\text{Ef-Tu}}$, and Sa$_{\text{Ef-Tu}}$ were searched for patters x-[HKR]-x(0,2)-[HKR]-x(0,2)-[HKR]-x and x-[HKR]-x(1,4)-[HKR]-x(1,4)-[HKR]-x using ScanProsite [144]. * indicates the motif (dKRHyaH) which is found in all three pathogens. $^{=}$ indicates the motifs that are highly homologous (up to three non-basic residues different) in all three pathogens.

Table S2A. Number of binding sites in full length and fragments of $\text{Mpn}_{\text{Ef-Tu}}$.

Analysis of the $\text{Mpn}_{\text{Ef-Tu}}$ for the putative protein-protein (P:P) and protein-nucleic acid interaction sites using ISIS [95].

$\text{Mpn}_{\text{Ef-Tu}}$ (Uniprot #: P23568)

Fragment number	**Full length**	**3**	**4**	**5**	**6**	**7**	**8**	**10**	**11**	**12**	**13**
Range (amino acid)	1-394	1-110	131-394	1-130	218-394	1-217	244-394	111-242	308-394	111-217	218-307
Exposed P:P	8	15	5	13	10	17	6	12	9	19	11
Buried P:P	6	5	2	7	5	2	5	3	6	2	0
DNA-binding	0	8	0	5	0	6	0	3	2	1	1

Table S2B. Number of binding sites in full length and fragments of $\text{Mhp}_{\text{Ef-Tu}}$.

Analysis of the $\text{Mhp}_{\text{Ef-Tu}}$ for the putative protein-protein (P:P) and protein-nucleic acid interaction sites using ISIS [95].

$\text{Mhp}_{\text{Ef-Tu}}$ (Uniprot #: Q4A9G1)

Fragment number	**Full length**	**1**	**4**	**5**	**6**
Range (amino acid)	Full	1-315	112-402	215-402	1-215
Exposed P:P	10	13	9	10	18
Buried P:P	2	3	1	3	4
DNA-binding	0	3	0	0	4

Table S2C. Number of binding sites in full length and fragments of $\text{Sa}_{\text{Ef-Tu}}$.

Analysis of the $\mathrm{Sa}_{\text{Ef-Tu}}$ for the putative protein-protein (P:P) and protein-nucleic acid interaction sites using ISIS [95].

$\mathrm{Sa}_{\text{Ef-Tu}}$ (Uniprot #: Q2G0N0)

Fragment number	**Full length**	**3**	**4**	**5**	**6**	**7**	**9**
Range (amino acid)	**Full**	**1-266**	**1-192**	**193-394**	**104-192**	**214-394**	**214-292**
Exposed P:P	10	13	10	7	12	5	10
Buried P:P	6	12	6	5	2	5	1
DNA-binding	0	3	4	0	2	0	1

Will be presented as “Supplementary file S9- Bioinformatics”

Supplementary Materials - Bioinformatics

Conserved/Non-conserved regions:

Analysis of conservation of amino acids in $\text{Mpn}_{\text{Ef-Tu}}$, $\text{Mhp}_{\text{Ef-Tu}}$, and $\text{Sa}_{\text{Ef-Tu}}$.

Degree of conservation in $\text{Mpn}_{\text{Ef-Tu}}$ was calculated by The ConSurf server [96]. Colours indicate degree of conservation of the amino acid across species. Red diamond sticks indicate predicted protein binding sites by ISIS [95,149]. Grey, yellow and purple circle sticks indicate predicted nucleotide, DNA and RNA binding regions, respectively by SomeNA [149,150]. Below the sticks are three rows: i) Blue and red bars indicate predicted beta-strand and helix secondary structures, respectively by REPROFSec [147,149], ii) Blue and yellow bars indicate predicted regions that are exposed and buried to solvent accessibilities, respectively by PROFAcc [147,149]. iii) Green bars indicate predicted disordered regions by Meta-Disorder (MD) [146,149]. Circled amino acids represent predicted binding sites. Amino acids indicated by a triangle indicate predicted nucleotide binding sites.

Legend:

The conservation scale:

1 2 3 4 5 6 7 8 9

Variable Average Conserved

e - An exposed residue according to the neural-network algorithm.

b - A buried residue according to the neural-network algorithm.

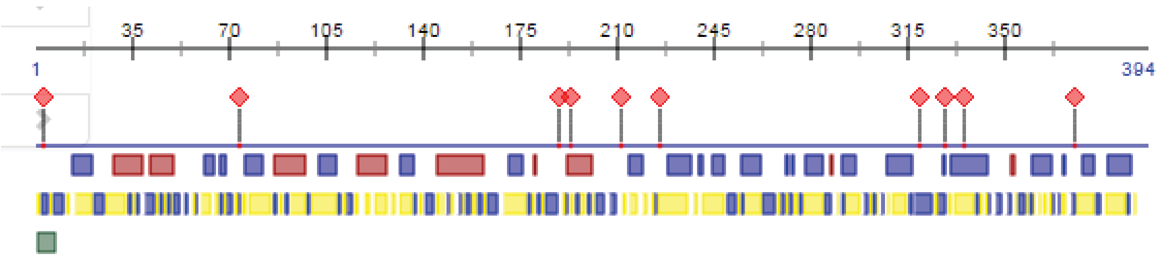
f - A predicted functional residue (highly conserved and exposed).

s - A predicted structural residue (highly conserved and buried).

X - Insufficient data - the calculation for this site was performed on less than 10% of the sequences.

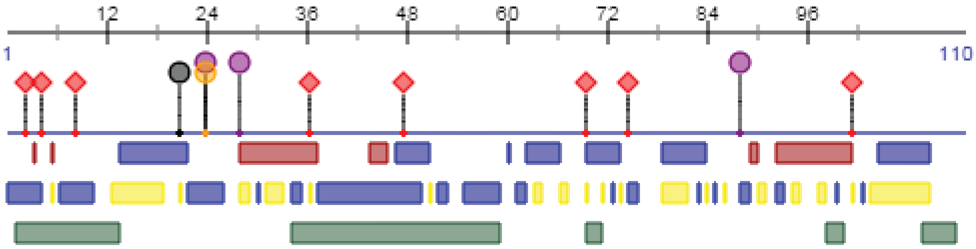
Mpn$_{\text{Ef-Tu}}$ (Uniprot #: P23568)

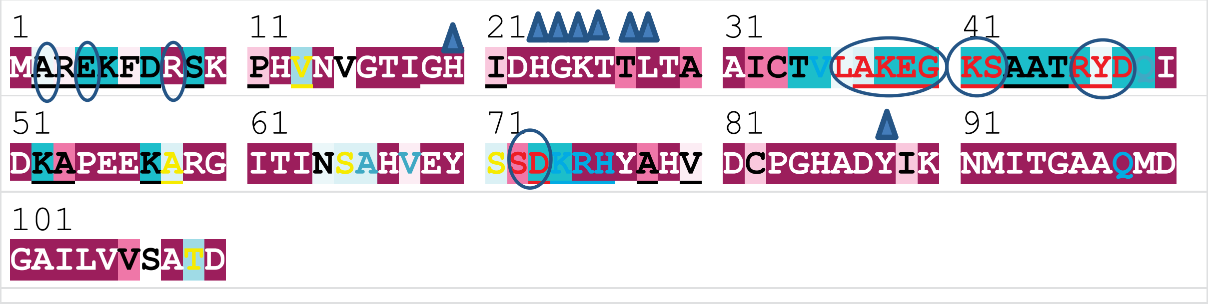
Full length protein: 1-394



1	11	21	31	41
MAREKFDRSK	PHVNVGTIGH	IDHGKTTLTA	AICTVLAKEG	KSAATRYDQI
51	61	71	81	91
DKAPEEKARG	ITINSAHVEY	SSDKRHYAHV	DCPGHADYIK	NMITGAAQMD
101	111	121	131	141
GAILVVSATD	SVMPQTREHI	LLARQVGVPR	MVVFLNKCDI	ATDEEVQELV
151	161	171	181	191
AEEVRDLLTS	YGFDGKNTPI	IYGSALKALE	GDPKWEAKIH	DIMNAVDEWI
201	211	221	231	241
PTPEREVDKP	FLLAIEDTMT	ITGRGTVVTG	RVERGELKVG	QEIEIVGLRP
251	261	271	281	291
IRKAVVTGIE	MFKKELDSAM	AGDNAGVLLR	GVDRKEVERG	QVLAKPGSIK
301	311	321	331	341
PHKKFKAEIY	ALKKEEGGRH	TGFLNGYRPQ	FYFRTTDVTG	SISLPENTEM
351	361	371	381	391
VLPGDNTSIT	VELIAPIACE	KGSKFSIREG	GRTVGAGSVT	EVLE

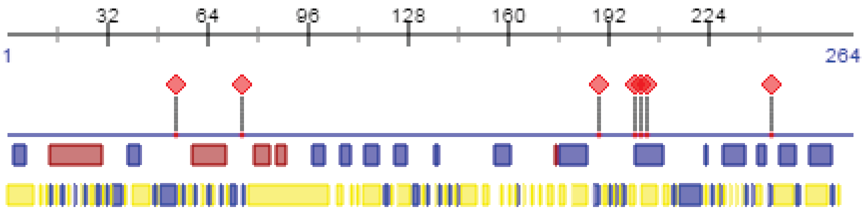
Fragment 3: 1-110





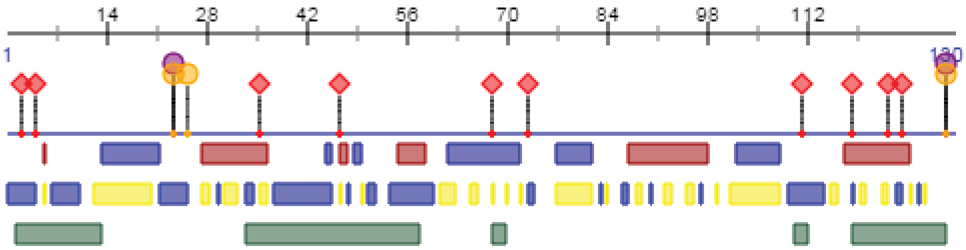
1	11	21	31	41
MAREKFDRSK	PHVNVGTIGH	IDHGKTTLTA	AICTVLAKEG	KSAATRYDQI
51	61	71	81	91
DKAPEEKARG	ITINSAHVEY	SSDKRHYAHV	DCPGHADYIK	NMITGAAQMD
101				
GAILVVSATD				

Fragment 4: 131-394



131	141	151	161	171
MVVFLNKCDI	ATDEEVQELV	AEEVRDLLTS	YGFDGKNTPI	IYGSALKALE
181	191	201	211	221
GDPKWEAKIH	DLMNAVDEWI	PTPEREVDKP	FLLAIEDTMT	ITGRGTVVTG
231	241	251	261	271
RVERGELKVG	QEIEIVGLRP	IRKAVVTGIE	MFKKELDSAM	AGDNAGVLLR
281	291	301	311	321
GVDRKEVERG	QVLAKPGSIK	PHKKFKAEIY	ALKKEEGGRH	TGFLNGYRPQ
331	341	351	361	371
FYFRTTDVTG	SISLPENTEM	VLPGDNTSIT	VELIAPIACE	KGSKFSIREG
381	391			
GRTVGAGSVT	EVLE			

Fragment 5: 1-130

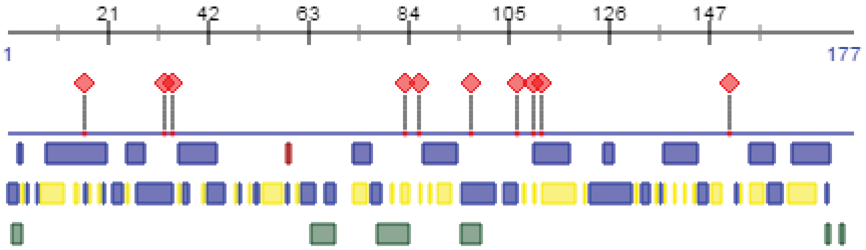


1 MAREKFDRSK 11 PHVNVGTIGH 21 IDHGKTTLTA 31 AICTVLAKEG 41 KSAATRYDQI

51 DKAPEEKARG 61 ITINSAHVEY 71 SSDKRHYAHV 81 DCPGHADYIK 91 NMITGAAQMD

101 GAILVVSATD 111 SVMPQTREHI 121 LLARQVGVPR

Fragment 6: 218-394



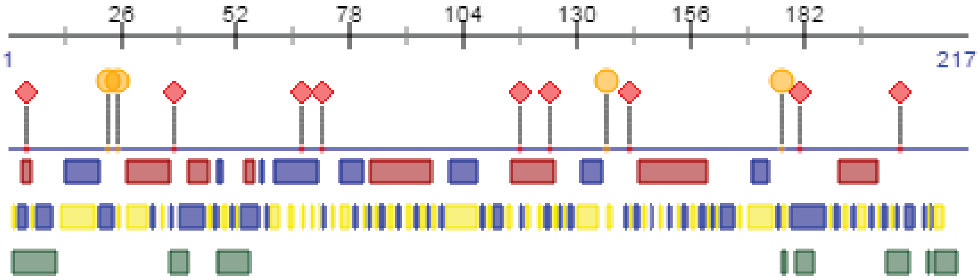
218 TMTITGRGTV 228 VTGRVERGEL 238 KVGQEIEIVG 248 LRPIRKAVVT 258 GIEMFKKELD

268 SAMAGDNAGV 278 LLRGVDRKEV 288 ERGQVLAKPG 298 SIKHKKFKA 308 EIYALKKEEG

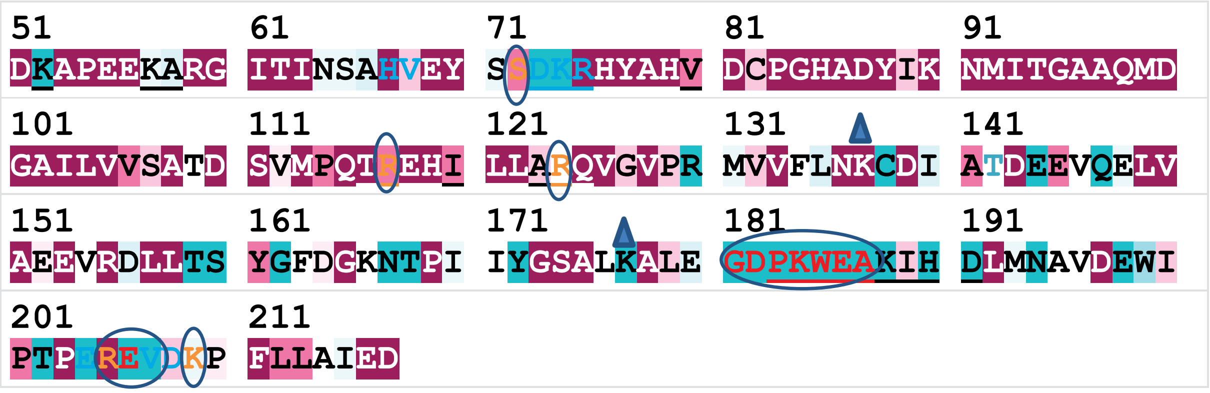
318 GRHTGFLNGY 328 RPQFYFRTTD 338 VTGSISLPEN 348 TEMVLPGDNT 358 SITVELIAPI

368 ACEKGSKFSI 378 REGGRTVGAG 388 SVTEVLPE

Fragment 7: 1-217

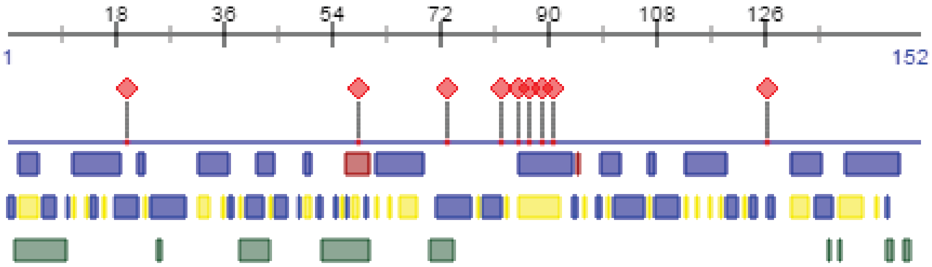


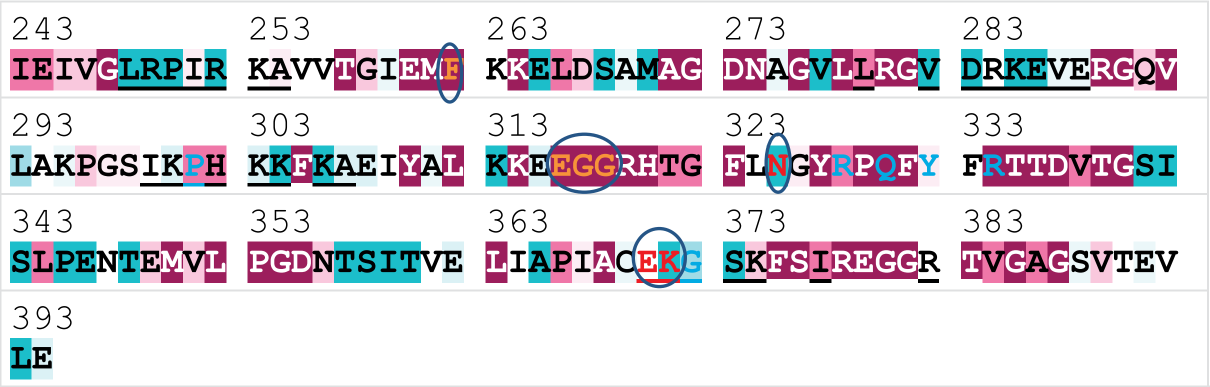
1 MAREKFDRSK 11 PHVNVGTIGH 21 IDHGKTTLTA 31 AICTVLAKEG 41 KSAATRYDQI



51	61	71	81	91
DKAPEEKARG	ITINSAHVEY	SSDKRHYAHV	DCPGHADYIK	NMITGAAQMD
101	111	121	131	141
GAILVVSATD	SVMPQTREHI	LLARQVGVPR	MVVFLNKCDI	ATDEEVQELV
151	161	171	181	191
AEEVRDLLTS	YGFDGKNTPI	IYGSALKALE	GDPKWEAKIH	DLMNAVDEWI
201	211			
PTPEREVDKP	FLLAIED			

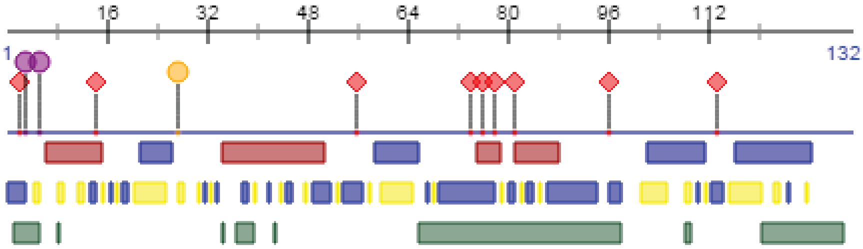
Fragment 8: 244-394





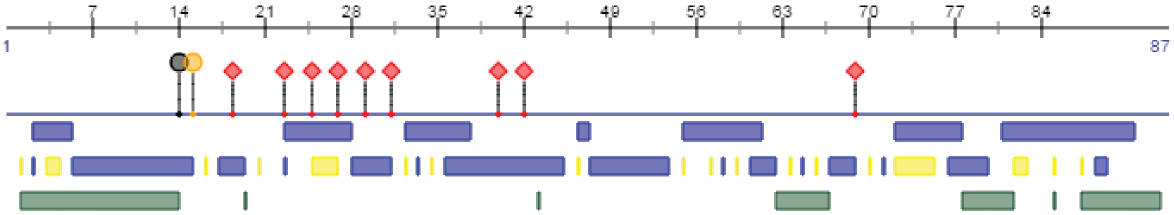
243	253	263	273	283
IEIVGLRPIR	KAVVTGIEMF	KKELDSAMAG	DNAGVLLRGV	DRKEVERGQV
293	303	313	323	333
LAKPGSIKPH	KKFKAEIYAL	KKEEGGRHTG	FLNGYRPQFY	FRTTDVTGSI
343	353	363	373	383
SLPENTEMVL	PGDNTSITVE	LIAPIACEKG	SKFSIREGGR	TVGAGSVTEV
393				
LE				

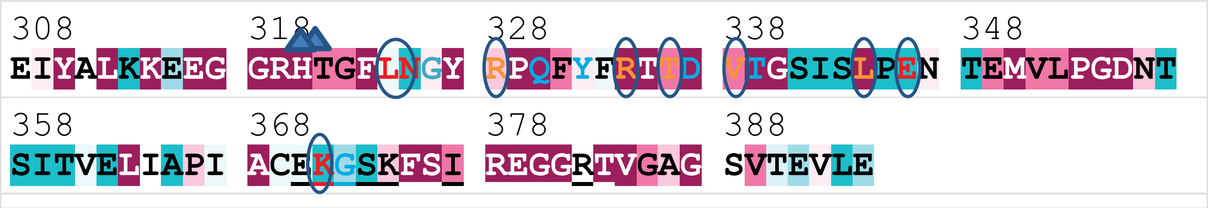
Fragment 10: 111-242



111 SVMPQTREHI	121 LLARQVGVPR	131 MVVFLNKCDI	141 ATDEEVQELV	151 AEEVRDLLTS
161 YGFDGKNTPI	171 IYGSALKALE	181 GDPKWEAKIH	191 DLMNAVDEWI	201 PTPEREVDKP
211 FLLAIEDTMT	221 ITGRGTVVTG	231 RVERGELKVG	QE	

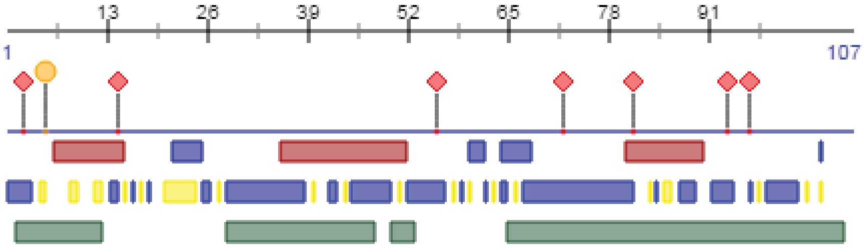
Fragment 11: 308-391

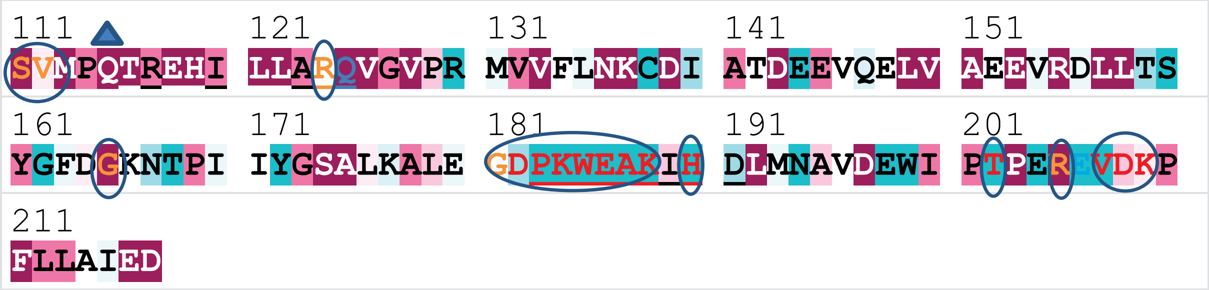




308 EIYALKKEEG	318 GRHTGFLNGY	328 RPQFYFRTTD	338 VTGSISLPEN	348 TEMVLPGDNT
358 SITVELIAPI	368 ACEKGSKFSI	378 REGGRTVGAG	388 SVTEVLE	

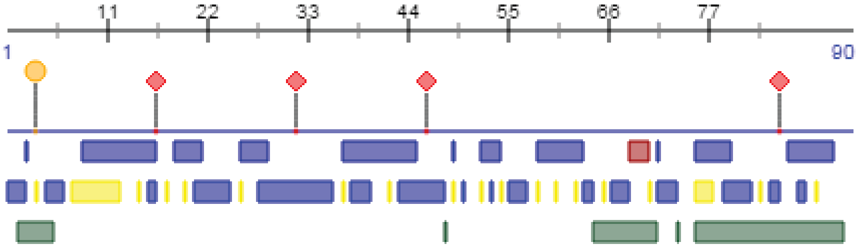
Fragment 12: 111-217





111 SVMPQTREHI	121 LLARQVGVPR	131 MVVFLNKCDI	141 ATDEEVQELV	151 AEEVRDLLTS
161 YGFDGKNTPI	171 IYGSALKALE	181 GDPKWEAKIH	191 DLMNAVDEWI	201 PTPEREVDKP
211 FLLAIED				

Fragment 13: 218-307

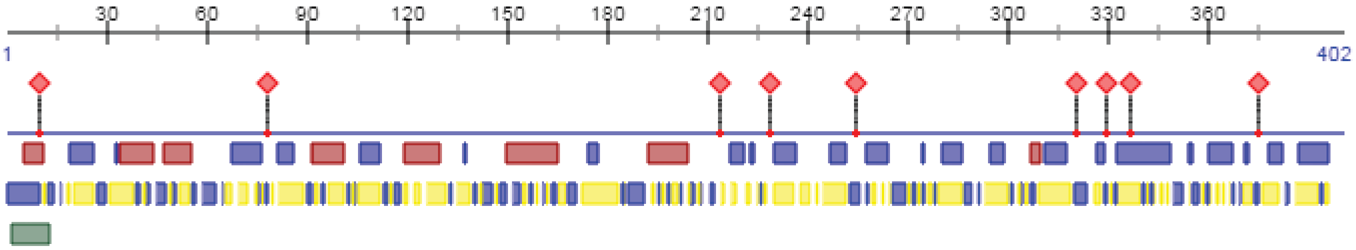


218 TMTITGRGTV 228 VTGRVERGEL 238 KVGQEIEIVG 248 LRPIRKAVVT 258 GIEMFKKELD

268 SAMAGDNAGV 278 LLRGVDRKEV 288 ERGQVLAKPG 298 SIKPHKKFKA

Mhp$_{Ef\text{-}Tu}$ (Uniprot #: Q4A9G1)

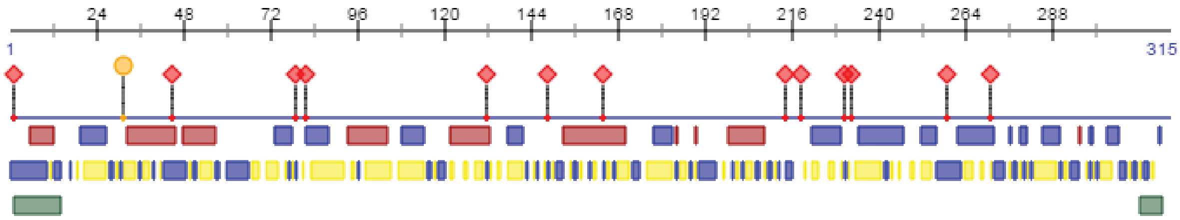
Full length protein: 1-402



```
1          11         21         31         41
MAVVKTTGKK DFDRSKEHIN IGTIGHVDHG KTTLTAAIST VLAKRGLAEA
eebeeebbee ebeeeeeebb bbbbbbbeeb ebebebbbbe bbbeeeeeeb
      s f     f f f s  sssss ffs fsfsf ss

51         61         71         81         91
KDYASIDAAP EEKARGITIN TAHIEYSTDK RHYAHVDCPG HADYIKNMIT
eebeebeebe eeeeebbbbb bbebebeeee ebbbbbbbee ebebbeebbb
     sf sf ff  fssss    f fs f   fssss s ff fsfs ffsss

101        111        121        131        141
GAAQMDGAIL VVAATDGPMP QTREHILLSK QVGVPKMVVF LNKIDLLEGE
bbbbbebbbb bbbbeeeeee ebeebbbbbe ebebebbbbb bbebeeeeee
sssssfsss  s  s fffff fsffs ss   fs sf   s   sf f f  f

151        161        171        181        191
EEMVDLVEVE IRELLSSYDF DGDNTPIIRG SARGALEGKP EWEAKVLELM
eebbebbeee beebbeeeeb eeeebebbeb bbbebbeeee eeeeebeebb
 f   ssf f  f ss  f   fff  f   s ss                 s

201        211        221        231        241
DAVDSYIDSP VREMDKPFLM AVEDVFTITG RGTVATGKVE RGQVKLNEEV
eebeeebeee eeeeeeebbb ebeebbbbbb ebebbebebe ebebebeeeb
   f   f f  f    fs s   ff   s s fsfs fsf f fs

251        261        271        281        291
EIVGYREEPK KTVITGIEMF NKNLQTAMAG DNAGVLLRGV DRKDIERGQV
ebbbbeeeee eeebebbebb eebbeebeee eebebbbebb eeeebeebeb
f  s           f  fss  f sf   ff ff f ssfs   f    fs s

301        311        321        331        341
IAKPKTIIPH TKFKAAIYAL KKEEGGRHTP FFKNYKPQFY FRTTDVTGGI
beeeeeeeee eebebebbbb eeeeeeeeee ebeeeeeebb bebeeeebeb
   f    ff        s s  f fffffff f   ffffs   fsffffs
```

```
351        361        371        381        391
EFEPGREMVI PGDNVDLTVE LIAPIAVEQG TKFSIREGGR TVGAGTVTEI
ebeebbebbb eeeebebebe bbbbbbbeeb bebbbeeeee bbbbbebbeb
 s     s s ffff       s  s s       sssffff  sss s

401
IK
ee
```

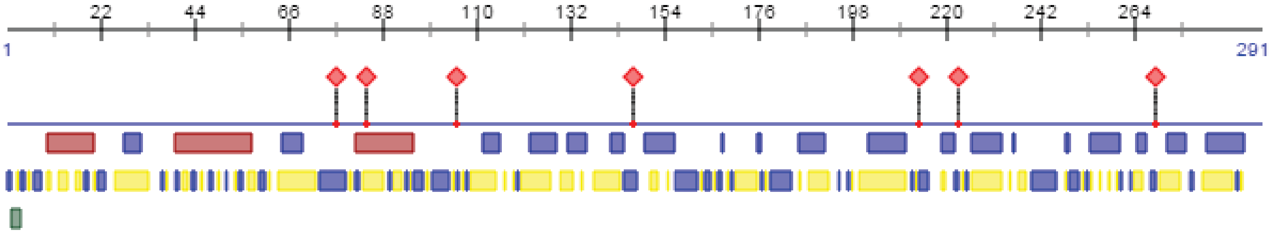
Fragment 1: 1-315



```
1          11         21         31         41
MAVVKTTGKK DFDRSKEHIN IGTIGHVDHG KTTLTAAIST VLAKRGLAEA
eebeeebbee ebeeeeeebb bbbbbbbeeb ebebebbbbe bbbeeeeeeb
      ssf     f f f s  sssss ffs fsfsfsss

51         61         71         81         91
KDYASIDAAP EEKARGITIN TAHIEYSTDK RHYAHVDCPG HADYIKNMIT
eebeebeebe eeeeebbbbb bbebebeeee ebbbbbbbee ebebbeebbb
     sf sf ff  fssss    f fs f   fssss s ff fsfs ffsss

101        111        121        131        141
GAAQMDGAIL VVAATDGPMP QTREHILLSK QVGVPKMVVF LNKIDLLEGE
bbbbbebbbb bbbbbbeeee ebeebbbbbe ebebebbbbb bbebeeeeee
sssssfs s  s  s ff ff fsffs ss f fs sf   s   sf f f  f

151        161        171        181        191
EEMVDLVEVE IRELLSSYDF DGDNTPIIRG SARGALEGKP EWEAKVLELM
eebbebbeee beebbeeeeb eeeebebbeb bbbebbeeee ebeeebeebb
 f   ssfff  f ss  f     ff f     ss                 s

201        211        221        231        241
DAVDSYIDSP VREMDKPFLM AVEDVFTITG RGTVATGKVE RGQVKLNEEV
ebbeeebeee eeeeeeebbb ebeebbbbbb ebebbebebe ebebeeeeeb
   f   f f  f    fs s   ff   s s fsfs fsf f fs

251        261        271        281        291
EIVGYREEPK KTVITGIEMF NKNLQTAMAG DNAGVLLRGV DRKDIERGQV
ebbbbeeeee eeebebbebb eebbeebeee eebebbbebb eeeebeebeb
```

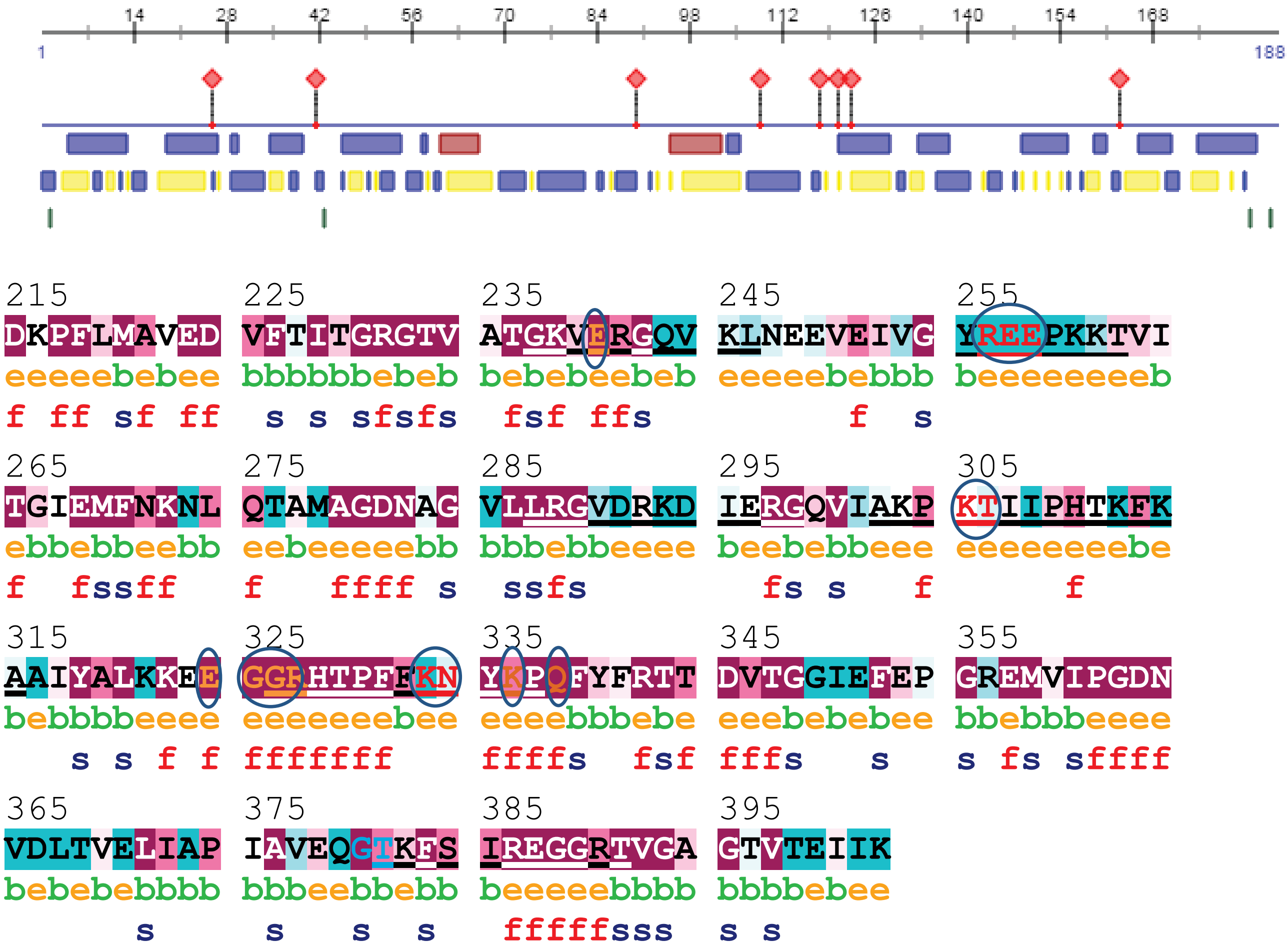
```
   s           f  fss  f sf   ff ff f ssfs        fs  s
301        311
IAKPKTIIPH TKFKA
beeeeeeeee eeeee
   f     f   f f
```

Fragment 4: 112-402



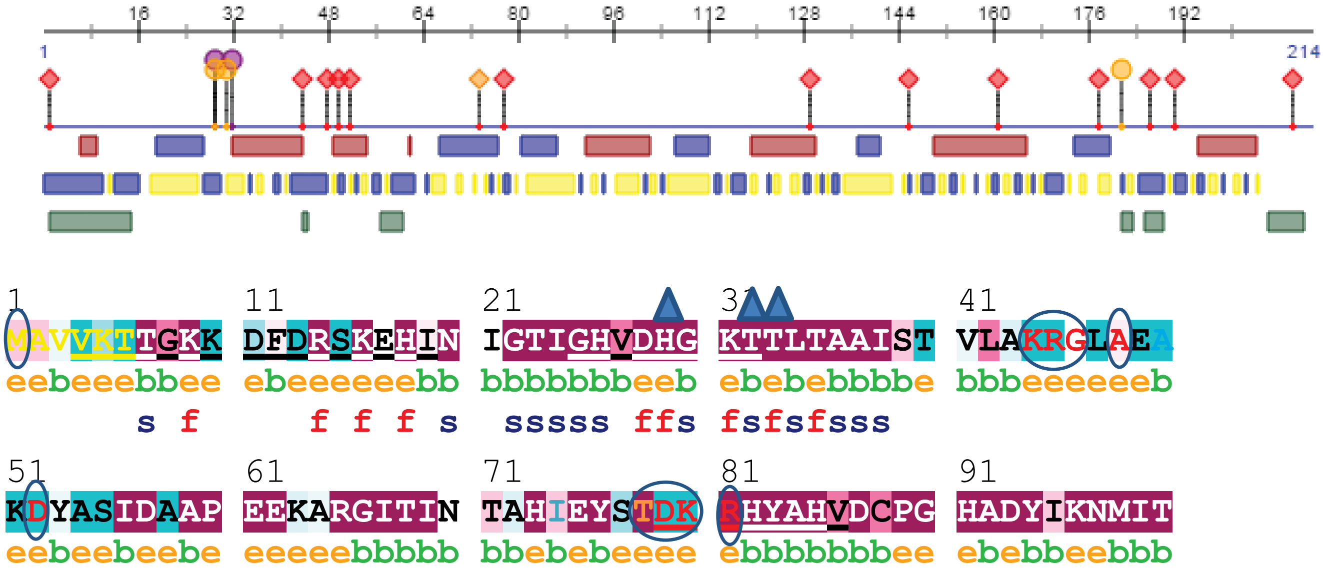
```
112        122        132        142        152
VAATDGPMPQ TREHILLSKQ VGVPKMVVFL NKIDLLEGEE EMVDLVEVEI
eeeeeeeeee beebbbbbee bebebbbbbb bebeeeeeee ebbebbeeeb
f f ffffff s fs ss  f s sf   s   sf f f  f  f   ssf f
162        172        182        192        202
RELLSSYDFD GDNTPIIRGS ARGALEGKPE WEAKVLELMD AVDSYIDSPV
eebbeeeebe eeebebbebb bbebbeeeee beeebeebbe bbeeebeeee
f ss       ff  f    s s  s              s     f   f f
212        222        232        242        252
REMDKPFLMA VEDVFTITGR GTVATGKVER GQVKLNEEVE IVGYREEPKK
eeeeeebbbe beebbbbbbe bebbebebee bebebeeebe bbbbeeeeee
f    fs s   ffs  s sf sfs fsf ff s        f   s
262        272        282        292        302
TVITGIEMFN KNLQTAMAGD NAGVLLRGVD RKDIERGQVI AKPKTIIPHT
eebebbebbe ebbeebeeee ebbbbbebbe eeebeebebb eeeeeeeeee
   f  fss  f sf   fff f s ssfs   f    fs s    f    ff
312        322        332        342        352
KFKAAIYALK KEEGGRHTPF FKNYKPQFYF RTTDVTGGIE FEPGREMVIP
ebebebbbbe eeeeeeeeee beeeeeebbb ebeeeebebe beebbebbbe
 s    s s  f ffffffff    ffffs   fsffffs    s    fs sf
362        372        382        392        402
GDNVDLTVEL IAPIAVEQGT KFSIREGGRT VGAGTVTEII K
eeebebebeb bbbbbbeebb ebbbeeeeeb bbbbebbebe e
fff      s   s s       s sffff s ss s
```

Fragment 5: 215-402



```
215        225        235        245        255
DKPFLMAVED VFTITGRGTV ATGKVERGQV KLNEEVEIVG YREEPKKTVI
eeeeebebee bbbbbbebeb bebebeebeb eeeeebebbb beeeeeeeeb
f ff sf ff  s s sfsfs  fsf ffs        f  s
265        275        285        295        305
TGIEMFNKNL QTAMAGDNAG VLLRGVDRKD IERGQVIAKP KTIIPHTKFK
ebbebbeebb eebeeeeebb bbbebbeeee beebebbeee eeeeeeeebe
f  fssff   f   ffff s  ssfs        fs s   f      f
315        325        335        345        355
AAIYALKKEE GGRHTPFFKN YKPQFYFRTT DVTGGIEFEP GREMVIPGDN
bebbbbeeee eeeeeeebee eeeebbbebe eeebebebee bbebbbeeee
   s s f f fffffff    ffffs  fsf fffs   s   s fs sffff
365        375        385        395
VDLTVELIAP IAVEQGTKFS IREGGRTVGA GTVTEIIK
bebebebbbb bbbeebbebb beeeeebbbb bbbbebee
      s     s   s  s   fffffsss  s s
```

Fragment 6: 1-215



```
1          11         21         31         41
MAVVKTTGKK DFDRSKEHIN IGTIGHVDHG KTTLTAAIST VLAKRGLAEA
eebeeebbee ebeeeeeebb bbbbbbbeeb ebebebbbbe bbbeeeeeeb
      s f     f f f s  sssss ffs fsfsfsss
51         61         71         81         91
KDYASIDAAP EEKARGITIN TAHIEYSTDK RHYAHVDCPG HADYIKNMIT
eebeebeebe eeeeebbbbb bbebebeeee ebbbbbbbee ebebbeebbb
```

```
     sf sf ff  fssss   f fs f    fssss s ff fsfs ffsss
101        111        121        131        141
GAAQMDGAIL VVAATDGPMP QTREHILLSK QVGVPKMVVF LNKIDLLEGE
bbbbbebbbb bbbbbeeeee ebeebbbbbe ebebebbbbb bbebeeeeee
sssssfs s  s  s ff ff fsffs ss   fs s    s   sf f f ff
151        161        171        181        191
EEMVDLVEVE IRELLSSYDF DGDNTPIIRG SARGALEGKP EWEAKVLELM
eebbebbeee beebbeeeeb eeeebebbeb bbbebbeeee ebeeebeebb
 f   ssf f  f ss  f    ff  f     ss                 s
201        211
DAVDSYIDSP VREM
ebbeebbeee eeee
   f   f f  f
```

Sa$_{Ef-Tu}$ (Uniprot #: Q2G0N0)

Full length protein: 1-394

1 MAKEKFDRSK 11 EHANIGTIGH 21 VDHGKTTLTA 31 AIATVLAKNG 41 DSVAQSYDMI

51 DNAPEEKERG 61 ITINTSHIEY 71 QTDKRHYAHV 81 DCPGHADYVK 91 NMITGAAQMD

101 GGILVVSAAD 111 GPMPQTREHI 121 LLSRNVGVPA 131 LVVFLNKVDM 141 VDDEELLELV

151 EMEVRDLLSE 161 YDFPGDDVPV 171 IAGSALKALE 181 GDAQYEEKIL 191 ELMEAVDTYI

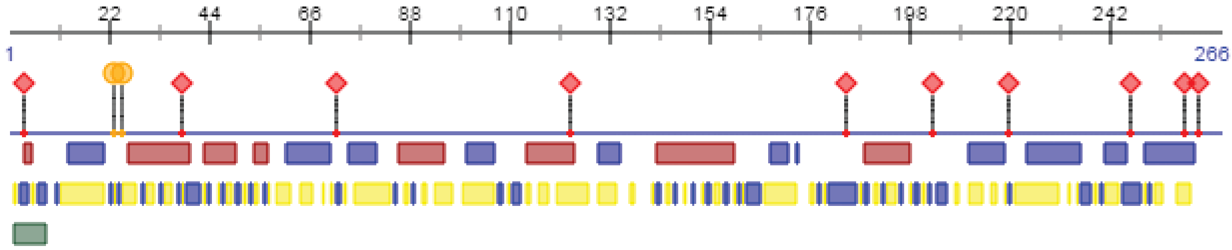
201 PTPERDSDKP 211 FMMPVEDVFS 221 ITGRGTVATG 231 RVERGQIKVG 241 EEVEIIGLHD

251 TSKTTVTGVE 261 MFRKLLDYAE 271 AGDNIGALLR 281 GVAREDVQRG 291 QVLAAPGSIT

301 PHTEFKAEVY 311 VLSKDEGGRH 321 TPFFSNYRPQ 331 FYFRTTDVTG 341 VVHLPEGTEM

351 VMPGDNVEMT 361 VELIAPIAIE 371 DGTRFSIREG 381 GRTVGSGVVT 391 EIIK

Fragment 3:1-266



1 MAKEKFDRSK 11 EHANIGTIGH 21 VDHGKTTLTA 31 AIATVLAKNG 41 DSVAQSYDMI

eeeeeeeeee eebbbbbbbb beebebebeb bbbebbbeee eeebeebeeb

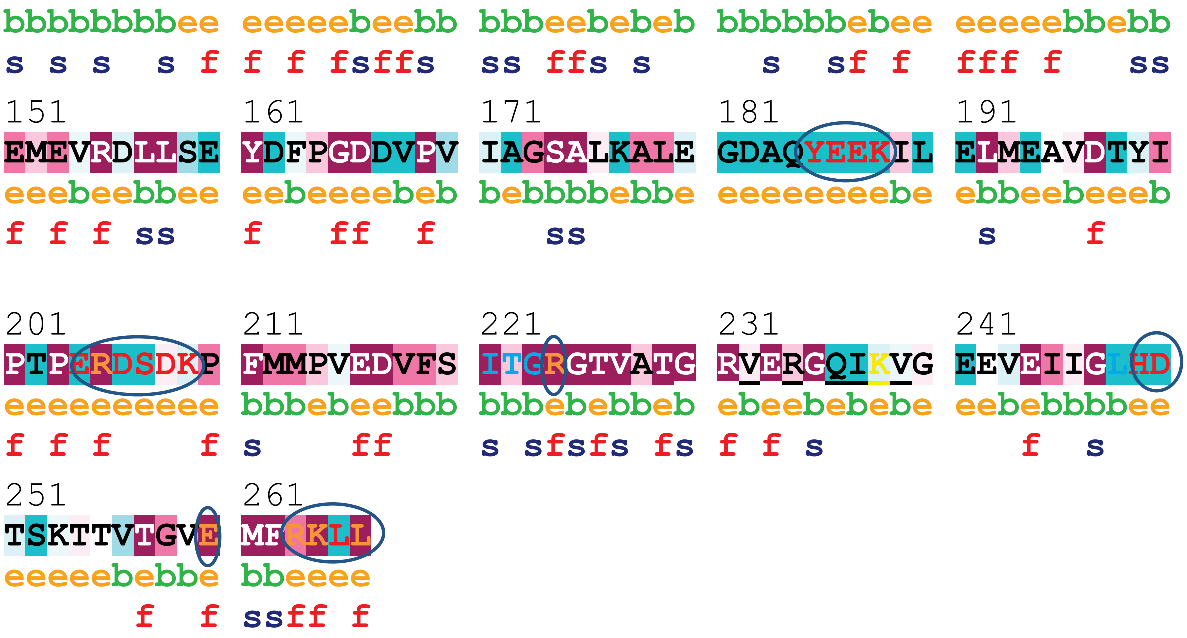
f f f f f s sssss ffsfsfsfs ss s

51 DNAPEEKERG 61 ITINTSHIEY 71 QTDKRHYAHV 81 DCPGHADYVK 91 NMITGAAQMD

eebeeeeeeb bbbbbbebeb eeeeebbbbb bbeeebebbe ebbbbbbbbe

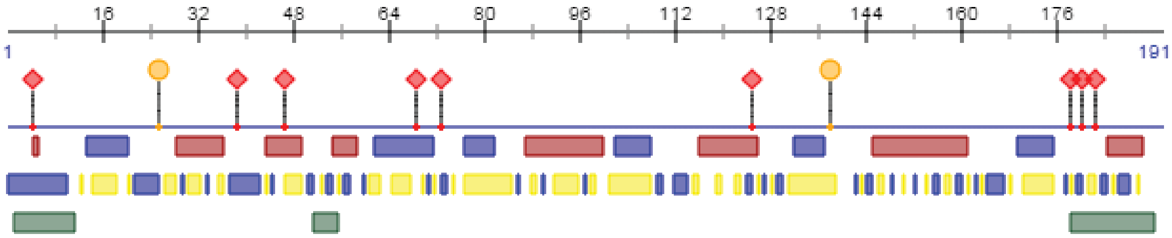
f sfff fs sss f fs f fssss ssfffsfs f fssssssssf

101 GGILVVSAAD 111 GPMPQTREHI 121 LLSRNVGVPA 131 LVVFLNKVDM 141 VDDEELLELV



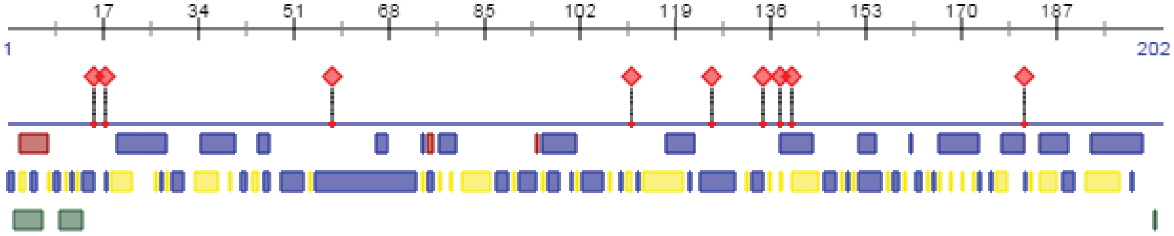
```
bbbbbbbbee eeeeebeebb bbbeebebeb bbbbbbebee eeeeebbebb
s s s   s f f f fsffs ss ffs s     s  sf f  fff f    ss
151        161        171        181        191
EMEVRDLLSE YDFPGDDVPV IAGSALKALE GDAQYEEKIL EIMEAVDTYI
eeebeebbee eebeeeebeb bebbbbebbe eeeeeeeebe ebbeebeeeb
f f f ss   f    ff  f    ss                  s    f

201        211        221        231        241
PTPERDSDKP FMMPVEDVFS ITGRGTVATG RVERGQIKVG EEVEIIGLHD
eeeeeeeeee bbbebeebbb bbbebebbeb ebeebebebe eebebbbbee
f f f    f s     ff   s sfsfs fs f f s         f  s
251        261
TSKTTVTGVE MFRKLL
eeeeebebbe bbeeee
      f  f ssff f
```

Fragment 4: 1-192



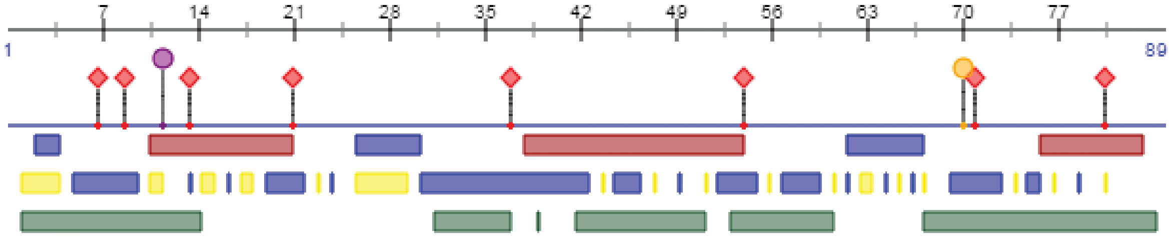
```
1          11         21         31         41
MAKEKFDRSK EHANIGTIGH VDHGKTTLTA AIATVLAKNG DSVAQSYDMI
eeeeeeeeee eebbbbbbbb beebebebeb bbbebbbeee eeebeebeeb
f f    f f  f s ssssss  ffsfsfsfs ss                   s 51
                  61         71         81         91
DNAPEEKERG ITINTSHIEY QTDKRHYAHV DCPGHADYVK NMITGAAQMD
eebeeeeeeb bbbbbbebeb eeeeebbbbb bbeeebebbe ebbbbbbbbe
f sfff  fs sss    f fs f  fssss  s fffsfs f fssssssssf101
                  111        121        131        141
GGILVVSAAD GPMPQTREHI LLSRNVGVPA LVVFLNKVDM VDDEELLELV
bbbbbbbbee eeeeebeebb bbbeebebeb bbbbbbebee eeeeebbebb
s s s   s f f fffsffs ss   fsfs      s  sf f  f f f    ss151
                  161        171        181        192
EMEVRDLLSE YDFPGDDVPV IAGSALKALE GDAQYEEKIL EL
eeebeebbee eebeeeebeb bebbbbebbe eeeeeeeeee ee
f f f ss   f    ff  f    ss
```

Fragment 5: 193-394



```
193        203        213        223        233
MEAVDTYIPT PERDSDKPFM MPVEDVFSIT GRGTVATGRV ERGQIKVGEE
eeebeeebee eeeeeeeebb bebeebbbbb bebebbebeb eebebebbee
    f   f  f f     s   f ff s s  sfsfs fsf  f s

243        253        263        273        283
VEIIGLHDTS KTTVTGVEMF RKLLDYAEAG DNIGALLRGV AREDVQRGQV
bebbbbeeee eeebebbebb eebbeebeee eebebbbebb eeeebeebeb
    s          f  fss ff  f   ff ff f s fs        fs s

293        303        313        323        333
LAAPGSITPH TEFKAEVYVL SKDEGGRHTP FFSNYRPQFY FRTTDVTGVV
beeeeebeee eebebebbbb eeeeeeeeee ebeeeeeebb bebeeeebeb
   f    ff   s      s  f fffffff f   ffffss  fsffffs

343        353        363        373        383
HLPEGTEMVM PGDNVEMTVE LIAPIAIEDG TRFSIREGGR TVGSGVVTEI
ebeebbebbb eeeebebebe bbbbbbbeeb bebbbeeeee bbbbbbbbeb
 s    fs s ffff            s       s sffff  sss s

393
IK
ee
```

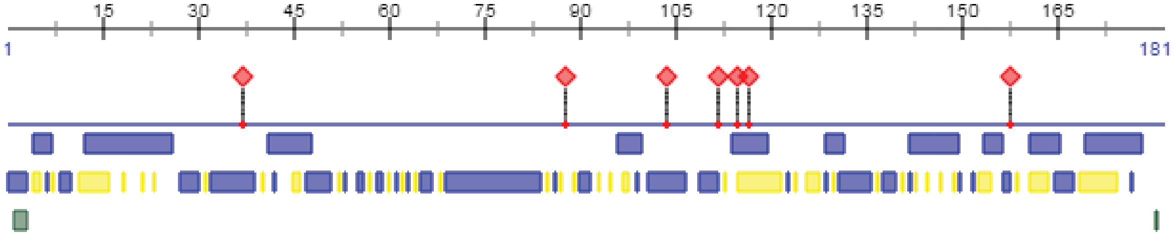
Fragment 6: 104-192



```
104        114        124        134        144
LVVSAADGPM PQTREHILLS RNVGVPALVV FLNKVDMVDD EELLELVEME
eebbbeeeee eebeebbbbb eebebebbbb bbbebeeeee eebbebbeee
ff  s ff f  fs fssss   fsfs    s   sf f f f  f   ssf f
```

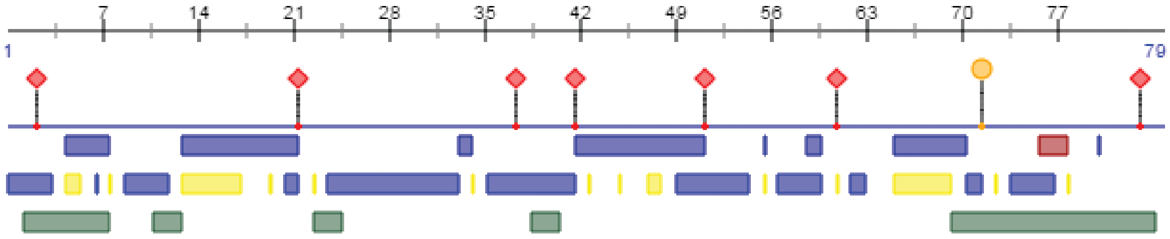
```
154        164        174        184
VRDLLSEYDF PGDDVPVIAG SALKALEGDA QYEEKILEL
beebbeeeeb eeeebebbeb bbbebbeeee ebeeebeee
 f  s       ff  f     ss  s  f          f
```

Fragment 7: 214-394



```
214        224        234        244        254
PVEDVFSITG RGTVATGRVE RGQIKVGEEV EIIGLHDTSK TTVTGVEMFR
eeeebbbbbb ebebbebebe ebebebbeeb ebbbbeeeee eebebbebbe
f ff s s s fsfs fsf f  s            s         f  fssf
264        274        284        294        304
KLLDYAEAGD NIGALLRGVA REDVQRGQVL AAPGSITPHT EFKAEVYVLS
ebbeeeeeee ebbbbbebbe eeebeebebb eeeeebeeee ebebebbbbe
f  f   fff f s s fs        fs s    f    ff   s    s s   31
4          324        334        344        354
KDEGGRHTPF FSNYRPQFYF RTTDVTGVVH LPEGTEMVMP GDNVEMTVEL
eeeeeeeeee beeeeeebbb ebeeeebebe beebbebbbe eeebebebeb
f ffffffff    ffffs   fsff fs    s     fs sf fff
364        374        384        394
IAPIAIEDGT RFSIREGGRT VGSGVVTEII K
bbbbbbeebb ebbbeeeeeb bbbbbbbebe e
    s       s  ffff s ss s
```

Fragment 9: 214-292



```
214        224        234        244        254
PVEDVFSITG RGTVATGRVE RGQIKVGEEV EIIGLHDTSK TTVTGVEMFR
eeeebbbbbb ebebbbbebe ebebebbeeb ebbbbeeeee eebebbebbe
f ff s s s fsfs ssf f  s        f  s             fs fss
```


264
KLLDYAEAGD
ebbeeeeeee
f sf fff
274
NIGALLRGVA
ebbbbbebbe
f s s fs
284
REDVQRGQV
eeeeeeeee
ffff

Will be presented as “Supplementary file S10- Experimental section”

S10. Supplementary Materials 3: Experimental Section

S10.1. Host and human proteins used in binding assays

Host proteins used for affinity chromatography include: purified fibronectin (Code: 341635) and plasminogen (Code: 528175) from human plasma supplied by Merck Millipore; plasminogen from human plasma (Code: P7999) bovine actin (Code: A3653) and fetuin (Code: F3004) supplied by Sigma.

Human proteins used for ELISA include: plasminogen (Code: P7999), lactoferrin (Code: L1294), laminin (Code: L6274), vitronectin (Code: SRP3186), plasma fibrinogen (Code: F3879) and plasma fibronectin (Code: 11051407001) supplied by Sigma.

S10.2. Peptide search parameters

Files were searched against the MSPnr100 database [151] with the following parameters. Fixed modifications: none. Variable modifications: propionamide, oxidized methionine, deamidation. Enzyme: semi-trypsin. Number of allowed missed cleavages: 3. Peptide mass tolerance: 100 ppm. MS/MS mass tolerance: 0.2 Da. Charge state: 2+, 3+ and 4+. For samples collected from the ‘Biotinylation enrichment of surface proteins’, ‘Avidin purification of A549 interacting proteins’ and ‘Avidin purification of PK-15 interacting proteins’, variable modifications also included NHS-LC-Biotin (K) and NHS-LC-Biotin (N-term). ‘Avidin purification of A549 interacting proteins’ was also searched against *homo sapiens* entries in MSPnr100 to identify biotinylated surface A549 proteins. ‘Avidin purification of PK-15 interacting proteins’ was also searched against *sus scrofa* entries in MSPnr100 to identify biotinylated surface PK-15 proteins.

S. aureus proteins were also searched against a *S. aureus* NCTC 8325 database derived from the published genome.

S10.3. Expression and purification of rMpn$_{Ef\text{-}Tu}$

Expression and purification of rMpn$_{\text{Ef-Tu}}$ was performed in one of two methods.

The first method was performed as described in [100]. In brief, the *M. pneumoniae tuf* gene (*MPN_665*) was amplified and cloned with a N-terminal hexahistadine tail into the plasmid vector pET30 (Merck Millipore) containing a kanamycin resistance gene. The recombinant construct was transformed in to BL21-DE3 competent *E. coli* cells (Merck Millipore), induced with 1 mM isopropyl-β-D-thiogalactosidase (IPTG, Roth) and purified under denaturing conditions with immobilized metal affinity chromatography Ni^{2+}-charged resin (Qiagen, Hilden, Germany) as described by the manufacturer. Elutions were concentrated using a 30 kDa Vivaspin centrifugal device (Sartorius, Göttingen, Germany). Recombinant protein was assayed and stored at -20°C. rMpn$_{\text{Ef-Tu}}$ was used to produce guinea pig antiserum as reported [100].

The second method was performed as described in [88] with modifications. In brief, the *M. pneumoniae tuf* gene (*MPN_665*) was synthesized with an N-terminal hexahistadine tail and cloned by Blue Heron Biotech (WA, USA) into a plasmid vector (PS100030) with an ampicillin resistance gene. The recombinant construct was transformed in to BL21-DE3 competent *E. coli* cells (Bioline, Eveleigh, Australia), induced with 1 mM isopropyl-β-D-thiogalactosidase (IPTG, Bioline) and purified under denaturing conditions with Profinity immobilized metal affinity chromatography Ni^{2+}-charged resin (Bio-Rad, Gladesville, Australia). BL21cells were lysed in 8 M Urea, 100 mM Na_2HCO_3, 10 mM Tris-HCl, pH 8 with 6 rounds of sonication for 30 seconds on ice. Following centrifugation, the supernatant was added to Ni2+ resin overnight at 4°C. The resin was then loaded onto a column, washed four times with 5 ml 8 M Urea, 100 mM Na_2HCO_3, 10 mM Tris-HCl, pH 6.3 and a 2-step elution: three times with 5 ml 8 M Urea, 100 mM Na_2HCO_3, 10 mM Tris-HCl, pH 5.9 and twice with 10 ml 8 M Urea, 100 mM Na_2HCO_3, 10 mM Tris-HCl, pH 4.5**.** Washes and elutions were monitored by SDS-PAGE. Elutions were concentrated using a 10 kDa Microsep™ centrifugal device (Pall, Port Washington, NY) and dialysed into PBS, 0.5% Tween 20 with 10,000 MWCO SnakeSkin® Dialysis Tubing (Thermo Fisher Scientific) at 4°C. Recombinant protein was assayed and stored at 4°C.

S10.4 LC-MS/MS of dimethyl labelled proteins

S10.4.1. LC-MS/MS (Sciex 5600) of dimethyl labelled proteins

Peptides from dimethyl labelled proteins described in section 1.16.1 were separated by nanoLC using an Ultimate nanoRSLC UPLC and autosampler system (Dionex, Amsterdam, Netherlands). Samples (2.5 µl) were concentrated and desalted onto a micro C18 precolumn (300 µm x 5 mm, Dionex) with H_2O:CH_3CN (98:2, 0.1 % TFA) at 15 µl/min. After a 4 min wash the pre-column was switched (Valco 10 port UPLC valve, Valco, Houston, TX) into line with a fritless nano column (75µ x ~15cm) containing C18AQ media (1.9µ, 120 Å Dr Maisch, Ammerbuch-Entringen Germany). Peptides were eluted using a linear gradient of H_2O:CH_3CN (98:2, 0.1 % formic acid) to H_2O:CH_3CN (64:36, 0.1 % formic acid) at 200 nl/min over 240 min. High voltage 2000 V was applied to low volume Titanium union (Valco) with the tip positioned ~ 0.5 cm from the curtain plate (T=150°C) of a 5600^+ mass spectrometer (Sciex, Toronto, Canada). Positive ions were generated by electrospray and the 5600^+ operated in information dependent acquisition mode (IDA).

A survey scan m/z 350-1750 was acquired (PWHH resolution ~30,000, 0.25 sec acquisition time) with autocalibration enabled (at ~6 hr intervals). Up to the 10 most abundant ions (>300 counts) with charge states > +2 and <+5 were sequentially isolated (width m/z ~3) and fragmented by CID with an optimal CE chosen based on m/z (product ion spectra were acquired at a resolution ~20,000 PWHH in 0.15 sec). M/z ratios selected for MS/MS were dynamically excluded for 30 or 45 seconds.

Peak lists were generated using Mascot Daemon/Mascot Distiller (Matrix Science, London, England) or ProteinPilot (Sciex, v4.5) using default parameters, and submitted to the database search program Mascot (version 2.5.1, Matrix Science). Search parameters were: Precursor tolerance 10 ppm and product ion tolerances ± 0.05 Da; oxidation (M), deamidation (NQ), propionamide (C), Dimethyl (K), Dimethyl (N-term) specified as variable modifications; enzyme specificity was semi-ArgC; 1 missed cleavage was possible and the non-redundant protein database from NCBI (Jan 2015) searched.

S10.4.2. LC-MS/MS (Thermo Scientific Q Exactive™) of dimethyl labelled proteins

Peptides from dimethyl labelled proteins described in section 1.18.1 were separated by nanoLC using an Ultimate nanoRSLC UPLC and autosampler system (Dionex, Amsterdam, Netherlands). Samples (2.5 µl) were concentrated and desalted onto a micro C18 precolumn (300 µm x 5 mm, Dionex) with H_2O:CH_3CN (98:2, 0.1 % TFA) at 15 µl/min. After a 4 min wash the pre-column was switched (Valco 10 port UPLC valve, Valco, Houston, TX) into line with a fritless nano column (75µ x ~35cm) containing C18AQ media (1.9µ, 120 Å Dr Maisch, Ammerbuch-Entringen Germany). Peptides were eluted using a linear gradient of H_2O:CH_3CN (98:2, 0.1 % formic acid) to H_2O:CH_3CN (64:36, 0.1 % formic acid) at 200 nl/min over 30 or

240 min. High voltage 2000 V was applied to low volume Titanium union (Valco) with the column oven heated to 45°C (Sonation, Biberach, Germany) and the tip positioned ~ 0.5 cm from the heated capillary (T=300°C) of a QExactive Plus mass spectrometer (Thermo Fisher Scientific, Bremen, Germany). Positive ions were generated by electrospray and the QExactive operated in data dependent acquisition mode (DDA).

A survey scan m/z 350-1750 was acquired (resolution = 70,000 at m/z 200, with an AGC target value of 10^6 ions) and lockmass was enabled (m/z 445.12003) Up to the 10 most abundant ions (>80,000 counts, underfill ratio 10%) with charge states > +2 and <+7 were sequentially isolated (width m/z 2.5) and fragmented by HCD (NCE = 30) with a AGC target of 10^5 ions (resolution = 17,500 at m/z 200). M/z ratios selected for MS/MS were dynamically excluded for 30 or 45 seconds.

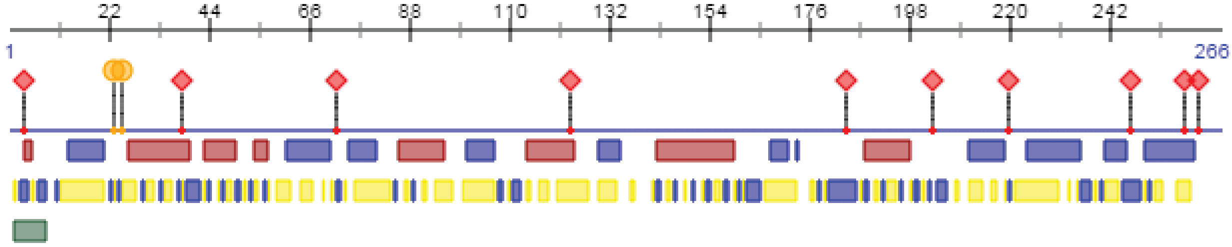
Peak lists were generated using Mascot Daemon/Mascot Distiller (Matrix Science, London, England) or Proteome Discoverer (Thermo Fisher Scientific, v1.4) using default parameters, and submitted to the database search program Mascot (version 2.5.1, Matrix Science). Search parameters were: Precursor tolerance 4 ppm and product ion tolerances ± 0.05 Da; oxidation (M), deamidation (NQ), propionamide (C), Dimethyl (K), Dimethyl (N-term) specified as variable modifications; enzyme specificity was semi-ArgC; 1 missed cleavage was possible and the non-redundant protein database from NCBI (Jan 2015) searched.

Item C.2 Residue analysis of *S. aureus* Ef-Tu (on next page) showing conserved, non-conserved, and disordered regions. Potential interaction sites are also noted. This analysis was performed by V. Jarocki.

Sa

1	11	21	31	41
MAKEKFDRSK	EHANIGTIGH	VDHGKTTLTA	AIATVLAKNG	DSVAQSYDMI
51	61	71	81	91
DNAPEEKERG	ITINTSHIEY	QTDKRHYAHV	DCPGHADYVK	NMITGAAQMD
101	111	121	131	141
GGILVVSAAD	GPMPQTREHI	LLSRNVGVPA	LVVFLNKVDM	VDDEELLELV
151	161	171	181	191
EMEVRDLLSE	YDFPGDDVPV	IAGSALKALE	GDAQYEEKIL	ELMEAVDTYI
201	211	221	231	241
PTPERDSDKP	FMMPVEDVFS	ITGRGTVATG	RVERGQIKVG	EEVEIIGLHD
251	261	271	281	291
TSKTTVTGVE	MFRKLLDYAE	AGDNIGALLR	GVAREDVQRG	QVLAAPGSIT
301	311	321	331	341
PHTEFKAEVY	VLSKDEGGRH	TPFFSNYRPQ	FYFRTTDVTG	VVHLPEGTEM
351	361	371	381	391
VMPGDNVEMT	VELIAPIAIE	DGTRFSIREG	GRTVGSGVVT	EIIK

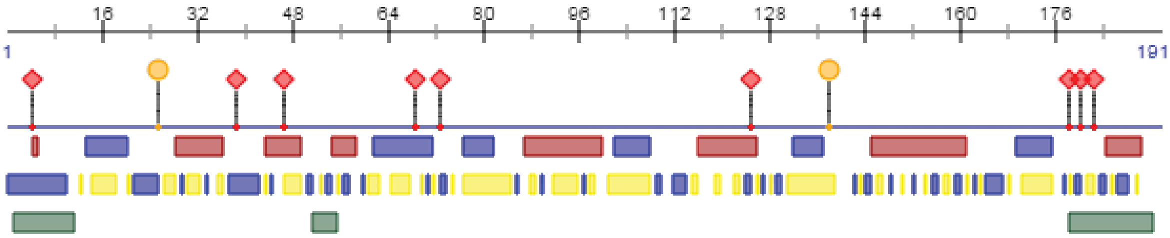
Fragment 3: 1-266



1	11	21	31	41
MAKEKFDRSK	EHANIGTIGH	VDHGKTTLTA	AIATVLAKNG	DSVAQSYDMI
eeeeeeeeee	eebbbbbbbb	beebebebeb	bbbebbbeee	eeebeebeeb
f f f f	f s sssss	ffsfsfsfs	ss	s
51	61	71	81	91
DNAPEEKERG	ITINTSHIEY	QTDKRHYAHV	DCPGHADYVK	NMITGAAQMD
eebeeeeeeb	bbbbbbebeb	eeeeebbbbb	bbeeebebbe	ebbbbbbbbe
f sfff fs	sss f fs	f fssss	ssfffsfs f	fssssssssf
101	111	121	131	141
GGILVVSAAD	GPMPQTREHI	LLSRNVGVPA	LVVFLNKVDM	VDDEELLELV

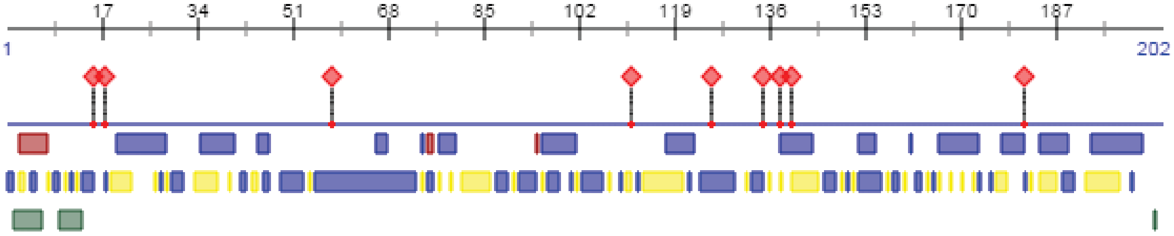
```
bbbbbbbbee eeeeebeebb bbbeebebeb bbbbbbebee eeeeebbebb
s s s  s f f f fsffs  ss ffs s     s  sf f  fff f   ss
151        161        171        181        191
EMEVRDLLSE YDFPGDDVPV IAGSALKALE GDAQYEEKIL ELMEAVDTYI
eeebeebbee eebeeeebeb bebbbbebbe eeeeeeeebe ebbeebeeeb
f f f ss   f   ff  f     ss                  s    f

201        211        221        231        241
PTPERDSDKP FMMPVEDVFS ITGRGTVATG RVERGQIKVG EEVEIIGLHD
eeeeeeeeee bbbebeebbb bbbebebbeb ebeebebebe eebebbbbee
f f f    f s    ff    s sfsfs fs f f s         f  s
251        261
TSKTTVTGVE MFRKLL
eeeeebebbe bbeeee
      f  f ssff f
```

Fragment 4: 1-192



```
1          11         21   ▲▲▲    31         41
MAKEKFDRSK EHANIGTIGH VDHGKTTLTA AIATVLAKNG DSVAQSYDMI
eeeeeeeeee eebbbbbbbb beebebebeb bbbebbbeee eeebeebeeb
f f    f f  f s sssss  ffsfsfsfs ss                  s 51
         61         71         81         91
DNAPEEKERG ITINTSHIEY QTDKRHYAHV DCPGHADYVK NMITGAAQMD
eebeeeeeeb bbbbbbebeb eeeeebbbbb bbeeebebbe ebbbbbbbbe
f sfff  fs sss   f fs  f  fssss  s fffsfs f fssssssssf101
        111        121        131      ▲ 141
GGILVVSAAD GPMPQTREHI LLSRNVGVPA LVVFLNKVDM VDDEELLELV
bbbbbbbbee eeeeebeebb bbbeebebeb bbbbbbebee eeeeebbebb
s s s  s f f f fsffs  ss  fsfs     s  sf f  f f f   ss151
        161        171        181        192
EMEVRDLLSE YDFPGDDVPV IAGSALKALE GDAQYEEKIL EL
eeebeebbee eebeeeebeb bebbbbebbe eeeeeeeeee ee
f f f ss   f   ff  f     ss
```

Fragment 5: 193-394



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193        203        213        223        233
MEAVDTYIPT PERDSDKPFM MPVEDVFSIT GRGTVATGRV ERGQIKVGEE
eeebeeebee eeeeeeeebb bebeebbbbb bebebbebeb eebebebbee
    f   f  f f     s   f ff s s  sfsfs fsf  f s

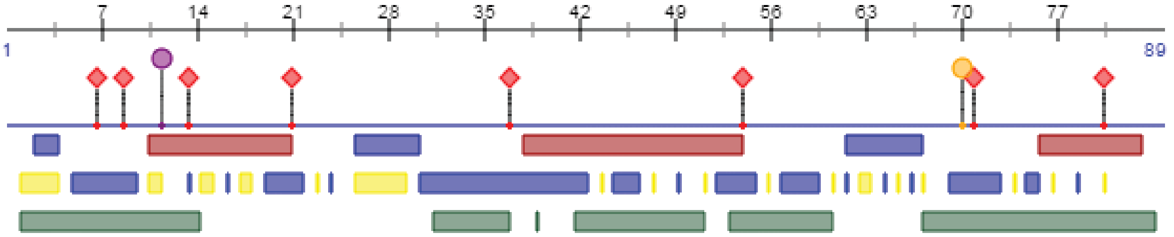
243        253        263        273        283
VEIIGLHDTS KTTVTGVEMF RKLLDYAEAG DNIGALLRGV AREDVQRGQV
bebbbbeeee eeebebbebb eebbeebeee eebebbbebb eeeebeebeb
    s          f  fss ff  f   ff ff f s fs        fs s

293        303        313        323        333
LAAPGSITPH TEFKAEVYVL SKDEGGRHTP FFSNYRPQFY FRTTDVTGVV
beeeeebeee eebebebbbb eeeeeeeeee ebeeeeeebb bebeeeebeb
   f    ff   s      s  f fffffff f   ffffss  fsffffs

343        353        363        373        383
HLPEGTEMVM PGDNVEMTVE LIAPIAIEDG TRFSIREGGR TVGSGVVTEI
ebeebbebbb eeeebebebe bbbbbbbeeb bebbbeeeee bbbbbbbbeb
 s    fs s ffff            s       s sffff  sss s

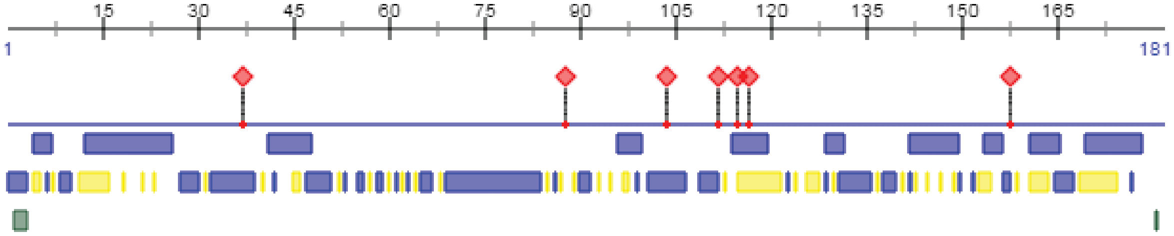
393
IK
ee
```

Fragment 6: 104-192

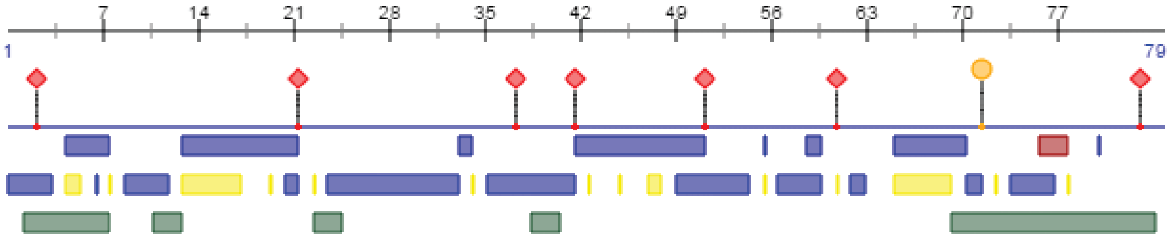


```
104        114        124        134        144
LVVSAADGPM PQTREHILLS RNVGVPALVV FLNKVDMVDD EELLELVEME
eebbbeeeee eebeebbbbb eebebebbbb bbbebeeeee eebbebbeee
ff  s ff f  fs fssss   fsfs    s   sf f f f  f   ssf f
```

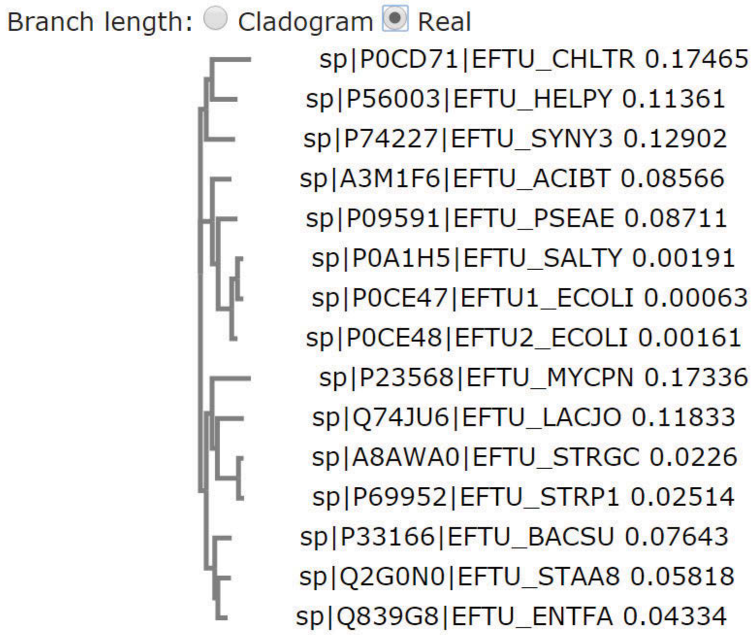
Fragment 7: 214-394



Fragment 9: 214-292




264
274
284
KLLDYAEAGD
NIGALLRGVA
REDVQRGQV
ebbeeeeeee
ebbbbbebbe
eeeeeeeee
f sf fff
f s s fs
ffff



Branch length: ○ Cladogram ● Real

```
sp|P0CD71|EFTU_CHLTR 0.17465
sp|P56003|EFTU_HELPY 0.11361
sp|P74227|EFTU_SYNY3 0.12902
sp|A3M1F6|EFTU_ACIBT 0.08566
sp|P09591|EFTU_PSEAE 0.08711
sp|P0A1H5|EFTU_SALTY 0.00191
sp|P0CE47|EFTU1_ECOLI 0.00063
sp|P0CE48|EFTU2_ECOLI 0.00161
sp|P23568|EFTU_MYCPN 0.17336
sp|Q74JU6|EFTU_LACJO 0.11833
sp|A8AWA0|EFTU_STRGC 0.0226
sp|P69952|EFTU_STRP1 0.02514
sp|P33166|EFTU_BACSU 0.07643
sp|Q2G0N0|EFTU_STAA8 0.05818
sp|Q839G8|EFTU_ENTFA 0.04334
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Figure C.1 Phylogeny tree output generated by Clustal Omega alignment [443] relating to all species shown in Figure 4.5.

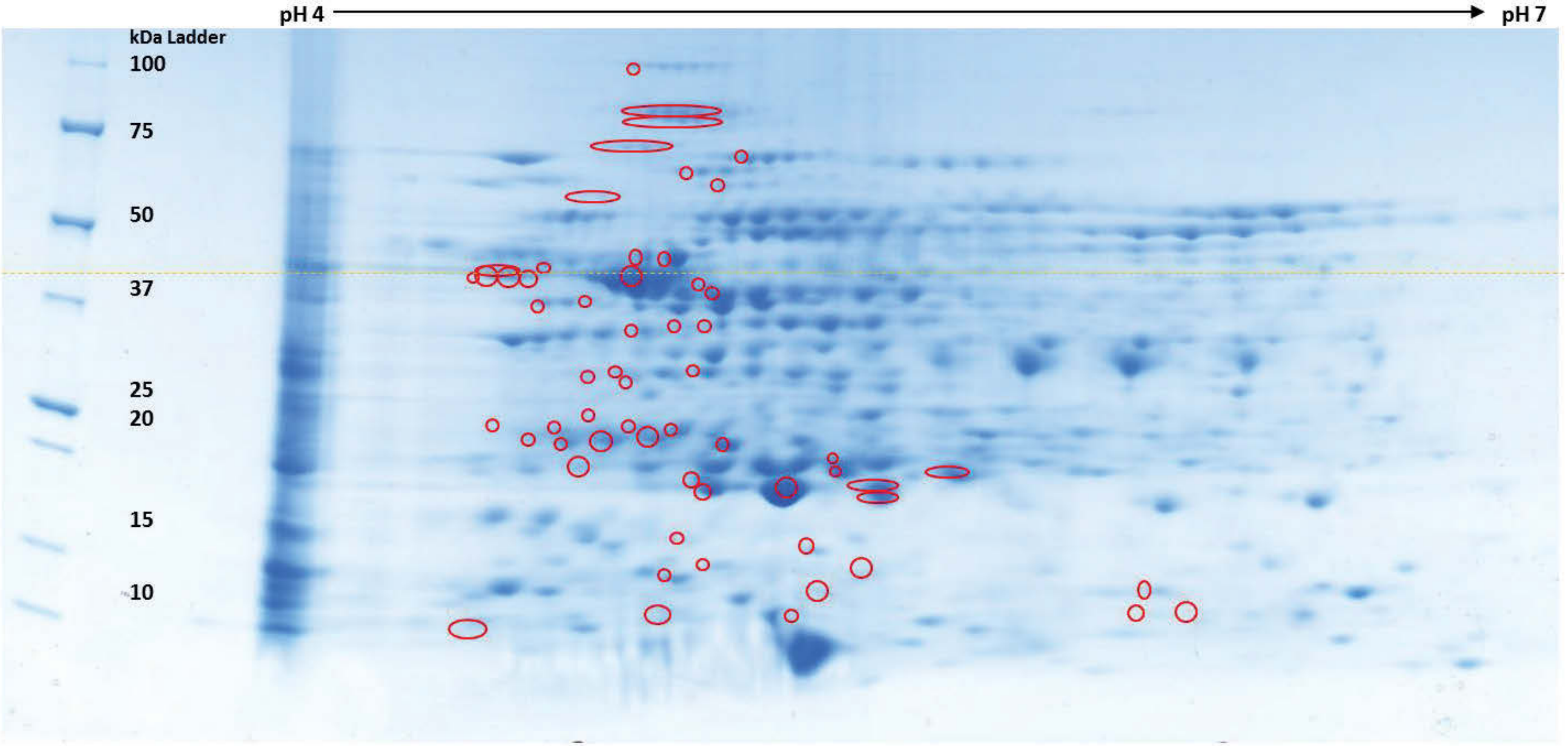

Figure C.2 2D-PAGE of WCL proteins showing all spots (in red) where Ef-Tu was identified. Yellow line depicts where Ef-Tu is expected to migrate on a gel (41 kDa).