

**CETZ1 IN CELL SHAPE CONTROL OF
HALOARCHAEA:
UNDERSTANDING THE FUNCTIONAL
DIVERGENCE OF TUBULIN SUPERFAMILY
PROTEINS**

Kariyawasam W. T. Roshali Thavindra de Silva

A thesis submitted in fulfilment of the requirements for the
degree of Doctor of Philosophy

The ithree Institute and School of Life Sciences, University of
Technology Sydney

November 2019

CERTIFICATE OF ORIGINAL AUTHORSHIP

I, Kariyawasam W. T. Roshali Thavindra de Silva declare that this thesis, is submitted in fulfilment of the requirements for the award of PhD, in the School of Life Sciences/ Faculty of Science at the University of Technology Sydney.

This thesis is wholly my own work unless otherwise reference or acknowledged. In addition, I certify that all information sources and literature used are indicated in the thesis.

This document has not been submitted for qualifications at any other academic institution.

This research is supported by the Australian Government Research Training Program.

Production Note:
Signature removed prior to publication.

Signature

Date: 02/09/2019

TABLE OF CONTENT

Certificate of Original Authorship	iii
List of Figures	viii
List of Tables	xi
Abbreviations	xii
Publications and Conference Proceedings	xiv
Acknowledgement	xv
Abstract	xvi
1 Introduction.....	18
1.1 Overview of the research problem	19
1.2 Cytoskeleton.....	20
1.3 Tubulin superfamily proteins	22
1.4 Microtubules.....	23
1.4.1 Relationship of tubulin structure and conformation with the function	24
1.4.2 Microtubule dynamics and regulation.....	28
1.4.3 Microtubule isoforms and post-translational modifications	33
1.5 Cell division in bacteria by FtsZ	34
1.5.1 FtsZ Polymerisation and structure	34
1.5.2 FtsZ controls prokaryotic cell division	35
1.6 Tubulins in archaea	39
1.6.1 Archaea	39
1.6.2 FtsZ and divergent tubulin superfamily members in archaea	41
1.6.3 Cell-structure-related euryarchaeota tubulin/FtsZ proteins (CetZ) in <i>Haloferax volcanii</i>	42
1.7 Aims of the present study	48
2 General Materials and Methods.....	49
2.1 Bacterial strains and plasmids	50
2.2 Growth media	51
2.3 Chemicals, reagents and solutions.....	53
2.4 Growth conditions and preparation of <i>E. coli</i> cells.....	55
2.4.1 Normal growth conditions for <i>E. coli</i>	55
2.4.2 Preparing chemically competent cells of <i>E. coli</i>	55
2.4.3 Preparing electrocompetent cells of <i>E. coli</i>	55
2.5 Transformation of <i>E. coli</i>	56

2.5.1	<i>E. coli</i> transformation by heat shock.....	56
2.5.2	<i>E. coli</i> transformation by electroporation.....	56
2.6	General growth conditions for <i>Haloferax volcanii</i>	57
2.7	<i>Haloferax volcanii</i> transformation	57
2.8	Common genetic techniques.....	58
2.8.1	Measuring DNA concentration and storage.....	58
2.8.2	Extraction of gDNA and plasmid DNA.....	58
2.8.3	Demethylation of plasmid DNA	58
2.8.4	Agarose gel electrophoresis	59
2.8.5	Polymerase chain reaction (PCR)	59
2.8.6	General cloning protocol.....	60
2.8.7	Sanger sequencing.....	61
2.9	General protein analysis techniques	61
2.9.1	Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) .	61
2.9.2	Western Blot.....	62
2.10	Common techniques used to analyse different cellular parameters	63
2.10.1	Imaging cell shapes using microscopy.....	63
2.10.2	Cell circularity analysis.....	64
2.10.3	Cell volume and cell count analysis by Coulter counter.....	64
3	Conditional Pleomorphology and Differentiation in the Model Archaeon <i>Haloferax volcanii</i>	65
3.1	Abstract	67
3.2	Introduction	67
3.3	Results	69
3.3.1	<i>H. volcanii</i> growth and pleomorphology in nutrient-limited batch culture ..	69
3.3.2	Improved growth of <i>H. volcanii</i> in TE-supplemented media	71
3.3.3	<i>H. volcanii</i> forms rods during the onset of growth in culture	73
3.3.4	The interplay between conditions controlling <i>H. volcanii</i> morphological development.....	75
3.3.5	Microfluidic flow chamber visualization of <i>H. volcanii</i> cellular development.....	76
3.3.6	Potential role of secreted signals in cell elongation during early growth .	78
3.3.7	Reversibility and specificity of the TE-starvation cell elongation response.	78

3.3.8	The requirement of tubulin-like protein CetZ1 for rod cell formation in batch culture.....	79
3.4	Discussion	82
3.5	Materials and Methods	85
3.5.1	Archaeal strains	85
3.5.2	Culture media and general growth conditions	85
3.5.3	Nutrient depletion in liquid cultures	86
3.5.4	Time-course studies of rod development	86
3.5.5	Microscopy.....	87
3.5.6	Coulter cytometry.....	88
3.5.7	Western blotting	88
4	Characterisation of CetZ1 localisation in <i>Haloferax volcanii</i> morphogenesis using a new knockout strain and fluorescent protein fusion	89
4.1	Introduction	91
4.1.1	<i>Haloferax volcanii</i> gene knockout system	91
4.1.2	The discovery of CetZ1 function in cell shape control	92
4.1.3	Previous studies of CetZ1 localisation in <i>Haloferax volcanii</i>	94
4.1.4	Designing functional fusion proteins in biology	95
4.1.5	Aims and the content of the results chapter	99
4.2	Results	100
4.2.1	Design, construction and complementation of CetZ1 knockout strains .	100
4.2.2	Design, construction and complementation of CetZ1 fluorescent protein fusions	109
4.2.3	The localisation of CetZ1 in <i>Haloferax volcanii</i> during morphogenesis	118
4.3	Discussion	125
4.4	Methods	128
4.4.1	Construction of plasmids containing the knock-out regions.....	128
4.4.2	Construction of knockout strains	129
4.4.3	Construction of vectors with CetZ1 fluorescent protein fusion.....	130
4.4.4	Testing the complementation of CetZ1 fluorescent fusion proteins	132
4.4.5	Motility assay	132
4.4.6	Early-log phase rod assay.....	133
5	Chapter 05: <i>In vivo</i> characterisation of CetZ1 function via site-directed mutagenesis	134
5.1	Introduction	135

5.2	Results	137
5.2.1	Use of CetZ1 site-directed mutants for identification of structural components in CetZ1 important for <i>Haloferx volcanii</i> motility and morphogenesis ..	137
5.2.2	CetZ1 localisation dynamics in the point mutants	146
5.3	Discussion	155
5.4	Methods	158
5.4.1	Construction of point mutants	158
5.4.2	Construction of fluorescent fusion proteins of CetZ1 point mutants	160
5.4.3	Early-log phase rod development.....	160
5.4.4	Live cell imaging.....	160
5.4.5	Cell volume and cell count analysis by Coulter counter.....	161
6	Analysis of <i>In Vitro</i> Interactions of CetZ1	162
6.1	Introduction	163
6.1.1	Models for subunit polymerisation	163
6.1.2	The polarity of the cytoskeletal filaments	165
6.2	Results	168
6.2.1	Optimisation of CetZ1 purification.....	168
6.2.2	Optimised condition for CetZ1 polymerisation	172
6.2.3	<i>In vitro</i> polymerisation of selected CetZ1 point mutants.....	178
6.2.4	CetZ1 aggregated multimers can directly bind to the lipids	181
6.3	Discussion	185
6.4	Methods	188
6.4.1	Overproduction of the protein and preparation of the cell lysate.....	188
6.4.2	The purification of untagged CetZ1	189
6.4.3	Purification of archaeal membrane lipids and liposome preparation.....	189
6.4.4	Ultracentrifuge co-sedimentation assay	190
6.4.5	Ultracentrifuge co-pelleting assay.....	191
6.4.6	90 ⁰ Light scattering assay.....	191
6.4.7	Malachite Green GTPase assay.....	192
7	Discussion.....	194
7.1	External signals that induce the <i>H. volcanii</i> rod formation	195
7.2	CetZ1 in modulating <i>H. volcanii</i> cell shape	198
8	Appendix: Supplementary Data.....	201
9	References.....	208

List of Figures

Figure 1.1: <i>Three main types of cytoskeletal components in cells.</i>	21
Figure 1.2: <i>Important structural features in tubulin heterodimer.</i>	24
Figure 1.3: <i>Straight and bent conformations of tubulin dimers and models proposed for the role of GTP in adapting these conformations into the microtubule lattice.</i>	26
Figure 1.4: <i>The structure of the γ- tubulin ring complex (γ- TuRC).</i>	28
Figure 1.5: <i>The effect of β:T238A mutation on microtubule dynamics.</i>	31
Figure 1.6: <i>Z ring formation in <i>Haloferax volcanii</i>, the model haloarchaeon used in this study.</i>	36
Figure 1.7: <i>An overview of cell division (left) apparatus and cell elongation (right) apparatus.</i>	37
Figure 1.8: <i>Different cell shapes in haloarchaea.</i>	40
Figure 1.9: <i>A phylogenetic overview of tubulin superfamily.</i>	43
Figure 1.10: <i>Evidence indicating <i>CetZ1</i> is not essential for cell division, and it is needed for the shapeshift form plate shape to rod shape.</i>	44
Figure 1.11: <i>Current evidence that displays <i>CetZ1</i> cytoskeletal dynamics.</i>	45
Figure 1.12: <i>Evidence showing <i>CetZ1</i> can assemble into a quaternary structure.</i>	47
Figure 3.1: <i>Effects of nutrient depletion on <i>H. volcanii</i> growth and morphology in liquid culture.</i>	70
Figure 3.2: <i>Media supplementation with trace elements (TE) solution improves growth and cell shape uniformity in <i>H. volcanii</i>.</i>	72
Figure 3.3: <i><i>H. volcanii</i> forms rods during the early stages of growth at low ODs in liquid batch culture.</i>	73
Figure 3.4: <i>Assays for <i>H. volcanii</i> reversible morphological transitions during the growth cycle.</i>	74
Figure 3.5: <i>Time-lapse microscopy of <i>H. volcanii</i> (H98 + pTA962) with and without trace elements.</i>	77
Figure 3.6: <i><i>CetZ1</i> is essential for rod development during early-growth after colony resuspension and during TE-depletion.</i>	80
Figure 4.1: <i>Summary of <i>H. volcanii</i> gene knockout system based on <i>pyrE2</i> genetic marker.</i>	92
Figure 4.2: <i>Motility and cell shape comparison of WT and <i>cetZ1</i> knockout cells.</i>	93
Figure 4.3: <i><i>CetZ1</i> localisation in the WT background.</i>	94
Figure 4.4: <i>Effect of linker rigidity on FRET efficiency and the separation between a CFP and YFP fusion protein.</i>	97
Figure 4.5: <i>Schematic representation of the <i>cetZ1</i> (HVO_2204) deletion construct.</i> ..	101
Figure 4.6: <i>Schematic representation showing the steps in the construction of new <i>cetZ1</i> knockout strains.</i>	103
Figure 4.7: <i>Diagnostic tests to confirm the Δ<i>cetZ1</i> strains</i>	104
Figure 4.8: <i>Complementation of <i>CetZ1</i> function in <i>cetZ1</i> in-frame and out-of-frame knockouts compared to <i>H. volcanii</i> H26 (WT) strain.</i>	106

Figure 4.9: Complementation of rod cell formation by <i>cetZ1</i> overexpression (4 mM tryptophan) during mid-log growth and <i>cetZ1</i> WT level expression (2 mM tryptophan) during early-log phase rod assay in the <i>cetZ1</i> in-frame knockout strain.	108
Figure 4.10: Plasmid design of the fluorescent vectors.	111
Figure 4.11: Screening of IF Δ <i>cetZ1</i> complementation by the fluorescently labelled <i>CetZ1</i>	113
Figure 4.12: The fluorescent (left) and phase-contrast (right) images of the cells from the early-log phase assay in <i>Hv</i> -YPCab+2 mM tryptophan for all <i>CetZ1</i> fusions with <i>G</i> linker in IF Δ <i>cetZ1</i>	115
Figure 4.13: Comparison of the complementation of Δ <i>cetZ1</i> by <i>CetZ1</i> -mTurquoise2 fusions and the original GFP fusion; <i>pIDJL40.CetZ1</i>	117
Figure 4.14: The localisation of new <i>CetZ1</i> -mTurquoise2 in motile rods and during supplementary expression.	119
Figure 4.15: <i>CetZ1</i> localisation during early-log phase assay and trace elements (TE) depletion assay.	121
Figure 4.16: <i>CetZ1</i> localisation imaged by 3D-SIM.	122
Figure 4.17: Selected time frames showing <i>CetZ1</i> localisation dynamics during morphogenesis.	123
Figure 5.1: Locations of the <i>CetZ1</i> point mutations designed to disrupt the lateral interaction, membrane interaction and GTP contact.	138
Figure 5.2: Expression and motility assays of strains expressing <i>CetZ1</i> point mutants.	141
Figure 5.3: Cell shapes observed in ID181 expressing the indicated <i>CetZ1</i> site-directed mutants (on <i>pTA962</i>) in the TE depletion assay.	143
Figure 5.4: Rod formation by <i>CetZ1</i> point mutants in the early-log phase assay.	144
Figure 5.5: <i>CetZ1</i> -mTurquoise2 localisation during early-log phase assay for point mutants that displayed decreased motility.	147
Figure 5.6: <i>CetZ1</i> -mTurquoise2 localisation during early-log phase assay for point mutants that displayed normal motility.	149
Figure 5.7: Comparison of distances of <i>CetZ1</i> localisations to the cell edge in different point mutants.	151
Figure 5.8: A comparison of the aspect ratio of the localisations in the double mutant (<i>R726E</i> , <i>K277E</i>) and <i>G108S</i> to the that of WT <i>CetZ1</i>	153
Figure 6.1: A schematic showing the differences in subunit assembly between 164	164
Figure 6.2: The two possible kinetic polarities for polymer growth. Tubulin shows the first top-end growth kinetics in which subunits add to the GTP-bound end of the polymer.	166
Figure 6.3: The optimisation of the protein purification buffer with different additives.	169
Figure 6.4: Buffer optimisation improved <i>CetZ1</i> purification.	170
Figure 6.5: SDS-PAGE analysis of the collected fractions from Ion Exchange and subsequent Gel Filtration.	171
Figure 6.6: Optimisation of <i>CetZ1</i> (12 μ M) in vitro polymerisation condition using 90 ^o light scattering assay.	173
Figure 6.7: The effect of pH on <i>CetZ1</i> (12 μ M) polymerisation.	174
Figure 6.8: Analysis of <i>CetZ1</i> GTP dependent polymerisation.	175
Figure 6.9: <i>CetZ1</i> displays cooperative polymerisation.	176

Figure 6.10: <i>Malachite Green Phosphate assay cannot detect CetZ1 GTPase activity.</i>	177
Figure 6.11: <i>Comparison of gel filtration chromatograms between (A) WT CetZ1 and CetZ1 point mutants, (B) CetZ1.M-loop, (C) CetZ1.E218A resulted during their purification.</i>	179
Figure 6.12: <i>Analysis of the polymerisation of CteZ1 point mutants, CetZ1, M-loop and CetZ1.E218A, via light scattering assay.</i>	180
Figure 6.13: <i>Haloferax volcanii lipids.</i>	181
Figure 6.14: <i>Analysis of CetZ1 lipid-binding via ultracentrifuge co-sedimentation assay.</i>	183

- **Supplementary Data Figure 1.** Reversal and specificity testing of TE starvation. *H. volcanii* (H98 + pTA962) colonies from Hv-Ca agar were resuspended in Hv-Ca liquid medium.
- **Supplementary Data Figure 2.** Effect of spent media on *H. volcanii* cell shape during on-set rod formation.
- **Supplementary Data Figure 3.** Inclusion body formation depending on the cells' history of starvation.
- **Supplementary Data Figure 4.** The growth differences in *H. volcanii* during TE depletion.
- **Supplementary Data Figure 5.** The CetZ1 localisation concerning the local curvature of the cell.
-
- **Supplementary Video 1.** *H. volcanii* cell shape change in Hv-Cab (+TE).
- **Supplementary Video 2.** *H. volcanii* cell shape change in Hv-Ca (-TE).
- **Supplementary Video 3.** *H. volcanii* cell shape change in Hv-YPC (-TE).
- **Supplementary Video 4.** *H. volcanii* cell shape change in Hv-YPCab (+TE).
- **Supplementary Video 5.** The localisation of CetZ1-mTq2 expressed in ID181 during early-log phase assay.
- **Supplementary Video 6.** The localisation of CetZ1-mTq2 expressed in ID181 during early-log phase assay.
- **Supplementary Video 7.** The localisation of CetZ1.R276E, K277E-mTq2 expressed in ID181 during early-log phase assay.
- **Supplementary Video 8.** The localisation of CetZ1.G108S-mTq2 expressed in ID181 during early-log phase assay.
- **Supplementary Video 9.** The localisation of CetZ1.C-terminal tail mutant-mTq2 expressed in ID181 during early-log phase assay.
- **Supplementary Video 10.** 3D-SIM images showing localisation of CetZ1-mTq2 expressed in ID181 during early-log phase assay.
- **Supplementary Video 11.** Z-stack of a 3D-SIM images showing localisation of CetZ1.G108G-mTq2 expressed in ID181 during early-phase assay.

LIST OF TABLES

Table 2.1 General Bacterial Strains Used in the Present Work	50
Table 2.2 General Archaea Strains Used in the Present Work	50
Table 2.3 General Plasmids Used in This Work	51
Table 2.4 Commonly Used Bacterial Growth Media.....	51
Table 2.5 Commonly Used Archaea Growth Media.....	52
Table 2.6 Commonly Used Chemicals in the Present Work.....	53
Table 2.7 Buffers and General Solutions Used in This Work.....	54
Table 2.8 Ingredients of SDS-PAGE Gels	62
Table 4.1 Primers Used for Amplification of Flanking Regions of <i>cetZ1</i> Deletions....	128
Table 4.2 Primers Used in Diagnostic PCR of <i>cetZ1</i> Deletion Strains.....	129
Table 4.3 Sequences of the Three Types of Linkers Used in This Study	130
Table 4.4 Primer Sequences Used for GFP Amplification and the Plasmid Sequence Confirmations.....	131
Table 5.1 Rod Formation of ID181 by CetZ1 with Point Mutations During Early-log Phase Assay.....	145
Table 5.2 Primers used to amplify the CetZ1 point mutations	159
Table 6.1 Protein Concentration Gradient used in Malachite Green Phosphate Assay	192

ABBREVIATIONS

AMP	Ampicillin
Å	Angstrom
BSA	Bovine Serum Albumin
BLAST	Basic local alignment search tool
DNA	deoxyribonucleic acid
g	Gram
GFP	Green fluorescent protein
GTP	Guanosine triphosphate
GDP	Guanosine diphosphate
h	Hour(s)
kb	Kilo base pair(s)
kDa	Kilodalton(s)
min	Minute(s)
ml	Millilitre(s)
MQW	Milli-Q water
OD	Optical Density
PBS	Phosphate Buffered Saline
PCR	Polymerase Chain Reaction
psi	Pounds per square inch
mRNA	Messenger Ribonucleic acid
M	Molar concentration
Mm	Millimolar concentration

MWCO	Molecular weight cut-off
n	nano
NCBI	National Centre for Biotechnology Information
RT	Room Temperature
rpm	Revolutions per minute
r.m.s.d	Root-mean-square deviation
SDS-PAGE	Sodium dodecyl sulfate polyacrylamide gel electrophoresis
sec	sec
TBS	Tris Buffered Saline
TEMED	N,N,N',N'-tetramethylethylenediamine
Tris	Tris(hydroxymethyl)methylamine
w	Weight
WT	Wild Type
v	Volume
μ	Micro

PUBLICATIONS AND CONFERENCE PROCEEDINGS

Journal Publications:

- **de Silva, R.T**, Halim, M. F., Pohlschroder, M., Duggin, I. G., ‘Cell shape differentiation in *Haloferax volcanii*’ Applied Environmental Biology (manuscript to be submitted).
- Liao, Y., Ithurbide, S., **de Silva, R. T**, Erdmann, S., Duggin, I. G. et al. (2018) ‘Archaeal cell biology: diverse functions of tubulin-like cytoskeletal proteins at the cell envelope’, Emerging Topics in Life Sciences. doi: 10.1042/etls20180026.

Conference Proceedings:

- **de Silva R.T**, Ithurbide S.I., Duggin I.G. (2019) “CetZ1 in cell shape control of haloarchaea: Understanding the functional divergence of tubulin superfamily protein” at Motile and Contractile Systems Gordon Research Conference, USA (**oral and poster presentation**).
- **de Silva R.T**, Ithurbide S.I., Duggin I.G. (2019) “CetZ1 in cell shape control of haloarchaea: Understanding the functional divergence of tubulin superfamily protein” at ASMMicrobe19, American Society of Microbiology, USA (**late breaker poster presentation**).
- **de Silva R.T**, Ithurbide S.I., Duggin I.G. (2018) “Metal starvation triggers CetZ1-dependent cell shape changes in haloarchaea” at Combio 2018, Sydney, Australia (**oral presentation**).
- **de Silva R.T**, Ithurbide S.I., Duggin I.G. (2018) “Metal starvation triggers CetZ1-dependent cell shape changes *Haloferax volcanii*” at Molecular biology of archaea: From mechanisms to ecology (MBoA6), EMBO Workshop, Vienna, Austria (**poster presentation**).

ACKNOWLEDGEMENT

I would like to convey my sincere thanks to all those who encouraged me and supported me in completing my research timely. First and foremost, I am deeply grateful to my supervisor A/Prof. Iain Duggin for all the opportunities, guidance, and support in my progression through the PhD. I deeply enjoyed all the insightful discussions. You have been an excellent mentor.

My warmest thanks to all my lab mates for making a wonderful vibe to work. I am grateful to Yan Liao, Greg Iosifidis, Taylor Corocher and Carly Italiano for proofreading my thesis. Also, I really enjoyed collaborating with Solenne Ithurbide to make the archaeal world colourful with a new set of fluorescent plasmids. The support received from my labmates, Tamika Blair, Dora Pittrich and Vinaya Shinde are much appreciated.

I would like to extend my thanks to UTS Microbial Imaging Facility. The MIF director A/Prof. Louise Cole and Dr Michael Johnson, for giving me excellent training and Dr Christian Evenhuis for his invaluable help in data analysis.

I am also grateful to itthree Director, Prof. Liz Harry, for her invaluable guidance which helped me to shape my research career, Dr Chris Rodrigues for giving me insightful advice to improve my research and to all my friends at the itthree institute. I must thank Shima Vahdat, Meggie Leung and Shannon Hawkins for making sure that all administrative works are completed timely. My appreciation also extends to Prof. Mecky Pohlschröder from the University of Pennsylvania for collaborating with our research.

I am grateful to all my thesis reviewers for spending their time reviewing my thesis. My warm thanks are due to Ransalu for his indispensable support. Thank you for your patience and encouragement. Last, but not least, I am also greatly indebted to my parents and friends for their affection.

K.W.T. Roshali Thavindra de Silva, itthree Institute, The University of Technology Sydney, 02 September 2019.

ABSTRACT

Cell shape dynamics are important for cell survival. Eukaryotic cytoskeletal protein tubulin plays essential roles in internal structure organisation and cell shape. However, the prokaryotic tubulin homologue, FtsZ, controls the assembly and function of the division ring. The origin of this functional disparity is still unclear. A third group of the tubulin superfamily, CetZ, has been recently identified in archaea and shows characteristics in common with both the tubulin and FtsZ. A conserved member, CetZ1, is required for cell shape changes (from plate to rod) during the development of motile cells in the archaeon, *Haloferax volcanii* (Duggin *et al.*, 2015).

The present study has defined additional culture conditions—metal nutrients depletion and early-log growth—that result in rod development, which has opened new ways of understanding cellular differentiation in archaea. A new Δ *cetZ1* strain, which can be complemented by resupply of CetZ1 on a plasmid, was also constructed. Using these culture conditions and Δ *cetZ1*, a functional CetZ1-mTurquoise2 fusion was identified after screening numerous fluorescent proteins and linker-peptide combinations. It displayed a patchy and dynamic localisation in discoid cells, then, during rod formation, displayed short dynamic filaments along the edges of the cell's long axis. During cell division, CetZ1 localises at the envelope around the division furrow; this differed significantly from FtsZ localisation pattern.

By using the CetZ1 and CetZ2 crystal structures as a guide, mutants were constructed to probe the functions and interactions of CetZ1 in *H. volcanii*. Mutation in the predicted CetZ1 membrane-interaction and self-association domains prevented rod development. The former displayed filament-like localisation detached from the cell edges, whereas the latter did not localise *in vivo*, consistent with the predictions. The GTPase mutants of CetZ1 prevented rod development but caused more intense and less dynamic localisation suggesting regulation of characteristic GTP-dependent dynamics is critical to CetZ1 function. CetZ1 *in vitro* studies revealed GTP-dependent polymerisation and these polymers were destabilised in predicted self-association mutant. Moreover, a mutation in the C-terminal tail displayed a decreased membrane localization.

These structure-function studies suggest CetZ1 forms polymers that has its longitudinal interactions controlled via the GTPase activity and the lateral interactions mediated by a

region similar to tubulin 'M-loop'. The dynamic localisation of CetZ1 to the cell edges via the C-terminal tail region is essential to modulate the cell shape. Finally, these discoveries support the notion that cell shape control by tubulin superfamily proteins could have predated the emergence of eukaryotic tubulins.