

Jan Lwe

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

135
papers

13,078
citations

61
h-index

114
g-index

153
ext. papers

15,043
ext. citations

13.6
avg, IF

6.51
L-index

| # | Paper | IF | Citations |
|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 135 | Clamping of DNA shuts the condensin neck gate.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2120006119 | 11.5 | 2 |
| 134 | Cryo-EM structure of MukBEF reveals DNA loop entrapment at chromosomal unloading sites. <i>Molecular Cell</i> , 2021 , 81, 4891-4906.e8 | 17.6 | 9 |
| 133 | High-resolution mapping of metal ions reveals principles of surface layer assembly in <i>Caulobacter crescentus</i> cells. <i>Structure</i> , 2021 , | 5.2 | 2 |
| 132 | Cell division in the archaeon <i>Haloferax volcanii</i> relies on two FtsZ proteins with distinct functions in division ring assembly and constriction. <i>Nature Microbiology</i> , 2021 , 6, 594-605 | 26.6 | 7 |
| 131 | Bacterial and archaeal cytoskeletons. <i>Current Biology</i> , 2021 , 31, R542-R546 | 6.3 | |
| 130 | Structure of the SARS-CoV-2 RNA-dependent RNA polymerase in the presence of favipiravir-RTP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118, | 11.5 | 63 |
| 129 | Folding of cohesin's coiled coil is important for Scc2/4-induced association with chromosomes. <i>ELife</i> , 2021 , 10, | 8.9 | 4 |
| 128 | Single-dose immunisation with a multimerised SARS-CoV-2 receptor binding domain (RBD) induces an enhanced and protective response in mice. <i>FEBS Letters</i> , 2021 , 595, 2323-2340 | 3.8 | 10 |
| 127 | Cryo-EM structure of the full-length Lon protease from <i>Thermus thermophilus</i> . <i>FEBS Letters</i> , 2021 , 595, 2691-2700 | 3.8 | 3 |
| 126 | FtsK in motion reveals its mechanism for double-stranded DNA translocation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 14202-14208 | 11.5 | 11 |
| 125 | Transport of DNA within cohesin involves clamping on top of engaged heads by Scc2 and entrapment within the ring by Scc3. <i>ELife</i> , 2020 , 9, | 8.9 | 25 |
| 124 | Author response: Transport of DNA within cohesin involves clamping on top of engaged heads by Scc2 and entrapment within the ring by Scc3 2020 , | | 3 |
| 123 | The structure of human thyroglobulin. <i>Nature</i> , 2020 , 578, 627-630 | 50.4 | 36 |
| 122 | Cryo-EM structures of holo condensin reveal a subunit flip-flop mechanism. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 743-751 | 17.6 | 47 |
| 121 | Identifying proteins bound to native mitotic ESC chromosomes reveals chromatin repressors are important for compaction. <i>Nature Communications</i> , 2020 , 11, 4118 | 17.4 | 8 |
| 120 | The structure of bactofilin filaments reveals their mode of membrane binding and lack of polarity. <i>Nature Microbiology</i> , 2019 , 4, 2357-2368 | 26.6 | 11 |
| 119 | Cryo-EM structure of the MinCD copolymeric filament from <i>Pseudomonas aeruginosa</i> at 3.1 Å resolution. <i>FEBS Letters</i> , 2019 , 593, 1915-1926 | 3.8 | 2 |

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|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|----|
| 118 | A folded conformation of MukBEF and cohesin. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 227-236 | 16.6 | 75 |
| 117 | Automated Protocols for Macromolecular Crystallization at the MRC Laboratory of Molecular Biology. <i>Journal of Visualized Experiments</i> , 2018 , | 1.6 | 6 |
| 116 | Cryo-EM reconstruction of Alfa from reveals the structure of a simplified actin-like filament at 3.4-Å resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 3458-3463 | 11.5 | 8 |
| 115 | Prokaryotic cytoskeletons: protein filaments organizing small cells. <i>Nature Reviews Microbiology</i> , 2018 , 16, 187-201 | 22.2 | 69 |
| 114 | FzIA, an essential regulator of FtsZ filament curvature, controls constriction rate during Caulobacter division. <i>Molecular Microbiology</i> , 2018 , 107, 180-197 | 4.1 | 13 |
| 113 | Structural Analysis of the Interaction between the Bacterial Cell Division Proteins FtsQ and FtsB. <i>MBio</i> , 2018 , 9, | 7.8 | 17 |
| 112 | Scc2 Is a Potent Activator of Cohesin's ATPase that Promotes Loading by Binding Scc1 without Pds5. <i>Molecular Cell</i> , 2018 , 70, 1134-1148.e7 | 17.6 | 71 |
| 111 | MreB filaments align along greatest principal membrane curvature to orient cell wall synthesis. <i>ELife</i> , 2018 , 7, | 8.9 | 95 |
| 110 | Structure of the hexagonal surface layer on Caulobacter crescentus cells. <i>Nature Microbiology</i> , 2017 , 2, 17059 | 26.6 | 60 |
| 109 | Overview of the Diverse Roles of Bacterial and Archaeal Cytoskeletons. <i>Sub-Cellular Biochemistry</i> , 2017 , 84, 1-26 | 5.5 | 8 |
| 108 | A Polymerization-Associated Structural Switch in FtsZ That Enables Treadmilling of Model Filaments. <i>MBio</i> , 2017 , 8, | 7.8 | 61 |
| 107 | Four-stranded mini microtubules formed by BtubAB show dynamic instability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E5950-E5958 | 11.5 | 15 |
| 106 | SnapShot: The Bacterial Cytoskeleton. <i>Cell</i> , 2016 , 166, 522-522.e1 | 56.2 | 4 |
| 105 | X-ray and cryo-EM structures of monomeric and filamentous actin-like protein MamK reveal changes associated with polymerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 13396-13401 | 11.5 | 19 |
| 104 | Crystal Structure of the Cohesin Gatekeeper Pds5 and in Complex with Kleisin Scc1. <i>Cell Reports</i> , 2016 , 14, 2108-2115 | 10.6 | 35 |
| 103 | Crenactin forms actin-like double helical filaments regulated by arcadin-2. <i>ELife</i> , 2016 , 5, | 8.9 | 23 |
| 102 | Activation of Xer-recombination at dif: structural basis of the FtsKEXerD interaction. <i>Scientific Reports</i> , 2016 , 6, 33357 | 4.9 | 10 |
| 101 | Structural Insights into Ring Formation of Cohesin and Related Smc Complexes. <i>Trends in Cell Biology</i> , 2016 , 26, 680-693 | 18.3 | 58 |

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|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----|
| 100 | Structures of actin-like ParM filaments show architecture of plasmid-segregating spindles. <i>Nature</i> , 2015 , 523, 106-10 | 50.4 | 57 |
| 99 | Reconstitution of a prokaryotic minus end-tracking system using TubRC centromeric complexes and tubulin-like protein TubZ filaments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E1845-50 | 11.5 | 27 |
| 98 | Advances in Single-Particle Electron Cryomicroscopy Structure Determination applied to Sub-tomogram Averaging. <i>Structure</i> , 2015 , 23, 1743-1753 | 5.2 | 142 |
| 97 | CetZ tubulin-like proteins control archaeal cell shape. <i>Nature</i> , 2015 , 519, 362-5 | 50.4 | 83 |
| 96 | Collaborative protein filaments. <i>EMBO Journal</i> , 2015 , 34, 2312-20 | 13 | 24 |
| 95 | Crystal structure of the Z-ring associated cell division protein ZapC from Escherichia coli. <i>FEBS Letters</i> , 2015 , 589, 3822-8 | 3.8 | 12 |
| 94 | Closing the cohesin ring: structure and function of its Smc3-kleisin interface. <i>Science</i> , 2014 , 346, 963-7 | 33.3 | 188 |
| 93 | The subtle allostery of microtubule dynamics. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 505-6 | 17.6 | 5 |
| 92 | A cylindrical specimen holder for electron cryo-tomography. <i>Ultramicroscopy</i> , 2014 , 137, 20-9 | 3.1 | 26 |
| 91 | Crenactin from Pyrobaculum calidifontis is closely related to actin in structure and forms steep helical filaments. <i>FEBS Letters</i> , 2014 , 588, 776-82 | 3.8 | 22 |
| 90 | LeoA, B and C from enterotoxigenic Escherichia coli (ETEC) are bacterial dynamins. <i>PLoS ONE</i> , 2014 , 9, e107211 | 3.7 | 24 |
| 89 | Structure and function of cohesin's Scc3/SA regulatory subunit. <i>FEBS Letters</i> , 2014 , 588, 3692-702 | 3.8 | 51 |
| 88 | MinCD cell division proteins form alternating copolymeric cytomotive filaments. <i>Nature Communications</i> , 2014 , 5, 5341 | 17.4 | 51 |
| 87 | Bacterial actin MreB forms antiparallel double filaments. <i>ELife</i> , 2014 , 3, e02634 | 8.9 | 106 |
| 86 | Architecture of the ring formed by the tubulin homologue FtsZ in bacterial cell division. <i>ELife</i> , 2014 , 3, e04601 | 8.9 | 169 |
| 85 | Do the divisome and elongasome share a common evolutionary past?. <i>Current Opinion in Microbiology</i> , 2013 , 16, 745-51 | 7.9 | 62 |
| 84 | Structure of the ParM filament at 8.5Å resolution. <i>Journal of Structural Biology</i> , 2013 , 184, 33-42 | 3.4 | 15 |
| 83 | Structure of the tubulin/FtsZ-like protein TubZ from Pseudomonas bacteriophage β Z. <i>Journal of Molecular Biology</i> , 2013 , 425, 2164-73 | 6.5 | 22 |

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|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----|
| 82 | The N-terminal membrane-spanning domain of the Escherichia coli DNA translocase FtsK hexamerizes at midcell. <i>MBio</i> , 2013 , 4, e00800-13 | 7.8 | 28 |
| 81 | Structural and genetic analyses reveal the protein SepF as a new membrane anchor for the Z ring. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E4601-10 | 11.5 | 80 |
| 80 | A bipolar spindle of antiparallel ParM filaments drives bacterial plasmid segregation. <i>Science</i> , 2012 , 338, 1334-7 | 33.3 | 70 |
| 79 | Localized dimerization and nucleoid binding drive gradient formation by the bacterial cell division inhibitor MipZ. <i>Molecular Cell</i> , 2012 , 46, 245-59 | 17.6 | 75 |
| 78 | FtsA forms actin-like protofilaments. <i>EMBO Journal</i> , 2012 , 31, 2249-60 | 13 | 173 |
| 77 | Superstructure of the centromeric complex of TubZRC plasmid partitioning systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 16522-7 | 11.5 | 24 |
| 76 | New insights into the mechanisms of cytomotive actin and tubulin filaments. <i>International Review of Cell and Molecular Biology</i> , 2011 , 292, 1-71 | 6 | 48 |
| 75 | Direct membrane binding by bacterial actin MreB. <i>Molecular Cell</i> , 2011 , 43, 478-87 | 17.6 | 181 |
| 74 | A positively charged channel within the Smc1/Smc3 hinge required for sister chromatid cohesion. <i>EMBO Journal</i> , 2011 , 30, 364-78 | 13 | 58 |
| 73 | A ferritin-based label for cellular electron cryotomography. <i>Structure</i> , 2011 , 19, 147-54 | 5.2 | 70 |
| 72 | Das bakterielle Zytoskelett. <i>BioSpektrum</i> , 2011 , 17, 396-398 | 0.1 | |
| 71 | Bacterial actin MreB assembles in complex with cell shape protein RodZ. <i>EMBO Journal</i> , 2010 , 29, 1081-90 | 13 | 113 |
| 70 | Features critical for membrane binding revealed by DivIVA crystal structure. <i>EMBO Journal</i> , 2010 , 29, 1988-2001 | 13 | 86 |
| 69 | The ParMRC system: molecular mechanisms of plasmid segregation by actin-like filaments. <i>Nature Reviews Microbiology</i> , 2010 , 8, 683-92 | 22.2 | 94 |
| 68 | Filament structure of bacterial tubulin homologue TubZ. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 19766-71 | 11.5 | 61 |
| 67 | Crystal structures of Bacillus subtilis Lon protease. <i>Journal of Molecular Biology</i> , 2010 , 401, 653-70 | 6.5 | 55 |
| 66 | Dynamain architecture--from monomer to polymer. <i>Current Opinion in Structural Biology</i> , 2010 , 20, 791-8 | 8.1 | 34 |
| 65 | Electron cryomicroscopy of E. coli reveals filament bundles involved in plasmid DNA segregation. <i>Science</i> , 2009 , 323, 509-12 | 33.3 | 86 |

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|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----|
| 64 | Evolution of cytomotive filaments: the cytoskeleton from prokaryotes to eukaryotes. <i>International Journal of Biochemistry and Cell Biology</i> , 2009 , 41, 323-9 | 5.6 | 103 |
| 63 | Structure of a bacterial dynamin-like protein lipid tube provides a mechanism for assembly and membrane curving. <i>Cell</i> , 2009 , 139, 1342-52 | 56.2 | 136 |
| 62 | Bacterial actin: architecture of the ParMRC plasmid DNA partitioning complex. <i>EMBO Journal</i> , 2008 , 27, 2230-8 | 13 | 48 |
| 61 | Structural and mutational analysis of the cell division protein FtsQ. <i>Molecular Microbiology</i> , 2008 , 68, 110-23 | 4.1 | 49 |
| 60 | Novel coiled-coil cell division factor ZapB stimulates Z ring assembly and cell division. <i>Molecular Microbiology</i> , 2008 , 68, 720-35 | 4.1 | 96 |
| 59 | Molecular mechanism of sequence-directed DNA loading and translocation by FtsK. <i>Molecular Cell</i> , 2008 , 31, 498-509 | 17.6 | 88 |
| 58 | Probing FtsZ and tubulin with C8-substituted GTP analogs reveals differences in their nucleotide binding sites. <i>Chemistry and Biology</i> , 2008 , 15, 189-99 | | 62 |
| 57 | Structural analysis of the ParR/parC plasmid partition complex. <i>EMBO Journal</i> , 2007 , 26, 4413-22 | 13 | 60 |
| 56 | Centromere pairing by a plasmid-encoded type I ParB protein. <i>Journal of Biological Chemistry</i> , 2007 , 282, 28216-25 | 5.4 | 22 |
| 55 | Structural insights into the conformational variability of FtsZ. <i>Journal of Molecular Biology</i> , 2007 , 373, 1229-42 | 6.5 | 135 |
| 54 | RF cloning: a restriction-free method for inserting target genes into plasmids. <i>Journal of Proteomics</i> , 2006 , 67, 67-74 | | 402 |
| 53 | Dynamic filaments of the bacterial cytoskeleton. <i>Annual Review of Biochemistry</i> , 2006 , 75, 467-92 | 29.1 | 169 |
| 52 | Double-stranded DNA translocation: structure and mechanism of hexameric FtsK. <i>Molecular Cell</i> , 2006 , 23, 457-69 | 17.6 | 185 |
| 51 | Dimeric structure of the cell shape protein MreC and its functional implications. <i>Molecular Microbiology</i> , 2006 , 62, 1631-42 | 4.1 | 79 |
| 50 | The FtsK gamma domain directs oriented DNA translocation by interacting with KOPS. <i>Nature Structural and Molecular Biology</i> , 2006 , 13, 965-72 | 17.6 | 83 |
| 49 | A bacterial dynamin-like protein. <i>Nature</i> , 2006 , 444, 766-9 | 50.4 | 182 |
| 48 | Crystal structure of the ubiquitin-like protein YukD from <i>Bacillus subtilis</i> . <i>FEBS Letters</i> , 2005 , 579, 3837-418 | | 19 |
| 47 | Bacterial chromosome segregation: structure and DNA binding of the Soj dimer--a conserved biological switch. <i>EMBO Journal</i> , 2005 , 24, 270-82 | 13 | 233 |

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|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----|
| 46 | Increasing complexity of the bacterial cytoskeleton. <i>Current Opinion in Cell Biology</i> , 2005 , 17, 75-81 | 9 | 80 |
| 45 | Robotic nanolitre protein crystallisation at the MRC Laboratory of Molecular Biology. <i>Progress in Biophysics and Molecular Biology</i> , 2005 , 88, 311-27 | 4.7 | 73 |
| 44 | Towards understanding the molecular basis of bacterial DNA segregation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005 , 360, 523-35 | 5.8 | 64 |
| 43 | Structure of bacterial tubulin BtubA/B: evidence for horizontal gene transfer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 9170-5 | 11.5 | 124 |
| 42 | Murein (peptidoglycan) binding property of the essential cell division protein FtsN from <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2004 , 186, 6728-37 | 3.5 | 92 |
| 41 | The structure of the AXH domain of spinocerebellar ataxin-1. <i>Journal of Biological Chemistry</i> , 2004 , 279, 3758-65 | 5.4 | 47 |
| 40 | Solution structure and domain architecture of the divisome protein FtsN. <i>Molecular Microbiology</i> , 2004 , 52, 651-60 | 4.1 | 60 |
| 39 | Structural analysis of the chromosome segregation protein Spo0J from <i>Thermus thermophilus</i> . <i>Molecular Microbiology</i> , 2004 , 53, 419-32 | 4.1 | 84 |
| 38 | Structural insights into FtsZ protofilament formation. <i>Nature Structural and Molecular Biology</i> , 2004 , 11, 1243-50 | 17.6 | 228 |
| 37 | Structural/functional homology between the bacterial and eukaryotic cytoskeletons. <i>Current Opinion in Cell Biology</i> , 2004 , 16, 24-31 | 9 | 68 |
| 36 | Molecules of the bacterial cytoskeleton. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2004 , 33, 177-98 | | 116 |
| 35 | Structure and stability of cohesin's Smc1-kleisin interaction. <i>Molecular Cell</i> , 2004 , 15, 951-64 | 17.6 | 246 |
| 34 | The crystal structure of ZapA and its modulation of FtsZ polymerisation. <i>Journal of Molecular Biology</i> , 2004 , 341, 839-52 | 6.5 | 105 |
| 33 | Structure of the Jab1/MPN domain and its implications for proteasome function. <i>Biochemistry</i> , 2003 , 42, 11460-5 | 3.2 | 100 |
| 32 | Crystal structure of the SOS cell division inhibitor Sula and in complex with FtsZ. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 7889-94 | 11.5 | 187 |
| 31 | The crystal structure of AF1521 a protein from <i>Archaeoglobus fulgidus</i> with homology to the non-histone domain of macroH2A. <i>Journal of Molecular Biology</i> , 2003 , 330, 503-11 | 6.5 | 97 |
| 30 | Prokaryotic DNA segregation by an actin-like filament. <i>EMBO Journal</i> , 2002 , 21, 3119-27 | 13 | 208 |
| 29 | F-actin-like filaments formed by plasmid segregation protein ParM. <i>EMBO Journal</i> , 2002 , 21, 6935-43 | 13 | 208 |

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|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|------|
| 28 | Molecular architecture of SMC proteins and the yeast cohesin complex. <i>Molecular Cell</i> , 2002 , 9, 773-88 | 17.6 | 565 |
| 27 | Distribution of the Escherichia coli structural maintenance of chromosomes (SMC)-like protein MukB in the cell. <i>Molecular Microbiology</i> , 2001 , 42, 1179-88 | 4.1 | 28 |
| 26 | Prokaryotic origin of the actin cytoskeleton. <i>Nature</i> , 2001 , 413, 39-44 | 50.4 | 646 |
| 25 | Crystal structure of the SMC head domain: an ABC ATPase with 900 residues antiparallel coiled-coil inserted. <i>Journal of Molecular Biology</i> , 2001 , 306, 25-35 | 6.5 | 132 |
| 24 | Conserved sequence motif at the C-terminus of the bacterial cell-division protein FtsA. <i>Biochimie</i> , 2001 , 83, 117-20 | 4.6 | 14 |
| 23 | Crystal structure of the bacterial cell division regulator MinD. <i>FEBS Letters</i> , 2001 , 492, 160-5 | 3.8 | 68 |
| 22 | Helical tubes of FtsZ from Methanococcus jannaschii. <i>Biological Chemistry</i> , 2000 , 381, 993-9 | 4.5 | 38 |
| 21 | 3D electron microscopy of the interaction of kinesin with tubulin. <i>Cell Structure and Function</i> , 1999 , 24, 277-84 | 2.2 | 10 |
| 20 | How Taxol stabilises microtubule structure. <i>Chemistry and Biology</i> , 1999 , 6, R65-9 | | 189 |
| 19 | Tubulin-like protofilaments in Ca ²⁺ -induced FtsZ sheets. <i>EMBO Journal</i> , 1999 , 18, 2364-71 | 13 | 197 |
| 18 | Crystal structure of the N-terminal domain of MukB: a protein involved in chromosome partitioning. <i>Structure</i> , 1999 , 7, 1181-7 | 5.2 | 48 |
| 17 | Crystal structure of the bacterial cell-division protein FtsZ. <i>Nature</i> , 1998 , 391, 203-6 | 50.4 | 730 |
| 16 | Crystal structure of the thermosome, the archaeal chaperonin and homolog of CCT. <i>Cell</i> , 1998 , 93, 125-38 | 36.2 | 375 |
| 15 | Crystal structure determination of FtsZ from Methanococcus jannaschii. <i>Journal of Structural Biology</i> , 1998 , 124, 235-43 | 3.4 | 41 |
| 14 | Structural investigation of proteasome inhibition. <i>Biological Chemistry</i> , 1997 , 378, 239-47 | 4.5 | 15 |
| 13 | Structure of 20S proteasome from yeast at 2.4 Å resolution. <i>Nature</i> , 1997 , 386, 463-71 | 50.4 | 1996 |
| 12 | Crystal structure of dimethyl sulfoxide reductase from Rhodobacter capsulatus at 1.88 Å resolution. <i>Journal of Molecular Biology</i> , 1996 , 263, 53-69 | 6.5 | 248 |
| 11 | Proteasome: from structure to function. <i>Current Opinion in Biotechnology</i> , 1996 , 7, 376-85 | 11.4 | 25 |

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|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|----|
| 10 | Preliminary X-ray crystallographic study of the proteasome from <i>Thermoplasma acidophilum</i> . <i>Journal of Molecular Biology</i> , 1993 , 234, 881-4 | 6.5 | 21 |
| 9 | The bacterial actin-like cell division protein FtsA forms curved antiparallel double filaments upon binding of FtsN | | 2 |
| 8 | A folded conformation of MukBEF and Cohesin | | 2 |
| 7 | A polymerisation-associated conformational switch in FtsZ that enables treadmilling | | 1 |
| 6 | MreB Filaments Create Rod Shape By Aligning Along Principal Membrane Curvature | | 2 |
| 5 | Two FtsZ proteins orchestrate archaeal cell division through distinct functions in ring assembly and constriction | | 10 |
| 4 | Multiple interactions between Scc1 and Scc2 activate cohesin's DNA dependent ATPase and replace Pds5 during loading | | 6 |
| 3 | Cryo-EM reconstruction of AlfA from <i>Bacillus subtilis</i> reveals the structure of a simplified actin-like filament at 3.4 Å resolution | | 1 |
| 2 | Single-dose immunisation with a multimerised SARS-CoV-2 receptor binding domain (RBD) induces an enhanced and protective response in mice | | 2 |
| 1 | Cryo-EM structure of MukBEF reveals DNA loop entrapment at chromosomal unloading sites | | 4 |