

# Jan LÄJwe

## List of Publications by Year in descending order

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Version: 2024-02-01

125  
papers

16,147  
citations

18887

64  
h-index

20625

120  
g-index

153  
all docs

153  
docs citations

153  
times ranked

12788  
citing authors

#	ARTICLE	IF	CITATIONS
1	High-resolution mapping of metal ions reveals principles of surface layer assembly in <i>Caulobacter crescentus</i> cells. <i>Structure</i> , 2022, 30, 215-228.e5.	1.6	12
2	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.	3.3	22
3	Asgard archaea shed light on the evolutionary origins of the eukaryotic ubiquitin-ESCRT machinery. <i>Nature Communications</i> , 2022, 13, .	5.8	27
4	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, .	3.3	144
5	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.	5.9	49
6	Bacterial and archaeal cytoskeletons. <i>Current Biology</i> , 2021, 31, R542-R546.	1.8	1
7	Folding of cohesin's coiled coil is important for Scc2/4-induced association with chromosomes. <i>ELife</i> , 2021, 10, .	2.8	37
8	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.	1.3	24
9	Cryo-EM structure of the full-length Lon protease from <i>Thermus thermophilus</i> . <i>FEBS Letters</i> , 2021, 595, 2691-2700.	1.3	9
10	Cryo-EM structure of MukBEF reveals DNA loop entrapment at chromosomal unloading sites. <i>Molecular Cell</i> , 2021, 81, 4891-4906.e8.	4.5	49
11	Cryo-EM structures of holo condensin reveal a subunit flip-flop mechanism. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 743-751.	3.6	90
12	Identifying proteins bound to native mitotic ESC chromosomes reveals chromatin repressors are important for compaction. <i>Nature Communications</i> , 2020, 11, 4118.	5.8	26
13	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.	3.3	35
14	The structure of human thyroglobulin. <i>Nature</i> , 2020, 578, 627-630.	13.7	81
15	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, .	2.8	67
16	The structure of bactofilin filaments reveals their mode of membrane binding and lack of polarity. <i>Nature Microbiology</i> , 2019, 4, 2357-2368.	5.9	30
17	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.	1.3	6
18	A folded conformation of MukBEF and cohesin. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 227-236.	3.6	121

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19	Automated Protocols for Macromolecular Crystallization at the MRC Laboratory of Molecular Biology. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	11
20	Cryo-EM reconstruction of AlfA from <i>Bacillus subtilis</i> 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.	3.3	11
21	Prokaryotic cytoskeletons: protein filaments organizing small cells. <i>Nature Reviews Microbiology</i> , 2018, 16, 187-201.	13.6	104
22	FzIA, an essential regulator of FtsZ filament curvature, controls constriction rate during <i>Caulobacter</i> division. <i>Molecular Microbiology</i> , 2018, 107, 180-197.	1.2	22
23	Structural Analysis of the Interaction between the Bacterial Cell Division Proteins FtsQ and FtsB. <i>MBio</i> , 2018, 9, .	1.8	40
24	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.	4.5	141
25	MreB filaments align along greatest principal membrane curvature to orient cell wall synthesis. <i>ELife</i> , 2018, 7, .	2.8	179
26	Structure of the hexagonal surface layer on <i>Caulobacter crescentus</i> cells. <i>Nature Microbiology</i> , 2017, 2, 17059.	5.9	85
27	Overview of the Diverse Roles of Bacterial and Archaeal Cytoskeletons. <i>Sub-Cellular Biochemistry</i> , 2017, 84, 1-26.	1.0	11
28	A Polymerization-Associated Structural Switch in FtsZ That Enables Treadmilling of Model Filaments. <i>MBio</i> , 2017, 8, .	1.8	91
29	Four-stranded mini microtubules formed by <i>Prostheco bacter</i> BtubAB show dynamic instability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5950-E5958.	3.3	26
30	Activation of Xer-recombination at dif: structural basis of the FtsK's XerD interaction. <i>Scientific Reports</i> , 2016, 6, 33357.	1.6	17
31	Structural Insights into Ring Formation of Cohesin and Related Smc Complexes. <i>Trends in Cell Biology</i> , 2016, 26, 680-693.	3.6	77
32	SnapShot: The Bacterial Cytoskeleton. <i>Cell</i> , 2016, 166, 522-522.e1.	13.5	6
33	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.	3.3	24
34	Crystal Structure of the Cohesin Gatekeeper Pds5 and in Complex with Kleisin Scc1. <i>Cell Reports</i> , 2016, 14, 2108-2115.	2.9	52
35	Crenactin forms actin-like double helical filaments regulated by arcadin-2. <i>ELife</i> , 2016, 5, .	2.8	39
36	Collaborative protein filaments. <i>EMBO Journal</i> , 2015, 34, 2312-2320.	3.5	30

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37	Crystal structure of the Z-ring associated cell division protein ZapC from <i>Escherichia coli</i> . FEBS Letters, 2015, 589, 3822-3828.	1.3	13
38	Structures of actin-like ParM filaments show architecture of plasmid-segregating spindles. Nature, 2015, 523, 106-110.	13.7	73
39	Reconstitution of a prokaryotic minus end-tracking system using TubRC centromeric complexes and tubulin-like protein TubZ filaments. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1845-50.	3.3	34
40	Advances in Single-Particle Electron Cryomicroscopy Structure Determination applied to Sub-tomogram Averaging. Structure, 2015, 23, 1743-1753.	1.6	189
41	CetZ tubulin-like proteins control archaeal cell shape. Nature, 2015, 519, 362-365.	13.7	138
42	LeoA, B and C from Enterotoxigenic <i>Escherichia coli</i> (ETEC) Are Bacterial Dynamins. PLoS ONE, 2014, 9, e107211.	1.1	42
43	Structure and function of cohesin's Scc3/SA regulatory subunit. FEBS Letters, 2014, 588, 3692-3702.	1.3	73
44	MinCD cell division proteins form alternating copolymeric cytomotive filaments. Nature Communications, 2014, 5, 5341.	5.8	64
45	Closing the cohesin ring: Structure and function of its Smc3-kleisin interface. Science, 2014, 346, 963-967.	6.0	255
46	The subtle allostery of microtubule dynamics. Nature Structural and Molecular Biology, 2014, 21, 505-506.	3.6	7
47	A cylindrical specimen holder for electron cryo-tomography. Ultramicroscopy, 2014, 137, 20-29.	0.8	31
48	Crenactin from <i>Pyrobaculum calidifontis</i> is closely related to actin in structure and forms steep helical filaments. FEBS Letters, 2014, 588, 776-782.	1.3	25
49	Bacterial actin MreB forms antiparallel double filaments. ELife, 2014, 3, e02634.	2.8	153
50	Architecture of the ring formed by the tubulin homologue FtsZ in bacterial cell division. ELife, 2014, 3, e04601.	2.8	218
51	Do the divisome and elongasome share a common evolutionary past?. Current Opinion in Microbiology, 2013, 16, 745-751.	2.3	91
52	Structure of the ParM filament at 8.5Å... resolution. Journal of Structural Biology, 2013, 184, 33-42.	1.3	20
53	Structure of the Tubulin/FtsZ-Like Protein TubZ from <i>Pseudomonas</i> Bacteriophage $\hat{\Gamma}$ KZ. Journal of Molecular Biology, 2013, 425, 2164-2173.	2.0	31
54	The N-Terminal Membrane-Spanning Domain of the <i>Escherichia coli</i> DNA Translocase FtsK Hexamerizes at Midcell. MBio, 2013, 4, e00800-13.	1.8	36

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55	Structural and genetic analyses reveal the protein SepF as a new membrane anchor for the Z ring. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4601-10.	3.3	116
56	FtsA forms actin-like protofilaments. EMBO Journal, 2012, 31, 2249-2260.	3.5	208
57	Superstructure of the centromeric complex of TubZR <i>C</i> plasmid partitioning systems. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16522-16527.	3.3	35
58	A Bipolar Spindle of Antiparallel ParM Filaments Drives Bacterial Plasmid Segregation. Science, 2012, 338, 1334-1337.	6.0	85
59	Localized Dimerization and Nucleoid Binding Drive Gradient Formation by the Bacterial Cell Division Inhibitor MipZ. Molecular Cell, 2012, 46, 245-259.	4.5	105
60	New Insights into the Mechanisms of Cytomotive Actin and Tubulin Filaments. International Review of Cell and Molecular Biology, 2011, 292, 1-71.	1.6	56
61	Direct Membrane Binding by Bacterial Actin MreB. Molecular Cell, 2011, 43, 478-487.	4.5	241
62	A positively charged channel within the Smc1/Smc3 hinge required for sister chromatid cohesion. EMBO Journal, 2011, 30, 364-378.	3.5	69
63	A Ferritin-Based Label for Cellular Electron Cryotomography. Structure, 2011, 19, 147-154.	1.6	92
64	Dynammin architecture from monomer to polymer. Current Opinion in Structural Biology, 2010, 20, 791-798.	2.6	41
65	Bacterial actin MreB assembles in complex with cell shape protein RodZ. EMBO Journal, 2010, 29, 1081-1090.	3.5	144
66	Features critical for membrane binding revealed by DivIVA crystal structure. EMBO Journal, 2010, 29, 1988-2001.	3.5	116
67	The ParMRC system: molecular mechanisms of plasmid segregation by actin-like filaments. Nature Reviews Microbiology, 2010, 8, 683-692.	13.6	115
68	Filament structure of bacterial tubulin homologue TubZ. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19766-19771.	3.3	71
69	Crystal Structures of Bacillus subtilis Lon Protease. Journal of Molecular Biology, 2010, 401, 653-670.	2.0	68
70	Electron Cryomicroscopy of <i>E. coli</i> Reveals Filament Bundles Involved in Plasmid DNA Segregation. Science, 2009, 323, 509-512.	6.0	93
71	Evolution of cytomotive filaments: The cytoskeleton from prokaryotes to eukaryotes. International Journal of Biochemistry and Cell Biology, 2009, 41, 323-329.	1.2	120
72	Structure of a Bacterial Dynammin-like Protein Lipid Tube Provides a Mechanism For Assembly and Membrane Curving. Cell, 2009, 139, 1342-1352.	13.5	163

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73	Probing FtsZ and Tubulin with C8-Substituted GTP Analogs Reveals Differences in Their Nucleotide Binding Sites. <i>Chemistry and Biology</i> , 2008, 15, 189-199.	6.2	74
74	Bacterial actin: architecture of the ParMRC plasmid DNA partitioning complex. <i>EMBO Journal</i> , 2008, 27, 2230-2238.	3.5	55
75	Structural and mutational analysis of the cell division protein FtsQ. <i>Molecular Microbiology</i> , 2008, 68, 110-123.	1.2	62
76	Novel coiled-coil cell division factor ZapB stimulates Z ring assembly and cell division. <i>Molecular Microbiology</i> , 2008, 68, 720-735.	1.2	113
77	Molecular Mechanism of Sequence-Directed DNA Loading and Translocation by FtsK. <i>Molecular Cell</i> , 2008, 31, 498-509.	4.5	97
78	Centromere Pairing by a Plasmid-encoded Type I ParB Protein. <i>Journal of Biological Chemistry</i> , 2007, 282, 28216-28225.	1.6	22
79	Structural Insights into the Conformational Variability of FtsZ. <i>Journal of Molecular Biology</i> , 2007, 373, 1229-1242.	2.0	156
80	Structural analysis of the ParR/parC plasmid partition complex. <i>EMBO Journal</i> , 2007, 26, 4413-4422.	3.5	71
81	Dynamic Filaments of the Bacterial Cytoskeleton. <i>Annual Review of Biochemistry</i> , 2006, 75, 467-492.	5.0	187
82	Double-Stranded DNA Translocation: Structure and Mechanism of Hexameric FtsK. <i>Molecular Cell</i> , 2006, 23, 457-469.	4.5	217
83	Dimeric structure of the cell shape protein MreC and its functional implications. <i>Molecular Microbiology</i> , 2006, 62, 1631-1642.	1.2	86
84	The FtsK $\hat{I}^3$ domain directs oriented DNA translocation by interacting with KOPS. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 965-972.	3.6	92
85	A bacterial dynamin-like protein. <i>Nature</i> , 2006, 444, 766-769.	13.7	203
86	RF cloning: A restriction-free method for inserting target genes into plasmids. <i>Journal of Proteomics</i> , 2006, 67, 67-74.	2.4	527
87	Bacterial chromosome segregation: structure and DNA binding of the Soj dimer ? a conserved biological switch. <i>EMBO Journal</i> , 2005, 24, 270-282.	3.5	286
88	Increasing complexity of the bacterial cytoskeleton. <i>Current Opinion in Cell Biology</i> , 2005, 17, 75-81.	2.6	89
89	Robotic nanolitre protein crystallisation at the MRC Laboratory of Molecular Biology. <i>Progress in Biophysics and Molecular Biology</i> , 2005, 88, 311-327.	1.4	86
90	Towards understanding the molecular basis of bacterial DNA segregation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005, 360, 523-535.	1.8	66

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91	Structure of bacterial tubulin BtubA/B: Evidence for horizontal gene transfer. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9170-9175.	3.3	141
92	Crystal structure of the ubiquitin-like protein YukD from Bacillus subtilis. FEBS Letters, 2005, 579, 3837-3841.	1.3	23
93	Murein (Peptidoglycan) Binding Property of the Essential Cell Division Protein FtsN from Escherichia coli. Journal of Bacteriology, 2004, 186, 6728-6737.	1.0	117
94	The Structure of the AXH Domain of Spinocerebellar Ataxin-1. Journal of Biological Chemistry, 2004, 279, 3758-3765.	1.6	55
95	Solution structure and domain architecture of the divisome protein FtsN. Molecular Microbiology, 2004, 52, 651-660.	1.2	72
96	Structural analysis of the chromosome segregation protein Spo0J from Thermus thermophilus. Molecular Microbiology, 2004, 53, 419-432.	1.2	100
97	Structural insights into FtsZ protofilament formation. Nature Structural and Molecular Biology, 2004, 11, 1243-1250.	3.6	265
98	Structural/functional homology between the bacterial and eukaryotic cytoskeletons. Current Opinion in Cell Biology, 2004, 16, 24-31.	2.6	74
99	Molecules of the Bacterial Cytoskeleton. Annual Review of Biophysics and Biomolecular Structure, 2004, 33, 177-198.	18.3	123
100	Structure and Stability of Cohesin's Smc1-Kleisin Interaction. Molecular Cell, 2004, 15, 951-964.	4.5	289
101	The Crystal Structure of ZapA and its Modulation of FtsZ Polymerisation. Journal of Molecular Biology, 2004, 341, 839-852.	2.0	118
102	Structure of the Jab1/MPN Domain and Its Implications for Proteasome Function. Biochemistry, 2003, 42, 11460-11465.	1.2	115
103	Crystal structure of the SOS cell division inhibitor Sula and in complex with FtsZ. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7889-7894.	3.3	221
104	The Crystal Structure of AF1521 a Protein from Archaeoglobus fulgidus with Homology to the Non-histone Domain of MacroH2A. Journal of Molecular Biology, 2003, 330, 503-511.	2.0	113
105	Molecular Architecture of SMC Proteins and the Yeast Cohesin Complex. Molecular Cell, 2002, 9, 773-788.	4.5	649
106	Distribution of the Escherichia coli structural maintenance of chromosomes (SMC)-like protein MukB in the cell. Molecular Microbiology, 2002, 42, 1179-1188.	1.2	34
107	Prokaryotic DNA segregation by an actin-like filament. EMBO Journal, 2002, 21, 3119-3127.	3.5	235
108	F-actin-like filaments formed by plasmid segregation protein ParM. EMBO Journal, 2002, 21, 6935-6943.	3.5	229

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109	Crystal structure of the SMC head domain: an ABC ATPase with 900 residues antiparallel coiled-coil inserted <sup>11</sup> Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 306, 25-35.	2.0	138
110	Conserved sequence motif at the C-terminus of the bacterial cell-division protein FtsA. <i>Biochimie</i> , 2001, 83, 117-120.	1.3	18
111	Crystal structure of the bacterial cell division regulator MinD. <i>FEBS Letters</i> , 2001, 492, 160-165.	1.3	73
112	Prokaryotic origin of the actin cytoskeleton. <i>Nature</i> , 2001, 413, 39-44.	13.7	759
113	Helical Tubes of FtsZ from <i>Methanococcus jannaschii</i> . <i>Biological Chemistry</i> , 2000, 381, 993-999.	1.2	40
114	3D Electron Microscopy of the Interaction of Kinesin with Tubulin. <i>Cell Structure and Function</i> , 1999, 24, 277-284.	0.5	12
115	How Taxol <sup>®</sup> stabilises microtubule structure. <i>Chemistry and Biology</i> , 1999, 6, R65-R69.	6.2	225
116	Tubulin-like protofilaments in Ca <sup>2+</sup> -induced FtsZ sheets. <i>EMBO Journal</i> , 1999, 18, 2364-2371.	3.5	206
117	Crystal structure of the N-terminal domain of MukB: a protein involved in chromosome partitioning. <i>Structure</i> , 1999, 7, 1181-1187.	1.6	49
118	Crystal structure of the bacterial cell-division protein FtsZ. <i>Nature</i> , 1998, 391, 203-206.	13.7	833
119	Crystal Structure of the Thermosome, the Archaeal Chaperonin and Homolog of CCT. <i>Cell</i> , 1998, 93, 125-138.	13.5	410
120	Crystal Structure Determination of FtsZ from <i>Methanococcus jannaschii</i> . <i>Journal of Structural Biology</i> , 1998, 124, 235-243.	1.3	43
121	Structural Investigation of Proteasome Inhibition. <i>Biological Chemistry</i> , 1997, 378, 239-47.	1.2	16
122	Structure of 20S proteasome from yeast at 2.4 Å... resolution. <i>Nature</i> , 1997, 386, 463-471.	13.7	2,214
123	Crystal Structure of Dimethyl Sulfoxide Reductase from <i>Rhodobacter capsulatus</i> at 1.88 Å... Resolution. <i>Journal of Molecular Biology</i> , 1996, 263, 53-69.	2.0	284
124	Proteasome: from structure to function. <i>Current Opinion in Biotechnology</i> , 1996, 7, 376-385.	3.3	26
125	Preliminary X-ray Crystallographic Study of the Proteasome from <i>Thermoplasma acidophilum</i> . <i>Journal of Molecular Biology</i> , 1993, 234, 881-884.	2.0	24