Jan LÃ¶we

List of Publications by Year
in descending order

125 papers	16,147 citations	16451 64 h-index	18130 120 g-index
153 all docs	153 docs citations	153 times ranked	11473 citing authors

#	Article	IF	Citations
1	Structure of 20S proteasome from yeast at 2.4Ã... resolution. Nature, 1997, 386, 463-471.	27.8	2,214
2	Crystal structure of the bacterial cell-division protein FtsZ. Nature, 1998, 391, 203-206.	27.8	833
3	Prokaryotic origin of the actin cytoskeleton. Nature, 2001, 413, 39-44.	27.8	759
4	Molecular Architecture of SMC Proteins and the Yeast Cohesin Complex. Molecular Cell, 2002, 9, 773-788.	9.7	649
5	RF cloning: A restriction-free method for inserting target genes into plasmids. Journal of Proteomics, 2006, 67, 67-74.	2.4	527
6	Crystal Structure of the Thermosome, the Archaeal Chaperonin and Homolog of CCT. Cell, 1998, 93, 125-138.	28.9	410
7	Structure and Stability of Cohesin's Smc1-Kleisin Interaction. Molecular Cell, 2004, 15, 951-964.	9.7	289
8	Bacterial chromosome segregation: structure and DNA binding of the Soj dimer ? a conserved biological switch. EMBO Journal, 2005, 24, 270-282.	7.8	286
9	Crystal Structure of Dimethyl Sulfoxide Reductase fromRhodobacter capsulatusat 1.88 Ã... Resolution. Journal of Molecular Biology, 1996, 263, 53-69.	4.2	284
10	Structural insights into FtsZ protofilament formation. Nature Structural and Molecular Biology, 2004, 11, 1243-1250.	8.2	265
11	Closing the cohesin ring: Structure and function of its Smc3-kleisin interface. Science, 2014, 346, 963-967.	12.6	255
12	Direct Membrane Binding by Bacterial Actin MreB. Molecular Cell, 2011, 43, 478-487.	9.7	241
13	Prokaryotic DNA segregation by an actin-like filament. EMBO Journal, 2002, 21, 3119-3127.	7.8	235
14	F-actin-like filaments formed by plasmid segregation protein ParM. EMBO Journal, 2002, 21, 6935-6943.	7.8	229
15	How TaxolÂ® stabilises microtubule structure. Chemistry and Biology, 1999, 6, R65-R69.	6.0	225
16	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.	7.1	221
17	Architecture of the ring formed by the tubulin homologue FtsZ in bacterial cell division. ELife, 2014, 3, e04601.	6.0	218
18	Double-Stranded DNA Translocation: Structure and Mechanism of Hexameric FtsK. Molecular Cell, 2006, 23, 457-469.	9.7	217

#	Article	IF	Citations
19	FtsA forms actin-like protofilaments. EMBO Journal, 2012, 31, 2249-2260.	7.8	208
20	Tubulin-like protofilaments in Ca2+-induced FtsZ sheets. EMBO Journal, 1999, 18, 2364-2371.	7.8	206
21	A bacterial dynamin-like protein. Nature, 2006, 444, 766-769.	27.8	203
22	Advances in Single-Particle Electron Cryomicroscopy Structure Determination applied to Sub-tomogram Averaging. Structure, 2015, 23, 1743-1753.	3.3	189
23	Dynamic Filaments of the Bacterial Cytoskeleton. Annual Review of Biochemistry, 2006, 75, 467-492.	11.1	187
24	MreB filaments align along greatest principal membrane curvature to orient cell wall synthesis. ELife, 2018, 7, .	6.0	179
25	Structure of a Bacterial Dynamin-like Protein Lipid Tube Provides a Mechanism For Assembly and Membrane Curving. Cell, 2009, 139, 1342-1352.	28.9	163
26	Structural Insights into the Conformational Variability of FtsZ. Journal of Molecular Biology, 2007, 373, 1229-1242.	4.2	156
27	Bacterial actin MreB forms antiparallel double filaments. ELife, 2014, 3, e02634.	6.0	153
28	Bacterial actin MreB assembles in complex with cell shape protein RodZ. EMBO Journal, 2010, 29, 1081-1090.	7.8	144
29	Structure of the SARS-CoV-2 RNA-dependent RNA polymerase in the presence of favipiravir-RTP. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	144
30	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.	7.1	141
31	Scc2 Is a Potent Activator of Cohesinâ€™s ATPase that Promotes Loading by Binding Scc1 without Pds5. Molecular Cell, 2018, 70, 1134-1148.e7.	9.7	141
32	Crystal structure of the SMC head domain: an ABC ATPase with 900 residues antiparallel coiled-coil inserted11Edited by R. Huber. Journal of Molecular Biology, 2001, 306, 25-35.	4.2	138
33	CetZ tubulin-like proteins control archaeal cell shape. Nature, 2015, 519, 362-365.	27.8	138
34	Molecules of the Bacterial Cytoskeleton. Annual Review of Biophysics and Biomolecular Structure, 2004, 33, 177-198.	18.3	123
35	A folded conformation of MukBEF and cohesin. Nature Structural and Molecular Biology, 2019, 26, 227-236.	8.2	121
36	Evolution of cytomotive filaments: The cytoskeleton from prokaryotes to eukaryotes. International Journal of Biochemistry and Cell Biology, 2009, 41, 323-329.	2.8	120

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37	The Crystal Structure of ZapA and its Modulation of FtsZ Polymerisation. Journal of Molecular Biology, 2004, 341, 839-852.	4.2	118
38	Murein (Peptidoglycan) Binding Property of the Essential Cell Division Protein FtsN from Escherichia coli. Journal of Bacteriology, 2004, 186, 6728-6737.	2.2	117
39	Features critical for membrane binding revealed by DivIVA crystal structure. EMBO Journal, 2010, 29, 1988-2001.	7.8	116
40	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.	7.1	116
41	Structure of the Jab1/MPN Domain and Its Implications for Proteasome Function. Biochemistry, 2003, 42, 11460-11465.	2.5	115
42	The ParMRC system: molecular mechanisms of plasmid segregation by actin-like filaments. Nature Reviews Microbiology, 2010, 8, 683-692.	28.6	115
43	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.	4.2	113
44	Novel coiledâ€coil cell division factor ZapB stimulates Z ring assembly and cell division. Molecular Microbiology, 2008, 68, 720-735.	2.5	113
45	Localized Dimerization and Nucleoid Binding Drive Gradient Formation by the Bacterial Cell Division Inhibitor MipZ. Molecular Cell, 2012, 46, 245-259.	9.7	105
46	Prokaryotic cytoskeletons: protein filaments organizing small cells. Nature Reviews Microbiology, 2018, 16, 187-201.	28.6	104
47	Structural analysis of the chromosome segregation protein Spo0J from Thermus thermophilus. Molecular Microbiology, 2004, 53, 419-432.	2.5	100
48	Molecular Mechanism of Sequence-Directed DNA Loading and Translocation by FtsK. Molecular Cell, 2008, 31, 498-509.	9.7	97
49	Electron Cryomicroscopy of <i>E. coli</i> Reveals Filament Bundles Involved in Plasmid DNA Segregation. Science, 2009, 323, 509-512.	12.6	93
50	The FtsK Î³ domain directs oriented DNA translocation by interacting with KOPS. Nature Structural and Molecular Biology, 2006, 13, 965-972.	8.2	92
51	A Ferritin-Based Label for Cellular Electron Cryotomography. Structure, 2011, 19, 147-154.	3.3	92
52	Do the divisome and elongasome share a common evolutionary past?. Current Opinion in Microbiology, 2013, 16, 745-751.	5.1	91
53	A Polymerization-Associated Structural Switch in FtsZ That Enables Treadmilling of Model Filaments. MBio, 2017, 8, .	4.1	91
54	Cryo-EM structures of holo condensin reveal a subunit flip-flop mechanism. Nature Structural and Molecular Biology, 2020, 27, 743-751.	8.2	90

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55	Increasing complexity of the bacterial cytoskeleton. Current Opinion in Cell Biology, 2005, 17, 75-81.	5.4	89
56	Robotic nanolitre protein crystallisation at the MRC Laboratory of Molecular Biology. Progress in Biophysics and Molecular Biology, 2005, 88, 311-327.	2.9	86
57	Dimeric structure of the cell shape protein MreC and its functional implications. Molecular Microbiology, 2006, 62, 1631-1642.	2.5	86
58	A Bipolar Spindle of Antiparallel ParM Filaments Drives Bacterial Plasmid Segregation. Science, 2012, 338, 1334-1337.	12.6	85
59	Structure of the hexagonal surface layer on Caulobacter crescentus cells. Nature Microbiology, 2017, 2, 17059.	13.3	85
60	The structure of human thyroglobulin. Nature, 2020, 578, 627-630.	27.8	81
61	Structural Insights into Ring Formation of Cohesin and Related Smc Complexes. Trends in Cell Biology, 2016, 26, 680-693.	7.9	77
62	Structural/functional homology between the bacterial and eukaryotic cytoskeletons. Current Opinion in Cell Biology, 2004, 16, 24-31.	5.4	74
63	Probing FtsZ and Tubulin with C8-Substituted GTP Analogs Reveals Differences in Their Nucleotide Binding Sites. Chemistry and Biology, 2008, 15, 189-199.	6.0	74
64	Crystal structure of the bacterial cell division regulator MinD. FEBS Letters, 2001, 492, 160-165.	2.8	73
65	Structure and function of cohesin's Scc3/SA regulatory subunit. FEBS Letters, 2014, 588, 3692-3702.	2.8	73
66	Structures of actin-like ParM filaments show architecture of plasmid-segregating spindles. Nature, 2015, 523, 106-110.	27.8	73
67	Solution structure and domain architecture of the divisome protein FtsN. Molecular Microbiology, 2004, 52, 651-660.	2.5	72
68	Structural analysis of the ParR/parC plasmid partition complex. EMBO Journal, 2007, 26, 4413-4422.	7.8	71
69	Filament structure of bacterial tubulin homologue TubZ. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19766-19771.	7.1	71
70	A positively charged channel within the Smc1/Smc3 hinge required for sister chromatid cohesion. EMBO Journal, 2011, 30, 364-378.	7.8	69
71	Crystal Structures of Bacillus subtilis Lon Protease. Journal of Molecular Biology, 2010, 401, 653-670.	4.2	68
72	Transport of DNA within cohesin involves clamping on top of engaged heads by Scc2 and entrapment within the ring by Scc3. ELife, 2020, 9, .	6.0	67

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73	Towards understanding the molecular basis of bacterial DNA segregation. Philosophical Transactions of the Royal Society B: Biological Sciences, 2005, 360, 523-535.	4.0	66
74	MinCD cell division proteins form alternating copolymeric cytomotive filaments. Nature Communications, 2014, 5, 5341.	12.8	64
75	Structural and mutational analysis of the cell division protein FtsQ. Molecular Microbiology, 2008, 68, 110-123.	2.5	62
76	New Insights into the Mechanisms of Cytomotive Actin and Tubulin Filaments. International Review of Cell and Molecular Biology, 2011, 292, 1-71.	3.2	56
77	The Structure of the AXH Domain of Spinocerebellar Ataxin-1. Journal of Biological Chemistry, 2004, 279, 3758-3765.	3.4	55
78	Bacterial actin: architecture of the ParMRC plasmid DNA partitioning complex. EMBO Journal, 2008, 27, 2230-2238.	7.8	55
79	Crystal Structure of the Cohesin Gatekeeper Pds5 and in Complex with Kleisin Scc1. Cell Reports, 2016, 14, 2108-2115.	6.4	52
80	Crystal structure of the N-terminal domain of MukB: a protein involved in chromosome partitioning. Structure, 1999, 7, 1181-1187.	3.3	49
81	Cell division in the archaeon Haloferax volcanii relies on two FtsZ proteins with distinct functions in division ring assembly and constriction. Nature Microbiology, 2021, 6, 594-605.	13.3	49
82	Cryo-EM structure of MukBEF reveals DNA loop entrapment at chromosomal unloading sites. Molecular Cell, 2021, 81, 4891-4906.e8.	9.7	49
83	Crystal Structure Determination of FtsZ fromMethanococcus jannaschii. Journal of Structural Biology, 1998, 124, 235-243.	2.8	43
84	LeoA, B and C from Enterotoxigenic Escherichia coli (ETEC) Are Bacterial Dynamins. PLoS ONE, 2014, 9, e107211.	2.5	42
85	Dynamin architectureâ€"from monomer to polymer. Current Opinion in Structural Biology, 2010, 20, 791-798.	5.7	41
86	Helical Tubes of FtsZ from Methanococcus jannaschii. Biological Chemistry, 2000, 381, 993-999.	2.5	40
87	Structural Analysis of the Interaction between the Bacterial Cell Division Proteins FtsQ and FtsB. MBio, 2018, 9, .	4.1	40
88	Crenactin forms actin-like double helical filaments regulated by arcadin-2. ELife, 2016, 5, .	6.0	39
89	Folding of cohesinâ€™s coiled coil is important for Scc2/4-induced association with chromosomes. ELife, 2021, 10, .	6.0	37
90	The N-Terminal Membrane-Spanning Domain of the Escherichia coli DNA Translocase FtsK Hexamerizes at Midcell. MBio, 2013, 4, e00800-13.	4.1	36

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91	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.	7.1	35
92	FtsK in motion reveals its mechanism for double-stranded DNA translocation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14202-14208.	7.1	35
93	Distribution of the Escherichia coli structural maintenance of chromosomes (SMC)-like protein MukB in the cell. Molecular Microbiology, 2002, 42, 1179-1188.	2.5	34
94	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.	7.1	34
95	Structure of the Tubulin/FtsZ-Like Protein TubZ from Pseudomonas Bacteriophage Î¦KZ. Journal of Molecular Biology, 2013, 425, 2164-2173.	4.2	31
96	A cylindrical specimen holder for electron cryo-tomography. Ultramicroscopy, 2014, 137, 20-29.	1.9	31
97	Collaborative protein filaments. EMBO Journal, 2015, 34, 2312-2320.	7.8	30
98	The structure of bactofilin filaments reveals their mode of membrane binding and lack of polarity. Nature Microbiology, 2019, 4, 2357-2368.	13.3	30
99	Asgard archaea shed light on the evolutionary origins of the eukaryotic ubiquitin-ESCRT machinery. Nature Communications, 2022, 13, .	12.8	27
100	Proteasome: from structure to function. Current Opinion in Biotechnology, 1996, 7, 376-385.	6.6	26
101	Four-stranded mini microtubules formed by <i>Prosthecobacter</i> BtubAB show dynamic instability. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5950-E5958.	7.1	26
102	Identifying proteins bound to native mitotic ESC chromosomes reveals chromatin repressors are important for compaction. Nature Communications, 2020, 11, 4118.	12.8	26
103	Crenactin from <i>Pyrobaculum calidifontis</i> is closely related to actin in structure and forms steep helical filaments. FEBS Letters, 2014, 588, 776-782.	2.8	25
104	Preliminary X-ray Crystallographic Study of the Proteasome from Thermoplasma acidophilum. Journal of Molecular Biology, 1993, 234, 881-884.	4.2	24
105	X-ray and cryo-EM structures of monomeric and filamentous actin-like protein MamK reveal changes associated with polymerization. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13396-13401.	7.1	24
106	Singleâ€dose immunisation with a multimerised SARSâ€CoVâ€2 receptor binding domain (RBD) induces an enhanced and protective response in mice. FEBS Letters, 2021, 595, 2323-2340.	2.8	24
107	Crystal structure of the ubiquitin-like protein YukD fromBacillus subtilis. FEBS Letters, 2005, 579, 3837-3841.	2.8	23
108	Centromere Pairing by a Plasmid-encoded Type I ParB Protein. Journal of Biological Chemistry, 2007, 282, 28216-28225.	3.4	22

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109	FzlA, an essential regulator of FtsZ filament curvature, controls constriction rate during <i>Caulobacter</i> division. Molecular Microbiology, 2018, 107, 180-197.	2.5	22
110	Clamping of DNA shuts the condensin neck gate. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2120006119.	7.1	22
111	Structure of the ParM filament at 8.5Ã… resolution. Journal of Structural Biology, 2013, 184, 33-42.	2.8	20
112	Conserved sequence motif at the C-terminus ofthe bacterial cell-division protein FtsA. Biochimie, 2001, 83, 117-120.	2.6	18
113	Activation of Xer-recombination at dif: structural basis of the FtsKÎ³â€“XerD interaction. Scientific Reports, 2016, 6, 33357.	3.3	17
114	Structural Investigation of Proteasome Inhibition. Biological Chemistry, 1997, 378, 239-47.	2.5	16
115	Crystal structure of the Zâ€ring associated cell division protein ZapC from <i>Escherichia coli</i>. FEBS Letters, 2015, 589, 3822-3828.	2.8	13
116	3D Electron Microscopy of the Interaction of Kinesin with Tubulin.. Cell Structure and Function, 1999, 24, 277-284.	1.1	12
117	High-resolution mapping of metal ions reveals principles of surface layer assembly in Caulobacter crescentus cells. Structure, 2022, 30, 215-228.e5.	3.3	12
118	Overview of the Diverse Roles of Bacterial and Archaeal Cytoskeletons. Sub-Cellular Biochemistry, 2017, 84, 1-26.	2.4	11
119	Automated Protocols for Macromolecular Crystallization at the MRC Laboratory of Molecular Biology. Journal of Visualized Experiments, 2018, , .	0.3	11
120	Cryo-EM reconstruction of AlfA from <i>Bacillus subtilis</i> reveals the structure of a simplified actin-like filament at 3.4-Ã… resolution. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3458-3463.	7.1	11
121	Cryoâ€EM structure of the fullâ€length Lon protease from <i>Thermus thermophilus</i>. FEBS Letters, 2021, 595, 2691-2700.	2.8	9
122	The subtle allostery of microtubule dynamics. Nature Structural and Molecular Biology, 2014, 21, 505-506.	8.2	7
123	SnapShot: The Bacterial Cytoskeleton. Cell, 2016, 166, 522-522.e1.	28.9	6
124	Cryoâ€<scp>EM</scp> structure of the Min<scp>CD</scp> copolymeric filament from <i>Pseudomonas aeruginosa</i> at 3.1 Ã… resolution. FEBS Letters, 2019, 593, 1915-1926.	2.8	6
125	Bacterial and archaeal cytoskeletons. Current Biology, 2021, 31, R542-R546.	3.9	1