

Werner KÃ¼hlbrandt

List of Publications by Year in descending order

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205
papers

22,077
citations

7551

77
h-index

10127

140
g-index

236
all docs

236
docs citations

236
times ranked

16675
citing authors

#	ARTICLE	IF	CITATIONS
1	Atomic model of plant light-harvesting complex by electron crystallography. <i>Nature</i> , 1994, 367, 614-621.	13.7	2,012
2	The Resolution Revolution. <i>Science</i> , 2014, 343, 1443-1444.	6.0	986
3	Mechanisms of photoprotection and nonphotochemical quenching in pea light-harvesting complex at 2.5 Å resolution. <i>EMBO Journal</i> , 2005, 24, 919-928.	3.5	731
4	Dimer ribbons of ATP synthase shape the inner mitochondrial membrane. <i>EMBO Journal</i> , 2008, 27, 1154-1160.	3.5	559
5	Biology, structure and mechanism of P-type ATPases. <i>Nature Reviews Molecular Cell Biology</i> , 2004, 5, 282-295.	16.1	498
6	Three-dimensional structure of plant light-harvesting complex determined by electron crystallography. <i>Nature</i> , 1991, 350, 130-134.	13.7	496
7	Structure and function of mitochondrial membrane protein complexes. <i>BMC Biology</i> , 2015, 13, 89.	1.7	459
8	Macromolecular organization of ATP synthase and complex I in whole mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14121-14126.	3.3	425
9	Structure of the yeast F ₁ F _o -ATP synthase dimer and its role in shaping the mitochondrial cristae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13602-13607.	3.3	413
10	Lipid-protein Interactions in Crystals of Plant Light-harvesting Complex. <i>Journal of Molecular Biology</i> , 1993, 234, 347-356.	2.0	358
11	Three-dimensional structure of the plant photosystem II reaction centre at 8 Å resolution. <i>Nature</i> , 1998, 396, 283-286.	13.7	340
12	Structure, mechanism, and regulation of the chloroplast ATP synthase. <i>Science</i> , 2018, 360, .	6.0	308
13	Two-dimensional crystallization of membrane proteins. <i>Quarterly Reviews of Biophysics</i> , 1992, 25, 1-49.	2.4	298
14	Aquaporin homologues in plants and mammals transport ammonia. <i>FEBS Letters</i> , 2004, 574, 31-36.	1.3	297
15	Horizontal membrane-intrinsic α -helices in the stator a-subunit of an F-type ATP synthase. <i>Nature</i> , 2015, 521, 237-240.	13.7	293
16	Arrangement of electron transport chain components in bovine mitochondrial supercomplex I ₁ III ₂ IV ₁ . <i>EMBO Journal</i> , 2011, 30, 4652-4664.	3.5	290
17	Protein Insertion into the Mitochondrial Inner Membrane by a Twin-Pore Translocase. <i>Science</i> , 2003, 299, 1747-1751.	6.0	272
18	Cross-strand binding of TFAM to a single mtDNA molecule forms the mitochondrial nucleoid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11288-11293.	3.3	266

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19	Structure and Mechanisms of F-Type ATP Synthases. <i>Annual Review of Biochemistry</i> , 2019, 88, 515-549.	5.0	266
20	Three-dimensional structure of the bacterial protein-translocation complex SecYEG. <i>Nature</i> , 2002, 418, 662-665.	13.7	237
21	Arrangement of Photosystem II and ATP Synthase in Chloroplast Membranes of Spinach and Pea. <i>Plant Cell</i> , 2010, 22, 1299-1312.	3.1	237
22	Structure of a Complete ATP Synthase Dimer Reveals the Molecular Basis of Inner Mitochondrial Membrane Morphology. <i>Molecular Cell</i> , 2016, 63, 445-456.	4.5	230
23	Amphipols From A to Z. <i>Annual Review of Biophysics</i> , 2011, 40, 379-408.	4.5	226
24	Cryo-EM enters a new era. <i>ELife</i> , 2014, 3, e03678.	2.8	214
25	Three-dimensional map of the plasma membrane H ⁺ -ATPase in the open conformation. <i>Nature</i> , 1998, 392, 840-843.	13.7	203
26	Age-dependent dissociation of ATP synthase dimers and loss of inner-membrane cristae in mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15301-15306.	3.3	203
27	Three-dimensional structure of the light-harvesting chlorophyll a/b protein complex. <i>Nature</i> , 1984, 307, 478-480.	13.7	196
28	Dimers of mitochondrial ATP synthase induce membrane curvature and self-assemble into rows. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4250-4255.	3.3	196
29	Protein denaturation at the air-water interface and how to prevent it. <i>ELife</i> , 2019, 8, .	2.8	196
30	Characterization of the translocon of the outer envelope of chloroplasts. <i>Journal of Cell Biology</i> , 2003, 160, 541-551.	2.3	195
31	Three-dimensional crystallization of membrane proteins. <i>Quarterly Reviews of Biophysics</i> , 1988, 21, 429-477.	2.4	182
32	Refolding of Escherichia coli produced membrane protein inclusion bodies immobilised by nickel chelating chromatography. <i>FEBS Letters</i> , 1998, 432, 21-26.	1.3	166
33	Rotary substates of mitochondrial ATP synthase reveal the basis of flexible F ₁ -F _o coupling. <i>Science</i> , 2019, 364, .	6.0	160
34	Two-dimensional structure of plant photosystem II at 8-Å... resolution. <i>Nature</i> , 1997, 389, 522-526.	13.7	159
35	Bacteriorhodopsin – the movie. <i>Nature</i> , 2000, 406, 569-570.	13.7	159
36	Structure of the monomeric outer-membrane porin OmpG in the open and closed conformation. <i>EMBO Journal</i> , 2006, 25, 3702-3713.	3.5	151

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37	Many wheels make light work. <i>Nature</i> , 1995, 374, 497-498.	13.7	142
38	Cryo-EM Structure of the TOM Core Complex from <i>Neurospora crassa</i> . <i>Cell</i> , 2017, 170, 693-700.e7.	13.5	138
39	Sequence conservation of light-harvesting and stress-response proteins in relation to the three-dimensional molecular structure of LHCII. <i>Photosynthesis Research</i> , 1995, 44, 139-148.	1.6	136
40	Atomic model of the F420-reducing [NiFe] hydrogenase by electron cryo-microscopy using a direct electron detector. <i>ELife</i> , 2014, 3, e01963.	2.8	132
41	Functional asymmetry and electron flow in the bovine respirasome. <i>ELife</i> , 2016, 5, .	2.8	130
42	Projection structure and oligomeric properties of a bacterial core protein translocase. <i>EMBO Journal</i> , 2001, 20, 2462-2471.	3.5	126
43	Crystallisation, structure and function of plant light-harvesting Complex II. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2009, 1787, 753-772.	0.5	126
44	Structure and autoregulation of a P4-ATPase lipid flippase. <i>Nature</i> , 2019, 571, 366-370.	13.7	126
45	Protein translocase of the outer mitochondrial membrane: role of import receptors in the structural organization of the TOM complex. <i>Journal of Molecular Biology</i> , 2002, 316, 657-666.	2.0	123
46	Central Role of Mic10 in the Mitochondrial Contact Site and Cristae Organizing System. <i>Cell Metabolism</i> , 2015, 21, 747-755.	7.2	120
47	CryoEM structures of membrane pore and prepore complex reveal cytolytic mechanism of <i>Pneumolysin</i> . <i>ELife</i> , 2017, 6, .	2.8	119
48	Conserved in situ arrangement of complex I and III ₂ in mitochondrial respiratory chain supercomplexes of mammals, yeast, and plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3024-3029.	3.3	119
49	Molecular Architecture of the Undecameric Rotor of a Bacterial Na ⁺ -ATP Synthase. <i>Journal of Molecular Biology</i> , 2002, 321, 307-316.	2.0	118
50	High-resolution electron crystallography of light-harvesting chlorophyll -protein complex in three different media. <i>Journal of Molecular Biology</i> , 1991, 217, 691-699.	2.0	116
51	Crystal structure of listeriolysin O reveals molecular details of oligomerization and pore formation. <i>Nature Communications</i> , 2014, 5, 3690.	5.8	116
52	Structure, Mechanism, and Regulation of the <i>Neurospora</i> Plasma Membrane H ⁺ -ATPase. <i>Science</i> , 2002, 297, 1692-1696.	6.0	115
53	Mutant Trimers of Light-Harvesting Complex II Exhibit Altered Pigment Content and Spectroscopic Features. <i>Biochemistry</i> , 1999, 38, 16214-16222.	1.2	114
54	Projection structure of NhaA, a secondary transporter from <i>Escherichia coli</i> , at 4.0 Å resolution. <i>EMBO Journal</i> , 1999, 18, 3558-3563.	3.5	113

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55	The state of detergent solubilised light-harvesting chlorophyll-a/b protein complex as monitored by picosecond time-resolved fluorescence and circular dichroism. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1987, 893, 349-364.	0.5	110
56	Spectroscopic characterization of three different monomeric forms of the main chlorophyll a/b binding protein from chloroplast membranes. <i>Biochemistry</i> , 1994, 33, 14775-14783.	1.2	110
57	Structural basis of Na ⁺ -independent and cooperative substrate/product antiport in CaiT. <i>Nature</i> , 2010, 467, 233-236.	13.7	110
58	High-resolution cryo-EM structures of respiratory complex I: Mechanism, assembly, and disease. <i>Science Advances</i> , 2019, 5, eaax9484.	4.7	109
59	Crystal structure of plant light-harvesting complex shows the active, energy-transmitting state. <i>EMBO Journal</i> , 2009, 28, 298-306.	3.5	108
60	Changes of mitochondrial ultrastructure and function during ageing in mice and <i>Drosophila</i> . <i>ELife</i> , 2017, 6, .	2.8	108
61	Molecular insights into lipid-assisted Ca ²⁺ regulation of the TRP channel Polycystin-2. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 123-130.	3.6	105
62	Structure of a type IV pilus machinery in the open and closed state. <i>ELife</i> , 2015, 4, .	2.8	103
63	Structure and function of the plant light-harvesting complex, LHC-II. <i>Current Opinion in Structural Biology</i> , 1994, 4, 519-528.	2.6	101
64	Controlled Unfolding and Refolding of a Single Sodium-proton Antiporter using Atomic Force Microscopy. <i>Journal of Molecular Biology</i> , 2004, 340, 1143-1152.	2.0	99
65	Direct interaction of the major light-harvesting complex II and PsbS in nonphotochemical quenching. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5452-5456.	3.3	98
66	Cryo-EM structure of respiratory complex I at work. <i>ELife</i> , 2018, 7, .	2.8	98
67	The structure of membrane crystals of the light-harvesting chlorophyll a/b protein complex.. <i>Journal of Cell Biology</i> , 1983, 96, 1414-1424.	2.3	97
68	Electron tomography of plant thylakoid membranes. <i>Journal of Experimental Botany</i> , 2011, 62, 2393-2402.	2.4	96
69	Structure and substrate ion binding in the sodium/proton antiporter PaNhaP. <i>ELife</i> , 2014, 3, e03579.	2.8	92
70	Loss of LRPPRC causes ATP synthase deficiency. <i>Human Molecular Genetics</i> , 2014, 23, 2580-2592.	1.4	91
71	Structure of outer membrane protein G in lipid bilayers. <i>Nature Communications</i> , 2017, 8, 2073.	5.8	91
72	Active site rearrangement and structural divergence in prokaryotic respiratory oxidases. <i>Science</i> , 2019, 366, 100-104.	6.0	90

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73	Assignment of Spectral Substructures to Pigment-Binding Sites in Higher Plant Light-Harvesting Complex LHC-II. <i>Biochemistry</i> , 2002, 41, 2281-2287.	1.2	89
74	A mitofusin-dependent docking ring complex triggers mitochondrial fusion in vitro. <i>ELife</i> , 2016, 5, .	2.8	87
75	Structure and assembly of the mitochondrial membrane remodelling GTPase Mgm1. <i>Nature</i> , 2019, 571, 429-433.	13.7	86
76	Locating ligand binding and activation of a single antiporter. <i>EMBO Reports</i> , 2005, 6, 668-674.	2.0	85
77	Cryo-Electron Microscopy Structure of a Yeast Mitochondrial Preprotein Translocase. <i>Journal of Molecular Biology</i> , 2008, 383, 1049-1057.	2.0	83
78	Structure and in situ organisation of the <i>Pyrococcus furiosus</i> archaeellum machinery. <i>ELife</i> , 2017, 6, .	2.8	83
79	Outer membrane continuity and septosome formation between vegetative cells in the filaments of <i>Anabaena</i> sp. PCC 7120. <i>Cellular Microbiology</i> , 2011, 13, 1744-1754.	1.1	81
80	Evidence for Structural Integrity in the Undecameric c-Rings Isolated from Sodium ATP Synthases. <i>Journal of Molecular Biology</i> , 2003, 325, 389-397.	2.0	80
81	Chloroplast Omp85 proteins change orientation during evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13841-13846.	3.3	80
82	Solid-State Magic-Angle Spinning NMR of Outer-Membrane Protein G from <i>Escherichia coli</i> . <i>ChemBioChem</i> , 2005, 6, 1679-1684.	1.3	79
83	Distribution of RNA and protein in crystalline eukaryotic ribosomes. <i>Journal of Molecular Biology</i> , 1982, 156, 431-448.	2.0	78
84	Rotary ATPases: A New Twist to an Ancient Machine. <i>Trends in Biochemical Sciences</i> , 2016, 41, 106-116.	3.7	78
85	The Three Isoforms of the Light-harvesting Complex II. <i>Journal of Biological Chemistry</i> , 2004, 279, 36884-36891.	1.6	77
86	Two-dimensional structure of light harvesting complex II (LHII) from the purple bacterium <i>Rhodovulum sulfidophilum</i> and comparison with LHII from <i>Rhodospseudomonas acidophila</i> . <i>Structure</i> , 1996, 4, 243-252.	1.6	75
87	Membrane perforation by the pore-forming toxin pneumolysin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13352-13357.	3.3	75
88	Structure and transport mechanism of the sodium/proton antiporter MjNhaP1. <i>ELife</i> , 2014, 3, e03583.	2.8	73
89	Two-dimensional structure of plant light-harvesting complex at 37 Å... resolution by electron crystallography. <i>Journal of Molecular Biology</i> , 1989, 207, 823-828.	2.0	72
90	Carotenoid Radical Cations as a Probe for the Molecular Mechanism of Nonphotochemical Quenching in Oxygenic Photosynthesis. <i>Journal of Physical Chemistry B</i> , 2007, 111, 3481-3487.	1.2	71

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91	Bovine F1Fo ATP synthase monomers bend the lipid bilayer in 2D membrane crystals. <i>ELife</i> , 2015, 4, e06119.	2.8	71
92	Projection Structure of Channelrhodopsin-2 at 6 Å Resolution by Electron Crystallography. <i>Journal of Molecular Biology</i> , 2011, 414, 86-95.	2.0	70
93	Two-dimensional crystallization of a membrane protein on a detergent-resistant lipid monolayer 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 308, 639-647.	2.0	68
94	First Insights into the Entry Process of Hyperthermophilic Archaeal Viruses. <i>Journal of Virology</i> , 2013, 87, 13379-13385.	1.5	66
95	High-resolution structure and dynamics of mitochondrial complex I Insights into the proton pumping mechanism. <i>Science Advances</i> , 2021, 7, eabj3221.	4.7	65
96	Photosystem II. <i>Current Opinion in Structural Biology</i> , 1999, 9, 469-475.	2.6	64
97	Accumulation of plant antenna complexes is regulated by post-transcriptional mechanisms in tobacco. <i>Plant Cell</i> , 1995, 7, 149-160.	3.1	63
98	Structure of the SecY Complex Unlocked by a Preprotein Mimic. <i>Cell Reports</i> , 2012, 1, 21-28.	2.9	63
99	Direct structural insight into the substrate-shuttling mechanism of yeast fatty acid synthase by electron cryomicroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9164-9169.	3.3	62
100	Helical arrays of U-shaped ATP synthase dimers form tubular cristae in ciliate mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8442-8447.	3.3	62
101	Visualizing active membrane protein complexes by electron cryotomography. <i>Nature Communications</i> , 2014, 5, 4129.	5.8	59
102	Structural basis of proton translocation and force generation in mitochondrial ATP synthase. <i>ELife</i> , 2017, 6, .	2.8	59
103	Consensus Structural Features of Purified Bacterial TatABC Complexes. <i>Journal of Molecular Biology</i> , 2003, 330, 277-286.	2.0	58
104	Mechanism of Na ⁺ -dependent citrate transport from the structure of an asymmetrical CitS dimer. <i>ELife</i> , 2015, 4, e09375.	2.8	58
105	Structure of GlnK1 with bound effectors indicates regulatory mechanism for ammonia uptake. <i>EMBO Journal</i> , 2007, 26, 589-599.	3.5	57
106	Three-dimensional crystals of the light-harvesting chlorophyll protein complex from pea chloroplasts. <i>Journal of Molecular Biology</i> , 1987, 194, 757-762.	2.0	54
107	pH-induced structural change in a sodium/proton antiporter from <i>Methanococcus jannaschii</i> . <i>EMBO Journal</i> , 2005, 24, 2720-2729.	3.5	54
108	Correlation of Car S ₁ Chl with Chl Chl S ₁ Energy Transfer Supports the Excitonic Model in Quenched Light Harvesting Complex II. <i>Journal of Physical Chemistry B</i> , 2010, 114, 15650-15655.	1.2	54

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109	Structure of the archaeal Na ⁺ /H ⁺ antiporter NhaP1 and functional role of transmembrane helix 1. <i>EMBO Journal</i> , 2011, 30, 439-449.	3.5	54
110	CryoEM at IUCr: a new era. <i>IUCr</i> , 2016, 3, 3-7.	1.0	54
111	Electron cryo-microscopy of biological specimens on conductive titanium-silicon metal glass films. <i>Ultramicroscopy</i> , 2008, 108, 698-705.	0.8	52
112	A ferredoxin bridge connects the two arms of plant mitochondrial complex I. <i>Plant Cell</i> , 2021, 33, 2072-2091.	3.1	52
113	Effect of surface roughness of carbon support films on high-resolution electron diffraction of two-dimensional protein crystals. <i>Ultramicroscopy</i> , 1991, 36, 307-318.	0.8	51
114	Discrimination of protein and nucleic acids by electron microscopy using contrast variation. <i>Ultramicroscopy</i> , 1982, 7, 221-231.	0.8	50
115	Cyclophilin D links programmed cell death and organismal aging in <i>Podospora anserina</i> . <i>Aging Cell</i> , 2010, 9, 761-775.	3.0	50
116	In situ structure of trypanosomal ATP synthase dimer reveals a unique arrangement of catalytic subunits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 992-997.	3.3	49
117	Observing Folding Pathways and Kinetics of a Single Sodium-proton Antiporter from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2006, 355, 2-8.	2.0	48
118	[2,3- ¹³ C]-labeling of Aromatic Residues Getting a Head Start in the Magic-Angle-Spinning NMR Assignment of Membrane Proteins. <i>Journal of the American Chemical Society</i> , 2008, 130, 408-409.	6.6	48
119	pH-Induced Conformational Change of the Î ² -Barrel-Forming Protein OmpG Reconstituted into Native <i>E. coli</i> Lipids. <i>Journal of Molecular Biology</i> , 2010, 396, 610-616.	2.0	48
120	Structure of Human Na ⁺ /H ⁺ Exchanger NHE1 Regulatory Region in Complex with Calmodulin and Ca ²⁺ . <i>Journal of Biological Chemistry</i> , 2011, 286, 40954-40961.	1.6	47
121	A 3D cellular context for the macromolecular world. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 841-845.	3.6	47
122	The crystal structure of an orthorhombic form of adenosine-5'-monophosphate. <i>Acta Crystallographica Section B: Structural Crystallography and Crystal Chemistry</i> , 1976, 32, 1850-1855.	0.4	46
123	Structure of light-harvesting chlorophyll protein complex from plant photosynthetic membranes at 7 Å... resolution in projection. <i>Journal of Molecular Biology</i> , 1988, 202, 849-864.	2.0	46
124	Projection Structure and Oligomeric State of the Osmoregulated Sodium/Glycine Betaine Symporter BetP of <i>Corynebacterium glutamicum</i> . <i>Journal of Molecular Biology</i> , 2004, 337, 1137-1147.	2.0	45
125	Self-assembly of the general membrane-remodeling protein PVAP into sevenfold virus-associated pyramids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3829-3834.	3.3	45
126	Comparison of H ⁺ -ATPase and Ca ²⁺ -ATPase suggests that a large conformational change initiates P-type ion pump reaction cycles. <i>Current Biology</i> , 1999, 9, 672-679.	1.8	44

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127	Structure of the P-type ATPases. <i>Current Opinion in Structural Biology</i> , 1998, 8, 510-516.	2.6	43
128	Projection Structure of yidC: A Conserved Mediator of Membrane Protein Assembly. <i>Journal of Molecular Biology</i> , 2008, 375, 901-907.	2.0	42
129	Light-Induced Helix Movements in Channelrhodopsin-2. <i>Journal of Molecular Biology</i> , 2015, 427, 341-349.	2.0	42
130	Projection structure of the monomeric porin OmpG at 6 Å resolution. <i>Journal of Molecular Biology</i> , 2001, 305, 71-77.	2.0	41
131	Conformations of NhaA, the Na/H Exchanger from <i>Escherichia coli</i> , in the pH-Activated and Ion-Translocating States. <i>Journal of Molecular Biology</i> , 2009, 386, 351-365.	2.0	40
132	Surface crystallisation of the plasma membrane H ⁺ -ATPase on a carbon support film for electron crystallography. <i>Journal of Molecular Biology</i> , 1999, 287, 961-968.	2.0	39
133	Molecular architecture of the Na ⁺ -type <i>scp</i> -ATPase rotor ring from <i>Burkholderia pseudomallei</i> . <i>EMBO Reports</i> , 2017, 18, 526-535.	2.0	39
134	The 3.7 Å... projection map of the glycerol facilitator GlpF: a variant of the aquaporin tetramer. <i>EMBO Reports</i> , 2000, 1, 183-189.	2.0	38
135	One Hairpin after the Other: Exploring Mechanical Unfolding Pathways of the Transmembrane Barrel Protein OmpG. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 8306-8308.	7.2	38
136	Structural basis for energy transduction by respiratory alternative complex III. <i>Nature Communications</i> , 2018, 9, 1728.	5.8	38
137	pH-Dependent Interactions Guide the Folding and Gate the Transmembrane Pore of the β ² -Barrel Membrane Protein OmpG. <i>Journal of Molecular Biology</i> , 2010, 397, 878-882.	2.0	37
138	Keeping It Simple, Transport Mechanism and pH Regulation in Na ⁺ /H ⁺ Exchangers. <i>Journal of Biological Chemistry</i> , 2014, 289, 13168-13176.	1.6	37
139	Structure and Function of Prokaryotic Glutamate Transporters from <i>Escherichia coli</i> and <i>Pyrococcus horikoshii</i> . <i>Biochemistry</i> , 2006, 45, 12796-12805.	1.2	35
140	Chlorophyllbis involved in long-wavelength spectral properties of light-harvesting complexes LHC I and LHC II. <i>FEBS Letters</i> , 2001, 499, 27-31.	1.3	34
141	Analysis of macromolecular structure and dynamics by electron cryo-microscopy. <i>Current Opinion in Chemical Biology</i> , 1999, 3, 537-543.	2.8	32
142	Human Leukotriene C4 Synthase at 4.5 Å... Resolution in Projection. <i>Structure</i> , 2004, 12, 2009-2014.	1.6	32
143	A comparison of the three isoforms of the light-harvesting complex II using transient absorption and time-resolved fluorescence measurements. <i>Photosynthesis Research</i> , 2006, 88, 269-285.	1.6	32
144	Protein Dynamics Tunes Excited State Positions in Light-Harvesting Complex II. <i>Journal of Physical Chemistry B</i> , 2015, 119, 3920-3930.	1.2	32

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145	Supramolecular organization of the human N-BAR domain in shaping the sarcolemma membrane. <i>Journal of Structural Biology</i> , 2016, 194, 375-382.	1.3	32
146	Mechanism of the electroneutral sodium/proton antiporter PaNhaP from transition-path shooting. <i>Nature Communications</i> , 2019, 10, 1742.	5.8	32
147	The 6.9-Å... Structure of GlpF: A Basis for Homology Modeling of the Glycerol Channel from <i>Escherichia coli</i> . <i>Journal of Structural Biology</i> , 2000, 132, 133-141.	1.3	30
148	Oligomeric Structure of the Carnitine Transporter CaiT from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 4795-4801.	1.6	30
149	Structural Asymmetry in a Trimeric Na ⁺ /Betaine Symporter, BetP, from <i>Corynebacterium glutamicum</i> . <i>Journal of Molecular Biology</i> , 2011, 407, 368-381.	2.0	30
150	Large scale expression, purification and 2D crystallization of recombinant plant plasma membrane H ⁺ -ATPase. <i>Journal of Molecular Biology</i> , 2001, 309, 465-476.	2.0	29
151	Properties of zeaxanthin and its radical cation bound to the minor light-harvesting complexes CP24, CP26 and CP29. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2009, 1787, 747-752.	0.5	29
152	Structure and function of bacterial light-harvesting complexes. <i>Structure</i> , 1995, 3, 521-525.	1.6	28
153	Correlation between the OmpG Secondary Structure and Its pH-Dependent Alterations Monitored by FTIR. <i>Journal of Molecular Biology</i> , 2010, 401, 56-67.	2.0	28
154	Energy-filtered transmission electron microscopy of biological samples on highly transparent carbon nanomembranes. <i>Ultramicroscopy</i> , 2011, 111, 342-349.	0.8	28
155	Membrane Structure of CtrA3, a Copper-transporting P-type-ATPase from <i>Aquifex aeolicus</i> . <i>Journal of Molecular Biology</i> , 2008, 378, 581-595.	2.0	27
156	Structure and Function of the FeoB G-Domain from <i>Methanococcus jannaschii</i> . <i>Journal of Molecular Biology</i> , 2009, 392, 405-419.	2.0	27
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