

Werner Khlbrandt

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.

205
papers

18,185
citations

72
h-index

130
g-index

236
ext. papers

20,454
ext. citations

12
avg, IF

7.27
L-index

#	Paper	IF	Citations
205	Forty years in cryoEM of membrane proteins.. <i>Microscopy (Oxford, England)</i> , 2022 , 71, i30-i50	1.3	2
204	Ca-mediated higher-order assembly of heterodimers in amino acid transport system b biogenesis and cystinuria.. <i>Nature Communications</i> , 2022 , 13, 2708	17.4	1
203	High-resolution structure and dynamics of mitochondrial complex I-Insights into the proton pumping mechanism. <i>Science Advances</i> , 2021 , 7, eabj3221	14.3	15
202	Structure of the hexameric fungal plasma membrane proton pump in its autoinhibited state. <i>Science Advances</i> , 2021 , 7, eabj5255	14.3	3
201	Devitrification reduces beam-induced movement in cryo-EM. <i>IUCrJ</i> , 2021 , 8, 186-194	4.7	5
200	A ferredoxin bridge connects the two arms of plant mitochondrial complex I. <i>Plant Cell</i> , 2021 , 33, 2072-2086	20.6	20
199	Molecular landscape of etioplast inner membranes in higher plants. <i>Nature Plants</i> , 2021 , 7, 514-523	11.5	10
198	Current limitations to high-resolution structure determination by single-particle cryoEM. <i>Quarterly Reviews of Biophysics</i> , 2021 , 54, e4	7	9
197	Conformational changes in the yeast mitochondrial ABC transporter Atm1 during the transport cycle.. <i>Science Advances</i> , 2021 , 7, eabk2392	14.3	0
196	The resolution revolution in cryoEM requires high-quality sample preparation: a rapid pipeline to a high-resolution map of yeast fatty acid synthase. <i>IUCrJ</i> , 2020 , 7, 220-227	4.7	7
195	Ion Binding and Selectivity of the Na/H Antiporter MjNhaP1 from Experiment and Simulation. <i>Journal of Physical Chemistry B</i> , 2020 , 124, 336-344	3.4	1
194	Reply to Desikan et al.: Micelle formation among various mechanisms of toxin pore formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 5109-5110	11.5	1
193	Active site rearrangement and structural divergence in prokaryotic respiratory oxidases. <i>Science</i> , 2019 , 366, 100-104	33.3	53
192	Noncovalent Functionalization of Carbon Substrates with Hydrogels Improves Structural Analysis of Vitrified Proteins by Electron Cryo-Microscopy. <i>ACS Nano</i> , 2019 , 13, 7185-7190	16.7	4
191	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	11.5	49
190	Rotary substates of mitochondrial ATP synthase reveal the basis of flexible F-F coupling. <i>Science</i> , 2019 , 364,	33.3	87
189	Structure and autoregulation of a P4-ATPase lipid flippase. <i>Nature</i> , 2019 , 571, 366-370	50.4	69

188	Mechanism of the electroneutral sodium/proton antiporter PaNhaP from transition-path shooting. <i>Nature Communications</i> , 2019 , 10, 1742	17.4	17
187	Structure and Mechanisms of F-Type ATP Synthases. <i>Annual Review of Biochemistry</i> , 2019 , 88, 515-549	29.1	121
186	Structure and assembly of the mitochondrial membrane remodelling GTPase Mgm1. <i>Nature</i> , 2019 , 571, 429-433	50.4	50
185	Cryo-EM structure of respiratory complex IV. <i>IUCrJ</i> , 2019 , 6, 773-780	4.7	3
184	Protein denaturation at the air-water interface and how to prevent it. <i>ELife</i> , 2019 , 8,	8.9	104
183	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	11.5	111
182	High-resolution cryo-EM structures of respiratory complex I: Mechanism, assembly, and disease. <i>Science Advances</i> , 2019 , 5, eaax9484	14.3	69
181	Conserved in situ arrangement of complex I and III 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	11.5	82
180	Structure of the catalytic F head of the F-F ATP synthase from. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E2906-E2907	11.5	1
179	Structural basis for energy transduction by respiratory alternative complex III. <i>Nature Communications</i> , 2018 , 9, 1728	17.4	25
178	Structure, mechanism, and regulation of the chloroplast ATP synthase. <i>Science</i> , 2018 , 360,	33.3	180
177	CryoEM structures of ATP synthase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018 , 1859, e3-e4	4.6	
176	Cryo-EM structure of respiratory complex I at work. <i>ELife</i> , 2018 , 7,	8.9	66
175	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	11.5	34
174	Molecular insights into lipid-assisted Ca regulation of the TRP channel Polycystin-2. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 123-130	17.6	79
173	Self-Perforated Hydrogel Nanomembranes Facilitate Structural Analysis of Proteins by Electron Cryo-Microscopy. <i>ACS Nano</i> , 2017 , 11, 6467-6473	16.7	9
172	Molecular architecture of the N-type ATPase rotor ring from. <i>EMBO Reports</i> , 2017 , 18, 526-535	6.5	28
171	Cryo-EM structure of the bifunctional secretin complex of. <i>ELife</i> , 2017 , 6,	8.9	18

170	Cryo-EM Structure of the TOM Core Complex from <i>Neurospora crassa</i> . <i>Cell</i> , 2017 , 170, 693-700.e7	56.2	105
169	Structure of outer membrane protein G in lipid bilayers. <i>Nature Communications</i> , 2017 , 8, 2073	17.4	69
168	CryoEM structures of membrane pore and prepore complex reveal cytolytic mechanism of Pneumolysin. <i>ELife</i> , 2017 , 6,	8.9	84
167	Changes of mitochondrial ultrastructure and function during ageing in mice and. <i>ELife</i> , 2017 , 6,	8.9	73
166	Structure and organisation of the archaellum machinery. <i>ELife</i> , 2017 , 6,	8.9	51
165	Structural basis of proton translocation and force generation in mitochondrial ATP synthase. <i>ELife</i> , 2017 , 6,	8.9	47
164	Cryo-EM structure of respiratory complex I reveals a link to mitochondrial sulfur metabolism. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016 , 1857, 1935-1942	4.6	22
163	Three in a row-how sodium ions cross the channel. <i>EMBO Journal</i> , 2016 , 35, 793-5	13	4
162	Supramolecular organization of the human N-BAR domain in shaping the sarcolemma membrane. <i>Journal of Structural Biology</i> , 2016 , 194, 375-82	3.4	22
161	Rotary ATPases: A New Twist to an Ancient Machine. <i>Trends in Biochemical Sciences</i> , 2016 , 41, 106-116	10.3	60
160	Functional asymmetry and electron flow in the bovine respirasome. <i>ELife</i> , 2016 , 5,	8.9	101
159	A mitofusin-dependent docking ring complex triggers mitochondrial fusion in vitro. <i>ELife</i> , 2016 , 5,	8.9	65
158	CryoEM at IUCrJ: a new era. <i>IUCrJ</i> , 2016 , 3, 3-7	4.7	45
157	Structure of a Complete ATP Synthase Dimer Reveals the Molecular Basis of Inner Mitochondrial Membrane Morphology. <i>Molecular Cell</i> , 2016 , 63, 445-56	17.6	182
156	Electrogenic Cation Binding in the Electroneutral Na ⁺ /H ⁺ Antiporter of <i>Pyrococcus abyssi</i> . <i>Journal of Biological Chemistry</i> , 2016 , 291, 26786-26793	5.4	10
155	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, 8442-7	11.5	46
154	Horizontal membrane-intrinsic helices in the stator a-subunit of an F-type ATP synthase. <i>Nature</i> , 2015 , 521, 237-40	50.4	235
153	Central role of Mic10 in the mitochondrial contact site and cristae organizing system. <i>Cell Metabolism</i> , 2015 , 21, 747-55	24.6	92

152	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, 11288-93	11.5	193
151	Structure and function of mitochondrial membrane protein complexes. <i>BMC Biology</i> , 2015 , 13, 89	7.3	284
150	Another Phase Plate in the Zoo: Reducing Charging and Optimizing the Design of Electrostatic Phase Plates. <i>Microscopy and Microanalysis</i> , 2015 , 21, 1941-1942	0.5	1
149	Structure of a type IV pilus machinery in the open and closed state. <i>ELife</i> , 2015 , 4,	8.9	77
148	Towards an optimum design for electrostatic phase plates. <i>Ultramicroscopy</i> , 2015 , 153, 22-31	3.1	12
147	Light-induced helix movements in channelrhodopsin-2. <i>Journal of Molecular Biology</i> , 2015 , 427, 341-9	6.5	31
146	Protein dynamics tunes excited state positions in light-harvesting complex II. <i>Journal of Physical Chemistry B</i> , 2015 , 119, 3920-30	3.4	29
145	Bovine F1Fo ATP synthase monomers bend the lipid bilayer in 2D membrane crystals. <i>ELife</i> , 2015 , 4, e06819	8.9	59
144	Author response: Structure of a type IV pilus machinery in the open and closed state 2015 ,		3
143	Mechanism of Na(+)-dependent citrate transport from the structure of an asymmetrical CitS dimer. <i>ELife</i> , 2015 , 4, e09375	8.9	42
142	Biochemistry. The resolution revolution. <i>Science</i> , 2014 , 343, 1443-4	33.3	687
141	Crystal structure of listeriolysin O reveals molecular details of oligomerization and pore formation. <i>Nature Communications</i> , 2014 , 5, 3690	17.4	87
140	Visualization of ATP synthase dimers in mitochondria by electron cryo-tomography. <i>Journal of Visualized Experiments</i> , 2014 , 51228	1.6	23
139	Atomic model of the F420-reducing [NiFe] hydrogenase by electron cryo-microscopy using a direct electron detector. <i>ELife</i> , 2014 , 3, e01963	8.9	106
138	Cryo-EM enters a new era. <i>ELife</i> , 2014 , 3, e03678	8.9	178
137	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, 3829-34	11.5	39
136	Loss of LRPPRC causes ATP synthase deficiency. <i>Human Molecular Genetics</i> , 2014 , 23, 2580-92	5.6	77
135	Visualizing active membrane protein complexes by electron cryotomography. <i>Nature Communications</i> , 2014 , 5, 4129	17.4	44

134	A 3D cellular context for the macromolecular world. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 841-5	17.6	33
133	Keeping it simple, transport mechanism and pH regulation in Na ⁺ /H ⁺ exchangers. <i>Journal of Biological Chemistry</i> , 2014 , 289, 13168-76	5.4	29
132	Structure and substrate ion binding in the sodium/proton antiporter PaNhaP. <i>ELife</i> , 2014 , 3, e03579	8.9	65
131	Structure and transport mechanism of the sodium/proton antiporter MjNhaP1. <i>ELife</i> , 2014 , 3, e03583	8.9	51
130	Author response: Structure and transport mechanism of the sodium/proton antiporter MjNhaP1 2014 ,		6
129	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, 5452-6	11.5	85
128	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, 15301-6	11.5	160
127	First insights into the entry process of hyperthermophilic archaeal viruses. <i>Journal of Virology</i> , 2013 , 87, 13379-85	6.6	48
126	Arginine oscillation explains Na ⁺ independence in the substrate/product antiporter CaiT. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 17296-301	11.5	15
125	Introduction to electron crystallography. <i>Methods in Molecular Biology</i> , 2013 , 955, 1-16	1.4	8
124	Practical aspects of Boersch phase contrast electron microscopy of biological specimens. <i>Ultramicroscopy</i> , 2012 , 116, 62-72	3.1	13
123	Structure of the SecY complex unlocked by a preprotein mimic. <i>Cell Reports</i> , 2012 , 1, 21-8	10.6	57
122	GREcon: A Method for the Lipid Reconstitution of Membrane Proteins. <i>Angewandte Chemie</i> , 2012 , 124, 8468-8472	3.6	2
121	GREcon: a method for the lipid reconstitution of membrane proteins. <i>Angewandte Chemie - International Edition</i> , 2012 , 51, 8343-7	16.4	16
120	Structure of the yeast F1Fo-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, 13602-7	11.5	330
119	Structure Of The Mitochondrial ATP Synthase And Its Role In Shaping Mitochondria Cristae. <i>Microscopy and Microanalysis</i> , 2012 , 18, 56-57	0.5	3
118	Amphipols from A to Z. <i>Annual Review of Biophysics</i> , 2011 , 40, 379-408	21.1	200
117	Structural asymmetry in a trimeric Na ⁺ /betaine symporter, BetP, from <i>Corynebacterium glutamicum</i> . <i>Journal of Molecular Biology</i> , 2011 , 407, 368-81	6.5	27

116	Projection structure of channelrhodopsin-2 at 6 Å resolution by electron crystallography. <i>Journal of Molecular Biology</i> , 2011 , 414, 86-95	6.5	60
115	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, 1744-54	3.9	62
114	Structure of the archaeal Na ⁺ /H ⁺ antiporter NhaP1 and functional role of transmembrane helix 1. <i>EMBO Journal</i> , 2011 , 30, 439-49	13	46
113	In-focus electron microscopy of frozen-hydrated biological samples with a Boersch phase plate. <i>Ultramicroscopy</i> , 2011 , 111, 1696-705	3.1	22
112	Energy-filtered transmission electron microscopy of biological samples on highly transparent carbon nanomembranes. <i>Ultramicroscopy</i> , 2011 , 111, 342-9	3.1	26
111	Single-walled carbon nanotubes and nanocrystalline graphene reduce beam-induced movements in high-resolution electron cryo-microscopy of ice-embedded biological samples. <i>Applied Physics Letters</i> , 2011 , 99, 133701	3.4	12
110	Electron tomography of plant thylakoid membranes. <i>Journal of Experimental Botany</i> , 2011 , 62, 2393-4027		86
109	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, 14121-6	11.5	341
108	Structure of human Na ⁺ /H ⁺ exchanger NHE1 regulatory region in complex with calmodulin and Ca ²⁺ . <i>Journal of Biological Chemistry</i> , 2011 , 286, 40954-61	5.4	41
107	Chloroplast Omp85 proteins change orientation during evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 13841-6	11.5	74
106	Arrangement of electron transport chain components in bovine mitochondrial supercomplex I1III2IV1. <i>EMBO Journal</i> , 2011 , 30, 4652-64	13	262
105	Cyclophilin D links programmed cell death and organismal aging in <i>Podospora anserina</i> . <i>Aging Cell</i> , 2010 , 9, 761-75	9.9	44
104	Structural basis of Na ⁽⁺⁾ -independent and cooperative substrate/product antiport in CaiT. <i>Nature</i> , 2010 , 467, 233-6	50.4	100
103	Arrangement of photosystem II and ATP synthase in chloroplast membranes of spinach and pea. <i>Plant Cell</i> , 2010 , 22, 1299-312	11.6	201
102	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, 9164-9	11.5	49
101	pH-induced conformational change of the beta-barrel-forming protein OmpG reconstituted into native <i>E. coli</i> lipids. <i>Journal of Molecular Biology</i> , 2010 , 396, 610-6	6.5	46
100	pH-dependent interactions guide the folding and gate the transmembrane pore of the beta-barrel membrane protein OmpG. <i>Journal of Molecular Biology</i> , 2010 , 397, 878-82	6.5	34
99	Correlation between the OmpG secondary structure and its pH-dependent alterations monitored by FTIR. <i>Journal of Molecular Biology</i> , 2010 , 401, 56-67	6.5	22

98	Correlation of Car S(1)-Chl with Chl - Car S(1) energy transfer supports the excitonic model in quenched light harvesting complex II. <i>Journal of Physical Chemistry B</i> , 2010 , 114, 15650-5	3.4	51
97	Dual energy landscape: the functional state of the β -barrel outer membrane protein G molds its unfolding energy landscape. <i>Proteomics</i> , 2010 , 10, 4151-62	4.8	14
96	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, 747-52	4.6	26
95	Crystallisation, structure and function of plant light-harvesting Complex II. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2009 , 1787, 753-72	4.6	114
94	Infrared spectroscopic study of the structural and functional properties of the Na(+)/H(+) antiporter MjNhaP1 from <i>Methanococcus jannaschii</i> . <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2009 , 1787, 730-7	4.6	8
93	One beta hairpin after the other: exploring mechanical unfolding pathways of the transmembrane beta-barrel protein OmpG. <i>Angewandte Chemie - International Edition</i> , 2009 , 48, 8306-8	16.4	36
92	Purification, crystallization and preliminary X-ray diffraction analysis of the FeoB G domain from <i>Methanococcus jannaschii</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009 , 65, 684-7		5
91	Crystal structure of plant light-harvesting complex shows the active, energy-transmitting state. <i>EMBO Journal</i> , 2009 , 28, 298-306	13	100
90	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, 351-65	6.5	33
89	Structure and function of the FeoB G-domain from <i>Methanococcus jannaschii</i> . <i>Journal of Molecular Biology</i> , 2009 , 392, 405-19	6.5	25
88	Dimer ribbons of ATP synthase shape the inner mitochondrial membrane. <i>EMBO Journal</i> , 2008 , 27, 1154-60	15	471
87	Projection structure of yidC: a conserved mediator of membrane protein assembly. <i>Journal of Molecular Biology</i> , 2008 , 375, 901-7	6.5	39
86	Membrane structure of CtrA3, a copper-transporting P-type-ATPase from <i>Aquifex aeolicus</i> . <i>Journal of Molecular Biology</i> , 2008 , 378, 581-95	6.5	26
85	Cryo-electron microscopy structure of a yeast mitochondrial preprotein translocase. <i>Journal of Molecular Biology</i> , 2008 , 383, 1049-57	6.5	69
84	[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, 408-9	16.4	46
83	Electron cryo-microscopy of biological specimens on conductive titanium-silicon metal glass films. <i>Ultramicroscopy</i> , 2008 , 108, 698-705	3.1	43
82	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, 3481-7	3.4	67
81	Structure of GlnK1 with bound effectors indicates regulatory mechanism for ammonia uptake. <i>EMBO Journal</i> , 2007 , 26, 589-99	13	53

80	Two-dimensional crystallization of human vitamin K-dependent gamma-glutamyl carboxylase. <i>Journal of Structural Biology</i> , 2007 , 157, 437-42	3.4	22
79	Oligomeric structure of the carnitine transporter CaiT from Escherichia coli. <i>Journal of Biological Chemistry</i> , 2006 , 281, 4795-801	5.4	30
78	Heterologously expressed GLT-1 associates in approximately 200-nm protein-lipid islands. <i>Biophysical Journal</i> , 2006 , 91, 3718-26	2.9	9
77	Structure and function of prokaryotic glutamate transporters from Escherichia coli and Pyrococcus horikoshii. <i>Biochemistry</i> , 2006 , 45, 12796-805	3.2	33
76	Observing folding pathways and kinetics of a single sodium-proton antiporter from Escherichia coli. <i>Journal of Molecular Biology</i> , 2006 , 355, 2-8	6.5	46
75	Structure of the monomeric outer-membrane porin OmpG in the open and closed conformation. <i>EMBO Journal</i> , 2006 , 25, 3702-13	13	131
74	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, 269-85	3.7	31
73	High-yield expression, reconstitution and structure of the recombinant, fully functional glutamate transporter GLT-1 from Rattus norvegicus. <i>Journal of Molecular Biology</i> , 2005 , 351, 598-613	6.5	25
72	Mechanisms of photoprotection and nonphotochemical quenching in pea light-harvesting complex at 2.5 Å resolution. <i>EMBO Journal</i> , 2005 , 24, 919-28	13	664
71	pH-induced structural change in a sodium/proton antiporter from Methanococcus jannaschii. <i>EMBO Journal</i> , 2005 , 24, 2720-9	13	50
70	Locating ligand binding and activation of a single antiporter. <i>EMBO Reports</i> , 2005 , 6, 668-74	6.5	77
69	Solid-state magic-angle spinning NMR of outer-membrane protein G from Escherichia coli. <i>ChemBioChem</i> , 2005 , 6, 1679-84	3.8	75
68	Structural differences in the inner part of photosystem II between higher plants and cyanobacteria. <i>Photosynthesis Research</i> , 2005 , 85, 3-13	3.7	19
67	The three isoforms of the light-harvesting complex II: spectroscopic features, trimer formation, and functional roles. <i>Journal of Biological Chemistry</i> , 2004 , 279, 36884-91	5.4	62
66	Biology, structure and mechanism of P-type ATPases. <i>Nature Reviews Molecular Cell Biology</i> , 2004 , 5, 282-95	48.7	420
65	Human leukotriene C(4) synthase at 4.5 Å resolution in projection. <i>Structure</i> , 2004 , 12, 2009-14	5.2	29
64	Aquaporin homologues in plants and mammals transport ammonia. <i>FEBS Letters</i> , 2004 , 574, 31-6	3.8	270
63	Projection structure and oligomeric state of the osmoregulated sodium/glycine betaine symporter BetP of Corynebacterium glutamicum. <i>Journal of Molecular Biology</i> , 2004 , 337, 1137-47	6.5	42

62	Controlled unfolding and refolding of a single sodium-proton antiporter using atomic force microscopy. <i>Journal of Molecular Biology</i> , 2004 , 340, 1143-52	6.5	90
61	Light-induced changes in the chemical bond structure of light-harvesting complex II probed by FTIR spectroscopy. <i>Biochemistry</i> , 2003 , 42, 10223-8	3.2	6
60	Protein insertion into the mitochondrial inner membrane by a twin-pore translocase. <i>Science</i> , 2003 , 299, 1747-51	33.3	242
59	Evidence for structural integrity in the undecameric c-rings isolated from sodium ATP synthases. <i>Journal of Molecular Biology</i> , 2003 , 325, 389-97	6.5	78
58	Consensus structural features of purified bacterial TatABC complexes. <i>Journal of Molecular Biology</i> , 2003 , 330, 277-86	6.5	56
57	Characterization of the translocon of the outer envelope of chloroplasts. <i>Journal of Cell Biology</i> , 2003 , 160, 541-51	7.3	180
56	Three-dimensional structure of the bacterial protein-translocation complex SecYEG. <i>Nature</i> , 2002 , 418, 662-5	50.4	223
55	Assignment of spectral substructures to pigment-binding sites in higher plant light-harvesting complex LHC-II. <i>Biochemistry</i> , 2002 , 41, 2281-7	3.2	84
54	Structure, mechanism, and regulation of the <i>Neurospora</i> plasma membrane H ⁺ -ATPase. <i>Science</i> , 2002 , 297, 1692-6	33.3	104
53	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, 657-66	6.5	114
52	Molecular architecture of the undecameric rotor of a bacterial Na ⁺ -ATP synthase. <i>Journal of Molecular Biology</i> , 2002 , 321, 307-16	6.5	106
51	Projection structure and oligomeric properties of a bacterial core protein translocase. <i>EMBO Journal</i> , 2001 , 20, 2462-71	13	109
50	Projection structure of the monomeric porin OmpG at 6 Å resolution. <i>Journal of Molecular Biology</i> , 2001 , 305, 71-7	6.5	38
49	Two-dimensional crystallization of a membrane protein on a detergent-resistant lipid monolayer. <i>Journal of Molecular Biology</i> , 2001 , 308, 639-47	6.5	62
48	Large scale expression, purification and 2D crystallization of recombinant plant plasma membrane H ⁺ -ATPase. <i>Journal of Molecular Biology</i> , 2001 , 309, 465-76	6.5	26
47	Chlorophyll b is involved in long-wavelength spectral properties of light-harvesting complexes LHC I and LHC II. <i>FEBS Letters</i> , 2001 , 499, 27-31	3.8	31
46	The 3.7 Å projection map of the glycerol facilitator GlpF: a variant of the aquaporin tetramer. <i>EMBO Reports</i> , 2000 , 1, 183-9	6.5	35
45	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, 133-41	3.4	28

44	Analysis of macromolecular structure and dynamics by electron cryo-microscopy. <i>Current Opinion in Chemical Biology</i> , 1999 , 3, 537-43	9.7	30
43	Projection structure of NhaA, a secondary transporter from Escherichia coli, at 4.0 Å resolution. <i>EMBO Journal</i> , 1999 , 18, 3558-63	13	107
42	Photosystem II. <i>Current Opinion in Structural Biology</i> , 1999 , 9, 469-75	8.1	60
41	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, 672-9	6.3	39
40	Purification and two-dimensional crystallization of highly active cytochrome b(6)f complex from spinach. <i>FEBS Letters</i> , 1999 , 463, 97-102	3.8	14
39	Mutant trimers of light-harvesting complex II exhibit altered pigment content and spectroscopic features. <i>Biochemistry</i> , 1999 , 38, 16214-22	3.2	106
38	Surface crystallisation of the plasma membrane H ⁺ -ATPase on a carbon support film for electron crystallography. <i>Journal of Molecular Biology</i> , 1999 , 287, 961-8	6.5	37
37	Three-dimensional map of the plasma membrane H ⁺ -ATPase in the open conformation. <i>Nature</i> , 1998 , 392, 840-3	50.4	188
36	Three-dimensional structure of the plant photosystem II reaction centre at 8 Å resolution. <i>Nature</i> , 1998 , 396, 283-6	50.4	305
35	Structure of the P-type ATPases. <i>Current Opinion in Structural Biology</i> , 1998 , 8, 510-6	8.1	40
34	Refolding of Escherichia coli produced membrane protein inclusion bodies immobilised by nickel chelating chromatography. <i>FEBS Letters</i> , 1998 , 432, 21-6	3.8	145
33	Picture story. Pumping ions. <i>Nature Structural Biology</i> , 1997 , 4, 773		2
32	Two-dimensional structure of plant photosystem II at 8-Å resolution. <i>Nature</i> , 1997 , 389, 522-526	50.4	151
31	Two-dimensional structure of light harvesting complex II (LHII) from the purple bacterium Rhodovulum sulfidophilum and comparison with LHII from Rhodospseudomonas acidophila. <i>Structure</i> , 1996 , 4, 243-52	5.2	69
30	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, 139-48	3.7	125
29	Accumulation of plant antenna complexes is regulated by post-transcriptional mechanisms in tobacco. <i>Plant Cell</i> , 1995 , 7, 149-60	11.6	61
28	Structure and function of bacterial light-harvesting complexes. <i>Structure</i> , 1995 , 3, 521-5	5.2	22
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26	Atomic model of plant light-harvesting complex by electron crystallography. <i>Nature</i> , 1994 , 367, 614-21	50.4	1820
25	Structure and function of the plant light-harvesting complex, LHC-II. <i>Current Opinion in Structural Biology</i> , 1994 , 4, 519-528	8.1	93
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23	Lipid-protein interactions in crystals of plant light-harvesting complex. <i>Journal of Molecular Biology</i> , 1993 , 234, 347-56	6.5	340
22	Two-dimensional crystallization of membrane proteins. <i>Quarterly Reviews of Biophysics</i> , 1992 , 25, 1-49	7	269
21	Three-dimensional electron diffraction of plant light-harvesting complex. <i>Biophysical Journal</i> , 1992 , 61, 287-97	2.9	18
20	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	3.1	45
19	Three-dimensional structure of plant light-harvesting complex determined by electron crystallography. <i>Nature</i> , 1991 , 350, 130-4	50.4	454
18	High-resolution electron crystallography of light-harvesting chlorophyll a/b-protein complex in three different media. <i>Journal of Molecular Biology</i> , 1991 , 217, 691-9	6.5	108
17	Two-dimensional structure of plant light-harvesting complex at 3.7 Å [corrected] resolution by electron crystallography. <i>Journal of Molecular Biology</i> , 1989 , 207, 823-8	6.5	64
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15	Chlorophyll dichroism of three-dimensional crystals of the light-harvesting chlorophyll a/b-protein complex. <i>FEBS Letters</i> , 1988 , 226, 275-279	3.8	5
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