

# Axel T Brunger

## 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.

251  
papers

29,752  
citations

90  
h-index

168  
g-index

301  
ext. papers

32,215  
ext. citations

10.7  
avg, IF

7.37  
L-index

#	Paper	IF	Citations
251	The protein-folding problem: Not yet solved.. <i>Science</i> , <b>2022</b> , 375, 507	33.3	6
250	Inhibition of calcium-triggered secretion by hydrocarbon-stapled peptides.. <i>Nature</i> , <b>2022</b> , 603, 949-956	50.4	3
249	Structural conservation among variants of the SARS-CoV-2 spike postfusion bundle.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2022</b> , 119, e2119467119	11.5	2
248	A feature-guided, focused 3D signal permutation method for subtomogram averaging.. <i>Journal of Structural Biology</i> , <b>2022</b> , 107851	3.4	0
247	Conformational dynamics of auto-inhibition in the ER calcium sensor STIM1. <i>ELife</i> , <b>2021</b> , 10,	8.9	4
246	Molecular Characterization of AMPA-Receptor-Containing Vesicles. <i>Frontiers in Molecular Neuroscience</i> , <b>2021</b> , 14, 754631	6.1	2
245	Prefused lysosomes cluster on autophagosomes regulated by VAMP8. <i>Cell Death and Disease</i> , <b>2021</b> , 12, 939	9.8	6
244	The AAA+ superfamily: a review of the structural and mechanistic principles of these molecular machines. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , <b>2021</b> , 1-32	8.7	7
243	Sec17/Sec18 can support membrane fusion without help from completion of SNARE zippering. <i>ELife</i> , <b>2021</b> , 10,	8.9	9
242	Role of Aberrant Spontaneous Neurotransmission in SNAP25-Associated Encephalopathies. <i>Neuron</i> , <b>2021</b> , 109, 59-72.e5	13.9	7
241	Deorphanizing FAM19A proteins as pan-neurexin ligands with an unusual biosynthetic binding mechanism. <i>Journal of Cell Biology</i> , <b>2020</b> , 219,	7.3	11
240	The pre-synaptic fusion machinery. <i>Current Opinion in Structural Biology</i> , <b>2019</b> , 54, 179-188	8.1	31
239	Structures of neurexophilin-neurexin complexes reveal a regulatory mechanism of alternative splicing. <i>EMBO Journal</i> , <b>2019</b> , 38, e101603	13	7
238	Resolving indexing ambiguities in X-ray free-electron laser diffraction patterns. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2019</b> , 75, 234-241	5.5	
237	Ca-Triggered Synaptic Vesicle Fusion Initiated by Release of Inhibition. <i>Trends in Cell Biology</i> , <b>2018</b> , 28, 631-645	18.3	28
236	NSF-mediated disassembly of on- and off-pathway SNARE complexes and inhibition by complexin. <i>ELife</i> , <b>2018</b> , 7,	8.9	18
235	Structural principles of SNARE complex recognition by the AAA+ protein NSF. <i>ELife</i> , <b>2018</b> , 7,	8.9	45

234	Molecular Mechanisms of Fast Neurotransmitter Release. <i>Annual Review of Biophysics</i> , <b>2018</b> , 47, 469-497. <small>21.1</small>	70
233	Conformational change of syntaxin linker region induced by Munc13s initiates SNARE complex formation in synaptic exocytosis. <i>EMBO Journal</i> , <b>2017</b> , 36, 816-829	13 47
232	Mechanistic Insights into NSF Mediated SNARE Complex Disassembly. <i>Biophysical Journal</i> , <b>2017</b> , 112, 31a	2.9
231	Morphologies of synaptic protein membrane fusion interfaces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 9110-9115	11.5 33
230	Molecular Mechanisms of Synaptic Vesicle Priming by Munc13 and Munc18. <i>Neuron</i> , <b>2017</b> , 95, 591-607. <small>10.9</small>	114
229	The primed SNARE-complex-in-synaptotagmin complex for neuronal exocytosis. <i>Nature</i> , <b>2017</b> , 548, 420-425. <small>35.4</small>	134
228	Expression of C1ql3 in Discrete Neuronal Populations Controls Efferent Synapse Numbers and Diverse Behaviors. <i>Neuron</i> , <b>2016</b> , 91, 1034-1051	13.9 50
227	Structure of photosystem II and substrate binding at room temperature. <i>Nature</i> , <b>2016</b> , 540, 453-457	50.4 260
226	N-terminal domain of complexin independently activates calcium-triggered fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E4698-707	11.5 28
225	C-terminal domain of mammalian complexin-1 localizes to highly curved membranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E7590-E7599	11.5 38
224	High-density grids for efficient data collection from multiple crystals. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2016</b> , 72, 2-11	5.5 52
223	Recent Advances in Deciphering the Structure and Molecular Mechanism of the AAA+ ATPase N-Ethylmaleimide-Sensitive Factor (NSF). <i>Journal of Molecular Biology</i> , <b>2016</b> , 428, 1912-26	6.5 36
222	: integration optimization, triage and analysis tool for the processing of XFEL diffraction images. <i>Journal of Applied Crystallography</i> , <b>2016</b> , 49, 1057-1064	3.8 17
221	Complexin induces a conformational change at the membrane-proximal C-terminal end of the SNARE complex. <i>ELife</i> , <b>2016</b> , 5,	8.9 26
220	Advances in X-ray free electron laser (XFEL) diffraction data processing applied to the crystal structure of the synaptotagmin-1 / SNARE complex. <i>ELife</i> , <b>2016</b> , 5,	8.9 18
219	Phosphorylation of residues inside the SNARE complex suppresses secretory vesicle fusion. <i>EMBO Journal</i> , <b>2016</b> , 35, 1810-21	13 24
218	Simultaneous single-molecule epigenetic imaging of DNA methylation and hydroxymethylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 4338-43	11.5 39
217	Atomic resolution experimental phase information reveals extensive disorder and bound 2-methyl-2,4-pentanediol in Ca(2+)-calmodulin. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2016</b> , 72, 83-92	5.5 5

216	De novo phasing with X-ray laser reveals mosquito larvicide BinAB structure. <i>Nature</i> , <b>2016</b> , 539, 43-47	50.4	73
215	Munc18a does not alter fusion rates mediated by neuronal SNAREs, synaptotagmin, and complexin. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 10518-34	5.4	15
214	Data Exploration Toolkit for serial diffraction experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 352-6		22
213	Capture and X-ray diffraction studies of protein microcrystals in a microfluidic trap array. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 928-40		51
212	Structures of C1q-like proteins reveal unique features among the C1q/TNF superfamily. <i>Structure</i> , <b>2015</b> , 23, 688-99	5.2	37
211	Towards reconstitution of membrane fusion mediated by SNAREs and other synaptic proteins. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , <b>2015</b> , 50, 231-41	8.7	42
210	A high-transparency, micro-patternable chip for X-ray diffraction analysis of microcrystals under native growth conditions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 1987-97		59
209	Architecture of the synaptotagmin-SNARE machinery for neuronal exocytosis. <i>Nature</i> , <b>2015</b> , 525, 62-7	50.4	192
208	ATG14 promotes membrane tethering and fusion of autophagosomes to endolysosomes. <i>Nature</i> , <b>2015</b> , 520, 563-6	50.4	339
207	Mechanistic insights into the recycling machine of the SNARE complex. <i>Nature</i> , <b>2015</b> , 518, 61-7	50.4	167
206	Enabling X-ray free electron laser crystallography for challenging biological systems from a limited number of crystals. <i>ELife</i> , <b>2015</b> , 4,	8.9	88
205	Mapping the conformational landscape of a dynamic enzyme by multitemperature and XFEL crystallography. <i>ELife</i> , <b>2015</b> , 4,	8.9	100
204	Tools to assist determination and validation of carbohydrate 3D structure data. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1273, 229-40	1.4	14
203	Goniometer-based femtosecond crystallography with X-ray free electron lasers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 17122-7	11.5	105
202	Direct visualization of trans-synaptic neurexin-neurologin interactions during synapse formation. <i>Journal of Neuroscience</i> , <b>2014</b> , 34, 15083-96	6.6	33
201	Deformable elastic network refinement for low-resolution macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2014</b> , 70, 2241-55		20
200	Complexin inhibits spontaneous release and synchronizes Ca <sup>2+</sup> -triggered synaptic vesicle fusion by distinct mechanisms. <i>ELife</i> , <b>2014</b> , 3, e03756	8.9	68
199	Complexin-1 enhances the on-rate of vesicle docking via simultaneous SNARE and membrane interactions. <i>Journal of the American Chemical Society</i> , <b>2013</b> , 135, 15274-7	16.4	38

198	Studying calcium-triggered vesicle fusion in a single vesicle-vesicle content and lipid-mixing system. <i>Nature Protocols</i> , <b>2013</b> , 8, 1-16	18.8	96
197	Advances, interactions, and future developments in the CNS, Phenix, and Rosetta structural biology software systems. <i>Annual Review of Biophysics</i> , <b>2013</b> , 42, 265-87	21.1	76
196	Properties of native brain $\beta$ synuclein. <i>Nature</i> , <b>2013</b> , 498, E4-6; discussion E6-7	50.4	207
195	Studying protein-reconstituted proteoliposome fusion with content indicators in vitro. <i>BioEssays</i> , <b>2013</b> , 35, 658-65	4.1	22
194	Ultrahigh-resolution imaging reveals formation of neuronal SNARE/Munc18 complexes in situ. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, E2812-20	11.5	84
193	Model morphing and sequence assignment after molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 2244-50		24
192	Processive ATP-driven substrate disassembly by the N-ethylmaleimide-sensitive factor (NSF) molecular machine. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 23436-45	5.4	30
191	Disassembly of all SNARE complexes by N-ethylmaleimide-sensitive factor (NSF) is initiated by a conserved 1:1 interaction between $\beta$ soluble NSF attachment protein (SNAP) and SNARE complex. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 24984-91	5.4	28
190	Native $\beta$ synuclein induces clustering of synaptic-vesicle mimics via binding to phospholipids and synaptobrevin-2/VAMP2. <i>ELife</i> , <b>2013</b> , 2, e00592	8.9	211
189	Gently does it for submicron crystals. <i>ELife</i> , <b>2013</b> , 2, e01662	8.9	3
188	Application of DEN refinement and automated model building to a difficult case of molecular-replacement phasing: the structure of a putative succinyl-diaminopimelate desuccinylase from <i>Corynebacterium glutamicum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 391-403		24
187	Improved crystallographic models through iterated local density-guided model deformation and reciprocal-space refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 861-70		33
186	Macromolecular Models by Single Molecule FRET. <i>NATO Science for Peace and Security Series B: Physics and Biophysics</i> , <b>2012</b> , 1-19	0.2	
185	A grid-enabled web service for low-resolution crystal structure refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 261-7		14
184	Improving the accuracy of macromolecular structure refinement at 7 Å resolution. <i>Structure</i> , <b>2012</b> , 20, 957-66	5.2	36
183	A novel evolutionarily conserved domain of cell-adhesion GPCRs mediates autoproteolysis. <i>EMBO Journal</i> , <b>2012</b> , 31, 1364-78	13	243
182	Beltless translocation domain of botulinum neurotoxin A embodies a minimum ion-conductive channel. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 1657-61	5.4	23
181	Synaptic proteins promote calcium-triggered fast transition from point contact to full fusion. <i>ELife</i> , <b>2012</b> , 1, e00109	8.9	128

180	Three-dimensional molecular modeling with single molecule FRET. <i>Journal of Structural Biology</i> , <b>2011</b> , 173, 497-505	3.4	84
179	Reintroducing electrostatics into macromolecular crystallographic refinement: application to neutron crystallography and DNA hydration. <i>Structure</i> , <b>2011</b> , 19, 523-33	5.2	30
178	A new generation of crystallographic validation tools for the protein data bank. <i>Structure</i> , <b>2011</b> , 19, 1395-412	5.4	335
177	Post-translational modifications and lipid binding profile of insect cell-expressed full-length mammalian synaptotagmin 1. <i>Biochemistry</i> , <b>2011</b> , 50, 9998-10012	3.2	25
176	In vitro system capable of differentiating fast Ca <sup>2+</sup> -triggered content mixing from lipid exchange for mechanistic studies of neurotransmitter release. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, E304-13	11.5	127
175	Single-molecule FRET-derived model of the synaptotagmin 1-SNARE fusion complex. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 318-24	17.6	157
174	Molecular mechanism of the synaptotagmin-SNARE interaction in Ca <sup>2+</sup> -triggered vesicle fusion. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 325-31	17.6	76
173	Super-resolution biomolecular crystallography with low-resolution data. <i>Nature</i> , <b>2010</b> , 464, 1218-22	50.4	243
172	Iterative structure-based peptide-like inhibitor design against the botulinum neurotoxin serotype A. <i>PLoS ONE</i> , <b>2010</b> , 5, e11378	3.7	22
171	The longin SNARE VAMP7/TI-VAMP adopts a closed conformation. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 17965-73	5.4	23
170	Polarizable atomic multipole x-ray refinement: hydration geometry and application to macromolecules. <i>Biophysical Journal</i> , <b>2010</b> , 98, 2984-92	2.9	24
169	Neurexins physically and functionally interact with GABA(A) receptors. <i>Neuron</i> , <b>2010</b> , 66, 403-16	13.9	121
168	A smooth and differentiable bulk-solvent model for macromolecular diffraction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2010</b> , 66, 1024-31		13
167	Interactions Between Botulinum Neurotoxins and Synaptic Vesicle Proteins <b>2009</b> , 41-52.e2		
166	Mechanistic insights into active site-associated polyubiquitination by the ubiquitin-conjugating enzyme Ube2g2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 3722-7	11.5	78
165	X-ray structure determination at low resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2009</b> , 65, 128-33		45
164	Polarizable atomic multipole X-ray refinement: application to peptide crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2009</b> , 65, 952-65		41
163	Neurologin-1 performs neurexin-dependent and neurexin-independent functions in synapse validation. <i>EMBO Journal</i> , <b>2009</b> , 28, 3244-55	13	99

162	Warren L. DeLano 21 June 1972-3 November 2009. <i>Nature Structural and Molecular Biology</i> , <b>2009</b> , 16, 1202-3	17.6	2
161	Receptor and substrate interactions of clostridial neurotoxins. <i>Toxicon</i> , <b>2009</b> , 54, 550-60	2.8	82
160	Single-molecule studies of the neuronal SNARE fusion machinery. <i>Annual Review of Biochemistry</i> , <b>2009</b> , 78, 903-28	29.1	87
159	Accessory proteins stabilize the acceptor complex for synaptobrevin, the 1:1 syntaxin/SNAP-25 complex. <i>Structure</i> , <b>2008</b> , 16, 308-20	5.2	131
158	Improved structures of full-length p97, an AAA ATPase: implications for mechanisms of nucleotide-dependent conformational change. <i>Structure</i> , <b>2008</b> , 16, 715-26	5.2	167
157	A potent peptidomimetic inhibitor of botulinum neurotoxin serotype A has a very different conformation than SNAP-25 substrate. <i>Structure</i> , <b>2008</b> , 16, 1588-97	5.2	54
156	Rab and Arl GTPase family members cooperate in the localization of the golgin GCC185. <i>Cell</i> , <b>2008</b> , 132, 286-98	56.2	138
155	The structure of the yeast plasma membrane SNARE complex reveals destabilizing water-filled cavities. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 1113-9	5.4	35
154	Highly specific interactions between botulinum neurotoxins and synaptic vesicle proteins. <i>Cellular and Molecular Life Sciences</i> , <b>2008</b> , 65, 2296-306	10.3	40
153	Crystal structure of a hyperactive Escherichia coli glycerol kinase mutant Gly230 --> Asp obtained using microfluidic crystallization devices. <i>Biochemistry</i> , <b>2007</b> , 46, 5722-31	3.2	24
152	Structural and biochemical studies of botulinum neurotoxin serotype C1 light chain protease: implications for dual substrate specificity. <i>Biochemistry</i> , <b>2007</b> , 46, 10685-93	3.2	45
151	Botulinum neurotoxin heavy chain belt as an intramolecular chaperone for the light chain. <i>PLoS Pathogens</i> , <b>2007</b> , 3, 1191-4	7.6	74
150	Ab initio molecular-replacement phasing for symmetric helical membrane proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2007</b> , 63, 188-96		14
149	Version 1.2 of the Crystallography and NMR system. <i>Nature Protocols</i> , <b>2007</b> , 2, 2728-33	18.8	1143
148	A ubiquitin ligase transfers preformed polyubiquitin chains from a conjugating enzyme to a substrate. <i>Nature</i> , <b>2007</b> , 446, 333-7	50.4	175
147	Crystallography: crystallographic evidence for deviating C3b structure. <i>Nature</i> , <b>2007</b> , 448, E1-2; discussion E2-3	50.4	33
146	Combining efficient conformational sampling with a deformable elastic network model facilitates structure refinement at low resolution. <i>Structure</i> , <b>2007</b> , 15, 1630-41	5.2	187
145	Transglutaminase 2 undergoes a large conformational change upon activation. <i>PLoS Biology</i> , <b>2007</b> , 5, e327	9.7	318

144	Structure and function of the yeast U-box-containing ubiquitin ligase Ufd2p. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 15599-606	11.5	47
143	Structures of neuroligin-1 and the neuroligin-1/neurexin-1 beta complex reveal specific protein-protein and protein-Ca <sup>2+</sup> interactions. <i>Neuron</i> , <b>2007</b> , 56, 992-1003	13.9	157
142	Inhibition of metalloprotease botulinum serotype A from a pseudo-peptide binding mode to a small molecule that is active in primary neurons. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 5004-5014	5.4	90
141	Conformation of the synaptobrevin transmembrane domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 8378-83	11.5	63
140	Ensemble molecular dynamics yields submillisecond kinetics and intermediates of membrane fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 11916-21	11.5	124
139	Neuronal SNAREs do not trigger fusion between synthetic membranes but do promote PEG-mediated membrane fusion. <i>Biophysical Journal</i> , <b>2006</b> , 90, 1661-75	2.9	125
138	Structural and functional comparisons of nucleotide pyrophosphatase/phosphodiesterase and alkaline phosphatase: implications for mechanism and evolution. <i>Biochemistry</i> , <b>2006</b> , 45, 9788-803	3.2	131
137	Central pore residues mediate the p97/VCP activity required for ERAD. <i>Molecular Cell</i> , <b>2006</b> , 22, 451-62	17.6	172
136	Considerations for the refinement of low-resolution crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2006</b> , 62, 923-32		62
135	Botulinum neurotoxin B recognizes its protein receptor with high affinity and specificity. <i>Nature</i> , <b>2006</b> , 444, 1092-5	50.4	193
134	The Structure of Nucleotide Pyrophosphatase/ Phosphodiesterase and Implications for Enzyme Evolution in the Alkaline Phosphatase Superfamily. <i>FASEB Journal</i> , <b>2006</b> , 20, A477	0.9	
133	A hybrid machine-learning approach for segmentation of protein localization data. <i>Bioinformatics</i> , <b>2005</b> , 21, 3778-86	7.2	10
132	2.3 A crystal structure of tetanus neurotoxin light chain. <i>Biochemistry</i> , <b>2005</b> , 44, 7450-7	3.2	43
131	Nucleotide dependent motion and mechanism of action of p97/VCP. <i>Journal of Molecular Biology</i> , <b>2005</b> , 347, 437-52	6.5	145
130	New insights into clostridial neurotoxin-SNARE interactions. <i>Trends in Molecular Medicine</i> , <b>2005</b> , 11, 377-81	11.5	67
129	Quantitative imaging of lymphocyte membrane protein reorganization and signaling. <i>Biophysical Journal</i> , <b>2005</b> , 88, 579-89	2.9	6
128	Structure and function of SNARE and SNARE-interacting proteins. <i>Quarterly Reviews of Biophysics</i> , <b>2005</b> , 38, 1-47	7	204
127	Single-molecule studies of synaptotagmin and complexin binding to the SNARE complex. <i>Biophysical Journal</i> , <b>2005</b> , 89, 690-702	2.9	86



126	Deformable modeling for improved calculation of molecular velocities from single-particle tracking <b>2005</b> , 208-11		
125	Refractive index-based determination of detergent concentration and its application to the study of membrane proteins. <i>Protein Science</i> , <b>2005</b> , 14, 2207-11	6.3	136
124	Exo84 and Sec5 are competitive regulatory Sec6/8 effectors to the RalA GTPase. <i>EMBO Journal</i> , <b>2005</b> , 24, 2064-74	13	121
123	Low-resolution crystallography is coming of age. <i>Structure</i> , <b>2005</b> , 13, 171-2	5.2	15
122	Structural basis of FFAT motif-mediated ER targeting. <i>Structure</i> , <b>2005</b> , 13, 1035-45	5.2	182
121	Automated crystallographic ligand building using the medial axis transform of an electron-density isosurface. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2005</b> , 61, 1354-63		12
120	X-ray scattering from unilamellar lipid vesicles. <i>Journal of Applied Crystallography</i> , <b>2005</b> , 38, 126-131	3.8	79
119	Substrate recognition strategy for botulinum neurotoxin serotype A. <i>Nature</i> , <b>2004</b> , 432, 925-9	50.4	277
118	Single molecule observation of liposome-bilayer fusion thermally induced by soluble N-ethyl maleimide sensitive-factor attachment protein receptors (SNAREs). <i>Biophysical Journal</i> , <b>2004</b> , 87, 3569-84	2.9	138
117	Exploring the structural dynamics of the E.coli chaperonin GroEL using translation-libration-screw crystallographic refinement of intermediate states. <i>Journal of Molecular Biology</i> , <b>2004</b> , 342, 229-45	6.5	88
116	Structure of a human A-type potassium channel interacting protein DPPX, a member of the dipeptidyl aminopeptidase family. <i>Journal of Molecular Biology</i> , <b>2004</b> , 343, 1055-65	6.5	83
115	Computational aspects of high-throughput crystallographic macromolecular structure determination. <i>Methods of Biochemical Analysis</i> , <b>2003</b> , 44, 75-87		1
114	High resolution structure, stability, and synaptotagmin binding of a truncated neuronal SNARE complex. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 8630-6	5.4	64
113	Automatic solution of heavy-atom substructures. <i>Methods in Enzymology</i> , <b>2003</b> , 374, 37-83	1.7	31
112	Structural basis of the interaction between RalA and Sec5, a subunit of the sec6/8 complex. <i>EMBO Journal</i> , <b>2003</b> , 22, 3267-78	13	94
111	Electron cryomicroscopy structure of N-ethyl maleimide sensitive factor at 11 A resolution. <i>EMBO Journal</i> , <b>2003</b> , 22, 4365-74	13	47
110	Role of the gamma-phosphate of ATP in triggering protein folding by GroEL-GroES: function, structure and energetics. <i>EMBO Journal</i> , <b>2003</b> , 22, 4877-87	13	110
109	Domain flexibility in the 1.75 A resolution structure of Pb <sup>2+</sup> -calmodulin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2003</b> , 59, 1782-92		27

108	Complete structure of p97/valosin-containing protein reveals communication between nucleotide domains. <i>Nature Structural and Molecular Biology</i> , <b>2003</b> , 10, 856-63	17.6	301
107	NSF and p97/VCP: similar at first, different at last. <i>FEBS Letters</i> , <b>2003</b> , 555, 126-33	3.8	64
106	Single-molecule studies of SNARE complex assembly reveal parallel and antiparallel configurations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 14800-5	11.5	109
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