

Axel T Brunger

List of Publications by Year in descending order

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257
papers

34,611
citations

2797

94
h-index

3822

178
g-index

301
all docs

301
docs citations

301
times ranked

26721
citing authors

#	ARTICLE	IF	CITATIONS
1	Free R value: a novel statistical quantity for assessing the accuracy of crystal structures. <i>Nature</i> , 1992, 355, 472-475.	13.7	4,116
2	Crystal structure of a SNARE complex involved in synaptic exocytosis at 2.4Å resolution. <i>Nature</i> , 1998, 395, 347-353.	13.7	2,191
3	Version 1.2 of the Crystallography and NMR system. <i>Nature Protocols</i> , 2007, 2, 2728-2733.	5.5	1,299
4	Stochastic boundary conditions for molecular dynamics simulations of ST2 water. <i>Chemical Physics Letters</i> , 1984, 105, 495-500.	1.2	548
5	Determination of three-dimensional structures of proteins by simulated annealing with interproton distance restraints. Application to crambin, potato carboxypeptidase inhibitor and barley serine proteinase inhibitor 2. <i>Protein Engineering, Design and Selection</i> , 1988, 2, 27-38.	1.0	513
6	Polar hydrogen positions in proteins: Empirical energy placement and neutron diffraction comparison. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 4, 148-156.	1.5	495
7	ATG14 promotes membrane tethering and fusion of autophagosomes to endolysosomes. <i>Nature</i> , 2015, 520, 563-566.	13.7	460
8	A New Generation of Crystallographic Validation Tools for the Protein Data Bank. <i>Structure</i> , 2011, 19, 1395-1412.	1.6	405
9	Crystallographic refinement by simulated annealing. <i>Journal of Molecular Biology</i> , 1988, 203, 803-816.	2.0	402
10	Torsion angle dynamics: Reduced variable conformational sampling enhances crystallographic structure refinement. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 19, 277-290.	1.5	379
11	Protein Hydration Observed by X-ray Diffraction. <i>Journal of Molecular Biology</i> , 1994, 243, 100-115.	2.0	379
12	Checking your imagination: applications of the free R value. <i>Structure</i> , 1996, 4, 897-904.	1.6	379
13	Transglutaminase 2 Undergoes a Large Conformational Change upon Activation. <i>PLoS Biology</i> , 2007, 5, e327.	2.6	369
14	A novel evolutionarily conserved domain of cell-adhesion GPCRs mediates autoproteolysis. <i>EMBO Journal</i> , 2012, 31, 1364-1378.	3.5	355
15	Active site dynamics in protein molecules: A stochastic boundary molecular-dynamics approach. <i>Biopolymers</i> , 1985, 24, 843-865.	1.2	347
16	Complete structure of p97/valosin-containing protein reveals communication between nucleotide domains. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 856-863.	3.6	347
17	Structural Basis of Rab Effector Specificity. <i>Cell</i> , 1999, 96, 363-374.	13.5	338
18	Structure of photosystem II and substrate binding at room temperature. <i>Nature</i> , 2016, 540, 453-457.	13.7	323

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19	Substrate recognition strategy for botulinum neurotoxin serotype A. <i>Nature</i> , 2004, 432, 925-929.	13.7	310
20	Structural Changes Are Associated with Soluble N-Ethylmaleimide-sensitive Fusion Protein Attachment Protein Receptor Complex Formation. <i>Journal of Biological Chemistry</i> , 1997, 272, 28036-28041.	1.6	308
21	The 1.0 Å... crystal structure of Ca ²⁺ -bound calmodulin: an analysis of disorder and implications for functionally relevant plasticity. <i>Journal of Molecular Biology</i> , 2000, 301, 1237-1256.	2.0	301
22	Torsion-Angle Molecular Dynamics as a New Efficient Tool for NMR Structure Calculation. <i>Journal of Magnetic Resonance</i> , 1997, 124, 154-164.	1.2	300
23	A dimerization motif for transmembrane α -helices. <i>Nature Structural Biology</i> , 1994, 1, 157-163.	9.7	294
24	Application of molecular dynamics with interproton distance restraints to three-dimensional protein structure determination. <i>Journal of Molecular Biology</i> , 1986, 191, 523-551.	2.0	288
25	[19] Free R value: Cross-validation in crystallography. <i>Methods in Enzymology</i> , 1997, 277, 366-396.	0.4	286
26	Native α -synuclein induces clustering of synaptic-vesicle mimics via binding to phospholipids and synaptobrevin-2/VAMP2. <i>ELife</i> , 2013, 2, e00592.	2.8	275
27	Properties of native brain α -synuclein. <i>Nature</i> , 2013, 498, E4-E6.	13.7	271
28	Architecture of the synaptotagmin-1 SNARE machinery for neuronal exocytosis. <i>Nature</i> , 2015, 525, 62-67.	13.7	268
29	Super-resolution biomolecular crystallography with low-resolution data. <i>Nature</i> , 2010, 464, 1218-1222.	13.7	267
30	Solution conformation of a heptadecapeptide comprising the DNA binding helix F of the cyclic AMP receptor protein of <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1985, 186, 435-455.	2.0	256
31	Structure and function of SNARE and SNARE-interacting proteins. <i>Quarterly Reviews of Biophysics</i> , 2005, 38, 1.	2.4	251
32	Folding intermediates of SNARE complex assembly. <i>Nature Structural Biology</i> , 1999, 6, 117-123.	9.7	242
33	The three-dimensional structure of α -1-purothionin in solution: combined use of nuclear magnetic resonance, distance geometry and restrained molecular dynamics. <i>EMBO Journal</i> , 1986, 5, 2729-2735.	3.5	241
34	Structure of the ATP-dependent oligomerization domain of N-ethylmaleimide sensitive factor complexed with ATP. <i>Nature Structural Biology</i> , 1998, 5, 803-811.	9.7	240
35	Identification of a Minimal Core of the Synaptic SNARE Complex Sufficient for Reversible Assembly and Disassembly. <i>Biochemistry</i> , 1998, 37, 10354-10362.	1.2	239
36	The primed SNARE-1 complexin-1 synaptotagmin complex for neuronal exocytosis. <i>Nature</i> , 2017, 548, 420-425.	13.7	229

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37	Interhelical hydrogen bonding drives strong interactions in membrane proteins. <i>Nature Structural Biology</i> , 2000, 7, 154-160.	9.7	226
38	Conformational variability in the refined structure of the chaperonin GroEL at 2.8 Å... resolution. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 1083-1094.	3.6	219
39	Botulinum neurotoxin B recognizes its protein receptor with high affinity and specificity. <i>Nature</i> , 2006, 444, 1092-1095.	13.7	219
40	Structural Basis of FFAT Motif-Mediated ER Targeting. <i>Structure</i> , 2005, 13, 1035-1045.	1.6	218
41	Mechanistic insights into the recycling machine of the SNARE complex. <i>Nature</i> , 2015, 518, 61-67.	13.7	216
42	Combining Efficient Conformational Sampling with a Deformable Elastic Network Model Facilitates Structure Refinement at Low Resolution. <i>Structure</i> , 2007, 15, 1630-1641.	1.6	213
43	Sampling and efficiency of metric matrix distance geometry: A novel partial metrization algorithm. <i>Journal of Biomolecular NMR</i> , 1992, 2, 33-56.	1.6	210
44	Refinement of the influenza virus hemagglutinin by simulated annealing. <i>Journal of Molecular Biology</i> , 1990, 212, 737-761.	2.0	204
45	Computational searching and mutagenesis suggest a structure for the pentameric transmembrane domain of phospholamban. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 154-162.	3.6	198
46	New applications of simulated annealing in X-ray crystallography and solution NMR. <i>Structure</i> , 1997, 5, 325-336.	1.6	197
47	Single-molecule FRET-derived model of the synaptotagmin I SNARE fusion complex. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 318-324.	3.6	194
48	Conformational changes of the multifunction p97 AAA ATPase during its ATPase cycle. <i>Nature Structural Biology</i> , 2002, 9, 950-957.	9.7	189
49	Central Pore Residues Mediate the p97/VCP Activity Required for ERAD. <i>Molecular Cell</i> , 2006, 22, 451-462.	4.5	188
50	A ubiquitin ligase transfers preformed polyubiquitin chains from a conjugating enzyme to a substrate. <i>Nature</i> , 2007, 446, 333-337.	13.7	187
51	Molecular Mechanisms of Synaptic Vesicle Priming by Munc13 and Munc18. <i>Neuron</i> , 2017, 95, 591-607.e10.	3.8	185
52	Improved Structures of Full-Length p97, an AAA ATPase: Implications for Mechanisms of Nucleotide-Dependent Conformational Change. <i>Structure</i> , 2008, 16, 715-726.	1.6	181
53	Crystal Structure of the Cytosolic C2a-C2b Domains of Synaptotagmin III. <i>Journal of Cell Biology</i> , 1999, 147, 589-598.	2.3	179
54	Structures of Neuroligin-1 and the Neuroligin-1/Neurexin-1 ^β Complex Reveal Specific Protein-Protein and Protein-Ca ²⁺ Interactions. <i>Neuron</i> , 2007, 56, 992-1003.	3.8	178

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55	The glycoporphin A transmembrane domain dimer: Sequence-specific propensity for a right-handed supercoil of helices. <i>Biochemistry</i> , 1992, 31, 12726-12732.	1.2	177
56	Algorithmic Challenges in Computational Molecular Biophysics. <i>Journal of Computational Physics</i> , 1999, 151, 9-48.	1.9	176
57	Crystal structure of the hCASK PDZ domain reveals the structural basis of class II PDZ domain target recognition. <i>Nature Structural Biology</i> , 1998, 5, 317-325.	9.7	172
58	A Structural Change Occurs upon Binding of Syntaxin to SNAP-25. <i>Journal of Biological Chemistry</i> , 1997, 272, 4582-4590.	1.6	167
59	Statistical analysis of predicted transmembrane α -helices. <i>BBA - Proteins and Proteomics</i> , 1998, 1429, 113-128.	2.1	166
60	Computational challenges for macromolecular structure determination by X-ray crystallography and solution NMR spectroscopy. <i>Quarterly Reviews of Biophysics</i> , 1993, 26, 49-125.	2.4	165
61	Epsin 1 Undergoes Nucleocytoplasmic Shuttling and Its Eps15 Interactor N-terminal Homology (NTH) Domain, Structurally Similar to Armadillo and Heat Repeats, Interacts with the Transcription Factor Promyelocytic Leukemia Zinc Finger Protein (PLZF). <i>Journal of Cell Biology</i> , 2000, 149, 537-546.	2.3	163
62	Structural and Functional Comparisons of Nucleotide Pyrophosphatase/Phosphodiesterase and Alkaline Phosphatase: Implications for Mechanism and Evolution. <i>Biochemistry</i> , 2006, 45, 9788-9803.	1.2	158
63	Refractive index-based determination of detergent concentration and its application to the study of membrane proteins. <i>Protein Science</i> , 2005, 14, 2207-2211.	3.1	157
64	Nucleotide Dependent Motion and Mechanism of Action of p97/VCP. <i>Journal of Molecular Biology</i> , 2005, 347, 437-452.	2.0	156
65	Neurexins Physically and Functionally Interact with GABA _A Receptors. <i>Neuron</i> , 2010, 66, 403-416.	3.8	154
66	Synaptic proteins promote calcium-triggered fast transition from point contact to full fusion. <i>ELife</i> , 2012, 1, e00109.	2.8	154
67	Single Molecule Observation of Liposome-Bilayer Fusion Thermally Induced by Soluble N-Ethyl Maleimide Sensitive-Factor Attachment Protein Receptors (SNAREs). <i>Biophysical Journal</i> , 2004, 87, 3569-3584.	0.2	153
68	Structure refinement of oligonucleotides by molecular dynamics with nuclear Overhauser effect interproton distance restraints: Application to 5'-d(C-G-T-A-C-G)-3'. <i>Journal of Molecular Biology</i> , 1986, 188, 455-475.	2.0	152
69	Accessory Proteins Stabilize the Acceptor Complex for Synaptobrevin, the 1:1 Syntaxin/SNAP-25 Complex. <i>Structure</i> , 2008, 16, 308-320.	1.6	151
70	Improved prediction for the structure of the dimeric transmembrane domain of glycoporphin A obtained through global searching. <i>Journal of Molecular Biology</i> , 1996, 26, 257-261.		149
71	Structural Characterization of the Intramolecular Interaction between the SH3 and Guanylate Kinase Domains of PSD-95. <i>Molecular Cell</i> , 2001, 8, 1313-1325.	4.5	149
72	Rab and Arl GTPase Family Members Cooperate in the Localization of the Golgin GCC185. <i>Cell</i> , 2008, 132, 286-298.	13.5	147

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73	Mapping the conformational landscape of a dynamic enzyme by multitemperature and XFEL crystallography. <i>ELife</i> , 2015, 4, .	2.8	143
74	In vitro system capable of differentiating fast Ca ²⁺ -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> , 2011, 108, E304-13.	3.3	142
75	Experimentally based orientational refinement of membrane protein models: a structure for the Influenza A M2 H + channel 1 Edited by G. von Heijne. <i>Journal of Molecular Biology</i> , 1999, 286, 951-962.	2.0	141
76	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> , 2006, 103, 11916-11921.	3.3	139
77	Neuronal SNAREs Do Not Trigger Fusion between Synthetic Membranes but Do Promote PEG-Mediated Membrane Fusion. <i>Biophysical Journal</i> , 2006, 90, 1661-1675.	0.2	134
78	Molecular Mechanisms of Fast Neurotransmitter Release. <i>Annual Review of Biophysics</i> , 2018, 47, 469-497.	4.5	133
79	The ENTH domain. <i>FEBS Letters</i> , 2002, 513, 11-18.	1.3	131
80	Role of the $\hat{\text{A}}$ -phosphate of ATP in triggering protein folding by GroEL-GroES: function, structure and energetics. <i>EMBO Journal</i> , 2003, 22, 4877-4887.	3.5	130
81	Exo84 and Sec5 are competitive regulatory Sec6/8 effectors to the RalA GTPase. <i>EMBO Journal</i> , 2005, 24, 2064-2074.	3.5	130
82	Conformational Variability of Solution Nuclear Magnetic Resonance Structures. <i>Journal of Molecular Biology</i> , 1995, 250, 80-93.	2.0	123
83	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> , 2014, 111, 17122-17127.	3.3	122
84	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> , 2003, 100, 14800-14805.	3.3	120
85	Neuroigin-1 performs neurexin-dependent and neurexin-independent functions in synapse validation. <i>EMBO Journal</i> , 2009, 28, 3244-3255.	3.5	120
86	Single-wavelength anomalous diffraction phasing revisited. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1413-1420.	2.5	116
87	Crystal Structure of the Vesicular Transport Protein Sec17. <i>Molecular Cell</i> , 1999, 4, 85-95.	4.5	114
88	Studying calcium-triggered vesicle fusion in a single vesicle-vesicle content and lipid-mixing system. <i>Nature Protocols</i> , 2013, 8, 1-16.	5.5	113
89	NSF N-Terminal Domain Crystal Structure. <i>Molecular Cell</i> , 1999, 4, 97-107.	4.5	112
90	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> , 2004, 342, 229-245.	2.0	109

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91	Enabling X-ray free electron laser crystallography for challenging biological systems from a limited number of crystals. <i>ELife</i> , 2015, 4, .	2.8	106
92	Exploration of disorder in protein structures by X-ray restrained molecular dynamics. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991, 10, 340-358.	1.5	105
93	Crystal Structures of a Rab Protein in its Inactive and Active Conformations. <i>Journal of Molecular Biology</i> , 2000, 304, 585-598.	2.0	103
94	Structural basis of the interaction between RalA and Sec5, a subunit of the sec6/8 complex. <i>EMBO Journal</i> , 2003, 22, 3267-3278.	3.5	103
95	[13] Crystallographic refinement by simulated annealing: Methods and applications. <i>Methods in Enzymology</i> , 1997, 277, 243-269.	0.4	102
96	Analysis of a Yeast SNARE Complex Reveals Remarkable Similarity to the Neuronal SNARE Complex and a Novel Function for the C Terminus of the SNAP-25 Homolog, Sec9. <i>Journal of Biological Chemistry</i> , 1997, 272, 16610-16617.	1.6	99
97	X-ray scattering from unilamellar lipid vesicles. <i>Journal of Applied Crystallography</i> , 2005, 38, 126-131.	1.9	98
98	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> , 2007, 282, 5004-5014.	1.6	98
99	Single-Molecule Studies of the Neuronal SNARE Fusion Machinery. <i>Annual Review of Biochemistry</i> , 2009, 78, 903-928.	5.0	98
100	De novo phasing with X-ray laser reveals mosquito larvicide BinAB structure. <i>Nature</i> , 2016, 539, 43-47.	13.7	98
101	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> , 2013, 110, E2812-20.	3.3	97
102	Automated modeling of coiled coils: application to the GCN4 dimerization region. <i>Protein Engineering, Design and Selection</i> , 1991, 4, 649-659.	1.0	95
103	Amino-acid substitutions in a surface turn modulate protein stability. <i>Nature Structural Biology</i> , 1996, 3, 54-58.	9.7	95
104	Structure of a Human A-type Potassium Channel Interacting Protein DPPX, a Member of the Dipeptidyl Aminopeptidase Family. <i>Journal of Molecular Biology</i> , 2004, 343, 1055-1065.	2.0	92
105	Single-Molecule Studies of Synaptotagmin and Complexin Binding to the SNARE Complex. <i>Biophysical Journal</i> , 2005, 89, 690-702.	0.2	92
106	Botulinum Neurotoxin Heavy Chain Belt as an Intramolecular Chaperone for the Light Chain. <i>PLoS Pathogens</i> , 2007, 3, e113.	2.1	92
107	Receptor and substrate interactions of clostridial neurotoxins. <i>Toxicon</i> , 2009, 54, 550-560.	0.8	92
108	Three-dimensional molecular modeling with single molecule FRET. <i>Journal of Structural Biology</i> , 2011, 173, 497-505.	1.3	92

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109	Molecular mechanism of the synaptotagmin-SNARE interaction in Ca ²⁺ -triggered vesicle fusion. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 325-331.	3.6	89
110	Complexin inhibits spontaneous release and synchronizes Ca ²⁺ -triggered synaptic vesicle fusion by distinct mechanisms. <i>ELife</i> , 2014, 3, e03756.	2.8	89
111	Advances, Interactions, and Future Developments in the CNS, Phenix, and Rosetta Structural Biology Software Systems. <i>Annual Review of Biophysics</i> , 2013, 42, 265-287.	4.5	88
112	A Revised Model for the Oligomeric State of the N-Ethylmaleimide-sensitive Fusion Protein, NSF. <i>Journal of Biological Chemistry</i> , 1998, 273, 15675-15681.	1.6	85
113	Structural insights into the molecular mechanism of Ca ²⁺ -dependent exocytosis. <i>Current Opinion in Neurobiology</i> , 2000, 10, 293-302.	2.0	85
114	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> , 2009, 106, 3722-3727.	3.3	84
115	Recent developments for the efficient crystallographic refinement of macromolecular structures. <i>Current Opinion in Structural Biology</i> , 1998, 8, 606-611.	2.6	83
116	Transmembrane signal transduction of the β 3 integrin. <i>Protein Science</i> , 2009, 11, 1800-1812.	3.1	78
117	Conformational change of syntaxin linker region induced by Munc13s initiates SNARE complex formation in synaptic exocytosis. <i>EMBO Journal</i> , 2017, 36, 816-829.	3.5	78
118	NSF and p97/VCP: similar at first, different at last. <i>FEBS Letters</i> , 2003, 555, 126-133.	1.3	77
119	Human ornithine aminotransferase complexed with L-canaline and gabaculine: structural basis for substrate recognition. <i>Structure</i> , 1997, 5, 1067-1075.	1.6	75
120	High Resolution Structure, Stability, and Synaptotagmin Binding of a Truncated Neuronal SNARE Complex. <i>Journal of Biological Chemistry</i> , 2003, 278, 8630-8636.	1.6	75
121	New insights into clostridial neurotoxin-SNARE interactions. <i>Trends in Molecular Medicine</i> , 2005, 11, 377-381.	3.5	75
122	Expression of C1q3 in Discrete Neuronal Populations Controls Efferent Synapse Numbers and Diverse Behaviors. <i>Neuron</i> , 2016, 91, 1034-1051.	3.8	75
123	Successful prediction of the coiled coil geometry of the GCN4 leucine zipper domain by simulated annealing: Comparison to the X-ray structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 133-146.	1.5	73
124	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> , 2015, 71, 1987-1997.	2.5	73
125	Conformation of the synaptobrevin transmembrane domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8378-8383.	3.3	72
126	The pre-synaptic fusion machinery. <i>Current Opinion in Structural Biology</i> , 2019, 54, 179-188.	2.6	72

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127	Do NOE distances contain enough information to assess the relative populations of multi-conformer structures?. <i>Journal of Biomolecular NMR</i> , 1996, 7, 72-6.	1.6	71
128	Thermal Motion and Conformational Disorder in Protein Crystal Structures: Comparison of Multi-Conformer and Time-Averaging Models. <i>Israel Journal of Chemistry</i> , 1994, 34, 165-175.	1.0	69
129	Solution conformations of human growth hormone releasing factor: comparison of the restrained molecular dynamics and distance geometry methods for a system without long-range distance data. <i>Protein Engineering, Design and Selection</i> , 1987, 1, 399-406.	1.0	68
130	Site-Directed Dichroism As a Method for Obtaining Rotational and Orientational Constraints for Oriented Polymers. <i>Journal of the American Chemical Society</i> , 1997, 119, 8973-8980.	6.6	68
131	Molecular Dynamics Applied to X-ray Structure Refinement. <i>Accounts of Chemical Research</i> , 2002, 35, 404-412.	7.6	68
132	STRUCTURAL PERSPECTIVES OF PHOSPHOLAMBAN, A HELICAL TRANSMEMBRANE PENTAMER. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1997, 26, 157-179.	18.3	67
133	Structural insights into the molecular mechanism of calcium-dependent vesicle-membrane fusion. <i>Current Opinion in Structural Biology</i> , 2001, 11, 163-173.	2.6	67
134	Considerations for the refinement of low-resolution crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 923-932.	2.5	67
135	Structural principles of SNARE complex recognition by the AAA+ protein NSF. <i>ELife</i> , 2018, 7, .	2.8	67
136	Thermodynamics of protein-peptide interactions in the ribonuclease-S system studied by molecular dynamics and free energy calculations. <i>Biochemistry</i> , 1992, 31, 8661-8674.	1.2	66
137	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> , 2016, 113, E7590-E7599.	3.3	66
138	Capture and X-ray diffraction studies of protein microcrystals in a microfluidic trap array. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 928-940.	2.5	64
139	Protein dynamics and distance determination by NOE measurements. <i>FEBS Letters</i> , 1988, 236, 71-76.	1.3	63
140	High-density grids for efficient data collection from multiple crystals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 2-11.	1.1	62
141	Structure of Proteins Involved in Synaptic Vesicle Fusion in Neurons. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2001, 30, 157-171.	18.3	61
142	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> , 2007, 104, 15599-15606.	3.3	59
143	Helix packing in proteins: Prediction and energetic analysis of dimeric, trimeric, and tetrameric GCN4 coiled coil structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 20, 105-123.	1.5	58
144	Are there dominant membrane protein families with a given number of helices?. , 1997, 28, 465-466.		58

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145	A Potent Peptidomimetic Inhibitor of Botulinum Neurotoxin Serotype A Has a Very Different Conformation than SNAP-25 Substrate. <i>Structure</i> , 2008, 16, 1588-1597.	1.6	57
146	Formation of a yeast SNARE complex is accompanied by significant structural changes. <i>FEBS Letters</i> , 1997, 415, 49-55.	1.3	56
147	Structures of C1q-like Proteins Reveal Unique Features among the C1q/TNF Superfamily. <i>Structure</i> , 2015, 23, 688-699.	1.6	56
148	Electron cryomicroscopy structure of N-ethyl maleimide sensitive factor at 11 Å resolution. <i>EMBO Journal</i> , 2003, 22, 4365-4374.	3.5	54
149	X-ray structure determination at low resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 128-133.	2.5	54
150	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> , 2016, 113, 4338-4343.	3.3	54
151	The AAA+ superfamily: a review of the structural and mechanistic principles of these molecular machines. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2022, 57, 156-187.	2.3	54
152	Simulation analysis of structures on the reaction pathway of RNase A. <i>Journal of the American Chemical Society</i> , 1990, 112, 3826-3831.	6.6	53
153	Conformational substrates and uncertainty in macromolecular free energy calculations. <i>The Journal of Physical Chemistry</i> , 1993, 97, 3409-3417.	2.9	52
154	Direct Visualization of <i>Trans</i> -Synaptic Neurexin-1/Neuroigin Interactions during Synapse Formation. <i>Journal of Neuroscience</i> , 2014, 34, 15083-15096.	1.7	51
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