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Protein Science

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Citation Report

#	ARTICLE	IF	CITATIONS
1	On the quest for the elusive mechanism of action of daptomycin: Binding, fusion, and oligomerization. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1490-1499.	1.1	18
2	Crystal Structure of <i>Borrelia turicatae</i> protein, BTA121, a differentially regulated gene in the tick-mammalian transmission cycle of relapsing fever spirochetes. <i>Scientific Reports</i> , 2017, 7, 15310.	1.6	2
3	Combining high-resolution cryo-electron microscopy and mutagenesis to develop cowpea mosaic virus for bionanotechnology. <i>Biochemical Society Transactions</i> , 2017, 45, 1263-1269.	1.6	11
4	Structural insights into the assembly and polyA signal recognition mechanism of the human CPSF complex. <i>ELife</i> , 2017, 6, .	2.8	71
5	Molecular structure of human KATP in complex with ATP and ADP. <i>ELife</i> , 2017, 6, .	2.8	141
6	Development of a Prototype System for Archiving Integrative/Hybrid Structure Models of Biological Macromolecules. <i>Structure</i> , 2018, 26, 894-904.e2.	1.6	81
7	Structural basis for ATP-dependent chromatin remodelling by the INO80 complex. <i>Nature</i> , 2018, 556, 386-390.	13.7	188
8	Evolutionary analysis of mitochondrially encoded proteins of toad-headed lizards, <i>Phrynocephalus</i> , along an altitudinal gradient. <i>BMC Genomics</i> , 2018, 19, 185.	1.2	19
9	Cryo-EM structure of the nucleosome containing the <i>ALB1</i> enhancer DNA sequence. <i>Open Biology</i> , 2018, 8, .	1.5	31
10	MolProbity: More and better reference data for improved atom structure validation. <i>Protein Science</i> , 2018, 27, 293-315.	3.1	2,776
11	Automating tasks in protein structure determination with the clipper python module. <i>Protein Science</i> , 2018, 27, 207-216.	3.1	6
12	Molecular structure of promoter-bound yeast TFIID. <i>Nature Communications</i> , 2018, 9, 4666.	5.8	32
13	Epitope-Based Peptide Vaccine Against Fructose-Bisphosphate Aldolase of <i>Madurella mycetomatis</i> Using Immunoinformatics Approaches. <i>Bioinformatics and Biology Insights</i> , 2018, 12, 117793221880970.	1.0	14
14	Type 9 secretion system structures reveal a new protein transport mechanism. <i>Nature</i> , 2018, 564, 77-82.	13.7	130
15	Structural Basis for Cholesterol Transport-like Activity of the Hedgehog Receptor Patched. <i>Cell</i> , 2018, 175, 1352-1364.e14.	13.5	197
16	Rigid-Body Fitting of Atomic Models on 3D Density Maps of Electron Microscopy. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1105, 219-235.	0.8	3
17	Structure of the type VI secretion system TssK-TssF-TssG baseplate subcomplex revealed by cryo-electron microscopy. <i>Nature Communications</i> , 2018, 9, 5385.	5.8	37
18	Cryo-EM structure of the native butyrylcholinesterase tetramer reveals a dimer of dimers stabilized by a superhelical assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13270-13275.	3.3	24

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19	Diving into chemical bonding: An immersive analysis of the electron charge rearrangement through virtual reality. <i>Journal of Computational Chemistry</i> , 2018, 39, 2607-2617.	1.5	30
20	The Structure and Dynamics of <i>C.Âlegans</i> Tubulin Reveals the Mechanistic Basis of Microtubule Growth. <i>Developmental Cell</i> , 2018, 47, 191-204.e8.	3.1	61
21	Substrate-engaged 26 <i>S&lt;/i&gt;</i> proteasome structures reveal mechanisms for ATP-hydrolysisâ€driven translocation. <i>Science</i> , 2018, 362, .	6.0	226
22	Structural basis for anthrax toxin receptor 1 recognition by Seneca Valley Virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10934-E10940.	3.3	21
23	Microtubule structure by cryo-EM: snapshots of dynamic instability. <i>Essays in Biochemistry</i> , 2018, 62, 737-751.	2.1	63
24	Cryo-EM structure of the Ebola virus nucleoproteinâ€RNA complex at 3.6Å... resolution. <i>Nature</i> , 2018, 563, 137-140.	13.7	94
25	Structure of the membrane-assembled retromer coat determined by cryo-electron tomography. <i>Nature</i> , 2018, 561, 561-564.	13.7	169
26	Structural basis of the filamin A actin-binding domain interaction with F-actin. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 918-927.	3.6	60
27	4D cell biology: big data image analytics and lattice light-sheet imaging reveal dynamics of clathrin-mediated endocytosis in stem cellâ€derived intestinal organoids. <i>Molecular Biology of the Cell</i> , 2018, 29, 2959-2968.	0.9	42
28	Evolutionary shift toward protein-based architecture in trypanosomal mitochondrial ribosomes. <i>Science</i> , 2018, 362, .	6.0	107
29	Structural basis for potent and broad inhibition of HIV-1 RT by thiophene[3,2-d]pyrimidine non-nucleoside inhibitors. <i>ELife</i> , 2018, 7, .	2.8	57
30	The nuclear actin-containing Arp8 module is a linker DNA sensor driving INO80 chromatin remodeling. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 823-832.	3.6	63
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32	Toxoplasma Parasite Twisting Motion Mechanically Induces Host Cell Membrane Fission to Complete Invasion within a Protective Vacuole. <i>Cell Host and Microbe</i> , 2018, 24, 81-96.e5.	5.1	44
33	ConfocalVR: Immersive Visualization for Confocal Microscopy. <i>Journal of Molecular Biology</i> , 2018, 430, 4028-4035.	2.0	50
34	Molecular Visualization on the Holodeck. <i>Journal of Molecular Biology</i> , 2018, 430, 3982-3996.	2.0	70
35	Anticipating innovations in structural biology. <i>Quarterly Reviews of Biophysics</i> , 2018, 51, e8.	2.4	6
36	ATP Synthase Diseases of Mitochondrial Genetic Origin. <i>Frontiers in Physiology</i> , 2018, 9, 329.	1.3	88

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38	Structure, mechanism, and regulation of the chloroplast ATP synthase. <i>Science</i> , 2018, 360, .	6.0	308
39	Mechanisms of Channel Block in Calcium-Permeable AMPA Receptors. <i>Neuron</i> , 2018, 99, 956-968.e4.	3.8	87
40	Semantics for an Integrative and Immersive Pipeline Combining Visualization and Analysis of Molecular Data. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	20
41	Visualizing late states of human 40S ribosomal subunit maturation. <i>Nature</i> , 2018, 558, 249-253.	13.7	118
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43	Structural basis for regulation of human acetyl-CoA carboxylase. <i>Nature</i> , 2018, 558, 470-474.	13.7	135
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47	Modelling structures in cryo-EM maps. <i>Current Opinion in Structural Biology</i> , 2019, 58, 105-114.	2.6	53
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49	Archiving and disseminating integrative structure models. <i>Journal of Biomolecular NMR</i> , 2019, 73, 385-398.	1.6	20
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51	Atomic structures of an entire contractile injection system in both the extended and contracted states. <i>Nature Microbiology</i> , 2019, 4, 1885-1894.	5.9	45
52	Optimised Molecular Graphics on the HoloLens. , 2019, , .		4
53	Understanding the molecular interaction of human argonaute2 and miR20a complex: A molecular dynamics approach. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 19915-19924.	1.2	10
54	Evolutionary compaction and adaptation visualized by the structure of the dormant microsporidian ribosome. <i>Nature Microbiology</i> , 2019, 4, 1798-1804.	5.9	60

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57	Structure of the <i>Helicobacter pylori</i> Cag type IV secretion system. <i>ELife</i> , 2019, 8, .	2.8	78
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62	Cryo_fit: Democratization of flexible fitting for cryo-EM. <i>Journal of Structural Biology</i> , 2019, 208, 1-6.	1.3	30
63	Phloretin protects against cardiac damage and remodeling via restoring SIRT1 and anti-inflammatory effects in the streptozotocin-induced diabetic mouse model. <i>Aging</i> , 2019, 11, 2822-2835.	1.4	55
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84	Mitoribosomal small subunit biogenesis in trypanosomes involves an extensive assembly machinery. <i>Science</i> , 2019, 365, 1144-1149.	6.0	61
85	The cryo-EM structure of the acid activatable pore-forming immune effector Macrophage-expressed gene 1. <i>Nature Communications</i> , 2019, 10, 4288.	5.8	65
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147	Transferrin receptor binds virus capsid with dynamic motion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20462-20471.	3.3	24
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