Andrej Å ali

List of Publications by Year
in descending order

282 papers	68,875 citations	1990 101 h-index	750 250 g-index
309 all docs	309 docs citations	309 times ranked	72216 citing authors

#	Article	IF	Citations
1	Comparative Protein Modelling by Satisfaction of Spatial Restraints. Journal of Molecular Biology, 1993, 234, 779-815.	2.0	11,892
2	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. Nature, 2020, 583, 459-468.	13.7	3,542
3	Comparative Protein Structure Modeling Using Modeller. Current Protocols in Bioinformatics, 2006, 15, Unit-5.6.	25.8	2,858
4	Comparative Protein Structure Modeling of Genes and Genomes. Annual Review of Biophysics and Biomolecular Structure, 2000, 29, 291-325.	18.3	2,811
5	Comparative Protein Structure Modeling Using MODELLER. Current Protocols in Bioinformatics, 2016, 54, 5.6.1-5.6.37.	25.8	2,248
6	Statistical potential for assessment and prediction of protein structures. Protein Science, 2006, 15, 2507-2524.	3.1	2,104
7	Modeling of loops in protein structures. Protein Science, 2000, 9, 1753-1773.	3.1	1,895
8	Modeller: Generation and Refinement of Homology-Based Protein Structure Models. Methods in Enzymology, 2003, 374, 461-491.	0.4	1,469
9	Protein Structure Prediction and Structural Genomics. Science, 2001, 294, 93-96.	6.0	1,445
10	Protein Structure Modeling with MODELLER. Methods in Molecular Biology, 2008, 426, 145-159.	0.4	1,187
11	Comparative Protein Structure Modeling Using MODELLER. Current Protocols in Protein Science, 2007, 50, Unit 2.9.	2.8	1,056
12	Evaluation of comparative protein modeling by MODELLER. Proteins: Structure, Function and Bioinformatics, 1995, 23, 318-326.	1.5	1,035
13	The molecular architecture of the nuclear pore complex. Nature, 2007, 450, 695-701.	13.7	947
14	RCSB Protein Data Bank: powerful new tools for exploring 3D structures of biological macromolecules for basic and applied research and education in fundamental biology, biomedicine, biotechnology, bioengineering and energy sciences. Nucleic Acids Research, 2021, 49, D437-D451.	6.5	918
15	Comparative Protein Structure Modeling Using MODELLER. Current Protocols in Bioinformatics, 2014, 47, 5.6.1-32.	25.8	860
16	Insights into Secondary Metabolism from a Global Analysis of Prokaryotic Biosynthetic Gene Clusters. Cell, 2014, 158, 412-421.	13.5	801
17	Protein Folding: A Perspective from Theory and Experiment. Angewandte Chemie - International Edition, 1998, 37, 868-893.	7.2	778
18	ModLoop: automated modeling of loops in protein structures. Bioinformatics, 2003, 19, 2500-2501.	1.8	707

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19	Global landscape of HIVâ€“human protein complexes. Nature, 2012, 481, 365-370.	13.7	651
20	Protein Structure Modeling with MODELLER. Methods in Molecular Biology, 2014, 1137, 1-15.	0.4	516
21	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, .	6.0	508
22	ModBase, a database of annotated comparative protein structure models, and associated resources. Nucleic Acids Research, 2011, 39, D465-D474.	6.5	506
23	UCSF Chimera, MODELLER, and IMP: An integrated modeling system. Journal of Structural Biology, 2012, 179, 269-278.	1.3	506
24	Determining the architectures of macromolecular assemblies. Nature, 2007, 450, 683-694.	13.7	499
25	The molecular sociology of the cell. Nature, 2007, 450, 973-982.	13.7	497
26	Accurate SAXS Profile Computation and its Assessment by Contrast Variation Experiments. Biophysical Journal, 2013, 105, 962-974.	0.2	489
27	FoXS: a web server for rapid computation and fitting of SAXS profiles. Nucleic Acids Research, 2010, 38, W540-W544.	6.5	474
28	From words to literature in structural proteomics. Nature, 2003, 422, 216-225.	13.7	473
29	Comparative Protein Structure Modeling Using MODELLER. Current Protocols in Protein Science, 2016, 86, 2.9.1-2.9.37.	2.8	471
30	Putting the Pieces Together: Integrative Modeling Platform Software for Structure Determination of Macromolecular Assemblies. PLoS Biology, 2012, 10, e1001244.	2.6	469
31	Structure of the 80S Ribosome from Saccharomyces cerevisiaeâ€”tRNA-Ribosome and Subunit-Subunit Interactions. Cell, 2001, 107, 373-386.	13.5	462
32	Integrative structure and functional anatomy of a nuclear pore complex. Nature, 2018, 555, 475-482.	13.7	435
33	FoXS, FoXSDock and MultiFoXS: Single-state and multi-state structural modeling of proteins and their complexes based on SAXS profiles. Nucleic Acids Research, 2016, 44, W424-W429.	6.5	427
34	Molecular architecture of the 26S proteasome holocomplex determined by an integrative approach. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1380-1387.	3.3	422
35	Tools for comparative protein structure modeling and analysis. Nucleic Acids Research, 2003, 31, 3375-3380.	6.5	406
36	Protein Structure Modeling with MODELLER. Methods in Molecular Biology, 2017, 1654, 39-54.	0.4	376

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37	Structural genomics: beyond the Human Genome Project. Nature Genetics, 1999, 23, 151-157.	9.4	369
38	Architecture of the Protein-Conducting Channel Associated with the Translating 80S Ribosome. Cell, 2001, 107, 361-372.	13.5	368
39	Components of Coated Vesicles and Nuclear Pore Complexes Share a Common Molecular Architecture. PLoS Biology, 2004, 2, e380.	2.6	357
40	Simple rules for passive diffusion through the nuclear pore complex. Journal of Cell Biology, 2016, 215, 57-76.	2.3	337
41	Protein Structure Fitting and Refinement Guided by Cryo-EM Density. Structure, 2008, 16, 295-307.	1.6	334
42	Vif hijacks CBF-Î² to degrade APOBEC3G and promote HIV-1 infection. Nature, 2012, 481, 371-375.	13.7	312
43	Statistical potentials for fold assessment. Protein Science, 2002, 11, 430-448.	3.1	304
44	Advances in comparative protein-structure modelling. Current Opinion in Structural Biology, 1997, 7, 206-214.	2.6	289
45	Ligand discovery from a dopamine D3 receptor homology model and crystal structure. Nature Chemical Biology, 2011, 7, 769-778.	3.9	285
46	Comparative protein structure modeling by iterative alignment, model building and model assessment. Nucleic Acids Research, 2003, 31, 3982-3992.	6.5	277
47	Derivation of rules for comparative protein modeling from a database of protein structure alignments. Protein Science, 1994, 3, 1582-1596.	3.1	275
48	ModBase, a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2014, 42, D336-D346.	6.5	275
49	Study of the Structural Dynamics of the E. coli 70S Ribosome Using Real-Space Refinement. Cell, 2003, 113, 789-801.	13.5	273
50	Crystal Structure of the Î´â€² Subunit of the Clamp-Loader Complex of E. coli DNA Polymerase III. Cell, 1997, 91, 335-345.	13.5	268
51	MODBASE: a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2006, 34, D291-D295.	6.5	265
52	A structural perspective on proteinâ€“protein interactions. Current Opinion in Structural Biology, 2004, 14, 313-324.	2.6	260
53	MODBASE, a database of annotated comparative protein structure models, and associated resources. Nucleic Acids Research, 2004, 32, 217D-222.	6.5	256
54	Nuclear Import Receptor Inhibits Phase Separation of FUS through Binding to Multiple Sites. Cell, 2018, 173, 693-705.e22.	13.5	253

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55	Simple fold composition and modular architecture of the nuclear pore complex. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2172-2177.	3.3	243
56	Integrative Structural Biology. Science, 2013, 339, 913-915.	6.0	216
57	Evaluation of comparative protein structure modeling by MODELLER-3. Proteins: Structure, Function and Bioinformatics, 1997, 29, 50-58.	1.5	207
58	2017 publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution: an update. Acta Crystallographica Section D: Structural Biology, 2017, 73, 710-728.	1.1	205
59	Integrating Diverse Data for Structure Determination of Macromolecular Assemblies. Annual Review of Biochemistry, 2008, 77, 443-477.	5.0	204
60	LS-SNP: large-scale annotation of coding non-synonymous SNPs based on multiple information sources. Bioinformatics, 2005, 21, 2814-2820.	1.8	202
61	Crystal structure of a eukaryotic phosphate transporter. Nature, 2013, 496, 533-536.	13.7	202
62	Principles for Integrative Structural Biology Studies. Cell, 2019, 177, 1384-1403.	13.5	201
63	Evidence for a Shared Nuclear Pore Complex Architecture That Is Conserved from the Last Common Eukaryotic Ancestor. Molecular and Cellular Proteomics, 2009, 8, 2119-2130.	2.5	200
64	Protein structure modeling for structural genomics. Nature Structural Biology, 2000, 7, 986-990.	9.7	199
65	Comparative Protein Structure Modeling: Introduction and Practical Examples with Modeller. , 2000, 143, 97-129.		193
66	Molecular Architecture of the 40Sâ‹…eIF1â‹…eIF3 Translation Initiation Complex. Cell, 2014, 158, 1123-1135.	13.5	193
67	CryptoSite: Expanding the Druggable Proteome by Characterization and Prediction of Cryptic Binding Sites. Journal of Molecular Biology, 2016, 428, 709-719.	2.0	190
68	Alignment of protein sequences by their profiles. Protein Science, 2004, 13, 1071-1087.	3.1	184
69	Opportunities and Challenges in Building a Spatiotemporal Multi-scale Model of the Human Pancreatic Î² Cell. Cell, 2018, 173, 11-19.	13.5	179
70	Function of human Rh based on structure of RhCG at 2.1Âå„«. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9638-9643.	3.3	178
71	Role of organic cation transporter 3 (SLC22A3) and its missense variants in the pharmacologic action of metformin. Pharmacogenetics and Genomics, 2010, 20, 687-699.	0.7	175
72	Structure-based ligand discovery for the Large-neutral Amino Acid Transporter 1, LAT-1. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5480-5485.	3.3	173

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73	PIBASE: a comprehensive database of structurally defined protein interfaces. Bioinformatics, 2005, 21, 1901-1907.	1.8	169
74	The Enzyme Function Initiative. Biochemistry, 2011, 50, 9950-9962.	1.2	169
75	Structural genomics: A pipeline for providing structures for the biologist. Protein Science, 2002, 11, 723-738.	3.1	168
76	A Systematic Computational Analysis of Biosynthetic Gene Cluster Evolution: Lessons for Engineering Biosynthesis. PLoS Computational Biology, 2014, 10, e1004016.	1.5	164
77	A composite score for predicting errors in protein structure models. Protein Science, 2006, 15, 1653-1666.	3.1	160
78	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. Structure, 2015, 23, 1156-1167.	1.6	159
79	Multiple Conformations of E. coli Hsp90 in Solution: Insights into the Conformational Dynamics of Hsp90. Structure, 2008, 16, 755-765.	1.6	154
80	MODBASE, a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2009, 37, D347-D354.	6.5	154
81	Structure-based model of allostery predicts coupling between distant sites. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4875-4880.	3.3	153
82	Structural Characterization by Cross-linking Reveals the Detailed Architecture of a Coatomer-related Heptameric Module from the Nuclear Pore Complex. Molecular and Cellular Proteomics, 2014, 13, 2927-2943.	2.5	152
83	Structural genomics of protein phosphatases. Journal of Structural and Functional Genomics, 2007, 8, 121-140.	1.2	148
84	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	1.5	148
85	Structure and Function of the Nuclear Pore Complex Cytoplasmic mRNA Export Platform. Cell, 2016, 167, 1215-1228.e25.	13.5	148
86	Evolution of modular intraflagellar transport from a coatomer-like progenitor. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6943-6948.	3.3	144
87	Comprehensive Molecular Structure of the Eukaryotic Ribosome. Structure, 2009, 17, 1591-1604.	1.6	140
88	Integration of Small-Angle X-Ray Scattering Data into Structural Modeling of Proteins and Their Assemblies. Journal of Molecular Biology, 2008, 382, 1089-1106.	2.0	139
89	How well can the accuracy of comparative protein structure models be predicted?. Protein Science, 2008, 17, 1881-1893.	3.1	138
90	Hostâ€“pathogen protein interactions predicted by comparative modeling. Protein Science, 2007, 16, 2585-2596.	3.1	136

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91	Molecular architecture of the yeast Mediator complex. ELife, 2015, 4, .	2.8	136
92	Molecular Docking Screens Using Comparative Models of Proteins. Journal of Chemical Information and Modeling, 2009, 49, 2512-2527.	2.5	132
93	Discovery of Potent, Selective Multidrug and Toxin Extrusion Transporter 1 (MATE1, SLC47A1) Inhibitors Through Prescription Drug Profiling and Computational Modeling. Journal of Medicinal Chemistry, 2013, 56, 781-795.	2.9	131
94	Structure-based discovery of prescription drugs that interact with the norepinephrine transporter, NET. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15810-15815.	3.3	120
95	Optimized atomic statistical potentials: assessment of protein interfaces and loops. Bioinformatics, 2013, 29, 3158-3166.	1.8	119
96	Inferential Optimization for Simultaneous Fitting of Multiple Components into a CryoEM Map of Their Assembly. Journal of Molecular Biology, 2009, 388, 180-194.	2.0	117
97	Packaging of Proteases and Proteoglycans in the Granules of Mast Cells and Other Hematopoietic Cells. Journal of Biological Chemistry, 1995, 270, 19524-19531.	1.6	116
98	A Conserved Coatomer-related Complex Containing Sec13 and Seh1 Dynamically Associates With the Vacuole in Saccharomyces cerevisiae. Molecular and Cellular Proteomics, 2011, 10, M110.006478.	2.5	115
99	Ring closure activates yeast Î³TuRC for species-specific microtubule nucleation. Nature Structural and Molecular Biology, 2015, 22, 132-137.	3.6	115
100	MODBASE, a database of annotated comparative protein structure models. Nucleic Acids Research, 2002, 30, 255-259.	6.5	114
101	A strategy for dissecting the architectures of native macromolecular assemblies. Nature Methods, 2015, 12, 1135-1138.	9.0	113
102	Structureâ€“function mapping of a heptameric module in the nuclear pore complex. Journal of Cell Biology, 2012, 196, 419-434.	2.3	110
103	Subnanometer-resolution electron cryomicroscopy-based domain models for the cytoplasmic region of skeletal muscle RyR channel. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9610-9615.	3.3	106
104	Recovering a Representative Conformational Ensemble from Underdetermined Macromolecular Structural Data. Journal of the American Chemical Society, 2013, 135, 16595-16609.	6.6	106
105	Refinement of Protein Structures by Iterative Comparative Modeling and CryoEM Density Fitting. Journal of Molecular Biology, 2006, 357, 1655-1668.	2.0	104
106	Evolution and Physics in Comparative Protein Structure Modeling. Accounts of Chemical Research, 2002, 35, 413-421.	7.6	103
107	Structure-Based Assessment of Missense Mutations in Human BRCA1. Cancer Research, 2004, 64, 3790-3797.	0.4	103
108	Cys-Scanning Disulfide Crosslinking and Bayesian Modeling Probe the Transmembrane Signaling Mechanism of the Histidine Kinase, PhoQ. Structure, 2014, 22, 1239-1251.	1.6	103

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109	Fold assessment for comparative protein structure modeling. Protein Science, 2007, 16, 2412-2426.	3.1	101
110	A phosphotyrosine switch regulates organic cation transporters. Nature Communications, 2016, 7, 10880.	5.8	100
111	Comparison of human solute carriers. Protein Science, 2010, 19, 412-428.	3.1	99
112	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a â€œPlug and Playâ€• Domain. Methods in Enzymology, 2018, 606, 1-71.	0.4	99
113	Immunoglobulin motif DNA recognition and heterodimerization of the PEBP2/CBF Runt domain. Nature Structural Biology, 1999, 6, 615-619.	9.7	97
114	Macromolecular docking restrained by a small angle X-ray scattering profile. Journal of Structural Biology, 2011, 173, 461-471.	1.3	97
115	Reliability of Assessment of Protein Structure Prediction Methods. Structure, 2002, 10, 435-440.	1.6	95
116	Molecular Details Underlying Dynamic Structures and Regulation of the Human 26S Proteasome. Molecular and Cellular Proteomics, 2017, 16, 840-854.	2.5	93
117	Structural characterization of components of protein assemblies by comparative modeling and electron cryo-microscopy. Journal of Structural Biology, 2005, 149, 191-203.	1.3	92
118	Integrative structural modeling with small angle X-ray scattering profiles. BMC Structural Biology, 2012, 12, 17.	2.3	92
119	High-resolution network biology: connecting sequence with function. Nature Reviews Genetics, 2013, 14, 865-879.	7.7	92
120	Integrative structure modeling with the Integrative Modeling Platform. Protein Science, 2018, 27, 245-258.	3.1	92
121	Mechanism of lid closure in the eukaryotic chaperonin TRiC/CCT. Nature Structural and Molecular Biology, 2008, 15, 746-753.	3.6	91
122	Uncertainty in integrative structural modeling. Current Opinion in Structural Biology, 2014, 28, 96-104.	2.6	91
123	Architecture of the Human and Yeast General Transcription and DNA Repair Factor TFIIH. Molecular Cell, 2015, 59, 794-806.	4.5	91
124	On a benderâ€”BARs, ESCRTs, COPs, and finally getting your coat. Journal of Cell Biology, 2011, 193, 963-972.	2.3	88
125	Comprehensive structure and functional adaptations of the yeast nuclear pore complex. Cell, 2022, 185, 361-378.e25.	13.5	87
126	Slide-and-exchange mechanism for rapid and selective transport through the nuclear pore complex. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2489-97.	3.3	85

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127	Molecular Modeling and Ligand Docking for Solute Carrier (SLC) Transporters. Current Topics in Medicinal Chemistry, 2013, 13, 843-856.	1.0	85
128	PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. Structure, 2017, 25, 1317-1318.	1.6	84
129	<scp>RCSB</scp> Protein Data Bank: Celebrating 50â€‰years of the <scp>PDB</scp> with new tools for understanding and visualizing biological macromolecules in <scp>3D</scp>. Protein Science, 2022, 31, 187-208.	3.1	84
130	Finding Cures for Tropical Diseases: Is Open Source an Answer?. PLoS Medicine, 2004, 1, e56.	3.9	82
131	Alignment of multiple protein structures based on sequence and structure features. Protein Engineering, Design and Selection, 2009, 22, 569-574.	1.0	82
132	The proteasome-interacting Ecm29 protein disassembles the 26S proteasome in response to oxidative stress. Journal of Biological Chemistry, 2017, 292, 16310-16320.	1.6	82
133	Development of a Prototype System for Archiving Integrative/Hybrid Structure Models of Biological Macromolecules. Structure, 2018, 26, 894-904.e2.	1.6	81
134	Protein Structure Modeling with MODELLER. Methods in Molecular Biology, 2021, 2199, 239-255.	0.4	81
135	A method for integrative structure determination of protein-protein complexes. Bioinformatics, 2012, 28, 3282-3289.	1.8	78
136	Modeling mutations in protein structures. Protein Science, 2007, 16, 2030-2041.	3.1	77
137	Report of the wwPDB Small-Angle Scattering Task Force: Data Requirements for Biomolecular Modeling and the PDB. Structure, 2013, 21, 875-881.	1.6	77
138	LigBase: a database of families of aligned ligand binding sites in known protein sequences and structures. Bioinformatics, 2002, 18, 200-201.	1.8	76
139	The structural dynamics of macromolecular processes. Current Opinion in Cell Biology, 2009, 21, 97-108.	2.6	74
140	Combining electron microscopy and comparative protein structure modeling. Current Opinion in Structural Biology, 2005, 15, 578-585.	2.6	73
141	Statistical Potential for Modeling and Ranking of Proteinâ€“Ligand Interactions. Journal of Chemical Information and Modeling, 2011, 51, 3078-3092.	2.5	69
142	Comparative Protein Structure Modeling and its Applications to Drug Discovery. Annual Reports in Medicinal Chemistry, 2004, 39, 259-276.	0.5	68
143	Assessing Exhaustiveness of Stochastic Sampling for Integrative Modeling of Macromolecular Structures. Biophysical Journal, 2017, 113, 2344-2353.	0.2	68
144	Integrative Structureâ€“Function Mapping of the Nucleoporin Nup133 Suggests a Conserved Mechanism for Membrane Anchoring of the Nuclear Pore Complex. Molecular and Cellular Proteomics, 2014, 13, 2911-2926.	2.5	67

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145	Immunoproteasome functions explained by divergence in cleavage specificity and regulation. ELife, 2017, 6, .	2.8	66
146	Integrative Structure Modeling of Macromolecular Assemblies from Proteomics Data. Molecular and Cellular Proteomics, 2010, 9, 1689-1702.	2.5	64
147	Coordinating the impact of structural genomics on the human Î±-helical transmembrane proteome. Nature Structural and Molecular Biology, 2013, 20, 135-138.	3.6	64
148	Molecular Architecture and Function of the SEA Complex, a Modulator of the TORC1 Pathway. Molecular and Cellular Proteomics, 2014, 13, 2855-2870.	2.5	64
149	Determining macromolecular assembly structures by molecular docking and fitting into an electron density map. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3205-3211.	1.5	63
150	Prediction of protease substrates using sequence and structure features. Bioinformatics, 2010, 26, 1714-1722.	1.8	61
151	Molecular Architecture of the Major Membrane Ring Component of the Nuclear Pore Complex. Structure, 2017, 25, 434-445.	1.6	61
152	Functional links between proteins. Nature, 1999, 402, 23-26.	13.7	60
153	Outcome of a Workshop on Archiving Structural Models of Biological Macromolecules. Structure, 2006, 14, 1211-1217.	1.6	60
154	Cross-activating c-Met/Î²1 integrin complex drives metastasis and invasive resistance in cancer. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8685-E8694.	3.3	60
155	High-Throughput Computational and Experimental Techniques in Structural Genomics. Genome Research, 2004, 14, 2145-2154.	2.4	59
156	Structure of Complement C3(H2O) Revealed By Quantitative Cross-Linking/Mass Spectrometry And Modeling. Molecular and Cellular Proteomics, 2016, 15, 2730-2743.	2.5	59
157	Variable gap penalty for protein sequenceâ€“structure alignment. Protein Engineering, Design and Selection, 2006, 19, 129-133.	1.0	58
158	Evolutionary constraints on structural similarity in orthologs and paralogs. Protein Science, 2009, 18, 1306-1315.	3.1	58
159	Scoring Largeâ€Scale Affinity Purification Mass Spectrometry Datasets with MiST. Current Protocols in Bioinformatics, 2015, 49, 8.19.1-8.19.16.	25.8	58
160	Discovery of Competitive and Noncompetitive Ligands of the Organic Cation Transporter 1 (OCT1;) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.9	58
161	Structural dynamics of the human COP9 signalosome revealed by cross-linking mass spectrometry and integrative modeling. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 4088-4098.	3.3	58
162	Functional Impact of Missense Variants in BRCA1 Predicted by Supervised Learning. PLoS Computational Biology, 2007, 3, e26.	1.5	57

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163	Protein complex compositions predicted by structural similarity. Nucleic Acids Research, 2006, 34, 2943-2952.	6.5	56
164	Selecting Optimum Eukaryotic Integral Membrane Proteins for Structure Determination by Rapid Expression and Solubilization Screening. Journal of Molecular Biology, 2009, 385, 820-830.	2.0	53
165	Structure, Dynamics, Evolution, and Function of a Major Scaffold Component in the Nuclear Pore Complex. Structure, 2013, 21, 560-571.	1.6	53
166	A Residue-Resolved Bayesian Approach to Quantitative Interpretation of Hydrogenâ€“Deuterium Exchange from Mass Spectrometry: Application to Characterizing Proteinâ€“Ligand Interactions. Journal of Physical Chemistry B, 2017, 121, 3493-3501.	1.2	52
167	The optimal size of a globular protein domain: A simple sphere-packing model. Chemical Physics Letters, 2005, 405, 224-228.	1.2	51
168	Toward an Integrated Structural Model of the 26S Proteasome. Molecular and Cellular Proteomics, 2010, 9, 1666-1677.	2.5	50
169	Limits of Ligand Selectivity from Docking to Models: In Silico Screening for A1 Adenosine Receptor Antagonists. PLoS ONE, 2012, 7, e49910.	1.1	50
170	Bayesian Weighing of Electron Cryo-Microscopy Data for Integrative Structural Modeling. Structure, 2019, 27, 175-188.e6.	1.6	50
171	High Selectivity of the Î³-Aminobutyric Acid Transporter 2 (GAT-2, SLC6A13) Revealed by Structure-based Approach. Journal of Biological Chemistry, 2012, 287, 37745-37756.	1.6	49
172	New York-Structural GenomiX Research Consortium (NYSGXRC): A Large Scale Center for the Protein Structure Initiative. Journal of Structural and Functional Genomics, 2005, 6, 225-232.	1.2	48
173	Impact of Mutations on the Allosteric Conformational Equilibrium. Journal of Molecular Biology, 2013, 425, 647-661.	2.0	48
174	Importin-9 wraps around the H2A-H2B core to act as nuclear importer and histone chaperone. ELife, 2019, 8, .	2.8	47
175	Regulatory Elements within the Prodomain of Falcipain-2, a Cysteine Protease of the Malaria Parasite Plasmodium falciparum. PLoS ONE, 2009, 4, e5694.	1.1	46
176	Classifying Variants of Undetermined Significance in BRCA2 with Protein Likelihood Ratios. Cancer Informatics, 2008, 6, CIN.S618.	0.9	45
177	Elucidating the Mechanism of Substrate Recognition by the Bacterial Hsp90 Molecular Chaperone. Journal of Molecular Biology, 2014, 426, 2393-2404.	2.0	45
178	From integrative structural biology to cell biology. Journal of Biological Chemistry, 2021, 296, 100743.	1.6	45
179	Assembly of macromolecular complexes by satisfaction of spatial restraints from electron microscopy images. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18821-18826.	3.3	44
180	The molecular architecture of the yeast spindle pole body core determined by Bayesian integrative modeling. Molecular Biology of the Cell, 2017, 28, 3298-3314.	0.9	44

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181	Structural basis of CD4 downregulation by HIV-1 Nef. Nature Structural and Molecular Biology, 2020, 27, 822-828.	3.6	44
182	The Overlap of Small Molecule and Protein Binding Sites within Families of Protein Structures. PLoS Computational Biology, 2010, 6, e1000668.	1.5	43
183	Insights into HIV-1 proviral transcription from integrative structure and dynamics of the Tat:AFF4:P-TEFb:TAR complex. ELife, 2016, 5, .	2.8	43
184	Regulation of Rvb1/Rvb2 by a Domain within the INO80 Chromatin Remodeling Complex Implicates the Yeast Rvbs as Protein Assembly Chaperones. Cell Reports, 2017, 19, 2033-2044.	2.9	43
185	Localization of protein-binding sites within families of proteins. Protein Science, 2005, 14, 2350-2360.	3.1	40
186	Minimalist Representations and the Importance of Nearest Neighbor Effects in Protein Folding Simulations. Journal of Molecular Biology, 2006, 363, 835-857.	2.0	40
187	Modeling of Proteins and Their Assemblies with the Integrative Modeling Platform. Methods in Molecular Biology, 2014, 1091, 277-295.	0.4	40
188	Structural Modeling of Protein Interactions by Analogy: Application to PSD-95. PLoS Computational Biology, 2006, 2, e153.	1.5	39
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