Andrej Å ali

List of Publications by Year
in descending order

282 papers	68,875 citations	1994 101 h-index	751 250 g-index
309 all docs	309 docs citations	309 times ranked	72216 citing authors

#	Article	IF	Citations
1	Integrative structure determination of histones H3 and H4 using genetic interactions. FEBS Journal, 2023, 290, 2565-2575.	4.7	0
2	<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.	7.6	84
3	From systems to structure â€” using genetic data to model protein structures. Nature Reviews Genetics, 2022, 23, 342-354.	16.3	14
4	Comprehensive structure and functional adaptations of the yeast nuclear pore complex. Cell, 2022, 185, 361-378.e25.	28.9	87
5	Soluble TREM2 inhibits secondary nucleation of AÎ² fibrillization and enhances cellular uptake of fibrillar AÎ². Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	14
6	Soft X-ray tomography to map and quantify organelle interactions at the mesoscale. Structure, 2022, 30, 510-521.e3.	3.3	22
7	Integration of software tools for integrative modeling of biomolecular systems. Journal of Structural Biology, 2022, 214, 107841.	2.8	7
8	Auto-segmentation and time-dependent systematic analysis of mesoscale cellular structure in Î²-cells during insulin secretion. PLoS ONE, 2022, 17, e0265567.	2.5	5
9	The YÎ¦ motif defines the structure-activity relationships of human 20S proteasome activators. Nature Communications, 2022, 13, 1226.	12.8	10
10	Doublecortin engages the microtubule lattice through a cooperative binding mode involving its C-terminal domain. ELife, 2022, 11, .	6.0	7
11	Using Integrative Modeling Platform to compute, validate, and archive a model of a protein complex structure. Protein Science, 2021, 30, 250-261.	7.6	31
12	IMProv: A Resource for Cross-link-Driven Structure Modeling that Accommodates Protein Dynamics. Molecular and Cellular Proteomics, 2021, 20, 100139.	3.8	6
13	Characterization of an A3G-VifHIV-1-CRL5-CBFÎ² Structure Using a Cross-linking Mass Spectrometry Pipeline for Integrative Modeling of Hostâ€“Pathogen Complexes. Molecular and Cellular Proteomics, 2021, 20, 100132.	3.8	4
14	The EBF1-PDGFRB T681I mutation is highly resistant to imatinib and dasatinib in vitro and detectable in clinical samples prior to treatment. Haematologica, 2021, 106, 2242-2245.	3.5	3
15	Global Protease Activity Profiling Identifies HER2-Driven Proteolysis in Breast Cancer. ACS Chemical Biology, 2021, 16, 712-723.	3.4	6
16	CM1-driven assembly and activation of yeast Î³-tubulin small complex underlies microtubule nucleation. ELife, 2021, 10, .	6.0	23
17	Integrative analysis reveals unique structural and functional features of the Smc5/6 complex. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	35
18	The active DNA-PK holoenzyme occupies a tensed state in a staggered synaptic complex. Structure, 2021, 29, 467-478.e6.	3.3	9

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19	Bayesian metamodeling of complex biological systems across varying representations. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	19
20	From integrative structural biology to cell biology. Journal of Biological Chemistry, 2021, 296, 100743.	3.4	45
21	Protein Structure Modeling with MODELLER. Methods in Molecular Biology, 2021, 2199, 239-255.	0.9	81
22	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.	14.5	918
23	New system for archiving integrative structures. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1486-1496.	2.3	22
24	Reversible phosphorylation of cyclin T1 promotes assembly and stability of P-TEFb. ELife, 2021, 10, .	6.0	14
25	Highly synergistic combinations of nanobodies that target SARS-CoV-2 and are resistant to escape. ELife, 2021, 10, .	6.0	36
26	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, .	12.6	508
27	Structural basis of CD4 downregulation by HIV-1 Nef. Nature Structural and Molecular Biology, 2020, 27, 822-828.	8.2	44
28	Visualizing subcellular rearrangements in intact Î² cells using soft x-ray tomography. Science Advances, 2020, 6, .	10.3	36
29	Genetic interaction mapping informs integrative structure determination of protein complexes. Science, 2020, 370, .	12.6	24
30	Enhancer Reprogramming within Pre-existing Topologically Associated Domains Promotes TGF-Î²-Induced EMT and Cancer Metastasis. Molecular Therapy, 2020, 28, 2083-2095.	8.2	22
31	Integrative structure and function of the yeast exocyst complex. Protein Science, 2020, 29, 1486-1501.	7.6	29
32	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. Nature, 2020, 583, 459-468.	27.8	3,542
33	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.	7.1	58
34	Crippling life support for SARS-CoV-2 and other viruses through synthetic lethality. Journal of Cell Biology, 2020, 219, .	5.2	20
35	Archiving and disseminating integrative structure models. Journal of Biomolecular NMR, 2019, 73, 385-398.	2.8	20
36	SSEThread: Integrative threading of the DNA-PKcs sequence based on data from chemical cross-linking and hydrogen deuterium exchange. Progress in Biophysics and Molecular Biology, 2019, 147, 92-102.	2.9	8

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37	Principles for Integrative Structural Biology Studies. Cell, 2019, 177, 1384-1403.	28.9	201
38	Glutamine Side Chain 13Câ•18O as a Nonperturbative IR Probe of Amyloid Fibril Hydration and Assembly. Journal of the American Chemical Society, 2019, 141, 7320-7326.	13.7	13
39	Optimizing model representation for integrative structure determination of macromolecular assemblies. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 540-545.	7.1	16
40	Bayesian Weighing of Electron Cryo-Microscopy Data for Integrative Structural Modeling. Structure, 2019, 27, 175-188.e6.	3.3	50
41	Modeling Biological Complexes Using Integrative Modeling Platform. Methods in Molecular Biology, 2019, 2022, 353-377.	0.9	34
42	Importin-9 wraps around the H2A-H2B core to act as nuclear importer and histone chaperone. ELife, 2019, 8, .	6.0	47
43	Development of a Prototype System for Archiving Integrative/Hybrid Structure Models of Biological Macromolecules. Structure, 2018, 26, 894-904.e2.	3.3	81
44	Nuclear Import Receptor Inhibits Phase Separation of FUS through Binding to Multiple Sites. Cell, 2018, 173, 693-705.e22.	28.9	253
45	Integrative structure and functional anatomy of a nuclear pore complex. Nature, 2018, 555, 475-482.	27.8	435
46	Opportunities and Challenges in Building a Spatiotemporal Multi-scale Model of the Human Pancreatic Î² Cell. Cell, 2018, 173, 11-19.	28.9	179
47	Integrative structure modeling with the Integrative Modeling Platform. Protein Science, 2018, 27, 245-258.	7.6	92
48	Integrative Structure Determination of Protein Complexes by Inferred Structural Equivalence. Biophysical Journal, 2018, 114, 61a.	0.5	1
49	Predicting CD4 T-cell epitopes based on antigen cleavage, MHCII presentation, and TCR recognition. PLoS ONE, 2018, 13, e0206654.	2.5	31
50	EpCAM homo-oligomerization is not the basis for its role in cell-cell adhesion. Scientific Reports, 2018, 8, 13269.	3.3	30
51	Architecture of Pol II(G) and molecular mechanism of transcription regulation by Gdown1. Nature Structural and Molecular Biology, 2018, 25, 859-867.	8.2	31
52	Prediction of enzymatic pathways by integrative pathway mapping. ELife, 2018, 7, .	6.0	30
53	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a â€œPlug and Playâ€• Domain. Methods in Enzymology, 2018, 606, 1-71.	1.0	99
54	Structure of the 80S Ribosome from Saccharomyces cerevisiaeâ€“tRNA-Ribosome and Subunit-Subunit Interactions. journal of hand surgery Asian-Pacific volume, The, 2018, , 286-299.	0.4	0

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55	Architecture of the Protein-Conducting Channel Associated with the Translating 80S Ribosome. journal of hand surgery Asian-Pacific volume, The, 2018, , 274-285.	0.4	0
56	Molecular Architecture of the Major Membrane Ring Component of the Nuclear Pore Complex. Structure, 2017, 25, 434-445.	3.3	61
57	Discovery of Competitive and Noncompetitive Ligands of the Organic Cation Transporter 1 (OCT1;) Tj ETQq1 1 0.784314 rgBT /Overl	6.4	58
58	Computational Discovery and Experimental Validation of Inhibitors of the Human Intestinal Transporter OATP2B1. Journal of Chemical Information and Modeling, 2017, 57, 1402-1413.	5.4	23
59	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.	6.4	43
60	Molecular Details Underlying Dynamic Structures and Regulation of the Human 26S Proteasome. Molecular and Cellular Proteomics, 2017, 16, 840-854.	3.8	93
61	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.	7.1	60
62	Protein Structure Modeling with MODELLER. Methods in Molecular Biology, 2017, 1654, 39-54.	0.9	376
63	The proteasome-interacting Ecm29 protein disassembles the 26S proteasome in response to oxidative stress. Journal of Biological Chemistry, 2017, 292, 16310-16320.	3.4	82
64	PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. Structure, 2017, 25, 1317-1318.	3.3	84
65	The molecular architecture of the yeast spindle pole body core determined by Bayesian integrative modeling. Molecular Biology of the Cell, 2017, 28, 3298-3314.	2.1	44
66	Assessing Exhaustiveness of Stochastic Sampling for Integrative Modeling of Macromolecular Structures. Biophysical Journal, 2017, 113, 2344-2353.	0.5	68
67	Human Concentrative Nucleoside Transporter 3 (hCNT3, SLC28A3) Forms a Cyclic Homotrimer. Biochemistry, 2017, 56, 3475-3483.	2.5	15
68	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.	2.6	52
69	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.	2.3	205
70	Reconstruction of 3D structures of MET antibodies from electron microscopy 2D class averages. PLoS ONE, 2017, 12, e0175758.	2.5	10
71	Immunoproteasome functions explained by divergence in cleavage specificity and regulation. ELife, 2017, 6, .	6.0	66
72	Insights into HIV-1 proviral transcription from integrative structure and dynamics of the Tat:AFF4:P-TEFb:TAR complex. ELife, 2016, 5, .	6.0	43

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73	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.	2.6	148
74	Editorial overview: Biophysical and molecular biological methods. Current Opinion in Structural Biology, 2016, 40, ix-xi.	5.7	0
75	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.	7.1	85
76	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.	14.5	427
77	Simple rules for passive diffusion through the nuclear pore complex. Journal of Cell Biology, 2016, 215, 57-76.	5.2	337
78	Guinea Pig Prion Protein Supports Rapid Propagation of Bovine Spongiform Encephalopathy and Variant Creutzfeldt-Jakob Disease Prions. Journal of Virology, 2016, 90, 9558-9569.	3.4	3
79	A phosphotyrosine switch regulates organic cation transporters. Nature Communications, 2016, 7, 10880.	12.8	100
80	Structure and Function of the Nuclear Pore Complex Cytoplasmic mRNA Export Platform. Cell, 2016, 167, 1215-1228.e25.	28.9	148
81	Comparative Protein Structure Modeling Using MODELLER. Current Protocols in Protein Science, 2016, 86, 2.9.1-2.9.37.	2.8	471
82	Clustering of disulfide-rich peptides provides scaffolds for hit discovery by phage display: application to interleukin-23. BMC Bioinformatics, 2016, 17, 481.	2.6	9
83	Comparative Protein Structure Modeling Using MODELLER. Current Protocols in Bioinformatics, 2016, 54, 5.6.1-5.6.37.	25.8	2,248
84	Structure of Complement C3(H2O) Revealed By Quantitative Cross-Linking/Mass Spectrometry And Modeling. Molecular and Cellular Proteomics, 2016, 15, 2730-2743.	3.8	59
85	CryptoSite: Expanding the Druggable Proteome by Characterization and Prediction of Cryptic Binding Sites. Journal of Molecular Biology, 2016, 428, 709-719.	4.2	190
86	Structure of Î³-tubulin small complex based on a cryo-EM map, chemical cross-links, and a remotely related structure. Journal of Structural Biology, 2016, 194, 303-310.	2.8	23
87	Structural Model of the Bilitranslocase Transmembrane Domain Supported by NMR and FRET Data. PLoS ONE, 2015, 10, e0135455.	2.5	8
88	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
89	Assembly and Molecular Architecture of the Phosphoinositide 3-Kinase p85Î± Homodimer. Journal of Biological Chemistry, 2015, 290, 30390-30405.	3.4	25
90	Topological Models of Heteromeric Protein Assemblies from Mass Spectrometry: Application to the Yeast eIF3:eIF5 Complex. Chemistry and Biology, 2015, 22, 117-128.	6.0	38

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91	Ring closure activates yeast Î³TuRC for species-specific microtubule nucleation. Nature Structural and Molecular Biology, 2015, 22, 132-137.	8.2	115
92	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. Structure, 2015, 23, 1156-1167.	3.3	159
93	A strategy for dissecting the architectures of native macromolecular assemblies. Nature Methods, 2015, 12, 1135-1138.	19.0	113
94	Small-Molecule Allosteric Modulators of the Protein Kinase PDK1 from Structure-Based Docking. Journal of Medicinal Chemistry, 2015, 58, 8285-8291.	6.4	32
95	Prion Proteinâ€"Antibody Complexes Characterized by Chromatography-Coupled Small-Angle X-Ray Scattering. Biophysical Journal, 2015, 109, 793-805.	0.5	33
96	Architecture of the Human and Yeast General Transcription and DNA Repair Factor TFIIH. Molecular Cell, 2015, 59, 794-806.	9.7	91
97	Prediction of Functionally Important Phospho-Regulatory Events in Xenopus laevis Oocytes. PLoS Computational Biology, 2015, 11, e1004362.	3.2	14
98	Molecular architecture of the yeast Mediator complex. ELife, 2015, 4, .	6.0	136
99	Protein Structure Modeling with MODELLER. Methods in Molecular Biology, 2014, 1137, 1-15.	0.9	516
100	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.	3.8	152
101	Determining Protein Complex Structures Based on a Bayesian Model of in Vivo FÃ¶rster Resonance Energy Transfer (FRET) Data. Molecular and Cellular Proteomics, 2014, 13, 2812-2823.	3.8	29
102	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.	3.8	67
103	Molecular Architecture and Function of the SEA Complex, a Modulator of the TORC1 Pathway. Molecular and Cellular Proteomics, 2014, 13, 2855-2870.	3.8	64
104	ModBase, a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2014, 42, D336-D346.	14.5	275
105	A Systematic Computational Analysis of Biosynthetic Gene Cluster Evolution: Lessons for Engineering Biosynthesis. PLoS Computational Biology, 2014, 10, e1004016.	3.2	164
106	Elucidating the Mechanism of Substrate Recognition by the Bacterial Hsp90 Molecular Chaperone. Journal of Molecular Biology, 2014, 426, 2393-2404.	4.2	45
107	Modeling of Proteins and Their Assemblies with the Integrative Modeling Platform. Methods in Molecular Biology, 2014, 1091, 277-295.	0.9	40
108	Uncertainty in integrative structural modeling. Current Opinion in Structural Biology, 2014, 28, 96-104.	5.7	91

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109	Comparative Protein Structure Modeling Using MODELLER. Current Protocols in Bioinformatics, 2014, 47, 5.6.1-32.	25.8	860
110	Molecular Architecture of Photoreceptor Phosphodiesterase Elucidated by Chemical Cross-Linking and Integrative Modeling. Journal of Molecular Biology, 2014, 426, 3713-3728.	4.2	37
111	Cys-Scanning Disulfide Crosslinking and Bayesian Modeling Probe the Transmembrane Signaling Mechanism of the Histidine Kinase, PhoQ. Structure, 2014, 22, 1239-1251.	3.3	103
112	Insights into Secondary Metabolism from a Global Analysis of Prokaryotic Biosynthetic Gene Clusters. Cell, 2014, 158, 412-421.	28.9	801
113	Molecular Architecture of the 40Sâ‹…eIF1â‹…eIF3 Translation Initiation Complex. Cell, 2014, 158, 1123-1135.	28.9	193
114	Prediction of Substrates for Glutathione Transferases by Covalent Docking. Journal of Chemical Information and Modeling, 2014, 54, 1687-1699.	5.4	20
115	SAXS Merge: an automated statistical method to merge SAXS profiles using Gaussian processes. Journal of Synchrotron Radiation, 2014, 21, 203-208.	2.4	15
116	Coordinating the impact of structural genomics on the human Î±-helical transmembrane proteome. Nature Structural and Molecular Biology, 2013, 20, 135-138.	8.2	64
117	Deamination of 6-Aminodeoxyfutalosine in Menaquinone Biosynthesis by Distantly Related Enzymes. Biochemistry, 2013, 52, 6525-6536.	2.5	12
118	Structure-Guided Discovery of New Deaminase Enzymes. Journal of the American Chemical Society, 2013, 135, 13927-13933.	13.7	16
119	High-resolution network biology: connecting sequence with function. Nature Reviews Genetics, 2013, 14, 865-879.	16.3	92
120	Accurate SAXS Profile Computation and its Assessment by Contrast Variation Experiments. Biophysical Journal, 2013, 105, 962-974.	0.5	489
121	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.	6.4	131
122	Assignment of Pterin Deaminase Activity to an Enzyme of Unknown Function Guided by Homology Modeling and Docking. Journal of the American Chemical Society, 2013, 135, 795-803.	13.7	32
123	Impact of Mutations on the Allosteric Conformational Equilibrium. Journal of Molecular Biology, 2013, 425, 647-661.	4.2	48
124	Integrative Structural Biology. Science, 2013, 339, 913-915.	12.6	216
125	Structure, Dynamics, Evolution, and Function of a Major Scaffold Component in the Nuclear Pore Complex. Structure, 2013, 21, 560-571.	3.3	53
126	Crystal structure of a eukaryotic phosphate transporter. Nature, 2013, 496, 533-536.	27.8	202

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127	Report of the wwPDB Small-Angle Scattering Task Force: Data Requirements for Biomolecular Modeling and the PDB. Structure, 2013, 21, 875-881.	3.3	77
128	Recovering a Representative Conformational Ensemble from Underdetermined Macromolecular Structural Data. Journal of the American Chemical Society, 2013, 135, 16595-16609.	13.7	106
129	Mapping Polymerization and Allostery of Hemoglobin S Using Point Mutations. Journal of Physical Chemistry B, 2013, 117, 13058-13068.	2.6	3
130	Optimized atomic statistical potentials: assessment of protein interfaces and loops. Bioinformatics, 2013, 29, 3158-3166.	4.1	119
131	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.	7.1	144
132	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.	7.1	173
133	Molecular Modeling and Ligand Docking for Solute Carrier (SLC) Transporters. Current Topics in Medicinal Chemistry, 2013, 13, 843-856.	2.1	85
134	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.	7.1	44
135	Limits of Ligand Selectivity from Docking to Models: In Silico Screening for A1 Adenosine Receptor Antagonists. PLoS ONE, 2012, 7, e49910.	2.5	50
136	Structureâ€“function mapping of a heptameric module in the nuclear pore complex. Journal of Cell Biology, 2012, 196, 419-434.	5.2	110
137	A method for integrative structure determination of protein-protein complexes. Bioinformatics, 2012, 28, 3282-3289.	4.1	78
138	UCSF Chimera, MODELLER, and IMP: An integrated modeling system. Journal of Structural Biology, 2012, 179, 269-278.	2.8	506
139	Vif hijacks CBF-Î² to degrade APOBEC3G and promote HIV-1 infection. Nature, 2012, 481, 371-375.	27.8	312
140	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.	7.1	422
141	Integrative structural modeling with small angle X-ray scattering profiles. BMC Structural Biology, 2012, 12, 17.	2.3	92
142	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.	3.4	49
143	Putting the Pieces Together: Integrative Modeling Platform Software for Structure Determination of Macromolecular Assemblies. PLoS Biology, 2012, 10, e1001244.	5.6	469
144	Atomic structure of the nuclear pore complex targeting domain of a Nup116 homologue from the yeast, Candida glabrata. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2110-2116.	2.6	7

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145	Global landscape of HIVâ€“human protein complexes. Nature, 2012, 481, 365-370.	27.8	651
146	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.	7.1	153
147	Virtual Ligand Screening Against Comparative Protein Structure Models. Methods in Molecular Biology, 2012, 819, 105-126.	0.9	11
148	Large scale analysis of synaptic phosphorylation and Oâ€GlcNAcylation reveals complex interplay between these postâ€translational modifications. FASEB Journal, 2012, 26, 978.2.	0.5	0
149	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.	7.1	120
150	The Enzyme Function Initiative. Biochemistry, 2011, 50, 9950-9962.	2.5	169
151	Enzymatic Deamination of the Epigenetic Base N-6-Methyladenine. Journal of the American Chemical Society, 2011, 133, 2080-2083.	13.7	24
152	Discovery of a Cytokinin Deaminase. ACS Chemical Biology, 2011, 6, 1036-1040.	3.4	15
153	Ligand discovery from a dopamine D3 receptor homology model and crystal structure. Nature Chemical Biology, 2011, 7, 769-778.	8.0	285
154	Macromolecular docking restrained by a small angle X-ray scattering profile. Journal of Structural Biology, 2011, 173, 461-471.	2.8	97
155	Macromolecular Assembly Structures by Comparative Modeling and Electron Microscopy. Methods in Molecular Biology, 2011, 857, 331-350.	0.9	4
156	Statistical Potential for Modeling and Ranking of Proteinâ€“Ligand Interactions. Journal of Chemical Information and Modeling, 2011, 51, 3078-3092.	5.4	69
157	Structure of the Câ€terminal domain of Saccharomyces cerevisiae Nup133, a component of the nuclear pore complex. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1672-1677.	2.6	16
158	Response to â€œPredictable difficulty or difficulty to predictâ€. Protein Science, 2011, 20, 4-5.	7.6	0
159	MultiFit: a web server for fitting multiple protein structures into their electron microscopy density map. Nucleic Acids Research, 2011, 39, W167-W170.	14.5	27
160	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.	3.8	115
161	On a benderâ€”BARs, ESCRTs, COPs, and finally getting your coat. Journal of Cell Biology, 2011, 193, 963-972.	5.2	88
162	ModBase, a database of annotated comparative protein structure models, and associated resources. Nucleic Acids Research, 2011, 39, D465-D474.	14.5	506

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163	Modeling of Proteins and Their Assemblies with the Integrative Modeling Platform. Methods in Molecular Biology, 2011, 781, 377-397.	0.9	18
164	Comparison of human solute carriers. Protein Science, 2010, 19, 412-428.	7.6	99
165	Functional hot spots in human ATPâ€binding cassette transporter nucleotide binding domains. Protein Science, 2010, 19, 2110-2121.	7.6	19
166	Structures of the autoproteolytic domain from the Saccharomyces cerevisiae nuclear pore complex component, Nup145. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1992-1998.	2.6	13
167	Determining macromolecular assembly structures by molecular docking and fitting into an electron density map. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3205-3211.	2.6	63
168	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.	7.1	178
169	FoXS: a web server for rapid computation and fitting of SAXS profiles. Nucleic Acids Research, 2010, 38, W540-W544.	14.5	474
170	The Overlap of Small Molecule and Protein Binding Sites within Families of Protein Structures. PLoS Computational Biology, 2010, 6, e1000668.	3.2	43
171	Toward an Integrated Structural Model of the 26S Proteasome. Molecular and Cellular Proteomics, 2010, 9, 1666-1677.	3.8	50
172	Prediction of protease substrates using sequence and structure features. Bioinformatics, 2010, 26, 1714-1722.	4.1	61
173	Integrative Structure Modeling of Macromolecular Assemblies from Proteomics Data. Molecular and Cellular Proteomics, 2010, 9, 1689-1702.	3.8	64
174	Role of organic cation transporter 3 (SLC22A3) and its missense variants in the pharmacologic action of metformin. Pharmacogenetics and Genomics, 2010, 20, 687-699.	1.5	175
175	Regulatory Elements within the Prodomain of Falcipain-2, a Cysteine Protease of the Malaria Parasite Plasmodium falciparum. PLoS ONE, 2009, 4, e5694.	2.5	46
176	MODBASE, a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2009, 37, D347-D354.	14.5	154
177	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.	3.8	200
178	A Kernel for Open Source Drug Discovery in Tropical Diseases. PLoS Neglected Tropical Diseases, 2009, 3, e418.	3.0	23
179	Alignment of multiple protein structures based on sequence and structure features. Protein Engineering, Design and Selection, 2009, 22, 569-574.	2.1	82
180	The structural dynamics of macromolecular processes. Current Opinion in Cell Biology, 2009, 21, 97-108.	5.4	74

#	Article	IF	Citations
181	Target selection and annotation for the structural genomics of the amidohydrolase and enolase superfamilies. Journal of Structural and Functional Genomics, 2009, 10, 107-125.	1.2	25
182	A survey of integral Î±-helical membrane proteins. Journal of Structural and Functional Genomics, 2009, 10, 269-280.	1.2	12
183	Evolutionary constraints on structural similarity in orthologs and paralogs. Protein Science, 2009, 18, 1306-1315.	7.6	58
184	Comprehensive Molecular Structure of the Eukaryotic Ribosome. Structure, 2009, 17, 1591-1604.	3.3	140
185	Selecting Optimum Eukaryotic Integral Membrane Proteins for Structure Determination by Rapid Expression and Solubilization Screening. Journal of Molecular Biology, 2009, 385, 820-830.	4.2	53
186	Inferential Optimization for Simultaneous Fitting of Multiple Components into a CryoEM Map of Their Assembly. Journal of Molecular Biology, 2009, 388, 180-194.	4.2	117
187	Protein Structure Modeling. NATO Science for Peace and Security Series A: Chemistry and Biology, 2009, , 139-151.	0.5	5
188	Molecular Docking Screens Using Comparative Models of Proteins. Journal of Chemical Information and Modeling, 2009, 49, 2512-2527.	5.4	132
189	Mechanism of lid closure in the eukaryotic chaperonin TRiC/CCT. Nature Structural and Molecular Biology, 2008, 15, 746-753.	8.2	91
190	Protein Structure Fitting and Refinement Guided by Cryo-EM Density. Structure, 2008, 16, 295-307.	3.3	334
191	Multiple Conformations of E. coli Hsp90 in Solution: Insights into the Conformational Dynamics of Hsp90. Structure, 2008, 16, 755-765.	3.3	154
192	How well can the accuracy of comparative protein structure models be predicted?. Protein Science, 2008, 17, 1881-1893.	7.6	138
193	Protein Structure Modeling with MODELLER. Methods in Molecular Biology, 2008, 426, 145-159.	0.9	1,187
194	Integrative Structure Determination of Protein Assemblies by Satisfaction of Spatial Restraints. Computational Biology, 2008, , 99-114.	0.2	6
195	Crystallographic Conformers of Actin in a Biologically Active Bundle of Filaments. Journal of Molecular Biology, 2008, 375, 331-336.	4.2	37
196	Integration of Small-Angle X-Ray Scattering Data into Structural Modeling of Proteins and Their Assemblies. Journal of Molecular Biology, 2008, 382, 1089-1106.	4.2	139
197	Integrating Diverse Data for Structure Determination of Macromolecular Assemblies. Annual Review of Biochemistry, 2008, 77, 443-477.	11.1	204
198	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.	7.1	106

#	Article	IF	Citations
199	Classifying Variants of Undetermined Significance in BRCA2 with Protein Likelihood Ratios. Cancer Informatics, 2008, 6, CIN.S618.	1.9	45
200	Structure Determination of Macromolecular Complexes by Experiment and Computation. Nucleic Acids and Molecular Biology, 2008, , 73-96.	0.2	1
201	Functional Impact of Missense Variants in BRCA1 Predicted by Supervised Learning. PLoS Computational Biology, 2007, 3, e26.	3.2	57
202	Determining the architectures of macromolecular assemblies. Nature, 2007, 450, 683-694.	27.8	499
203	The molecular architecture of the nuclear pore complex. Nature, 2007, 450, 695-701.	27.8	947
204	The molecular sociology of the cell. Nature, 2007, 450, 973-982.	27.8	497
205	The AnnoLite and AnnoLyze programs for comparative annotation of protein structures. BMC Bioinformatics, 2007, 8, S4.	2.6	36
206	Comparative Protein Structure Modeling Using MODELLER. Current Protocols in Protein Science, 2007, 50, Unit 2.9.	2.8	1,056
207	Modeling mutations in protein structures. Protein Science, 2007, 16, 2030-2041.	7.6	77
208	Fold assessment for comparative protein structure modeling. Protein Science, 2007, 16, 2412-2426.	7.6	101
209	Hostâ€“pathogen protein interactions predicted by comparative modeling. Protein Science, 2007, 16, 2585-2596.	7.6	136
210	Structural genomics of protein phosphatases. Journal of Structural and Functional Genomics, 2007, 8, 121-140.	1.2	148
211	Protein interactions and disease phenotypes in the ABC transporter superfamily. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2007, , 51-63.	0.7	4
212	Variable gap penalty for protein sequenceâ€“structure alignment. Protein Engineering, Design and Selection, 2006, 19, 129-133.	2.1	58
213	Comparative Protein Structure Modeling Using Modeller. Current Protocols in Bioinformatics, 2006, 15, Unit-5.6.	25.8	2,858
214	Refinement of Protein Structures by Iterative Comparative Modeling and CryoEM Density Fitting. Journal of Molecular Biology, 2006, 357, 1655-1668.	4.2	104
215	Minimalist Representations and the Importance of Nearest Neighbor Effects in Protein Folding Simulations. Journal of Molecular Biology, 2006, 363, 835-857.	4.2	40
216	A composite score for predicting errors in protein structure models. Protein Science, 2006, 15, 1653-1666.	7.6	160

#	Article	IF	Citations
217	Localization of binding sites in protein structures by optimization of a composite scoring function. Protein Science, 2006, 15, 2366-2380.	7.6	21
218	Statistical potential for assessment and prediction of protein structures. Protein Science, 2006, 15, 2507-2524.	7.6	2,104
219	Outcome of a Workshop on Archiving Structural Models of Biological Macromolecules. Structure, 2006, 14, 1211-1217.	3.3	60
220	Protein complex compositions predicted by structural similarity. Nucleic Acids Research, 2006, 34, 2943-2952.	14.5	56
221	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.	7.1	243
222	Structural Modeling of Protein Interactions by Analogy: Application to PSD-95. PLoS Computational Biology, 2006, 2, e153.	3.2	39
223	PharmGKB Submission Update: IV. PMT Submissions of Genetic Variations in ATP-Binding Cassette Transporters to the PharmGKB Network. Pharmacological Reviews, 2006, 58, 1-2.	16.0	18
224	MODBASE: a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2006, 34, D291-D295.	14.5	265
225	The optimal size of a globular protein domain: A simple sphere-packing model. Chemical Physics Letters, 2005, 405, 224-228.	2.6	51
226	Localization of protein-binding sites within families of proteins. Protein Science, 2005, 14, 2350-2360.	7.6	40
227	Comparative Protein Structure Modeling. , 2005, , 831-860.		15
228	Structural Characterization of Assemblies from Overall Shape and Subcomplex Compositions. Structure, 2005, 13, 435-445.	3.3	27
229	Macromolecular Assemblies Highlighted. Structure, 2005, 13, 339-341.	3.3	5
230	Combining electron microscopy and comparative protein structure modeling. Current Opinion in Structural Biology, 2005, 15, 578-585.	5.7	73
231	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
232	LS-SNP: large-scale annotation of coding non-synonymous SNPs based on multiple information sources. Bioinformatics, 2005, 21, 2814-2820.	4.1	202
233	PIBASE: a comprehensive database of structurally defined protein interfaces. Bioinformatics, 2005, 21, 1901-1907.	4.1	169
234	Detecting remotely related proteins by their interactions and sequence similarity. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7151-7156.	7.1	26

#	Article	IF	Citations
235	Structural characterization of components of protein assemblies by comparative modeling and electron cryo-microscopy. Journal of Structural Biology, 2005, 149, 191-203.	2.8	92
236	Characterization of Protein Hubs by Inferring Interacting Motifs from Protein Interactions. PLoS Computational Biology, 2005, preprint, e178.	3.2	0
237	Stereochemical Criteria for Prediction of the Effects of Proline Mutations on Protein Stability. PLoS Computational Biology, 2005, preprint, e241.	3.2	0
238	Structure-Based Assessment of Missense Mutations in Human BRCA1. Cancer Research, 2004, 64, 3790-3797.	0.9	103
239	High-Throughput Computational and Experimental Techniques in Structural Genomics. Genome Research, 2004, 14, 2145-2154.	5.5	59
240	Finding Cures for Tropical Diseases: Is Open Source an Answer?. PLoS Medicine, 2004, 1, e56.	8.4	82
241	Components of Coated Vesicles and Nuclear Pore Complexes Share a Common Molecular Architecture. PLoS Biology, 2004, 2, e380.	5.6	357
242	A structural perspective on proteinâ€“protein interactions. Current Opinion in Structural Biology, 2004, 14, 313-324.	5.7	260
243	Alignment of protein sequences by their profiles. Protein Science, 2004, 13, 1071-1087.	7.6	184
244	Comparative Protein Structure Modeling and its Applications to Drug Discovery. Annual Reports in Medicinal Chemistry, 2004, 39, 259-276.	0.9	68
245	A structural perspective on protein?protein interactions. Current Opinion in Structural Biology, 2004, 14, 313-313.	5.7	0
246	Detection of homologous proteins by an intermediate sequence search. Protein Science, 2004, 13, 54-62.	7.6	35
247	MODBASE, a database of annotated comparative protein structure models, and associated resources. Nucleic Acids Research, 2004, 32, 217D-222.	14.5	256
248	From words to literature in structural proteomics. Nature, 2003, 422, 216-225.	27.8	473
249	Modeling Protein Structure from its Sequence. Current Protocols in Bioinformatics, 2003, 3, 5.1.1.	25.8	6
250	Comparative protein structure modeling by iterative alignment, model building and model assessment. Nucleic Acids Research, 2003, 31, 3982-3992.	14.5	277
251	Modeller: Generation and Refinement of Homology-Based Protein Structure Models. Methods in Enzymology, 2003, 374, 461-491.	1.0	1,469
252	Study of the Structural Dynamics of the E. coli 70S Ribosome Using Real-Space Refinement. Cell, 2003, 113, 789-801.	28.9	273

#	Article	IF	Citations
253	Tools for comparative protein structure modeling and analysis. Nucleic Acids Research, 2003, 31, 3375-3380.	14.5	406
254	ModLoop: automated modeling of loops in protein structures. Bioinformatics, 2003, 19, 2500-2501.	4.1	707
255	LigBase: a database of families of aligned ligand binding sites in known protein sequences and structures. Bioinformatics, 2002, 18, 200-201.	4.1	76
256	MODBASE, a database of annotated comparative protein structure models. Nucleic Acids Research, 2002, 30, 255-259.	14.5	114
257	Evolution and Physics in Comparative Protein Structure Modeling. Accounts of Chemical Research, 2002, 35, 413-421.	15.6	103
258	Reliability of Assessment of Protein Structure Prediction Methods. Structure, 2002, 10, 435-440.	3.3	95
259	Structural genomics: A pipeline for providing structures for the biologist. Protein Science, 2002, 11, 723-738.	7.6	168
260	Statistical potentials for fold assessment. Protein Science, 2002, 11, 430-448.	7.6	304
261	Protein Structure Prediction and Structural Genomics. Science, 2001, 294, 93-96.	12.6	1,445
262	Structure of the 80S Ribosome from Saccharomyces cerevisiaeâ€"tRNA-Ribosome and Subunit-Subunit Interactions. Cell, 2001, 107, 373-386.	28.9	462
263	Architecture of the Protein-Conducting Channel Associated with the Translating 80S Ribosome. Cell, 2001, 107, 361-372.	28.9	368
264	1H, 13C, 15N resonance assignments and fold verification of a circular permuted variant of the potent HIV-inactivating protein cyanovirin-N. Journal of Biomolecular NMR, 2001, 19, 289-290.	2.8	15
265	Target practice. , 2001, 8, 482-484.		21
266	Response to Paoli. Nature Structural Biology, 2001, 8, 745-745.	9.7	3
267	Protein structure modeling for structural genomics. Nature Structural Biology, 2000, 7, 986-990.	9.7	199
268	Modeling of loops in protein structures. Protein Science, 2000, 9, 1753-1773.	7.6	1,895
269	Comparative Protein Structure Modeling of Genes and Genomes. Annual Review of Biophysics and Biomolecular Structure, 2000, 29, 291-325.	18.3	2,811
270	Comparative Protein Structure Modeling: Introduction and Practical Examples with Modeller. , 2000, 143, 97-129.		193

#	Article	IF	Citations
271	Immunoglobulin motif DNA recognition and heterodimerization of the PEBP2/CBF Runt domain. Nature Structural Biology, 1999, 6, 615-619.	9.7	97
272	Structural genomics: beyond the Human Genome Project. Nature Genetics, 1999, 23, 151-157.	21.4	369
273	Functional links between proteins. Nature, 1999, 402, 23-26.	27.8	60
274	Protein Folding: A Perspective from Theory and Experiment. Angewandte Chemie - International Edition, 1998, 37, 868-893.	13.8	778
275	Advances in comparative protein-structure modelling. Current Opinion in Structural Biology, 1997, 7, 206-214.	5.7	289
276	Crystal Structure of the Î´â€² Subunit of the Clamp-Loader Complex of E. coli DNA Polymerase III. Cell, 1997, 91, 335-345.	28.9	268
277	Evaluation of comparative protein structure modeling by MODELLER-3. Proteins: Structure, Function and Bioinformatics, 1997, 29, 50-58.	2.6	207
278	Protein dynamics: From the native to the unfolded state and back again. Molecular Engineering, 1995, 5, 55-70.	0.2	1
279	Evaluation of comparative protein modeling by MODELLER. Proteins: Structure, Function and Bioinformatics, 1995, 23, 318-326.	2.6	1,035
280	Packaging of Proteases and Proteoglycans in the Granules of Mast Cells and Other Hematopoietic Cells. Journal of Biological Chemistry, 1995, 270, 19524-19531.	3.4	116
281	Derivation of rules for comparative protein modeling from a database of protein structure alignments. Protein Science, 1994, 3, 1582-1596.	7.6	275
282	Comparative Protein Modelling by Satisfaction of Spatial Restraints. Journal of Molecular Biology, 1993, 234, 779-815.	4.2	11,892