Andrej Sali

List of Publications by Citations

283 papers	53,614 citations	99 h-index	230 g-index
309 ext. papers	61,853 ext. citations	11.8 avg, IF	7.9 L-index

#	Paper	IF	Citations
283	Comparative protein modelling by satisfaction of spatial restraints. *Journal of Molecular Biology*, **1993**, 234, 779-815	6.5	10363
282	Comparative protein structure modeling of genes and genomes. *Annual Review of Biophysics and Biomolecular Structure*, **2000**, 29, 291-325		2439
281	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. *Nature*, **2020**, 583, 459-468	50.4	2142
280	Comparative protein structure modeling using Modeller. *Current Protocols in Bioinformatics*, **2006**, Chapter 5, Unit-5.6	24.2	1717
279	Statistical potential for assessment and prediction of protein structures. *Protein Science*, **2006**, 15, 2507-24	6.3	1714
278	Modeling of loops in protein structures. *Protein Science*, **2000**, 9, 1753-73	6.3	1586
277	Comparative Protein Structure Modeling Using MODELLER. *Current Protocols in Bioinformatics*, **2016**, 54, 5.6.1-5.6.37	24.2	1267
276	Protein structure prediction and structural genomics. *Science*, **2001**, 294, 93-6	33.3	1235
275	Modeller: generation and refinement of homology-based protein structure models. *Methods in Enzymology*, **2003**, 374, 461-91	1.7	1226
274	Evaluation of comparative protein modeling by MODELLER. *Proteins: Structure, Function and Bioinformatics*, **1995**, 23, 318-26	4.2	930
273	The molecular architecture of the nuclear pore complex. *Nature*, **2007**, 450, 695-701	50.4	830
272	Comparative protein structure modeling using MODELLER. *Current Protocols in Protein Science*, **2007**, Chapter 2, Unit 2.9	3.1	790
271	Comparative Protein Structure Modeling Using MODELLER. *Current Protocols in Bioinformatics*, **2014**, 47, 5.6.1-32	24.2	754
270	Protein structure modeling with MODELLER. *Methods in Molecular Biology*, **2008**, 426, 145-59	1.4	723
269	Protein Folding: A Perspective from Theory and Experiment. *Angewandte Chemie - International Edition*, **1998**, 37, 868-893	16.4	693
268	Insights into secondary metabolism from a global analysis of prokaryotic biosynthetic gene clusters. *Cell*, **2014**, 158, 412-421	56.2	587
267	ModLoop: automated modeling of loops in protein structures. *Bioinformatics*, **2003**, 19, 2500-1	7.2	566

266	Global landscape of HIV-human protein complexes. *Nature*, **2011**, 481, 365-70	50.4	507
265	Determining the architectures of macromolecular assemblies. *Nature*, **2007**, 450, 683-94	50.4	437
264	The molecular sociology of the cell. *Nature*, **2007**, 450, 973-82	50.4	424
263	Structure of the 80S ribosome from Saccharomyces cerevisiae--tRNA-ribosome and subunit-subunit interactions. *Cell*, **2001**, 107, 373-86	56.2	417
262	From words to literature in structural proteomics. *Nature*, **2003**, 422, 216-25	50.4	412
261	Protein structure modeling with MODELLER. *Methods in Molecular Biology*, **2014**, 1137, 1-15	1.4	406
260	FoXS: a web server for rapid computation and fitting of SAXS profiles. *Nucleic Acids Research*, **2010**, 38, W540-4	20.1	403
259	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, 1380-7	11.5	380
258	UCSF Chimera, MODELLER, and IMP: an integrated modeling system. *Journal of Structural Biology*, **2012**, 179, 269-78	3.4	373
257	Putting the pieces together: integrative modeling platform software for structure determination of macromolecular assemblies. *PLoS Biology*, **2012**, 10, e1001244	9.7	362
256	Accurate SAXS profile computation and its assessment by contrast variation experiments. *Biophysical Journal*, **2013**, 105, 962-74	2.9	359
255	Tools for comparative protein structure modeling and analysis. *Nucleic Acids Research*, **2003**, 31, 3375-80	20.1	350
254	Structural genomics: beyond the human genome project. *Nature Genetics*, **1999**, 23, 151-7	36.3	336
253	Architecture of the protein-conducting channel associated with the translating 80S ribosome. *Cell*, **2001**, 107, 361-72	56.2	335
252	Components of coated vesicles and nuclear pore complexes share a common molecular architecture. *PLoS Biology*, **2004**, 2, e380	9.7	318
251	Comparative Protein Structure Modeling Using MODELLER. *Current Protocols in Protein Science*, **2016**, 86, 2.9.1-2.9.37	3.1	301
250	Integrative structure and functional anatomy of a nuclear pore complex. *Nature*, **2018**, 555, 475-482	50.4	280
249	Protein Structure Modeling with MODELLER. *Methods in Molecular Biology*, **2017**, 1654, 39-54	1.4	276

248	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	20.1	273
247	Statistical potentials for fold assessment. *Protein Science*, **2002**, 11, 430-48	6.3	270
246	Vif hijacks CBF-β to degrade APOBEC3G and promote HIV-1 infection. *Nature*, **2011**, 481, 371-5	50.4	268
245	Advances in comparative protein-structure modelling. *Current Opinion in Structural Biology*, **1997**, 7, 206-14	8.1	266
244	Protein structure fitting and refinement guided by cryo-EM density. *Structure*, **2008**, 16, 295-307	5.2	266
243	Derivation of rules for comparative protein modeling from a database of protein structure alignments. *Protein Science*, **1994**, 3, 1582-96	6.3	261
242	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. *Science*, **2020**, 370,	33.3	261
241	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, W424-9	20.1	260
240	ModBase, a database of annotated comparative protein structure models, and associated resources. *Nucleic Acids Research*, **2011**, 39, D465-74	20.1	252
239	Study of the structural dynamics of the E coli 70S ribosome using real-space refinement. *Cell*, **2003**, 113, 789-801	56.2	252
238	Ligand discovery from a dopamine D3 receptor homology model and crystal structure. *Nature Chemical Biology*, **2011**, 7, 769-78	11.7	250
237	Comparative protein structure modeling by iterative alignment, model building and model assessment. *Nucleic Acids Research*, **2003**, 31, 3982-92	20.1	245
236	MODBASE: a database of annotated comparative protein structure models and associated resources. *Nucleic Acids Research*, **2006**, 34, D291-5	20.1	237
235	Crystal structure of the delta' subunit of the clamp-loader complex of E. coli DNA polymerase III. *Cell*, **1997**, 91, 335-45	56.2	235
234	MODBASE, a database of annotated comparative protein structure models, and associated resources. *Nucleic Acids Research*, **2004**, 32, D217-22	20.1	233
233	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, 2172-7	11.5	231
232	A structural perspective on protein-protein interactions. *Current Opinion in Structural Biology*, **2004**, 14, 313-24	8.1	221
231	ModBase, a database of annotated comparative protein structure models and associated resources. *Nucleic Acids Research*, **2014**, 42, D336-46	20.1	207

230	Simple rules for passive diffusion through the nuclear pore complex. *Journal of Cell Biology*, **2016**, 215, 57-76	7.3	199
229	LS-SNP: large-scale annotation of coding non-synonymous SNPs based on multiple information sources. *Bioinformatics*, **2005**, 21, 2814-20	7.2	193
228	Integrating diverse data for structure determination of macromolecular assemblies. *Annual Review of Biochemistry*, **2008**, 77, 443-77	29.1	183
227	Nuclear Import Receptor Inhibits Phase Separation of FUS through Binding to Multiple Sites. *Cell*, **2018**, 173, 693-705.e22	56.2	177
226	Biochemistry. Integrative structural biology. *Science*, **2013**, 339, 913-5	33.3	177
225	Protein structure modeling for structural genomics. *Nature Structural Biology*, **2000**, 7 Suppl, 986-90		176
224	Alignment of protein sequences by their profiles. *Protein Science*, **2004**, 13, 1071-87	6.3	171
223	Crystal structure of a eukaryotic phosphate transporter. *Nature*, **2013**, 496, 533-6	50.4	170
222	Evidence for a shared nuclear pore complex architecture that is conserved from the last common eukaryotic ancestor. *Molecular and Cellular Proteomics*, **2009**, 8, 2119-30	7.6	169
221	Evaluation of comparative protein structure modeling by MODELLER-3. *Proteins: Structure, Function and Bioinformatics*, **1997**, 29, 50-58	4.2	168
220	Comparative protein structure modeling. Introduction and practical examples with modeller. *Methods in Molecular Biology*, **2000**, 143, 97-129	1.4	166
219	Molecular architecture of the 40S?eIF1?eIF3 translation initiation complex. *Cell*, **2014**, 158, 1123-1135	56.2	157
218	Function of human Rh based on structure of RhCG at 2.1 A. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 9638-43	11.5	153
217	Structural genomics: a pipeline for providing structures for the biologist. *Protein Science*, **2002**, 11, 723-38	3.3	153
216	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	5.5	145
215	Role of organic cation transporter 3 (SLC22A3) and its missense variants in the pharmacologic action of metformin. *Pharmacogenetics and Genomics*, **2010**, 20, 687-99	1.9	145
214	MODBASE, a database of annotated comparative protein structure models and associated resources. *Nucleic Acids Research*, **2009**, 37, D347-54	20.1	143
213	A composite score for predicting errors in protein structure models. *Protein Science*, **2006**, 15, 1653-66	6.3	141

212	PIBASE: a comprehensive database of structurally defined protein interfaces. *Bioinformatics*, **2005**, 21, 1901-7	7.2	141
211	The Enzyme Function Initiative. *Biochemistry*, **2011**, 50, 9950-62	3.2	140
210	Multiple conformations of E. coli Hsp90 in solution: insights into the conformational dynamics of Hsp90. *Structure*, **2008**, 16, 755-65	5.2	140
209	A SARS-CoV-2-Human Protein-Protein Interaction Map Reveals Drug Targets and Potential Drug-Repurposing **2020**,		133
208	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. *Structure*, **2015**, 23, 1156-67	5.2	131
207	Comprehensive molecular structure of the eukaryotic ribosome. *Structure*, **2009**, 17, 1591-1604	5.2	130
206	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, 5480-5	11.5	129
205	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, 4875-80	11.5	128
204	Structural genomics of protein phosphatases. *Journal of Structural and Functional Genomics*, **2007**, 8, 121-40		125
203	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, 2927-43	7.6	122
202	A systematic computational analysis of biosynthetic gene cluster evolution: lessons for engineering biosynthesis. *PLoS Computational Biology*, **2014**, 10, e1004016	5	118
201	Integration of small-angle X-ray scattering data into structural modeling of proteins and their assemblies. *Journal of Molecular Biology*, **2008**, 382, 1089-106	6.5	118
200	Molecular docking screens using comparative models of proteins. *Journal of Chemical Information and Modeling*, **2009**, 49, 2512-27	6.1	116
199	How well can the accuracy of comparative protein structure models be predicted?. *Protein Science*, **2008**, 17, 1881-93	6.3	112
198	Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 323-48	4.2	111
197	Structure and Function of the Nuclear Pore Complex Cytoplasmic mRNA Export Platform. *Cell*, **2016**, 167, 1215-1228.e25	56.2	110
196	CryptoSite: Expanding the Druggable Proteome by Characterization and Prediction of Cryptic Binding Sites. *Journal of Molecular Biology*, **2016**, 428, 709-719	6.5	110
195	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, 6943-8	11.5	110

194	Host pathogen protein interactions predicted by comparative modeling. *Protein Science*, **2007**, 16, 2585-96	6.3	110
193	Principles for Integrative Structural Biology Studies. *Cell*, **2019**, 177, 1384-1403	56.2	108
192	Molecular architecture of the yeast Mediator complex. *ELife*, **2015**, 4,	8.9	107
191	Packaging of proteases and proteoglycans in the granules of mast cells and other hematopoietic cells. A cluster of histidines on mouse mast cell protease 7 regulates its binding to heparin serglycin proteoglycans. *Journal of Biological Chemistry*, **1995**, 270, 19524-31	5.4	105
190	Inferential optimization for simultaneous fitting of multiple components into a CryoEM map of their assembly. *Journal of Molecular Biology*, **2009**, 388, 180-94	6.5	103
189	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, 15810-5	11.5	101
188	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	8.3	100
187	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, 9610-5	11.5	98
186	Evolution and physics in comparative protein structure modeling. *Accounts of Chemical Research*, **2002**, 35, 413-21	24.3	97
185	Ring closure activates yeast γTuRC for species-specific microtubule nucleation. *Nature Structural and Molecular Biology*, **2015**, 22, 132-7	17.6	95
184	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	7.6	95
183	Structure-function mapping of a heptameric module in the nuclear pore complex. *Journal of Cell Biology*, **2012**, 196, 419-34	7.3	95
182	A strategy for dissecting the architectures of native macromolecular assemblies. *Nature Methods*, **2015**, 12, 1135-8	21.6	94
181	Refinement of protein structures by iterative comparative modeling and CryoEM density fitting. *Journal of Molecular Biology*, **2006**, 357, 1655-68	6.5	93
180	Structure-based assessment of missense mutations in human BRCA1: implications for breast and ovarian cancer predisposition. *Cancer Research*, **2004**, 64, 3790-7	10.1	92
179	Recovering a representative conformational ensemble from underdetermined macromolecular structural data. *Journal of the American Chemical Society*, **2013**, 135, 16595-609	16.4	88
178	Optimized atomic statistical potentials: assessment of protein interfaces and loops. *Bioinformatics*, **2013**, 29, 3158-66	7.2	88
177	Macromolecular docking restrained by a small angle X-ray scattering profile. *Journal of Structural Biology*, **2011**, 173, 461-71	3.4	88

176	Reliability of assessment of protein structure prediction methods. *Structure*, **2002**, 10, 435-40	5.2	87
175	Immunoglobulin motif DNA recognition and heterodimerization of the PEBP2/CBF Runt domain. *Nature Structural Biology*, **1999**, 6, 615-9		86
174	Cys-scanning disulfide crosslinking and bayesian modeling probe the transmembrane signaling mechanism of the histidine kinase, PhoQ. *Structure*, **2014**, 22, 1239-1251	5.2	83
173	Comparison of human solute carriers. *Protein Science*, **2010**, 19, 412-28	6.3	83
172	Integrative structural modeling with small angle X-ray scattering profiles. *BMC Structural Biology*, **2012**, 12, 17	2.7	80
171	Fold assessment for comparative protein structure modeling. *Protein Science*, **2007**, 16, 2412-26	6.3	80
170	MODBASE, a database of annotated comparative protein structure models. *Nucleic Acids Research*, **2002**, 30, 255-9	20.1	80
169	Response to Predictable difficulty or difficulty to predict *Protein Science*, **2011**, 20, 4-5	6.3	78
168	Evolution: On a bender--BARs, ESCRTs, COPs, and finally getting your coat. *Journal of Cell Biology*, **2011**, 193, 963-72	7.3	78
167	Structural characterization of components of protein assemblies by comparative modeling and electron cryo-microscopy. *Journal of Structural Biology*, **2005**, 149, 191-203	3.4	78
166	Architecture of the Human and Yeast General Transcription and DNA Repair Factor TFIIH. *Molecular Cell*, **2015**, 59, 794-806	17.6	75
165	Mechanism of lid closure in the eukaryotic chaperonin TRiC/CCT. *Nature Structural and Molecular Biology*, **2008**, 15, 746-53	17.6	75
164	A phosphotyrosine switch regulates organic cation transporters. *Nature Communications*, **2016**, 7, 10880	17.4	74
163	Alignment of multiple protein structures based on sequence and structure features. *Protein Engineering, Design and Selection*, **2009**, 22, 569-74	1.9	71
162	A method for integrative structure determination of protein-protein complexes. *Bioinformatics*, **2012**, 28, 3282-9	7.2	69
161	LigBase: a database of families of aligned ligand binding sites in known protein sequences and structures. *Bioinformatics*, **2002**, 18, 200-1	7.2	69
160	Uncertainty in integrative structural modeling. *Current Opinion in Structural Biology*, **2014**, 28, 96-104	8.1	68
159	Molecular Details Underlying Dynamic Structures and Regulation of the Human 26S Proteasome. *Molecular and Cellular Proteomics*, **2017**, 16, 840-854	7.6	67

158	The structural dynamics of macromolecular processes. *Current Opinion in Cell Biology*, **2009**, 21, 97-108	9	67
157	Modeling mutations in protein structures. *Protein Science*, **2007**, 16, 2030-41	6.3	66
156	High-resolution network biology: connecting sequence with function. *Nature Reviews Genetics*, **2013**, 14, 865-79	30.1	65
155	Report of the wwPDB Small-Angle Scattering Task Force: data requirements for biomolecular modeling and the PDB. *Structure*, **2013**, 21, 875-81	5.2	65
154	Molecular modeling and ligand docking for solute carrier (SLC) transporters. *Current Topics in Medicinal Chemistry*, **2013**, 13, 843-56	3	65
153	Integrative structure modeling with the Integrative Modeling Platform. *Protein Science*, **2018**, 27, 245-258	3	63
152	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a "Plug and Play" Domain. *Methods in Enzymology*, **2018**, 606, 1-71	1.7	63
151	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	11.5	63
150	Combining electron microscopy and comparative protein structure modeling. *Current Opinion in Structural Biology*, **2005**, 15, 578-85	8.1	62
149	Statistical potential for modeling and ranking of protein-ligand interactions. *Journal of Chemical Information and Modeling*, **2011**, 51, 3078-92	6.1	61
148	The proteasome-interacting Ecm29 protein disassembles the 26S proteasome in response to oxidative stress. *Journal of Biological Chemistry*, **2017**, 292, 16310-16320	5.4	60
147	PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. *Structure*, **2017**, 25, 1317-1318	5.2	58
146	Integrative structure modeling of macromolecular assemblies from proteomics data. *Molecular and Cellular Proteomics*, **2010**, 9, 1689-702	7.6	58
145	Coordinating the impact of structural genomics on the human α-helical transmembrane proteome. *Nature Structural and Molecular Biology*, **2013**, 20, 135-8	17.6	57
144	Determining macromolecular assembly structures by molecular docking and fitting into an electron density map. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 3205-11	4.2	56
143	Comparative Protein Structure Modeling and its Applications to Drug Discovery. *Annual Reports in Medicinal Chemistry*, **2004**, 39, 259-276	1.6	56
142	Development of a Prototype System for Archiving Integrative/Hybrid Structure Models of Biological Macromolecules. *Structure*, **2018**, 26, 894-904.e2	5.2	54
141	Integrative structure-function mapping of the nucleoporin Nup133 suggests a conserved mechanism for membrane anchoring of the nuclear pore complex. *Molecular and Cellular Proteomics*, **2014**, 13, 2911-26	7.6	54

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139	Variable gap penalty for protein sequence-structure alignment. *Protein Engineering, Design and Selection*, **2006**, 19, 129-33	1.9	53
138	Molecular architecture and function of the SEA complex, a modulator of the TORC1 pathway. *Molecular and Cellular Proteomics*, **2014**, 13, 2855-70	7.6	52
137	Selecting optimum eukaryotic integral membrane proteins for structure determination by rapid expression and solubilization screening. *Journal of Molecular Biology*, **2009**, 385, 820-30	6.5	51
136	Evolutionary constraints on structural similarity in orthologs and paralogs. *Protein Science*, **2009**, 18, 1306-15	6.3	50
135	Protein complex compositions predicted by structural similarity. *Nucleic Acids Research*, **2006**, 34, 2943-52	20.1	50
134	Prediction of protease substrates using sequence and structure features. *Bioinformatics*, **2010**, 26, 1714-22	7.2	49
133	Outcome of a workshop on archiving structural models of biological macromolecules. *Structure*, **2006**, 14, 1211-7	5.2	49
132	Structure, dynamics, evolution, and function of a major scaffold component in the nuclear pore complex. *Structure*, **2013**, 21, 560-71	5.2	48
131	Toward an integrated structural model of the 26S proteasome. *Molecular and Cellular Proteomics*, **2010**, 9, 1666-77	7.6	48
130	High-throughput computational and experimental techniques in structural genomics. *Genome Research*, **2004**, 14, 2145-54	9.7	48
129	Functional impact of missense variants in BRCA1 predicted by supervised learning. *PLoS Computational Biology*, **2007**, 3, e26	5	47
128	The optimal size of a globular protein domain: A simple sphere-packing model. *Chemical Physics Letters*, **2005**, 405, 224-228	2.5	47
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126	Limits of ligand selectivity from docking to models: in silico screening for A(1) adenosine receptor antagonists. *PLoS ONE*, **2012**, 7, e49910	3.7	46
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124	Regulatory elements within the prodomain of Falcipain-2, a cysteine protease of the malaria parasite Plasmodium falciparum. *PLoS ONE*, **2009**, 4, e5694	3.7	42
123	High selectivity of the γ-aminobutyric acid transporter 2 (GAT-2, SLC6A13) revealed by structure-based approach. *Journal of Biological Chemistry*, **2012**, 287, 37745-56	5.4	41

122	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, 18821-6	11.5	40
121	Classifying Variants of Undetermined Significance in BRCA2 with protein likelihood ratios. *Cancer Informatics*, **2008**, 6, 203-16	2.4	40
120	New York-Structural GenomiX Research Consortium (NYSGXRC): a large scale center for the protein structure initiative. *Journal of Structural and Functional Genomics*, **2005**, 6, 225-32		40
119	Discovery of Competitive and Noncompetitive Ligands of the Organic Cation Transporter 1 (OCT1; SLC22A1). *Journal of Medicinal Chemistry*, **2017**, 60, 2685-2696	8.3	39
118	Opportunities and Challenges in Building a Spatiotemporal Multi-scale Model of the Human Pancreatic □Cell. *Cell*, **2018**, 173, 11-19	56.2	39
117	Assessing Exhaustiveness of Stochastic Sampling for Integrative Modeling of Macromolecular Structures. *Biophysical Journal*, **2017**, 113, 2344-2353	2.9	39
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115	Impact of mutations on the allosteric conformational equilibrium. *Journal of Molecular Biology*, **2013**, 425, 647-61	6.5	38
114	Scoring Large-Scale Affinity Purification Mass Spectrometry Datasets with MiST. *Current Protocols in Bioinformatics*, **2015**, 49, 8.19.1-8.19.16	24.2	38
113	Elucidating the mechanism of substrate recognition by the bacterial Hsp90 molecular chaperone. *Journal of Molecular Biology*, **2014**, 426, 2393-404	6.5	37
112	Minimalist representations and the importance of nearest neighbor effects in protein folding simulations. *Journal of Molecular Biology*, **2006**, 363, 835-57	6.5	37
111	Immunoproteasome functions explained by divergence in cleavage specificity and regulation. *ELife*, **2017**, 6,	8.9	37
110	Structural modeling of protein interactions by analogy: application to PSD-95. *PLoS Computational Biology*, **2006**, 2, e153	5	36
109	A Residue-Resolved Bayesian Approach to Quantitative Interpretation of Hydrogen-Deuterium Exchange from Mass Spectrometry: Application to Characterizing Protein-Ligand Interactions. *Journal of Physical Chemistry B*, **2017**, 121, 3493-3501	3.4	35
108	Localization of protein-binding sites within families of proteins. *Protein Science*, **2005**, 14, 2350-60	6.3	35
107	Molecular architecture of photoreceptor phosphodiesterase elucidated by chemical cross-linking and integrative modeling. *Journal of Molecular Biology*, **2014**, 426, 3713-3728	6.5	34
106	Topological models of heteromeric protein assemblies from mass spectrometry: application to the yeast eIF3:eIF5 complex. *Chemistry and Biology*, **2015**, 22, 117-28		34
105	Detection of homologous proteins by an intermediate sequence search. *Protein Science*, **2004**, 13, 54-62	6.3	33

104	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	10.6	32
103	The molecular architecture of the yeast spindle pole body core determined by Bayesian integrative modeling. *Molecular Biology of the Cell*, **2017**, 28, 3298-3314	3.5	32
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101	The AnnoLite and AnnoLyze programs for comparative annotation of protein structures. *BMC Bioinformatics*, **2007**, 8 Suppl 4, S4	3.6	32
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99	Prion Protein-Antibody Complexes Characterized by Chromatography-Coupled Small-Angle X-Ray Scattering. *Biophysical Journal*, **2015**, 109, 793-805	2.9	28
98	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	11.5	28
97	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	16.4	28
96	Insights into HIV-1 proviral transcription from integrative structure and dynamics of the Tat:AFF4:P-TEFb:TAR complex. *ELife*, **2016**, 5,	8.9	28
95	Protein Structure Modeling with MODELLER. *Methods in Molecular Biology*, **2021**, 2199, 239-255	1.4	28
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93	Structural characterization of assemblies from overall shape and subcomplex compositions. *Structure*, **2005**, 13, 435-45	5.2	25
92	Target selection and annotation for the structural genomics of the amidohydrolase and enolase superfamilies. *Journal of Structural and Functional Genomics*, **2009**, 10, 107-25		24
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