Andrej Sali

List of Publications by Year in Descending Order

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	Soluble TREM2 inhibits secondary nucleation of A fibrillization and enhances cellular uptake of fibrillar A *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	2
282	Soft X-ray tomography to map and quantify organelle interactions at the mesoscale.. *Structure*, **2022**,	5.2	2
281	Integration of software tools for integrative modeling of biomolecular systems.. *Journal of Structural Biology*, **2022**, 107841	3.4	0
280	Auto-segmentation and time-dependent systematic analysis of mesoscale cellular structure in cells during insulin secretion.. *PLoS ONE*, **2022**, 17, e0265567	3.7	1
279	The Y motif defines the structure-activity relationships of human 20S proteasome activators.. *Nature Communications*, **2022**, 13, 1226	17.4	4
278	Doublecortin engages the microtubule lattice through a cooperative binding mode involving its C-terminal domain.. *ELife*, **2022**, 11,	8.9	2
277	Comprehensive structure and functional adaptations of the yeast nuclear pore complex.. *Cell*, **2021**,	56.2	18
276	Highly synergistic combinations of nanobodies that target SARS-CoV-2 and are resistant to escape. *ELife*, **2021**, 10,	8.9	3
275	New system for archiving integrative structures. *Acta Crystallographica Section D: Structural Biology*, **2021**, 77, 1486-1496	5.5	2
274	RCSB Protein Data Bank: Celebrating 50 years of the PDB with new tools for understanding and visualizing biological macromolecules in 3D. *Protein Science*, **2021**,	6.3	11
273	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
272	Global Protease Activity Profiling Identifies HER2-Driven Proteolysis in Breast Cancer. *ACS Chemical Biology*, **2021**, 16, 712-723	4.9	5
271	Nanobody Repertoires for Exposing Vulnerabilities of SARS-CoV-2 **2021**,		4
270	CM1-driven assembly and activation of yeast tubulin small complex underlies microtubule nucleation. *ELife*, **2021**, 10,	8.9	5
269	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,	11.5	10
268	The active DNA-PK holoenzyme occupies a tensed state in a staggered synaptic complex. *Structure*, **2021**, 29, 467-478.e6	5.2	6
267	Using Integrative Modeling Platform to compute, validate, and archive a model of a protein complex structure. *Protein Science*, **2021**, 30, 250-261	6.3	11

266	IMProv: A Resource for Cross-link-Driven Structure Modeling that Accommodates Protein Dynamics. *Molecular and Cellular Proteomics*, **2021**, 20, 100139	7.6	0
265	Characterization of an A3G-Vif-CRL5-CBF Structure Using a Cross-linking Mass Spectrometry Pipeline for Integrative Modeling of Host-Pathogen Complexes. *Molecular and Cellular Proteomics*, **2021**, 20, 100132	7.6	1
264	The T681I mutation is highly resistant to imatinib and dasatinib and detectable in clinical samples prior to treatment. *Haematologica*, **2021**, 106, 2242-2245	6.6	2
263	Bayesian metamodeling of complex biological systems across varying representations. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	3
262	From integrative structural biology to cell biology. *Journal of Biological Chemistry*, **2021**, 296, 100743	5.4	13
261	Protein Structure Modeling with MODELLER. *Methods in Molecular Biology*, **2021**, 2199, 239-255	1.4	28
260	Visualizing subcellular rearrangements in intact cells using soft x-ray tomography. *Science Advances*, **2020**, 6,	14.3	10
259	Genetic interaction mapping informs integrative structure determination of protein complexes. *Science*, **2020**, 370,	33.3	11
258	Enhancer Reprogramming within Pre-existing Topologically Associated Domains Promotes TGF-Induced EMT and Cancer Metastasis. *Molecular Therapy*, **2020**, 28, 2083-2095	11.7	8
257	Integrative structure and function of the yeast exocyst complex. *Protein Science*, **2020**, 29, 1486-1501	6.3	10
256	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. *Nature*, **2020**, 583, 459-468	50.4	2142
255	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
254	Crippling life support for SARS-CoV-2 and other viruses through synthetic lethality. *Journal of Cell Biology*, **2020**, 219,	7.3	9
253	A SARS-CoV-2-Human Protein-Protein Interaction Map Reveals Drug Targets and Potential Drug-Repurposing **2020**,		133
252	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. *Science*, **2020**, 370,	33.3	261
251	Structural basis of CD4 downregulation by HIV-1 Nef. *Nature Structural and Molecular Biology*, **2020**, 27, 822-828	17.6	18
250	Principles for Integrative Structural Biology Studies. *Cell*, **2019**, 177, 1384-1403	56.2	108
249	Glutamine Side Chain C?O as a Nonperturbative IR Probe of Amyloid Fibril Hydration and Assembly. *Journal of the American Chemical Society*, **2019**, 141, 7320-7326	16.4	10

248	Archiving and disseminating integrative structure models. *Journal of Biomolecular NMR*, **2019**, 73, 385-398	3	9
247	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	4.7	6
246	Importin-9 wraps around the H2A-H2B core to act as nuclear importer and histone chaperone. *ELife*, **2019**, 8,	8.9	21
245	Modeling Biological Complexes Using Integrative Modeling Platform. *Methods in Molecular Biology*, **2019**, 2022, 353-377	1.4	17
244	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	11.5	6
243	Bayesian Weighing of Electron Cryo-Microscopy Data for Integrative Structural Modeling. *Structure*, **2019**, 27, 175-188.e6	5.2	24
242	Development of a Prototype System for Archiving Integrative/Hybrid Structure Models of Biological Macromolecules. *Structure*, **2018**, 26, 894-904.e2	5.2	54
241	Nuclear Import Receptor Inhibits Phase Separation of FUS through Binding to Multiple Sites. *Cell*, **2018**, 173, 693-705.e22	56.2	177
240	Integrative structure and functional anatomy of a nuclear pore complex. *Nature*, **2018**, 555, 475-482	50.4	280
239	Opportunities and Challenges in Building a Spatiotemporal Multi-scale Model of the Human Pancreatic □Cell. *Cell*, **2018**, 173, 11-19	56.2	39
238	Integrative structure modeling with the Integrative Modeling Platform. *Protein Science*, **2018**, 27, 245-258	3	63
237	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
236	Structure of the 80S Ribosome from Saccharomyces cerevisiae□RNA-Ribosome and Subunit-Subunit Interactions. *journal of hand surgery Asian-Pacific volume, The*, **2018**, 286-299	0.5	
235	Architecture of the Protein-Conducting Channel Associated with the Translating 80S Ribosome. *journal of hand surgery Asian-Pacific volume, The*, **2018**, 274-285	0.5	
234	Predicting CD4 T-cell epitopes based on antigen cleavage, MHCII presentation, and TCR recognition. *PLoS ONE*, **2018**, 13, e0206654	3.7	17
233	EpCAM homo-oligomerization is not the basis for its role in cell-cell adhesion. *Scientific Reports*, **2018**, 8, 13269	4.9	20
232	Architecture of Pol II(G) and molecular mechanism of transcription regulation by Gdown1. *Nature Structural and Molecular Biology*, **2018**, 25, 859-867	17.6	16
231	Prediction of enzymatic pathways by integrative pathway mapping. *ELife*, **2018**, 7,	8.9	22

230	Molecular Architecture of the Major Membrane Ring Component of the Nuclear Pore Complex. *Structure*, **2017**, 25, 434-445	5.2	31
229	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
228	Computational Discovery and Experimental Validation of Inhibitors of the Human Intestinal Transporter OATP2B1. *Journal of Chemical Information and Modeling*, **2017**, 57, 1402-1413	6.1	13
227	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
226	Molecular Details Underlying Dynamic Structures and Regulation of the Human 26S Proteasome. *Molecular and Cellular Proteomics*, **2017**, 16, 840-854	7.6	67
225	Cross-activating c-Met/β1 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	11.5	42
224	Protein Structure Modeling with MODELLER. *Methods in Molecular Biology*, **2017**, 1654, 39-54	1.4	276
223	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
222	Reconstruction of 3D structures of MET antibodies from electron microscopy 2D class averages. *PLoS ONE*, **2017**, 12, e0175758	3.7	6
221	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
220	PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. *Structure*, **2017**, 25, 1317-1318	5.2	58
219	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
218	Assessing Exhaustiveness of Stochastic Sampling for Integrative Modeling of Macromolecular Structures. *Biophysical Journal*, **2017**, 113, 2344-2353	2.9	39
217	Human Concentrative Nucleoside Transporter 3 (hCNT3, SLC28A3) Forms a Cyclic Homotrimer. *Biochemistry*, **2017**, 56, 3475-3483	3.2	9
216	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
215	Immunoproteasome functions explained by divergence in cleavage specificity and regulation. *ELife*, **2017**, 6,	8.9	37
214	Guinea Pig Prion Protein Supports Rapid Propagation of Bovine Spongiform Encephalopathy and Variant Creutzfeldt-Jakob Disease Prions. *Journal of Virology*, **2016**, 90, 9558-9569	6.6	2
213	A phosphotyrosine switch regulates organic cation transporters. *Nature Communications*, **2016**, 7, 10880	17.4	74

212	Structure and Function of the Nuclear Pore Complex Cytoplasmic mRNA Export Platform. *Cell*, **2016**, 167, 1215-1228.e25	56.2	110
211	Comparative Protein Structure Modeling Using MODELLER. *Current Protocols in Protein Science*, **2016**, 86, 2.9.1-2.9.37	3.1	301
210	Clustering of disulfide-rich peptides provides scaffolds for hit discovery by phage display: application to interleukin-23. *BMC Bioinformatics*, **2016**, 17, 481	3.6	6
209	Comparative Protein Structure Modeling Using MODELLER. *Current Protocols in Bioinformatics*, **2016**, 54, 5.6.1-5.6.37	24.2	1267
208	Structure of Complement C3(H2O) Revealed By Quantitative Cross-Linking/Mass Spectrometry And Modeling. *Molecular and Cellular Proteomics*, **2016**, 15, 2730-43	7.6	46
207	CryptoSite: Expanding the Druggable Proteome by Characterization and Prediction of Cryptic Binding Sites. *Journal of Molecular Biology*, **2016**, 428, 709-719	6.5	110
206	Structure of Ɛtubulin small complex based on a cryo-EM map, chemical cross-links, and a remotely related structure. *Journal of Structural Biology*, **2016**, 194, 303-10	3.4	15
205	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
204	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
203	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
202	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
201	Simple rules for passive diffusion through the nuclear pore complex. *Journal of Cell Biology*, **2016**, 215, 57-76	7.3	199
200	Ring closure activates yeast ΓTuRC for species-specific microtubule nucleation. *Nature Structural and Molecular Biology*, **2015**, 22, 132-7	17.6	95
199	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. *Structure*, **2015**, 23, 1156-67	5.2	131
198	A strategy for dissecting the architectures of native macromolecular assemblies. *Nature Methods*, **2015**, 12, 1135-8	21.6	94
197	Small-Molecule Allosteric Modulators of the Protein Kinase PDK1 from Structure-Based Docking. *Journal of Medicinal Chemistry*, **2015**, 58, 8285-8291	8.3	19
196	Prion Protein-Antibody Complexes Characterized by Chromatography-Coupled Small-Angle X-Ray Scattering. *Biophysical Journal*, **2015**, 109, 793-805	2.9	28
195	Architecture of the Human and Yeast General Transcription and DNA Repair Factor TFIIH. *Molecular Cell*, **2015**, 59, 794-806	17.6	75

194	Structural Model of the Bilitranslocase Transmembrane Domain Supported by NMR and FRET Data. *PLoS ONE*, **2015**, 10, e0135455	3.7	7
193	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
192	Assembly and Molecular Architecture of the Phosphoinositide 3-Kinase p85Homodimer. *Journal of Biological Chemistry*, **2015**, 290, 30390-405	5.4	17
191	Topological models of heteromeric protein assemblies from mass spectrometry: application to the yeast eIF3:eIF5 complex. *Chemistry and Biology*, **2015**, 22, 117-28		34
190	Prediction of Functionally Important Phospho-Regulatory Events in Xenopus laevis Oocytes. *PLoS Computational Biology*, **2015**, 11, e1004362	5	14
189	Molecular architecture of the yeast Mediator complex. *ELife*, **2015**, 4,	8.9	107
188	Modeling of proteins and their assemblies with the Integrative Modeling Platform. *Methods in Molecular Biology*, **2014**, 1091, 277-95	1.4	25
187	Uncertainty in integrative structural modeling. *Current Opinion in Structural Biology*, **2014**, 28, 96-104	8.1	68
186	Comparative Protein Structure Modeling Using MODELLER. *Current Protocols in Bioinformatics*, **2014**, 47, 5.6.1-32	24.2	754
185	Molecular architecture of photoreceptor phosphodiesterase elucidated by chemical cross-linking and integrative modeling. *Journal of Molecular Biology*, **2014**, 426, 3713-3728	6.5	34
184	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
183	Insights into secondary metabolism from a global analysis of prokaryotic biosynthetic gene clusters. *Cell*, **2014**, 158, 412-421	56.2	587
182	Molecular architecture of the 40S?eIF1?eIF3 translation initiation complex. *Cell*, **2014**, 158, 1123-1135	56.2	157
181	Prediction of substrates for glutathione transferases by covalent docking. *Journal of Chemical Information and Modeling*, **2014**, 54, 1687-99	6.1	15
180	Protein structure modeling with MODELLER. *Methods in Molecular Biology*, **2014**, 1137, 1-15	1.4	406
179	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
178	Determining protein complex structures based on a Bayesian model of in vivo Fster resonance energy transfer (FRET) data. *Molecular and Cellular Proteomics*, **2014**, 13, 2812-23	7.6	22
177	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

176	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
175	ModBase, a database of annotated comparative protein structure models and associated resources. *Nucleic Acids Research*, **2014**, 42, D336-46	20.1	207
174	A systematic computational analysis of biosynthetic gene cluster evolution: lessons for engineering biosynthesis. *PLoS Computational Biology*, **2014**, 10, e1004016	5	118
173	Elucidating the mechanism of substrate recognition by the bacterial Hsp90 molecular chaperone. *Journal of Molecular Biology*, **2014**, 426, 2393-404	6.5	37
172	SAXS Merge: an automated statistical method to merge SAXS profiles using Gaussian processes. *Journal of Synchrotron Radiation*, **2014**, 21, 203-8	2.4	12
171	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
170	Deamination of 6-aminodeoxyfutalosine in menaquinone biosynthesis by distantly related enzymes. *Biochemistry*, **2013**, 52, 6525-36	3.2	9
169	Structure-guided discovery of new deaminase enzymes. *Journal of the American Chemical Society*, **2013**, 135, 13927-33	16.4	13
168	High-resolution network biology: connecting sequence with function. *Nature Reviews Genetics*, **2013**, 14, 865-79	30.1	65
167	Accurate SAXS profile computation and its assessment by contrast variation experiments. *Biophysical Journal*, **2013**, 105, 962-74	2.9	359
166	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
165	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
164	Impact of mutations on the allosteric conformational equilibrium. *Journal of Molecular Biology*, **2013**, 425, 647-61	6.5	38
163	Biochemistry. Integrative structural biology. *Science*, **2013**, 339, 913-5	33.3	177
162	Structure, dynamics, evolution, and function of a major scaffold component in the nuclear pore complex. *Structure*, **2013**, 21, 560-71	5.2	48
161	Crystal structure of a eukaryotic phosphate transporter. *Nature*, **2013**, 496, 533-6	50.4	170
160	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
159	Recovering a representative conformational ensemble from underdetermined macromolecular structural data. *Journal of the American Chemical Society*, **2013**, 135, 16595-609	16.4	88

158	Mapping polymerization and allostery of hemoglobin S using point mutations. *Journal of Physical Chemistry B*, **2013**, 117, 13058-68	3.4	3
157	Optimized atomic statistical potentials: assessment of protein interfaces and loops. *Bioinformatics*, **2013**, 29, 3158-66	7.2	88
156	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
155	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
154	Molecular modeling and ligand docking for solute carrier (SLC) transporters. *Current Topics in Medicinal Chemistry*, **2013**, 13, 843-56	3	65
153	UCSF Chimera, MODELLER, and IMP: an integrated modeling system. *Journal of Structural Biology*, **2012**, 179, 269-78	3.4	373
152	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
151	Integrative structural modeling with small angle X-ray scattering profiles. *BMC Structural Biology*, **2012**, 12, 17	2.7	80
150	High selectivity of the □aminobutyric acid transporter 2 (GAT-2, SLC6A13) revealed by structure-based approach. *Journal of Biological Chemistry*, **2012**, 287, 37745-56	5.4	41
149	Putting the pieces together: integrative modeling platform software for structure determination of macromolecular assemblies. *PLoS Biology*, **2012**, 10, e1001244	9.7	362
148	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, 2110-6	4.2	6
147	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
146	Macromolecular assembly structures by comparative modeling and electron microscopy. *Methods in Molecular Biology*, **2012**, 857, 331-50	1.4	4
145	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
144	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
143	Structure-function mapping of a heptameric module in the nuclear pore complex. *Journal of Cell Biology*, **2012**, 196, 419-34	7.3	95
142	A method for integrative structure determination of protein-protein complexes. *Bioinformatics*, **2012**, 28, 3282-9	7.2	69
141	Virtual ligand screening against comparative protein structure models. *Methods in Molecular Biology*, **2012**, 819, 105-26	1.4	11

140	Large scale analysis of synaptic phosphorylation and O-GlcNAcylation reveals complex interplay between these post-translational modifications. *FASEB Journal*, **2012**, 26, 978.2	0.9	
139	Vif hijacks CBF-β to degrade APOBEC3G and promote HIV-1 infection. *Nature*, **2011**, 481, 371-5	50.4	268
138	Global landscape of HIV-human protein complexes. *Nature*, **2011**, 481, 365-70	50.4	507
137	Discovery of a cytokinin deaminase. *ACS Chemical Biology*, **2011**, 6, 1036-40	4.9	15
136	Ligand discovery from a dopamine D3 receptor homology model and crystal structure. *Nature Chemical Biology*, **2011**, 7, 769-78	11.7	250
135	Macromolecular docking restrained by a small angle X-ray scattering profile. *Journal of Structural Biology*, **2011**, 173, 461-71	3.4	88
134	Statistical potential for modeling and ranking of protein-ligand interactions. *Journal of Chemical Information and Modeling*, **2011**, 51, 3078-92	6.1	61
133	Structure of the C-terminal domain of Saccharomyces cerevisiae Nup133, a component of the nuclear pore complex. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79, 1672-7	4.2	16
132	Response to Predictable difficulty or difficulty to predict. *Protein Science*, **2011**, 20, 4-5	6.3	78
131	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
130	The Enzyme Function Initiative. *Biochemistry*, **2011**, 50, 9950-62	3.2	140
129	Enzymatic deamination of the epigenetic base N-6-methyladenine. *Journal of the American Chemical Society*, **2011**, 133, 2080-3	16.4	22
128	MultiFit: a web server for fitting multiple protein structures into their electron microscopy density map. *Nucleic Acids Research*, **2011**, 39, W167-70	20.1	21
127	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
126	Evolution: On a bender--BARs, ESCRTs, COPs, and finally getting your coat. *Journal of Cell Biology*, **2011**, 193, 963-72	7.3	78
125	ModBase, a database of annotated comparative protein structure models, and associated resources. *Nucleic Acids Research*, **2011**, 39, D465-74	20.1	252
124	Modeling of proteins and their assemblies with the integrative modeling platform. *Methods in Molecular Biology*, **2011**, 781, 377-97	1.4	16
123	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

122	FoXS: a web server for rapid computation and fitting of SAXS profiles. *Nucleic Acids Research*, **2010**, 38, W540-4	20.1	403
121	The overlap of small molecule and protein binding sites within families of protein structures. *PLoS Computational Biology*, **2010**, 6, e1000668	5	39
120	Toward an integrated structural model of the 26S proteasome. *Molecular and Cellular Proteomics*, **2010**, 9, 1666-77	7.6	48
119	Prediction of protease substrates using sequence and structure features. *Bioinformatics*, **2010**, 26, 1714-22	7.2	49
118	Integrative structure modeling of macromolecular assemblies from proteomics data. *Molecular and Cellular Proteomics*, **2010**, 9, 1689-702	7.6	58
117	Comparison of human solute carriers. *Protein Science*, **2010**, 19, 412-28	6.3	83
116	Functional hot spots in human ATP-binding cassette transporter nucleotide binding domains. *Protein Science*, **2010**, 19, 2110-21	6.3	15
115	Structures of the autoproteolytic domain from the Saccharomyces cerevisiae nuclear pore complex component, Nup145. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 1992-8	4.2	9
114	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
113	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
112	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
111	MODBASE, a database of annotated comparative protein structure models and associated resources. *Nucleic Acids Research*, **2009**, 37, D347-54	20.1	143
110	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
109	A kernel for open source drug discovery in tropical diseases. *PLoS Neglected Tropical Diseases*, **2009**, 3, e418	4.8	20
108	Alignment of multiple protein structures based on sequence and structure features. *Protein Engineering, Design and Selection*, **2009**, 22, 569-74	1.9	71
107	The structural dynamics of macromolecular processes. *Current Opinion in Cell Biology*, **2009**, 21, 97-108	9	67
106	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
105	A survey of integral alpha-helical membrane proteins. *Journal of Structural and Functional Genomics*, **2009**, 10, 269-80		12

104	Evolutionary constraints on structural similarity in orthologs and paralogs. *Protein Science*, **2009**, 18, 1306-15	6.3	50
103	Comprehensive molecular structure of the eukaryotic ribosome. *Structure*, **2009**, 17, 1591-1604	5.2	130
102	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
101	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
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5	CM1-driven assembly and activation of Yeast □Tubulin Small Complex underlies microtubule nucleation		1
4	Structure of complement C3(H2O) revealed by quantitative cross-linking/mass spectrometry and modeling		1
3	Bayesian metamodeling of complex biological systems across varying representations		1
2	A quantitative map of nuclear pore assembly reveals two distinct mechanisms		2
1	Integrative analysis reveals unique features of the Smc5/6 complex		2