

Michael R Sawaya

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

201
papers

22,051
citations

71
h-index

147
g-index

227
ext. papers

25,293
ext. citations

12.9
avg, IF

6.68
L-index

#	Paper	IF	Citations
201	Extended β -Strands Contribute to Reversible Amyloid Formation.. <i>ACS Nano</i> , 2022 ,	16.7	2
200	Amyloid fibrils in disease FTLD-TDP are composed of TMEM106B not TDP-43.. <i>Nature</i> , 2022 ,	50.4	5
199	Cryo-EM structure of RNA-induced tau fibrils reveals a small C-terminal core that may nucleate fibril formation.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2119952119	11.5	0
198	Atomic View of an Amyloid Dodecamer Exhibiting Selective Cellular Toxic Vulnerability in Acute Brain Slices.. <i>Protein Science</i> , 2021 ,	6.3	1
197	Intrinsic electronic conductivity of individual atomically resolved amyloid crystals reveals micrometer-long hole hopping via tyrosines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	15
196	Inhibition of amyloid formation of the Nucleoprotein of SARS-CoV-2 2021 ,		6
195	Structural characterization of hexameric shell proteins from two types of choline-utilization bacterial microcompartments. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021 , 77, 275-285	1.1	0
194	Cryo-EM structures of hIAPP fibrils seeded by patient-extracted fibrils reveal new polymorphs and conserved fibril cores. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 724-730	17.6	3
193	The expanding amyloid family: Structure, stability, function, and pathogenesis. <i>Cell</i> , 2021 , 184, 4857-4873	36.2	23
192	Ab Initio Determination of Peptide Structures by MicroED. <i>Methods in Molecular Biology</i> , 2021 , 2215, 329-348	1.4	1
191	Cryo-EM structure and inhibitor design of human IAPP (amylin) fibrils. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 653-659	17.6	41
190	Crystal structure of a conformational antibody that binds tau oligomers and inhibits pathological seeding by extracts from donors with Alzheimer's disease. <i>Journal of Biological Chemistry</i> , 2020 , 295, 10662-10676	5.4	5
189	Serial femtosecond crystallography on in vivo-grown crystals drives elucidation of mosquitoicidal Cyt1Aa bioactivation cascade. <i>Nature Communications</i> , 2020 , 11, 1153	17.4	11
188	The β -Synuclein hereditary mutation E46K unlocks a more stable, pathogenic fibril structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 3592-3602	11.5	57
187	Cryo-EM structure of a human prion fibril with a hydrophobic, protease-resistant core. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 417-423	17.6	37
186	Fragment-based determination of a proteinase K structure from MicroED data using ARCIMBOLDO_SHREDDER. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020 , 76, 703-712	5.5	6
185	Symmetry breaking and structural polymorphism in a bacterial microcompartment shell protein for choline utilization. <i>Protein Science</i> , 2020 , 29, 2201-2212	6.3	7

184	Isobutanol production freed from biological limits using synthetic biochemistry. <i>Nature Communications</i> , 2020 , 11, 4292	17.4	24
183	CryoEM structure of the low-complexity domain of hnRNPA2 and its conversion to pathogenic amyloid. <i>Nature Communications</i> , 2020 , 11, 4090	17.4	36
182	Non-proteinaceous hydrolase comprised of a phenylalanine metallo-supramolecular amyloid-like structure. <i>Nature Catalysis</i> , 2019 , 2, 977-985	36.5	65
181	Cryo-EM structures of four polymorphic TDP-43 amyloid cores. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 619-627	17.6	103
180	Structure and mechanism of TagA, a novel membrane-associated glycosyltransferase that produces wall teichoic acids in pathogenic bacteria. <i>PLoS Pathogens</i> , 2019 , 15, e1007723	7.6	13
179	Structure of amyloid- β (20-34) with Alzheimer β -associated isomerization at Asp23 reveals a distinct protofilament interface. <i>Nature Communications</i> , 2019 , 10, 3357	17.4	25
178	Structure-based inhibitors halt prion-like seeding by Alzheimer β disease-and tauopathy-derived brain tissue samples. <i>Journal of Biological Chemistry</i> , 2019 , 294, 16451-16464	5.4	23
177	Structures of fibrils formed by β synuclein hereditary disease mutant H50Q reveal new polymorphs. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 1044-1052	17.6	62
176	Homochiral and racemic MicroED structures of a peptide repeat from the ice-nucleation protein InaZ. <i>IUCrJ</i> , 2019 , 6, 197-205	4.7	8
175	Structure-based inhibitors of amyloid beta core suggest a common interface with tau. <i>ELife</i> , 2019 , 8,	8.9	34
174	Structure and Mechanism of LcpA, a Phosphotransferase That Mediates Glycosylation of a Gram-Positive Bacterial Cell Wall-Anchored Protein. <i>MBio</i> , 2019 , 10,	7.8	9
173	Mechanically rigid supramolecular assemblies formed from an Fmoc-guanine conjugated peptide nucleic acid. <i>Nature Communications</i> , 2019 , 10, 5256	17.4	9
172	Structural Variability of EspG Chaperones from Mycobacterial ESX-1, ESX-3, and ESX-5 Type VII Secretion Systems. <i>Journal of Molecular Biology</i> , 2019 , 431, 289-307	6.5	13
171	Transition of Metastable Cross- β Crystals into Cross- β Fibrils by β -Turn Flipping. <i>Journal of the American Chemical Society</i> , 2019 , 141, 363-369	16.4	11
170	Atomic structures of corkscrew-forming segments of SOD1 reveal varied oligomer conformations. <i>Protein Science</i> , 2018 , 27, 1231-1242	6.3	11
169	Crystal structures of amyloidogenic segments of human transthyretin. <i>Protein Science</i> , 2018 , 27, 1295-1303	13	15
168	Atomic structures of low-complexity protein segments reveal kinked β sheets that assemble networks. <i>Science</i> , 2018 , 359, 698-701	33.3	220
167	Distal amyloid β -protein fragments template amyloid assembly. <i>Protein Science</i> , 2018 , 27, 1181-1190	6.3	6

166	Common fibrillar spines of amyloid- β and human islet amyloid polypeptide revealed by microelectron diffraction and structure-based inhibitors. <i>Journal of Biological Chemistry</i> , 2018 , 293, 2888-2902	5.4	31
165	Sub- β gstr β cryo-EM structure of a prion protofibril reveals a polar clasp. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 131-134	17.6	56
164	Atomic-level evidence for packing and positional amyloid polymorphism by segment from TDP-43 RRM2. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 311-319	17.6	63
163	Atomic insights into the genesis of cellular filaments by globular proteins. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 705-714	17.6	4
162	computation of the PDB to audit diffraction anisotropy of soluble and membrane proteins. <i>Data in Brief</i> , 2018 , 19, 753-757	1.2	1
161	Ultrafast Time-Resolved Studies on Fluorescein for Recognition Strands Architecture in Amyloid Fibrils. <i>Journal of Physical Chemistry B</i> , 2018 , 122, 8-18	3.4	5
160	Inhibiting amyloid- β cytotoxicity through its interaction with the cell surface receptor LILRB2 by structure-based design. <i>Nature Chemistry</i> , 2018 , 10, 1213-1221	17.6	24
159	Identification of two principal amyloid-driving segments in variable domains of Ig light chains in systemic light-chain amyloidosis. <i>Journal of Biological Chemistry</i> , 2018 , 293, 19659-19671	5.4	19
158	Cryo-EM of full-length β synuclein reveals fibril polymorphs with a common structural kernel. <i>Nature Communications</i> , 2018 , 9, 3609	17.4	267
157	Atomic structures of TDP-43 LCD segments and insights into reversible or pathogenic aggregation. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 463-471	17.6	116
156	Structural Studies of Amyloid Proteins at the Molecular Level. <i>Annual Review of Biochemistry</i> , 2017 , 86, 69-95	29.1	264
155	The cytotoxic PSM β reveals a cross- β amyloid-like fibril. <i>Science</i> , 2017 , 355, 831-833	33.3	154
154	Atomic-resolution structures from fragmented protein crystals with the cryoEM method MicroED. <i>Nature Methods</i> , 2017 , 14, 399-402	21.6	109
153	Flow-aligned, single-shot fiber diffraction using a femtosecond X-ray free-electron laser. <i>Cytoskeleton</i> , 2017 , 74, 472-481	2.4	10
152	Atomic structure of a toxic, oligomeric segment of SOD1 linked to amyotrophic lateral sclerosis (ALS). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 8770-8775	11.5	60
151	Catastrophic disassembly of actin filaments via Mical-mediated oxidation. <i>Nature Communications</i> , 2017 , 8, 2183	17.4	41
150	X-ray diffraction reveals the intrinsic difference in the physical properties of membrane and soluble proteins. <i>Scientific Reports</i> , 2017 , 7, 17013	4.9	7
149	Atomic structures of fibrillar segments of hIAPP suggest tightly mated β -sheets are important for cytotoxicity. <i>ELife</i> , 2017 , 6,	8.9	76

148	Ab initio structure determination from prion nanocrystals at atomic resolution by MicroED. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 11232-11236	11.5	66
147	Crystal Structures of IAPP Amyloidogenic Segments Reveal a Novel Packing Motif of Out-of-Register Beta Sheets. <i>Journal of Physical Chemistry B</i> , 2016 , 120, 5810-6	3.4	46
146	Distinct C9orf72-Associated Dipeptide Repeat Structures Correlate with Neuronal Toxicity. <i>PLoS ONE</i> , 2016 , 11, e0165084	3.7	24
145	Crystal Structure and Bioinformatics Inferred Function of Protein A2617 from <i>Methylobium petroleiphilum</i> . <i>FASEB Journal</i> , 2016 , 30, 601.9	0.9	
144	Crystal Structure of the <i>Streptomyces coelicolor</i> Sortase E1 Transpeptidase Provides Insight into the Binding Mode of the Novel Class E Sorting Signal. <i>PLoS ONE</i> , 2016 , 11, e0167763	3.7	15
143	The function of the PduJ microcompartment shell protein is determined by the genomic position of its encoding gene. <i>Molecular Microbiology</i> , 2016 , 101, 770-83	4.1	24
142	Three-Dimensional Determination of the Coordinates of Individual Atoms in Materials. <i>Microscopy and Microanalysis</i> , 2016 , 22, 916-917	0.5	
141	Progress in low-resolution ab initio phasing with CrowdPhase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 446-53	5.5	3
140	De novo phasing with X-ray laser reveals mosquito larvicide BinAB structure. <i>Nature</i> , 2016 , 539, 43-47	50.4	73
139	A PII-Like Protein Regulated by Bicarbonate: Structural and Biochemical Studies of the Carboxysome-Associated CPII Protein. <i>Journal of Molecular Biology</i> , 2016 , 428, 4013-4030	6.5	8
138	Implications for Alzheimer's disease of an atomic resolution structure of amyloid- β (1-42) fibrils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 9398-400	11.5	24
137	Selective molecular transport through the protein shell of a bacterial microcompartment organelle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 2990-5	11.5	90
136	Biochemical and Structural Basis for Controlling Chemical Modularity in Fungal Polyketide Biosynthesis. <i>Journal of the American Chemical Society</i> , 2015 , 137, 9885-93	16.4	44
135	Indexing amyloid peptide diffraction from serial femtosecond crystallography: new algorithms for sparse patterns. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 357-66		12
134	Structure of the Angiotensin receptor revealed by serial femtosecond crystallography. <i>Cell</i> , 2015 , 161, 833-44	56.2	262
133	Toxicity of eosinophil MBP is repressed by intracellular crystallization and promoted by extracellular aggregation. <i>Molecular Cell</i> , 2015 , 57, 1011-1021	17.6	62
132	Three-dimensional coordinates of individual atoms in materials revealed by electron tomography. <i>Nature Materials</i> , 2015 , 14, 1099-103	27	131
131	Uncovering the Mechanism of Aggregation of Human Transthyretin. <i>Journal of Biological Chemistry</i> , 2015 , 290, 28932-43	5.4	85

130	Structural Organization of Insulin Fibrils Based on Polarized Raman Spectroscopy: Evaluation of Existing Models. <i>Journal of the American Chemical Society</i> , 2015 , 137, 11312-20	16.4	22
129	Structure of the toxic core of β synuclein from invisible crystals. <i>Nature</i> , 2015 , 525, 486-90	50.4	393
128	Structural analysis of mevalonate-3-kinase provides insight into the mechanisms of isoprenoid pathway decarboxylases. <i>Protein Science</i> , 2015 , 24, 212-20	6.3	13
127	Inhibition by small-molecule ligands of formation of amyloid fibrils of an immunoglobulin light chain variable domain. <i>ELife</i> , 2015 , 4, e10935	8.9	36
126	(Quasi-)racemic X-ray structures of glycosylated and non-glycosylated forms of the chemokine Ser-CCL1 prepared by total chemical synthesis. <i>Angewandte Chemie - International Edition</i> , 2014 , 53, 5194-8	16.4	50
125	The role of distant mutations and allosteric regulation on LovD active site dynamics. <i>Nature Chemical Biology</i> , 2014 , 10, 431-6	11.7	132
124	Factors that drive peptide assembly from native to amyloid structures: experimental and theoretical analysis of [leu-5]-enkephalin mutants. <i>Journal of Physical Chemistry B</i> , 2014 , 118, 7247-56	3.4	23
123	Protein crystal structure obtained at 2.9 Å resolution from injecting bacterial cells into an X-ray free-electron laser beam. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 12769-74	11.5	84
122	Identification of a unique Fe-S cluster binding site in a glycyl-radical type microcompartment shell protein. <i>Journal of Molecular Biology</i> , 2014 , 426, 3287-3304	6.5	16
121	Alanine scanning mutagenesis identifies an asparagine-arginine-lysine triad essential to assembly of the shell of the Pdu microcompartment. <i>Journal of Molecular Biology</i> , 2014 , 426, 2328-45	6.5	46
120	(Quasi-)Racemic X-ray Structures of Glycosylated and Non-Glycosylated Forms of the Chemokine Ser-CCL1 Prepared by Total Chemical Synthesis. <i>Angewandte Chemie</i> , 2014 , 126, 5294-5298	3.6	11
119	Structural and computational studies of the <i>Staphylococcus aureus</i> sortase B-substrate complex reveal a substrate-stabilized oxyanion hole. <i>Journal of Biological Chemistry</i> , 2014 , 289, 8891-902	5.4	29
118	Aggregation-triggering segments of SOD1 fibril formation support a common pathway for familial and sporadic ALS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 197-201	11.5	92
117	Structure-based design of functional amyloid materials. <i>Journal of the American Chemical Society</i> , 2014 , 136, 18044-51	16.4	82
116	Novel mechanism of heme capture by Hbp2, the hemoglobin-binding hemophore from <i>Listeria monocytogenes</i> . <i>Journal of Biological Chemistry</i> , 2014 , 289, 34886-99	5.4	23
115	Formation of amyloid fibers by monomeric light chain variable domains. <i>Journal of Biological Chemistry</i> , 2014 , 289, 27513-25	5.4	25
114	Structure of the methanofuran/methanopterin-biosynthetic enzyme MJ1099 from <i>Methanocaldococcus jannaschii</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1472-9	1.1	2
113	The structured core domain of B-crystallin can prevent amyloid fibrillation and associated toxicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E1562-70	11.5	154

112	CrowdPhase: crowdsourcing the phase problem. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 1538-48		8
111	Methods to refine macromolecular structures in cases of severe diffraction anisotropy. <i>Methods in Molecular Biology</i> , 2014 , 1091, 205-14	1.4	7
110	Towards three-dimensional structural determination of amorphous materials at atomic resolution. <i>Physical Review B</i> , 2013 , 88,	3.3	15
109	Uncovering the enzymes that catalyze the final steps in oxytetracycline biosynthesis. <i>Journal of the American Chemical Society</i> , 2013 , 135, 7138-41	16.4	61
108	Amyloid Structures at the Atomic Level: Insights from Crystallography 2013 , 21-38		
107	Structure and flexibility of nanoscale protein cages designed by symmetric self-assembly. <i>Journal of the American Chemical Society</i> , 2013 , 135, 7738-43	16.4	76
106	Heterologous expression of mycobacterial Esx complexes in Escherichia coli for structural studies is facilitated by the use of maltose binding protein fusions. <i>PLoS ONE</i> , 2013 , 8, e81753	3.7	15
105	Out-of-register β -sheets suggest a pathway to toxic amyloid aggregates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 20913-8	11.5	149
104	The crystal structure of the Rv0301-Rv0300 VapBC-3 toxin-antitoxin complex from M. tuberculosis reveals a Mg ²⁺ ion in the active site and a putative RNA-binding site. <i>Protein Science</i> , 2012 , 21, 1754-67	6.3	46
103	Cell-free formation of RNA granules: low complexity sequence domains form dynamic fibers within hydrogels. <i>Cell</i> , 2012 , 149, 753-67	56.2	1300
102	Structural states and dynamics of the D-loop in actin. <i>Biophysical Journal</i> , 2012 , 103, 930-9	2.9	32
101	Single-wavelength phasing strategy for quasi-racemic protein crystal diffraction data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 62-8		9
100	Ribonuclease A suggests how proteins self-chaperone against amyloid fiber formation. <i>Protein Science</i> , 2012 , 21, 26-37	6.3	21
99	Atomic view of a toxic amyloid small oligomer. <i>Science</i> , 2012 , 335, 1228-31	33.3	440
98	Computational design of self-assembling protein nanomaterials with atomic level accuracy. <i>Science</i> , 2012 , 336, 1171-4	33.3	473
97	Multiple forms of Spire-actin complexes and their functional consequences. <i>Journal of Biological Chemistry</i> , 2012 , 287, 10684-10692	5.4	20
96	β -microglobulin forms three-dimensional domain-swapped amyloid fibrils with disulfide linkages. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 49-55	17.6	93
95	Characteristics of amyloid-related oligomers revealed by crystal structures of macrocyclic β -sheet mimics. <i>Journal of the American Chemical Society</i> , 2011 , 133, 6736-44	16.4	73

94	Molecular basis for amyloid-beta polymorphism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 16938-43	11.5	306
93	Synthetic symmetrization in the crystallization and structure determination of CclA from <i>Thermotoga maritima</i> . <i>Protein Science</i> , 2011 , 20, 168-78	6.3	18
92	Structures of segments of β -synuclein fused to maltose-binding protein suggest intermediate states during amyloid formation. <i>Protein Science</i> , 2011 , 20, 996-1004	6.3	22
91	An approach to crystallizing proteins by metal-mediated synthetic symmetrization. <i>Protein Science</i> , 2011 , 20, 1876-90	6.3	54
90	Crystal structure of the central coiled-coil domain from human liprin- β . <i>Biochemistry</i> , 2011 , 50, 3807-15	3.2	2
89	Macrocyclic β -sheet peptides that inhibit the aggregation of a tau-protein-derived hexapeptide. <i>Journal of the American Chemical Society</i> , 2011 , 133, 3144-57	16.4	98
88	Atomic structures suggest determinants of transmission barriers in mammalian prion disease. <i>Biochemistry</i> , 2011 , 50, 2456-63	3.2	45
87	Discovery and characterization of a unique mycobacterial heme acquisition system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 5051-6	11.5	152
86	Structural and biochemical characterization of the salicylyl-acyltransferase SsfX3 from a tetracycline biosynthetic pathway. <i>Journal of Biological Chemistry</i> , 2011 , 286, 41539-41551	5.4	12
85	Towards a pharmacophore for amyloid. <i>PLoS Biology</i> , 2011 , 9, e1001080	9.7	159
84	Structural insight into the mechanisms of transport across the <i>Salmonella enterica</i> Pdu microcompartment shell. <i>Journal of Biological Chemistry</i> , 2010 , 285, 37838-46	5.4	108
83	An introduction to biomolecular graphics. <i>PLoS Computational Biology</i> , 2010 , 6, e1000918	5	30
82	Crystallographic studies of prion protein (PrP) segments suggest how structural changes encoded by polymorphism at residue 129 modulate susceptibility to human prion disease. <i>Journal of Biological Chemistry</i> , 2010 , 285, 29671-5	5.4	50
81	Structure and mechanisms of a protein-based organelle in <i>Escherichia coli</i> . <i>Science</i> , 2010 , 327, 81-4	33.3	171
80	Total chemical synthesis and X-ray structure of kalitoxin by racemic protein crystallography. <i>Chemical Communications</i> , 2010 , 46, 8174-6	5.8	42
79	X-ray crystallographic structure of an artificial beta-sheet dimer. <i>Journal of the American Chemical Society</i> , 2010 , 132, 11622-8	16.4	36
78	Two amyloid States of the prion protein display significantly different folding patterns. <i>Journal of Molecular Biology</i> , 2010 , 400, 908-21	6.5	56
77	Multidimensional structure-activity relationship of a protein in its aggregated states. <i>Angewandte Chemie - International Edition</i> , 2010 , 49, 3904-8	16.4	46

76	Apo and ligand-bound structures of ModA from the archaeon <i>Methanosarcina acetivorans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 242-50		11
75	Crystal structures of truncated alphaA and alphaB crystallins reveal structural mechanisms of polydispersity important for eye lens function. <i>Protein Science</i> , 2010 , 19, 1031-43	6.3	244
74	Structure of the dimerization domain of DiGeorge critical region 8. <i>Protein Science</i> , 2010 , 19, 1354-65	6.3	45
73	Determination of the X-ray structure of the snake venom protein omwaprin by total chemical synthesis and racemic protein crystallography. <i>Protein Science</i> , 2010 , 19, 1840-9	6.3	45
72	Atomic structures of IAPP (amylin) fusions suggest a mechanism for fibrillation and the role of insulin in the process. <i>Protein Science</i> , 2009 , 18, 1521-30	6.3	172
71	Structure of a mutant human purine nucleoside phosphorylase with the prodrug, 2-fluoro-2Rdeoxyadenosine and the cytotoxic drug, 2-fluoroadenine. <i>Protein Science</i> , 2009 , 18, 1107-14	6.3	10
70	Analysis of lattice-translocation disorder in the layered hexagonal structure of carboxysome shell protein CsoS1C. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009 , 65, 980-8		33
69	Molecular mechanisms for protein-encoded inheritance. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 973-8	17.6	218
68	Directed evolution and structural characterization of a simvastatin synthase. <i>Chemistry and Biology</i> , 2009 , 16, 1064-74		63
67	Functional amyloids as natural storage of peptide hormones in pituitary secretory granules. <i>Science</i> , 2009 , 325, 328-32	33.3	728
66	Molecular basis for insulin fibril assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 18990-5	11.5	290
65	Crystal structure of human fibrinogen. <i>Biochemistry</i> , 2009 , 48, 3877-86	3.2	231
64	Insights from multiple structures of the shell proteins from the beta-carboxysome. <i>Protein Science</i> , 2009 , 18, 108-20	6.3	78
63	Regulation of enzyme localization by polymerization: polymer formation by the SAM domain of diacylglycerol kinase delta1. <i>Structure</i> , 2008 , 16, 380-7	5.2	53
62	Structure of the PduU shell protein from the Pdu microcompartment of <i>Salmonella</i> . <i>Structure</i> , 2008 , 16, 1324-32	5.2	82
61	Atomic-level models of the bacterial carboxysome shell. <i>Science</i> , 2008 , 319, 1083-6	33.3	310
60	Atomic structure of the cross-beta spine of islet amyloid polypeptide (amylin). <i>Protein Science</i> , 2008 , 17, 1467-74	6.3	281
59	Structures and functional implications of an AMP-binding cystathionine beta-synthase domain protein from a hyperthermophilic archaeon. <i>Journal of Molecular Biology</i> , 2008 , 380, 181-92	6.5	22

58	The Tim8-Tim13 complex has multiple substrate binding sites and binds cooperatively to Tim23. <i>Journal of Molecular Biology</i> , 2008 , 382, 1144-56	6.5	53
57	A double S shape provides the structural basis for the extraordinary binding specificity of Dscam isoforms. <i>Cell</i> , 2008 , 134, 1007-18	56.2	86
56	Bacterial inclusion bodies contain amyloid-like structure. <i>PLoS Biology</i> , 2008 , 6, e195	9.7	159
55	Connecting actin monomers by iso-peptide bond is a toxicity mechanism of the <i>Vibrio cholerae</i> MARTX toxin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 18537-42	11.5	57
54	Multiple crystal structures of actin dimers and their implications for interactions in the actin filament. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008 , 64, 454-65		16
53	Structure of the RuBisCO chaperone RbcX from <i>Synechocystis</i> sp. PCC6803. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007 , 63, 1109-12		16
52	Atomic structures of amyloid cross-beta spines reveal varied steric zippers. <i>Nature</i> , 2007 , 447, 453-7	50.4	1785
51	Structural analysis of CsoS1A and the protein shell of the <i>Halothiobacillus neapolitanus</i> carboxysome. <i>PLoS Biology</i> , 2007 , 5, e144	9.7	118
50	Characterizing a crystal from an initial native dataset. <i>Methods in Molecular Biology</i> , 2007 , 364, 95-120	1.4	10
49	Deposition diseases and 3D domain swapping. <i>Structure</i> , 2006 , 14, 811-24	5.2	180
48	Toward the structural genomics of complexes: crystal structure of a PE/PPE protein complex from <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 8060-5	11.5	602
47	The structure of beta-carbonic anhydrase from the carboxysomal shell reveals a distinct subclass with one active site for the price of two. <i>Journal of Biological Chemistry</i> , 2006 , 281, 7546-55	5.4	133
46	The crystal structure of the primary Ca ²⁺ sensor of the Na ⁺ /Ca ²⁺ exchanger reveals a novel Ca ²⁺ binding motif. <i>Journal of Biological Chemistry</i> , 2006 , 281, 21577-21581	5.4	88
45	Crystal Structure Refinement 2006 ,		224
44	The structural biology of protein aggregation diseases: Fundamental questions and some answers. <i>Accounts of Chemical Research</i> , 2006 , 39, 568-75	24.3	153
43	Regulation by oligomerization in a mycobacterial folate biosynthetic enzyme. <i>Journal of Molecular Biology</i> , 2005 , 349, 61-72	6.5	32
42	Structure of the cross-beta spine of amyloid-like fibrils. <i>Nature</i> , 2005 , 435, 773-8	50.4	1791
41	Amyloid-like fibrils of ribonuclease A with three-dimensional domain-swapped and native-like structure. <i>Nature</i> , 2005 , 437, 266-9	50.4	224

40	Crystal structures of a tetrahedral open pore ferritin from the hyperthermophilic archaeon <i>Archaeoglobus fulgidus</i> . <i>Structure</i> , 2005 , 13, 637-48	5.2	98
39	Crystal structure of a RuBisCO-like protein from the green sulfur bacterium <i>Chlorobium tepidum</i> . <i>Structure</i> , 2005 , 13, 779-89	5.2	31
38	Crystal structure of the restriction-modification system control element C.BclI and mapping of its binding site. <i>Structure</i> , 2005 , 13, 1837-47	5.2	27
37	The 1.70 angstroms X-ray crystal structure of <i>Mycobacterium tuberculosis</i> phosphoglycerate mutase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 309-15		10
36	The crystal structure of a cross-linked actin dimer suggests a detailed molecular interface in F-actin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 13105-10	11.5	51
35	Structural organization of a Sex-comb-on-midleg/polyhomeotic copolymer. <i>Journal of Biological Chemistry</i> , 2005 , 280, 27769-75	5.4	67
34	Protein structures forming the shell of primitive bacterial organelles. <i>Science</i> , 2005 , 309, 936-8	33.3	354
33	An amyloid-forming segment of beta2-microglobulin suggests a molecular model for the fibril. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 10584-9	11.5	209
32	Derepression by depolymerization; structural insights into the regulation of Yan by Mae. <i>Cell</i> , 2004 , 118, 163-73	56.2	80
31	Crystal structure of the <i>Mycobacterium tuberculosis</i> dUTPase: insights into the catalytic mechanism. <i>Journal of Molecular Biology</i> , 2004 , 341, 503-17	6.5	71
30	Structural and EPR characterization of the soluble form of cytochrome c-550 and of the psbV2 gene product from the cyanobacterium <i>Thermosynechococcus elongatus</i> . <i>Plant and Cell Physiology</i> , 2003 , 44, 697-706	4.9	34
29	The crystal structure of a cyanobacterial water-soluble carotenoid binding protein. <i>Structure</i> , 2003 , 11, 55-65	5.2	191
28	The crystal structure of the first enzyme in the pantothenate biosynthetic pathway, ketopantoate hydroxymethyltransferase, from <i>M. tuberculosis</i> . <i>Structure</i> , 2003 , 11, 753-64	5.2	32
27	Structure of superoxide dismutase from <i>Pyrobaculum aerophilum</i> presents a challenging case in molecular replacement with multiple molecules, pseudo-symmetry and twinning. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 2191-9		16
26	Granulysin crystal structure and a structure-derived lytic mechanism. <i>Journal of Molecular Biology</i> , 2003 , 325, 355-65	6.5	131
25	The crystal structure of the bifunctional primase-helicase of bacteriophage T7. <i>Molecular Cell</i> , 2003 , 12, 1113-23	17.6	123
24	Crystal structure of a major secreted protein of <i>Mycobacterium tuberculosis</i> -MPT63 at 1.5-Å resolution. <i>Protein Science</i> , 2002 , 11, 2887-93	6.3	32
23	Structure of a Nudix protein from <i>Pyrobaculum aerophilum</i> reveals a dimer with two intersubunit beta-sheets. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 571-8		15

22	Structure of cytochrome c6 from <i>Arthrospira maxima</i> : an assembly of 24 subunits in a nearly symmetric shell. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 1104-10		4
21	Dimerization allows DNA target site recognition by the NarL response regulator. <i>Nature Structural Biology</i> , 2002 , 9, 771-8		137
20	Crystal structure of human L-isoaspartyl methyltransferase. <i>Journal of Biological Chemistry</i> , 2002 , 277, 10642-6	5.4	20
19	Thiol-disulfide exchange in an immunoglobulin-like fold: structure of the N-terminal domain of DsbD. <i>Biochemistry</i> , 2002 , 41, 6920-7	3.2	62
18	Structural basis of non-specific lipid binding in maize lipid-transfer protein complexes revealed by high-resolution X-ray crystallography. <i>Journal of Molecular Biology</i> , 2001 , 308, 263-78	6.5	145
17	Crystal structure of a protein repair methyltransferase from <i>Pyrococcus furiosus</i> with its L-isoaspartyl peptide substrate. <i>Journal of Molecular Biology</i> , 2001 , 313, 1103-16	6.5	50
16	Structures of cytochrome c-549 and cytochrome c6 from the cyanobacterium <i>Arthrospira maxima</i> . <i>Biochemistry</i> , 2001 , 40, 9215-25	3.2	61
15	Crystal structure of T7 gene 4 ring helicase indicates a mechanism for sequential hydrolysis of nucleotides. <i>Cell</i> , 2000 , 101, 589-600	56.2	427
14	An open and closed case for all polymerases. <i>Structure</i> , 1999 , 7, R31-5	5.2	258
13	Crystal structure of the helicase domain from the replicative helicase-primase of bacteriophage T7. <i>Cell</i> , 1999 , 99, 167-77	56.2	256
12	Crystal structures of human DNA polymerase beta complexed with gapped and nicked DNA: evidence for an induced fit mechanism. <i>Biochemistry</i> , 1997 , 36, 11205-15	3.2	582
11	Loop and subdomain movements in the mechanism of <i>Escherichia coli</i> dihydrofolate reductase: crystallographic evidence. <i>Biochemistry</i> , 1997 , 36, 586-603	3.2	581
10	A structural basis for metal ion mutagenicity and nucleotide selectivity in human DNA polymerase beta. <i>Biochemistry</i> , 1996 , 35, 12762-77	3.2	158
9	Characterization of the metal ion binding helix-hairpin-helix motifs in human DNA polymerase beta by X-ray structural analysis. <i>Biochemistry</i> , 1996 , 35, 12778-87	3.2	80
8	Crystal structures of human DNA polymerase beta complexed with DNA: implications for catalytic mechanism, processivity, and fidelity. <i>Biochemistry</i> , 1996 , 35, 12742-61	3.2	256
7	Crystallization of the A alpha subunit of protein phosphatase 2A. <i>Protein Science</i> , 1996 , 5, 1198-200	6.3	1
6	Isomorphous crystal structures of <i>Escherichia coli</i> dihydrofolate reductase complexed with folate, 5-deazafolate, and 5,10-dideazatetrahydrofolate: mechanistic implications. <i>Biochemistry</i> , 1995 , 34, 2710-23	3.2	71
5	Cryo-EM Structures of Four Polymorphic TDP-43 Amyloid Cores		1

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| 4 | The cryoEM structure of the fibril-forming low-complexity domain of hnRNPA2 reveals distinct differences from pathogenic amyloid and shows how mutation converts it to the pathogenic form | 1 |
| 3 | Homochiral and racemic MicroED structures of a peptide from the ice nucleation protein InaZ | 2 |
| 2 | Cryo-EM structures of β -synuclein fibrils with the H50Q hereditary mutation reveal new polymorphs | 2 |
| 1 | Identifying amyloid-related diseases by mapping mutations in low-complexity protein domains to pathologies. <i>Nature Structural and Molecular Biology</i> , | 17.6 1 |