

# Michael R Sawaya

## List of Publications by Citations

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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	Structure of the cross-beta spine of amyloid-like fibrils. <i>Nature</i> , <b>2005</b> , 435, 773-8	50.4	1791
200	Atomic structures of amyloid cross-beta spines reveal varied steric zippers. <i>Nature</i> , <b>2007</b> , 447, 453-7	50.4	1785
199	Cell-free formation of RNA granules: low complexity sequence domains form dynamic fibers within hydrogels. <i>Cell</i> , <b>2012</b> , 149, 753-67	56.2	1300
198	Functional amyloids as natural storage of peptide hormones in pituitary secretory granules. <i>Science</i> , <b>2009</b> , 325, 328-32	33.3	728
197	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> , <b>2006</b> , 103, 8060-5	11.5	602
196	Crystal structures of human DNA polymerase beta complexed with gapped and nicked DNA: evidence for an induced fit mechanism. <i>Biochemistry</i> , <b>1997</b> , 36, 11205-15	3.2	582
195	Loop and subdomain movements in the mechanism of <i>Escherichia coli</i> dihydrofolate reductase: crystallographic evidence. <i>Biochemistry</i> , <b>1997</b> , 36, 586-603	3.2	581
194	Computational design of self-assembling protein nanomaterials with atomic level accuracy. <i>Science</i> , <b>2012</b> , 336, 1171-4	33.3	473
193	Atomic view of a toxic amyloid small oligomer. <i>Science</i> , <b>2012</b> , 335, 1228-31	33.3	440
192	Crystal structure of T7 gene 4 ring helicase indicates a mechanism for sequential hydrolysis of nucleotides. <i>Cell</i> , <b>2000</b> , 101, 589-600	56.2	427
191	Structure of the toxic core of $\beta$ synuclein from invisible crystals. <i>Nature</i> , <b>2015</b> , 525, 486-90	50.4	393
190	Protein structures forming the shell of primitive bacterial organelles. <i>Science</i> , <b>2005</b> , 309, 936-8	33.3	354
189	Atomic-level models of the bacterial carboxysome shell. <i>Science</i> , <b>2008</b> , 319, 1083-6	33.3	310
188	Molecular basis for amyloid-beta polymorphism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 16938-43	11.5	306
187	Molecular basis for insulin fibril assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 18990-5	11.5	290
186	Atomic structure of the cross-beta spine of islet amyloid polypeptide (amylin). <i>Protein Science</i> , <b>2008</b> , 17, 1467-74	6.3	281
185	Cryo-EM of full-length $\beta$ synuclein reveals fibril polymorphs with a common structural kernel. <i>Nature Communications</i> , <b>2018</b> , 9, 3609	17.4	267

184	Structural Studies of Amyloid Proteins at the Molecular Level. <i>Annual Review of Biochemistry</i> , <b>2017</b> , 86, 69-95	29.1	264
183	Structure of the Angiotensin receptor revealed by serial femtosecond crystallography. <i>Cell</i> , <b>2015</b> , 161, 833-44	56.2	262
182	An open and closed case for all polymerases. <i>Structure</i> , <b>1999</b> , 7, R31-5	5.2	258
181	Crystal structure of the helicase domain from the replicative helicase-primase of bacteriophage T7. <i>Cell</i> , <b>1999</b> , 99, 167-77	56.2	256
180	Crystal structures of human DNA polymerase beta complexed with DNA: implications for catalytic mechanism, processivity, and fidelity. <i>Biochemistry</i> , <b>1996</b> , 35, 12742-61	3.2	256
179	Crystal structures of truncated alphaA and alphaB crystallins reveal structural mechanisms of polydispersity important for eye lens function. <i>Protein Science</i> , <b>2010</b> , 19, 1031-43	6.3	244
178	Crystal structure of human fibrinogen. <i>Biochemistry</i> , <b>2009</b> , 48, 3877-86	3.2	231
177	Crystal Structure Refinement <b>2006</b> ,		224
176	Amyloid-like fibrils of ribonuclease A with three-dimensional domain-swapped and native-like structure. <i>Nature</i> , <b>2005</b> , 437, 266-9	50.4	224
175	Atomic structures of low-complexity protein segments reveal kinked $\beta$ sheets that assemble networks. <i>Science</i> , <b>2018</b> , 359, 698-701	33.3	220
174	Molecular mechanisms for protein-encoded inheritance. <i>Nature Structural and Molecular Biology</i> , <b>2009</b> , 16, 973-8	17.6	218
173	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> , <b>2004</b> , 101, 10584-9	11.5	209
172	The crystal structure of a cyanobacterial water-soluble carotenoid binding protein. <i>Structure</i> , <b>2003</b> , 11, 55-65	5.2	191
171	Deposition diseases and 3D domain swapping. <i>Structure</i> , <b>2006</b> , 14, 811-24	5.2	180
170	Atomic structures of IAPP (amylin) fusions suggest a mechanism for fibrillation and the role of insulin in the process. <i>Protein Science</i> , <b>2009</b> , 18, 1521-30	6.3	172
169	Structure and mechanisms of a protein-based organelle in Escherichia coli. <i>Science</i> , <b>2010</b> , 327, 81-4	33.3	171
168	Towards a pharmacophore for amyloid. <i>PLoS Biology</i> , <b>2011</b> , 9, e1001080	9.7	159
167	Bacterial inclusion bodies contain amyloid-like structure. <i>PLoS Biology</i> , <b>2008</b> , 6, e195	9.7	159

166	A structural basis for metal ion mutagenicity and nucleotide selectivity in human DNA polymerase beta. <i>Biochemistry</i> , <b>1996</b> , 35, 12762-77	3.2	158
165	The cytotoxic PSM $\beta$ reveals a cross- $\beta$ amyloid-like fibril. <i>Science</i> , <b>2017</b> , 355, 831-833	33.3	154
164	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> , <b>2014</b> , 111, E1562-70	11.5	154
163	The structural biology of protein aggregation diseases: Fundamental questions and some answers. <i>Accounts of Chemical Research</i> , <b>2006</b> , 39, 568-75	24.3	153
162	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> , <b>2011</b> , 108, 5051-6	11.5	152
161	Out-of-register $\beta$ -sheets suggest a pathway to toxic amyloid aggregates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 20913-8	11.5	149
160	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> , <b>2001</b> , 308, 263-78	6.5	145
159	Dimerization allows DNA target site recognition by the NarL response regulator. <i>Nature Structural Biology</i> , <b>2002</b> , 9, 771-8		137
158	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> , <b>2006</b> , 281, 7546-55	5.4	133
157	The role of distant mutations and allosteric regulation on LovD active site dynamics. <i>Nature Chemical Biology</i> , <b>2014</b> , 10, 431-6	11.7	132
156	Three-dimensional coordinates of individual atoms in materials revealed by electron tomography. <i>Nature Materials</i> , <b>2015</b> , 14, 1099-103	27	131
155	Granulysin crystal structure and a structure-derived lytic mechanism. <i>Journal of Molecular Biology</i> , <b>2003</b> , 325, 355-65	6.5	131
154	The crystal structure of the bifunctional primase-helicase of bacteriophage T7. <i>Molecular Cell</i> , <b>2003</b> , 12, 1113-23	17.6	123
153	Structural analysis of CsoS1A and the protein shell of the Halothiobacillus neapolitanus carboxysome. <i>PLoS Biology</i> , <b>2007</b> , 5, e144	9.7	118
152	Atomic structures of TDP-43 LCD segments and insights into reversible or pathogenic aggregation. <i>Nature Structural and Molecular Biology</i> , <b>2018</b> , 25, 463-471	17.6	116
151	Atomic-resolution structures from fragmented protein crystals with the cryoEM method MicroED. <i>Nature Methods</i> , <b>2017</b> , 14, 399-402	21.6	109
150	Structural insight into the mechanisms of transport across the Salmonella enterica Pdu microcompartment shell. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 37838-46	5.4	108
149	Cryo-EM structures of four polymorphic TDP-43 amyloid cores. <i>Nature Structural and Molecular Biology</i> , <b>2019</b> , 26, 619-627	17.6	103

148	Macrocyclic $\beta$ -sheet peptides that inhibit the aggregation of a tau-protein-derived hexapeptide. <i>Journal of the American Chemical Society</i> , <b>2011</b> , 133, 3144-57	16.4	98
147	Crystal structures of a tetrahedral open pore ferritin from the hyperthermophilic archaeon <i>Archaeoglobus fulgidus</i> . <i>Structure</i> , <b>2005</b> , 13, 637-48	5.2	98
146	$\beta$ microglobulin forms three-dimensional domain-swapped amyloid fibrils with disulfide linkages. <i>Nature Structural and Molecular Biology</i> , <b>2011</b> , 18, 49-55	17.6	93
145	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> , <b>2014</b> , 111, 197-201	11.5	92
144	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> , <b>2015</b> , 112, 2990-5	11.5	90
143	The crystal structure of the primary $\text{Ca}^{2+}$ sensor of the $\text{Na}^{+}/\text{Ca}^{2+}$ exchanger reveals a novel $\text{Ca}^{2+}$ binding motif. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 21577-21581	5.4	88
142	A double S shape provides the structural basis for the extraordinary binding specificity of Dscam isoforms. <i>Cell</i> , <b>2008</b> , 134, 1007-18	56.2	86
141	Uncovering the Mechanism of Aggregation of Human Transthyretin. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 28932-43	5.4	85
140	Protein crystal structure obtained at 2.9 $\text{\AA}$ 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> , <b>2014</b> , 111, 12769-74	11.5	84
139	Structure-based design of functional amyloid materials. <i>Journal of the American Chemical Society</i> , <b>2014</b> , 136, 18044-51	16.4	82
138	Structure of the PduU shell protein from the Pdu microcompartment of Salmonella. <i>Structure</i> , <b>2008</b> , 16, 1324-32	5.2	82
137	Derepression by depolymerization; structural insights into the regulation of Yan by Mae. <i>Cell</i> , <b>2004</b> , 118, 163-73	56.2	80
136	Characterization of the metal ion binding helix-hairpin-helix motifs in human DNA polymerase beta by X-ray structural analysis. <i>Biochemistry</i> , <b>1996</b> , 35, 12778-87	3.2	80
135	Insights from multiple structures of the shell proteins from the beta-carboxysome. <i>Protein Science</i> , <b>2009</b> , 18, 108-20	6.3	78
134	Structure and flexibility of nanoscale protein cages designed by symmetric self-assembly. <i>Journal of the American Chemical Society</i> , <b>2013</b> , 135, 7738-43	16.4	76
133	Atomic structures of fibrillar segments of hIAPP suggest tightly mated $\beta$ -sheets are important for cytotoxicity. <i>ELife</i> , <b>2017</b> , 6,	8.9	76
132	Characteristics of amyloid-related oligomers revealed by crystal structures of macrocyclic $\beta$ -sheet mimics. <i>Journal of the American Chemical Society</i> , <b>2011</b> , 133, 6736-44	16.4	73
131	De novo phasing with X-ray laser reveals mosquito larvicide BinAB structure. <i>Nature</i> , <b>2016</b> , 539, 43-47	50.4	73

130	Crystal structure of the Mycobacterium tuberculosis dUTPase: insights into the catalytic mechanism. <i>Journal of Molecular Biology</i> , <b>2004</b> , 341, 503-17	6.5	71
129	Isomorphous crystal structures of Escherichia coli dihydrofolate reductase complexed with folate, 5-deazafofolate, and 5,10-dideazatetrahydrofolate: mechanistic implications. <i>Biochemistry</i> , <b>1995</b> , 34, 2710-23	3.3	71
128	Structural organization of a Sex-comb-on-midleg/polyhomeotic copolymer. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 27769-75	5.4	67
127	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> , <b>2016</b> , 113, 11232-11236	11.5	66
126	Non-proteinaceous hydrolase comprised of a phenylalanine metallo-supramolecular amyloid-like structure. <i>Nature Catalysis</i> , <b>2019</b> , 2, 977-985	36.5	65
125	Atomic-level evidence for packing and positional amyloid polymorphism by segment from TDP-43 RRM2. <i>Nature Structural and Molecular Biology</i> , <b>2018</b> , 25, 311-319	17.6	63
124	Directed evolution and structural characterization of a simvastatin synthase. <i>Chemistry and Biology</i> , <b>2009</b> , 16, 1064-74		63
123	Toxicity of eosinophil MBP is repressed by intracellular crystallization and promoted by extracellular aggregation. <i>Molecular Cell</i> , <b>2015</b> , 57, 1011-1021	17.6	62
122	Structures of fibrils formed by $\beta$ -synuclein hereditary disease mutant H50Q reveal new polymorphs. <i>Nature Structural and Molecular Biology</i> , <b>2019</b> , 26, 1044-1052	17.6	62
121	Thiol-disulfide exchange in an immunoglobulin-like fold: structure of the N-terminal domain of DsbD. <i>Biochemistry</i> , <b>2002</b> , 41, 6920-7	3.2	62
120	Uncovering the enzymes that catalyze the final steps in oxytetracycline biosynthesis. <i>Journal of the American Chemical Society</i> , <b>2013</b> , 135, 7138-41	16.4	61
119	Structures of cytochrome c-549 and cytochrome c6 from the cyanobacterium <i>Arthrospira maxima</i> . <i>Biochemistry</i> , <b>2001</b> , 40, 9215-25	3.2	61
118	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> , <b>2017</b> , 114, 8770-8775	11.5	60
117	The $\beta$ -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> , <b>2020</b> , 117, 3592-3602	11.5	57
116	Connecting actin monomers by iso-peptide bond is a toxicity mechanism of the Vibrio cholerae MARTX toxin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 18537-42	11.5	57
115	Sub- $\beta$ -sheet cryo-EM structure of a prion protofibril reveals a polar clasp. <i>Nature Structural and Molecular Biology</i> , <b>2018</b> , 25, 131-134	17.6	56
114	Two amyloid States of the prion protein display significantly different folding patterns. <i>Journal of Molecular Biology</i> , <b>2010</b> , 400, 908-21	6.5	56
113	An approach to crystallizing proteins by metal-mediated synthetic symmetrization. <i>Protein Science</i> , <b>2011</b> , 20, 1876-90	6.3	54

112	Regulation of enzyme localization by polymerization: polymer formation by the SAM domain of diacylglycerol kinase delta1. <i>Structure</i> , <b>2008</b> , 16, 380-7	5.2	53
111	The Tim8-Tim13 complex has multiple substrate binding sites and binds cooperatively to Tim23. <i>Journal of Molecular Biology</i> , <b>2008</b> , 382, 1144-56	6.5	53
110	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> , <b>2005</b> , 102, 13105-10	11.5	51
109	(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> , <b>2014</b> , 53, 5194-8	16.4	50
108	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> , <b>2010</b> , 285, 29671-5	5.4	50
107	Crystal structure of a protein repair methyltransferase from <i>Pyrococcus furiosus</i> with its L-isoaspartyl peptide substrate. <i>Journal of Molecular Biology</i> , <b>2001</b> , 313, 1103-16	6.5	50
106	Crystal Structures of IAPP Amyloidogenic Segments Reveal a Novel Packing Motif of Out-of-Register Beta Sheets. <i>Journal of Physical Chemistry B</i> , <b>2016</b> , 120, 5810-6	3.4	46
105	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> , <b>2014</b> , 426, 2328-45	6.5	46
104	The crystal structure of the Rv0301-Rv0300 VapBC-3 toxin-antitoxin complex from <i>M. tuberculosis</i> reveals a Mg <sup>2+</sup> ion in the active site and a putative RNA-binding site. <i>Protein Science</i> , <b>2012</b> , 21, 1754-67	6.3	46
103	Multidimensional structure-activity relationship of a protein in its aggregated states. <i>Angewandte Chemie - International Edition</i> , <b>2010</b> , 49, 3904-8	16.4	46
102	Atomic structures suggest determinants of transmission barriers in mammalian prion disease. <i>Biochemistry</i> , <b>2011</b> , 50, 2456-63	3.2	45
101	Structure of the dimerization domain of DiGeorge critical region 8. <i>Protein Science</i> , <b>2010</b> , 19, 1354-65	6.3	45
100	Determination of the X-ray structure of the snake venom protein omwaprin by total chemical synthesis and racemic protein crystallography. <i>Protein Science</i> , <b>2010</b> , 19, 1840-9	6.3	45
99	Biochemical and Structural Basis for Controlling Chemical Modularity in Fungal Polyketide Biosynthesis. <i>Journal of the American Chemical Society</i> , <b>2015</b> , 137, 9885-93	16.4	44
98	Total chemical synthesis and X-ray structure of kaliotoxin by racemic protein crystallography. <i>Chemical Communications</i> , <b>2010</b> , 46, 8174-6	5.8	42
97	Cryo-EM structure and inhibitor design of human IAPP (amylin) fibrils. <i>Nature Structural and Molecular Biology</i> , <b>2020</b> , 27, 653-659	17.6	41
96	Catastrophic disassembly of actin filaments via Mical-mediated oxidation. <i>Nature Communications</i> , <b>2017</b> , 8, 2183	17.4	41
95	Cryo-EM structure of a human prion fibril with a hydrophobic, protease-resistant core. <i>Nature Structural and Molecular Biology</i> , <b>2020</b> , 27, 417-423	17.6	37

94	X-ray crystallographic structure of an artificial beta-sheet dimer. <i>Journal of the American Chemical Society</i> , <b>2010</b> , 132, 11622-8	16.4	36
93	Inhibition by small-molecule ligands of formation of amyloid fibrils of an immunoglobulin light chain variable domain. <i>ELife</i> , <b>2015</b> , 4, e10935	8.9	36
92	CryoEM structure of the low-complexity domain of hnRNPA2 and its conversion to pathogenic amyloid. <i>Nature Communications</i> , <b>2020</b> , 11, 4090	17.4	36
91	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> , <b>2003</b> , 44, 697-706	4.9	34
90	Structure-based inhibitors of amyloid beta core suggest a common interface with tau. <i>ELife</i> , <b>2019</b> , 8,	8.9	34
89	Analysis of lattice-translocation disorder in the layered hexagonal structure of carboxysome shell protein CsoS1C. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2009</b> , 65, 980-8		33
88	Structural states and dynamics of the D-loop in actin. <i>Biophysical Journal</i> , <b>2012</b> , 103, 930-9	2.9	32
87	Crystal structure of a major secreted protein of <i>Mycobacterium tuberculosis</i> -MPT63 at 1.5-Å resolution. <i>Protein Science</i> , <b>2002</b> , 11, 2887-93	6.3	32
86	Regulation by oligomerization in a mycobacterial folate biosynthetic enzyme. <i>Journal of Molecular Biology</i> , <b>2005</b> , 349, 61-72	6.5	32
85	The crystal structure of the first enzyme in the pantothenate biosynthetic pathway, ketopantoate hydroxymethyltransferase, from <i>M. tuberculosis</i> . <i>Structure</i> , <b>2003</b> , 11, 753-64	5.2	32
84	Common fibrillar spines of amyloid- $\beta$ and human islet amyloid polypeptide revealed by microelectron diffraction and structure-based inhibitors. <i>Journal of Biological Chemistry</i> , <b>2018</b> , 293, 2888-2902	5.4	31
83	Crystal structure of a RuBisCO-like protein from the green sulfur bacterium <i>Chlorobium tepidum</i> . <i>Structure</i> , <b>2005</b> , 13, 779-89	5.2	31
82	An introduction to biomolecular graphics. <i>PLoS Computational Biology</i> , <b>2010</b> , 6, e1000918	5	30
81	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> , <b>2014</b> , 289, 8891-902	5.4	29
80	Crystal structure of the restriction-modification system control element C.BclI and mapping of its binding site. <i>Structure</i> , <b>2005</b> , 13, 1837-47	5.2	27
79	Structure of amyloid- $\beta$ (20-34) with Alzheimer- $\beta$ -associated isomerization at Asp23 reveals a distinct protofilament interface. <i>Nature Communications</i> , <b>2019</b> , 10, 3357	17.4	25
78	Formation of amyloid fibers by monomeric light chain variable domains. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 27513-25	5.4	25
77	Distinct C9orf72-Associated Dipeptide Repeat Structures Correlate with Neuronal Toxicity. <i>PLoS ONE</i> , <b>2016</b> , 11, e0165084	3.7	24



76	Isobutanol production freed from biological limits using synthetic biochemistry. <i>Nature Communications</i> , <b>2020</b> , 11, 4292	17.4	24
75	The function of the PduJ microcompartment shell protein is determined by the genomic position of its encoding gene. <i>Molecular Microbiology</i> , <b>2016</b> , 101, 770-83	4.1	24
74	Implications for Alzheimer's disease of an atomic resolution structure of amyloid- $\beta$ (1-42) fibrils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 9398-400	11.5	24
73	Inhibiting amyloid- $\beta$ cytotoxicity through its interaction with the cell surface receptor LirB2 by structure-based design. <i>Nature Chemistry</i> , <b>2018</b> , 10, 1213-1221	17.6	24
72	Structure-based inhibitors halt prion-like seeding by Alzheimer's disease-and tauopathy-derived brain tissue samples. <i>Journal of Biological Chemistry</i> , <b>2019</b> , 294, 16451-16464	5.4	23
71	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> , <b>2014</b> , 118, 7247-56	3.4	23
70	Novel mechanism of heme capture by Hbp2, the hemoglobin-binding hemophore from <i>Listeria monocytogenes</i> . <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 34886-99	5.4	23
69	The expanding amyloid family: Structure, stability, function, and pathogenesis. <i>Cell</i> , <b>2021</b> , 184, 4857-4873	36.2	23
68	Structural Organization of Insulin Fibrils Based on Polarized Raman Spectroscopy: Evaluation of Existing Models. <i>Journal of the American Chemical Society</i> , <b>2015</b> , 137, 11312-20	16.4	22
67	Structures of segments of $\beta$ synuclein fused to maltose-binding protein suggest intermediate states during amyloid formation. <i>Protein Science</i> , <b>2011</b> , 20, 996-1004	6.3	22
66	Structures and functional implications of an AMP-binding cystathionine beta-synthase domain protein from a hyperthermophilic archaeon. <i>Journal of Molecular Biology</i> , <b>2008</b> , 380, 181-92	6.5	22
65	Ribonuclease A suggests how proteins self-chaperone against amyloid fiber formation. <i>Protein Science</i> , <b>2012</b> , 21, 26-37	6.3	21
64	Multiple forms of Spire-actin complexes and their functional consequences. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 10684-10692	5.4	20
63	Crystal structure of human L-isoaspartyl methyltransferase. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 10642-6	5.4	20
62	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> , <b>2018</b> , 293, 19659-19671	5.4	19
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