

David Eisenberg

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261
papers

43,654
citations

96
h-index

208
g-index

282
ext. papers

49,118
ext. citations

13.2
avg. IF

7.52
L-index

#	Paper	IF	Citations
261	Assessment of protein models with three-dimensional profiles. <i>Nature</i> , 1992 , 356, 83-5	50.4	2511
260	Structure of the cross-beta spine of amyloid-like fibrils. <i>Nature</i> , 2005 , 435, 773-8	50.4	1791
259	Atomic structures of amyloid cross-beta spines reveal varied steric zippers. <i>Nature</i> , 2007 , 447, 453-7	50.4	1785
258	Solvation energy in protein folding and binding. <i>Nature</i> , 1986 , 319, 199-203	50.4	1673
257	The Database of Interacting Proteins: 2004 update. <i>Nucleic Acids Research</i> , 2004 , 32, D449-51	20.1	1532
256	VERIFY3D: assessment of protein models with three-dimensional profiles. <i>Methods in Enzymology</i> , 1997 , 277, 396-404	1.7	1402
255	Detecting protein function and protein-protein interactions from genome sequences. <i>Science</i> , 1999 , 285, 751-3	33.3	1397
254	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
253	DIP, the Database of Interacting Proteins: a research tool for studying cellular networks of protein interactions. <i>Nucleic Acids Research</i> , 2002 , 30, 303-5	20.1	1196
252	The amyloid state of proteins in human diseases. <i>Cell</i> , 2012 , 148, 1188-203	56.2	1192
251	The helical hydrophobic moment: a measure of the amphiphilicity of a helix. <i>Nature</i> , 1982 , 299, 371-4	50.4	895
250	A combined algorithm for genome-wide prediction of protein function. <i>Nature</i> , 1999 , 402, 83-6	50.4	773
249	Functional amyloids as natural storage of peptide hormones in pituitary secretory granules. <i>Science</i> , 2009 , 325, 328-32	33.3	728
248	3D domain swapping: a mechanism for oligomer assembly. <i>Protein Science</i> , 1995 , 4, 2455-68	6.3	678
247	The Sorcerer II Global Ocean Sampling expedition: expanding the universe of protein families. <i>PLoS Biology</i> , 2007 , 5, e16	9.7	638
246	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
245	Protein function in the post-genomic era. <i>Nature</i> , 2000 , 405, 823-6	50.4	590

244	3D domain swapping: as domains continue to swap. <i>Protein Science</i> , 2002 , 11, 1285-99	6.3	587
243	Identifying the amyloids, proteins capable of forming amyloid-like fibrils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 3487-92	11.5	575
242	The primary mechanism of attenuation of bacillus Calmette-Guerin is a loss of secreted lytic function required for invasion of lung interstitial tissue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 12420-5	11.5	555
241	Protein interactions: two methods for assessment of the reliability of high throughput observations. <i>Molecular and Cellular Proteomics</i> , 2002 , 1, 349-56	7.6	486
240	Atomic solvation parameters applied to molecular dynamics of proteins in solution. <i>Protein Science</i> , 1992 , 1, 227-35	6.3	453
239	Atomic view of a toxic amyloid small oligomer. <i>Science</i> , 2012 , 335, 1228-31	33.3	440
238	Structure of the toxic core of β -synuclein from invisible crystals. <i>Nature</i> , 2015 , 525, 486-90	50.4	393
237	Sequence-structure analysis of FAD-containing proteins. <i>Protein Science</i> , 2001 , 10, 1712-28	6.3	355
236	Structure-based design of non-natural amino-acid inhibitors of amyloid fibril formation. <i>Nature</i> , 2011 , 475, 96-100	50.4	341
235	An amyloid-forming peptide from the yeast prion Sup35 reveals a dehydrated beta-sheet structure for amyloid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 2375-80	11.5	327
234	The 3D profile method for identifying fibril-forming segments of proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 4074-8	11.5	325
233	Crystal structure of human BPI and two bound phospholipids at 2.4 angstrom resolution. <i>Science</i> , 1997 , 276, 1861-4	33.3	317
232	A census of protein repeats. <i>Journal of Molecular Biology</i> , 1999 , 293, 151-60	6.5	313
231	Recent atomic models of amyloid fibril structure. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 260-5	8.1	312
230	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
229	The activities of amyloids from a structural perspective. <i>Nature</i> , 2016 , 539, 227-235	50.4	294
228	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
227	Novel subunit-subunit interactions in the structure of glutamine synthetase. <i>Nature</i> , 1986 , 323, 304-9	50.4	282

226	Atomic structure of the cross-beta spine of islet amyloid polypeptide (amylin). <i>Protein Science</i> , 2008 , 17, 1467-74	6.3	281
225	Protein fold recognition using sequence-derived predictions. <i>Protein Science</i> , 1996 , 5, 947-55	6.3	279
224	Propagation of Tau Aggregates and Neurodegeneration. <i>Annual Review of Neuroscience</i> , 2017 , 40, 189-210		278
223	Amyloid nomenclature 2018: recommendations by the International Society of Amyloidosis (ISA) nomenclature committee. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2018 , 25, 215-219	2.7	278
222	Structure-function relationships of glutamine synthetases. <i>BBA - Proteins and Proteomics</i> , 2000 , 1477, 122-45		276
221	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
220	Structural Studies of Amyloid Proteins at the Molecular Level. <i>Annual Review of Biochemistry</i> , 2017 , 86, 69-95	29.1	264
219	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
218	Profile analysis. <i>Methods in Enzymology</i> , 1990 , 183, 146-59	1.7	234
217	Prolinks: a database of protein functional linkages derived from coevolution. <i>Genome Biology</i> , 2004 , 5, R35	18.3	230
216	Toxic fibrillar oligomers of amyloid- β have cross- β structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 7717-22	11.5	226
215	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
214	Atomic structures of low-complexity protein segments reveal kinked β -sheets that assemble networks. <i>Science</i> , 2018 , 359, 698-701	33.3	220
213	Molecular mechanisms for protein-encoded inheritance. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 973-8	17.6	218
212	A domain-swapped RNase A dimer with implications for amyloid formation. <i>Nature Structural Biology</i> , 2001 , 8, 211-4		216
211	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
210	Three-dimensional cluster analysis identifies interfaces and functional residue clusters in proteins. <i>Journal of Molecular Biology</i> , 2001 , 307, 1487-502	6.5	206
209	Toward rational protein crystallization: A Web server for the design of crystallizable protein variants. <i>Protein Science</i> , 2007 , 16, 1569-76	6.3	205

208	Unique transcriptome signature of Mycobacterium tuberculosis in pulmonary tuberculosis. <i>Infection and Immunity</i> , 2006 , 74, 1233-42	3.7	194
207	A Designed Inhibitor of p53 Aggregation Rescues p53 Tumor Suppression in Ovarian Carcinomas. <i>Cancer Cell</i> , 2016 , 29, 90-103	24.3	192
206	Deposition diseases and 3D domain swapping. <i>Structure</i> , 2006 , 14, 811-24	5.2	180
205	Amyloid β -sheet mimics that antagonize protein aggregation and reduce amyloid toxicity. <i>Nature Chemistry</i> , 2012 , 4, 927-33	17.6	174
204	The discovery of the alpha-helix and beta-sheet, the principal structural features of proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 11207-10	11.5	173
203	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
202	Refined structure of monomeric diphtheria toxin at 2.3 Å resolution. <i>Protein Science</i> , 1994 , 3, 1464-75	6.3	172
201	Structural models of amyloid-like fibrils. <i>Advances in Protein Chemistry</i> , 2006 , 73, 235-82		162
200	A missing link in cupredoxins: crystal structure of cucumber stellacyanin at 1.6 Å resolution. <i>Protein Science</i> , 1996 , 5, 2175-83	6.3	162
199	Refined structure of dimeric diphtheria toxin at 2.0 Å resolution. <i>Protein Science</i> , 1994 , 3, 1444-63	6.3	161
198	Towards a pharmacophore for amyloid. <i>PLoS Biology</i> , 2011 , 9, e1001080	9.7	159
197	Bacterial inclusion bodies contain amyloid-like structure. <i>PLoS Biology</i> , 2008 , 6, e195	9.7	159
196	Genomic evidence that the intracellular proteins of archaeal microbes contain disulfide bonds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 9679-84	11.5	159
195	Structure-based inhibitors of tau aggregation. <i>Nature Chemistry</i> , 2018 , 10, 170-176	17.6	159
194	GXXXG and GXXXA motifs stabilize FAD and NAD(P)-binding Rossmann folds through C(alpha)-H...O hydrogen bonds and van der waals interactions. <i>Journal of Molecular Biology</i> , 2002 , 323, 69-76	6.5	155
193	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
192	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
191	Inference of protein function from protein structure. <i>Structure</i> , 2005 , 13, 121-30	5.2	153

190	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
189	A 3D-1D substitution matrix for protein fold recognition that includes predicted secondary structure of the sequence. <i>Journal of Molecular Biology</i> , 1997 , 267, 1026-38	6.5	144
188	Half a century of amyloids: past, present and future. <i>Chemical Society Reviews</i> , 2020 , 49, 5473-5509	58.5	142
187	Defensins promote fusion and lysis of negatively charged membranes. <i>Protein Science</i> , 1993 , 2, 1301-12	6.3	138
186	Secondary structure-based profiles: use of structure-conserving scoring tables in searching protein sequence databases for structural similarities. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991 , 10, 229-39	4.2	135
185	Seeded conversion of recombinant prion protein to a disulfide-bonded oligomer by a reduction-oxidation process. <i>Nature Structural and Molecular Biology</i> , 2003 , 10, 725-30	17.6	130
184	The crystal structure of the designed trimeric coiled coil coil-VaLd: implications for engineering crystals and supramolecular assemblies. <i>Protein Science</i> , 1997 , 6, 80-8	6.3	128
183	The crystal structure of phosphinothricin in the active site of glutamine synthetase illuminates the mechanism of enzymatic inhibition. <i>Biochemistry</i> , 2001 , 40, 1903-12	3.2	128
182	Computational methods of analysis of protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2003 , 13, 377-82	8.1	125
181	Amyloid nomenclature 2020: update and recommendations by the International Society of Amyloidosis (ISA) nomenclature committee. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2020 , 27, 217-222	2.7	123
180	The design, synthesis, and crystallization of an alpha-helical peptide. <i>Proteins: Structure, Function and Bioinformatics</i> , 1986 , 1, 16-22	4.2	121
179	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
178	A systematic screen of beta(2)-microglobulin and insulin for amyloid-like segments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 4079-82	11.5	115
177	Use of logic relationships to decipher protein network organization. <i>Science</i> , 2004 , 306, 2246-9	33.3	115
176	Cooperative hydrogen bonding in amyloid formation. <i>Protein Science</i> , 2007 , 16, 761-4	6.3	114
175	Atomic-resolution structures from fragmented protein crystals with the cryoEM method MicroED. <i>Nature Methods</i> , 2017 , 14, 399-402	21.6	109
174	An interfacial mechanism and a class of inhibitors inferred from two crystal structures of the Mycobacterium tuberculosis 30 kDa major secretory protein (Antigen 85B), a mycolyl transferase. <i>Journal of Molecular Biology</i> , 2001 , 307, 671-81	6.5	109
173	Structure and proposed activity of a member of the VapBC family of toxin-antitoxin systems. VapBC-5 from Mycobacterium tuberculosis. <i>Journal of Biological Chemistry</i> , 2009 , 284, 276-283	5.4	108

172	The BPI/LBP family of proteins: a structural analysis of conserved regions. <i>Protein Science</i> , 1998 , 7, 906-1043	14.3	107
171	Inferring protein domain interactions from databases of interacting proteins. <i>Genome Biology</i> , 2005 , 6, R89	18.3	107
170	Structural model for the reaction mechanism of glutamine synthetase, based on five crystal structures of enzyme-substrate complexes. <i>Biochemistry</i> , 1994 , 33, 675-81	3.2	107
169	TDP-43 and RNA form amyloid-like myo-granules in regenerating muscle. <i>Nature</i> , 2018 , 563, 508-513	50.4	104
168	Cryo-EM structures of four polymorphic TDP-43 amyloid cores. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 619-627	17.6	103
167	The most highly amphiphilic alpha-helices include two amino acid segments in human immunodeficiency virus glycoprotein 41. <i>Biopolymers</i> , 1990 , 29, 171-7	2.2	103
166	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
165	Structures of the two 3D domain-swapped RNase A trimers. <i>Protein Science</i> , 2002 , 11, 371-80	6.3	96
164	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
163	Cross-beta order and diversity in nanocrystals of an amyloid-forming peptide. <i>Journal of Molecular Biology</i> , 2003 , 330, 1165-75	6.5	93
162	Bioinformatic identification of potential autocrine signaling loops in cancers from gene expression profiles. <i>Nature Genetics</i> , 2001 , 29, 295-300	36.3	93
161	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
160	The crystal structure of a heptameric archaeal Sm protein: Implications for the eukaryotic snRNP core. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 5532-7	11.5	91
159	Subunit asymmetry in the three-dimensional structure of a human CuZnSOD mutant found in familial amyotrophic lateral sclerosis. <i>Protein Science</i> , 1998 , 7, 545-55	6.3	90
158	Short protein segments can drive a non-fibrillizing protein into the amyloid state. <i>Protein Engineering, Design and Selection</i> , 2009 , 22, 531-6	1.9	89
157	Assigning amino acid sequences to 3-dimensional protein folds. <i>FASEB Journal</i> , 1996 , 10, 126-36	0.9	87
156	The TB structural genomics consortium: a resource for Mycobacterium tuberculosis biology. <i>Tuberculosis</i> , 2003 , 83, 223-49	2.6	86
155	Uncovering the Mechanism of Aggregation of Human Transthyretin. <i>Journal of Biological Chemistry</i> , 2015 , 290, 28932-43	5.4	85

154	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
153	Sliding-layer conformational change limited by the quaternary structure of plant RuBisCO. <i>Nature</i> , 1987 , 329, 354-6	50.4	83
152	Designed amyloid fibers as materials for selective carbon dioxide capture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 191-6	11.5	82
151	Structure-based design of functional amyloid materials. <i>Journal of the American Chemical Society</i> , 2014 , 136, 18044-51	16.4	82
150	Discovery of the ammonium substrate site on glutamine synthetase, a third cation binding site. <i>Protein Science</i> , 1995 , 4, 2358-65	6.3	82
149	Runaway domain swapping in amyloid-like fibrils of T7 endonuclease I. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 8042-7	11.5	81
148	Inference of protein function and protein linkages in Mycobacterium tuberculosis based on prokaryotic genome organization: a combined computational approach. <i>Genome Biology</i> , 2003 , 4, R59	18.3	79
147	Structure-based discovery of fiber-binding compounds that reduce the cytotoxicity of amyloid beta. <i>ELife</i> , 2013 , 2, e00857	8.9	79
146	Ketones block amyloid entry and improve cognition in an Alzheimer's model. <i>Neurobiology of Aging</i> , 2016 , 39, 25-37	5.6	77
145	Protein interaction databases. <i>Current Opinion in Biotechnology</i> , 2001 , 12, 334-9	11.4	76
144	Atomic structures of fibrillar segments of hIAPP suggest tightly mated β-sheets are important for cytotoxicity. <i>ELife</i> , 2017 , 6,	8.9	76
143	Crystal structures of a pantothenate synthetase from M. tuberculosis and its complexes with substrates and a reaction intermediate. <i>Protein Science</i> , 2003 , 12, 1097-108	6.3	74
142	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
141	De novo phasing with X-ray laser reveals mosquito larvicide BinAB structure. <i>Nature</i> , 2016 , 539, 43-47	50.4	73
140	Thermodynamics of melittin tetramerization determined by circular dichroism and implications for protein folding. <i>Protein Science</i> , 1992 , 1, 641-53	6.3	69
139	Multicopy crystallographic refinement of a relaxed glutamine synthetase from Mycobacterium tuberculosis highlights flexible loops in the enzymatic mechanism and its regulation. <i>Biochemistry</i> , 2002 , 41, 9863-72	3.2	68
138	Amyloid β-Protein C-Terminal Fragments: Formation of Cylindrins and β-Barrels. <i>Journal of the American Chemical Society</i> , 2016 , 138, 549-57	16.4	67
137	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

136	Non-proteinaceous hydrolase comprised of a phenylalanine metallo-supramolecular amyloid-like structure. <i>Nature Catalysis</i> , 2019 , 2, 977-985	36.5	65
135	Inverted protein structure prediction. <i>Current Opinion in Structural Biology</i> , 1993 , 3, 437-444	8.1	65
134	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
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	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
131	Hydrophobicity and amphiphilicity in protein structure. <i>Journal of Cellular Biochemistry</i> , 1986 , 31, 11-7	4.7	61
130	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
129	The TB structural genomics consortium: providing a structural foundation for drug discovery. <i>Current Drug Targets Infectious Disorders</i> , 2002 , 2, 121-41		60
128	Mycobacterium tuberculosis gene expression profiling within the context of protein networks. <i>Microbes and Infection</i> , 2006 , 8, 747-57	9.3	59
127	Local moves: an efficient algorithm for simulation of protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 23, 73-82	4.2	58
126	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
125	Sub-angstrom 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
124	A novel inhibitor of Mycobacterium tuberculosis pantothenate synthetase. <i>Journal of Biomolecular Screening</i> , 2007 , 12, 100-5		56
123	Crystal structure of activated tobacco rubisco complexed with the reaction-intermediate analogue 2-carboxy-arabinitol 1,5-bisphosphate. <i>Protein Science</i> , 1993 , 2, 1136-46	6.3	54
122	Unusual conformation of nicotinamide adenine dinucleotide (NAD) bound to diphtheria toxin: a comparison with NAD bound to the oxidoreductase enzymes. <i>Protein Science</i> , 1997 , 6, 2084-96	6.3	51
121	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
120	Predicting structures for genome proteins. <i>Current Opinion in Structural Biology</i> , 1999 , 9, 208-11	8.1	49
119	A model for oxidative modification of glutamine synthetase, based on crystal structures of mutant H269N and the oxidized enzyme. <i>Biochemistry</i> , 1993 , 32, 7999-8003	3.2	49

118	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
117	The crystal structure of the Rv0301-Rv0300 VapBC-3 toxin-antitoxin complex from <i>M. tuberculosis</i> 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
116	Visualization and interpretation of protein networks in <i>Mycobacterium tuberculosis</i> based on hierarchical clustering of genome-wide functional linkage maps. <i>Nucleic Acids Research</i> , 2003 , 31, 7099-109	10.1	46
115	Atomic structures suggest determinants of transmission barriers in mammalian prion disease. <i>Biochemistry</i> , 2011 , 50, 2456-63	3.2	45
114	Crystal structure of the pantothenate synthetase from <i>Mycobacterium tuberculosis</i> , snapshots of the enzyme in action. <i>Biochemistry</i> , 2006 , 45, 1554-61	3.2	44
113	The 1.7 Å crystal structure of BPI: a study of how two dissimilar amino acid sequences can adopt the same fold. <i>Journal of Molecular Biology</i> , 2000 , 299, 1019-34	6.5	44
112	The three-dimensional structure of human bactericidal/permeability-increasing protein: implications for understanding protein-lipopolysaccharide interactions. <i>Biochemical Pharmacology</i> , 1999 , 57, 225-9	6	44
111	Amyloid seeding of transthyretin by ex vivo cardiac fibrils and its inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E6741-E6750	11.5	43
110	Structure and assembly of an augmented Sm-like archaeal protein 14-mer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 4539-44	11.5	42
109	The oligomerization and ligand-binding properties of Sm-like archaeal proteins (SmAPs). <i>Protein Science</i> , 2003 , 12, 832-47	6.3	42
108	Interactions of nucleotides with fully unadenylylated glutamine synthetase from <i>Salmonella typhimurium</i> . <i>Biochemistry</i> , 1994 , 33, 11184-8	3.2	42
107	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
106	Centrosymmetric bilayers in the 0.75 Å resolution structure of a designed alpha-helical peptide, D,L-Alpha-1. <i>Protein Science</i> , 1999 , 8, 1410-22	6.3	41
105	A study of combined structure/sequence profiles. <i>Folding & Design</i> , 1996 , 1, 451-61		40
104	A molecular model for membrane fusion based on solution studies of an amphiphilic peptide from HIV gp41. <i>Protein Science</i> , 1992 , 1, 1454-64	6.3	40
103	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
102	Structure-Based Peptide Inhibitor Design of Amyloid- β Aggregation. <i>Frontiers in Molecular Neuroscience</i> , 2019 , 12, 54	6.1	36
101	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

100	Detecting distant relatives of mammalian LPS-binding and lipid transport proteins. <i>Protein Science</i> , 1998 , 7, 1643-6	6.3	36
99	Draft crystal structure of the vault shell at 9-A resolution. <i>PLoS Biology</i> , 2007 , 5, e318	9.7	36
98	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
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