

David Eisenberg

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.

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	Extended β -Strands Contribute to Reversible Amyloid Formation.. <i>ACS Nano</i> , 2022 ,	16.7	2
260	Amyloid fibrils in disease FTLD-TDP are composed of TMEM106B not TDP-43.. <i>Nature</i> , 2022 ,	50.4	5
259	Bioinformatic identification of TRK-fused gene protein (TFG) as a previously unrecognized amyloidogenic protein.. <i>Journal of Biological Chemistry</i> , 2022 , 101920	5.4	1
258	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
257	Atomic View of an Amyloid Dodecamer Exhibiting Selective Cellular Toxic Vulnerability in Acute Brain Slices.. <i>Protein Science</i> , 2021 ,	6.3	1
256	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
255	Inhibition of amyloid formation of the Nucleoprotein of SARS-CoV-2 2021 ,		6
254	Prevalence and species distribution of the low-complexity, amyloid-like, reversible, kinked segment structural motif in amyloid-like fibrils. <i>Journal of Biological Chemistry</i> , 2021 , 297, 101194	5.4	6
253	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
252	The expanding amyloid family: Structure, stability, function, and pathogenesis. <i>Cell</i> , 2021 , 184, 4857-4873	36.2	23
251	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
250	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
249	Half a century of amyloids: past, present and future. <i>Chemical Society Reviews</i> , 2020 , 49, 5473-5509	58.5	142
248	The 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
247	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
246	Inhibition of synucleinopathic seeding by rationally designed inhibitors. <i>ELife</i> , 2020 , 9,	8.9	29
245	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

244	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
243	Non-proteinaceous hydrolase comprised of a phenylalanine metallo-supramolecular amyloid-like structure. <i>Nature Catalysis</i> , 2019 , 2, 977-985	36.5	65
242	Cryo-EM structures of four polymorphic TDP-43 amyloid cores. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 619-627	17.6	103
241	Structure-Based Peptide Inhibitor Design of Amyloid- β Aggregation. <i>Frontiers in Molecular Neuroscience</i> , 2019 , 12, 54	6.1	36
240	A pair of peptides inhibits seeding of the hormone transporter transthyretin into amyloid fibrils. <i>Journal of Biological Chemistry</i> , 2019 , 294, 6130-6141	5.4	16
239	Structure of amyloid- β (20-34) with Alzheimer's-associated isomerization at Asp23 reveals a distinct protofilament interface. <i>Nature Communications</i> , 2019 , 10, 3357	17.4	25
238	Structure-based inhibitors halt prion-like seeding by Alzheimer's disease-and tauopathy-derived brain tissue samples. <i>Journal of Biological Chemistry</i> , 2019 , 294, 16451-16464	5.4	23
237	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
236	Structure-based inhibitors of amyloid beta core suggest a common interface with tau. <i>ELife</i> , 2019 , 8,	8.9	34
235	Targeting Misfolded p53 and p53 Aggregation to Overcome Resistance to Apoptosis in Acute Myeloid Leukemia. <i>Blood</i> , 2019 , 134, 3786-3786	2.2	
234	Mechanically rigid supramolecular assemblies formed from an Fmoc-guanine conjugated peptide nucleic acid. <i>Nature Communications</i> , 2019 , 10, 5256	17.4	9
233	Atomic structures of corkscrew-forming segments of SOD1 reveal varied oligomer conformations. <i>Protein Science</i> , 2018 , 27, 1231-1242	6.3	11
232	Crystal structures of amyloidogenic segments of human transthyretin. <i>Protein Science</i> , 2018 , 27, 1295-1303	6.3	15
231	Atomic structures of low-complexity protein segments reveal kinked β -sheets that assemble networks. <i>Science</i> , 2018 , 359, 698-701	33.3	220
230	Distal amyloid β -protein fragments template amyloid assembly. <i>Protein Science</i> , 2018 , 27, 1181-1190	6.3	6
229	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, 28882-2902	5.4	31
228	Sub- β -sheet 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
227	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

226	Paul D. Boyer (1918-2018). <i>Science</i> , 2018 , 361, 334	33.3	
225	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
224	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
223	Structure-based inhibitors of tau aggregation. <i>Nature Chemistry</i> , 2018 , 10, 170-176	17.6	159
222	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
221	Inhibiting amyloid- β cytotoxicity through its interaction with the cell surface receptor LirB2 by structure-based design. <i>Nature Chemistry</i> , 2018 , 10, 1213-1221	17.6	24
220	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
219	TDP-43 and RNA form amyloid-like myo-granules in regenerating muscle. <i>Nature</i> , 2018 , 563, 508-513	50.4	104
218	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
217	Assessment of the effects of transthyretin peptide inhibitors in Drosophila models of neuropathic ATTR. <i>Neurobiology of Disease</i> , 2018 , 120, 118-125	7.5	7
216	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
215	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
214	Toward the Atomic Structure of PrP. <i>Cold Spring Harbor Perspectives in Biology</i> , 2017 , 9,	10.2	15
213	Structural Studies of Amyloid Proteins at the Molecular Level. <i>Annual Review of Biochemistry</i> , 2017 , 86, 69-95	29.1	264
212	Atomic-resolution structures from fragmented protein crystals with the cryoEM method MicroED. <i>Nature Methods</i> , 2017 , 14, 399-402	21.6	109
211	Flow-aligned, single-shot fiber diffraction using a femtosecond X-ray free-electron laser. <i>Cytoskeleton</i> , 2017 , 74, 472-481	2.4	10
210	In memoriam-Rainer Jaenicke. <i>Protein Science</i> , 2017 , 26, 394-395	6.3	
209	Asparagine and glutamine ladders promote cross-species prion conversion. <i>Journal of Biological Chemistry</i> , 2017 , 292, 19076-19086	5.4	15

208	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
207	Propagation of Tau Aggregates and Neurodegeneration. <i>Annual Review of Neuroscience</i> , 2017 , 40, 189-210		278
206	Taking the measure of MicroED. <i>Current Opinion in Structural Biology</i> , 2017 , 46, 79-86	8.1	26
205	Atomic structures of fibrillar segments of hIAPP suggest tightly mated β -sheets are important for cytotoxicity. <i>ELife</i> , 2017 , 6,	8.9	76
204	Preparation of Crystalline Samples of Amyloid Fibrils and Oligomers. <i>Methods in Molecular Biology</i> , 2016 , 1345, 201-10	1.4	5
203	The Formation, function and regulation of amyloids: insights from structural biology. <i>Journal of Internal Medicine</i> , 2016 , 280, 164-76	10.8	32
202	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
201	The activities of amyloids from a structural perspective. <i>Nature</i> , 2016 , 539, 227-235	50.4	294
200	Structures of EccB1 and EccD1 from the core complex of the mycobacterial ESX-1 type VII secretion system. <i>BMC Structural Biology</i> , 2016 , 16, 5	2.7	22
199	Ketones block amyloid entry and improve cognition in an Alzheimer's model. <i>Neurobiology of Aging</i> , 2016 , 39, 25-37	5.6	77
198	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
197	A Designed Inhibitor of p53 Aggregation Rescues p53 Tumor Suppression in Ovarian Carcinomas. <i>Cancer Cell</i> , 2016 , 29, 90-103	24.3	192
196	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
195	Targeting Aggregation of Wild-Type p53 and Mutant p53 with ReACp53 As a Novel Therapeutic Concept for AML. <i>Blood</i> , 2016 , 128, 3944-3944	2.2	1
194	De novo phasing with X-ray laser reveals mosquito larvicide BinAB structure. <i>Nature</i> , 2016 , 539, 43-47	50.4	73
193	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
192	Perspective on SOD1 mediated toxicity in Amyotrophic Lateral Sclerosis. <i>Postepy Biochemii</i> , 2016 , 62, 362-369	0	21
191	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

190	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
189	Uncovering the Mechanism of Aggregation of Human Transthyretin. <i>Journal of Biological Chemistry</i> , 2015 , 290, 28932-43	5.4	85
188	Structure of the toxic core of β -synuclein from invisible crystals. <i>Nature</i> , 2015 , 525, 486-90	50.4	393
187	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
186	The Amyloid State of Proteins. <i>FASEB Journal</i> , 2015 , 29, 218.1	0.9	
185	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
184	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
183	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
182	A proposed mechanism for the promotion of prion conversion involving a strictly conserved tyrosine residue in the Ω - Ω loop of PrPC. <i>Journal of Biological Chemistry</i> , 2014 , 289, 10660-10667	5.4	31
181	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
180	Structure-based design of functional amyloid materials. <i>Journal of the American Chemical Society</i> , 2014 , 136, 18044-51	16.4	82
179	Formation of amyloid fibers by monomeric light chain variable domains. <i>Journal of Biological Chemistry</i> , 2014 , 289, 27513-25	5.4	25
178	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
177	Salvage or recovery of failed targets by mutagenesis to reduce surface entropy. <i>Methods in Molecular Biology</i> , 2014 , 1140, 201-9	1.4	12
176	Amyloid Structures at the Atomic Level: Insights from Crystallography 2013 , 21-38		
175	Comparative proteomics identifies the cell-associated lethality of M. tuberculosis RelBE-like toxin-antitoxin complexes. <i>Structure</i> , 2013 , 21, 627-37	5.2	17
174	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
173	Structure-based discovery of fiber-binding compounds that reduce the cytotoxicity of amyloid beta. <i>ELife</i> , 2013 , 2, e00857	8.9	79

172	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
171	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
170	Amyloid β -sheet mimics that antagonize protein aggregation and reduce amyloid toxicity. <i>Nature Chemistry</i> , 2012 , 4, 927-33	17.6	174
169	The amyloid state of proteins in human diseases. <i>Cell</i> , 2012 , 148, 1188-203	56.2	1192
168	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
167	Ribonuclease A suggests how proteins self-chaperone against amyloid fiber formation. <i>Protein Science</i> , 2012 , 21, 26-37	6.3	21
166	Atomic view of a toxic amyloid small oligomer. <i>Science</i> , 2012 , 335, 1228-31	33.3	440
165	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
164	Structure-based design of non-natural amino-acid inhibitors of amyloid fibril formation. <i>Nature</i> , 2011 , 475, 96-100	50.4	341
163	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
162	The TB Structural Genomics Consortium: a decade of progress. <i>Tuberculosis</i> , 2011 , 91, 155-72	2.6	33
161	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
160	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
159	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
158	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
157	Atomic structures suggest determinants of transmission barriers in mammalian prion disease. <i>Biochemistry</i> , 2011 , 50, 2456-63	3.2	45
156	Towards a pharmacophore for amyloid. <i>PLoS Biology</i> , 2011 , 9, e1001080	9.7	159
155	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

154	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
153	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
152	Multidimensional Structure-Activity Relationship of a Protein in Its Aggregated States. <i>Angewandte Chemie</i> , 2010 , 122, 3996-4000	3.6	3
151	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
150	The crystal structure of the Mycobacterium tuberculosis Rv3019c-Rv3020c ESX complex reveals a domain-swapped heterotetramer. <i>Protein Science</i> , 2010 , 19, 1692-703	6.3	24
149	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
148	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
147	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
146	Molecular mechanisms for protein-encoded inheritance. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 973-8	17.6	218
145	Functional amyloids as natural storage of peptide hormones in pituitary secretory granules. <i>Science</i> , 2009 , 325, 328-32	33.3	728
144	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
143	Inferring molecular function: contributions from functional linkages. <i>Trends in Genetics</i> , 2008 , 24, 587-908.5		4
142	The structure of a fibril-forming sequence, NNQQNY, in the context of a globular fold. <i>Protein Science</i> , 2008 , 17, 1617-23	6.3	16
141	Atomic structure of the cross-beta spine of islet amyloid polypeptide (amylin). <i>Protein Science</i> , 2008 , 17, 1467-74	6.3	281
140	Bacterial inclusion bodies contain amyloid-like structure. <i>PLoS Biology</i> , 2008 , 6, e195	9.7	159
139	Identifying cognate binding pairs among a large set of paralogs: the case of PE/PPE proteins of Mycobacterium tuberculosis. <i>PLoS Computational Biology</i> , 2008 , 4, e1000174	5	29
138	Annotating proteins with generalized functional linkages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 17700-5	11.5	11
137	Cooperative hydrogen bonding in amyloid formation. <i>Protein Science</i> , 2007 , 16, 761-4	6.3	114

136	The Sorcerer II Global Ocean Sampling expedition: expanding the universe of protein families. <i>PLoS Biology</i> , 2007 , 5, e16	9.7	638
135	Atomic structures of amyloid cross-beta spines reveal varied steric zippers. <i>Nature</i> , 2007 , 447, 453-7	50.4	1785
134	A novel inhibitor of Mycobacterium tuberculosis pantothenate synthetase. <i>Journal of Biomolecular Screening</i> , 2007 , 12, 100-5		56
133	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
132	The mechanism of the amyloidogenic conversion of T7 endonuclease I. <i>Journal of Biological Chemistry</i> , 2007 , 282, 14968-74	5.4	7
131	Draft crystal structure of the vault shell at 9-A resolution. <i>PLoS Biology</i> , 2007 , 5, e318	9.7	36
130	The protein network as a tool for finding novel drug targets. <i>Progress in Drug Research Fortschritte Der Arzneimittelforschung Progres Des Recherches Pharmaceutiques</i> , 2007 , 64, 191, 193-215		10
129	Recent atomic models of amyloid fibril structure. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 260-5	8.1	312
128	Deposition diseases and 3D domain swapping. <i>Structure</i> , 2006 , 14, 811-24	5.2	180
127	Toward the structural genomics of complexes: crystal structure of a PE/PPE protein complex from Mycobacterium tuberculosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 8060-5	11.5	602
126	Bioinformatic challenges for the next decade(s). <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006 , 361, 525-7	5.8	7
125	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
124	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
123	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
122	Unique transcriptome signature of Mycobacterium tuberculosis in pulmonary tuberculosis. <i>Infection and Immunity</i> , 2006 , 74, 1233-42	3.7	194
121	Structural models of amyloid-like fibrils. <i>Advances in Protein Chemistry</i> , 2006 , 73, 235-82		162
120	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
119	Crystal structure of the pantothenate synthetase from Mycobacterium tuberculosis, snapshots of the enzyme in action. <i>Biochemistry</i> , 2006 , 45, 1554-61	3.2	44

118	Mycobacterium tuberculosis gene expression profiling within the context of protein networks. <i>Microbes and Infection</i> , 2006 , 8, 747-57	9.3	59
117	Regulation by oligomerization in a mycobacterial folate biosynthetic enzyme. <i>Journal of Molecular Biology</i> , 2005 , 349, 61-72	6.5	32
116	Inferring protein domain interactions from databases of interacting proteins. <i>Genome Biology</i> , 2005 , 6, R89	18.3	107
115	Detection of parallel functional modules by comparative analysis of genome sequences. <i>Nature Biotechnology</i> , 2005 , 23, 253-60	44.5	27
114	Structure of the cross-beta spine of amyloid-like fibrils. <i>Nature</i> , 2005 , 435, 773-8	50.4	1791
113	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
112	Utilizing logical relationships in genomic data to decipher cellular processes. <i>FEBS Journal</i> , 2005 , 272, 5110-8	5.7	32
111	Inference of protein function from protein structure. <i>Structure</i> , 2005 , 13, 121-30	5.2	153
110	A Web-Based Comparative Genomics Tutorial for Investigating Microbial Genomes. <i>Journal of Microbiology and Biology Education</i> , 2004 , 5, 30-35		1
109	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
108	The Database of Interacting Proteins: 2004 update. <i>Nucleic Acids Research</i> , 2004 , 32, D449-51	20.1	1532
107	PFIT and PFRIT: bioinformatic algorithms for detecting glycosidase function from structure and sequence. <i>Protein Science</i> , 2004 , 13, 221-9	6.3	1
106	DPANN: improved sequence to structure alignments following fold recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 528-38	4.2	8
105	Use of logic relationships to decipher protein network organization. <i>Science</i> , 2004 , 306, 2246-9	33.3	115
104	Prolinks: a database of protein functional linkages derived from coevolution. <i>Genome Biology</i> , 2004 , 5, R35	18.3	230
103	A web-based comparative genomics tutorial for investigating microbial genomes. <i>Journal of Microbiology and Biology Education</i> , 2004 , 5, 30-5		2
102	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
101	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

100	John T. Edsall as tutor and teacher. <i>Biophysical Chemistry</i> , 2003 , 100, 91-3	3.5	
99	Computational methods of analysis of protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2003 , 13, 377-82	8.1	125
98	The TB structural genomics consortium: a resource for Mycobacterium tuberculosis biology. <i>Tuberculosis</i> , 2003 , 83, 223-49	2.6	86
97	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
96	The oligomerization and ligand-binding properties of Sm-like archaeal proteins (SmAPs). <i>Protein Science</i> , 2003 , 12, 832-47	6.3	42
95	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
94	Structure and function of an archaeal homolog of survival protein E (SurEalpha): an acid phosphatase with purine nucleotide specificity. <i>Journal of Molecular Biology</i> , 2003 , 326, 1559-75	6.5	26
93	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
92	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
91	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
90	Visualization and interpretation of protein networks in Mycobacterium tuberculosis based on hierarchical clustering of genome-wide functional linkage maps. <i>Nucleic Acids Research</i> , 2003 , 31, 7099-109	11.1	46
89	Crystal structure of a major secreted protein of Mycobacterium tuberculosis-MPT63 at 1.5-A resolution. <i>Protein Science</i> , 2002 , 11, 2887-93	6.3	32
88	Structures of the two 3D domain-swapped RNase A trimers. <i>Protein Science</i> , 2002 , 11, 371-80	6.3	96
87	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
86	The directional atomic solvation energy: an atom-based potential for the assignment of protein sequences to known folds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 16041-6	11.5	27
85	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
84	Describing biological protein interactions in terms of protein states and state transitions: the LiveDIP database. <i>Molecular and Cellular Proteomics</i> , 2002 , 1, 104-16	7.6	31
83	The TB structural genomics consortium: providing a structural foundation for drug discovery. <i>Current Drug Targets Infectious Disorders</i> , 2002 , 2, 121-41		60

82	Multicopy crystallographic refinement of a relaxed glutamine synthetase from <i>Mycobacterium tuberculosis</i> highlights flexible loops in the enzymatic mechanism and its regulation. <i>Biochemistry</i> , 2002 , 41, 9863-72	3.2	68
81	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
80	3D domain swapping: as domains continue to swap. <i>Protein Science</i> , 2002 , 11, 1285-99	6.3	587
79	A hierarchic approach to the design of hexameric helical barrels. <i>Journal of Molecular Biology</i> , 2002 , 319, 243-53	6.5	29
78	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
77	Motif-based fold assignment. <i>Protein Science</i> , 2001 , 10, 2460-9	6.3	6
76	Protein interaction databases. <i>Current Opinion in Biotechnology</i> , 2001 , 12, 334-9	11.4	76
75	Sequence-structure analysis of FAD-containing proteins. <i>Protein Science</i> , 2001 , 10, 1712-28	6.3	355
74	A domain-swapped RNase A dimer with implications for amyloid formation. <i>Nature Structural Biology</i> , 2001 , 8, 211-4		216
73	Bioinformatic identification of potential autocrine signaling loops in cancers from gene expression profiles. <i>Nature Genetics</i> , 2001 , 29, 295-300	36.3	93
72	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
71	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
70	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
69	An interfacial mechanism and a class of inhibitors inferred from two crystal structures of the <i>Mycobacterium tuberculosis</i> 30 kDa major secretory protein (Antigen 85B), a mycolyl transferase. <i>Journal of Molecular Biology</i> , 2001 , 307, 671-81	6.5	109
68	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
67	3D structure and significance of the GPhiXXG helix packing motif in tetramers of the E1beta subunit of pyruvate dehydrogenase from the archeon <i>Pyrobaculum aerophilum</i> . <i>Biochemistry</i> , 2001 , 40, 14484-92	3.2	19
66	Turning a reference inside-out: Commentary on an article by Stevens and Arkin entitled: Are membrane proteins inside-out proteins? (<i>Proteins</i> 1999;36:135-143). <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 38, 121-122	4.2	16
65	Protein function in the post-genomic era. <i>Nature</i> , 2000 , 405, 823-6	50.4	590

64	Structure-function relationships of glutamine synthetases. <i>BBA - Proteins and Proteomics</i> , 2000 , 1477, 122-45		276
63	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
62	Characterization of high-order diphtheria toxin oligomers. <i>Biochemistry</i> , 2000 , 39, 15901-9	3.2	21
61	Preliminary crystallographic studies on glutamine synthetase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 865-8		4
60	A combined algorithm for genome-wide prediction of protein function. <i>Nature</i> , 1999 , 402, 83-6	50.4	773
59	Packed protein bilayers in the 0.90 Å resolution structure of a designed alpha helical bundle. <i>Protein Science</i> , 1999 , 8, 1400-9	6.3	34
58	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
57	Detecting protein function and protein-protein interactions from genome sequences. <i>Science</i> , 1999 , 285, 751-3	33.3	1397
56	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
55	Predicting structures for genome proteins. <i>Current Opinion in Structural Biology</i> , 1999 , 9, 208-11	8.1	49
54	A census of protein repeats. <i>Journal of Molecular Biology</i> , 1999 , 293, 151-60	6.5	313
53	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
52	The BPI/LBP family of proteins: a structural analysis of conserved regions. <i>Protein Science</i> , 1998 , 7, 906-14	6.3	107
51	Detecting distant relatives of mammalian LPS-binding and lipid transport proteins. <i>Protein Science</i> , 1998 , 7, 1643-6	6.3	36
50	Crystal structure of human BPI and two bound phospholipids at 2.4 angstrom resolution. <i>Science</i> , 1997 , 276, 1861-4	33.3	317
49	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
48	VERIFY3D: assessment of protein models with three-dimensional profiles. <i>Methods in Enzymology</i> , 1997 , 277, 396-404	1.7	1402
47	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

46	Fold assignments for amino acid sequences of the CASP2 experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 29, 113-122	4.2	16
45	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
44	Assigning amino acid sequences to 3-dimensional protein folds. <i>FASEB Journal</i> , 1996 , 10, 126-36	0.9	87
43	Crystallization of a designed peptide from a molten globule ensemble. <i>Folding & Design</i> , 1996 , 1, 57-64		22
42	A study of combined structure/sequence profiles. <i>Folding & Design</i> , 1996 , 1, 451-61		40
41	Protein fold recognition using sequence-derived predictions. <i>Protein Science</i> , 1996 , 5, 947-55	6.3	279
40	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
39	Local moves: an efficient algorithm for simulation of protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 23, 73-82	4.2	58
38	Crystallization of the chaperone protein SecB. <i>Protein Science</i> , 1995 , 4, 1651-3	6.3	4
37	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
36	3D domain swapping: a mechanism for oligomer assembly. <i>Protein Science</i> , 1995 , 4, 2455-68	6.3	678
35	Crystal structure of the unactivated ribulose 1,5-bisphosphate carboxylase/oxygenase complexed with a transition state analog, 2-carboxy-D-arabinitol 1,5-bisphosphate. <i>Protein Science</i> , 1994 , 3, 64-9	6.3	22
34	The three-dimensional profile method using residue preference as a continuous function of residue environment. <i>Protein Science</i> , 1994 , 3, 687-95	6.3	35
33	Refined structure of dimeric diphtheria toxin at 2.0 Å resolution. <i>Protein Science</i> , 1994 , 3, 1444-63	6.3	161
32	Refined structure of monomeric diphtheria toxin at 2.3 Å resolution. <i>Protein Science</i> , 1994 , 3, 1464-75	6.3	172
31	Max Perutz's achievements: how did he do it?. <i>Protein Science</i> , 1994 , 3, 1625-8	6.3	15
30	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
29	Interactions of nucleotides with fully unadenylylated glutamine synthetase from <i>Salmonella typhimurium</i> . <i>Biochemistry</i> , 1994 , 33, 11184-8	3.2	42

28	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
27	Inverted protein structure prediction. <i>Current Opinion in Structural Biology</i> , 1993 , 3, 437-444	8.1	65
26	Extending the diffraction limit of protein crystals: the example of glutamine synthetase from <i>Salmonella typhimurium</i> in the presence of its cofactor ATP. <i>Protein Science</i> , 1993 , 2, 470-1	6.3	5
25	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
24	Defensins promote fusion and lysis of negatively charged membranes. <i>Protein Science</i> , 1993 , 2, 1301-12	6.3	138
23	Atomic solvation parameters applied to molecular dynamics of proteins in solution. <i>Protein Science</i> , 1992 , 1, 227-35	6.3	453
22	Thermodynamics of melittin tetramerization determined by circular dichroism and implications for protein folding. <i>Protein Science</i> , 1992 , 1, 641-53	6.3	69
21	X-ray grade crystals of a designed alpha-helical coiled coil. <i>Protein Science</i> , 1992 , 1, 956-7	6.3	11
20	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
19	Assessment of protein models with three-dimensional profiles. <i>Nature</i> , 1992 , 356, 83-5	50.4	2511
18	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
17	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
16	Profile analysis. <i>Methods in Enzymology</i> , 1990 , 183, 146-59	1.7	234
15	Sliding-layer conformational change limited by the quaternary structure of plant RuBisCO. <i>Nature</i> , 1987 , 329, 354-6	50.4	83
14	Hydrophobicity and amphiphilicity in protein structure. <i>Journal of Cellular Biochemistry</i> , 1986 , 31, 11-7	4.7	61
13	The design, synthesis, and crystallization of an alpha-helical peptide. <i>Proteins: Structure, Function and Bioinformatics</i> , 1986 , 1, 16-22	4.2	121
12	Solvation energy in protein folding and binding. <i>Nature</i> , 1986 , 319, 199-203	50.4	1673
11	Novel subunit-subunit interactions in the structure of glutamine synthetase. <i>Nature</i> , 1986 , 323, 304-9	50.4	282

10	The helical hydrophobic moment: a measure of the amphiphilicity of a helix. <i>Nature</i> , 1982 , 299, 371-4	50.4	895
9	The Curies' Nobel Prizes. <i>Science</i> , 1982 , 215, 348-348	33.3	
8	Assessment of the effects of transthyretin peptide inhibitors in <i>Drosophila</i> models of neuropathic ATTR		1
7	A structure-based model for the electrostatic interaction of the N-terminus of protein tau with the fibril core of Alzheimer's Disease filaments		1
6	Cryo-EM Structures of Four Polymorphic TDP-43 Amyloid Cores		1
5	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
4	The prevalence and distribution in genomes of low-complexity, amyloid-like, reversible, kinked segment (LARKS), a common structural motif in amyloid-like fibrils		2
3	Exploring Mechanisms of Inhibition of Amyloid Seeding of Transthyretin		1
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