

David Eisenberg

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8345583/publications.pdf>

Version: 2024-02-01

254
papers

53,726
citations

1883

102
h-index

1310

224
g-index

282
all docs

282
docs citations

282
times ranked

42975
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Assessment of protein models with three-dimensional profiles. <i>Nature</i> , 1992, 356, 83-85. | 13.7 | 2,958 |
| 2 | Atomic structures of amyloid cross- β^2 spines reveal varied steric zippers. <i>Nature</i> , 2007, 447, 453-457. | 13.7 | 2,066 |
| 3 | Structure of the cross- β^2 spine of amyloid-like fibrils. <i>Nature</i> , 2005, 435, 773-778. | 13.7 | 2,034 |
| 4 | The Database of Interacting Proteins: 2004 update. <i>Nucleic Acids Research</i> , 2004, 32, 449D-451. | 6.5 | 1,918 |
| 5 | Solvation energy in protein folding and binding. <i>Nature</i> , 1986, 319, 199-203. | 13.7 | 1,867 |
| 6 | [20] VERIFY3D: Assessment of protein models with three-dimensional profiles. <i>Methods in Enzymology</i> , 1997, 277, 396-404. | 0.4 | 1,839 |
| 7 | Cell-free Formation of RNA Granules: Low Complexity Sequence Domains Form Dynamic Fibers within Hydrogels. <i>Cell</i> , 2012, 149, 753-767. | 13.5 | 1,725 |
| 8 | Detecting Protein Function and Protein-Protein Interactions from Genome Sequences. <i>Science</i> , 1999, 285, 751-753. | 6.0 | 1,595 |
| 9 | The Amyloid State of Proteins in Human Diseases. <i>Cell</i> , 2012, 148, 1188-1203. | 13.5 | 1,496 |
| 10 | DIP, the Database of Interacting Proteins: a research tool for studying cellular networks of protein interactions. <i>Nucleic Acids Research</i> , 2002, 30, 303-305. | 6.5 | 1,487 |
| 11 | The helical hydrophobic moment: a measure of the amphiphilicity of a helix. <i>Nature</i> , 1982, 299, 371-374. | 13.7 | 1,019 |
| 12 | Functional Amyloids As Natural Storage of Peptide Hormones in Pituitary Secretory Granules. <i>Science</i> , 2009, 325, 328-332. | 6.0 | 903 |
| 13 | A combined algorithm for genome-wide prediction of protein function. <i>Nature</i> , 1999, 402, 83-86. | 13.7 | 879 |
| 14 | 3D domain swapping: A mechanism for oligomer assembly. <i>Protein Science</i> , 1995, 4, 2455-2468. | 3.1 | 742 |
| 15 | The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. <i>PLoS Biology</i> , 2007, 5, e16. | 2.6 | 736 |
| 16 | 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, 3487-3492. | 3.3 | 708 |
| 17 | Protein function in the post-genomic era. <i>Nature</i> , 2000, 405, 823-826. | 13.7 | 690 |
| 18 | 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, 8060-8065. | 3.3 | 683 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | The primary mechanism of attenuation of bacillus Calmette-Guerin is a loss of secreted lytic function required for invasion of lung interstitial tissue. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12420-12425. | 3.3 | 656 |
| 20 | 3D domain swapping: As domains continue to swap. Protein Science, 2002, 11, 1285-1299. | 3.1 | 648 |
| 21 | Protein Interactions. Molecular and Cellular Proteomics, 2002, 1, 349-356. | 2.5 | 570 |
| 22 | Structure of the toxic core of $\hat{\alpha}$ -synuclein from invisible crystals. Nature, 2015, 525, 486-490. | 13.7 | 528 |
| 23 | Atomic View of a Toxic Amyloid Small Oligomer. Science, 2012, 335, 1228-1231. | 6.0 | 518 |
| 24 | Atomic solvation parameters applied to molecular dynamics of proteins in solution. Protein Science, 1992, 1, 227-235. | 3.1 | 507 |
| 25 | Cryo-EM of full-length $\hat{\alpha}$ -synuclein reveals fibril polymorphs with a common structural kernel. Nature Communications, 2018, 9, 3609. | 5.8 | 468 |
| 26 | Propagation of Tau Aggregates and Neurodegeneration. Annual Review of Neuroscience, 2017, 40, 189-210. | 5.0 | 453 |
| 27 | Structural Studies of Amyloid Proteins at the Molecular Level. Annual Review of Biochemistry, 2017, 86, 69-95. | 5.0 | 419 |
| 28 | Amyloid nomenclature 2018: recommendations by the International Society of Amyloidosis (ISA) nomenclature committee. Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis, 2018, 25, 215-219. | 1.4 | 417 |
| 29 | Sequence-structure analysis of FAD-containing proteins. Protein Science, 2001, 10, 1712-1728. | 3.1 | 412 |
| 30 | Structure-based design of non-natural amino-acid inhibitors of amyloid fibril formation. Nature, 2011, 475, 96-100. | 13.7 | 394 |
| 31 | The activities of amyloids from a structural perspective. Nature, 2016, 539, 227-235. | 13.7 | 386 |
| 32 | A census of protein repeats. Journal of Molecular Biology, 1999, 293, 151-160. | 2.0 | 385 |
| 33 | Molecular basis for amyloid- $\hat{\beta}$ polymorphism. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16938-16943. | 3.3 | 383 |
| 34 | Atomic structures of low-complexity protein segments reveal kinked $\hat{\beta}$ sheets that assemble networks. Science, 2018, 359, 698-701. | 6.0 | 376 |
| 35 | An amyloid-forming peptide from the yeast prion Sup35 reveals a dehydrated $\hat{\alpha}$ -sheet structure for amyloid. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 2375-2380. | 3.3 | 375 |
| 36 | The 3D profile method for identifying fibril-forming segments of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4074-4078. | 3.3 | 372 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 37 | Recent atomic models of amyloid fibril structure. <i>Current Opinion in Structural Biology</i> , 2006, 16, 260-265. | 2.6 | 354 |
| 38 | Crystal Structure of Human BPI and Two Bound Phospholipids at 2.4Å Resolution. <i>Science</i> , 1997, 276, 1861-1864. | 6.0 | 352 |
| 39 | Half a century of amyloids: past, present and future. <i>Chemical Society Reviews</i> , 2020, 49, 5473-5509. | 18.7 | 345 |
| 40 | Molecular basis for insulin fibril assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18990-18995. | 3.3 | 341 |
| 41 | [9] Profile analysis. <i>Methods in Enzymology</i> , 1990, 183, 146-159. | 0.4 | 337 |
| 42 | Structure-function relationships of glutamine synthetases. <i>BBA - Proteins and Proteomics</i> , 2000, 1477, 122-145. | 2.1 | 322 |
| 43 | Novel subunit-subunit interactions in the structure of glutamine synthetase. <i>Nature</i> , 1986, 323, 304-309. | 13.7 | 320 |
| 44 | Atomic structure of the cross- β spine of islet amyloid polypeptide (amylin). <i>Protein Science</i> , 2008, 17, 1467-1474. | 3.1 | 313 |
| 45 | Protein fold recognition using sequence-derived predictions. <i>Protein Science</i> , 1996, 5, 947-955. | 3.1 | 299 |
| 46 | 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, 7717-7722. | 3.3 | 286 |
| 47 | Prolinks: a database of protein functional linkages derived from coevolution. <i>Genome Biology</i> , 2004, 5, R35. | 13.9 | 276 |
| 48 | A Designed Inhibitor of p53 Aggregation Rescues p53 Tumor Suppression in Ovarian Carcinomas. <i>Cancer Cell</i> , 2016, 29, 90-103. | 7.7 | 273 |
| 49 | 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. | 1.4 | 265 |
| 50 | Crystal structures of truncated alphaA and alphaB crystallins reveal structural mechanisms of polydispersity important for eye lens function. <i>Protein Science</i> , 2010, 19, 1031-1043. | 3.1 | 264 |
| 51 | Molecular mechanisms for protein-encoded inheritance. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 973-978. | 3.6 | 250 |
| 52 | Toward rational protein crystallization: A Web server for the design of crystallizable protein variants. <i>Protein Science</i> , 2007, 16, 1569-1576. | 3.1 | 247 |
| 53 | Structure-based inhibitors of tau aggregation. <i>Nature Chemistry</i> , 2018, 10, 170-176. | 6.6 | 246 |
| 54 | A domain-swapped RNase A dimer with implications for amyloid formation. <i>Nature Structural Biology</i> , 2001, 8, 211-214. | 9.7 | 240 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 55 | Amyloid-like fibrils of ribonuclease A with three-dimensional domain-swapped and native-like structure. <i>Nature</i> , 2005, 437, 266-269. | 13.7 | 239 |
| 56 | Unique Transcriptome Signature of <i>Mycobacterium tuberculosis</i> in Pulmonary Tuberculosis. <i>Infection and Immunity</i> , 2006, 74, 1233-1242. | 1.0 | 234 |
| 57 | The discovery of the $\hat{\alpha}$ -helix and $\hat{\alpha}$ -sheet, the principal structural features of proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 11207-11210. | 3.3 | 228 |
| 58 | Three-dimensional cluster analysis identifies interfaces and functional residue clusters in proteins ¹¹ Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 2001, 307, 1487-1502. | 2.0 | 226 |
| 59 | An amyloid-forming segment of $\hat{\alpha}$ 2-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, 10584-10589. | 3.3 | 220 |
| 60 | Amyloid $\hat{\beta}$ -sheet mimics that antagonize protein aggregation and reduce amyloid toxicity. <i>Nature Chemistry</i> , 2012, 4, 927-933. | 6.6 | 213 |
| 61 | Cryo-EM structures of four polymorphic TDP-43 amyloid cores. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 619-627. | 3.6 | 205 |
| 62 | Deposition Diseases and 3D Domain Swapping. <i>Structure</i> , 2006, 14, 811-824. | 1.6 | 195 |
| 63 | Refined structure of monomelic diphtheria toxin at 2.3 Å... resolution. <i>Protein Science</i> , 1994, 3, 1464-1475. | 3.1 | 192 |
| 64 | Bacterial Inclusion Bodies Contain Amyloid-Like Structure. <i>PLoS Biology</i> , 2008, 6, e195. | 2.6 | 189 |
| 65 | 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, 1521-1530. | 3.1 | 186 |
| 66 | Towards a Pharmacophore for Amyloid. <i>PLoS Biology</i> , 2011, 9, e1001080. | 2.6 | 184 |
| 67 | Out-of-register $\hat{\beta}$ -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, 20913-20918. | 3.3 | 184 |
| 68 | Structural Models of Amyloid-Like Fibrils. <i>Advances in Protein Chemistry</i> , 2006, 73, 235-282. | 4.4 | 183 |
| 69 | 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. | 3.6 | 183 |
| 70 | Refined structure of dimeric diphtheria toxin at 2.0 Å... resolution. <i>Protein Science</i> , 1994, 3, 1444-1463. | 3.1 | 181 |
| 71 | A missing link in cupredoxins: Crystal structure of cucumber stellacyanin at 1.6 Å... resolution. <i>Protein Science</i> , 1996, 5, 2175-2183. | 3.1 | 181 |
| 72 | The structured core domain of $\hat{\beta}$ -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. | 3.3 | 181 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 73 | Inference of Protein Function from Protein Structure. <i>Structure</i> , 2005, 13, 121-130. | 1.6 | 175 |
| 74 | The Structural Biology of Protein Aggregation Diseases: Fundamental Questions and Some Answers. <i>Accounts of Chemical Research</i> , 2006, 39, 568-575. | 7.6 | 173 |
| 75 | GXXXG and GXXXA Motifs Stabilize FAD and NAD(P)-binding Rossmann Folds Through C α -H α -O Hydrogen Bonds and van der Waals Interactions. <i>Journal of Molecular Biology</i> , 2002, 323, 69-76. | 2.0 | 168 |
| 76 | 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, 9679-9684. | 3.3 | 167 |
| 77 | The expanding amyloid family: Structure, stability, function, and pathogenesis. <i>Cell</i> , 2021, 184, 4857-4873. | 13.5 | 166 |
| 78 | TDP-43 and RNA form amyloid-like myo-granules in regenerating muscle. <i>Nature</i> , 2018, 563, 508-513. | 13.7 | 163 |
| 79 | Defensins promote fusion and lysis of negatively charged membranes. <i>Protein Science</i> , 1993, 2, 1301-1312. | 3.1 | 160 |
| 80 | 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, 229-239. | 1.5 | 159 |
| 81 | 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, 1026-1038. | 2.0 | 159 |
| 82 | The Crystal Structure of Phosphinothricin in the Active Site of Glutamine Synthetase Illuminates the Mechanism of Enzymatic Inhibition. <i>Biochemistry</i> , 2001, 40, 1903-1912. | 1.2 | 158 |
| 83 | Atomic-resolution structures from fragmented protein crystals with the cryoEM method MicroED. <i>Nature Methods</i> , 2017, 14, 399-402. | 9.0 | 158 |
| 84 | Non-proteinaceous hydrolase comprised of a phenylalanine metallo-supramolecular amyloid-like structure. <i>Nature Catalysis</i> , 2019, 2, 977-985. | 16.1 | 142 |
| 85 | 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, 725-730. | 3.6 | 140 |
| 86 | Use of Logic Relationships to Decipher Protein Network Organization. <i>Science</i> , 2004, 306, 2246-2249. | 6.0 | 140 |
| 87 | The crystal structure of the designed trimeric coiled coil coil _a L _d : Implications for engineering crystals and supramolecular assemblies. <i>Protein Science</i> , 1997, 6, 80-88. | 3.1 | 138 |
| 88 | The design, synthesis, and crystallization of an alpha-helical peptide. <i>Proteins: Structure, Function and Bioinformatics</i> , 1986, 1, 16-22. | 1.5 | 137 |
| 89 | Computational methods of analysis of protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2003, 13, 377-382. | 2.6 | 136 |
| 90 | Inferring protein domain interactions from databases of interacting proteins. <i>Genome Biology</i> , 2005, 6, R89. | 13.9 | 128 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 91 | Structural model for the reaction mechanism of glutamine synthetase, based on five crystal structures of enzyme-substrate complexes. <i>Biochemistry</i> , 1994, 33, 675-681. | 1.2 | 127 |
| 92 | Cooperative hydrogen bonding in amyloid formation. <i>Protein Science</i> , 2007, 16, 761-764. | 3.1 | 127 |
| 93 | 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. | 3.6 | 127 |
| 94 | The BPI/LBP family of proteins: A structural analysis of conserved regions. <i>Protein Science</i> , 1998, 7, 906-914. | 3.1 | 125 |
| 95 | A systematic screen of beta2-microglobulin and insulin for amyloid-like segments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4079-4082. | 3.3 | 125 |
| 96 | Bioinformatic identification of potential autocrine signaling loops in cancers from gene expression profiles. <i>Nature Genetics</i> , 2001, 29, 295-300. | 9.4 | 122 |
| 97 | 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. | 3.3 | 122 |
| 98 | 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. | 3.3 | 122 |
| 99 | Structure and Proposed Activity of a Member of the VapBC Family of Toxin-Antitoxin Systems. <i>Journal of Biological Chemistry</i> , 2009, 284, 276-283. | 1.6 | 118 |
| 100 | Uncovering the Mechanism of Aggregation of Human Transthyretin. <i>Journal of Biological Chemistry</i> , 2015, 290, 28932-28943. | 1.6 | 117 |
| 101 | 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. Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 2001, 307, 671-681. | 2.0 | 115 |
| 102 | Macrocyclic β -Sheet Peptides That Inhibit the Aggregation of a Tau-Protein-Derived Hexapeptide. <i>Journal of the American Chemical Society</i> , 2011, 133, 3144-3157. | 6.6 | 114 |
| 103 | The most highly amphiphilic β -helices include two amino acid segments in human immunodeficiency virus glycoprotein 41. <i>Biopolymers</i> , 1990, 29, 171-177. | 1.2 | 112 |
| 104 | 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, 12769-12774. | 3.3 | 111 |
| 105 | Discovery of the ammonium substrate site on glutamine synthetase, A third cation binding site. <i>Protein Science</i> , 1995, 4, 2358-2365. | 3.1 | 108 |
| 106 | Structures of the two 3D domain-swapped RNase A trimers. <i>Protein Science</i> , 2009, 11, 371-380. | 3.1 | 107 |
| 107 | Ketones block amyloid entry and improve cognition in an Alzheimer's model. <i>Neurobiology of Aging</i> , 2016, 39, 25-37. | 1.5 | 107 |
| 108 | β 2-microglobulin forms three-dimensional domain-swapped amyloid fibrils with disulfide linkages. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 49-55. | 3.6 | 105 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 109 | 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. | 3.3 | 104 |
| 110 | Inference of protein function and protein linkages in <i>Mycobacterium tuberculosis</i> based on prokaryotic genome organization: a combined computational approach. <i>Genome Biology</i> , 2003, 4, R59. | 13.9 | 103 |
| 111 | Cross-beta Order and Diversity in Nanocrystals of an Amyloid-forming Peptide. <i>Journal of Molecular Biology</i> , 2003, 330, 1165-1175. | 2.0 | 102 |
| 112 | Structure-Based Design of Functional Amyloid Materials. <i>Journal of the American Chemical Society</i> , 2014, 136, 18044-18051. | 6.6 | 102 |
| 113 | Assigning amino acid sequences to 3-dimensional protein folds. <i>FASEB Journal</i> , 1996, 10, 126-136. | 0.2 | 101 |
| 114 | Subunit asymmetry in the three-dimensional structure of a human CuZnSOD mutant found in familial amyotrophic lateral sclerosis. <i>Protein Science</i> , 1998, 7, 545-555. | 3.1 | 101 |
| 115 | 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, 5532-5537. | 3.3 | 100 |
| 116 | Short protein segments can drive a non-fibrillizing protein into the amyloid state. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 531-536. | 1.0 | 99 |
| 117 | De novo phasing with X-ray laser reveals mosquito larvicide BinAB structure. <i>Nature</i> , 2016, 539, 43-47. | 13.7 | 98 |
| 118 | Cryo-EM structure and inhibitor design of human IAPP (amylin) fibrils. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 653-659. | 3.6 | 98 |
| 119 | The TB structural genomics consortium: a resource for <i>Mycobacterium tuberculosis</i> biology. <i>Tuberculosis</i> , 2003, 83, 223-249. | 0.8 | 95 |
| 120 | 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. | 3.3 | 95 |
| 121 | Atomic structures of fibrillar segments of hIAPP suggest tightly mated β^2 -sheets are important for cytotoxicity. <i>ELife</i> , 2017, 6, . | 2.8 | 95 |
| 122 | Structure-based discovery of fiber-binding compounds that reduce the cytotoxicity of amyloid beta. <i>ELife</i> , 2013, 2, e00857. | 2.8 | 94 |
| 123 | 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, 191-196. | 3.3 | 93 |
| 124 | Sliding-layer conformational change limited by the quaternary structure of plant RuBisCO. <i>Nature</i> , 1987, 329, 354-356. | 13.7 | 91 |
| 125 | Amyloid β^2 -Protein C-Terminal Fragments: Formation of Cylindrins and β^2 -Barrels. <i>Journal of the American Chemical Society</i> , 2016, 138, 549-557. | 6.6 | 91 |
| 126 | Protein interaction databases. <i>Current Opinion in Biotechnology</i> , 2001, 12, 334-339. | 3.3 | 89 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 127 | 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. | 3.6 | 89 |
| 128 | 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, 8042-8047. | 3.3 | 88 |
| 129 | Toxicity of Eosinophil MBP Is Repressed by Intracellular Crystallization and Promoted by Extracellular Aggregation. <i>Molecular Cell</i> , 2015, 57, 1011-1021. | 4.5 | 88 |
| 130 | Sub-Ångström cryo-EM structure of a prion protofibril reveals a polar clasp. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 131-134. | 3.6 | 87 |
| 131 | Amyloid fibrils in FTL-D-TDP are composed of TMEM106B and not TDP-43. <i>Nature</i> , 2022, 605, 304-309. | 13.7 | 85 |
| 132 | Characteristics of Amyloid-Related Oligomers Revealed by Crystal Structures of Macrocyclic β -Sheet Mimics. <i>Journal of the American Chemical Society</i> , 2011, 133, 6736-6744. | 6.6 | 84 |
| 133 | Crystal structures of a pantothenate synthetase from <i>M. tuberculosis</i> and its complexes with substrates and a reaction intermediate. <i>Protein Science</i> , 2003, 12, 1097-1108. | 3.1 | 83 |
| 134 | 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, 9863-9872. | 1.2 | 82 |
| 135 | CryoEM structure of the low-complexity domain of hnRNPA2 and its conversion to pathogenic amyloid. <i>Nature Communications</i> , 2020, 11, 4090. | 5.8 | 81 |
| 136 | Structure-based inhibitors of amyloid beta core suggest a common interface with tau. <i>ELife</i> , 2019, 8, . | 2.8 | 81 |
| 137 | Thermodynamics of melittin tetramerization determined by circular dichroism and implications for protein folding. <i>Protein Science</i> , 1992, 1, 641-653. | 3.1 | 75 |
| 138 | Hydrophobicity and amphiphilicity in protein structure. <i>Journal of Cellular Biochemistry</i> , 1986, 31, 11-17. | 1.2 | 73 |
| 139 | Inverted protein structure prediction. <i>Current Opinion in Structural Biology</i> , 1993, 3, 437-444. | 2.6 | 73 |
| 140 | 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. | 3.6 | 73 |
| 141 | The TB Structural Genomics Consortium: Providing a Structural Foundation for Drug Discovery. <i>Current Drug Targets Infectious Disorders</i> , 2002, 2, 121-141. | 2.1 | 66 |
| 142 | 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. | 3.3 | 66 |
| 143 | Local moves: An efficient algorithm for simulation of protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 23, 73-82. | 1.5 | 64 |
| 144 | <i>Mycobacterium tuberculosis</i> gene expression profiling within the context of protein networks. <i>Microbes and Infection</i> , 2006, 8, 747-757. | 1.0 | 64 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 145 | Crystal structure of activated tobacco rubisco complexed with the reaction intermediate analogue 2-carboxy- β -D-xylofuranose 5-bisphosphate. <i>Protein Science</i> , 1993, 2, 1136-1146. | 3.1 | 61 |
| 146 | A Novel Inhibitor of <i>Mycobacterium tuberculosis</i> Pantothenate Synthetase. <i>Journal of Biomolecular Screening</i> , 2007, 12, 100-105. | 2.6 | 61 |
| 147 | Crystal Structures of IAPP Amyloidogenic Segments Reveal a Novel Packing Motif of Out-of-Register Beta Sheets. <i>Journal of Physical Chemistry B</i> , 2016, 120, 5810-5816. | 1.2 | 61 |
| 148 | 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, 29671-29675. | 1.6 | 58 |
| 149 | Structure-Based Peptide Inhibitor Design of Amyloid- β Aggregation. <i>Frontiers in Molecular Neuroscience</i> , 2019, 12, 54. | 1.4 | 58 |
| 150 | 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, 7099-7109. | 6.5 | 55 |
| 151 | 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. | 1.2 | 54 |
| 152 | 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, 2084-2096. | 3.1 | 54 |
| 153 | The crystal structure of the Rv0301-Rv0300 VapBC 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, 1754-1767. | 3.1 | 54 |
| 154 | Inhibition of synucleinopathic seeding by rationally designed inhibitors. <i>ELife</i> , 2020, 9, . | 2.8 | 54 |
| 155 | Atomic Structures Suggest Determinants of Transmission Barriers in Mammalian Prion Disease. <i>Biochemistry</i> , 2011, 50, 2456-2463. | 1.2 | 53 |
| 156 | The formation, function and regulation of amyloids: insights from structural biology. <i>Journal of Internal Medicine</i> , 2016, 280, 164-176. | 2.7 | 53 |
| 157 | Predicting structures for genome proteins. <i>Current Opinion in Structural Biology</i> , 1999, 9, 208-211. | 2.6 | 52 |
| 158 | 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. | 1.6 | 51 |
| 159 | The 1.7 Å... crystal structure of BPI: a study of how two dissimilar amino acid sequences can adopt the same fold 1 Edited by D. Rees. <i>Journal of Molecular Biology</i> , 2000, 299, 1019-1034. | 2.0 | 50 |
| 160 | Crystal Structure of the Pantothenate Synthetase from <i>Mycobacterium tuberculosis</i> , Snapshots of the Enzyme in Action. <i>Biochemistry</i> , 2006, 45, 1554-1561. | 1.2 | 50 |
| 161 | Common fibrillar spines of amyloid- β and human islet amyloid polypeptide revealed by microelectron diffraction and structure-based inhibitors. <i>Journal of Biological Chemistry</i> , 2018, 293, 2888-2902. | 1.6 | 50 |
| 162 | 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, 4539-4544. | 3.3 | 49 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 163 | The Evolving Role of 3D Domain Swapping in Proteins. <i>Structure</i> , 2004, 12, 1339-1341. | 1.6 | 49 |
| 164 | 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. | 3.6 | 48 |
| 165 | Inhibition by small-molecule ligands of formation of amyloid fibrils of an immunoglobulin light chain variable domain. <i>ELife</i> , 2015, 4, e10935. | 2.8 | 48 |
| 166 | Interactions of Nucleotides with Fully Unadenylylated Glutamine Synthetase from <i>Salmonella typhimurium</i> . <i>Biochemistry</i> , 1994, 33, 11184-11188. | 1.2 | 47 |
| 167 | The three-dimensional structure of human bactericidal/permeability-increasing protein. <i>Biochemical Pharmacology</i> , 1999, 57, 225-229. | 2.0 | 47 |
| 168 | The oligomerization and ligand-binding properties of Sm-like archaeal proteins (SmAPs). <i>Protein Science</i> , 2003, 12, 832-847. | 3.1 | 47 |
| 169 | Inhibiting amyloid- β^2 cytotoxicity through its interaction with the cell surface receptor LirB2 by structure-based design. <i>Nature Chemistry</i> , 2018, 10, 1213-1221. | 6.6 | 46 |
| 170 | Structure of amyloid- β^2 (20-34) with Alzheimer's-associated isomerization at Asp23 reveals a distinct protofilament interface. <i>Nature Communications</i> , 2019, 10, 3357. | 5.8 | 45 |
| 171 | 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, . | 3.3 | 45 |
| 172 | A molecular model for membrane fusion based on solution studies of an amphiphilic peptide from HIV gp41. <i>Protein Science</i> , 1992, 1, 1454-1464. | 3.1 | 43 |
| 173 | Centrosymmetric bilayers in the 0.75 Å resolution structure of a designed alpha-helical peptide, D, L- α . <i>Protein Science</i> , 1999, 8, 1410-1422. | 3.1 | 43 |
| 174 | Draft Crystal Structure of the Vault Shell at 9-Å... Resolution. <i>PLoS Biology</i> , 2007, 5, e318. | 2.6 | 43 |
| 175 | A study of combined structure/sequence profiles. <i>Folding & Design</i> , 1996, 1, 451-461. | 4.5 | 42 |
| 176 | Detecting distant relatives of mammalian LPS-binding and lipid transport proteins. <i>Protein Science</i> , 1998, 7, 1643-1646. | 3.1 | 40 |
| 177 | Regulation by Oligomerization in a Mycobacterial Folate Biosynthetic Enzyme. <i>Journal of Molecular Biology</i> , 2005, 349, 61-72. | 2.0 | 39 |
| 178 | X-ray Crystallographic Structure of an Artificial β^2 -Sheet Dimer. <i>Journal of the American Chemical Society</i> , 2010, 132, 11622-11628. | 6.6 | 39 |
| 179 | The TB Structural Genomics Consortium: A decade of progress. <i>Tuberculosis</i> , 2011, 91, 155-172. | 0.8 | 39 |
| 180 | The three-dimensional profile method using residue preference as a continuous function of residue environment. <i>Protein Science</i> , 1994, 3, 687-695. | 3.1 | 38 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 181 | 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. | 3.3 | 38 |
| 182 | Identifying Cognate Binding Pairs among a Large Set of Paralogs: The Case of PE/PPE Proteins of <i>Mycobacterium tuberculosis</i> . <i>PLoS Computational Biology</i> , 2008, 4, e1000174. | 1.5 | 37 |
| 183 | Crystal structure of a major secreted protein of <i>Mycobacterium tuberculosis</i> -MPT63 at 1.5-Å resolution. <i>Protein Science</i> , 2009, 11, 2887-2893. | 3.1 | 37 |
| 184 | Formation of Amyloid Fibers by Monomeric Light Chain Variable Domains. <i>Journal of Biological Chemistry</i> , 2014, 289, 27513-27525. | 1.6 | 37 |
| 185 | A Proposed Mechanism for the Promotion of Prion Conversion Involving a Strictly Conserved Tyrosine Residue in the $\beta 2\text{-}\beta 3$ Loop of PrPC. <i>Journal of Biological Chemistry</i> , 2014, 289, 10660-10667. | 1.6 | 37 |
| 186 | Describing Biological Protein Interactions in Terms of Protein States and State Transitions. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 104-116. | 2.5 | 35 |
| 187 | Taking the measure of MicroED. <i>Current Opinion in Structural Biology</i> , 2017, 46, 79-86. | 2.6 | 35 |
| 188 | Packed protein bilayers in the 0.90 Å resolution structure of a designed alpha helical bundle. <i>Protein Science</i> , 1999, 8, 1400-1409. | 3.1 | 34 |
| 189 | Utilizing logical relationships in genomic data to decipher cellular processes. <i>FEBS Journal</i> , 2005, 272, 5110-5118. | 2.2 | 33 |
| 190 | A pair of peptides inhibits seeding of the hormone transporter transthyretin into amyloid fibrils. <i>Journal of Biological Chemistry</i> , 2019, 294, 6130-6141. | 1.6 | 33 |
| 191 | A Hierarchic Approach to the Design of Hexameric Helical Barrels. <i>Journal of Molecular Biology</i> , 2002, 319, 243-253. | 2.0 | 32 |
| 192 | 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. | 3.1 | 32 |
| 193 | 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. | 1.6 | 32 |
| 194 | Detection of parallel functional modules by comparative analysis of genome sequences. <i>Nature Biotechnology</i> , 2005, 23, 253-260. | 9.4 | 30 |
| 195 | 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, 16041-16046. | 3.3 | 29 |
| 196 | Structure and Function of an Archaeal Homolog of Survival Protein E (SurE): An Acid Phosphatase with Purine Nucleotide Specificity. <i>Journal of Molecular Biology</i> , 2003, 326, 1559-1575. | 2.0 | 28 |
| 197 | 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. | 1.6 | 28 |
| 198 | The crystal structure of the <i>Mycobacterium tuberculosis</i> Rv3019c-Rv3020c ESX complex reveals a domain-swapped heterotetramer. <i>Protein Science</i> , 2010, 19, 1692-1703. | 3.1 | 27 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 199 | Comparative Proteomics Identifies the Cell-Associated Lethality of M.Âtuberculosis RelBE-like Toxin-Antitoxin Complexes. <i>Structure</i> , 2013, 21, 627-637. | 1.6 | 27 |
| 200 | Implications for Alzheimerâ€™s disease of an atomic resolution structure of amyloid-Î²(1â€“42) fibrils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9398-9400. | 3.3 | 27 |
| 201 | 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. | 2.3 | 27 |
| 202 | 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, 7247-7256. | 1.2 | 26 |
| 203 | Crystallization of a designed peptide from a molten globule ensemble. <i>Folding & Design</i> , 1996, 1, 57-64. | 4.5 | 25 |
| 204 | Crystal structure of the unactivated ribulose 1, 5â€bisphosphate carboxylase/oxygenase complexed with a transition state analog, 2â€carboxyâ€Dâ€arabinitol 1, 5â€bisphosphate. <i>Protein Science</i> , 1994, 3, 64-69. | 3.1 | 24 |
| 205 | Ribonuclease A suggests how proteins selfâ€chaperone against amyloid fiber formation. <i>Protein Science</i> , 2012, 21, 26-37. | 3.1 | 24 |
| 206 | Mechanically rigid supramolecular assemblies formed from an Fmoc-guanine conjugated peptide nucleic acid. <i>Nature Communications</i> , 2019, 10, 5256. | 5.8 | 24 |
| 207 | Characterization of High-Order Diphtheria Toxin Oligomersâ€. <i>Biochemistry</i> , 2000, 39, 15901-15909. | 1.2 | 23 |
| 208 | Asparagine and glutamine ladders promote cross-species prion conversion. <i>Journal of Biological Chemistry</i> , 2017, 292, 19076-19086. | 1.6 | 23 |
| 209 | Perspective on SOD1 mediated toxicity in Amyotrophic Lateral Sclerosis. <i>Postepy Biochemii</i> , 2016, 62, 362-369. | 0.5 | 22 |
| 210 | 3D Structure and Significance of the GÎ XXG Helix Packing Motif in Tetramers of the E1Î² Subunit of Pyruvate Dehydrogenase from the Archeon <i>Pyrobaculum aerophilum</i> â€,â€j. <i>Biochemistry</i> , 2001, 40, 14484-14492. | 1.2 | 21 |
| 211 | Heterologous Expression of Mycobacterial Esx Complexes in <i>Escherichia coli</i> for Structural Studies Is Facilitated by the Use of Maltose Binding Protein Fusions. <i>PLoS ONE</i> , 2013, 8, e81753. | 1.1 | 21 |
| 212 | Toward the Atomic Structure of PrP^{Sc}. <i>Cold Spring Harbor Perspectives in Biology</i> , 2017, 9, a031336. | 2.3 | 21 |
| 213 | Atomic structures of corkscrewâ€forming segments of SOD1 reveal varied oligomer conformations. <i>Protein Science</i> , 2018, 27, 1231-1242. | 3.1 | 21 |
| 214 | 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. | 1.6 | 21 |
| 215 | The structure of a fibrilâ€forming sequence, NNQQNY, in the context of a globular fold. <i>Protein Science</i> , 2008, 17, 1617-1623. | 3.1 | 20 |
| 216 | Crystal structures of amyloidogenic segments of human transthyretin. <i>Protein Science</i> , 2018, 27, 1295-1303. | 3.1 | 20 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 217 | Fold assignments for amino acid sequences of the CASP2 experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 113-122. | 1.5 | 19 |
| 218 | 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. | 1.5 | 18 |
| 219 | Indexing amyloid peptide diffraction from serial femtosecond crystallography: new algorithms for sparse patterns. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 357-366. | 2.5 | 18 |
| 220 | Max Perutz's achievements: How did he do it?. <i>Protein Science</i> , 1994, 3, 1625-1628. | 3.1 | 16 |
| 221 | Taming tangled tau. <i>Nature</i> , 2017, 547, 170-171. | 13.7 | 16 |
| 222 | The protein network as a tool for finding novel drug targets. , 2007, 64, 191-215. | | 14 |
| 223 | Annotating proteins with generalized functional linkages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17700-17705. | 3.3 | 14 |
| 224 | Extended β -Strands Contribute to Reversible Amyloid Formation. <i>ACS Nano</i> , 2022, 16, 2154-2163. | 7.3 | 14 |
| 225 | Salvage or Recovery of Failed Targets by Mutagenesis to Reduce Surface Entropy. <i>Methods in Molecular Biology</i> , 2014, 1140, 201-209. | 0.4 | 13 |
| 226 | Flow-aligned, single-shot fiber diffraction using a femtosecond X-ray free-electron laser. <i>Cytoskeleton</i> , 2017, 74, 472-481. | 1.0 | 12 |
| 227 | X-ray grade crystals of a designed α -helical coiled coil. <i>Protein Science</i> , 1992, 1, 956-957. | 3.1 | 11 |
| 228 | Assessment of the effects of transthyretin peptide inhibitors in <i>Drosophila</i> models of neuropathic ATTR. <i>Neurobiology of Disease</i> , 2018, 120, 118-125. | 2.1 | 11 |
| 229 | Identifying amyloid-related diseases by mapping mutations in low-complexity protein domains to pathologies. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 529-536. | 3.6 | 11 |
| 230 | Bioinformatic challenges for the next decade(s). <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 525-527. | 1.8 | 10 |
| 231 | DPANN: Improved sequence to structure alignments following fold recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 528-538. | 1.5 | 9 |
| 232 | 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, 470-471. | 3.1 | 8 |
| 233 | Atomic view of an amyloid dodecamer exhibiting selective cellular toxic vulnerability in acute brain slices. <i>Protein Science</i> , 2021, , . | 3.1 | 8 |
| 234 | The Mechanism of the Amyloidogenic Conversion of T7 Endonuclease I. <i>Journal of Biological Chemistry</i> , 2007, 282, 14968-14974. | 1.6 | 7 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 235 | Distal amyloid β -protein fragments template amyloid assembly. <i>Protein Science</i> , 2018, 27, 1181-1190. | 3.1 | 7 |
| 236 | Motif-based fold assignment. <i>Protein Science</i> , 2001, 10, 2460-2469. | 3.1 | 6 |
| 237 | Preparation of Crystalline Samples of Amyloid Fibrils and Oligomers. <i>Methods in Molecular Biology</i> , 2016, 1345, 201-210. | 0.4 | 6 |
| 238 | Ultrafast Time-Resolved Studies on Fluorescein for Recognition Strands Architecture in Amyloid Fibrils. <i>Journal of Physical Chemistry B</i> , 2018, 122, 8-18. | 1.2 | 6 |
| 239 | Preliminary crystallographic studies on glutamine synthetase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 865-868. | 2.5 | 5 |
| 240 | Inferring molecular function: contributions from functional linkages. <i>Trends in Genetics</i> , 2008, 24, 587-590. | 2.9 | 5 |
| 241 | Atomic insights into the genesis of cellular filaments by globular proteins. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 705-714. | 3.6 | 5 |
| 242 | Crystallization of the chaperone protein SecB. <i>Protein Science</i> , 1995, 4, 1651-1653. | 3.1 | 4 |
| 243 | Bioinformatic identification of previously unrecognized amyloidogenic proteins. <i>Journal of Biological Chemistry</i> , 2022, 298, 101920. | 1.6 | 4 |
| 244 | A web-based comparative genomics tutorial for investigating microbial genomes. <i>Journal of Microbiology and Biology Education</i> , 2004, 5, 30-5. | 0.2 | 3 |
| 245 | 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. | 0.6 | 2 |
| 246 | A Web-Based Comparative Genomics Tutorial for Investigating Microbial Genomes. <i>Journal of Microbiology and Biology Education</i> , 2004, 5, 30-35. | 0.2 | 1 |
| 247 | PFIT and PFRIT: Bioinformatic algorithms for detecting glycosidase function from structure and sequence. <i>Protein Science</i> , 2004, 13, 221-229. | 3.1 | 1 |
| 248 | The Amyloid State of Proteins. <i>FASEB Journal</i> , 2015, 29, 218.1. | 0.2 | 1 |
| 249 | John T. Edsall as tutor and teacher. <i>Biophysical Chemistry</i> , 2002, 100, 91-93. | 1.5 | 0 |
| 250 | Phylogenetic profiling. , 2005, , . | | 0 |
| 251 | In memoriam Rainer Jaenicke. <i>Protein Science</i> , 2017, 26, 394-395. | 3.1 | 0 |
| 252 | Paul D. Boyer (1918-2018). <i>Science</i> , 2018, 361, 334-334. | 6.0 | 0 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 253 | The Curies' Nobel Prizes. <i>Science</i> , 1982, 215, 348-348. | 6.0 | 0 |
| 254 | Targeting Misfolded p53 and p53 Aggregation to Overcome Resistance to Apoptosis in Acute Myeloid Leukemia. <i>Blood</i> , 2019, 134, 3786-3786. | 0.6 | 0 |