

George N Phillips Jr

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242
papers

12,917
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59
h-index

106
g-index

252
ext. papers

13,965
ext. citations

6.6
avg, IF

6.12
L-index

#	Paper	IF	Citations
242	The molecular structure of green fluorescent protein. <i>Nature Biotechnology</i> , 1996 , 14, 1246-51	44.5	1258
241	Watching a protein as it functions with 150-ps time-resolved x-ray crystallography. <i>Science</i> , 2003 , 300, 1944-7	33.3	674
240	Mechanism of NO-induced oxidation of myoglobin and hemoglobin. <i>Biochemistry</i> , 1996 , 35, 6976-83	3.2	567
239	High-resolution crystal structures of distal histidine mutants of sperm whale myoglobin. <i>Journal of Molecular Biology</i> , 1993 , 234, 140-55	6.5	364
238	Crystal structure of photolysed carbonmonoxy-myoglobin. <i>Nature</i> , 1994 , 371, 808-12	50.4	333
237	Structural determinants of the stretching frequency of CO bound to myoglobin. <i>Biochemistry</i> , 1994 , 33, 1433-46	3.2	326
236	Restructuring the crystalline cellulose hydrogen bond network enhances its depolymerization rate. <i>Journal of the American Chemical Society</i> , 2011 , 133, 11163-74	16.4	272
235	Myoglobin discriminates between O ₂ , NO, and CO by electrostatic interactions with the bound ligand. <i>Journal of Biological Inorganic Chemistry</i> , 1997 , 2, 544-552	3.7	251
234	Bound CO Is A Molecular Probe of Electrostatic Potential in the Distal Pocket of Myoglobin. <i>Journal of Physical Chemistry B</i> , 1999 , 103, 8817-8829	3.4	235
233	Kinetic pathways and barriers for ligand binding to myoglobin. <i>Journal of Biological Chemistry</i> , 1996 , 271, 17593-6	5.4	227
232	Dynamics of proteins in crystals: comparison of experiment with simple models. <i>Biophysical Journal</i> , 2002 , 83, 723-32	2.9	218
231	Molecular structure of dihydroorotase: a paradigm for catalysis through the use of a binuclear metal center. <i>Biochemistry</i> , 2001 , 40, 6989-97	3.2	171
230	Structures and analysis of highly homologous psychrophilic, mesophilic, and thermophilic adenylate kinases. <i>Journal of Biological Chemistry</i> , 2004 , 279, 28202-8	5.4	163
229	Structure and mechanism of mouse cysteine dioxygenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 3084-9	11.5	157
228	Effects of the location of distal histidine in the reaction of myoglobin with hydrogen peroxide. <i>Journal of Biological Chemistry</i> , 1999 , 274, 2838-44	5.4	149
227	Structure and dynamics of green fluorescent protein. <i>Current Opinion in Structural Biology</i> , 1997 , 7, 821-8.1	8.1	148
226	Crystal structure of a nonsymbiotic plant hemoglobin. <i>Structure</i> , 2000 , 8, 1005-14	5.2	148

225	Ensemble refinement of protein crystal structures: validation and application. <i>Structure</i> , 2007 , 15, 1040-52	5.2	146
224	Crystal structure of tropomyosin at 7 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 38, 49-59	4.2	146
223	Identification of transcribed sequences in <i>Arabidopsis thaliana</i> by using high-resolution genome tiling arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 4453-8	11.5	136
222	Nonhuman genetics. Genomic basis for the convergent evolution of electric organs. <i>Science</i> , 2014 , 344, 1522-5	33.3	128
221	The closed conformation of a highly flexible protein: the structure of <i>E. coli</i> adenylate kinase with bound AMP and AMPPNP. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994 , 19, 183-98	4.2	123
220	Characterization of recombinant soybean leghemoglobin a and apolar distal histidine mutants. <i>Journal of Molecular Biology</i> , 1997 , 266, 1032-42	6.5	122
219	Probing substates in sperm whale myoglobin using high-pressure crystallography. <i>Structure</i> , 2002 , 10, 51-60	5.2	121
218	Structure of myoglobin-ethyl isocyanide. Histidine as a swinging door for ligand entry. <i>Journal of Molecular Biology</i> , 1989 , 207, 459-63	6.5	116
217	Inhibition of human pancreatic ribonuclease by the human ribonuclease inhibitor protein. <i>Journal of Molecular Biology</i> , 2007 , 368, 434-49	6.5	113
216	Drop-on-demand sample delivery for studying biocatalysts in action at X-ray free-electron lasers. <i>Nature Methods</i> , 2017 , 14, 443-449	21.6	107
215	Glycosyltransferase structural biology and its role in the design of catalysts for glycosylation. <i>Current Opinion in Biotechnology</i> , 2011 , 22, 800-8	11.4	107
214	Nitric oxide myoglobin: Crystal structure and analysis of ligand geometry. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998 , 30, 352-356	4.2	107
213	Structure of the oxygen sensor in <i>Bacillus subtilis</i> : signal transduction of chemotaxis by control of symmetry. <i>Structure</i> , 2003 , 11, 1097-110	5.2	104
212	Protocols for production of selenomethionine-labeled proteins in 2-L polyethylene terephthalate bottles using auto-induction medium. <i>Protein Expression and Purification</i> , 2005 , 40, 256-67	2	99
211	Crystal structure of myoglobin from a synthetic gene. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990 , 7, 358-65	4.2	99
210	Optimization and evaluation of a coarse-grained model of protein motion using x-ray crystal data. <i>Biophysical Journal</i> , 2006 , 91, 2760-7	2.9	93
209	A model from electron microscopy for the molecular structure of fibrinogen and fibrin. <i>Nature</i> , 1981 , 289, 263-7	50.4	92
208	Crystal structures of <i>Bacillus stearothermophilus</i> adenylate kinase with bound Ap5A, Mg ²⁺ Ap5A, and Mn ²⁺ Ap5A reveal an intermediate lid position and six coordinate octahedral geometry for bound Mg ²⁺ and Mn ²⁺ . <i>Proteins: Structure, Function and Bioinformatics</i> , 1998 , 32, 276-88	4.2	90

207	Structural basis for selective activation of ABA receptors. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 1109-13	17.6	88
206	Protein structural variation in computational models and crystallographic data. <i>Structure</i> , 2007 , 15, 169-72	5.2	86
205	The structural biology of enzymes involved in natural product glycosylation. <i>Natural Product Reports</i> , 2012 , 29, 1201-37	15.1	81
204	A photo-labile thioether linkage to phycoviolobin provides the foundation for the blue/green photocycles in DXCF-cyanobacteriochromes. <i>Structure</i> , 2013 , 21, 88-97	5.2	80
203	Structural consequences of effector protein complex formation in a diiron hydroxylase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 19194-8	11.5	80
202	Project management system for structural and functional proteomics: Sesame. <i>Journal of Structural and Functional Genomics</i> , 2003 , 4, 11-23		80
201	Many local motions cooperate to produce the adenylate kinase conformational transition. <i>Journal of Molecular Biology</i> , 2010 , 400, 618-31	6.5	78
200	Understanding protein flexibility through dimensionality reduction. <i>Journal of Computational Biology</i> , 2003 , 10, 617-34	1.7	77
199	Perturbation of the Fe-D2 Bond by Nearby Residues in Heme Pocket: Observation of Fe-O2 Raman Bands for Oxymyoglobin Mutants. <i>Journal of the American Chemical Society</i> , 1996 , 118, 7845-7846	16.4	76
198	Structural enzymology using X-ray free electron lasers. <i>Structural Dynamics</i> , 2017 , 4, 044003	3.2	75
197	Enzyme intermediates captured "on the fly" by mix-and-inject serial crystallography. <i>BMC Biology</i> , 2018 , 16, 59	7.3	73
196	Waterproofing the heme pocket. Role of proximal amino acid side chains in preventing hemin loss from myoglobin. <i>Journal of Biological Chemistry</i> , 2001 , 276, 9093-100	5.4	72
195	Motions of calmodulin characterized using both Bragg and diffuse X-ray scattering. <i>Structure</i> , 1997 , 5, 1599-612	5.2	71
194	Molecular mechanisms of calcium and magnesium binding to parvalbumin. <i>Biophysical Journal</i> , 2002 , 82, 1133-46	2.9	71
193	Structure and dynamics of the water around myoglobin. <i>Protein Science</i> , 1995 , 4, 149-58	6.3	70
192	Roles of static and dynamic domains in stability and catalysis of adenylate kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 2132-7	11.5	70
191	Metal-ion affinity and specificity in EF-hand proteins: coordination geometry and domain plasticity in parvalbumin. <i>Structure</i> , 1999 , 7, 1269-78	5.2	69
190	Application of elastic network models to proteins in the crystalline state. <i>Biophysical Journal</i> , 2009 , 96, 464-75	2.9	68

189	Structure of tropomyosin at 9 angstroms resolution. <i>Journal of Molecular Biology</i> , 1992 , 227, 441-52	6.5	67
188	Structural analysis of fish versus mammalian hemoglobins: effect of the heme pocket environment on autooxidation and hemin loss. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 75, 217-30	4.2	66
187	High-throughput purification and quality assurance of <i>Arabidopsis thaliana</i> proteins for eukaryotic structural genomics. <i>Journal of Structural and Functional Genomics</i> , 2005 , 6, 143-7		65
186	Automatic domain decomposition of proteins by a Gaussian Network Model. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 57, 725-33	4.2	62
185	Structure of aspartoacylase, the brain enzyme impaired in Canavan disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 456-61	11.5	60
184	A double mutant of sperm whale myoglobin mimics the structure and function of elephant myoglobin. <i>Journal of Biological Chemistry</i> , 1995 , 270, 20763-74	5.4	60
183	Evolution of substrate specificity in bacterial AA10 lytic polysaccharide monooxygenases. <i>Biotechnology for Biofuels</i> , 2014 , 7, 109	7.8	59
182	Biophysical and kinetic characterization of HemAT, an aerotaxis receptor from <i>Bacillus subtilis</i> . <i>Biophysical Journal</i> , 2005 , 88, 2801-14	2.9	59
181	Adaptive evolution of threonine deaminase in plant defense against insect herbivores. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 5897-902	11.5	57
180	Structures of thermophilic and mesophilic adenylate kinases from the genus <i>Methanococcus</i> . <i>Journal of Molecular Biology</i> , 2003 , 330, 1087-99	6.5	56
179	Biochemical characterization and crystal structures of a fungal family 3 β -glucosidase, Cel3A from <i>Hypocrea jecorina</i> . <i>Journal of Biological Chemistry</i> , 2014 , 289, 31624-37	5.4	54
178	Identifying and engineering ion pairs in adenylate kinases. Insights from molecular dynamics simulations of thermophilic and mesophilic homologues. <i>Journal of Biological Chemistry</i> , 2005 , 280, 30943-8	5.4	53
177	Structures of two <i>Arabidopsis thaliana</i> major latex proteins represent novel helix-grip folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 76, 237-43	4.2	52
176	Comparison of cell-based and cell-free protocols for producing target proteins from the <i>Arabidopsis thaliana</i> genome for structural studies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 59, 633-43	4.2	52
175	Time-dependent atomic coordinates for the dissociation of carbon monoxide from myoglobin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 776-83		50
174	Construction of an atomic model for tropomyosin and implications for interactions with actin. <i>Journal of Molecular Biology</i> , 1986 , 192, 128-31	6.5	49
173	Comparison of apo- and heme-bound crystal structures of a truncated human heme oxygenase-2. <i>Journal of Biological Chemistry</i> , 2007 , 282, 37624-31	5.4	48
172	Bis-methionyl coordination in the crystal structure of the heme-binding domain of the streptococcal cell surface protein Shp. <i>Journal of Molecular Biology</i> , 2007 , 374, 374-83	6.5	48

171	Biochemical and structural insights of the early glycosylation steps in calicheamicin biosynthesis. <i>Chemistry and Biology</i> , 2008 , 15, 842-53		47
170	Structure and mechanism of the rebeccamycin sugar 4QO-methyltransferase RebM. <i>Journal of Biological Chemistry</i> , 2008 , 283, 22628-36	5.4	46
169	High resolution crystal structures of the deoxy, oxy, and aquomet forms of cobalt myoglobin. <i>Journal of Biological Chemistry</i> , 1996 , 271, 25419-22	5.4	46
168	Complete set of glycosyltransferase structures in the calicheamicin biosynthetic pathway reveals the origin of regiospecificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 17649-54	11.5	44
167	Generation of Size-Controlled, Submicrometer Protein Crystals. <i>Chemistry of Materials</i> , 2005 , 17, 2679-2686	6.6	44
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165	The structure and NO binding properties of the nitrophorin-like heme-binding protein from <i>Arabidopsis thaliana</i> gene locus At1g79260.1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 917-31	4.2	41
164	Solution and crystal structures of a sperm whale myoglobin triple mutant that mimics the sulfide-binding hemoglobin from <i>Lucina pectinata</i> . <i>Journal of Biological Chemistry</i> , 1998 , 273, 9517-26	5.4	39
163	Structural and evolutionary relationships of "AT-less" type I polyketide synthase ketosynthases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 12693-8	11.5	38
162	Characterizing global substates of myoglobin. <i>Structure</i> , 1998 , 6, 587-94	5.2	38
161	Asymmetric sulfoxidation and amine binding by H64D/V68A and H64D/V68S Mb: mechanistic insight into the chiral discrimination step. <i>Journal of the American Chemical Society</i> , 2002 , 124, 8506-7	16.4	38
160	X-ray structure of ILL2, an auxin-conjugate amidohydrolase from <i>Arabidopsis thaliana</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 74, 61-71	4.2	37
159	Structure and dynamics of UDP-glucose pyrophosphorylase from <i>Arabidopsis thaliana</i> with bound UDP-glucose and UTP. <i>Journal of Molecular Biology</i> , 2007 , 366, 830-41	6.5	37
158	Structure of an ETHE1-like protein from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 964-70		37
157	The structure of fibrinogen and fibrin: II. Architecture of the fibrin clot. <i>Annals of the New York Academy of Sciences</i> , 1983 , 408, 367-79	6.5	37
156	A tRNA splicing operon: Archease endows RtcB with dual GTP/ATP cofactor specificity and accelerates RNA ligation. <i>Nucleic Acids Research</i> , 2014 , 42, 3931-42	20.1	36
155	Bioinformatic method for protein thermal stabilization by structural entropy optimization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 9594-7	11.5	36
154	Bis-methionine ligation to heme iron in the streptococcal cell surface protein Shp facilitates rapid hemin transfer to HtsA of the HtsABC transporter. <i>Journal of Biological Chemistry</i> , 2007 , 282, 31380-8	5.4	36

153	Sampling of the native conformational ensemble of myoglobin via structures in different crystalline environments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 70, 353-62	4.2	35
152	Structure and interactions of the first three RNA recognition motifs of splicing factor prp24. <i>Journal of Molecular Biology</i> , 2007 , 367, 1447-58	6.5	34
151	Mechanical properties of tropomyosin and implications for muscle regulation 1996 , 38, 89-95		34
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149	Structural basis for catalysis by onconase. <i>Journal of Molecular Biology</i> , 2008 , 375, 165-77	6.5	33
148	What is the pitch of the alpha-helical coiled coil?. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992 , 14, 425-9	4.2	33
147	Structure and specificity of a permissive bacterial C-prenyltransferase. <i>Nature Chemical Biology</i> , 2017 , 13, 366-368	11.7	32
146	Structural characterization of human Uch37. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 649-54	4.2	32
145	Structures of the noncanonical RNA ligase RtcB reveal the mechanism of histidine guanylylation. <i>Biochemistry</i> , 2013 , 52, 2518-25	3.2	32
144	The crystal structure of BlmI as a model for nonribosomal peptide synthetase peptidyl carrier proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 1210-8	4.2	31
143	Expanding the nucleotide and sugar 1-phosphate promiscuity of nucleotidyltransferase RmlA via directed evolution. <i>Journal of Biological Chemistry</i> , 2011 , 286, 13235-43	5.4	31
142	The structure of fibrinogen and fibrin: I. Electron microscopy and X-ray crystallography of fibrinogen. <i>Annals of the New York Academy of Sciences</i> , 1983 , 408, 194-213	6.5	31
141	Reader domain specificity and lysine demethylase-4 family function. <i>Nature Communications</i> , 2016 , 7, 13387	17.4	30
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139	Structure, dynamics, and specificity of endoglucanase D from <i>Clostridium cellulovorans</i> . <i>Journal of Molecular Biology</i> , 2013 , 425, 4267-85	6.5	30
138	Evaluating elastic network models of crystalline biological molecules with temperature factors, correlated motions, and diffuse x-ray scattering. <i>Biophysical Journal</i> , 2010 , 99, 2616-25	2.9	30
137	Multi-scale surface descriptors. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2009 , 15, 1201-8		30
136	Crystal structure of ADP/AMP complex of <i>Escherichia coli</i> adenylate kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 62, 555-6	4.2	30

135	Molecular engineering of myoglobin: influence of residue 68 on the rate and the enantioselectivity of oxidation reactions catalyzed by H64D/V68X myoglobin. <i>Biochemistry</i> , 2003 , 42, 10174-81	3.2	29
134	Assignment of the nucleotide binding sites and the mechanism of substrate inhibition of <i>Escherichia coli</i> adenylate kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991 , 9, 28-36	4.2	29
133	Structure of the ent-Copalyl Diphosphate Synthase PtmT2 from <i>Streptomyces platensis</i> CB00739, a Bacterial Type II Diterpene Synthase. <i>Journal of the American Chemical Society</i> , 2016 , 138, 10905-15	16.4	29
132	Structural Basis of Stereospecificity in the Bacterial Enzymatic Cleavage of β Aryl Ether Bonds in Lignin. <i>Journal of Biological Chemistry</i> , 2016 , 291, 5234-46	5.4	27
131	Structure and substrate specificity of a eukaryotic fucosidase from <i>Fusarium graminearum</i> . <i>Journal of Biological Chemistry</i> , 2014 , 289, 25624-38	5.4	27
130	Small-scale, semi-automated purification of eukaryotic proteins for structure determination. <i>Journal of Structural and Functional Genomics</i> , 2007 , 8, 153-66		27
129	Motions of tropomyosin: characterization of anisotropic motions and coupled displacements in crystals. <i>Biophysical Journal</i> , 1986 , 49, 76-8	2.9	27
128	Functional AdoMet Isosteres Resistant to Classical AdoMet Degradation Pathways. <i>ACS Chemical Biology</i> , 2016 , 11, 2484-91	4.9	27
127	Large-scale motions in the adenylate kinase solution ensemble: coarse-grained simulations and comparison with solution X-ray scattering. <i>Chemical Physics</i> , 2012 , 396, 84-91	2.3	26
126	Creating protein models from electron-density maps using particle-filtering methods. <i>Bioinformatics</i> , 2007 , 23, 2851-8	7.2	26
125	Pro-metastatic collagen lysyl hydroxylase dimer assemblies stabilized by Fe-binding. <i>Nature Communications</i> , 2018 , 9, 512	17.4	25
124	Functional evolution of ribonuclease inhibitor: insights from birds and reptiles. <i>Journal of Molecular Biology</i> , 2014 , 426, 3041-56	6.5	25
123	The Center for Eukaryotic Structural Genomics. <i>Journal of Structural and Functional Genomics</i> , 2009 , 10, 165-79		25
122	Structure and mechanism of an ADP-glucose phosphorylase from <i>Arabidopsis thaliana</i> . <i>Biochemistry</i> , 2006 , 45, 3154-62	3.2	25
121	Membrane association, mechanism of action, and structure of <i>Arabidopsis</i> embryonic factor 1 (FAC1). <i>Journal of Biological Chemistry</i> , 2006 , 281, 14939-47	5.4	24
120	Study of global motions in proteins by weighted masses molecular dynamics: Adenylate kinase as a test case. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 25, 79-88	4.2	24
119	Crystal structure of SsfS6, the putative C-glycosyltransferase involved in SF2575 biosynthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 1277-82	4.2	23
118	Structure of pyrimidine 5'Nucleotidase type 1. Insight into mechanism of action and inhibition during lead poisoning. <i>Journal of Biological Chemistry</i> , 2006 , 281, 20521-9	5.4	23

117	Structural characterization of CalO2: a putative orsellinic acid P450 oxidase in the calicheamicin biosynthetic pathway. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 74, 50-60	4.2	22
116	Analysis of diffuse scattering and relation to molecular motion. <i>Methods in Enzymology</i> , 1997 , 277, 407-327		22
115	Structure of the bifunctional acyltransferase/decarboxylase LnmK from the leinamycin biosynthetic pathway revealing novel activity for a double-hot-dog fold. <i>Biochemistry</i> , 2013 , 52, 902-11	3.2	21
114	Structure-guided functional characterization of enediyne self-sacrifice resistance proteins, CalU16 and CalU19. <i>ACS Chemical Biology</i> , 2014 , 9, 2347-58	4.9	20
113	Structure of cellobiose phosphorylase from <i>Clostridium thermocellum</i> in complex with phosphate. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 1345-9		20
112	Structure of the C-terminal heme-binding domain of THAP domain containing protein 4 from <i>Homo sapiens</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 1337-41	4.2	20
111	Apoglobin Stability Is the Major Factor Governing both Cell-free and in Vivo Expression of Holomyoglobin. <i>Journal of Biological Chemistry</i> , 2015 , 290, 23479-95	5.4	19
110	Structural characterization of the mitomycin 7-O-methyltransferase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 2181-8	4.2	19
109	SOMoRe: a multi-dimensional search and optimization approach to molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 304-14		19
108	Conformational variation of calcium-bound troponin C. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 37, 510-1	4.2	19
107	Straight-chain alkyl isocyanides open the distal histidine gate in crystal structures of myoglobin. <i>Biochemistry</i> , 2010 , 49, 4977-86	3.2	18
106	Interconversion of functional motions between mesophilic and thermophilic adenylate kinases. <i>PLoS Computational Biology</i> , 2011 , 7, e1002103	5	18
105	Structure of T4moC, the Rieske-type ferredoxin component of toluene 4-monooxygenase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 476-82		18
104	X-ray structure of Arabidopsis At2g06050, 12-oxophytodienoate reductase isoform 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 58, 243-5	4.2	18
103	X-ray structure of Danio rerio secretagoin: A hexa-EF-hand calcium sensor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 76, 477-83	4.2	17
102	Crystal structure of Arabidopsis thaliana cytokinin dehydrogenase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 70, 303-6	4.2	17
101	A probabilistic approach to protein backbone tracing in electron density maps. <i>Bioinformatics</i> , 2006 , 22, e81-9	7.2	17
100	Kinetic proofreading by the cavity system of myoglobin: protection from poisoning. <i>BioEssays</i> , 2004 , 26, 422-33	4.1	17

99	Automated Illustration of Molecular Flexibility. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2012 , 18, 132-45	4	16
98	Crystallographic analysis of active site contributions to regiospecificity in the diiron enzyme toluene 4-monooxygenase. <i>Biochemistry</i> , 2012 , 51, 1101-13	3.2	16
97	Stabilization of myoglobin by multiple alanine substitutions in helical positions. <i>Protein Science</i> , 1994 , 3, 1430-5	6.3	16
96	Crystal Structures of SgcE6 and SgcC, the Two-Component Monooxygenase That Catalyzes Hydroxylation of a Carrier Protein-Tethered Substrate during the Biosynthesis of the Eneidyne Antitumor Antibiotic C-1027 in <i>Streptomyces globisporus</i> . <i>Biochemistry</i> , 2016 , 55, 5142-54	3.2	15
95	Natural separation of the acyl-CoA ligase reaction results in a non-adenylating enzyme. <i>Nature Chemical Biology</i> , 2018 , 14, 730-737	11.7	15
94	Structural characterization of CalO1: a putative orsellinic acid methyltransferase in the calicheamicin-biosynthetic pathway. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011 , 67, 197-203		15
93	Mechanism of Human Apohemoglobin Unfolding. <i>Biochemistry</i> , 2017 , 56, 1444-1459	3.2	14
92	Resistance to Eneidyne Antitumor Antibiotics by Sequestration. <i>Cell Chemical Biology</i> , 2018 , 25, 1075-1085.e4		14
91	Characterization and Crystal Structure of a Nonheme Diiron Monooxygenase Involved in Platensimycin and Platencin Biosynthesis. <i>Journal of the American Chemical Society</i> , 2019 , 141, 12406-12412	16.4	14
90	Crystal structure of At2g03760, a putative steroid sulfotransferase from <i>Arabidopsis thaliana</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 57, 854-7	4.2	14
89	Biochemical and Structural Characterization of TtnD, a Prenylated FMN-Dependent Decarboxylase from the Tautomycetin Biosynthetic Pathway. <i>ACS Chemical Biology</i> , 2018 , 13, 2728-2738	4.9	14
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