

# George N Phillips Jr

## List of Publications by Year in descending order

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243  
papers

14,890  
citations

17405

63  
h-index

22764

112  
g-index

252  
all docs

252  
docs citations

252  
times ranked

14743  
citing authors

#	ARTICLE	IF	CITATIONS
1	The molecular structure of green fluorescent protein. <i>Nature Biotechnology</i> , 1996, 14, 1246-1251.	9.4	1,407
2	Watching a Protein as it Functions with 150-ps Time-Resolved X-ray Crystallography. <i>Science</i> , 2003, 300, 1944-1947.	6.0	726
3	Mechanism of NO-Induced Oxidation of Myoglobin and Hemoglobin. <i>Biochemistry</i> , 1996, 35, 6976-6983.	1.2	625
4	High-Resolution Crystal Structures of Distal Histidine Mutants of Sperm Whale Myoglobin. <i>Journal of Molecular Biology</i> , 1993, 234, 140-155.	2.0	390
5	Crystal structure of photolysed carbonmonoxy-myoglobin. <i>Nature</i> , 1994, 371, 808-812.	13.7	354
6	Structural Determinants of the Stretching Frequency of CO Bound to Myoglobin. <i>Biochemistry</i> , 1994, 33, 1433-1446.	1.2	341
7	Restructuring the Crystalline Cellulose Hydrogen Bond Network Enhances Its Depolymerization Rate. <i>Journal of the American Chemical Society</i> , 2011, 133, 11163-11174.	6.6	321
8	Myoglobin discriminates between O <sub>2</sub> , NO, and CO by electrostatic interactions with the bound ligand. <i>Journal of Biological Inorganic Chemistry</i> , 1997, 2, 544-552.	1.1	265
9	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.	1.2	250
10	Kinetic Pathways and Barriers for Ligand Binding to Myoglobin. <i>Journal of Biological Chemistry</i> , 1996, 271, 17593-17596.	1.6	240
11	Dynamics of Proteins in Crystals: Comparison of Experiment with Simple Models. <i>Biophysical Journal</i> , 2002, 83, 723-732.	0.2	240
12	Molecular Structure of Dihydroorotase: A Paradigm for Catalysis through the Use of a Binuclear Metal Center. <i>Biochemistry</i> , 2001, 40, 6989-6997.	1.2	189
13	Genomic basis for the convergent evolution of electric organs. <i>Science</i> , 2014, 344, 1522-1525.	6.0	181
14	Structures and Analysis of Highly Homologous Psychrophilic, Mesophilic, and Thermophilic Adenylate Kinases. <i>Journal of Biological Chemistry</i> , 2004, 279, 28202-28208.	1.6	178
15	Structure and mechanism of mouse cysteine dioxygenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 3084-3089.	3.3	174
16	Crystal structure of tropomyosin at 7 1/2 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 38, 49-59.	1.5	164
17	Crystal structure of a nonsymbiotic plant hemoglobin. <i>Structure</i> , 2000, 8, 1005-1014.	1.6	164
18	Ensemble Refinement of Protein Crystal Structures: Validation and Application. <i>Structure</i> , 2007, 15, 1040-1052.	1.6	164

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19	Effects of the Location of Distal Histidine in the Reaction of Myoglobin with Hydrogen Peroxide. <i>Journal of Biological Chemistry</i> , 1999, 274, 2838-2844.	1.6	162
20	Structure and dynamics of green fluorescent protein. <i>Current Opinion in Structural Biology</i> , 1997, 7, 821-827.	2.6	161
21	Drop-on-demand sample delivery for studying biocatalysts in action at X-ray free-electron lasers. <i>Nature Methods</i> , 2017, 14, 443-449.	9.0	150
22	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, 4453-4458.	3.3	147
23	Probing Substates in Sperm Whale Myoglobin Using High-Pressure Crystallography. <i>Structure</i> , 2002, 10, 51-60.	1.6	143
24	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, 183-198.	1.5	139
25	Glycosyltransferase structural biology and its role in the design of catalysts for glycosylation. <i>Current Opinion in Biotechnology</i> , 2011, 22, 800-808.	3.3	136
26	Characterization of recombinant soybean leghemoglobin a and apolar distal histidine mutants. <i>Journal of Molecular Biology</i> , 1997, 266, 1032-1042.	2.0	133
27	Inhibition of Human Pancreatic Ribonuclease by the Human Ribonuclease Inhibitor Protein. <i>Journal of Molecular Biology</i> , 2007, 368, 434-449.	2.0	130
28	Structure of myoglobin-ethyl isocyanide histidine as a swinging door for ligand entry. <i>Journal of Molecular Biology</i> , 1989, 207, 459-463.	2.0	127
29	Enzyme intermediates captured on the fly by mix-and-inject serial crystallography. <i>BMC Biology</i> , 2018, 16, 59.	1.7	117
30	Crystal structure of myoglobin from a synthetic gene. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 7, 358-365.	1.5	113
31	Structure of the Oxygen Sensor in <i>Bacillus subtilis</i> . <i>Structure</i> , 2003, 11, 1097-1110.	1.6	113
32	Nitric oxide myoglobin: Crystal structure and analysis of ligand geometry. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 30, 352-356.	1.5	111
33	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, 256-267.	0.6	104
34	Structural basis for selective activation of ABA receptors. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1109-1113.	3.6	104
35	A model from electron microscopy for the molecular structure of fibrinogen and fibrin. <i>Nature</i> , 1981, 289, 263-267.	13.7	100
36	Crystal structures of <i>Bacillus stearothermophilus</i> adenylate kinase with bound Ap5A, Mg <sup>2+</sup> Ap5A, and Mn <sup>2+</sup> Ap5A reveal an intermediate lid position and six coordinate octahedral geometry for bound Mg <sup>2+</sup> and Mn <sup>2+</sup> . , 1998, 32, 276-288.		99

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37	Optimization and Evaluation of a Coarse-Grained Model of Protein Motion Using X-Ray Crystal Data. <i>Biophysical Journal</i> , 2006, 91, 2760-2767.	0.2	99
38	The structural biology of enzymes involved in natural product glycosylation. <i>Natural Product Reports</i> , 2012, 29, 1201.	5.2	99
39	Motions of calmodulin characterized using both Bragg and diffuse X-ray scattering. <i>Structure</i> , 1997, 5, 1599-1612.	1.6	95
40	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, 19194-19198.	3.3	92
41	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.	1.6	92
42	Structural enzymology using X-ray free electron lasers. <i>Structural Dynamics</i> , 2017, 4, 044003.	0.9	92
43	Understanding Protein Flexibility through Dimensionality Reduction. <i>Journal of Computational Biology</i> , 2003, 10, 617-634.	0.8	91
44	Protein Structural Variation in Computational Models and Crystallographic Data. <i>Structure</i> , 2007, 15, 169-177.	1.6	90
45	Metal-ion affinity and specificity in EF-hand proteins: coordination geometry and domain plasticity in parvalbumin. <i>Structure</i> , 1999, 7, 1269-1278.	1.6	88
46	Project management system for structural and functional proteomics: Sesame. <i>Journal of Structural and Functional Genomics</i> , 2003, 4, 11-23.	1.2	88
47	Molecular Mechanisms of Calcium and Magnesium Binding to Parvalbumin. <i>Biophysical Journal</i> , 2002, 82, 1133-1146.	0.2	85
48	Many Local Motions Cooperate to Produce the Adenylate Kinase Conformational Transition. <i>Journal of Molecular Biology</i> , 2010, 400, 618-631.	2.0	85
49	Waterproofing the Heme Pocket. <i>Journal of Biological Chemistry</i> , 2001, 276, 9093-9100.	1.6	84
50	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, 217-230.	1.5	79
51	Perturbation of the Fe <sup>2+</sup> -O <sub>2</sub> Bond by Nearby Residues in Heme Pocket: Observation of $\nu_{1/2}$ Fe-O <sub>2</sub> Raman Bands for Oxy-myoglobin Mutants. <i>Journal of the American Chemical Society</i> , 1996, 118, 7845-7846.	6.6	78
52	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, 2132-2137.	3.3	78
53	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, 5897-5902.	3.3	75
54	Application of Elastic Network Models to Proteins in the Crystalline State. <i>Biophysical Journal</i> , 2009, 96, 464-475.	0.2	74

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55	Structure and dynamics of the water around myoglobin. <i>Protein Science</i> , 1995, 4, 149-158.	3.1	73
56	Automatic domain decomposition of proteins by a Gaussian Network Model. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 725-733.	1.5	71
57	Structure of tropomyosin at 9 Å...ngstroms resolution. <i>Journal of Molecular Biology</i> , 1992, 227, 441-452.	2.0	69
58	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, 456-461.	3.3	69
59	Evolution of substrate specificity in bacterial AA10 lytic polysaccharide monooxygenases. <i>Biotechnology for Biofuels</i> , 2014, 7, 109.	6.2	69
60	Structures of two <i>Arabidopsis thaliana</i> major latex proteins represent novel helix-grip folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 237-243.	1.5	68
61	Biochemical Characterization and Crystal Structures of a Fungal Family 3 $\beta$ -Glucosidase, Cel3A from <i>Hypocrea jecorina</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 31624-31637.	1.6	68
62	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, 143-147.	1.2	67
63	Biophysical and Kinetic Characterization of HemAT, an Aerotaxis Receptor from <i>Bacillus subtilis</i> . <i>Biophysical Journal</i> , 2005, 88, 2801-2814.	0.2	67
64	A Double Mutant of Sperm Whale Myoglobin Mimics the Structure and Function of Elephant Myoglobin. <i>Journal of Biological Chemistry</i> , 1995, 270, 20763-20774.	1.6	64
65	Structures of Thermophilic and Mesophilic Adenylate Kinases from the Genus <i>Methanococcus</i> . <i>Journal of Molecular Biology</i> , 2003, 330, 1087-1099.	2.0	58
66	Identifying and Engineering Ion Pairs in Adenylate Kinases. <i>Journal of Biological Chemistry</i> , 2005, 280, 30943-30948.	1.6	58
67	High Resolution Crystal Structures of the Deoxy, Oxy, and Aquomet Forms of Cobalt Myoglobin. <i>Journal of Biological Chemistry</i> , 1996, 271, 25419-25422.	1.6	57
68	Structure and Mechanism of the Rebeccamycin Sugar 4-O-Methyltransferase RebM. <i>Journal of Biological Chemistry</i> , 2008, 283, 22628-22636.	1.6	57
69	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, 633-643.	1.5	56
70	Comparison of Apo- and Heme-bound Crystal Structures of a Truncated Human Heme Oxygenase-2. <i>Journal of Biological Chemistry</i> , 2007, 282, 37624-37631.	1.6	56
71	Structures of the Noncanonical RNA Ligase RtcB Reveal the Mechanism of Histidine Guanylylation. <i>Biochemistry</i> , 2013, 52, 2518-2525.	1.2	56
72	Functional Evolution of Ribonuclease Inhibitor: Insights from Birds and Reptiles. <i>Journal of Molecular Biology</i> , 2014, 426, 3041-3056.	2.0	56

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73	Structural and evolutionary relationships of $\alpha$ -AT-less type I polyketide synthase ketosynthases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12693-12698.	3.3	55
74	Construction of an atomic model for tropomyosin and implications for interactions with actin. <i>Journal of Molecular Biology</i> , 1986, 192, 128-131.	2.0	53
75	Time-dependent atomic coordinates for the dissociation of carbon monoxide from myoglobin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 776-783.	2.5	53
76	Biochemical and Structural Insights of the Early Glycosylation Steps in Calicheamicin Biosynthesis. <i>Chemistry and Biology</i> , 2008, 15, 842-853.	6.2	51
77	Structural Basis for Catalysis by Onconase. <i>Journal of Molecular Biology</i> , 2008, 375, 165-177.	2.0	51
78	A tRNA splicing operon: Archease endows RtcB with dual GTP/ATP cofactor specificity and accelerates RNA ligation. <i>Nucleic Acids Research</i> , 2014, 42, 3931-3942.	6.5	50
79	Structure of the <i>ent</i> -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, 10905-10915.	6.6	50
80	Structure and specificity of a permissive bacterial C-prenyltransferase. <i>Nature Chemical Biology</i> , 2017, 13, 366-368.	3.9	50
81	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, 374-383.	2.0	49
82	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, 917-931.	1.5	49
83	Generation of Size-Controlled, Submicrometer Protein Crystals. <i>Chemistry of Materials</i> , 2005, 17, 2679-2686.	3.2	48
84	Phe-46(CD4) orients the distal histidine for hydrogen bonding to bound ligands in sperm whale myoglobin. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 322-339.	1.5	47
85	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, 17649-17654.	3.3	47
86	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, 9517-9526.	1.6	45
87	Sampling of the native conformational ensemble of myoglobin via structures in different crystalline environments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 353-362.	1.5	45
88	Reader domain specificity and lysine demethylase-4 family function. <i>Nature Communications</i> , 2016, 7, 13387.	5.8	45
89	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, 830-841.	2.0	43
90	THE STRUCTURE OF FIBRINOGEN AND FIBRIN: II. ARCHITECTURE OF THE FIBRIN CLOT. <i>Annals of the New York Academy of Sciences</i> , 1983, 408, 367-379.	1.8	42

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91	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.	1.5	42
92	Structure, Dynamics, and Specificity of Endoglucanase D from <i>Clostridium cellulovorans</i> . <i>Journal of Molecular Biology</i> , 2013, 425, 4267-4285.	2.0	41
93	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, 8506-8507.	6.6	40
94	Structure of an ETHE1-like protein from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 964-970.	2.5	40
95	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, 9594-9597.	3.3	40
96	Structural Basis of Stereospecificity in the Bacterial Enzymatic Cleavage of $\hat{I}^2$ -Aryl Ether Bonds in Lignin. <i>Journal of Biological Chemistry</i> , 2016, 291, 5234-5246.	1.6	40
97	Characterizing global substates of myoglobin. <i>Structure</i> , 1998, 6, 587-594.	1.6	39
98	What is the pitch of the $\hat{I}^{\pm}$ -helical coiled coil?. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 14, 425-429.	1.5	38
99	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, 31380-31388.	1.6	38
100	Structure of Human J-type Co-chaperone HscB Reveals a Tetracysteine Metal-binding Domain. <i>Journal of Biological Chemistry</i> , 2008, 283, 30184-30192.	1.6	38
101	Evaluating Elastic Network Models of Crystalline Biological Molecules with Temperature Factors, Correlated Motions, and Diffuse X-Ray Scattering. <i>Biophysical Journal</i> , 2010, 99, 2616-2625.	0.2	38
102	Mechanical properties of tropomyosin and implications for muscle regulation. , 1996, 38, 89-95.		37
103	Multi-Scale Surface Descriptors. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2009, 15, 1201-1208.	2.9	37
104	Expanding the Nucleotide and Sugar 1-Phosphate Promiscuity of Nucleotidyltransferase RmlA via Directed Evolution. <i>Journal of Biological Chemistry</i> , 2011, 286, 13235-13243.	1.6	37
105	Structure and Interactions of the First Three RNA Recognition Motifs of Splicing Factor Prp24. <i>Journal of Molecular Biology</i> , 2007, 367, 1447-1458.	2.0	36
106	Understanding molecular recognition of promiscuity of thermophilic methionine adenosyltransferase s<sc>MAT</sc> from <i>Sulfolobus solfataricus</i> . <i>FEBS Journal</i> , 2014, 281, 4224-4239.	2.2	36
107	Functional AdoMet Isosteres Resistant to Classical AdoMet Degradation Pathways. <i>ACS Chemical Biology</i> , 2016, 11, 2484-2491.	1.6	36
108	Crystal structure of ADP/AMP complex of <i>Escherichia coli</i> adenylate kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 555-556.	1.5	35

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109	Structural characterization of human Uch37. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 649-654.	1.5	34
110	Pro-metastatic collagen lysyl hydroxylase dimer assemblies stabilized by Fe <sup>2+</sup> -binding. <i>Nature Communications</i> , 2018, 9, 512.	5.8	34
111	Moving beyond static snapshots: Protein dynamics and the Protein Data Bank. <i>Journal of Biological Chemistry</i> , 2021, 296, 100749.	1.6	34
112	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.	1.5	33
113	The Center for Eukaryotic Structural Genomics. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 165-179.	1.2	33
114	The crystal structure of BlmI as a model for nonribosomal peptide synthetase peptidyl carrier proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1210-1218.	1.5	33
115	Structure and Substrate Specificity of a Eukaryotic Fucosidase from <i>Fusarium graminearum</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 25624-25638.	1.6	33
116	Creating protein models from electron-density maps using particle-filtering methods. <i>Bioinformatics</i> , 2007, 23, 2851-2858.	1.8	32
117	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.	0.9	32
118	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.	1.8	31
119	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, 10174-10181.	1.2	31
120	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, 902-911.	1.2	31
121	[21] Analysis of diffuse scattering and relation to molecular motion. <i>Methods in Enzymology</i> , 1997, 277, 407-432.	0.4	30
122	Apoglobin Stability Is the Major Factor Governing both Cell-free and in Vivo Expression of Holomyoglobin. <i>Journal of Biological Chemistry</i> , 2015, 290, 23479-23495.	1.6	30
123	Membrane Association, Mechanism of Action, and Structure of Arabidopsis Embryonic Factor 1 (FAC1). <i>Journal of Biological Chemistry</i> , 2006, 281, 14939-14947.	1.6	29
124	Unique patterns of transcript and miRNA expression in the South American strong voltage electric eel ( <i>Electrophorus electricus</i> ). <i>BMC Genomics</i> , 2015, 16, 243.	1.2	29
125	Motions of Tropomyosin. <i>Biophysical Journal</i> , 1986, 49, 76-78.	0.2	28
126	Structure and Mechanism of an ADP-Glucose Phosphorylase from <i>Arabidopsis thaliana</i> . <i>Biochemistry</i> , 2006, 45, 3154-3162.	1.2	28



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127	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, 1337-1341.	1.5	28
128	Small-scale, semi-automated purification of eukaryotic proteins for structure determination. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 153-166.	1.2	27
129	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.	1.5	27
130	Structural characterization of the mitomycin 7-O-methyltransferase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2181-2188.	1.5	26
131	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.	1.5	26
132	Conformational variation of calcium-bound troponin C. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 510-511.	1.5	25
133	Structure of Pyrimidine 5'-Nucleotidase Type 1. <i>Journal of Biological Chemistry</i> , 2006, 281, 20521-20529.	1.6	25
134	Structure of cellobiose phosphorylase from <i>Clostridium thermocellum</i> in complex with phosphate. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1345-1349.	0.7	25
135	Crystal structure of SsfS6, the putative C-glycosyltransferase involved in SF2575 biosynthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1277-1282.	1.5	24
136	Structure-Guided Functional Characterization of Eneidyne Self-Sacrifice Resistance Proteins, CalU16 and CalU19. <i>ACS Chemical Biology</i> , 2014, 9, 2347-2358.	1.6	24
137	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.	6.6	23
138	X-ray structure of <i>Danio rerio</i> secretagogin: A hexameric hand calcium sensor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 477-483.	1.5	22
139	X-ray structure of Arabidopsis At2g06050, 12-oxophytodienoate reductase isoform 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 243-245.	1.5	21
140	Automated Illustration of Molecular Flexibility. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2012, 18, 132-145.	2.9	21
141	Resistance to Eneidyne Antitumor Antibiotics by Sequestration. <i>Cell Chemical Biology</i> , 2018, 25, 1075-1085.e4.	2.5	21
142	Natural separation of the acyl-CoA ligase reaction results in a non-adenylating enzyme. <i>Nature Chemical Biology</i> , 2018, 14, 730-737.	3.9	21
143	SOMoRe: a multi-dimensional search and optimization approach to molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 304-314.	2.5	20
144	A probabilistic approach to protein backbone tracing in electron density maps. <i>Bioinformatics</i> , 2006, 22, e81-e89.	1.8	20

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145	Crystal structure of <i>Arabidopsis thaliana</i> cytokinin dehydrogenase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 303-306.	1.5	20
146	Methionine Adenosyltransferase Engineering to Enable Bioorthogonal Platforms for AdoMet-Utilizing Enzymes. <i>ACS Chemical Biology</i> , 2020, 15, 695-705.	1.6	20
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