

George N Phillips Jr

List of Publications by Year in descending order

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243
papers

14,890
citations

17440

63
h-index

22166

113
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.	17.5	1,407
2	Watching a Protein as it Functions with 150-ps Time-Resolved X-ray Crystallography. <i>Science</i> , 2003, 300, 1944-1947.	12.6	726
3	Mechanism of NO-Induced Oxidation of Myoglobin and Hemoglobin. <i>Biochemistry</i> , 1996, 35, 6976-6983.	2.5	625
4	High-Resolution Crystal Structures of Distal Histidine Mutants of Sperm Whale Myoglobin. <i>Journal of Molecular Biology</i> , 1993, 234, 140-155.	4.2	390
5	Crystal structure of photolysed carbonmonoxy-myoglobin. <i>Nature</i> , 1994, 371, 808-812.	27.8	354
6	Structural Determinants of the Stretching Frequency of CO Bound to Myoglobin. <i>Biochemistry</i> , 1994, 33, 1433-1446.	2.5	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.	13.7	321
8	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.	2.6	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.	2.6	250
10	Kinetic Pathways and Barriers for Ligand Binding to Myoglobin. <i>Journal of Biological Chemistry</i> , 1996, 271, 17593-17596.	3.4	240
11	Dynamics of Proteins in Crystals: Comparison of Experiment with Simple Models. <i>Biophysical Journal</i> , 2002, 83, 723-732.	0.5	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.	2.5	189
13	Genomic basis for the convergent evolution of electric organs. <i>Science</i> , 2014, 344, 1522-1525.	12.6	181
14	Structures and Analysis of Highly Homologous Psychrophilic, Mesophilic, and Thermophilic Adenylate Kinases. <i>Journal of Biological Chemistry</i> , 2004, 279, 28202-28208.	3.4	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.	7.1	174
16	Crystal structure of tropomyosin at 7 1/2 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 38, 49-59.	2.6	164
17	Crystal structure of a nonsymbiotic plant hemoglobin. <i>Structure</i> , 2000, 8, 1005-1014.	3.3	164
18	Ensemble Refinement of Protein Crystal Structures: Validation and Application. <i>Structure</i> , 2007, 15, 1040-1052.	3.3	164

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19	Effects of the Location of Distal Histidine in the Reaction of Myoglobin with Hydrogen Peroxide. Journal of Biological Chemistry, 1999, 274, 2838-2844.	3.4	162
20	Structure and dynamics of green fluorescent protein. Current Opinion in Structural Biology, 1997, 7, 821-827.	5.7	161
21	Drop-on-demand sample delivery for studying biocatalysts in action at X-ray free-electron lasers. Nature Methods, 2017, 14, 443-449.	19.0	150
22	Identification of transcribed sequences in Arabidopsis thaliana by using high-resolution genome tiling arrays. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4453-4458.	7.1	147
23	Probing Substates in Sperm Whale Myoglobin Using High-Pressure Crystallography. Structure, 2002, 10, 51-60.	3.3	143
24	The closed conformation of a highly flexible protein: The structure of E. coli adenylate kinase with bound AMP and AMPPNP. Proteins: Structure, Function and Bioinformatics, 1994, 19, 183-198.	2.6	139
25	Glycosyltransferase structural biology and its role in the design of catalysts for glycosylation. Current Opinion in Biotechnology, 2011, 22, 800-808.	6.6	136
26	Characterization of recombinant soybean leghemoglobin a and apolar distal histidine mutants. Journal of Molecular Biology, 1997, 266, 1032-1042.	4.2	133
27	Inhibition of Human Pancreatic Ribonuclease by the Human Ribonuclease Inhibitor Protein. Journal of Molecular Biology, 2007, 368, 434-449.	4.2	130
28	Structure of myoglobin-ethyl isocyanide histidine as a swinging door for ligand entry. Journal of Molecular Biology, 1989, 207, 459-463.	4.2	127
29	Enzyme intermediates captured <i>in situ</i> by mix-and-inject serial crystallography. BMC Biology, 2018, 16, 59.	3.8	117
30	Crystal structure of myoglobin from a synthetic gene. Proteins: Structure, Function and Bioinformatics, 1990, 7, 358-365.	2.6	113
31	Structure of the Oxygen Sensor in Bacillus subtilis. Structure, 2003, 11, 1097-1110.	3.3	113
32	Nitric oxide myoglobin: Crystal structure and analysis of ligand geometry. Proteins: Structure, Function and Bioinformatics, 1998, 30, 352-356.	2.6	111
33	Protocols for production of selenomethionine-labeled proteins in 2-L polyethylene terephthalate bottles using auto-induction medium. Protein Expression and Purification, 2005, 40, 256-267.	1.3	104
34	Structural basis for selective activation of ABA receptors. Nature Structural and Molecular Biology, 2010, 17, 1109-1113.	8.2	104
35	A model from electron microscopy for the molecular structure of fibrinogen and fibrin. Nature, 1981, 289, 263-267.	27.8	100
36	Crystal structures of Bacillus stearothermophilus adenylate kinase with bound Ap5A, Mg2+ Ap5A, and Mn2+ Ap5A reveal an intermediate lid position and six coordinate octahedral geometry for bound Mg2+ and Mn2+. Proteins: Structure, Function and Bioinformatics, 1998, 32, 276-288.	2.6	99

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37	Optimization and Evaluation of a Coarse-Grained Model of Protein Motion Using X-Ray Crystal Data. Biophysical Journal, 2006, 91, 2760-2767.	0.5	99
38	The structural biology of enzymes involved in natural product glycosylation. Natural Product Reports, 2012, 29, 1201.	10.3	99
39	Motions of calmodulin characterized using both Bragg and diffuse X-ray scattering. Structure, 1997, 5, 1599-1612.	3.3	95
40	Structural consequences of effector protein complex formation in a diiron hydroxylase. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 19194-19198.	7.1	92
41	A Photo-Labile Thioether Linkage to Phycoviolobilin Provides the Foundation for the Blue/Green Photocycles in DXCF-Cyanobacteriochromes. Structure, 2013, 21, 88-97.	3.3	92
42	Structural enzymology using X-ray free electron lasers. Structural Dynamics, 2017, 4, 044003.	2.3	92
43	Understanding Protein Flexibility through Dimensionality Reduction. Journal of Computational Biology, 2003, 10, 617-634.	1.6	91
44	Protein Structural Variation in Computational Models and Crystallographic Data. Structure, 2007, 15, 169-177.	3.3	90
45	Metal-ion affinity and specificity in EF-hand proteins: coordination geometry and domain plasticity in parvalbumin. Structure, 1999, 7, 1269-1278.	3.3	88
46	Project management system for structural and functional proteomics: Sesame. Journal of Structural and Functional Genomics, 2003, 4, 11-23.	1.2	88
47	Molecular Mechanisms of Calcium and Magnesium Binding to Parvalbumin. Biophysical Journal, 2002, 82, 1133-1146.	0.5	85
48	Many Local Motions Cooperate to Produce the Adenylate Kinase Conformational Transition. Journal of Molecular Biology, 2010, 400, 618-631.	4.2	85
49	Waterproofing the Heme Pocket. Journal of Biological Chemistry, 2001, 276, 9093-9100.	3.4	84
50	Structural analysis of fish versus mammalian hemoglobins: Effect of the heme pocket environment on autooxidation and heme loss. Proteins: Structure, Function and Bioinformatics, 2009, 75, 217-230.	2.6	79
51	Perturbation of the Fe ²⁺ -O ₂ Bond by Nearby Residues in Heme Pocket: Observation of $\nu_{1/2}$ Fe-O ₂ Raman Bands for Oxy myoglobin Mutants. Journal of the American Chemical Society, 1996, 118, 7845-7846.	13.7	78
52	Roles of static and dynamic domains in stability and catalysis of adenylate kinase. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2132-2137.	7.1	78
53	Adaptive evolution of threonine deaminase in plant defense against insect herbivores. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5897-5902.	7.1	75
54	Application of Elastic Network Models to Proteins in the Crystalline State. Biophysical Journal, 2009, 96, 464-475.	0.5	74

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55	Structure and dynamics of the water around myoglobin. <i>Protein Science</i> , 1995, 4, 149-158.	7.6	73
56	Automatic domain decomposition of proteins by a Gaussian Network Model. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 725-733.	2.6	71
57	Structure of tropomyosin at 9 Å...ngstroms resolution. <i>Journal of Molecular Biology</i> , 1992, 227, 441-452.	4.2	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.	7.1	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.	2.6	68
61	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, 31624-31637.	3.4	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.	0.5	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.	3.4	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.	4.2	58
66	Identifying and Engineering Ion Pairs in Adenylate Kinases. <i>Journal of Biological Chemistry</i> , 2005, 280, 30943-30948.	3.4	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.	3.4	57
68	Structure and Mechanism of the Rebeccamycin Sugar 4'-O-Methyltransferase RebM. <i>Journal of Biological Chemistry</i> , 2008, 283, 22628-22636.	3.4	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.	2.6	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.	3.4	56
71	Structures of the Noncanonical RNA Ligase RtcB Reveal the Mechanism of Histidine Guanylylation. <i>Biochemistry</i> , 2013, 52, 2518-2525.	2.5	56
72	Functional Evolution of Ribonuclease Inhibitor: Insights from Birds and Reptiles. <i>Journal of Molecular Biology</i> , 2014, 426, 3041-3056.	4.2	56

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73	Structural and evolutionary relationships of α -type I polyketide synthase ketosynthases. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12693-12698.	7.1	55
74	Construction of an atomic model for tropomyosin and implications for interactions with actin. Journal of Molecular Biology, 1986, 192, 128-131.	4.2	53
75	Time-dependent atomic coordinates for the dissociation of carbon monoxide from myoglobin. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 776-783.	2.5	53
76	Biochemical and Structural Insights of the Early Glycosylation Steps in Calicheamicin Biosynthesis. Chemistry and Biology, 2008, 15, 842-853.	6.0	51
77	Structural Basis for Catalysis by Onconase. Journal of Molecular Biology, 2008, 375, 165-177.	4.2	51
78	A tRNA splicing operon: Archease endows RtcB with dual GTP/ATP cofactor specificity and accelerates RNA ligation. Nucleic Acids Research, 2014, 42, 3931-3942.	14.5	50
79	Structure of the <i>ent</i> -Copalyl Diphosphate Synthase PtmT2 from <i>Streptomyces platensis</i> CB00739, a Bacterial Type II Diterpene Synthase. Journal of the American Chemical Society, 2016, 138, 10905-10915.	13.7	50
80	Structure and specificity of a permissive bacterial C-prenyltransferase. Nature Chemical Biology, 2017, 13, 366-368.	8.0	50
81	Bis-methionyl Coordination in the Crystal Structure of the Heme-binding Domain of the Streptococcal Cell Surface Protein Shp. Journal of Molecular Biology, 2007, 374, 374-383.	4.2	49
82	The structure and NO binding properties of the nitrophorin-like heme-binding protein from <i>Arabidopsis thaliana</i> gene locus At1g79260.1. Proteins: Structure, Function and Bioinformatics, 2010, 78, 917-931.	2.6	49
83	Generation of Size-Controlled, Submicrometer Protein Crystals. Chemistry of Materials, 2005, 17, 2679-2686.	6.7	48
84	Phe-46(CD4) orients the distal histidine for hydrogen bonding to bound ligands in sperm whale myoglobin. Proteins: Structure, Function and Bioinformatics, 1995, 22, 322-339.	2.6	47
85	Complete set of glycosyltransferase structures in the calicheamicin biosynthetic pathway reveals the origin of regioselectivity. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17649-17654.	7.1	47
86	Solution and Crystal Structures of a Sperm Whale Myoglobin Triple Mutant That Mimics the Sulfide-binding Hemoglobin from <i>Lucina pectinata</i> . Journal of Biological Chemistry, 1998, 273, 9517-9526.	3.4	45
87	Sampling of the native conformational ensemble of myoglobin via structures in different crystalline environments. Proteins: Structure, Function and Bioinformatics, 2008, 70, 353-362.	2.6	45
88	Reader domain specificity and lysine demethylase-4 family function. Nature Communications, 2016, 7, 13387.	12.8	45
89	Structure and Dynamics of UDP-Glucose Pyrophosphorylase from <i>Arabidopsis thaliana</i> with Bound UDP-Glucose and UTP. Journal of Molecular Biology, 2007, 366, 830-841.	4.2	43
90	THE STRUCTURE OF FIBRINOGEN AND FIBRIN: II. ARCHITECTURE OF THE FIBRIN CLOT. Annals of the New York Academy of Sciences, 1983, 408, 367-379.	3.8	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.	2.6	42
92	Structure, Dynamics, and Specificity of Endoglucanase D from <i>Clostridium cellulovorans</i> . <i>Journal of Molecular Biology</i> , 2013, 425, 4267-4285.	4.2	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.	13.7	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.	7.1	40
96	Structural Basis of Stereospecificity in the Bacterial Enzymatic Cleavage of β^2 -Aryl Ether Bonds in Lignin. <i>Journal of Biological Chemistry</i> , 2016, 291, 5234-5246.	3.4	40
97	Characterizing global substates of myoglobin. <i>Structure</i> , 1998, 6, 587-594.	3.3	39
98	What is the pitch of the α -helical coiled coil?. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 14, 425-429.	2.6	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.	3.4	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.	3.4	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.	0.5	38
102	Mechanical properties of tropomyosin and implications for muscle regulation. <i>Biopolymers</i> , 1996, 38, 89-95.	2.4	37
103	Multi-Scale Surface Descriptors. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2009, 15, 1201-1208.	4.4	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.	3.4	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.	4.2	36
106	Understanding molecular recognition of promiscuity of thermophilic methionine adenosyltransferase MAT from <i>Sulfolobus solfataricus</i> . <i>FEBS Journal</i> , 2014, 281, 4224-4239.	4.7	36
107	Functional AdoMet Isosteres Resistant to Classical AdoMet Degradation Pathways. <i>ACS Chemical Biology</i> , 2016, 11, 2484-2491.	3.4	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.	2.6	35

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109	Structural characterization of human Uch37. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 649-654.	2.6	34
110	Pro-metastatic collagen lysyl hydroxylase dimer assemblies stabilized by Fe ²⁺ -binding. <i>Nature Communications</i> , 2018, 9, 512.	12.8	34
111	Moving beyond static snapshots: Protein dynamics and the Protein Data Bank. <i>Journal of Biological Chemistry</i> , 2021, 296, 100749.	3.4	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.	2.6	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.	2.6	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.	3.4	33
116	Creating protein models from electron-density maps using particle-filtering methods. <i>Bioinformatics</i> , 2007, 23, 2851-2858.	4.1	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.	1.9	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.	3.8	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.	2.5	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.	2.5	31
121	[21] Analysis of diffuse scattering and relation to molecular motion. <i>Methods in Enzymology</i> , 1997, 277, 407-432.	1.0	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.	3.4	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.	3.4	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.	2.8	29
125	Motions of Tropomyosin. <i>Biophysical Journal</i> , 1986, 49, 76-78.	0.5	28
126	Structure and Mechanism of an ADP-Glucose Phosphorylase from <i>Arabidopsis thaliana</i> . <i>Biochemistry</i> , 2006, 45, 3154-3162.	2.5	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.	2.6	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.	2.6	27
130	Structural characterization of the mitomycin 7-O-methyltransferase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2181-2188.	2.6	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.	2.6	26
132	Conformational variation of calcium-bound troponin C. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 510-511.	2.6	25
133	Structure of Pyrimidine 5'-Nucleotidase Type 1. <i>Journal of Biological Chemistry</i> , 2006, 281, 20521-20529.	3.4	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.	2.6	24
136	Structure-Guided Functional Characterization of Eneidine Self-Sacrifice Resistance Proteins, CalU16 and CalU19. <i>ACS Chemical Biology</i> , 2014, 9, 2347-2358.	3.4	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.	13.7	23
138	X-ray structure of <i>Danio rerio</i> secretagogin: A hexameric hand and calcium sensor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 477-483.	2.6	22
139	X-ray structure of Arabidopsis At2g06050, 12-oxophytodienoate reductase isoform 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 243-245.	2.6	21
140	Automated Illustration of Molecular Flexibility. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2012, 18, 132-145.	4.4	21
141	Resistance to Eneidine Antitumor Antibiotics by Sequestration. <i>Cell Chemical Biology</i> , 2018, 25, 1075-1085.e4.	5.2	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.	8.0	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.	4.1	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.	2.6	20
146	Methionine Adenosyltransferase Engineering to Enable Bioorthogonal Platforms for AdoMet-Utilizing Enzymes. <i>ACS Chemical Biology</i> , 2020, 15, 695-705.	3.4	20
147	Stabilization of myoglobin by multiple alanine substitutions in helical positions. <i>Protein Science</i> , 1994, 3, 1430-1435.	7.6	19
148	Structure of T4moC, the Rieske-type ferredoxin component of toluene 4-monooxygenase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 476-482.	2.5	19
149	Protein structure determination using a database of interatomic distance probabilities. <i>Protein Science</i> , 1999, 8, 2720-2727.	7.6	19
150	Straight-Chain Alkyl Isocyanides Open the Distal Histidine Gate in Crystal Structures of Myoglobin,. <i>Biochemistry</i> , 2010, 49, 4977-4986.	2.5	19
151	Interconversion of Functional Motions between Mesophilic and Thermophilic Adenylate Kinases. <i>PLoS Computational Biology</i> , 2011, 7, e1002103.	3.2	19
152	Crystallographic Analysis of Active Site Contributions to Regiospecificity in the Diiron Enzyme Toluene 4-Monooxygenase. <i>Biochemistry</i> , 2012, 51, 1101-1113.	2.5	19
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