

# George N Phillips Jr

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

242  
papers

12,917  
citations

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 crystal structure of DynF from the dynemicin-biosynthesis pathway of <i>Micromonospora chersina</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2022</b> , 78, 1-7	1.1	0
241	The Structure of the PEX4-PEX22 Peroxin Complex-Insights Into Ubiquitination at the Peroxisomal Membrane.. <i>Frontiers in Cell and Developmental Biology</i> , <b>2022</b> , 10, 838923	5.7	0
240	Structure and Function of a Dual Reductase-Dehydratase Enzyme System Involved in -Terphenyl Biosynthesis. <i>ACS Chemical Biology</i> , <b>2021</b> ,	4.9	1
239	Pump-Probe Circular Dichroism Spectroscopy of Cyanobacteriochrome TePixJ Yields: Insights into Its Photoconversion. <i>Journal of Physical Chemistry B</i> , <b>2021</b> , 125, 202-210	3.4	0
238	A collagen glucosyltransferase drives lung adenocarcinoma progression in mice. <i>Communications Biology</i> , <b>2021</b> , 4, 482	6.7	3
237	Moving beyond static snapshots: Protein dynamics and the Protein Data Bank. <i>Journal of Biological Chemistry</i> , <b>2021</b> , 296, 100749	5.4	7
236	Structural basis of the stereoselective formation of the spirooxindole ring in the biosynthesis of citrinadins. <i>Nature Communications</i> , <b>2021</b> , 12, 4158	17.4	3
235	Structural characterization of DynU16, a START/Bet v1-like protein involved in dynemicin biosynthesis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2021</b> , 77, 328-333	1.1	0
234	phage ferredoxin: structural characterization and electron transfer to cyanobacterial sulfite reductases. <i>Journal of Biological Chemistry</i> , <b>2020</b> , 295, 10610-10623	5.4	3
233	The Interplay between Molten Globules and Heme Disassembly Defines Human Hemoglobin Disassembly. <i>Biophysical Journal</i> , <b>2020</b> , 118, 1381-1400	2.9	6
232	Methionine Adenosyltransferase Engineering to Enable Bioorthogonal Platforms for AdoMet-Utilizing Enzymes. <i>ACS Chemical Biology</i> , <b>2020</b> , 15, 695-705	4.9	10
231	Crystal Structure of Xylosidase from in Complex with a Hydrolyzed Xyloglucan Product and New Insights in Accurately Predicting Substrate Specificities of GH31 Family Glycosidases. <i>ACS Sustainable Chemistry and Engineering</i> , <b>2020</b> , 8, 2540-2547	8.3	6
230	Molecular-replacement phasing using predicted protein structures from. <i>IUCrJ</i> , <b>2020</b> , 7, 1168-1178	4.7	4
229	Photoreversible interconversion of a phytochrome photosensory module in the crystalline state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 300-307	11.5	12
228	Covalent Capture of Collagen Triple Helices Using Lysine-Aspartate and Lysine-Glutamate Pairs. <i>Biomacromolecules</i> , <b>2020</b> , 21, 3772-3781	6.9	6
227	Plant hydraulics and agrichemical genomics. <i>Science</i> , <b>2019</b> , 366, 416-417	33.3	1
226	Target highlights in CASP13: Experimental target structures through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2019</b> , 87, 1037-1057	4.2	9

225	Characterization and Crystal Structure of a Nonheme Diiron Monooxygenase Involved in Platensimycin and Platencin Biosynthesis. <i>Journal of the American Chemical Society</i> , <b>2019</b> , 141, 12406-12412	16.4	14
224	Pro-metastatic collagen lysyl hydroxylase dimer assemblies stabilized by Fe-binding. <i>Nature Communications</i> , <b>2018</b> , 9, 512	17.4	25
223	Structural Insights into the Free-Standing Condensation Enzyme SgcC5 Catalyzing Ester-Bond Formation in the Biosynthesis of the Eneidyne Antitumor Antibiotic C-1027. <i>Biochemistry</i> , <b>2018</b> , 57, 3278-3288	3.2	9
222	Resistance to Eneidyne Antitumor Antibiotics by Sequestration. <i>Cell Chemical Biology</i> , <b>2018</b> , 25, 1075-1085.e4	11.7	14
221	Enzyme intermediates captured "on the fly" by mix-and-inject serial crystallography. <i>BMC Biology</i> , <b>2018</b> , 16, 59	7.3	73
220	Natural separation of the acyl-CoA ligase reaction results in a non-adenylating enzyme. <i>Nature Chemical Biology</i> , <b>2018</b> , 14, 730-737	11.7	15
219	Structural Proteomics <b>2018</b> , 99-128		
218	Biochemical and Structural Characterization of TtnD, a Prenylated FMN-Dependent Decarboxylase from the Tautomycetin Biosynthetic Pathway. <i>ACS Chemical Biology</i> , <b>2018</b> , 13, 2728-2738	4.9	14
217	Structural enzymology using X-ray free electron lasers. <i>Structural Dynamics</i> , <b>2017</b> , 4, 044003	3.2	75
216	OleD Loki as a Catalyst for Tertiary Amine and Hydroxamate Glycosylation. <i>ChemBioChem</i> , <b>2017</b> , 18, 363-367	3.8	4
215	Mechanism of Human Apohemoglobin Unfolding. <i>Biochemistry</i> , <b>2017</b> , 56, 1444-1459	3.2	14
214	A scalable lysyl hydroxylase 2 expression system and luciferase-based enzymatic activity assay. <i>Archives of Biochemistry and Biophysics</i> , <b>2017</b> , 618, 45-51	4.1	10
213	Drop-on-demand sample delivery for studying biocatalysts in action at X-ray free-electron lasers. <i>Nature Methods</i> , <b>2017</b> , 14, 443-449	21.6	107
212	Structure and specificity of a permissive bacterial C-prenyltransferase. <i>Nature Chemical Biology</i> , <b>2017</b> , 13, 366-368	11.7	32
211	Crystal Structure of Thioesterase SgcE10 Supporting Common Polyene Intermediates in 9- and 10-Membered Eneidyne Core Biosynthesis. <i>ACS Omega</i> , <b>2017</b> , 2, 5159-5169	3.9	5
210	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> , <b>2016</b> , 55, 5142-54	3.2	15
209	Crystal structure of SgcJ, an NTF2-like superfamily protein involved in biosynthesis of the nine-membered enediyne antitumor antibiotic C-1027. <i>Journal of Antibiotics</i> , <b>2016</b> , 69, 731-740	3.7	9
208	Reader domain specificity and lysine demethylase-4 family function. <i>Nature Communications</i> , <b>2016</b> , 7, 13387	17.4	30

207	Structural dynamics of a methionine lyase for calicheamicin biosynthesis: Rotation of the conserved tyrosine stacking with pyridoxal phosphate. <i>Structural Dynamics</i> , <b>2016</b> , 3, 034702	3-2	4
206	Structural Basis of Stereospecificity in the Bacterial Enzymatic Cleavage of Aryl Ether Bonds in Lignin. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 5234-46	5-4	27
205	Loop dynamics of thymidine diphosphate-rhamnose 3O-methyltransferase (CalS11), an enzyme in calicheamicin biosynthesis. <i>Structural Dynamics</i> , <b>2016</b> , 3, 012004	3-2	4
204	Preface to Special Topic on Protein Dynamics: Beyond Static Snapshots in Structural Biology. <i>Structural Dynamics</i> , <b>2016</b> , 3, 011901	3-2	
203	Functional AdoMet Isosteres Resistant to Classical AdoMet Degradation Pathways. <i>ACS Chemical Biology</i> , <b>2016</b> , 11, 2484-91	4-9	27
202	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> , <b>2016</b> , 138, 10905-15	16-4	29
201	Expression platforms for producing eukaryotic proteins: a comparison of E. coli cell-based and wheat germ cell-free synthesis, affinity and solubility tags, and cloning strategies. <i>Journal of Structural and Functional Genomics</i> , <b>2015</b> , 16, 67-80		10
200	Molecular dynamics simulation of a psychrophilic adenylate kinase <b>2015</b> , 58, 209-212		2
199	Unique patterns of transcript and miRNA expression in the South American strong voltage electric eel ( <i>Electrophorus electricus</i> ). <i>BMC Genomics</i> , <b>2015</b> , 16, 243	4-5	13
198	Apoglobin Stability Is the Major Factor Governing both Cell-free and in Vivo Expression of Holomyoglobin. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 23479-95	5-4	19
197	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> , <b>2015</b> , 112, 12693-8	11-5	38
196	Crystal structure of the protein At3g01520, a eukaryotic universal stress protein-like protein from <i>Arabidopsis thaliana</i> in complex with AMP. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2015</b> , 83, 1368-73	4-2	12
195	Structural characterization of AtmS13, a putative sugar aminotransferase involved in indolocarbazole AT2433 aminopentose biosynthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2015</b> , 83, 1547-54	4-2	9
194	Structural Basis for the Stereochemical Control of Amine Installation in Nucleotide Sugar Aminotransferases. <i>ACS Chemical Biology</i> , <b>2015</b> , 10, 2048-56	4-9	8
193	Structural Characterization of CalS8, a TDP-D-Glucose Dehydrogenase Involved in Calicheamicin Aminodideoxypentose Biosynthesis. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 26249-58	5-4	2
192	Crystal Structure of the Zorbamycin-Binding Protein ZbmA, the Primary Self-Resistance Element in <i>Streptomyces flavoviridis</i> ATCC21892. <i>Biochemistry</i> , <b>2015</b> , 54, 6842-51	3-2	8
191	Structure of a cupin protein Plu4264 from <i>Photobacterium luminescens</i> subsp. <i>laumondii</i> TTO1 at 1.35 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2015</b> , 83, 383-8	4-2	2
190	LucY: A Versatile New Fluorescent Reporter Protein. <i>PLoS ONE</i> , <b>2015</b> , 10, e0124272	3-7	3

189	An integrated approach for thermal stabilization of a mesophilic adenylate kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2014</b> , 82, 1947-59	4.2	11
188	Understanding molecular recognition of promiscuity of thermophilic methionine adenosyltransferase sMAT from <i>Sulfolobus solfataricus</i> . <i>FEBS Journal</i> , <b>2014</b> , 281, 4224-39	5.7	30
187	Effectiveness and limitations of local structural entropy optimization in the thermal stabilization of mesophilic and thermophilic adenylate kinases. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2014</b> , 82, 2631-42	4.2	5
186	Structure-guided functional characterization of enediene self-sacrifice resistance proteins, CalU16 and CalU19. <i>ACS Chemical Biology</i> , <b>2014</b> , 9, 2347-58	4.9	20
185	Functional evolution of ribonuclease inhibitor: insights from birds and reptiles. <i>Journal of Molecular Biology</i> , <b>2014</b> , 426, 3041-56	6.5	25
184	Structure and substrate specificity of a eukaryotic fucosidase from <i>Fusarium graminearum</i> . <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 25624-38	5.4	27
183	Structure of RNA 3'phosphate cyclase bound to substrate RNA. <i>Rna</i> , <b>2014</b> , 20, 1560-6	5.8	2
182	Nonhuman genetics. Genomic basis for the convergent evolution of electric organs. <i>Science</i> , <b>2014</b> , 344, 1522-5	33.3	128
181	A tRNA splicing operon: Archease endows RtcB with dual GTP/ATP cofactor specificity and accelerates RNA ligation. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 3931-42	20.1	36
180	Biochemical characterization and crystal structures of a fungal family 3 $\beta$ -glucosidase, Cel3A from <i>Hypocrea jecorina</i> . <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 31624-37	5.4	54
179	The crystal structure of Blm1 as a model for nonribosomal peptide synthetase peptidyl carrier proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2014</b> , 82, 1210-8	4.2	31
178	Evolution of substrate specificity in bacterial AA10 lytic polysaccharide monooxygenases. <i>Biotechnology for Biofuels</i> , <b>2014</b> , 7, 109	7.8	59
177	Using a commodity high-definition television for collaborative structural biology. <i>Journal of Applied Crystallography</i> , <b>2014</b> , 47, 1153-1157	3.8	12
176	Crystal structure of human protein N-terminal glutamine amidohydrolase, an initial component of the N-end rule pathway. <i>PLoS ONE</i> , <b>2014</b> , 9, e111142	3.7	7
175	A photo-labile thioether linkage to phycoviolobin provides the foundation for the blue/green photocycles in DXCF-cyanobacteriochromes. <i>Structure</i> , <b>2013</b> , 21, 88-97	5.2	80
174	Structures of the noncanonical RNA ligase RtcB reveal the mechanism of histidine guanylation. <i>Biochemistry</i> , <b>2013</b> , 52, 2518-25	3.2	32
173	Allosteric activation transitions in enzymes and biomolecular motors: insights from atomistic and coarse-grained simulations. <i>Topics in Current Chemistry</i> , <b>2013</b> , 337, 139-64		11
172	Structure, dynamics, and specificity of endoglucanase D from <i>Clostridium cellulovorans</i> . <i>Journal of Molecular Biology</i> , <b>2013</b> , 425, 4267-85	6.5	30

171	Structure of the bifunctional acyltransferase/decarboxylase LnmK from the leinamycin biosynthetic pathway revealing novel activity for a double-hot-dog fold. <i>Biochemistry</i> , <b>2013</b> , 52, 902-11	3.2	21
170	Structural and functional characterization of CalS11, a TDP-rhamnose 3O-methyltransferase involved in calicheamicin biosynthesis. <i>ACS Chemical Biology</i> , <b>2013</b> , 8, 1632-9	4.9	10
169	Crystal structure of the protein from Arabidopsis thaliana gene At5g06450, a putative DnaQ-like exonuclease domain-containing protein with homohexameric assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2013</b> , 81, 1669-1675	4.2	5
168	Crystal structure of SsfS6, the putative C-glycosyltransferase involved in SF2575 biosynthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2013</b> , 81, 1277-82	4.2	23
167	Automated Illustration of Molecular Flexibility. <i>IEEE Transactions on Visualization and Computer Graphics</i> , <b>2012</b> , 18, 132-45	4	16
166	Redox, haem and CO in enzymatic catalysis and regulation. <i>Biochemical Society Transactions</i> , <b>2012</b> , 40, 501-7	5.1	10
165	Crystallographic analysis of active site contributions to regioselectivity in the diiron enzyme toluene 4-monooxygenase. <i>Biochemistry</i> , <b>2012</b> , 51, 1101-13	3.2	16
164	Local functional descriptors for surface comparison based binding prediction. <i>BMC Bioinformatics</i> , <b>2012</b> , 13, 314	3.6	3
163	The structural biology of enzymes involved in natural product glycosylation. <i>Natural Product Reports</i> , <b>2012</b> , 29, 1201-37	15.1	81
162	Structural characterization of human Uch37. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2012</b> , 80, 649-54	4.2	32
161	Crystal structure of tandem ACT domain-containing protein ACTP from Galdieria sulphuraria. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2012</b> , 80, 2105-2109	4.2	2
160	Large-scale motions in the adenylate kinase solution ensemble: coarse-grained simulations and comparison with solution X-ray scattering. <i>Chemical Physics</i> , <b>2012</b> , 396, 84-91	2.3	26
159	Restructuring the crystalline cellulose hydrogen bond network enhances its depolymerization rate. <i>Journal of the American Chemical Society</i> , <b>2011</b> , 133, 11163-74	16.4	272
158	Glycosyltransferase structural biology and its role in the design of catalysts for glycosylation. <i>Current Opinion in Biotechnology</i> , <b>2011</b> , 22, 800-8	11.4	107
157	Structural characterization of CalO1: a putative orsellinic acid methyltransferase in the calicheamicin-biosynthetic pathway. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2011</b> , 67, 197-203		15
156	Structure of cellobiose phosphorylase from Clostridium thermocellum in complex with phosphate. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2011</b> , 67, 1345-9		20
155	Structural architecture of Galdieria sulphuraria DCN1L. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79, 1329-36	4.2	3
154	Structure of the C-terminal heme-binding domain of THAP domain containing protein 4 from Homo sapiens. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79, 1337-41	4.2	20

153	Structural characterization of the mitomycin 7-O-methyltransferase. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79, 2181-8	4.2	19
152	Crystal structure of <i>Arabidopsis thaliana</i> 12-oxophytodienoate reductase isoform 3 in complex with 8-iso prostaglandin A(1). <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79, 3236-41	4.2	2
151	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> , <b>2011</b> , 108, 5897-902	11.5	57
150	Expanding the nucleotide and sugar 1-phosphate promiscuity of nucleotidyltransferase RmlA via directed evolution. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 13235-43	5.4	31
149	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> , <b>2011</b> , 108, 17649-54	11.5	44
148	Interconversion of functional motions between mesophilic and thermophilic adenylate kinases. <i>PLoS Computational Biology</i> , <b>2011</b> , 7, e1002103	5	18
147	Structural basis for selective activation of ABA receptors. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 1109-13	17.6	88
146	Evaluating elastic network models of crystalline biological molecules with temperature factors, correlated motions, and diffuse x-ray scattering. <i>Biophysical Journal</i> , <b>2010</b> , 99, 2616-25	2.9	30
145	Straight-chain alkyl isocyanides open the distal histidine gate in crystal structures of myoglobin. <i>Biochemistry</i> , <b>2010</b> , 49, 4977-86	3.2	18
144	Many local motions cooperate to produce the adenylate kinase conformational transition. <i>Journal of Molecular Biology</i> , <b>2010</b> , 400, 618-31	6.5	78
143	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> , <b>2010</b> , 78, 917-31	4.2	41
142	Crystal structure of an eIF4G-like protein from <i>Danio rerio</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2010</b> , 78, 1803-6	4.2	2
141	Novel procedure for thermal equilibration in molecular dynamics simulation. <i>Molecular Simulation</i> , <b>2009</b> , 35, 349-357	2	9
140	Plant science. How plant cells go to sleep for a long, long time. <i>Science</i> , <b>2009</b> , 326, 1356-7	33.3	6
139	The Center for Eukaryotic Structural Genomics. <i>Journal of Structural and Functional Genomics</i> , <b>2009</b> , 10, 165-79		25
138	X-ray structure of ILL2, an auxin-conjugate amidohydrolase from <i>Arabidopsis thaliana</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2009</b> , 74, 61-71	4.2	37
137	Structural characterization of CalO2: a putative orsellinic acid P450 oxidase in the calicheamicin biosynthetic pathway. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2009</b> , 74, 50-60	4.2	22
136	Discovery of sarcosine dimethylglycine methyltransferase from <i>Galdieria sulphuraria</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2009</b> , 74, 368-77	4.2	10

135	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> , <b>2009</b> , 75, 217-30	4.2	66
134	X-ray structure of Danio rerio secretagoin: A hexa-EF-hand calcium sensor. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2009</b> , 76, 477-83	4.2	17
133	Structures of two Arabidopsis thaliana major latex proteins represent novel helix-grip folds. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2009</b> , 76, 237-43	4.2	52
132	Application of elastic network models to proteins in the crystalline state. <i>Biophysical Journal</i> , <b>2009</b> , 96, 464-75	2.9	68
131	Multi-scale surface descriptors. <i>IEEE Transactions on Visualization and Computer Graphics</i> , <b>2009</b> , 15, 1201-8		30
130	Spherical-harmonic decomposition for molecular recognition in electron-density maps. <i>International Journal of Data Mining and Bioinformatics</i> , <b>2009</b> , 3, 205-27	0.5	4
129	Describing protein conformational ensembles: beyond static snapshots. <i>F1000 Biology Reports</i> , <b>2009</b> , 1, 38		4
128	Structure of human J-type co-chaperone HscB reveals a tetracysteine metal-binding domain. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 30184-92	5.4	33
127	Structural basis for catalysis by onconase. <i>Journal of Molecular Biology</i> , <b>2008</b> , 375, 165-77	6.5	33
126	Optimal design of thermally stable proteins. <i>Bioinformatics</i> , <b>2008</b> , 24, 2339-43	7.2	10
125	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> , <b>2008</b> , 105, 19194-8	11.5	80
124	Structure and mechanism of the rebeccamycin sugar 4QO-methyltransferase RebM. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 22628-36	5.4	46
123	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> , <b>2008</b> , 105, 9594-7	11.5	36
122	Structure and dynamics of gamma-SNAP: insight into flexibility of proteins from the SNAP family. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 70, 93-104	4.2	11
121	Sampling of the native conformational ensemble of myoglobin via structures in different crystalline environments. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 70, 353-62	4.2	35
120	Crystal structure of Arabidopsis thaliana cytokinin dehydrogenase. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 70, 303-6	4.2	17
119	Crystal structure of Homo sapiens protein LOC79017. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 70, 588-91	4.2	
118	X-ray structure of a soluble Rieske-type ferredoxin from Mus musculus. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2008</b> , 64, 933-40		4



117	Structural and functional characterization of a novel phosphatase from the Arabidopsis thaliana gene locus At1g05000. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 73, 241-53	4.2	13
116	Biochemical and structural insights of the early glycosylation steps in calicheamicin biosynthesis. <i>Chemistry and Biology</i> , <b>2008</b> , 15, 842-53		47
115	Protein structural variation in computational models and crystallographic data. <i>Structure</i> , <b>2007</b> , 15, 169-72		86
114	Ensemble refinement of protein crystal structures: validation and application. <i>Structure</i> , <b>2007</b> , 15, 1040-52		146
113	Structures of proteins of biomedical interest from the Center for Eukaryotic Structural Genomics. <i>Journal of Structural and Functional Genomics</i> , <b>2007</b> , 8, 73-84		9
112	Small-scale, semi-automated purification of eukaryotic proteins for structure determination. <i>Journal of Structural and Functional Genomics</i> , <b>2007</b> , 8, 153-66		27
111	A graphical approach to tracking and reporting target status in structural genomics. <i>Journal of Structural and Functional Genomics</i> , <b>2007</b> , 8, 209-16		4
110	Effect of low-complexity regions on protein structure determination. <i>Journal of Structural and Functional Genomics</i> , <b>2007</b> , 8, 217-26		10
109	Comparison of apo- and heme-bound crystal structures of a truncated human heme oxygenase-2. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 37624-31	5.4	48
108	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> , <b>2007</b> , 104, 456-61	11.5	60
107	Bis-methionine ligation to heme iron in the streptococcal cell surface protein Shp facilitates rapid heme transfer to HtsA of the HtsABC transporter. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 31380-8	5.4	36
106	Creating protein models from electron-density maps using particle-filtering methods. <i>Bioinformatics</i> , <b>2007</b> , 23, 2851-8	7.2	26
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