

# P Andrew Karplus

## 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.

154 papers	12,818 citations	58 h-index	112 g-index
158 ext. papers	13,964 ext. citations	6.3 avg, IF	6.67 L-index

#	Paper	IF	Citations
154	Creating a Selective Nanobody Against 3-Nitrotyrosine Containing Proteins.. <i>Frontiers in Chemistry</i> , <b>2022</b> , 10, 835229	5	0
153	Nanobody assemblies with fully flexible topology enabled by genetically encoded tetrazine amino acids.. <i>Science Advances</i> , <b>2022</b> , 8, eabm6909	14.3	0
152	Modifying the resolving cysteine affects the structure and hydrogen peroxide reactivity of peroxiredoxin 2. <i>Journal of Biological Chemistry</i> , <b>2021</b> , 296, 100494	5.4	2
151	A complete Fourier-synthesis-based backbone-conformation-dependent library for proteins. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2021</b> , 77, 249-266	5.5	
150	Overcoming Near-Cognate Suppression in a Release Factor 1-Deficient Host with an Improved Nitro-Tyrosine tRNA Synthetase. <i>Journal of Molecular Biology</i> , <b>2020</b> , 432, 4690-4704	6.5	10
149	Immobilization of Proteins with Controlled Load and Orientation. <i>ACS Applied Materials &amp; Interfaces</i> , <b>2019</b> , 11, 36391-36398	9.5	20
148	Substrate Specificity in Thiol Dioxygenases. <i>Biochemistry</i> , <b>2019</b> , 58, 2398-2407	3.2	20
147	Structure and role for active site lid of lactate monooxygenase from Mycobacterium smegmatis. <i>Protein Science</i> , <b>2019</b> , 28, 135-149	6.3	10
146	Automated NMR resonance assignments and structure determination using a minimal set of 4D spectra. <i>Nature Communications</i> , <b>2018</b> , 9, 384	17.4	23
145	Differential Kinetics of Two-Cysteine Peroxiredoxin Disulfide Formation Reveal a Novel Model for Peroxide Sensing. <i>Biochemistry</i> , <b>2018</b> , 57, 3416-3424	3.2	47
144	Experimentally Dissecting the Origins of Peroxiredoxin Catalysis. <i>Antioxidants and Redox Signaling</i> , <b>2018</b> , 28, 521-536	8.4	20
143	Structural insights into a thermostable variant of human carbonic anhydrase II. <i>Protein Science</i> , <b>2018</b> , 27, 573-577	6.3	6
142	Ensemblator v3: Robust atom-level comparative analyses and classification of protein structure ensembles. <i>Protein Science</i> , <b>2018</b> , 27, 41-50	6.3	8
141	The mitotic kinesin-14 KlpA contains a context-dependent directionality switch. <i>Nature Communications</i> , <b>2017</b> , 8, 13999	17.4	27
140	Evolution and Distribution of C-Cyclitol Synthases in Prokaryotes and Eukaryotes. <i>ACS Chemical Biology</i> , <b>2017</b> , 12, 979-988	4.9	15
139	The sedoheptulose 7-phosphate cyclases and their emerging roles in biology and ecology. <i>Natural Product Reports</i> , <b>2017</b> , 34, 945-956	15.1	11
138	High-resolution studies of hydride transfer in the ferredoxin:NADP reductase superfamily. <i>FEBS Journal</i> , <b>2017</b> , 284, 3302-3319	5.7	10

137	Backbone chemical shift assignments for <i>Xanthomonas campestris</i> peroxiredoxin Q in the reduced and oxidized states: a dramatic change in backbone dynamics. <i>Biomolecular NMR Assignments</i> , <b>2016</b> , 10, 57-61	0.7	8
136	NMR structure of the HIV-1 reverse transcriptase thumb subdomain. <i>Journal of Biomolecular NMR</i> , <b>2016</b> , 66, 273-280	3	3
135	On the reliability of peptide nonplanarity seen in ultra-high resolution crystal structures. <i>Protein Science</i> , <b>2016</b> , 25, 926-32	6.3	7
134	The Anchored Flexibility Model in LC8 Motif Recognition: Insights from the Chica Complex. <i>Biochemistry</i> , <b>2016</b> , 55, 199-209	3.2	21
133	A new default restraint library for the protein backbone in Phenix: a conformation-dependent geometry goes mainstream. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2016</b> , 72, 176-9	5.5	27
132	Beyond basins: $\phi$ preferences of a residue depend heavily on the $\psi$ values of its neighbors. <i>Protein Science</i> , <b>2016</b> , 25, 1757-62	6.3	5
131	Peroxiredoxin Catalysis at Atomic Resolution. <i>Structure</i> , <b>2016</b> , 24, 1668-1678	5.2	30
130	Structure-Based Insights into the Role of the Cys-Tyr Crosslink and Inhibitor Recognition by Mammalian Cysteine Dioxygenase. <i>Journal of Molecular Biology</i> , <b>2016</b> , 428, 3999-4012	6.5	25
129	Structure and proposed mechanism of L-glycerophosphate oxidase from <i>Mycoplasma pneumoniae</i> . <i>FEBS Journal</i> , <b>2015</b> , 282, 3030-42	5.7	15
128	Assessing and maximizing data quality in macromolecular crystallography. <i>Current Opinion in Structural Biology</i> , <b>2015</b> , 34, 60-8	8.1	142
127	Peroxiredoxins: guardians against oxidative stress and modulators of peroxide signaling. <i>Trends in Biochemical Sciences</i> , <b>2015</b> , 40, 435-45	10.3	322
126	ChSeq: A database of chameleon sequences. <i>Protein Science</i> , <b>2015</b> , 24, 1075-86	6.3	32
125	Native proteins trap high-energy transit conformations. <i>Science Advances</i> , <b>2015</b> , 1, e1501188	14.3	10
124	A primer on peroxiredoxin biochemistry. <i>Free Radical Biology and Medicine</i> , <b>2015</b> , 80, 183-90	7.8	79
123	Structures of Arg- and Gln-type bacterial cysteine dioxygenase homologs. <i>Protein Science</i> , <b>2015</b> , 24, 154-61	6.3	20
122	Mammalian Cysteine Dioxygenase <b>2015</b> , 1-11		0
121	Rationally engineered flavin-dependent oxidase reveals steric control of dioxygen reduction. <i>FEBS Journal</i> , <b>2015</b> , 282, 3060-74	5.7	27
120	Residue-level global and local ensemble-ensemble comparisons of protein domains. <i>Protein Science</i> , <b>2015</b> , 24, 1528-42	6.3	7

119	Kinetic mechanism of L-glycerophosphate oxidase from <i>Mycoplasma pneumoniae</i> . <i>FEBS Journal</i> , <b>2015</b> , 282, 3043-59	5.7	10
118	Dissecting peroxiredoxin catalysis: separating binding, peroxidation, and resolution for a bacterial AhpC. <i>Biochemistry</i> , <b>2015</b> , 54, 1567-75	3.2	45
117	De novo synthesis of a sunscreen compound in vertebrates. <i>ELife</i> , <b>2015</b> , 4,	8.9	50
116	Structural basis of improved second-generation 3-nitro-tyrosine tRNA synthetases. <i>Biochemistry</i> , <b>2014</b> , 53, 1916-24	3.2	37
115	Tuning of peroxiredoxin catalysis for various physiological roles. <i>Biochemistry</i> , <b>2014</b> , 53, 7693-705	3.2	90
114	Crystal structure of <i>Escherichia coli</i> SsuE: defining a general catalytic cycle for FMN reductases of the flavodoxin-like superfamily. <i>Biochemistry</i> , <b>2014</b> , 53, 3509-19	3.2	21
113	Structure of a sedoheptulose 7-phosphate cyclase: ValA from <i>Streptomyces hygroscopicus</i> . <i>Biochemistry</i> , <b>2014</b> , 53, 4250-60	3.2	11
112	Conformation-dependent backbone geometry restraints set a new standard for protein crystallographic refinement. <i>FEBS Journal</i> , <b>2014</b> , 281, 4061-71	5.7	29
111	Gleaning unexpected fruits from hard-won synthetases: probing principles of permissivity in non-canonical amino acid-tRNA synthetases. <i>ChemBioChem</i> , <b>2014</b> , 15, 1810-9	3.8	25
110	Evaluating peroxiredoxin sensitivity toward inactivation by peroxide substrates. <i>Methods in Enzymology</i> , <b>2013</b> , 527, 21-40	1.7	27
109	Cysteine dioxygenase structures from pH4 to 9: consistent cys-persulfenate formation at intermediate pH and a Cys-bound enzyme at higher pH. <i>Journal of Molecular Biology</i> , <b>2013</b> , 425, 3121-36	6.5	52
108	Sulfenic Acids and Peroxiredoxins in Oxidant Defense and Signaling <b>2013</b> , 85-118		3
107	The sensitive balance between the fully folded and locally unfolded conformations of a model peroxiredoxin. <i>Biochemistry</i> , <b>2013</b> , 52, 8708-21	3.2	45
106	Data Processing: How Good Are My Data Really?. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , <b>2013</b> , 59-68	0.1	
105	Observed octameric assembly of a <i>Plasmodium yoelii</i> peroxiredoxin can be explained by the replacement of native "ball-and-socket" interacting residues by an affinity tag. <i>Protein Science</i> , <b>2013</b> , 22, 1445-52	6.3	10
104	Mapping the active site helix-to-strand conversion of CxxxxC peroxiredoxin Q enzymes. <i>Biochemistry</i> , <b>2012</b> , 51, 7638-50	3.2	22
103	Peroxiredoxins in parasites. <i>Antioxidants and Redox Signaling</i> , <b>2012</b> , 17, 608-33	8.4	69
102	motifs: a purely conformation-based fine-grained enumeration of protein parts at the two-residue level. <i>Journal of Molecular Biology</i> , <b>2012</b> , 416, 78-93	6.5	19

101	Peroxiredoxins as molecular triage agents, sacrificing themselves to enhance cell survival during a peroxide attack. <i>Molecular Cell</i> , <b>2012</b> , 45, 275-8	17.6	16
100	The tumor suppressor merlin controls growth in its open state, and phosphorylation converts it to a less-active more-closed state. <i>Developmental Cell</i> , <b>2012</b> , 22, 703-5	10.2	44
99	Linking crystallographic model and data quality. <i>Science</i> , <b>2012</b> , 336, 1030-3	33.3	1329
98	Nonplanar peptide bonds in proteins are common and conserved but not biased toward active sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 449-53	11.5	51
97	Structure-based insights into the catalytic power and conformational dexterity of peroxiredoxins. <i>Antioxidants and Redox Signaling</i> , <b>2011</b> , 15, 795-815	8.4	236
96	Symerythrin structures at atomic resolution and the origins of rubrerythrins and the ferritin-like superfamily. <i>Journal of Molecular Biology</i> , <b>2011</b> , 413, 177-94	6.5	16
95	Cysteine-based redox switches in enzymes. <i>Antioxidants and Redox Signaling</i> , <b>2011</b> , 14, 1065-77	8.4	272
94	Thiol dioxygenases: unique families of cupin proteins. <i>Amino Acids</i> , <b>2011</b> , 41, 91-102	3.5	76
93	Conformational studies of the robust 2-Cys peroxiredoxin <i>Salmonella typhimurium</i> AhpC by solution phase hydrogen/deuterium (H/D) exchange monitored by electrospray ionization mass spectrometry. <i>International Journal of Mass Spectrometry</i> , <b>2011</b> , 302, 93-100	1.9	7
92	A conformation-dependent stereochemical library improves crystallographic refinement even at atomic resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2011</b> , 67, 699-706		22
91	A diiron protein autogenerates a valine-phenylalanine cross-link. <i>Science</i> , <b>2011</b> , 332, 929	33.3	12
90	Iron-containing urease in a pathogenic bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 13095-9	11.5	53
89	The crystal structure of dynein intermediate chain-light chain roadblock complex gives new insights into dynein assembly. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 22566-75	5.4	36
88	Protein Geometry Database: a flexible engine to explore backbone conformations and their relationships to covalent geometry. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D320-5	20.1	28
87	Engineering of fluorescent reporters into redox domains to monitor electron transfers. <i>Methods in Enzymology</i> , <b>2010</b> , 474, 1-21	1.7	5
86	A fresh look at the Ramachandran plot and the occurrence of standard structures in proteins. <i>Biomolecular Concepts</i> , <b>2010</b> , 1, 271-283	3.7	151
85	Structural evidence that peroxiredoxin catalytic power is based on transition-state stabilization. <i>Journal of Molecular Biology</i> , <b>2010</b> , 402, 194-209	6.5	136
84	Evolutionary origin of a secondary structure: $\beta$ helices as cryptic but widespread insertional variations of $\beta$ helices that enhance protein functionality. <i>Journal of Molecular Biology</i> , <b>2010</b> , 404, 232-46	6.5	113

83	Using a conformation-dependent stereochemical library improves crystallographic refinement of proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2010</b> , 66, 834-42		32
82	Multivalency in the assembly of intrinsically disordered Dynein intermediate chain. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 33115-21	5.4	57
81	Conformation dependence of backbone geometry in proteins. <i>Structure</i> , <b>2009</b> , 17, 1316-25	5.2	79
80	On the occurrence of linear groups in proteins. <i>Protein Science</i> , <b>2009</b> , 18, 1321-5	6.3	32
79	Structural, thermodynamic, and kinetic effects of a phosphomimetic mutation in dynein light chain LC8. <i>Biochemistry</i> , <b>2009</b> , 48, 11381-9	3.2	10
78	Crystal structure and catalytic properties of Bacillus anthracis CoADR-RHD: implications for flavin-linked sulfur trafficking. <i>Biochemistry</i> , <b>2009</b> , 48, 9650-67	3.2	20
77	Redox-dependent dynamics of a dual thioredoxin fold protein: evolution of specialized folds. <i>Biochemistry</i> , <b>2009</b> , 48, 5984-93	3.2	9
76	Structural changes common to catalysis in the Tpx peroxiredoxin subfamily. <i>Journal of Molecular Biology</i> , <b>2009</b> , 393, 867-81	6.5	42
75	Catalytic cycle of human glutathione reductase near 1 Å resolution. <i>Journal of Molecular Biology</i> , <b>2008</b> , 382, 371-84	6.5	76
74	The interplay of ligand binding and quaternary structure in the diverse interactions of dynein light chain LC8. <i>Journal of Molecular Biology</i> , <b>2008</b> , 384, 954-66	6.5	33
73	Structure of alpha-glycerophosphate oxidase from Streptococcus sp.: a template for the mitochondrial alpha-glycerophosphate dehydrogenase. <i>Biochemistry</i> , <b>2008</b> , 47, 965-77	3.2	21
72	A putative Fe <sup>2+</sup> -bound persulfenate intermediate in cysteine dioxygenase. <i>Biochemistry</i> , <b>2008</b> , 47, 11390-2	3.2	72
71	Cysteine pK(a) values for the bacterial peroxiredoxin AhpC. <i>Biochemistry</i> , <b>2008</b> , 47, 12860-8	3.2	90
70	Substrate specificity and redox potential of AhpC, a bacterial peroxiredoxin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 8209-14	11.5	126
69	Isolation of Legume Glycosyltransferases and Active Site Mapping of the Phaseolus lunatus Zeatin O-glucosyltransferase ZOG1. <i>Journal of Plant Growth Regulation</i> , <b>2008</b> , 27, 192-201	4.7	11
68	A forward-looking suggestion for resolving the stereochemical restraints debate: ideal geometry functions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2008</b> , 64, 335-6		14
67	Self-masking in an intact ERM-merlin protein: an active role for the central alpha-helical domain. <i>Journal of Molecular Biology</i> , <b>2007</b> , 365, 1446-59	6.5	89
66	Structure and dynamics of LC8 complexes with KXTQT-motif peptides: swallow and dynein intermediate chain compete for a common site. <i>Journal of Molecular Biology</i> , <b>2007</b> , 371, 457-68	6.5	70

65	Structural characterization of zinc-deficient human superoxide dismutase and implications for ALS. <i>Journal of Molecular Biology</i> , <b>2007</b> , 373, 877-90	6.5	107
64	Structural survey of the peroxiredoxins. <i>Sub-Cellular Biochemistry</i> , <b>2007</b> , 44, 41-60	5.5	74
63	Song: Chymotrypsin (to the tune of "eight days a week," by the beatles)*. <i>Biochemistry and Molecular Biology Education</i> , <b>2006</b> , 34, 287	1.3	0
62	Song: Enzymes speed reactions (to the tune of "we will rock you," by queen)*S. <i>Biochemistry and Molecular Biology Education</i> , <b>2006</b> , 34, 286	1.3	
61	Song: Learn about the buffer (generic rap)*. <i>Biochemistry and Molecular Biology Education</i> , <b>2006</b> , 34, 285	1.3	
60	Identification and characterization of bacterial cysteine dioxygenases: a new route of cysteine degradation for eubacteria. <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 5561-9	3.5	81
59	Crystal structure of mammalian cysteine dioxygenase. A novel mononuclear iron center for cysteine thiol oxidation. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 18723-33	5.4	131
58	Structure of coenzyme A-disulfide reductase from <i>Staphylococcus aureus</i> at 1.54 Å resolution. <i>Biochemistry</i> , <b>2006</b> , 45, 11278-89	3.2	35
57	Urease <b>2006</b> ,		1
56	In-house sulfur SAD phasing: a case study of the effects of data quality and resolution cutoffs. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2006</b> , 62, 707-16		25
55	Crystal structure of a novel <i>Plasmodium falciparum</i> 1-Cys peroxiredoxin. <i>Journal of Molecular Biology</i> , <b>2005</b> , 346, 1021-34	6.5	81
54	Analysis of the link between enzymatic activity and oligomeric state in AhpC, a bacterial peroxiredoxin. <i>Biochemistry</i> , <b>2005</b> , 44, 10583-92	3.2	174
53	Oxidized and synchrotron cleaved structures of the disulfide redox center in the N-terminal domain of <i>Salmonella typhimurium</i> AhpF. <i>Protein Science</i> , <b>2005</b> , 14, 2414-20	6.3	38
52	Structure of Ptr ToxA: an RGD-containing host-selective toxin from <i>Pyrenophora tritici-repentis</i> . <i>Plant Cell</i> , <b>2005</b> , 17, 3190-202	11.6	85
51	The EBP50-moesin interaction involves a binding site regulated by direct masking on the FERM domain. <i>Journal of Cell Science</i> , <b>2004</b> , 117, 1547-52	5.3	60
50	Protein sulfenic acids in redox signaling. <i>Annual Review of Pharmacology and Toxicology</i> , <b>2004</b> , 44, 325-47	17.9	511
49	Structural Aspects of Plant Ferredoxin : NADP(+) Oxidoreductases. <i>Photosynthesis Research</i> , <b>2004</b> , 81, 303-15	3.7	34
48	Structure of the active N-terminal domain of Ezrin. Conformational and mobility changes identify keystone interactions. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 4949-56	5.4	85



47	Peroxiredoxin evolution and the regulation of hydrogen peroxide signaling. <i>Science</i> , <b>2003</b> , 300, 650-3	33.3	1132
46	Crystallization and preliminary crystallographic analysis of the soluble alpha-glycerophosphate oxidase from <i>Streptococcus</i> sp. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2002</b> , 58, 165-6		2
45	The role of glutamine 114 in old yellow enzyme. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 2138-45	5.4	38
44	Dimers to doughnuts: redox-sensitive oligomerization of 2-cysteine peroxiredoxins. <i>Biochemistry</i> , <b>2002</b> , 41, 5493-504	3.2	296
43	Crystal structure of the antioxidant enzyme glutathione reductase inactivated by peroxynitrite. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 2779-84	5.4	102
42	Structure of intact AhpF reveals a mirrored thioredoxin-like active site and implies large domain rotations during catalysis. <i>Biochemistry</i> , <b>2001</b> , 40, 3900-11	3.2	47
41	Biochemical and crystallographic characterization of ferredoxin-NADP(+) reductase from nonphotosynthetic tissues. <i>Biochemistry</i> , <b>2001</b> , 40, 14501-8	3.2	50
40	AhpF and other NADH:peroxiredoxin oxidoreductases, homologues of low Mr thioredoxin reductase. <i>FEBS Journal</i> , <b>2000</b> , 267, 6126-33		108
39	Kinetic and structural characterization of urease active site variants. <i>Biochemistry</i> , <b>2000</b> , 39, 8575-84	3.2	86
38	Flt3 ligand structure and unexpected commonalities of helical bundles and cystine knots. <i>Nature Structural Biology</i> , <b>2000</b> , 7, 486-91		61
37	The insect immune protein scolexin is a novel serine proteinase homolog. <i>Protein Science</i> , <b>1999</b> , 8, 242-86.3		26
36	The flavin environment in old yellow enzyme. An evaluation of insights from spectroscopic and artificial flavin studies. <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 9357-62	5.4	22
35	A productive NADP+ binding mode of ferredoxin-NADP + reductase revealed by protein engineering and crystallographic studies. <i>Nature Structural Biology</i> , <b>1999</b> , 6, 847-53		158
34	Enzyme inactivation through sulphhydryl oxidation by physiologic NO-carriers. <i>Nature Structural Biology</i> , <b>1998</b> , 5, 267-71		140
33	Crystal structures of two mutants that have implications for the folding of bovine pancreatic ribonuclease A. <i>Protein Science</i> , <b>1998</b> , 7, 1255-8	6.3	36
32	Trypanocidal bisbenzylisoquinoline alkaloids are inhibitors of trypanothione reductase. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , <b>1998</b> , 13, 1-9		24
31	Chemical rescue of <i>Klebsiella aerogenes</i> urease variants lacking the carbamylated-lysine nickel ligand. <i>Biochemistry</i> , <b>1998</b> , 37, 6214-20	3.2	45
30	On the active site of Old Yellow Enzyme. Role of histidine 191 and asparagine 194. <i>Journal of Biological Chemistry</i> , <b>1998</b> , 273, 32753-62	5.4	105



29	Probing the function of the invariant glutamyl residue 312 in spinach ferredoxin-NADP+ reductase. <i>Journal of Biological Chemistry</i> , <b>1998</b> , 273, 34008-15	5.4	48
28	Roles of the catalytic domain and two cellulose binding domains of <i>Thermomonospora fusca</i> E4 in cellulose hydrolysis. <i>Journal of Bacteriology</i> , <b>1998</b> , 180, 1709-14	3.5	172
27	Structures of Cys319 variants and acetohydroxamate-inhibited <i>Klebsiella aerogenes</i> urease. <i>Biochemistry</i> , <b>1997</b> , 36, 8164-72	3.2	196
26	70 Years of Crystalline Urease: What Have We Learned?. <i>Accounts of Chemical Research</i> , <b>1997</b> , 30, 330-337	4.3	311
25	Improved R-factors for diffraction data analysis in macromolecular crystallography. <i>Nature Structural Biology</i> , <b>1997</b> , 4, 269-75		720
24	Structure and mechanism of endo/exocellulase E4 from <i>Thermomonospora fusca</i> . <i>Nature Structural Biology</i> , <b>1997</b> , 4, 810-8		309
23	Hydrophobicity regained. <i>Protein Science</i> , <b>1997</b> , 6, 1302-7	6.3	160
22	Backbone makes a significant contribution to the electrostatics of alpha/beta-barrel proteins. <i>Protein Science</i> , <b>1997</b> , 6, 1849-57	6.3	12
21	Structures of the <i>Klebsiella aerogenes</i> urease apoenzyme and two active-site mutants. <i>Biochemistry</i> , <b>1996</b> , 35, 10616-26	3.2	90
20	Crystal structure of thermostable family 5 endocellulase E1 from <i>Acidothermus cellulolyticus</i> in complex with cellotetraose. <i>Biochemistry</i> , <b>1996</b> , 35, 10648-60	3.2	223
19	Refined crystal structure and mutagenesis of human granulocyte-macrophage colony-stimulating factor. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1996</b> , 26, 304-13	4.2	50
18	Charge is the major discriminating factor for glutathione reductase versus trypanothione reductase inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , <b>1996</b> , 4, 1247-53	3.4	63
17	Experimentally observed conformation-dependent geometry and hidden strain in proteins. <i>Protein Science</i> , <b>1996</b> , 5, 1406-20	6.3	214
16	Kinetics and crystallographic analysis of human glutathione reductase in complex with a xanthene inhibitor. <i>Journal of Biological Chemistry</i> , <b>1996</b> , 271, 8101-7	5.4	64
15	Refined crystal structure and mutagenesis of human granulocyte-macrophage colony-stimulating factor <b>1996</b> , 26, 304		2
14	Consensus preferred hydration sites in six FKBP12-drug complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 23, 1-11	4.2	16
13	Urease activity in the crystalline state. <i>Protein Science</i> , <b>1995</b> , 4, 2234-6	6.3	16
12	Flavoprotein structure and mechanism. 8. Structure-function relations for old yellow enzyme. <i>FASEB Journal</i> , <b>1995</b> , 9, 1518-26	0.9	96

11	Involvement of serine 96 in the catalytic mechanism of ferredoxin-NADP+ reductase: structure-function relationship as studied by site-directed mutagenesis and X-ray crystallography. <i>Biochemistry</i> , <b>1995</b> , 34, 8371-9	3.2	67
10	Structure-Function Studies of Endo-1,4- $\beta$ -glucanase E2 from <i>Thermomonospora fusca</i> . <i>ACS Symposium Series</i> , <b>1994</b> , 66-74	0.4	
9	Structure-function relations for ferredoxin reductase. <i>Journal of Bioenergetics and Biomembranes</i> , <b>1994</b> , 26, 89-99	3.7	104
8	Crystal structure of the catalytic domain of a thermophilic endocellulase. <i>Biochemistry</i> , <b>1993</b> , 32, 9906-16	2	202
7	Structural prototypes for an extended family of flavoprotein reductases: comparison of phthalate dioxygenase reductase with ferredoxin reductase and ferredoxin. <i>Protein Science</i> , <b>1993</b> , 2, 2112-33	6.3	164
6	Low-resolution structure of recombinant human granulocyte-macrophage colony stimulating factor. <i>Journal of Molecular Biology</i> , <b>1991</b> , 221, 55-60	6.5	22
5	STRUCTURE/FUNCTION OF SPINACH FERREDOXIN:NADP+ OXIDOREDUCTASE <b>1991</b> , 449-456		3
4	A crystallographic study of the glutathione binding site of glutathione reductase at 0.3-nm resolution. <i>FEBS Journal</i> , <b>1989</b> , 178, 693-703		130
3	Inhibition of human glutathione reductase by the nitrosourea drugs 1,3-bis(2-chloroethyl)-1-nitrosourea and 1-(2-chloroethyl)-3-(2-hydroxyethyl)-1-nitrosourea. A crystallographic analysis. <i>FEBS Journal</i> , <b>1988</b> , 171, 193-8		66
2	Crystallographic analysis of the binding of NADPH, NADPH fragments, and NADPH analogues to glutathione reductase. <i>Biochemistry</i> , <b>1988</b> , 27, 4465-74	3.2	128
1	Amino acid sequence of spinach ferredoxin:NADP+ oxidoreductase. <i>Biochemistry</i> , <b>1984</b> , 23, 6576-83	3.2	109