

Paul Karplus

List of Publications by Year in descending order

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91
papers

14,753
citations

34493

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92
times ranked

18177
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluating Peroxiredoxin Sensitivity Toward Inactivation by Peroxide Substrates. <i>Methods in Enzymology</i> , 2013, 527, 21-40.	0.4	31
2	Better models by discarding data?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1215-1222.	2.5	202
3	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> , 2013, 425, 3121-3136.	2.0	59
4	Observed octameric assembly of a <i>Plasmodium yoelii</i> peroxiredoxin can be explained by the replacement of native α -ball-and-socket-interacting residues by an affinity tag. <i>Protein Science</i> , 2013, 22, 1445-1452.	3.1	10
5	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> , 2012, 109, 449-453.	3.3	63
6	Peroxiredoxins in Parasites. <i>Antioxidants and Redox Signaling</i> , 2012, 17, 608-633.	2.5	83
7	(β , γ) ₂ Motifs: A Purely Conformation-Based Fine-Grained Enumeration of Protein Parts at the Two-Residue Level. <i>Journal of Molecular Biology</i> , 2012, 416, 78-93.	2.0	25
8	Peroxiredoxins as Molecular Triage Agents, Sacrificing Themselves to Enhance Cell Survival During a Peroxide Attack. <i>Molecular Cell</i> , 2012, 45, 275-278.	4.5	18
9	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> , 2012, 22, 703-705.	3.1	56
10	Linking Crystallographic Model and Data Quality. <i>Science</i> , 2012, 336, 1030-1033.	6.0	1,637
11	Structure-based Insights into the Catalytic Power and Conformational Dexterity of Peroxiredoxins. <i>Antioxidants and Redox Signaling</i> , 2011, 15, 795-815.	2.5	289
12	Symerythrin Structures at Atomic Resolution and the Origins of Rubrerythrins and the Ferritin-Like Superfamily. <i>Journal of Molecular Biology</i> , 2011, 413, 177-194.	2.0	16
13	Cysteine-Based Redox Switches in Enzymes. <i>Antioxidants and Redox Signaling</i> , 2011, 14, 1065-1077.	2.5	327
14	Thiol dioxygenases: unique families of cupin proteins. <i>Amino Acids</i> , 2011, 41, 91-102.	1.2	98
15	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> , 2011, 302, 93-100.	0.7	8
16	A conformation-dependent stereochemical library improves crystallographic refinement even at atomic resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 699-706.	2.5	25
17	A Diiron Protein Autogenerates a Valine-Phenylalanine Cross-Link. <i>Science</i> , 2011, 332, 929-929.	6.0	16
18	Iron-containing urease in a pathogenic bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13095-13099.	3.3	64

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19	Using a conformation-dependent stereochemical library improves crystallographic refinement of proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 834-842.	2.5	36
20	The Crystal Structure of Dynein Intermediate Chain-Light Chain Roadblock Complex Gives New Insights into Dynein Assembly. <i>Journal of Biological Chemistry</i> , 2010, 285, 22566-22575.	1.6	39
21	Engineering of Fluorescent Reporters into Redox Domains to Monitor Electron Transfers. <i>Methods in Enzymology</i> , 2010, 474, 1-21.	0.4	5
22	Structural Evidence that Peroxiredoxin Catalytic Power Is Based on Transition-State Stabilization. <i>Journal of Molecular Biology</i> , 2010, 402, 194-209.	2.0	156
23	Evolutionary Origin of a Secondary Structure: Î±-Helices as Cryptic but Widespread Insertional Variations of Î±-Helices That Enhance Protein Functionality. <i>Journal of Molecular Biology</i> , 2010, 404, 232-246.	2.0	143
24	Characterization of Sulfoxxygenation and Structural Implications of Human Flavin-Containing Monooxygenase Isoform 2 (FMO2.1) Variants S195L and N413K. <i>Drug Metabolism and Disposition</i> , 2009, 37, 1785-1791.	1.7	10
25	Multivalency in the Assembly of Intrinsically Disordered Dynein Intermediate Chain. <i>Journal of Biological Chemistry</i> , 2009, 284, 33115-33121.	1.6	66
26	Conformation Dependence of Backbone Geometry in Proteins. <i>Structure</i> , 2009, 17, 1316-1325.	1.6	94
27	On the occurrence of linear groups in proteins. <i>Protein Science</i> , 2009, 18, 1321-1325.	3.1	37
28	Structure of the Cdt1 C-terminal domain: Conservation of the winged helix fold in replication licensing factors. <i>Protein Science</i> , 2009, 18, 2252-2264.	3.1	33
29	Typical 2â€Cys peroxiredoxins â€ structures, mechanisms and functions. <i>FEBS Journal</i> , 2009, 276, 2469-2477.	2.2	401
30	Structural Changes Common to Catalysis in the Tpx Peroxiredoxin Subfamily. <i>Journal of Molecular Biology</i> , 2009, 393, 867-881.	2.0	51
31	A forward-looking suggestion for resolving the stereochemical restraints debate: ideal geometry functions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 335-336.	2.5	14
32	Catalytic Cycle of Human Glutathione Reductase Near 1Å.. Resolution. <i>Journal of Molecular Biology</i> , 2008, 382, 371-384.	2.0	97
33	The Interplay of Ligand Binding and Quaternary Structure in the Diverse Interactions of Dynein Light Chain LC8. <i>Journal of Molecular Biology</i> , 2008, 384, 954-966.	2.0	36
34	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> , 2008, 105, 8209-8214.	3.3	146
35	The Arg-Gly-Aspâ€Containing, Solvent-Exposed Loop of Ptr ToxA Is Required for Internalization. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 315-325.	1.4	79
36	Self-masking in an Intact ERM-merlin Protein: An Active Role for the Central Î±-Helical Domain. <i>Journal of Molecular Biology</i> , 2007, 365, 1446-1459.	2.0	111

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37	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> , 2007, 371, 457-468.	2.0	75
38	Structural Characterization of Zinc-deficient Human Superoxide Dismutase and Implications for ALS. <i>Journal of Molecular Biology</i> , 2007, 373, 877-890.	2.0	122
39	C-terminal truncation of rabbit flavin-containing monooxygenase isoform 2 enhances solubility. <i>Archives of Biochemistry and Biophysics</i> , 2006, 450, 149-156.	1.4	6
40	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> , 2006, 62, 707-716.	2.5	26
41	Song: Chymotrypsin (to the tune of "eight days a week," by the Beatles). <i>Biochemistry and Molecular Biology Education</i> , 2006, 34, 287-287.	0.5	1
42	Song: Enzymes speed reactions (to the tune of "we will rock you," by Queen). <i>Biochemistry and Molecular Biology Education</i> , 2006, 34, 286-286.	0.5	0
43	Song: Learn about the buffer (generic rap). <i>Biochemistry and Molecular Biology Education</i> , 2006, 34, 285-285.	0.5	0
44	Identification and Characterization of Bacterial Cysteine Dioxygenases: a New Route of Cysteine Degradation for Eubacteria. <i>Journal of Bacteriology</i> , 2006, 188, 5561-5569.	1.0	92
45	Crystal Structure of Mammalian Cysteine Dioxygenase. <i>Journal of Biological Chemistry</i> , 2006, 281, 18723-18733.	1.6	148
46	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> , 2005, 14, 2414-2420.	3.1	39
47	Structure of Ptr ToxA: An RGD-Containing Host-Selective Toxin from <i>Pyrenophora tritici-repentis</i> . <i>Plant Cell</i> , 2005, 17, 3190-3202.	3.1	119
48	Crystal Structure of a Novel <i>Plasmodium falciparum</i> 1-Cys Peroxiredoxin. <i>Journal of Molecular Biology</i> , 2005, 346, 1021-1034.	2.0	92
49	A Novel Mechanism of Chemoprotection by Sulforaphane. <i>Cancer Research</i> , 2004, 64, 5767-5774.	0.4	477
50	The EBP50-moesin interaction involves a binding site regulated by direct masking on the FERM domain. <i>Journal of Cell Science</i> , 2004, 117, 1547-1552.	1.2	68
51	PROTEINSULFENICACIDS IN REDOX SIGNALING. <i>Annual Review of Pharmacology and Toxicology</i> , 2004, 44, 325-347.	4.2	542
52	Structural Aspects of Plant Ferredoxin : NADP+Oxidoreductases. <i>Photosynthesis Research</i> , 2004, 81, 303-315.	1.6	37
53	Glutathione Reductase of the Malarial Parasite <i>Plasmodium falciparum</i> : Crystal Structure and Inhibitor Development. <i>Journal of Molecular Biology</i> , 2003, 328, 893-907.	2.0	120
54	Peroxiredoxin Evolution and the Regulation of Hydrogen Peroxide Signaling. <i>Science</i> , 2003, 300, 650-653.	6.0	1,236

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55	Structure of the Active N-terminal Domain of Ezrin. <i>Journal of Biological Chemistry</i> , 2003, 278, 4949-4956.	1.6	95
56	The Role of Glutamine 114 in Old Yellow Enzyme. <i>Journal of Biological Chemistry</i> , 2002, 277, 2138-2145.	1.6	42
57	Synthesis and Characterization of Photolabile o-Nitrobenzyl Derivatives of Urea. <i>Journal of Organic Chemistry</i> , 2002, 67, 8827-8831.	1.7	19
58	Crystal Structure of the Antioxidant Enzyme Glutathione Reductase Inactivated by Peroxynitrite. <i>Journal of Biological Chemistry</i> , 2002, 277, 2779-2784.	1.6	113
59	Relatedness of baculovirus and gypsy retrotransposon envelope proteins. <i>BMC Evolutionary Biology</i> , 2001, 1, 1.	3.2	82
60	AhpF and other NADH:peroxiredoxin oxidoreductases, homologues of low Mr thioredoxin reductase. <i>FEBS Journal</i> , 2000, 267, 6126-6133.	0.2	118
61	Competition between C-terminal Tyrosine and Nicotinamide Modulates Pyridine Nucleotide Affinity and Specificity in Plant Ferredoxin-NADP+ Reductase. <i>Journal of Biological Chemistry</i> , 2000, 275, 10472-10476.	1.6	81
62	Site-Directed Mutagenesis Improves Catalytic Efficiency and Thermostability of Escherichia coli pH 2.5 Acid Phosphatase/Phytase Expressed in Pichia pastoris. <i>Archives of Biochemistry and Biophysics</i> , 2000, 382, 105-112.	1.4	109
63	Structure of the ERM Protein Moesin Reveals the FERM Domain Fold Masked by an Extended Actin Binding Tail Domain. <i>Cell</i> , 2000, 101, 259-270.	13.5	555
64	The Flavin Environment in Old Yellow Enzyme. <i>Journal of Biological Chemistry</i> , 1999, 274, 9357-9362.	1.6	25
65	A productive NADP+ binding mode of ferredoxin-NADP + reductase revealed by protein engineering and crystallographic studies. <i>Nature Structural Biology</i> , 1999, 6, 847-853.	9.7	181
66	Characterization of metal-substituted Klebsiella aerogenes urease. <i>Journal of Biological Inorganic Chemistry</i> , 1999, 4, 468-477.	1.1	34
67	Enzyme inactivation through sulfhydryl oxidation by physiologic NO-carriers. <i>Nature Structural Biology</i> , 1998, 5, 267-271.	9.7	147
68	On the Active Site of Old Yellow Enzyme. <i>Journal of Biological Chemistry</i> , 1998, 273, 32753-32762.	1.6	111
69	Probing the Function of the Invariant Glutamyl Residue 312 in Spinach Ferredoxin-NADP+ Reductase. <i>Journal of Biological Chemistry</i> , 1998, 273, 34008-34015.	1.6	52
70	Improved R-factors for diffraction data analysis in macromolecular crystallography. <i>Nature Structural Biology</i> , 1997, 4, 269-275.	9.7	786
71	Structure and mechanism of endo/exocellulase E4 from Thermomonospora fusca. <i>Nature Structural Biology</i> , 1997, 4, 810-818.	9.7	349
72	Refined crystal structure and mutagenesis of human granulocyte-macrophage colony-stimulating factor., 1996, 26, 304-313.		57

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73	Charge is the major discriminating factor for glutathione reductase versus trypanothione reductase inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 1996, 4, 1247-1253.	1.4	66
74	Kinetics and Crystallographic Analysis of Human Glutathione Reductase in Complex with a Xanthene Inhibitor. <i>Journal of Biological Chemistry</i> , 1996, 271, 8101-8107.	1.6	73
75	Characterization of the Mononickel Metallocenter in H134A Mutant Urease. <i>Journal of Biological Chemistry</i> , 1996, 271, 18632-18637.	1.6	33
76	Overexpression of <i>Crithidia fasciculata</i> trypanothione reductase and crystallization using a novel geometry. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 337-341.	2.5	2
77	Consensus preferred hydration sites in six FKBP12-drug complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 23, 1-11.	1.5	18
78	Probing the Roles of Active Site Residues in D-Xylose Isomerase. <i>Journal of Biological Chemistry</i> , 1995, 270, 22895-22906.	1.6	66
79	Refined Crystal Structure of Spinach Ferredoxin Reductase at 1.7 Å... Resolution: Oxidized, Reduced and 2-Phospho-5-AMP Bound States. <i>Journal of Molecular Biology</i> , 1995, 247, 125-145.	2.0	196
80	Structure-function relations for ferredoxin reductase. <i>Journal of Bioenergetics and Biomembranes</i> , 1994, 26, 89-99.	1.0	110
81	Structural comparisons among the short-chain helical cytokines. <i>Structure</i> , 1994, 2, 159-173.	1.6	162
82	Atomic Structures of the Human Immunophilin FKBP-12 Complexes with FK506 and Rapamycin. <i>Journal of Molecular Biology</i> , 1993, 229, 105-124.	2.0	1,158
83	Crystallization of Old Yellow Enzyme Illustrates an Effective Strategy for Increasing Protein Crystal Size. <i>Journal of Molecular Biology</i> , 1993, 234, 502-507.	2.0	7
84	Preliminary crystallographic studies of urease from jack bean and from <i>Klebsiella aerogenes</i> . <i>Journal of Molecular Biology</i> , 1992, 227, 934-937.	2.0	53
85	Low-resolution structure of recombinant human granulocyte-macrophage colony stimulating factor. <i>Journal of Molecular Biology</i> , 1991, 221, 55-60.	2.0	23
86	Atomic structure of FKBP-FK506, an immunophilin-immunosuppressant complex. <i>Science</i> , 1991, 252, 839-842.	6.0	638
87	Novel fold and putative receptor binding site of granulocyte-macrophage colony-stimulating factor. <i>Science</i> , 1991, 254, 1779-1782.	6.0	218
88	A crystallographic study of the glutathione binding site of glutathione reductase at 0.3-nm resolution. <i>FEBS Journal</i> , 1989, 178, 693-703.	0.2	143
89	Substrate binding and catalysis by glutathione reductase as derived from refined enzyme: Substrate crystal structures at 2 Å... resolution. <i>Journal of Molecular Biology</i> , 1989, 210, 163-180.	2.0	299
90	Refined structure of porcine cytosolic adenylate kinase at 2.1 Å... resolution. <i>Journal of Molecular Biology</i> , 1988, 199, 359-371.	2.0	251

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91	Refined structure of glutathione reductase at 1.54 Å... resolution. Journal of Molecular Biology, 1987, 195, 701-729.	2.0	498