

Paul 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.

91
papers

13,069
citations

52
h-index

92
g-index

92
ext. papers

13,936
ext. citations

8.1
avg. IF

6.5
L-index

#	Paper	IF	Citations
91	Evaluating peroxiredoxin sensitivity toward inactivation by peroxide substrates. <i>Methods in Enzymology</i> , 2013 , 527, 21-40	1.7	27
90	Better models by discarding data?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 1215-22		183
89	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, 3121-36	6.5	52
88	Observed octameric assembly of a Plasmodium yoelii peroxiredoxin can be explained by the replacement of native "ball-and-socket" interacting residues by an affinity tag. <i>Protein Science</i> , 2013 , 22, 1445-52	6.3	10
87	Peroxiredoxins in parasites. <i>Antioxidants and Redox Signaling</i> , 2012 , 17, 608-33	8.4	69
86	Ⓜ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	6.5	19
85	Peroxiredoxins as molecular triage agents, sacrificing themselves to enhance cell survival during a peroxide attack. <i>Molecular Cell</i> , 2012 , 45, 275-8	17.6	16
84	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, 703-5	10.2	44
83	Linking crystallographic model and data quality. <i>Science</i> , 2012 , 336, 1030-3	33.3	1329
82	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, 449-53	11.5	51
81	Structure-based insights into the catalytic power and conformational dexterity of peroxiredoxins. <i>Antioxidants and Redox Signaling</i> , 2011 , 15, 795-815	8.4	236
80	Symerythrin structures at atomic resolution and the origins of rubrerythrins and the ferritin-like superfamily. <i>Journal of Molecular Biology</i> , 2011 , 413, 177-94	6.5	16
79	Cysteine-based redox switches in enzymes. <i>Antioxidants and Redox Signaling</i> , 2011 , 14, 1065-77	8.4	272
78	Thiol dioxygenases: unique families of cupin proteins. <i>Amino Acids</i> , 2011 , 41, 91-102	3.5	76
77	Conformational studies of the robust 2-Cys peroxiredoxin Salmonella typhimurium 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	1.9	7
76	A conformation-dependent stereochemical library improves crystallographic refinement even at atomic resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011 , 67, 699-706		22
75	A diiron protein autogenerates a valine-phenylalanine cross-link. <i>Science</i> , 2011 , 332, 929	33.3	12

74	Iron-containing urease in a pathogenic bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 13095-9	11.5	53
73	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, 22566-75	5.4	36
72	Engineering of fluorescent reporters into redox domains to monitor electron transfers. <i>Methods in Enzymology</i> , 2010 , 474, 1-21	1.7	5
71	Structural evidence that peroxiredoxin catalytic power is based on transition-state stabilization. <i>Journal of Molecular Biology</i> , 2010 , 402, 194-209	6.5	136
70	Evolutionary origin of a secondary structure: α helices as cryptic but widespread insertional variations of α helices that enhance protein functionality. <i>Journal of Molecular Biology</i> , 2010 , 404, 232-46	6.5	113
69	Using a conformation-dependent stereochemical library improves crystallographic refinement of proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010 , 66, 834-42		32
68	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, 1785-91	4	9
67	Multivalency in the assembly of intrinsically disordered Dynein intermediate chain. <i>Journal of Biological Chemistry</i> , 2009 , 284, 33115-21	5.4	57
66	Conformation dependence of backbone geometry in proteins. <i>Structure</i> , 2009 , 17, 1316-25	5.2	79
65	On the occurrence of linear groups in proteins. <i>Protein Science</i> , 2009 , 18, 1321-5	6.3	32
64	Structure of the Cdt1 C-terminal domain: conservation of the winged helix fold in replication licensing factors. <i>Protein Science</i> , 2009 , 18, 2252-64	6.3	28
63	Typical 2-Cys peroxiredoxins--structures, mechanisms and functions. <i>FEBS Journal</i> , 2009 , 276, 2469-77	5.7	361
62	Structural changes common to catalysis in the Tpx peroxiredoxin subfamily. <i>Journal of Molecular Biology</i> , 2009 , 393, 867-81	6.5	42
61	Catalytic cycle of human glutathione reductase near 1 Å resolution. <i>Journal of Molecular Biology</i> , 2008 , 382, 371-84	6.5	76
60	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, 954-66	6.5	33
59	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, 8209-14	11.5	126
58	The Arg-Gly-Asp-containing, solvent-exposed loop of Ptr ToxA is required for internalization. <i>Molecular Plant-Microbe Interactions</i> , 2008 , 21, 315-25	3.6	65
57	A forward-looking suggestion for resolving the stereochemical restraints debate: ideal geometry functions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008 , 64, 335-6		14

56	Self-masking in an intact ERM-merlin protein: an active role for the central alpha-helical domain. <i>Journal of Molecular Biology</i> , 2007 , 365, 1446-59	6.5	89
55	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, 457-68	6.5	70
54	Structural characterization of zinc-deficient human superoxide dismutase and implications for ALS. <i>Journal of Molecular Biology</i> , 2007 , 373, 877-90	6.5	107
53	Song: Chymotrypsin (to the tune of "eight days a week," by the beatles)*. <i>Biochemistry and Molecular Biology Education</i> , 2006 , 34, 287	1.3	0
52	Song: Enzymes speed reactions (to the tune of "we will rock you," by queen)*S. <i>Biochemistry and Molecular Biology Education</i> , 2006 , 34, 286	1.3	
51	Song: Learn about the buffer (generic rap)*. <i>Biochemistry and Molecular Biology Education</i> , 2006 , 34, 285	1.3	
50	Identification and characterization of bacterial cysteine dioxygenases: a new route of cysteine degradation for eubacteria. <i>Journal of Bacteriology</i> , 2006 , 188, 5561-9	3.5	81
49	Crystal structure of mammalian cysteine dioxygenase. A novel mononuclear iron center for cysteine thiol oxidation. <i>Journal of Biological Chemistry</i> , 2006 , 281, 18723-33	5.4	131
48	C-Terminal truncation of rabbit flavin-containing monooxygenase isoform 2 enhances solubility. <i>Archives of Biochemistry and Biophysics</i> , 2006 , 450, 149-56	4.1	6
47	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, 707-16		25
46	Crystal structure of a novel Plasmodium falciparum 1-Cys peroxiredoxin. <i>Journal of Molecular Biology</i> , 2005 , 346, 1021-34	6.5	81
45	Oxidized and synchrotron cleaved structures of the disulfide redox center in the N-terminal domain of Salmonella typhimurium AhpF. <i>Protein Science</i> , 2005 , 14, 2414-20	6.3	38
44	Structure of Ptr ToxA: an RGD-containing host-selective toxin from Pyrenophora tritici-repentis. <i>Plant Cell</i> , 2005 , 17, 3190-202	11.6	85
43	A novel mechanism of chemoprotection by sulforaphane: inhibition of histone deacetylase. <i>Cancer Research</i> , 2004 , 64, 5767-74	10.1	427
42	The EBP50-moesin interaction involves a binding site regulated by direct masking on the FERM domain. <i>Journal of Cell Science</i> , 2004 , 117, 1547-52	5.3	60
41	Protein sulfenic acids in redox signaling. <i>Annual Review of Pharmacology and Toxicology</i> , 2004 , 44, 325-47	7.9	511
40	Structural Aspects of Plant Ferredoxin : NADP(+) Oxidoreductases. <i>Photosynthesis Research</i> , 2004 , 81, 303-15	3.7	34
39	Structure of the active N-terminal domain of Ezrin. Conformational and mobility changes identify keystone interactions. <i>Journal of Biological Chemistry</i> , 2003 , 278, 4949-56	5.4	85

38	Glutathione reductase of the malarial parasite Plasmodium falciparum: crystal structure and inhibitor development. <i>Journal of Molecular Biology</i> , 2003 , 328, 893-907	6.5	108
37	Peroxiredoxin evolution and the regulation of hydrogen peroxide signaling. <i>Science</i> , 2003 , 300, 650-3	33.3	1132
36	The role of glutamine 114 in old yellow enzyme. <i>Journal of Biological Chemistry</i> , 2002 , 277, 2138-45	5.4	38
35	Synthesis and characterization of photolabile o-nitrobenzyl derivatives of urea. <i>Journal of Organic Chemistry</i> , 2002 , 67, 8827-31	4.2	19
34	Crystal structure of the antioxidant enzyme glutathione reductase inactivated by peroxyxynitrite. <i>Journal of Biological Chemistry</i> , 2002 , 277, 2779-84	5.4	102
33	Relatedness of baculovirus and gypsy retrotransposon envelope proteins. <i>BMC Evolutionary Biology</i> , 2001 , 1, 1	3	61
32	AhpF and other NADH:peroxiredoxin oxidoreductases, homologues of low Mr thioredoxin reductase. <i>FEBS Journal</i> , 2000 , 267, 6126-33		108
31	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, 10472-6	5.4	74
30	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, 105-12	4.1	99
29	Structure of the ERM protein moesin reveals the FERM domain fold masked by an extended actin binding tail domain. <i>Cell</i> , 2000 , 101, 259-70	56.2	498
28	The flavin environment in old yellow enzyme. An evaluation of insights from spectroscopic and artificial flavin studies. <i>Journal of Biological Chemistry</i> , 1999 , 274, 9357-62	5.4	22
27	A productive NADP+ binding mode of ferredoxin-NADP + reductase revealed by protein engineering and crystallographic studies. <i>Nature Structural Biology</i> , 1999 , 6, 847-53		158
26	Characterization of metal-substituted Klebsiella aerogenes urease. <i>Journal of Biological Inorganic Chemistry</i> , 1999 , 4, 468-77	3.7	28
25	Enzyme inactivation through sulphhydryl oxidation by physiologic NO-carriers. <i>Nature Structural Biology</i> , 1998 , 5, 267-71		140
24	On the active site of Old Yellow Enzyme. Role of histidine 191 and asparagine 194. <i>Journal of Biological Chemistry</i> , 1998 , 273, 32753-62	5.4	105
23	Probing the function of the invariant glutamyl residue 312 in spinach ferredoxin-NADP+ reductase. <i>Journal of Biological Chemistry</i> , 1998 , 273, 34008-15	5.4	48
22	Improved R-factors for diffraction data analysis in macromolecular crystallography. <i>Nature Structural Biology</i> , 1997 , 4, 269-75		720
21	Structure and mechanism of endo/exocellulase E4 from Thermomonospora fusca. <i>Nature Structural Biology</i> , 1997 , 4, 810-8		309

20	Refined crystal structure and mutagenesis of human granulocyte-macrophage colony-stimulating factor. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 26, 304-13	4.2	50
19	Charge is the major discriminating factor for glutathione reductase versus trypanothione reductase inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 1996 , 4, 1247-53	3.4	63
18	Kinetics and crystallographic analysis of human glutathione reductase in complex with a xanthene inhibitor. <i>Journal of Biological Chemistry</i> , 1996 , 271, 8101-7	5.4	64
17	Characterization of the mononickel metalcenter in H134A mutant urease. <i>Journal of Biological Chemistry</i> , 1996 , 271, 18632-7	5.4	31
16	Consensus preferred hydration sites in six FKBP12-drug complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 23, 1-11	4.2	16
15	Probing the roles of active site residues in D-xylose isomerase. <i>Journal of Biological Chemistry</i> , 1995 , 270, 22895-906	5.4	62
14	Refined crystal structure of spinach ferredoxin reductase at 1.7 Å resolution: oxidized, reduced and 2Qphospho-5QAMP bound states. <i>Journal of Molecular Biology</i> , 1995 , 247, 125-45	6.5	177
13	Overexpression of <i>Crithidia fasciculata</i> trypanothione reductase and crystallization using a novel geometry. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995 , 51, 337-41		2
12	Structure-function relations for ferredoxin reductase. <i>Journal of Bioenergetics and Biomembranes</i> , 1994 , 26, 89-99	3.7	104
11	Structural comparisons among the short-chain helical cytokines. <i>Structure</i> , 1994 , 2, 159-73	5.2	151
10	Atomic structures of the human immunophilin FKBP-12 complexes with FK506 and rapamycin. <i>Journal of Molecular Biology</i> , 1993 , 229, 105-24	6.5	1079
9	Crystallization of Old Yellow Enzyme illustrates an effective strategy for increasing protein crystal size. <i>Journal of Molecular Biology</i> , 1993 , 234, 502-7	6.5	6
8	Preliminary crystallographic studies of urease from jack bean and from <i>Klebsiella aerogenes</i> . <i>Journal of Molecular Biology</i> , 1992 , 227, 934-7	6.5	47
7	Atomic structure of FKBP-FK506, an immunophilin-immunosuppressant complex. <i>Science</i> , 1991 , 252, 839-42	33.3	582
6	Novel fold and putative receptor binding site of granulocyte-macrophage colony-stimulating factor. <i>Science</i> , 1991 , 254, 1779-82	33.3	201
5	Low-resolution structure of recombinant human granulocyte-macrophage colony stimulating factor. <i>Journal of Molecular Biology</i> , 1991 , 221, 55-60	6.5	22
4	A crystallographic study of the glutathione binding site of glutathione reductase at 0.3-nm resolution. <i>FEBS Journal</i> , 1989 , 178, 693-703		130
3	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, 163-80	6.5	272

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| 2 | Refined structure of porcine cytosolic adenylate kinase at 2.1 Å resolution. <i>Journal of Molecular Biology</i> , 1988 , 199, 359-71 | 6.5 | 231 |
| 1 | Refined structure of glutathione reductase at 1.54 Å resolution. <i>Journal of Molecular Biology</i> , 1987 , 195, 701-29 | 6.5 | 442 |