

Peter C E Moody

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.

83

papers

4,596

citations

36

h-index

67

g-index

90

ext. papers

4,961

ext. citations

8.6

avg, IF

4.98

L-index

#	Paper	IF	Citations
83	XFEL Crystal Structures of Peroxidase Compound II. <i>Angewandte Chemie - International Edition</i> , 2021 , 60, 14578-14585	16.4	8
82	XFEL Crystal Structures of Peroxidase Compound II. <i>Angewandte Chemie</i> , 2021 , 133, 14699-14706	3.6	
81	Crystal structures of a dual coenzyme specific glyceraldehyde-3-phosphate dehydrogenase from the enteric pathogen <i>Campylobacter jejuni</i> . <i>Journal of Molecular Structure</i> , 2021 , 1242, 130820	3.4	2
80	Visualizing the protons in a metalloenzyme electron proton transfer pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 6484-6490	11.5	16
79	Activity of fructose-1,6-bisphosphatase from. <i>Biochemistry and Cell Biology</i> , 2020 , 98, 518-524	3.6	1
78	Heme peroxidase-Trapping intermediates by cryo neutron crystallography. <i>Methods in Enzymology</i> , 2020 , 634, 379-389	1.7	1
77	Discovery of a heme-binding domain in a neuronal voltage-gated potassium channel. <i>Journal of Biological Chemistry</i> , 2020 , 295, 13277-13286	5.4	6
76	Heme binding to human CLOCK affects interactions with the E-box. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 19911-19916	11.5	16
75	A mechanism for CO regulation of ion channels. <i>Nature Communications</i> , 2018 , 9, 907	17.4	27
74	Reply to Mortensen et al.: The zymogen form of complement component C1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E3867-E3868	11.5	1
73	The role of Ala134 in controlling substrate binding and reactivity in ascorbate peroxidase. <i>Journal of Inorganic Biochemistry</i> , 2018 , 180, 230-234	4.2	5
72	The Nature and Reactivity of Ferryl Heme in Compounds I and II. <i>Accounts of Chemical Research</i> , 2018 , 51, 427-435	24.3	72
71	Structure of the C1r-C1s interaction of the C1 complex of complement activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 768-773	11.5	25
70	The rise of neutron cryo-crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018 , 74, 792-799	5.5	7
69	Combining X-ray and neutron crystallography with spectroscopy. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017 , 73, 141-147	5.5	15
68	Structural and spectroscopic characterisation of a heme peroxidase from sorghum. <i>Journal of Biological Inorganic Chemistry</i> , 2016 , 21, 63-70	3.7	12
67	Direct visualization of a Fe(IV)-OH intermediate in a heme enzyme. <i>Nature Communications</i> , 2016 , 7, 13445.4	5.4	47

66	A heme-binding domain controls regulation of ATP-dependent potassium channels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 3785-90	11.5	36
65	The Crystal Structure of Pneumolysin at 2.0 Å Resolution Reveals the Molecular Packing of the Pre-pore Complex. <i>Scientific Reports</i> , 2015 , 5, 13293	4.9	37
64	Molecular basis of sugar recognition by collectin-K1 and the effects of mutations associated with 3MC syndrome. <i>BMC Biology</i> , 2015 , 13, 27	7.3	35
63	Chapter 3: Understanding the Reactivity and Interactions of Peroxidases with Substrates. <i>2-Oxoglutarate-Dependent Oxygenases</i> , 2015 , 47-60	1.8	2
62	Heme enzymes. Neutron cryo-crystallography captures the protonation state of ferryl heme in a peroxidase. <i>Science</i> , 2014 , 345, 193-7	33.3	115
61	Redox-linked domain movements in the catalytic cycle of cytochrome p450 reductase. <i>Structure</i> , 2013 , 21, 1581-9	5.2	57
60	Structure of Cu(I)-bound DJ-1 reveals a biscysteinate metal binding site at the homodimer interface: insights into mutational inactivation of DJ-1 in Parkinsonism. <i>Journal of the American Chemical Society</i> , 2013 , 135, 15974-7	16.4	14
59	Probing the conformational mobility of the active site of a heme peroxidase. <i>Dalton Transactions</i> , 2013 , 42, 3170-5	4.3	3
58	Structural basis of the C1q/C1s interaction and its central role in assembly of the C1 complex of complement activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 13916-20	11.5	77
57	Crystal structure of guaiacol and phenol bound to a heme peroxidase. <i>FEBS Journal</i> , 2012 , 279, 1632-9	5.7	23
56	How is the distal pocket of a heme protein optimized for binding of tryptophan?. <i>FEBS Journal</i> , 2012 , 279, 4501-9	5.7	20
55	Structural basis of mannan-binding lectin recognition by its associated serine protease MASP-1: implications for complement activation. <i>Structure</i> , 2011 , 19, 1635-43	5.2	53
54	Expression, purification, crystallization and preliminary X-ray analysis of wild-type and of an active-site mutant of glyceraldehyde-3-phosphate dehydrogenase from <i>Campylobacter jejuni</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 72-5		1
53	Proton delivery to ferryl heme in a heme peroxidase: enzymatic use of the Grothuss mechanism. <i>Journal of the American Chemical Society</i> , 2011 , 133, 15376-83	16.4	31
52	Nature of the ferryl heme in compounds I and II. <i>Journal of Biological Chemistry</i> , 2011 , 286, 1260-8	5.4	81
51	Comparison of the regulation, metabolic functions, and roles in virulence of the glyceraldehyde-3-phosphate dehydrogenase homologues gapA and gapB in <i>Staphylococcus aureus</i> . <i>Infection and Immunity</i> , 2010 , 78, 5223-32	3.7	52
50	An analysis of substrate binding interactions in the heme peroxidase enzymes: a structural perspective. <i>Archives of Biochemistry and Biophysics</i> , 2010 , 500, 13-20	4.1	57
49	Evidence for heme oxygenase activity in a heme peroxidase. <i>Biochemistry</i> , 2009 , 48, 4738-46	3.2	5

48	Iron oxidation state modulates active site structure in a heme peroxidase. <i>Biochemistry</i> , 2008 , 47, 4403-9	3.2	11
47	The role of serine 167 in human indoleamine 2,3-dioxygenase: a comparison with tryptophan 2,3-dioxygenase. <i>Biochemistry</i> , 2008 , 47, 4761-9	3.2	58
46	Engineering the substrate specificity and reactivity of a heme protein: creation of an ascorbate binding site in cytochrome c peroxidase. <i>Biochemistry</i> , 2008 , 47, 13933-41	3.2	21
45	The tuberculosis prodrug isoniazid bound to activating peroxidases. <i>Journal of Biological Chemistry</i> , 2008 , 283, 6193-200	5.4	59
44	Expression, purification, crystallization and preliminary X-ray analysis of an NADP-dependent glyceraldehyde-3-phosphate dehydrogenase from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 723-6		1
43	Expression, purification, crystallization and preliminary X-ray analysis of an NAD-dependent glyceraldehyde-3-phosphate dehydrogenase from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 727-9		1
42	The redox properties of ascorbate peroxidase. <i>Biochemistry</i> , 2007 , 46, 8017-23	3.2	30
41	Filling a hole in cytochrome P450 BM3 improves substrate binding and catalytic efficiency. <i>Journal of Molecular Biology</i> , 2007 , 373, 633-51	6.5	64
40	Conformational mobility in the active site of a heme peroxidase. <i>Journal of Biological Chemistry</i> , 2006 , 281, 24512-20	5.4	22
39	Interaction of ascorbate peroxidase with substrates: a mechanistic and structural analysis. <i>Biochemistry</i> , 2006 , 45, 7808-17	3.2	40
38	Enzyme-catalyzed mechanism of isoniazid activation in class I and class III peroxidases. <i>Journal of Biological Chemistry</i> , 2004 , 279, 39000-9	5.4	45
37	The structure and mechanism of serine acetyltransferase from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2004 , 279, 40729-36	5.4	75
36	Atomic resolution structures and solution behavior of enzyme-substrate complexes of <i>Enterobacter cloacae</i> PB2 pentaerythritol tetranitrate reductase. Multiple conformational states and implications for the mechanism of nitroaromatic explosive degradation. <i>Journal of Biological Chemistry</i> , 2004 , 279, 30563-72	5.4	37
35	Crystal structure of the ascorbate peroxidase-salicylhydroxamic acid complex. <i>Biochemistry</i> , 2004 , 43, 8644-51	3.2	50
34	Defining substrate specificity and catalytic mechanism in ascorbate peroxidase. <i>Biochemical Society Symposia</i> , 2004 , 27-38		12
33	Crystal structure of the ascorbate peroxidase-ascorbate complex. <i>Nature Structural and Molecular Biology</i> , 2003 , 10, 303-7	17.6	147
32	A new framework for understanding substrate binding and functional diversity in haem peroxidases. <i>Dalton Transactions</i> , 2003 , 4208	4.3	10
31	Crystal structure of bacterial morphinone reductase and properties of the C191A mutant enzyme. <i>Journal of Biological Chemistry</i> , 2002 , 277, 30976-83	5.4	61

30	Kinetic and structural basis of reactivity of pentaerythritol tetranitrate reductase with NADPH, 2-cyclohexenone, nitroesters, and nitroaromatic explosives. <i>Journal of Biological Chemistry</i> , 2002 , 277, 21906-12	5.4	69
29	Effects of environment on flavin reactivity in morphinone reductase: analysis of enzymes displaying differential charge near the N-1 atom and C-2 carbonyl region of the active-site flavin. <i>Biochemical Journal</i> , 2001 , 359, 315-23	3.8	10
28	Effects of environment on flavin reactivity in morphinone reductase: analysis of enzymes displaying differential charge near the N-1 atom and C-2 carbonyl region of the active-site flavin. <i>Biochemical Journal</i> , 2001 , 359, 315-323	3.8	15
27	Crystal structure of pentaerythritol tetranitrate reductase: "flipped" binding geometries for steroid substrates in different redox states of the enzyme. <i>Journal of Molecular Biology</i> , 2001 , 310, 433-47	6.5	92
26	Degradation of explosives by nitrate ester reductases. <i>Biochemical Society Symposia</i> , 2001 , 68, 143-53		10
25	Serine acetyltransferase from <i>Escherichia coli</i> is a dimer of trimers. <i>Journal of Biological Chemistry</i> , 2000 , 275, 461-6	5.4	45
24	Crystal structure of the human O(6)-alkylguanine-DNA alkyltransferase. <i>Nucleic Acids Research</i> , 2000 , 28, 393-401	20.1	93
23	DNA-binding mechanism of the <i>Escherichia coli</i> Ada O(6)-alkylguanine-DNA alkyltransferase. <i>Nucleic Acids Research</i> , 2000 , 28, 3710-8	20.1	14
22	Analysis and characterization of data from twinned crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 1750-8		16
21	Crystal structure of <i>Trematomus newnesi</i> haemoglobin re-opens the root effect question. <i>Journal of Molecular Biology</i> , 1999 , 287, 897-906	6.5	65
20	The structure of the exo-beta-(1,3)-glucanase from <i>Candida albicans</i> in native and bound forms: relationship between a pocket and groove in family 5 glycosyl hydrolases. <i>Journal of Molecular Biology</i> , 1999 , 294, 771-83	6.5	80
19	Crystallization and preliminary diffraction studies of pentaerythritol tetranitrate reductase from <i>Enterobacter cloacae</i> PB2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 675-7		7
18	Reductive and oxidative half-reactions of morphinone reductase from <i>Pseudomonas putida</i> M10: a kinetic and thermodynamic analysis. <i>Biochemistry</i> , 1998 , 37, 7598-607	3.2	45
17	Ligand-induced conformational change in penicillin acylase. <i>Journal of Molecular Biology</i> , 1998 , 284, 463-75		93
16	A modulator of rho family G proteins, rhoGDI, binds these G proteins via an immunoglobulin-like domain and a flexible N-terminal arm. <i>Structure</i> , 1997 , 5, 623-33	5.2	98
15	The potential role of glycine-160 of human O6-alkylguanine-DNA alkyltransferase in reaction with O6-benzylguanine as determined by site-directed mutagenesis and molecular modelling comparisons. <i>BBA - Proteins and Proteomics</i> , 1997 , 1342, 90-102		6
14	Crystallization and preliminary diffraction studies of morphinone reductase, a flavoprotein involved in the degradation of morphine alkaloids. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997 , 53, 619-21		2
13	Crystallization and preliminary diffraction studies of NodL, a rhizobial O-acetyl-transferase involved in the host-specific nodulation of legume roots. <i>Protein Science</i> , 1996 , 5, 538-41	6.3	7

12	Penicillin acylase has a single-amino-acid catalytic centre. <i>Nature</i> , 1995 , 373, 264-8	50.4	420
11	A protein catalytic framework with an N-terminal nucleophile is capable of self-activation. <i>Nature</i> , 1995 , 378, 416-9	50.4	557
10	X-ray crystallographic studies on hexameric insulins in the presence of helix-stabilizing agents, thiocyanate, methylparaben, and phenol. <i>Biochemistry</i> , 1995 , 34, 15553-63	3.2	72
9	The crystal structure of a major secreted aspartic proteinase from <i>Candida albicans</i> in complexes with two inhibitors. <i>Structure</i> , 1995 , 3, 1261-71	5.2	103
8	The high-resolution crystal structure of a parallel-stranded guanine tetraplex. <i>Science</i> , 1994 , 265, 520-4	33.3	461
7	Crystal structure of an extracellular fragment of the rat CD4 receptor containing domains 3 and 4. <i>Structure</i> , 1994 , 2, 469-81	5.2	23
6	Crystallization of inhibited aspartic proteinase from <i>Candida albicans</i> . <i>Journal of Molecular Biology</i> , 1993 , 234, 1266-9	6.5	14
5	Insulin assembly: its modification by protein engineering and ligand binding. <i>Philosophical Transactions of the Royal Society: Physical and Engineering Sciences</i> , 1993 , 345, 153-164		6
4	Crystal structure of the aspartic acid-199----asparagine mutant of chloramphenicol acetyltransferase to 2.35-A resolution: structural consequences of disruption of a buried salt bridge. <i>Biochemistry</i> , 1990 , 29, 11261-5	3.2	27
3	Crystallization of O6-methylguanine-DNA methyltransferase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1988 , 200, 751-2	6.5	10
2	Structure of chloramphenicol acetyltransferase at 1.75-A resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1988 , 85, 4133-7	11.5	151
1	Structure of holo-glyceraldehyde-3-phosphate dehydrogenase from <i>Bacillus stearothermophilus</i> at 1.8 A resolution. <i>Journal of Molecular Biology</i> , 1987 , 193, 171-87	6.5	276