

Carrie M Wilmot

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.

79
papers

2,267
citations

29
h-index

45
g-index

84
ext. papers

2,468
ext. citations

6.2
avg, IF

4.59
L-index

#	Paper	IF	Citations
79	Structure-Based Design and Biological Evaluation of Novel Caspase-2 Inhibitors Based on the Peptide AcVDVAD-CHO and the Caspase-2-Mediated Tau Cleavage Sequence YKPD314.. <i>ACS Pharmacology and Translational Science</i> , 2022 , 5, 20-40	5.9	1
78	Larger active site in an ancestral hydroxynitrile lyase increases catalytically promiscuous esterase activity. <i>PLoS ONE</i> , 2020 , 15, e0235341	3.7	5
77	Complexation of the nickel and cobalt transcriptional regulator RcnR with DNA. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020 , 76, 25-30	1.1	1
76	Discovery of Hydroxylase Activity for PqqB Provides a Missing Link in the Pyrroloquinoline Quinone Biosynthetic Pathway. <i>Journal of the American Chemical Society</i> , 2019 , 141, 4398-4405	16.4	20
75	X-ray and EPR Characterization of the Auxiliary Fe-S Clusters in the Radical SAM Enzyme PqqE. <i>Biochemistry</i> , 2018 , 57, 1306-1315	3.2	21
74	The role of OleA His285 in orchestration of long-chain acyl-coenzyme A substrates. <i>FEBS Letters</i> , 2018 , 592, 987-998	3.8	3
73	Active Multienzyme Assemblies for Long-Chain Olefinic Hydrocarbon Biosynthesis. <i>Journal of Bacteriology</i> , 2017 , 199,	3.5	15
72	Nuclear Magnetic Resonance Structure and Binding Studies of PqqD, a Chaperone Required in the Biosynthesis of the Bacterial Dehydrogenase Cofactor Pyrroloquinoline Quinone. <i>Biochemistry</i> , 2017 , 56, 2735-2746	3.2	30
71	β-Lactone Synthetase Found in the Olefin Biosynthesis Pathway. <i>Biochemistry</i> , 2017 , 56, 348-351	3.2	38
70	OleA Glu117 is key to condensation of two fatty-acyl coenzyme A substrates in long-chain olefin biosynthesis. <i>Biochemical Journal</i> , 2017 , 474, 3871-3886	3.8	4
69	Crystal structures reveal metal-binding plasticity at the metallo-β-lactamase active site of PqqB from <i>Pseudomonas putida</i> . <i>Journal of Biological Inorganic Chemistry</i> , 2017 , 22, 1089-1097	3.7	8
68	(1)H, (13)C, and (15)N resonance assignments and secondary structure information for <i>Methylobacterium extorquens</i> PqqD and the complex of PqqD with PqqA. <i>Biomolecular NMR Assignments</i> , 2016 , 10, 385-9	0.7	6
67	Acoustic Injectors for Drop-On-Demand Serial Femtosecond Crystallography. <i>Structure</i> , 2016 , 24, 631-649.2	4.2	69
66	Substrate Trapping in Crystals of the Thiolase OleA Identifies Three Channels That Enable Long Chain Olefin Biosynthesis. <i>Journal of Biological Chemistry</i> , 2016 , 291, 26698-26706	5.4	18
65	MauG, a Diheme Enzyme Involved in the Synthesis of the Enzyme Cofactor, Tryptophan Tryptophylquinone 2016 , 1-30		5
64	A T67A mutation in the proximal pocket of the high-spin heme of MauG stabilizes formation of a mixed-valent FeII/FeIII state and enhances charge resonance stabilization of the bis-FeIV state. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2015 , 1847, 709-16	4.6	4
63	Hydrocarbon Biosynthesis in Microorganisms 2015 , 13-31		2

62	Quaternary Structure Defines a Large Class of Amyloid- β Oligomers Neutralized by Sequestration. <i>Cell Reports</i> , 2015 , 11, 1760-71	10.6	106
61	Site-directed mutagenesis of Gln103 reveals the influence of this residue on the redox properties and stability of MauG. <i>Biochemistry</i> , 2014 , 53, 1342-9	3.2	9
60	A molecular threading mechanism underlies Jumonji lysine demethylase KDM2A regulation of methylated H3K36. <i>Genes and Development</i> , 2014 , 28, 1758-71	12.6	51
59	Standardization of β -L-iduronidase enzyme assay with Michaelis-Menten kinetics. <i>Molecular Genetics and Metabolism</i> , 2014 , 111, 113-5	3.7	11
58	Oxidative damage in MauG: implications for the control of high-valent iron species and radical propagation pathways. <i>Biochemistry</i> , 2013 , 52, 9447-55	3.2	24
57	Diradical intermediate within the context of tryptophan tryptophylquinone biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 4569-73	11.5	44
56	MauG: a di-heme enzyme required for methylamine dehydrogenase maturation. <i>Dalton Transactions</i> , 2013 , 42, 3127-35	4.3	6
55	Structural analysis of aliphatic versus aromatic substrate specificity in a copper amine oxidase from <i>Hansenula polymorpha</i> . <i>Biochemistry</i> , 2013 , 52, 2291-301	3.2	10
54	A Trp199Glu MauG variant reveals a role for Trp199 interactions with pre-methylamine dehydrogenase during tryptophan tryptophylquinone biosynthesis. <i>FEBS Letters</i> , 2013 , 587, 1736-41	3.8	2
53	Posttranslational biosynthesis of the protein-derived cofactor tryptophan tryptophylquinone. <i>Annual Review of Biochemistry</i> , 2013 , 82, 531-50	29.1	34
52	Carboxyl group of Glu113 is required for stabilization of the diferrous and bis-Fe(IV) states of MauG. <i>Biochemistry</i> , 2013 , 52, 6358-67	3.2	13
51	Reactivity and Structure in the CDE Protein Superfamily: From O ₂ Generation to Peroxidase Chemistry and Beyond. <i>Handbook of Porphyrin Science</i> , 2013 , 441-470	0.3	1
50	Structural snapshots from the oxidative half-reaction of a copper amine oxidase: implications for O ₂ activation. <i>Journal of Biological Chemistry</i> , 2013 , 288, 28409-17	5.4	15
49	Structures of MauG in complex with quinol and quinone MADH. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 69, 738-43		4
48	Polysaccharide monooxygenases: giving a boost to biofuel production. <i>Structure</i> , 2012 , 20, 938-40	5.2	1
47	The precursor form of <i>Hansenula polymorpha</i> copper amine oxidase 1 in complex with CuI and Coll. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012 , 68, 501-10		4
46	Proline 107 is a major determinant in maintaining the structure of the distal pocket and reactivity of the high-spin heme of MauG. <i>Biochemistry</i> , 2012 , 51, 1598-606	3.2	30
45	Crystal structures of <i>Xanthomonas campestris</i> OleA reveal features that promote head-to-head condensation of two long-chain fatty acids. <i>Biochemistry</i> , 2012 , 51, 4138-46	3.2	23

44	Geometric and electronic structures of the His-Fe(IV)=O and His-Fe(IV)-Tyr hemes of MauG. <i>Journal of Biological Inorganic Chemistry</i> , 2012 , 17, 1241-55	3.7	20
43	Cofactor biosynthesis through protein post-translational modification. <i>Current Opinion in Chemical Biology</i> , 2012 , 16, 54-9	9.7	16
42	The role of protein crystallography in defining the mechanisms of biogenesis and catalysis in copper amine oxidase. <i>International Journal of Molecular Sciences</i> , 2012 , 13, 5375-405	6.3	31
41	Mutagenesis of tryptophan ¹⁹⁹ suggests that hopping is required for MauG-dependent tryptophan tryptophylquinone biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 16956-61	11.5	60
40	Chlorite dismutases, DyPs, and EfeB: 3 microbial heme enzyme families comprise the CDE structural superfamily. <i>Journal of Molecular Biology</i> , 2011 , 408, 379-98	6.5	71
39	Structural analysis of a Ni-methyl species in methyl-coenzyme M reductase from <i>Methanothermobacter marburgensis</i> . <i>Journal of the American Chemical Society</i> , 2011 , 133, 5626-8	16.4	38
38	Crystal structures of CO and NO adducts of MauG in complex with pre-methylamine dehydrogenase: implications for the mechanism of dioxygen activation. <i>Biochemistry</i> , 2011 , 50, 2931-8	3.2	20
37	The tightly bound calcium of MauG is required for tryptophan tryptophylquinone cofactor biosynthesis. <i>Biochemistry</i> , 2011 , 50, 144-50	3.2	17
36	In crystallo posttranslational modification within a MauG/pre-methylamine dehydrogenase complex. <i>Science</i> , 2010 , 327, 1392-4	33.3	106
35	Structural insight into methyl-coenzyme M reductase chemistry using coenzyme B analogues. <i>Biochemistry</i> , 2010 , 49, 7683-93	3.2	36
34	Kinetic and structural analysis of substrate specificity in two copper amine oxidases from <i>Hansenula polymorpha</i> . <i>Biochemistry</i> , 2010 , 49, 2540-50	3.2	32
33	Functional importance of tyrosine 294 and the catalytic selectivity for the bis-Fe(IV) state of MauG revealed by replacement of this axial heme ligand with histidine. <i>Biochemistry</i> , 2010 , 49, 9783-91	3.2	38
32	Structural features promoting dioxygen production by <i>Dechloromonas aromatica</i> chlorite dismutase. <i>Journal of Biological Inorganic Chemistry</i> , 2010 , 15, 879-88	3.7	53
31	Cloning, purification, crystallization and preliminary X-ray diffraction of the OleC protein from <i>Stenotrophomonas maltophilia</i> involved in head-to-head hydrocarbon biosynthesis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1108-10		10
30	Crystallization and preliminary X-ray diffraction of chlorite dismutase from <i>Dechloromonas aromatica</i> RCB. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009 , 65, 818-21		6
29	Uncovering novel biochemistry in the mechanism of tryptophan tryptophylquinone cofactor biosynthesis. <i>Current Opinion in Chemical Biology</i> , 2009 , 13, 469-74	9.7	25
28	Exploring molecular oxygen pathways in <i>Hansenula polymorpha</i> copper-containing amine oxidase. <i>Journal of Biological Chemistry</i> , 2007 , 282, 17767-76	5.4	70
27	Tracking X-ray-derived redox changes in crystals of a methylamine dehydrogenase/amicyanin complex using single-crystal UV/Vis microspectrophotometry. <i>Journal of Synchrotron Radiation</i> , 2007 , 14, 92-8	2.4	31

26	Synergy within structural biology of single crystal optical spectroscopy and X-ray crystallography. <i>Current Opinion in Structural Biology</i> , 2007 , 17, 580-6	8.1	24
25	Biochemistry. An ancient and intimate partnership. <i>Science</i> , 2007 , 316, 379-80	33.3	2
24	Mechanistic possibilities in MauG-dependent tryptophan tryptophylquinone biosynthesis. <i>Biochemistry</i> , 2006 , 45, 13276-83	3.2	45
23	Isotope labeling studies reveal the order of oxygen incorporation into the tryptophan tryptophylquinone cofactor of methylamine dehydrogenase. <i>Journal of the American Chemical Society</i> , 2006 , 128, 12416-7	16.4	22
22	Prokaryotic Copper Amine Oxidases 2006 ,		1
21	MauG-dependent in vitro biosynthesis of tryptophan tryptophylquinone in methylamine dehydrogenase. <i>Journal of the American Chemical Society</i> , 2005 , 127, 8258-9	16.4	48
20	Active site aspartate residues are critical for tryptophan tryptophylquinone biogenesis in methylamine dehydrogenase. <i>Journal of Biological Chemistry</i> , 2005 , 280, 17392-6	5.4	15
19	Further insights into quinone cofactor biogenesis: probing the role of mauG in methylamine dehydrogenase tryptophan tryptophylquinone formation. <i>Biochemistry</i> , 2004 , 43, 5494-502	3.2	76
18	Medical implications from the crystal structure of a copper-containing amine oxidase complexed with the antidepressant drug tranylcypromine. <i>FEBS Letters</i> , 2004 , 576, 301-5	3.8	17
17	Copper-containing amine oxidases. Biogenesis and catalysis; a structural perspective. <i>Archives of Biochemistry and Biophysics</i> , 2004 , 428, 22-31	4.1	95
16	Catching catalysis in the act: using single crystal kinetics to trap methylamine dehydrogenase reaction intermediates. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2003 , 1647, 381-9	4	7
15	MauG, a novel diheme protein required for tryptophan tryptophylquinone biogenesis. <i>Biochemistry</i> , 2003 , 42, 7318-25	3.2	113
14	Understanding quinone cofactor biogenesis in methylamine dehydrogenase through novel cofactor generation. <i>Biochemistry</i> , 2003 , 42, 3224-30	3.2	20
13	Cryocrystallography of metalloprotein reaction intermediates. <i>Current Opinion in Chemical Biology</i> , 2002 , 6, 202-7	9.7	17
12	Crystallization and preliminary X-ray structure determination of jack bean urease with a bound antibody fragment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 374-6		30
11	Defining redox state of X-ray crystal structures by single-crystal ultraviolet-visible microspectrophotometry. <i>Methods in Enzymology</i> , 2002 , 353, 301-18	1.7	29
10	Probing the catalytic mechanism of Escherichia coli amine oxidase using mutational variants and a reversible inhibitor as a substrate analogue. <i>Biochemical Journal</i> , 2002 , 365, 809-16	3.8	24
9	Oxygen activation in the copper-containing quinoprotein amine oxidase. <i>Biochemical Society Transactions</i> , 2000 , 28, A77-A77	5.1	

8	Analyzing protein functions in four dimensions. <i>Nature Structural Biology</i> , 2000 , 7, 1006-12		60
7	Investigation into the mechanism of λ_{max} shifts and their dependence on pH for the 2-hydrazinopyridine derivatives of two copper amine oxidases. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2000 , 8, 17-25		12
6	The active site base controls cofactor reactivity in Escherichia coli amine oxidase: x-ray crystallographic studies with mutational variants. <i>Biochemistry</i> , 1999 , 38, 8217-27	3.2	84
5	Catalytic mechanism of the quinoenzyme amine oxidase from Escherichia coli: exploring the reductive half-reaction. <i>Biochemistry</i> , 1997 , 36, 1608-20	3.2	144
4	Structure and mechanism of galactose oxidase: catalytic role of tyrosine 495. <i>Journal of Biological Inorganic Chemistry</i> , 1997 , 2, 327-335	3.7	34
3	Tyrosine 495 is a key residue in the active site of galactose oxidase. <i>Biochemical Society Transactions</i> , 1995 , 23, 510S	5.1	17
2	Preliminary studies of two active site mutants of galactose oxidase. <i>Biochemical Society Transactions</i> , 1993 , 21 (Pt 3), 319S	5.1	4
1	Crystallization studies of glycosylated and unglycosylated human recombinant interleukin-2. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992 , 12, 24-30	4.2	9