

Carrie M Wilmot

List of Publications by Year in descending order

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78
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2,605
citations

159358

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docs citations

84
times ranked

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#	ARTICLE	IF	CITATIONS
1	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 YKPVD314. <i>ACS Pharmacology and Translational Science</i> , 2022, 5, 20-40.	2.5	9
2	Larger active site in an ancestral hydroxynitrile lyase increases catalytically promiscuous esterase activity. <i>PLoS ONE</i> , 2020, 15, e0235341.	1.1	13
3	Complexation of the nickel and cobalt transcriptional regulator RcnR with DNA. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 25-30.	0.4	1
4	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.	6.6	28
5	X-ray and EPR Characterization of the Auxiliary Fe-S Clusters in the Radical SAM Enzyme PqqE. <i>Biochemistry</i> , 2018, 57, 1306-1315.	1.2	31
6	The role of OleA His285 in orchestration of long-chain acyl-coenzyme A substrates. <i>FEBS Letters</i> , 2018, 592, 987-998.	1.3	4
7	Active Multienzyme Assemblies for Long-Chain Olefinic Hydrocarbon Biosynthesis. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	18
8	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.	1.2	39
9	$\hat{\text{I}}^2$ -Lactone Synthetase Found in the Olefin Biosynthesis Pathway. <i>Biochemistry</i> , 2017, 56, 348-351.	1.2	45
10	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.	1.7	4
11	Crystal structures reveal metal-binding plasticity at the metallo- $\hat{\text{I}}^2$ -lactamase active site of PqqB from <i>Pseudomonas putida</i> . <i>Journal of Biological Inorganic Chemistry</i> , 2017, 22, 1089-1097.	1.1	10
12	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.	1.6	21
13	MauG, a Diheme Enzyme Involved in the Synthesis of the Enzyme Cofactor, Tryptophan Tryptophylquinone. , 2016, , 1-30.		8
14	^1H , ^{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, 385-389.	0.4	8
15	Acoustic Injectors for Drop-On-Demand Serial Femtosecond Crystallography. <i>Structure</i> , 2016, 24, 631-640.	1.6	88
16	Quaternary Structure Defines a Large Class of Amyloid- $\hat{\text{I}}^2$ Oligomers Neutralized by Sequestration. <i>Cell Reports</i> , 2015, 11, 1760-1771.	2.9	141
17	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, 709-716.	0.5	4
18	Hydrocarbon Biosynthesis in Microorganisms. , 2015, , 13-31.		3

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19	Standardization of \pm -L-iduronidase enzyme assay with Michaelis-Menten kinetics. <i>Molecular Genetics and Metabolism</i> , 2014, 111, 113-115.	0.5	13
20	Site-Directed Mutagenesis of Gln103 Reveals the Influence of This Residue on the Redox Properties and Stability of MauG. <i>Biochemistry</i> , 2014, 53, 1342-1349.	1.2	10
21	A molecular threading mechanism underlies Jumonji lysine demethylase KDM2A regulation of methylated H3K36. <i>Genes and Development</i> , 2014, 28, 1758-1771.	2.7	83
22	Oxidative Damage in MauG: Implications for the Control of High-Valent Iron Species and Radical Propagation Pathways. <i>Biochemistry</i> , 2013, 52, 9447-9455.	1.2	25
23	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, 4569-4573.	3.3	51
24	MauG: a di-heme enzyme required for methylamine dehydrogenase maturation. <i>Dalton Transactions</i> , 2013, 42, 3127-3135.	1.6	9
25	Structural Analysis of Aliphatic versus Aromatic Substrate Specificity in a Copper Amine Oxidase from <i>Hansenula polymorpha</i> . <i>Biochemistry</i> , 2013, 52, 2291-2301.	1.2	10
26	A Trp199Glu MauG variant reveals a role for Trp199 interactions with pre-methylamine dehydrogenase during tryptophan tryptophylquinone biosynthesis. <i>FEBS Letters</i> , 2013, 587, 1736-1741.	1.3	3
27	Posttranslational Biosynthesis of the Protein-Derived Cofactor Tryptophan Tryptophylquinone. <i>Annual Review of Biochemistry</i> , 2013, 82, 531-550.	5.0	36
28	Carboxyl Group of Glu113 Is Required for Stabilization of the Diferrous and Bis-Fe ^{IV} States of MauG. <i>Biochemistry</i> , 2013, 52, 6358-6367.	1.2	14
29	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
30	Structural Snapshots from the Oxidative Half-reaction of a Copper Amine Oxidase. <i>Journal of Biological Chemistry</i> , 2013, 288, 28409-28417.	1.6	18
31	Structures of MauG in complex with quinol and quinone MADH. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 738-743.	0.7	5
32	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, 5375-5405.	1.8	39
33	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, 1598-1606.	1.2	30
34	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, 4138-4146.	1.2	26
35	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, 1241-1255.	1.1	20
36	Cofactor biosynthesis through protein post-translational modification. <i>Current Opinion in Chemical Biology</i> , 2012, 16, 54-59.	2.8	17

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37	Polysaccharide Monooxygenases: Giving a Boost to Biofuel Production. <i>Structure</i> , 2012, 20, 938-940.	1.6	1
38	The precursor form of <i>Hansenula polymorpha</i> copper amine oxidase 1 in complex with Cu ^I and Co ^{II} . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 501-510.	0.7	4
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, 5626-5628.	6.6	44
40	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, 2931-2938.	1.2	20
41	The Tightly Bound Calcium of MauG Is Required for Tryptophan Tryptophylquinone Cofactor Biosynthesis. <i>Biochemistry</i> , 2011, 50, 144-150.	1.2	17
42	Mutagenesis of tryptophan199 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, 16956-16961.	3.3	65
43	Chlorite Dismutases, DyPs, and EfeB: 3 Microbial Heme Enzyme Families Comprise the CDE Structural Superfamily. <i>Journal of Molecular Biology</i> , 2011, 408, 379-398.	2.0	77
44	Structural features promoting dioxygen production by <i>Dechloromonas aromatica</i> chlorite dismutase. <i>Journal of Biological Inorganic Chemistry</i> , 2010, 15, 879-888.	1.1	57
45	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, 1108-1110.	0.7	11
46	In Crystallo Posttranslational Modification Within a MauG/Pre-Methylamine Dehydrogenase Complex. <i>Science</i> , 2010, 327, 1392-1394.	6.0	117
47	Structural Insight into Methyl-Coenzyme M Reductase Chemistry Using Coenzyme B Analogues. <i>Biochemistry</i> , 2010, 49, 7683-7693.	1.2	55
48	Kinetic and Structural Analysis of Substrate Specificity in Two Copper Amine Oxidases from <i>Hansenula polymorpha</i> . <i>Biochemistry</i> , 2010, 49, 2540-2550.	1.2	36
49	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, 9783-9791.	1.2	42
50	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, 818-821.	0.7	6
51	Uncovering novel biochemistry in the mechanism of tryptophan tryptophylquinone cofactor biosynthesis. <i>Current Opinion in Chemical Biology</i> , 2009, 13, 469-474.	2.8	29
52	BIOCHEMISTRY: An Ancient and Intimate Partnership. <i>Science</i> , 2007, 316, 379-380.	6.0	2
53	Exploring Molecular Oxygen Pathways in <i>Hansenula polymorpha</i> Copper-containing Amine Oxidase. <i>Journal of Biological Chemistry</i> , 2007, 282, 17767-17776.	1.6	76
54	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, 92-98.	1.0	37

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55	Synergy within structural biology of single crystal optical spectroscopy and X-ray crystallography. <i>Current Opinion in Structural Biology</i> , 2007, 17, 580-586.	2.6	25
56	Mechanistic Possibilities in MauG-Dependent Tryptophan Tryptophylquinone Biosynthesis. <i>Biochemistry</i> , 2006, 45, 13276-13283.	1.2	45
57	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, 12416-12417.	6.6	23
58	Active Site Aspartate Residues Are Critical for Tryptophan Tryptophylquinone Biogenesis in Methylamine Dehydrogenase. <i>Journal of Biological Chemistry</i> , 2005, 280, 17392-17396.	1.6	15
59	MauG-Dependent in Vitro Biosynthesis of Tryptophan Tryptophylquinone in Methylamine Dehydrogenase. <i>Journal of the American Chemical Society</i> , 2005, 127, 8258-8259.	6.6	52
60	Further Insights into Quinone Cofactor Biogenesis: Probing the Role of mauG in Methylamine Dehydrogenase Tryptophan Tryptophylquinone Formation. <i>Biochemistry</i> , 2004, 43, 5494-5502.	1.2	76
61	Medical implications from the crystal structure of a copper-containing amine oxidase complexed with the antidepressant drug tranylcypromine. <i>FEBS Letters</i> , 2004, 576, 301-305.	1.3	19
62	Copper-containing amine oxidases. Biogenesis and catalysis; a structural perspective. <i>Archives of Biochemistry and Biophysics</i> , 2004, 428, 22-31.	1.4	105
63	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, 381-389.	1.1	9
64	MauG, a Novel Diheme Protein Required for Tryptophan Tryptophylquinone Biogenesis. <i>Biochemistry</i> , 2003, 42, 7318-7325.	1.2	123
65	Understanding Quinone Cofactor Biogenesis in Methylamine Dehydrogenase through Novel Cofactor Generation. <i>Biochemistry</i> , 2003, 42, 3224-3230.	1.2	21
66	Defining Redox State of X-Ray Crystal Structures by Single-Crystal Ultraviolet-Visible Microspectrophotometry. <i>Methods in Enzymology</i> , 2002, 353, 301-318.	0.4	32
67	Probing the catalytic mechanism of <i>Escherichia coli</i> amine oxidase using mutational variants and a reversible inhibitor as a substrate analogue. <i>Biochemical Journal</i> , 2002, 365, 809-816.	1.7	27
68	Cryocrystallography of metalloprotein reaction intermediates. <i>Current Opinion in Chemical Biology</i> , 2002, 6, 202-207.	2.8	19
69	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, 374-376.	2.5	31
70	Oxygen activation in the copper-containing quinoprotein amine oxidase. <i>Biochemical Society Transactions</i> , 2000, 28, A77-A77.	1.6	0
71	Analyzing protein functions in four dimensions. <i>Nature Structural Biology</i> , 2000, 7, 1006-1012.	9.7	69
72	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.	1.8	14

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73	The Active Site Base Controls Cofactor Reactivity in <i>Escherichia coli</i> Amine Oxidase: X-ray Crystallographic Studies with Mutational Variants. <i>Biochemistry</i> , 1999, 38, 8217-8227.	1.2	92
74	Catalytic Mechanism of the Quinoenzyme Amine Oxidase from <i>Escherichia coli</i> : Exploring the Reductive Half-Reaction. <i>Biochemistry</i> , 1997, 36, 1608-1620.	1.2	154
75	Structure and mechanism of galactose oxidase: catalytic role of tyrosine 495. <i>Journal of Biological Inorganic Chemistry</i> , 1997, 2, 327-335.	1.1	40
76	Tyrosine 495 is a key residue in the active site of Galactose oxidase. <i>Biochemical Society Transactions</i> , 1995, 23, 510S-510S.	1.6	18
77	Preliminary studies of two active site mutants of galactose oxidase. <i>Biochemical Society Transactions</i> , 1993, 21, 319S-319S.	1.6	5
78	Crystallization studies of glycosylated and unglycosylated human recombinant interleukin-2. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 12, 24-30.	1.5	9