

Michael E P Murphy

List of Publications by Year in descending order

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106
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7,735
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66343

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docs citations

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times ranked

7529
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#	ARTICLE	IF	CITATIONS
1	Sequence Divergence in the Arginase Domain of Ornithine Decarboxylase/Arginase in <i>Fusobacteriaceae</i> Leads to Loss of Function in Oral Associated Species. <i>Biochemistry</i> , 2022, 61, 1378-1391.	2.5	2
2	Peptidoglycan binding by a pocket on the accessory NTF2-domain of Pgp2 directs helical cell shape of <i>Campylobacter jejuni</i> . <i>Journal of Biological Chemistry</i> , 2021, 296, 100528.	3.4	5
3	Structural and functional analysis of lignostilbene dioxygenases from <i>Sphingobium</i> sp. SYK-6. <i>Journal of Biological Chemistry</i> , 2021, 296, 100758.	3.4	7
4	Biophysical characterization of the ETV6 PNT domain polymerization interfaces. <i>Journal of Biological Chemistry</i> , 2021, 296, 100284.	3.4	2
5	A copper site is required for iron transport by the periplasmic proteins P19 and FetP. <i>Metallomics</i> , 2020, 12, 1530-1541.	2.4	5
6	Smoking Prevalence and Secondhand Smoke Exposure during Pregnancy and Postpartum—Establishing Risks to Health and Human Rights before Developing a Tailored Programme for Smoking Cessation. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 1838.	2.6	12
7	A bacterial surface layer protein exploits multistep crystallization for rapid self-assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 388-394.	7.1	18
8	Introduction of the Menaquinone Biosynthetic Pathway into <i>Rhodobacter sphaeroides</i> and <i>de Novo</i> Synthesis of Menaquinone for Incorporation into Heterologously Expressed Integral Membrane Proteins. <i>ACS Synthetic Biology</i> , 2020, 9, 1190-1200.	3.8	7
9	Identification of functionally important residues and structural features in a bacterial lignostilbene dioxygenase. <i>Journal of Biological Chemistry</i> , 2019, 294, 12911-12920.	3.4	10
10	The heme-sensitive regulator SbnI has a bifunctional role in staphyloferrin B production by <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 11622-11636.	3.4	11
11	Structural insight into the high reduction potentials observed for <i>Fusobacterium nucleatum</i> flavodoxin. <i>Protein Science</i> , 2019, 28, 1460-1472.	7.6	3
12	<i>Staphylococcus aureus</i> heme and siderophore-iron acquisition pathways. <i>BioMetals</i> , 2019, 32, 409-424.	4.1	42
13	Peptides Containing meso-Oxo-Diaminopimelic Acid as Substrates for the Cell-Shape-Determining Proteases Csd6 and Pgp2. <i>ChemBioChem</i> , 2019, 20, 1591-1598.	2.6	10
14	SbnI is a free serine kinase that generates -phospho-l-serine for staphyloferrin B biosynthesis in. <i>Journal of Biological Chemistry</i> , 2018, 293, 6147-6160.	3.4	12
15	Structure-function analyses reveal key features in <i>Staphylococcus aureus</i> IsdB-associated unfolding of the heme-binding pocket of human hemoglobin. <i>Journal of Biological Chemistry</i> , 2018, 293, 177-190.	3.4	55
16	Crystallographic study of dioxygen chemistry in a copper-containing nitrite reductase from <i>Geobacillus thermodenitrificans</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 769-777.	2.3	2
17	Metal- and Serine-Dependent Meta-Cleavage Product Hydrolases Utilize Similar Nucleophile-Activation Strategies. <i>ACS Catalysis</i> , 2018, 8, 11622-11632.	11.2	6
18	Investigating the <i>Campylobacter jejuni</i> Transcriptional Response to Host Intestinal Extracts Reveals the Involvement of a Widely Conserved Iron Uptake System. <i>MBio</i> , 2018, 9, .	4.1	24

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19	Repression of branched-chain amino acid synthesis in <i>Staphylococcus aureus</i> is mediated by isoleucine via CodY, and by a leucine-rich attenuator peptide. <i>PLoS Genetics</i> , 2018, 14, e1007159.	3.5	55
20	Iron Uptake Oxidoreductase (IruO) Uses a Flavin Adenine Dinucleotide Semiquinone Intermediate for Iron-Siderophore Reduction. <i>ACS Chemical Biology</i> , 2017, 12, 1778-1786.	3.4	20
21	Antibiotic Capture by Bacterial Lipocalins Uncovers an Extracellular Mechanism of Intrinsic Antibiotic Resistance. <i>MBio</i> , 2017, 8, .	4.1	31
22	The bacterial meta-cleavage hydrolase LigY belongs to the amidohydrolase superfamily, not to the β -hydrolase superfamily. <i>Journal of Biological Chemistry</i> , 2017, 292, 18290-18302.	3.4	11
23	Surface-layer protein from <i>Caulobacter crescentus</i> : expression, purification and X-ray crystallographic analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 677-680.	0.8	4
24	Deciphering the Substrate Specificity of SbnA, the Enzyme Catalyzing the First Step in Staphyloferrin B Biosynthesis. <i>Biochemistry</i> , 2016, 55, 927-939.	2.5	22
25	A Bacterial Cell Shape-Determining Inhibitor. <i>ACS Chemical Biology</i> , 2016, 11, 981-991.	3.4	16
26	Redox-coupled proton transfer mechanism in nitrite reductase revealed by femtosecond crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2928-2933.	7.1	88
27	The B-type Channel Is a Major Route for Iron Entry into the Ferroxidase Center and Central Cavity of Bacterioferritin. <i>Journal of Biological Chemistry</i> , 2015, 290, 3732-3739.	3.4	24
28	A Single-Crystal EPR Study at 95 GHz of the Type-2 Copper Site of Nitrite Reductase From <i>Alcaligenes faecalis</i> . <i>Applied Magnetic Resonance</i> , 2015, 46, 411-420.	1.2	1
29	Helical Shape of <i>Helicobacter pylori</i> Requires an Atypical Glutamine as a Zinc Ligand in the Carboxypeptidase Csd4. <i>Journal of Biological Chemistry</i> , 2015, 290, 3622-3638.	3.4	17
30	A Ferric Peroxo Intermediate in the Oxidation of Heme by IsdI. <i>Biochemistry</i> , 2015, 54, 2613-2621.	2.5	14
31	A Diatom Ferritin Optimized for Iron Oxidation but Not Iron Storage. <i>Journal of Biological Chemistry</i> , 2015, 290, 28416-28427.	3.4	31
32	The Fate of Intracellular Metal Ions in Microbes. , 2015, , 39-56.		1
33	SbnG, a Citrate Synthase in <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 33797-33807.	3.4	18
34	Structural and kinetic properties of <i>Rhodobacter sphaeroides</i> photosynthetic reaction centers containing exclusively Zn-coordinated bacteriochlorophyll as bacteriochlorin cofactors. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 366-374.	1.0	9
35	Hemoglobin Binding and Catalytic Heme Extraction by IsdB Near Iron Transporter Domains. <i>Biochemistry</i> , 2014, 53, 2286-2294.	2.5	23
36	Steric Mechanism of Auto-Inhibitory Regulation of Specific and Non-Specific DNA Binding by the ETS Transcriptional Repressor ETV6. <i>Journal of Molecular Biology</i> , 2014, 426, 1390-1406.	4.2	44

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37	Synthesis of L-2,3-Diaminopropionic Acid, a Siderophore and Antibiotic Precursor. <i>Chemistry and Biology</i> , 2014, 21, 379-388.	6.0	60
38	Improved Manganese-Oxidizing Activity of DypB, a Peroxidase from a Lignolytic Bacterium. <i>ACS Chemical Biology</i> , 2013, 8, 700-706.	3.4	89
39	The Mannoprotein Cig1 Supports Iron Acquisition From Heme and Virulence in the Pathogenic Fungus <i>Cryptococcus neoformans</i> . <i>Journal of Infectious Diseases</i> , 2013, 207, 1339-1347.	4.0	96
40	Role of <i>Rhodobacter sphaeroides</i> Photosynthetic Reaction Center Residue M214 in the Composition, Absorbance Properties, and Conformations of H _A and B _A Cofactors. <i>Biochemistry</i> , 2013, 52, 2206-2217.	2.5	17
41	IruO Is a Reductase for Heme Degradation by IsdI and IsdG Proteins in <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 25749-25759.	3.4	23
42	Mechanism of Ferrous Iron Binding and Oxidation by Ferritin from a Pennate Diatom. <i>Journal of Biological Chemistry</i> , 2013, 288, 14917-14925.	3.4	53
43	Inactivation of the Heme Degrading Enzyme IsdI by an Active Site Substitution That Diminishes Heme Ruffling. <i>Journal of Biological Chemistry</i> , 2012, 287, 34179-34188.	3.4	31
44	Distal Heme Pocket Residues of B-type Dye-decolorizing Peroxidase. <i>Journal of Biological Chemistry</i> , 2012, 287, 10623-10630.	3.4	90
45	Discovery of an Iron-Regulated Citrate Synthase in <i>Staphylococcus aureus</i> . <i>Chemistry and Biology</i> , 2012, 19, 1568-1578.	6.0	30
46	Monomer-Dimer Control and Crystal Engineering in TASPs. <i>Chemistry - A European Journal</i> , 2012, 18, 11409-11416.	3.3	2
47	Unique Heme-Iron Coordination by the Hemoglobin Receptor IsdB of <i>Staphylococcus aureus</i> . <i>Biochemistry</i> , 2011, 50, 5443-5452.	2.5	79
48	Characterization of Dye-Decolorizing Peroxidases from <i>Rhodococcus jostii</i> RHA1. <i>Biochemistry</i> , 2011, 50, 5108-5119.	2.5	144
49	Iron-Coordinating Tyrosine Is a Key Determinant of NEAT Domain Heme Transfer. <i>Journal of Molecular Biology</i> , 2011, 413, 684-698.	4.2	47
50	Characterization of a Dipartite Iron Uptake System from Uropathogenic <i>Escherichia coli</i> Strain F11. <i>Journal of Biological Chemistry</i> , 2011, 286, 25317-25330.	3.4	34
51	Electronic properties of the highly ruffled heme bound to the heme degrading enzyme IsdI. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13071-13076.	7.1	48
52	Structural biology of heme binding in the <i>Staphylococcus aureus</i> Isd system. <i>Journal of Inorganic Biochemistry</i> , 2010, 104, 341-348.	3.5	125
53	The IsdG family of haem oxygenases degrades haem to a novel chromophore. <i>Molecular Microbiology</i> , 2010, 75, 1529-1538.	2.5	138
54	The <i>Staphylococcus aureus</i> Siderophore Receptor HtsA Undergoes Localized Conformational Changes to Enclose Staphyloferrin A in an Arginine-rich Binding Pocket. <i>Journal of Biological Chemistry</i> , 2010, 285, 11162-11171.	3.4	65

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55	Directed evolution of copper nitrite reductase to a chromogenic reductant. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 137-145.	2.1	22
56	Specificity of Staphyloferrin B Recognition by the SirA Receptor from <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 34579-34588.	3.4	56
57	Structure and Function of P19, a High-Affinity Iron Transporter of the Human Pathogen <i>Campylobacter jejuni</i> . <i>Journal of Molecular Biology</i> , 2010, 401, 590-604.	4.2	35
58	Iron core mineralisation in prokaryotic ferritins. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2010, 1800, 732-744.	2.4	97
59	Structural and Mechanistic Studies of a Stabilized Subunit Dimer Variant of <i>Escherichia coli</i> Bacterioferritin Identify Residues Required for Core Formation. <i>Journal of Biological Chemistry</i> , 2009, 284, 18873-18881.	3.4	23
60	Crystallographic characterization of the passenger domain of the <i>Bordetella</i> autotransporter BrkA. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 608-611.	0.7	3
61	Characterization of staphyloferrin A biosynthetic and transport mutants in <i>Staphylococcus aureus</i> . <i>Molecular Microbiology</i> , 2009, 72, 947-963.	2.5	120
62	Ferritin is used for iron storage in bloom-forming marine pennate diatoms. <i>Nature</i> , 2009, 457, 467-470.	27.8	287
63	X-ray Crystal Analysis of a TASP: Structural Insights of a Cavitein Dimer. <i>Journal of the American Chemical Society</i> , 2009, 131, 7421-7429.	13.7	24
64	Conserved Active Site Residues Limit Inhibition of a Copper-Containing Nitrite Reductase by Small Molecules. <i>Biochemistry</i> , 2008, 47, 4452-4460.	2.5	26
65	Ruffling of Metalloporphyrins Bound to IsdG and IsdI, Two Heme-degrading Enzymes in <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 30957-30963.	3.4	97
66	Heme Coordination by <i>Staphylococcus aureus</i> IsdE. <i>Journal of Biological Chemistry</i> , 2007, 282, 28815-28822.	3.4	86
67	Stable Copper ^{II} Nitrosyl Formation by Nitrite Reductase in Either Oxidation State. <i>Biochemistry</i> , 2007, 46, 12366-12374.	2.5	45
68	Effect of the Methionine Ligand on the Reorganization Energy of the Type-1 Copper Site of Nitrite Reductase. <i>Journal of the American Chemical Society</i> , 2007, 129, 519-525.	13.7	25
69	Haem recognition by a <i>Staphylococcus aureus</i> NEAT domain. <i>Molecular Microbiology</i> , 2007, 63, 139-149.	2.5	142
70	Type-2 copper-containing enzymes. <i>Cellular and Molecular Life Sciences</i> , 2007, 64, 2887-2899.	5.4	126
71	A Rearranging Ligand Enables Allosteric Control of Catalytic Activity in Copper-containing Nitrite Reductase. <i>Journal of Molecular Biology</i> , 2006, 358, 1081-1093.	4.2	12
72	Cofacial Heme Binding is Linked to Dimerization by a Bacterial Heme Transport Protein. <i>Journal of Molecular Biology</i> , 2006, 362, 1108-1119.	4.2	45

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73	Structures of Ternary Complexes of BphK, a Bacterial Glutathione S-Transferase That Reductively Dechlorinates Polychlorinated Biphenyl Metabolites. <i>Journal of Biological Chemistry</i> , 2006, 281, 30933-30940.	3.4	23
74	Anion-independent Iron Coordination by the <i>Campylobacter jejuni</i> Ferric Binding Protein. <i>Journal of Biological Chemistry</i> , 2005, 280, 9283-9290.	3.4	36
75	Characterization of a Nucleotide-Binding Domain Associated with Neisserial Iron Transport. <i>Journal of Bacteriology</i> , 2004, 186, 3266-3269.	2.2	2
76	Side-On Copper-Nitrosyl Coordination by Nitrite Reductase. <i>Science</i> , 2004, 304, 867-870.	12.6	218
77	A Caged Lanthanide Complex as a Paramagnetic Shift Agent for Protein NMR. <i>Chemistry - A European Journal</i> , 2004, 10, 3252-3260.	3.3	93
78	Specificity of the Synergistic Anion for Iron Binding by Ferric Binding Protein from <i>Neisseria gonorrhoeae</i> . <i>Biochemistry</i> , 2004, 43, 9195-9203.	2.5	12
79	Directing the mode of nitrite binding to a copper-containing nitrite reductase from <i>Alcaligenes faecalis</i> S-6: Characterization of an active site isoleucine. <i>Protein Science</i> , 2003, 12, 248-256.	7.6	38
80	Reconstitution of the Type-1 Active Site of the H145G/A Variants of Nitrite Reductase by Ligand Insertion. <i>Biochemistry</i> , 2003, 42, 4075-4083.	2.5	37
81	S-Nitrosation of Ca ²⁺ -Loaded and Ca ²⁺ -Free Recombinant Calbindin D28K from Human Brain. <i>Biochemistry</i> , 2002, 41, 6185-6192.	2.5	18
82	Crystal structure of the soluble domain of the major anaerobically induced outer membrane protein (AniA) from pathogenic <i>Neisseria</i> : a new class of copper-containing nitrite reductases. <i>Journal of Molecular Biology</i> , 2002, 315, 1111-1127.	4.2	101
83	Alternate Substrate Binding Modes to Two Mutant (D98N and H255N) Forms of Nitrite Reductase from <i>Alcaligenes faecalis</i> S-6: Structural Model of a Transient Catalytic Intermediate. <i>Biochemistry</i> , 2001, 40, 9132-9141.	2.5	67
84	A Single-Crystal Electron Paramagnetic Resonance Study at 95 GHz of the Type 1 Copper Site of the Green Nitrite Reductase of <i>Alcaligenes faecalis</i> . <i>Journal of Physical Chemistry B</i> , 2001, 105, 2236-2243.	2.6	17
85	Structure and Site-directed Mutagenesis of a Flavoprotein from <i>Escherichia coli</i> That Reduces Nitrocompounds. <i>Journal of Biological Chemistry</i> , 2001, 276, 2816-2823.	3.4	89
86	Catalytic Roles for Two Water Bridged Residues (Asp-98 and His-255) in the Active Site of Copper-containing Nitrite Reductase. <i>Journal of Biological Chemistry</i> , 2000, 275, 23957-23964.	3.4	115
87	Carbon Monoxide Binding to Copper-Containing Nitrite Reductase from <i>Alcaligenes faecalis</i> . <i>Journal of Physical Chemistry B</i> , 2000, 104, 10738-10742.	2.6	28
88	Crystal structures of two mutants (K206Q, H207E) of the N-lobe of human transferrin with increased affinity for iron. <i>Protein Science</i> , 2000, 9, 49-52.	7.6	26
89	X-ray Crystallography and Mass Spectroscopy Reveal that the N-lobe of Human Transferrin Expressed in <i>Pichia pastoris</i> Is Folded Correctly but Is Glycosylated on Serine-32. <i>Biochemistry</i> , 1999, 38, 2535-2541.	2.5	25
90	Consequences of factor IX mutations in 26 families with haemophilia B. <i>British Journal of Haematology</i> , 1998, 100, 58-61.	2.5	11

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91	A domain mutations in 65 haemophilia A families and molecular modelling of dysfunctional factor VIII proteins. <i>British Journal of Haematology</i> , 1998, 103, 1051-1060.	2.5	34
92	Two High-Resolution Crystal Structures of the Recombinant N-Lobe of Human Transferrin Reveal a Structural Change Implicated in Iron Release. <i>Biochemistry</i> , 1998, 37, 7919-7928.	2.5	242
93	1.8 Å... crystal structure of the major NAD(P)H:FMN oxidoreductase of a bioluminescent bacterium, <i>Vibrio fischeri</i> : overall structure, cofactor and substrate-analog binding, and comparison with related flavoproteins. <i>Journal of Molecular Biology</i> , 1998, 280, 259-273.	4.2	86
94	On the Mechanism of Nitrite Reductase: Complex between Pseudoazurin and Nitrite Reductase from <i>A. Cycloclastes</i> . , 1998, , 115-128.		3
95	Structure of Nitrite Bound to Copper-containing Nitrite Reductase from <i>Alcaligenes faecalis</i> . <i>Journal of Biological Chemistry</i> , 1997, 272, 28455-28460.	3.4	195
96	Loss of Tolerance to Exogenous and Endogenous Factor VIII in a Mild Hemophilia A Patient With an Arg593 to Cys Mutation. <i>Blood</i> , 1997, 90, 1902-1910.	1.4	77
97	Structural comparison of cupredoxin domains: Domain recycling to construct proteins with novel functions. <i>Protein Science</i> , 1997, 6, 761-770.	7.6	118
98	Site-directed mutagenesis of azurin from <i>Pseudomonas aeruginosa</i> enhances the formation of an electron-transfer complex with a copper-containing nitrite reductase from <i>Alcaligenes faecalis</i> S-6. <i>FEBS Letters</i> , 1996, 394, 87-90.	2.8	27
99	Structure of <i>Alcaligenes faecalis</i> Nitrite Reductase and a Copper Site Mutant, M150E, That Contains Zinc. <i>Biochemistry</i> , 1995, 34, 12107-12117.	2.5	102
100	Replacements in a conserved leucine cluster in the hydrophobic heme pocket of cytochrome <i>c</i> . <i>Protein Science</i> , 1995, 4, 198-208.	7.6	15
101	Raster3D Version 2.0. A program for photorealistic molecular graphics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994, 50, 869-873.	2.5	2,205
102	X-ray Structure and Site-Directed Mutagenesis of a Nitrite Reductase from <i>Alcaligenes Faecalis</i> S-6: Roles of Two Copper Atoms in Nitrite Reduction. <i>Biochemistry</i> , 1994, 33, 5246-5252.	2.5	185
103	The structure and function of omega loop A replacements in cytochrome <i>c</i> . <i>Protein Science</i> , 1993, 2, 1429-1440.	7.6	27
104	Structure determination and analysis of yeast iso-2-cytochrome c and a composite mutant protein. <i>Journal of Molecular Biology</i> , 1992, 227, 160-176.	4.2	46
105	Structure of recombinant human renin, a target for cardiovascular-active drugs, at 2.5 Å resolution. <i>Science</i> , 1989, 243, 1346-1351.	12.6	234
106	Comparative molecular model building of two serine proteinases from cytotoxic T lymphocytes. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 4, 190-204.	2.6	78