

Megan J Maher

List of Publications by Year in descending order

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62
papers

1,739
citations

257450

24
h-index

302126

39
g-index

67
all docs

67
docs citations

67
times ranked

2418
citing authors

#	ARTICLE	IF	CITATIONS
1	Dysregulation of <i>Streptococcus pneumoniae</i> zinc homeostasis breaks ampicillin resistance in a pneumonia infection model. <i>Cell Reports</i> , 2022, 38, 110202.	6.4	18
2	Mitochondrial COA7 is a heme-binding protein with disulfide reductase activity, which acts in the early stages of complex IV assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	12
3	Structural and Functional Investigation of the Periplasmic Arsenate-Binding Protein ArrX from <i>Chrysiogenes arsenatis</i> . <i>Biochemistry</i> , 2021, 60, 465-476.	2.5	5
4	Insane in the membrane: developments in protein folding, protein transport, and signaling by GPCRs. <i>Current Opinion in Structural Biology</i> , 2021, 69, vi-viii.	5.7	0
5	The structural basis of bacterial manganese import. <i>Science Advances</i> , 2021, 7, .	10.3	17
6	What Role Does COA6 Play in Cytochrome C Oxidase Biogenesis: A Metallochaperone or Thiol Oxidoreductase, or Both?. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6983.	4.1	11
7	Human glutaredoxin-1 can transfer copper to isolated metal binding domains of the P1B-type ATPase, ATP7B. <i>Scientific Reports</i> , 2020, 10, 4157.	3.3	7
8	Structural and functional characterizations of the C-terminal domains of CzcD proteins. <i>Journal of Inorganic Biochemistry</i> , 2020, 208, 111087.	3.5	12
9	Zinc-binding to the cytoplasmic PAS domain regulates the essential Walk histidine kinase of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2019, 10, 3067.	12.8	38
10	The purification of the ĩfFpvI/FpvR20 and ĩfPvdS/FpvR20 protein complexes is facilitated at room temperature. <i>Protein Expression and Purification</i> , 2019, 160, 11-18.	1.3	1
11	The crystal structure of the CopC protein from <i>Pseudomonas fluorescens</i> reveals amended classifications for the CopC protein family. <i>Journal of Inorganic Biochemistry</i> , 2019, 195, 194-200.	3.5	17
12	The structure and activity of the glutathione reductase from <i>Streptococcus pneumoniae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 54-61.	0.8	8
13	High-resolution crystal structure of the reduced Grx1 from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 392-396.	0.8	3
14	Structural and functional characterization of the mitochondrial complex IV assembly factor Coa6. <i>Life Science Alliance</i> , 2019, 2, e201900458.	2.8	15
15	Crystal structure of bacterial succinate:quinone oxidoreductase flavoprotein SdhA in complex with its assembly factor SdhE. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2982-2987.	7.1	15
16	The central active site arginine in sulfite oxidizing enzymes alters kinetic properties by controlling electron transfer and redox interactions. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018, 1859, 19-27.	1.0	7
17	The crystal structures of a copper-bound metallochaperone from <i>Saccharomyces cerevisiae</i> . <i>Journal of Inorganic Biochemistry</i> , 2017, 177, 368-374.	3.5	3
18	Integrated activities of two alternative sigma factors coordinate iron acquisition and uptake by <i>Pseudomonas aeruginosa</i> . <i>Molecular Microbiology</i> , 2017, 106, 891-904.	2.5	13

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19	Dysregulation of transition metal ion homeostasis is the molecular basis for cadmium toxicity in <i>Streptococcus pneumoniae</i> . <i>Nature Communications</i> , 2015, 6, 6418.	12.8	117
20	COA6 is a mitochondrial complex IV assembly factor critical for biogenesis of mtDNA-encoded COX2. <i>Human Molecular Genetics</i> , 2015, 24, 5404-5415.	2.9	89
21	Structural basis of interprotein electron transfer in bacterial sulfite oxidation. <i>ELife</i> , 2015, 4, e09066.	6.0	19
22	Exploring the correlation between the sequence composition of the nucleotide binding G5 loop of the FeoB GTPase domain (NFeoB) and intrinsic rate of GDP release. <i>Bioscience Reports</i> , 2014, 34, e00158.	2.4	10
23	A GTPase Chimera Illustrates an Uncoupled Nucleotide Affinity and Release Rate, Providing Insight into the Activation Mechanism. <i>Biophysical Journal</i> , 2014, 107, L45-L48.	0.5	4
24	Structural and functional analysis of a FeoB A143S G5 loop mutant explains the accelerated GDP release rate. <i>FEBS Journal</i> , 2014, 281, 2254-2265.	4.7	12
25	The bacterial SoxAX cytochromes. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 977-992.	5.4	29
26	Structure of an atypical FeoB G-domain reveals a putative domain-swapped dimer. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 399-404.	0.7	12
27	The structure of the yeast NADH dehydrogenase (Ndi1) reveals overlapping binding sites for water- and lipid-soluble substrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15247-15252.	7.1	88
28	The cation-independent G-proteins: In a class of their own. <i>FEBS Letters</i> , 2012, 586, 2218-2224.	2.8	37
29	The X-ray crystal structure of a pseudoazurin from <i>Sinorhizobium meliloti</i> . <i>Journal of Inorganic Biochemistry</i> , 2012, 115, 148-154.	3.5	9
30	Molecular Basis of the Cooperative Binding of Cu(I) and Cu(II) to the CopK Protein from <i>Cupriavidus metallidurans</i> CH34. <i>Biochemistry</i> , 2011, 50, 9237-9247.	2.5	18
31	The Initiation of GTP Hydrolysis by the G-Domain of FeoB: Insights from a Transition-State Complex Structure. <i>PLoS ONE</i> , 2011, 6, e23355.	2.5	34
32	A suite of Switch I and Switch II mutant structures from the G-protein domain of FeoB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 973-980.	2.5	14
33	The structure of an N11A mutant of the G-protein domain of FeoB. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1511-1515.	0.7	8
34	Insights into Structure and Function of the Active Site of SoxAX Cytochromes. <i>Journal of Biological Chemistry</i> , 2011, 286, 24872-24881.	3.4	19
35	Potassium-activated GTPase Reaction in the G Protein-coupled Ferrous Iron Transporter B. <i>Journal of Biological Chemistry</i> , 2010, 285, 14594-14602.	3.4	51
36	Structural basis of GDP release and gating in G protein coupled Fe ²⁺ transport. <i>EMBO Journal</i> , 2009, 28, 2677-2685.	7.8	43

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37	Crystal structure of A3B3 complex of V-ATPase from <i>Thermus thermophilus</i> . <i>EMBO Journal</i> , 2009, 28, 3771-3779.	7.8	59
38	Unprecedented Binding Cooperativity between Cu ^I and Cu ^{II} in the Copper Resistance Protein CopK from <i>Cupriavidus metallidurans</i> CH34: Implications from Structural Studies by NMR Spectroscopy and X-Ray Crystallography. <i>Journal of the American Chemical Society</i> , 2009, 131, 3549-3564.	13.7	38
39	Crystal Structure of the Acid-Induced Arginine Decarboxylase from <i>Escherichia coli</i> : Reversible Decamer Assembly Controls Enzyme Activity. <i>Biochemistry</i> , 2009, 48, 3915-3927.	2.5	48
40	Thioredoxin A Active-Site Mutants Form Mixed Disulfide Dimers That Resemble Enzyme-Substrate Reaction Intermediates. <i>Journal of Molecular Biology</i> , 2008, 379, 520-534.	4.2	20
41	Structures of Ligand-free and Inhibitor Complexes of Dihydroorotase from <i>Escherichia coli</i> : Implications for Loop Movement in Inhibitor Design. <i>Journal of Molecular Biology</i> , 2007, 370, 812-825.	4.2	35
42	Kinetic and Structural Analysis of Mutant <i>Escherichia coli</i> Dihydroorotases: A Flexible Loop Stabilizes the Transition State. <i>Biochemistry</i> , 2007, 46, 10538-10550.	2.5	16
43	Structure of the T109S mutant of <i>Escherichia coli</i> dihydroorotase complexed with the inhibitor 5-fluoroorotate: catalytic activity is reflected by the crystal form. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 154-161.	0.7	11
44	Intermolecular Transfer of Copper Ions from the CopC Protein of <i>Pseudomonas syringae</i> . Crystal Structures of Fully Loaded Cu ₂ Cu ₂ Forms. <i>Journal of the American Chemical Society</i> , 2006, 128, 5834-5850.	13.7	121
45	CopC Protein from <i>Pseudomonas syringae</i> : Intermolecular Transfer of Copper from Both the Copper(I) and Copper(II) Sites. <i>Inorganic Chemistry</i> , 2005, 44, 5203-5205.	4.0	36
46	Dihydroorotase from <i>Escherichia coli</i> : Loop Movement and Cooperativity between Subunits. <i>Journal of Molecular Biology</i> , 2005, 348, 523-533.	4.2	30
47	Tandem LIM domains provide synergistic binding in the LMO4:Ldb1 complex. <i>EMBO Journal</i> , 2004, 23, 3589-3598.	7.8	84
48	Metal-substituted derivatives of the rubredoxin from <i>Clostridium pasteurianum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 298-303.	2.5	35
49	Structure of <i>Escherichia coli</i> aminopeptidase P in complex with the inhibitor apstatin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1770-1779.	2.5	29
50	X-ray Absorption Spectroscopy of Selenate Reductase. <i>Inorganic Chemistry</i> , 2004, 43, 402-404.	4.0	35
51	Structure of the Prolidase from <i>Pyrococcus furiosus</i> . <i>Biochemistry</i> , 2004, 43, 2771-2783.	2.5	87
52	Crystallization of hamster dihydroorotase: involvement of a disulfide-linked tetrameric form. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 381-384.	2.5	5
53	Crystallization of FLINC4, an intramolecular LMO4-Ldb1 complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1484-1486.	2.5	10
54	Auracyanin B structure in space group P65. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1545-1550.	2.5	7

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55	Crystallization and preliminary X-ray analysis of the selenate reductase from <i>Thauera selenatis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 706-708.	2.5	9
56	Crystallization of <i>Pichia pastoris</i> lysyl oxidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2177-2179.	2.5	4
57	Crystal structure of auracyanin, a blue-copper protein from the green thermophilic photosynthetic bacterium <i>Chloroflexus aurantiacus</i> 11 Edited by R Huber. <i>Journal of Molecular Biology</i> , 2001, 306, 47-67.	4.2	50
58	Crystallization and characterization of the prolidase from <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 428-430.	2.5	15
59	Mutation of the surface valine residues 8 and 44 in the rubredoxin from <i>Clostridium pasteurianum</i> : solvent access versus structural changes as determinants of reversible potential. <i>Journal of Biological Inorganic Chemistry</i> , 2000, 5, 75-84.	2.6	32
60	The dependence of reversible potentials on the form of modification of edge plane pyrolytic graphite electrodes in voltammetric studies on rubredoxin and ferredoxin from <i>Clostridium pasteurianum</i> . <i>Electrochemistry Communications</i> , 1999, 1, 309-314.	4.7	15
61	Rubredoxin from <i>Clostridium pasteurianum</i> . Structures of G10A, G43A and G10VG43A mutant proteins. Mutation of conserved glycine 10 to valine causes the 9-10 peptide link to invert. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 962-968.	2.5	8
62	The Rubredoxin from <i>Clostridium pasteurianum</i> : Mutation of the Iron Cysteine Ligands to Serine. Crystal and Molecular Structures of Oxidized and Dithionite-Treated Forms of the Cys42Ser Mutant. <i>Journal of the American Chemical Society</i> , 1998, 120, 4135-4150.	13.7	81