

Maria Selmer

List of Publications by Year in descending order

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37
papers

2,762
citations

430754

18
h-index

345118

36
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41
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41
docs citations

41
times ranked

2475
citing authors

#	ARTICLE	IF	CITATIONS
1	Structures and kinetics of Thermotoga maritima MetY reveal new insights into the predominant sulfurylation enzyme of bacterial methionine biosynthesis. Journal of Biological Chemistry, 2021, 296, 100797.	1.6	14
2	Structure and mechanism of a phage-encoded SAM lyase revises catalytic function of enzyme family. ELife, 2021, 10, .	2.8	15
3	Structure and kinetics of indole-3-glycerol phosphate synthase from Pseudomonas aeruginosa: Decarboxylation is not essential for indole formation. Journal of Biological Chemistry, 2020, 295, 15948-15956.	1.6	1
4	Structure and Characterization of Phosphoglucomutase 5 from Atlantic and Baltic Herring An Inactive Enzyme with Intact Substrate Binding. Biomolecules, 2020, 10, 1631.	1.8	4
5	Oligomerization and characteristics of phosphoenolpyruvate carboxylase in Synechococcus PCC 7002. Scientific Reports, 2020, 10, 3607.	1.6	4
6	Structural Recognition of Spectinomycin by Resistance Enzyme ANT(9) from Enterococcus faecalis. Antimicrobial Agents and Chemotherapy, 2020, 64, .	1.4	5
7	Crystal structure of ErmE - 23S rRNA methyltransferase in macrolide resistance. Scientific Reports, 2019, 9, 14607.	1.6	9
8	A bacteriophage enzyme induces bacterial metabolic perturbation that confers a novel promiscuous function. Nature Ecology and Evolution, 2018, 2, 1321-1330.	3.4	19
9	Structural mechanism of AadA, a dual-specificity aminoglycoside adenylyltransferase from Salmonella enterica. Journal of Biological Chemistry, 2018, 293, 11481-11490.	1.6	26
10	Structural and functional innovations in the real-time evolution of new (12±)8 barrel enzymes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4727-4732.	3.3	26
11	Two proofreading steps amplify the accuracy of genetic code translation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13744-13749.	3.3	48
12	Structure of AadA from Salmonella enterica: a monomeric aminoglycoside (3±)(9) adenylyltransferase. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2267-2277.	2.5	16
13	Two-step Ligand Binding in a (12±)8 Barrel Enzyme. Journal of Biological Chemistry, 2015, 290, 24657-24668.	1.6	16
14	Resistance to 12-Lactam Antibiotics Conferred by Point Mutations in Penicillin-Binding Proteins PBP3, PBP4 and PBP6 in Salmonella enterica. PLoS ONE, 2014, 9, e97202.	1.1	40
15	Energetic Pathway Sampling in a Protein Interaction Domain. Structure, 2013, 21, 1193-1202.	1.6	38
16	Structural and functional insights into the molecular mechanism of rRNA m6A methyltransferase RlmJ. Nucleic Acids Research, 2013, 41, 9537-9548.	6.5	21
17	Purification, crystallization and preliminary X-ray diffraction analysis of the 23S rRNA methyltransferase RlmJ from Escherichia coli. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1001-1003.	0.7	2
18	Mechanism of Elongation Factor-G-mediated Fusidic Acid Resistance and Fitness Compensation in Staphylococcus aureus. Journal of Biological Chemistry, 2012, 287, 30257-30267.	1.6	32

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19	Crystal structure of RlmM, the 2'-O-ribose methyltransferase for C2498 of Escherichia coli 23S rRNA. Nucleic Acids Research, 2012, 40, 10507-10520.	6.5	13
20	Structure and function of FusB: an elongation factor G-binding fusidic acid resistance protein active in ribosomal translocation and recycling. Open Biology, 2012, 2, 120016.	1.5	23
21	Tolerance of Protein Folding to a Circular Permutation in a PDZ Domain. PLoS ONE, 2012, 7, e50055.	1.1	12
22	Ribosome engineering to promote new crystal forms. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 578-583.	2.5	26
23	<i>Staphylococcus aureus</i> elongation factor G structure and analysis of a target for fusidic acid. FEBS Journal, 2010, 277, 3789-3803.	2.2	47
24	The Plastic Energy Landscape of Protein Folding. Journal of Biological Chemistry, 2010, 285, 18051-18059.	1.6	20
25	The Structure of the Ribosome with Elongation Factor G Trapped in the Posttranslocational State. Science, 2009, 326, 694-699.	6.0	465
26	Crystallographic studies of ribosomal frameshifting. FASEB Journal, 2009, 23, .	0.2	0
27	Exit Biology: Battle for the Nascent Chain. Structure, 2008, 16, 498-500.	1.6	8
28	Structures of tRNAs with an expanded anticodon loop in the decoding center of the 30S ribosomal subunit. Rna, 2007, 13, 817-823.	1.6	52
29	Crystal structure of the ribosome recycling factor bound to the ribosome. Nature Structural and Molecular Biology, 2007, 14, 733-737.	3.6	99
30	Structure of the 70S Ribosome Complexed with mRNA and tRNA. Science, 2006, 313, 1935-1942.	6.0	1,186
31	Crystal Structures of the Ribosome in Complex with Release Factors RF1 and RF2 Bound to a Cognate Stop Codon. Cell, 2005, 123, 1255-1266.	13.5	239
32	Structure of the L1 protuberance in the ribosome. Nature Structural Biology, 2003, 10, 104-108.	9.7	84
33	Is tRNA Binding or tRNA Mimicry Mandatory for Translation Factors?. Current Protein and Peptide Science, 2002, 3, 133-141.	0.7	9
34	Preparation of a crystallizable mRNA-binding fragment of Moorella thermoacetica elongation factor SelB. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1871-1873.	2.5	3
35	Post-termination complex disassembly by ribosome recycling factor, a functional tRNA mimic. EMBO Journal, 2002, 21, 2272-2281.	3.5	97
36	Structure of ribosomal protein TL5 complexed with RNA provides new insights into the CTC family of stress proteins. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 968-976.	2.5	38

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37	Crystallization and preliminary X-ray analysis of <i>Thermotoga maritima</i> ribosome recycling factor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 2049-2050.	2.5	5