

# Maria Selmer

## List of Publications by Year in descending order

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Version: 2024-02-01

37  
papers

2,762  
citations

430754

18  
h-index

345118

36  
g-index

41  
all docs

41  
docs citations

41  
times ranked

2475  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of the 70S Ribosome Complexed with mRNA and tRNA. <i>Science</i> , 2006, 313, 1935-1942.	6.0	1,186
2	The Structure of the Ribosome with Elongation Factor G Trapped in the Posttranslocational State. <i>Science</i> , 2009, 326, 694-699.	6.0	465
3	Crystal Structures of the Ribosome in Complex with Release Factors RF1 and RF2 Bound to a Cognate Stop Codon. <i>Cell</i> , 2005, 123, 1255-1266.	13.5	239
4	Crystal structure of the ribosome recycling factor bound to the ribosome. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 733-737.	3.6	99
5	Post-termination complex disassembly by ribosome recycling factor, a functional tRNA mimic. <i>EMBO Journal</i> , 2002, 21, 2272-2281.	3.5	97
6	Structure of the L1 protuberance in the ribosome. <i>Nature Structural Biology</i> , 2003, 10, 104-108.	9.7	84
7	Structures of tRNAs with an expanded anticodon loop in the decoding center of the 30S ribosomal subunit. <i>Rna</i> , 2007, 13, 817-823.	1.6	52
8	Two proofreading steps amplify the accuracy of genetic code translation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13744-13749.	3.3	48
9	<i>Staphylococcus aureus</i> elongation factor G structure and analysis of a target for fusidic acid. <i>FEBS Journal</i> , 2010, 277, 3789-3803.	2.2	47
10	Resistance to $\beta$ -Lactam Antibiotics Conferred by Point Mutations in Penicillin-Binding Proteins PBP3, PBP4 and PBP6 in <i>Salmonella enterica</i> . <i>PLoS ONE</i> , 2014, 9, e97202.	1.1	40
11	Structure of ribosomal protein TL5 complexed with RNA provides new insights into the CTC family of stress proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 968-976.	2.5	38
12	Energetic Pathway Sampling in a Protein Interaction Domain. <i>Structure</i> , 2013, 21, 1193-1202.	1.6	38
13	Mechanism of Elongation Factor-G-mediated Fusidic Acid Resistance and Fitness Compensation in <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 30257-30267.	1.6	32
14	Ribosome engineering to promote new crystal forms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 578-583.	2.5	26
15	Structural and functional innovations in the real-time evolution of new $\beta$ barrel enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4727-4732.	3.3	26
16	Structural mechanism of AadA, a dual-specificity aminoglycoside adenylyltransferase from <i>Salmonella enterica</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 11481-11490.	1.6	26
17	Structure and function of FusB: an elongation factor G-binding fusidic acid resistance protein active in ribosomal translocation and recycling. <i>Open Biology</i> , 2012, 2, 120016.	1.5	23
18	Structural and functional insights into the molecular mechanism of rRNA m6A methyltransferase RlmJ. <i>Nucleic Acids Research</i> , 2013, 41, 9537-9548.	6.5	21

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19	The Plastic Energy Landscape of Protein Folding. <i>Journal of Biological Chemistry</i> , 2010, 285, 18051-18059.	1.6	20
20	A bacteriophage enzyme induces bacterial metabolic perturbation that confers a novel promiscuous function. <i>Nature Ecology and Evolution</i> , 2018, 2, 1321-1330.	3.4	19
21	Structure of AadA from <i>Salmonella enterica</i> : a monomeric aminoglycoside (3-adenylyltransferase). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2267-2277.	2.5	16
22	Two-step Ligand Binding in a (12±)8 Barrel Enzyme. <i>Journal of Biological Chemistry</i> , 2015, 290, 24657-24668.	1.6	16
23	Structure and mechanism of a phage-encoded SAM lyase revises catalytic function of enzyme family. <i>ELife</i> , 2021, 10, .	2.8	15
24	Structures and kinetics of <i>Thermotoga maritima</i> MetY reveal new insights into the predominant sulfurylation enzyme of bacterial methionine biosynthesis. <i>Journal of Biological Chemistry</i> , 2021, 296, 100797.	1.6	14
25	Crystal structure of RlmM, the 2-O-ribose methyltransferase for C2498 of <i>Escherichia coli</i> 23S rRNA. <i>Nucleic Acids Research</i> , 2012, 40, 10507-10520.	6.5	13
26	Tolerance of Protein Folding to a Circular Permutation in a PDZ Domain. <i>PLoS ONE</i> , 2012, 7, e50055.	1.1	12
27	Is tRNA Binding or tRNA Mimicry Mandatory for Translation Factors?. <i>Current Protein and Peptide Science</i> , 2002, 3, 133-141.	0.7	9
28	Crystal structure of ErmE - 23S rRNA methyltransferase in macrolide resistance. <i>Scientific Reports</i> , 2019, 9, 14607.	1.6	9
29	Exit Biology: Battle for the Nascent Chain. <i>Structure</i> , 2008, 16, 498-500.	1.6	8
30	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
31	Structural Recognition of Spectinomycin by Resistance Enzyme ANT(9) from <i>Enterococcus faecalis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	5
32	Structure and Characterization of Phosphoglucomutase 5 from Atlantic and Baltic Herring: An Inactive Enzyme with Intact Substrate Binding. <i>Biomolecules</i> , 2020, 10, 1631.	1.8	4
33	Oligomerization and characteristics of phosphoenolpyruvate carboxylase in <i>Synechococcus</i> PCC 7002. <i>Scientific Reports</i> , 2020, 10, 3607.	1.6	4
34	Preparation of a crystallizable mRNA-binding fragment of <i>Moorella thermoacetica</i> elongation factor SelB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1871-1873.	2.5	3
35	Purification, crystallization and preliminary X-ray diffraction analysis of the 23S rRNA methyltransferase RlmJ from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1001-1003.	0.7	2
36	Structure and kinetics of indole-3-glycerol phosphate synthase from <i>Pseudomonas aeruginosa</i> : Decarboxylation is not essential for indole formation. <i>Journal of Biological Chemistry</i> , 2020, 295, 15948-15956.	1.6	1

#	ARTICLE	IF	CITATIONS
37	Crystallographic studies of ribosomal frameshifting. FASEB Journal, 2009, 23, .	0.2	0