

# Emmanuelle Schmitt

## List of Publications by Year in descending order

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66  
papers

2,813  
citations

147801

31  
h-index

189892

50  
g-index

68  
all docs

68  
docs citations

68  
times ranked

2551  
citing authors

#	ARTICLE	IF	CITATIONS
1	Role of aIF5B in archaeal translation initiation. <i>Nucleic Acids Research</i> , 2022, 50, 6532-6548.	14.5	10
2	Bulges in left-handed G-quadruplexes. <i>Nucleic Acids Research</i> , 2021, 49, 1724-1736.	14.5	13
3	Recognition of different base tetrads by RHAU (DHX36): X-ray crystal structure of the G4 recognition motif bound to the 3' end tetrad of a DNA G-quadruplex. <i>Journal of Structural Biology</i> , 2020, 209, 107399.	2.8	11
4	Use of <sup>35</sup> S-methionine as an amino acid substrate of Escherichia coli methionyl-tRNA synthetase. <i>Journal of Structural Biology</i> , 2020, 209, 107435.	2.8	5
5	Structural basis of the interaction between cyclodipeptide synthases and aminoacylated tRNA substrates. <i>Rna</i> , 2020, 26, 1589-1602.	3.5	10
6	Recent Advances in Archaeal Translation Initiation. <i>Frontiers in Microbiology</i> , 2020, 11, 584152.	3.5	23
7	Cryo-EM study of an archaeal 30S initiation complex gives insights into evolution of translation initiation. <i>Communications Biology</i> , 2020, 3, 58.	4.4	27
8	Adaptive landscape flattening allows the design of both enzyme: Substrate binding and catalytic power. <i>PLoS Computational Biology</i> , 2020, 16, e1007600.	3.2	13
9	NMR solution and X-ray crystal structures of a DNA molecule containing both right- and left-handed parallel-stranded G-quadruplexes. <i>Nucleic Acids Research</i> , 2019, 47, 8272-8281.	14.5	30
10	Start Codon Recognition in Eukaryotic and Archaeal Translation Initiation: A Common Structural Core. <i>International Journal of Molecular Sciences</i> , 2019, 20, 939.	4.1	14
11	A Minimal Sequence for Left-Handed G-Quadruplex Formation. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 2331-2335.	13.8	41
12	A Minimal Sequence for Left-Handed G-Quadruplex Formation. <i>Angewandte Chemie</i> , 2019, 131, 2353-2357.	2.0	5
13	Structural basis for partition of the cyclodipeptide synthases into two subfamilies. <i>Journal of Structural Biology</i> , 2018, 203, 17-26.	2.8	13
14	Role of aIF1 in <i>Pyrococcus abyssi</i> translation initiation. <i>Nucleic Acids Research</i> , 2018, 46, 11061-11074.	14.5	7
15	The trimeric coiled-coil HSBP1 protein promotes WASH complex assembly at centrosomes. <i>EMBO Journal</i> , 2018, 37, .	7.8	22
16	Cyclization Reaction Catalyzed by Cyclodipeptide Synthases Relies on a Conserved Tyrosine Residue. <i>Scientific Reports</i> , 2018, 8, 7031.	3.3	8
17	The structure of an <i>E. coli</i> tRNA <sup>fMet</sup> A <sub>1</sub> shows an unusual conformation of the A <sub>1</sub> -U <sub>72</sub> base pair. <i>Rna</i> , 2017, 23, 673-682.	3.5	10
18	Cryo-EM study of start codon selection during archaeal translation initiation. <i>Nature Communications</i> , 2016, 7, 13366.	12.8	25

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19	Identification of a second GTP-bound magnesium ion in archaeal initiation factor 2. <i>Nucleic Acids Research</i> , 2015, 43, 2946-2957.	14.5	28
20	Structure of a left-handed DNA G-quadruplex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2729-2733.	7.1	109
21	Cdc123, a Cell Cycle Regulator Needed for eIF2 Assembly, Is an ATP-Grasp Protein with Unique Features. <i>Structure</i> , 2015, 23, 1596-1608.	3.3	16
22	Unravelling the mechanism of non-ribosomal peptide synthesis by cyclodipeptide synthases. <i>Nature Communications</i> , 2014, 5, 5141.	12.8	54
23	Capturing the mutational landscape of the beta-lactamase TEM-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13067-13072.	7.1	228
24	Roles of yeast eIF2 <sup>1</sup> and eIF2 <sup>2</sup> subunits in the binding of the initiator methionyl-tRNA. <i>Nucleic Acids Research</i> , 2013, 41, 1047-1057.	14.5	17
25	Structure of the ternary initiation complex eIF2-GDPNP-methionylated initiator tRNA. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 450-454.	8.2	63
26	Translation Initiation. <i>EcoSal Plus</i> , 2011, 4, .	5.4	5
27	Intrinsic resistance to aminoglycosides in <i>Enterococcus faecium</i> is conferred by the 16S rRNA m <sup>C1404</sup> -specific methyltransferase EfmM. <i>Rna</i> , 2011, 17, 251-262.	3.5	42
28	tRNA Binding Properties of Eukaryotic Translation Initiation Factor 2 from <i>Encephalitozoon cuniculi</i> . <i>Biochemistry</i> , 2010, 49, 8680-8688.	2.5	12
29	Eukaryotic and archaeal translation initiation factor 2: A heterotrimeric tRNA carrier. <i>FEBS Letters</i> , 2010, 584, 405-412.	2.8	73
30	Discovery of <i>Escherichia coli</i> methionyl-tRNA synthetase mutants for efficient labeling of proteins with azidonorleucine in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15285-15290.	7.1	114
31	Structural Bases for 16 S rRNA Methylation Catalyzed by ArmA and RmtB Methyltransferases. <i>Journal of Molecular Biology</i> , 2009, 388, 570-582.	4.2	41
32	Switching from an Induced-Fit to a Lock-and-Key Mechanism in an Aminoacyl-tRNA Synthetase with Modified Specificity. <i>Journal of Molecular Biology</i> , 2009, 394, 843-851.	4.2	17
33	A unique conformation of the anticodon stem-loop is associated with the capacity of tRNA <sup>fMet</sup> to initiate protein synthesis. <i>Nucleic Acids Research</i> , 2008, 36, 4894-4901.	14.5	45
34	Structure of an archaeal heterotrimeric initiation factor 2 reveals a nucleotide state between the GTP and the GDP states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18445-18450.	7.1	71
35	Protection-Based Assays to Measure Aminoacyl-tRNA Binding to Translation Initiation Factors. <i>Methods in Enzymology</i> , 2007, 430, 265-281.	1.0	26
36	Structural Switch of the <sup>3</sup> Subunit in an Archaeal eIF2 <sup>1</sup> <sup>3</sup> Heterodimer. <i>Structure</i> , 2006, 14, 119-128.	3.3	61

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37	Structural Basis of RNA-Dependent Recruitment of Glutamine to the Genetic Code. <i>Science</i> , 2006, 312, 1950-1954.	12.6	80
38	Structural Basis for tRNA-Dependent Amidotransferase Function. <i>Structure</i> , 2005, 13, 1421-1433.	3.3	44
39	Initiator tRNA Binding by eIF5B, the Eukaryotic/Archaeal Homologue of Bacterial Initiation Factor IF2. <i>Biochemistry</i> , 2005, 44, 15594-15601.	2.5	44
40	Crystal Structure at 1.8 Å... Resolution and Identification of Active Site Residues of <i>Sulfolobus solfataricus</i> Peptidyl-tRNA Hydrolase. <i>Biochemistry</i> , 2005, 44, 4294-4301.	2.5	20
41	Structure-Function Relationships of the Intact eIF2 $\beta$ Subunit from the Archaeon <i>Pyrococcus abyssi</i> . <i>Biochemistry</i> , 2005, 44, 8749-8756.	2.5	22
42	Functional Molecular Mapping of Archaeal Translation Initiation Factor 2. <i>Journal of Biological Chemistry</i> , 2004, 279, 15984-15993.	3.4	64
43	Three-Dimensional Structure of Methionyl-tRNA Synthetase from <i>Pyrococcus abyssi</i> . <i>Biochemistry</i> , 2004, 43, 2635-2644.	2.5	27
44	Mitochondrial Methionyl-tRNA <sup>Met</sup> Formyltransferase from <i>Saccharomyces cerevisiae</i> : A Gene Disruption and tRNA Substrate Specificity. <i>Biochemistry</i> , 2003, 42, 932-939.	2.5	19
45	Use of Analogues of Methionine and Methionyl Adenylate to Sample Conformational Changes During Catalysis in <i>Escherichia coli</i> Methionyl-tRNA Synthetase. <i>Journal of Molecular Biology</i> , 2003, 332, 59-72.	4.2	73
46	Structure and Function of the C-Terminal Domain of Methionyl-tRNA Synthetase. <i>Biochemistry</i> , 2002, 41, 13003-13011.	2.5	30
47	The large subunit of initiation factor eIF2 is a close structural homologue of elongation factors. <i>EMBO Journal</i> , 2002, 21, 1821-1832.	7.8	88
48	Recognition of tRNAs by Methionyl-tRNA Transformylase from Mammalian Mitochondria. <i>Journal of Biological Chemistry</i> , 2001, 276, 20064-20068.	3.4	34
49	Structure of Crystallized-Tyr-tRNA <sup>Tyr</sup> Deacylase. <i>Journal of Biological Chemistry</i> , 2001, 276, 47285-47290.	3.4	52
50	The many routes of bacterial transfer RNAs after aminoacylation. <i>Current Opinion in Structural Biology</i> , 2000, 10, 95-101.	5.7	14
51	Crystallization and preliminary X-ray analysis of <i>Escherichia coli</i> methionyl-tRNA <sup>Met</sup> formyltransferase complexed with formyl-methionyl-tRNA <sup>Met</sup> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 332-334.	2.5	22
52	Receptor Site for the 5'-Phosphate of Elongator tRNAs Governs Substrate Selection by Peptidyl-tRNA Hydrolase. <i>Biochemistry</i> , 1999, 38, 4982-4987.	2.5	36
53	Crystal structure of <i>Escherichia coli</i> methionyl-tRNA synthetase highlights species-specific features. <i>Journal of Molecular Biology</i> , 1999, 294, 1287-1297.	4.2	107
54	Crystal structure of aspartyl-tRNA synthetase from <i>Pyrococcus kodakaraensis</i> KOD: archaeon specificity and catalytic mechanism of adenylate formation. <i>EMBO Journal</i> , 1998, 17, 5227-5237.	7.8	118

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55	Crystal structure of methionyl-tRNA <sup>fMet</sup> transformylase complexed with the initiator formyl-methionyl-tRNA <sup>fMet</sup> . EMBO Journal, 1998, 17, 6819-6826.	7.8	129
56	General Structure/Function Properties of Microbial Methionyl-Trna Synthetases. FEBS Journal, 1997, 246, 539-547.	0.2	14
57	Crystal structure at 1.2Å resolution and active site mapping of Escherichia coli peptidyl-tRNA hydrolase. EMBO Journal, 1997, 16, 4760-4769.	7.8	86
58	Molecular recognition governing the initiation of translation in Escherichia coli. A review. Biochimie, 1996, 78, 543-554.	2.6	52
59	Structure of crystalline Escherichia coli methionyl-tRNA <sup>(f)Met</sup> formyltransferase: comparison with glycylamide ribonucleotide formyltransferase.. EMBO Journal, 1996, 15, 4749-4758.	7.8	66
60	Crystallization and preliminary X-ray analysis of Escherichia coli methionyl-tRNA <sup>fMet</sup> formyltransferase. Proteins: Structure, Function and Bioinformatics, 1996, 25, 139-141.	2.6	12
61	Structure of crystalline Escherichia coli methionyl-tRNA <sup>(f)Met</sup> formyltransferase: comparison with glycylamide ribonucleotide formyltransferase. EMBO Journal, 1996, 15, 4749-58.	7.8	31
62	Transition state stabilization by the $\alpha$ -high $\alpha$ ™ motif of class I aminoacyl-tRNA synthetases: the case of Escherichia coli methionyl-tRNA synthetase. Nucleic Acids Research, 1995, 23, 4793-4798.	14.5	29
63	Methionyl-tRNA Synthetase Needs an Intact and Mobile 332KMSKS336 Motif in Catalysis of Methionyl Adenylate Formation. Journal of Molecular Biology, 1994, 242, 566-577.	4.2	43
64	Two Acidic Residues of Escherichia coli Methionyl-tRNA Synthetase Act as Negative Discriminants Towards the Binding of Non-cognate tRNA Anticodons. Journal of Molecular Biology, 1993, 233, 615-628.	4.2	55
65	Structural and biochemical characterization of the Escherichia coli argE gene product. Journal of Bacteriology, 1992, 174, 2323-2331.	2.2	58
66	Methionyl-tRNA synthetase from Bacillus stearothermophilus: structural and functional identities with the Escherichia coli enzyme. Nucleic Acids Research, 1991, 19, 3673-3681.	14.5	34