

Tilman Schirmer

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

3,223
citations

279798

23
h-index

395702

33
g-index

44
all docs

44
docs citations

44
times ranked

2720
citing authors

#	ARTICLE	IF	CITATIONS
1	Cell cycle-dependent dynamic localization of a bacterial response regulator with a novel di-guanylate cyclase output domain. <i>Genes and Development</i> , 2004, 18, 715-727.	5.9	554
2	Structural basis of activity and allosteric control of diguanylate cyclase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 17084-17089.	7.1	428
3	Structural and mechanistic determinants of c-di-GMP signalling. <i>Nature Reviews Microbiology</i> , 2009, 7, 724-735.	28.6	413
4	Structure of BeF3 ⁺ -Modified Response Regulator PleD: Implications for Diguanylate Cyclase Activation, Catalysis, and Feedback Inhibition. <i>Structure</i> , 2007, 15, 915-927.	3.3	209
5	Second messenger signalling governs <i>Escherichia coli</i> biofilm induction upon ribosomal stress. <i>Molecular Microbiology</i> , 2009, 72, 1500-1516.	2.5	183
6	Regulatory Cohesion of Cell Cycle and Cell Differentiation through Interlinked Phosphorylation and Second Messenger Networks. <i>Molecular Cell</i> , 2011, 43, 550-560.	9.7	169
7	Adenylylation control by intra- or intermolecular active-site obstruction in Fic proteins. <i>Nature</i> , 2012, 482, 107-110.	27.8	149
8	C-di-GMP Synthesis: Structural Aspects of Evolution, Catalysis and Regulation. <i>Journal of Molecular Biology</i> , 2016, 428, 3683-3701.	4.2	114
9	Crystal Structures of YkuL and Its Complex with Second Messenger Cyclic Di-GMP Suggest Catalytic Mechanism of Phosphodiester Bond Cleavage by EAL Domains. <i>Journal of Biological Chemistry</i> , 2009, 284, 13174-13184.	3.4	96
10	Structure and Signaling Mechanism of a Zinc-Sensory Diguanylate Cyclase. <i>Structure</i> , 2013, 21, 1149-1157.	3.3	95
11	Adenylylation of Gyrase and Topo IV by FicT Toxins Disrupts Bacterial DNA Topology. <i>Cell Reports</i> , 2015, 12, 1497-1507.	6.4	92
12	Crystal Structure of the Major Celery Allergen Api g 1: Molecular Analysis of Cross-reactivity. <i>Journal of Molecular Biology</i> , 2005, 351, 1101-1109.	4.2	75
13	Cyclic di-GMP mediates a histidine kinase/phosphatase switch by noncovalent domain cross-linking. <i>Science Advances</i> , 2016, 2, e1600823.	10.3	69
14	Cyclic di-GMP differentially tunes a bacterial flagellar motor through a novel class of CheY-like regulators. <i>ELife</i> , 2017, 6, .	6.0	62
15	Inherent Regulation of EAL Domain-catalyzed Hydrolysis of Second Messenger Cyclic di-GMP. <i>Journal of Biological Chemistry</i> , 2014, 289, 6978-6990.	3.4	60
16	Fic domain-catalyzed adenylylation: Insight provided by the structural analysis of the type IV secretion system effector BepA. <i>Protein Science</i> , 2011, 20, 492-499.	7.6	50
17	Expression and Genetic Activation of Cyclic Di-GMP-Specific Phosphodiesterases in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2016, 198, 448-462.	2.2	48
18	Structure of the N-Terminal Gyrase B Fragment in Complex with ADP \cdot ...Pi Reveals Rigid-Body Motion Induced by ATP Hydrolysis. <i>PLoS ONE</i> , 2014, 9, e107289.	2.5	46

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19	Efficient Enzymatic Production of the Bacterial Second Messenger c-di-GMP by the Diguanylate Cyclase YdeH from <i>E. coli</i> . <i>Applied Biochemistry and Biotechnology</i> , 2011, 163, 71-79.	2.9	43
20	An Alternative Active Site Architecture for O ₂ Activation in the Ergothioneine Biosynthetic EgtB from <i>Chloracidobacterium thermophilum</i> . <i>Journal of the American Chemical Society</i> , 2019, 141, 5275-5285.	13.7	39
21	Precise timing of transcription by c-di-GMP coordinates cell cycle and morphogenesis in <i>Caulobacter</i> . <i>Nature Communications</i> , 2020, 11, 816.	12.8	38
22	Conserved Inhibitory Mechanism and Competent ATP Binding Mode for Adenylyltransferases with Fic Fold. <i>PLoS ONE</i> , 2013, 8, e64901.	2.5	32
23	Hybrid histidine kinase activation by cyclic di-GMP-mediated domain liberation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1000-1008.	7.1	28
24	Intrinsic regulation of FIC-domain AMP-transferases by oligomerization and automodification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E529-37.	7.1	27
25	Reciprocal growth control by competitive binding of nucleotide second messengers to a metabolic switch in <i>Caulobacter crescentus</i> . <i>Nature Microbiology</i> , 2021, 6, 59-72.	13.3	23
26	Intercepting second-messenger signaling by rationally designed peptides sequestering c-di-GMP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17211-17220.	7.1	20
27	The BID Domain of Type IV Secretion Substrates Forms a Conserved Four-Helix Bundle Topped with a Hook. <i>Structure</i> , 2017, 25, 203-211.	3.3	15
28	Activation mechanism of a small prototypic Rec-GGDEF diguanylate cyclase. <i>Nature Communications</i> , 2021, 12, 2162.	12.8	14
29	Structural basis for selective AMPylation of Rac-subfamily GTPases by <i>Bartonella</i> effector protein 1 (Bep1). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	7
30	Crystal Structure of the <i>Escherichia coli</i> Fic Toxin-Like Protein in Complex with Its Cognate Antitoxin. <i>PLoS ONE</i> , 2016, 11, e0163654.	2.5	6
31	Evolutionary Diversification of Host-Targeted <i>Bartonella</i> Effectors Proteins Derived from a Conserved FicTA Toxin-Antitoxin Module. <i>Microorganisms</i> , 2021, 9, 1645.	3.6	5
32	Acquisition of enzymatic progress curves in real time by quenching-free ion exchange chromatography. <i>Analytical Biochemistry</i> , 2022, 639, 114523.	2.4	3
33	Making, Breaking, and Sensing of Cyclic Di-GMP: Structural, Thermodynamic, and Evolutionary Principles. , 0, , 76-95.		2
34	Combinatorial mutagenesis analysis of residues in the channel constriction loop L3 and neighbouring β -strands in the LamB glycoporin of <i>Escherichia coli</i> . <i>Molecular Membrane Biology</i> , 1996, 13, 41-48.	2.0	1
35	Structure-Function Relationships in Sugar-Specific Porins. , 2005, , 169-181.		0