

Robert Schnell

List of Publications by Year in descending order

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31
papers

866
citations

430874

18
h-index

477307

29
g-index

31
all docs

31
docs citations

31
times ranked

1432
citing authors

#	ARTICLE	IF	CITATIONS
1	Siroheme- and [Fe4-S4]-dependent NirA from Mycobacterium tuberculosis Is a Sulfite Reductase with a Covalent Cys-Tyr Bond in the Active Site. <i>Journal of Biological Chemistry</i> , 2005, 280, 27319-27328.	3.4	97
2	Structural Insights into Catalysis and Inhibition of O-Acetylserine Sulfhydrylase from Mycobacterium tuberculosis. <i>Journal of Biological Chemistry</i> , 2007, 282, 23473-23481.	3.4	82
3	A secretagogin locus of the mammalian hypothalamus controls stress hormone release. <i>EMBO Journal</i> , 2015, 34, 36-54.	7.8	75
4	A TRPV1 secretagogin regulatory axis controls pancreatic cell survival by modulating protein turnover. <i>EMBO Journal</i> , 2017, 36, 2107-2125.	7.8	52
5	Peptidoglycan Remodeling in Mycobacterium tuberculosis: Comparison of Structures and Catalytic Activities of RipA and RipB. <i>Journal of Molecular Biology</i> , 2011, 413, 247-260.	4.2	50
6	Inhibitors of the Cysteine Synthase CysM with Antibacterial Potency against Dormant Mycobacterium tuberculosis. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 6848-6859.	6.4	45
7	Discovery of an Allosteric Inhibitor Binding Site in 3-Oxo-acyl-ACP Reductase from Pseudomonas aeruginosa. <i>ACS Chemical Biology</i> , 2013, 8, 2518-2527.	3.4	38
8	Structure of LdtMt2, an L,D-transpeptidase from Mycobacterium tuberculosis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 432-441.	2.5	36
9	Binding and processing of lactam antibiotics by the transpeptidase LdtMt2 from Mycobacterium tuberculosis. <i>FEBS Journal</i> , 2017, 284, 725-741.	4.7	35
10	The AEROPATH project targeting Pseudomonas aeruginosa: crystallographic studies for assessment of potential targets in early-stage drug discovery. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 25-34.	0.7	30
11	Structural and Functional Characterization of the BcsG Subunit of the Cellulose Synthase in Salmonella typhimurium. <i>Journal of Molecular Biology</i> , 2018, 430, 3170-3189.	4.2	29
12	Pyridoxal-phosphate dependent mycobacterial cysteine synthases: Structure, mechanism and potential as drug targets. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1175-1183.	2.3	28
13	Engineering of Ancestors as a Tool to Elucidate Structure, Mechanism, and Specificity of Extant Terpene Cyclase. <i>Journal of the American Chemical Society</i> , 2021, 143, 3794-3807.	13.7	28
14	The structure of the N-terminal module of the cell wall hydrolase RipA and its role in regulating catalytic activity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 912-923.	2.6	26
15	1.9 Å structure of the signal receiver domain of the putative response regulator NarL from Mycobacterium tuberculosis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 1096-1100.	0.7	24
16	Structural enzymology of sulphur metabolism in Mycobacterium tuberculosis. <i>Biochemical and Biophysical Research Communications</i> , 2010, 396, 33-38.	2.1	22
17	RipD (Rv1566c) from Mycobacterium tuberculosis: adaptation of an NlpC/p60 domain to a non-catalytic peptidoglycan-binding function. <i>Biochemical Journal</i> , 2014, 457, 33-41.	3.7	21
18	CysK2 from Mycobacterium tuberculosis Is an O ² -Phospho-Serine-Dependent S-Sulfocysteine Synthase. <i>Journal of Bacteriology</i> , 2014, 196, 3410-3420.	2.2	21

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19	Tetrahydrodipicolinate N-Succinyltransferase and Dihydrodipicolinate Synthase from <i>Pseudomonas aeruginosa</i> : Structure Analysis and Gene Deletion. <i>PLoS ONE</i> , 2012, 7, e31133.	2.5	20
20	Secretagogin protects Pdx1 from proteasomal degradation to control a transcriptional program required for I ² cell specification. <i>Molecular Metabolism</i> , 2018, 14, 108-120.	6.5	19
21	Structural characterization of substrate and inhibitor binding to farnesyl pyrophosphate synthase from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 721-731.	2.5	17
22	Profiling of in vitro activities of urea-based inhibitors against cysteine synthases from <i>Mycobacterium tuberculosis</i> . <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017, 27, 4582-4587.	2.2	13
23	A FabG inhibitor targeting an allosteric binding site inhibits several orthologs from Gram-negative ESKAPE pathogens. <i>Bioorganic and Medicinal Chemistry</i> , 2021, 30, 115898.	3.0	12
24	GABAergic Terminals Are a Source of Galanin to Modulate Cholinergic Neuron Development in the Neonatal Forebrain. <i>Cerebral Cortex</i> , 2014, 24, 3277-3288.	2.9	10
25	Crystal structure of NirD, the small subunit of the nitrite reductase NirbD from <i>Mycobacterium tuberculosis</i> at 2.0 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2799-2803.	2.6	9
26	Crystal Structures of the Kinase Domain of the Sulfate-Activating Complex in <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2015, 10, e0121494.	2.5	9
27	N-Thio-β-lactams targeting L,D-transpeptidase-2, with activity against drug-resistant strains of <i>Mycobacterium tuberculosis</i> . <i>Cell Chemical Biology</i> , 2021, 28, 1321-1332.e5.	5.2	8
28	Substrate Channel Flexibility in <i>Pseudomonas aeruginosa</i> MurB Accommodates Two Distinct Substrates. <i>PLoS ONE</i> , 2013, 8, e66936.	2.5	5
29	Structures of <i>Pseudomonas aeruginosa</i> β ² -ketoacyl-(acyl-carrier-protein) synthase II (FabF) and a C164Q mutant provide templates for antibacterial drug discovery and identify a buried potassium ion and a ligand-binding site that is an artefact of the crystal form. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1020-1026.	0.8	4
30	Lead derivatization of ethyl 6-bromo-2-((dimethylamino)methyl)-5-hydroxy-1-phenyl-1H-indole-3-carboxylate and 5-bromo-2-(thiophene-2-carboxamido) benzoic acid as FabG inhibitors targeting ESKAPE pathogens. <i>European Journal of Medicinal Chemistry</i> , 2021, , 113976.	5.5	1
31	Crystal structure of the flavoenzyme PA4991 from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 105-111.	0.8	0