Robert Schnell

List of Publications by Citations

31 papers	626 citations	16 h-index	24 g-index
31 ext. papers	769 ext. citations	5.6 avg, IF	3.61 L-index

#	Paper	IF	Citations
31	Siroheme- and [Fe4-S4]-dependent NirA from Mycobacterium tuberculosis is a sulfite reductase with a covalent Cys-Tyr bond in the active site. *Journal of Biological Chemistry*, **2005**, 280, 27319-28	5.4	84
30	Structural insights into catalysis and inhibition of O-acetylserine sulfhydrylase from Mycobacterium tuberculosis. Crystal structures of the enzyme alpha-aminoacrylate intermediate and an enzyme-inhibitor complex. *Journal of Biological Chemistry*, **2007**, 282, 23473-81	5.4	77
29	A secretagogin locus of the mammalian hypothalamus controls stress hormone release. *EMBO Journal*, **2015**, 34, 36-54	13	46
28	Peptidoglycan remodeling in Mycobacterium tuberculosis: comparison of structures and catalytic activities of RipA and RipB. *Journal of Molecular Biology*, **2011**, 413, 247-60	6.5	41
27	Inhibitors of the Cysteine Synthase CysM with Antibacterial Potency against Dormant Mycobacterium tuberculosis. *Journal of Medicinal Chemistry*, **2016**, 59, 6848-59	8.3	33
26	A TRPV1-to-secretagogin regulatory axis controls pancreatic β cell survival by modulating protein turnover. *EMBO Journal*, **2017**, 36, 2107-2125	13	31
25	The AEROPATH project targeting Pseudomonas aeruginosa: crystallographic studies for assessment of potential targets in early-stage drug discovery. *Acta Crystallographica Section F: Structural Biology Communications*, **2013**, 69, 25-34		28
24	Structure of LdtMt2, an L,D-transpeptidase from Mycobacterium tuberculosis. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 432-41		26
23	Discovery of an allosteric inhibitor binding site in 3-Oxo-acyl-ACP reductase from Pseudomonas aeruginosa. *ACS Chemical Biology*, **2013**, 8, 2518-27	4.9	26
22	Binding and processing of β lactam antibiotics by the transpeptidase Ldt from Mycobacterium tuberculosis. *FEBS Journal*, **2017**, 284, 725-741	5.7	22
21	1.9 A structure of the signal receiver domain of the putative response regulator NarL from Mycobacterium tuberculosis. *Acta Crystallographica Section F: Structural Biology Communications*, **2008**, 64, 1096-100		22
20	Structural enzymology of sulphur metabolism in Mycobacterium tuberculosis. *Biochemical and Biophysical Research Communications*, **2010**, 396, 33-8	3.4	21
19	Structural and Functional Characterization of the BcsG Subunit of the Cellulose Synthase in Salmonella typhimurium. *Journal of Molecular Biology*, **2018**, 430, 3170-3189	6.5	19
18	The structure of the N-terminal module of the cell wall hydrolase RipA and its role in regulating catalytic activity. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86, 912-923	4.2	16
17	RipD (Rv1566c) from Mycobacterium tuberculosis: adaptation of an NlpC/p60 domain to a non-catalytic peptidoglycan-binding function. *Biochemical Journal*, **2014**, 457, 33-41	3.8	16
16	CysK2 from Mycobacterium tuberculosis is an O-phospho-L-serine-dependent S-sulfocysteine synthase. *Journal of Bacteriology*, **2014**, 196, 3410-20	3.5	16
15	Tetrahydrodipicolinate N-succinyltransferase and dihydrodipicolinate synthase from Pseudomonas aeruginosa: structure analysis and gene deletion. *PLoS ONE*, **2012**, 7, e31133	3.7	15

List of Publications

14	Pyridoxal-phosphate dependent mycobacterial cysteine synthases: Structure, mechanism and potential as drug targets. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2015**, 1854, 1175-83	4	14
13	Structural characterization of substrate and inhibitor binding to farnesyl pyrophosphate synthase from Pseudomonas aeruginosa. *Acta Crystallographica Section D: Biological Crystallography*, **2015**, 71, 721-31		11
12	Secretagogin protects Pdx1 from proteasomal degradation to control a transcriptional program required for β cell specification. *Molecular Metabolism*, **2018**, 14, 108-120	8.8	10
11	Profiling of in vitro activities of urea-based inhibitors against cysteine synthases from Mycobacterium tuberculosis. *Bioorganic and Medicinal Chemistry Letters*, **2017**, 27, 4582-4587	2.9	10
10	GABAergic terminals are a source of galanin to modulate cholinergic neuron development in the neonatal forebrain. *Cerebral Cortex*, **2014**, 24, 3277-88	5.1	8
9	Engineering of Ancestors as a Tool to Elucidate Structure, Mechanism, and Specificity of Extant Terpene Cyclase. *Journal of the American Chemical Society*, **2021**, 143, 3794-3807	16.4	8
8	Crystal structure of NirD, the small subunit of the nitrite reductase NirbD from Mycobacterium tuberculosis at 2.0 Å resolution. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 2799-803	4.2	7
7	A FabG inhibitor targeting an allosteric binding site inhibits several orthologs from Gram-negative ESKAPE pathogens. *Bioorganic and Medicinal Chemistry*, **2021**, 30, 115898	3.4	7
6	Crystal structures of the kinase domain of the sulfate-activating complex in Mycobacterium tuberculosis. *PLoS ONE*, **2015**, 10, e0121494	3.7	4
5	Structures of Pseudomonas aeruginosa β-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. *Acta Crystallographica Section F, Structural Biology Communications*, **2015**, 71, 1020-6	1.1	3
4	Substrate Channel Flexibility in Pseudomonas aeruginosa MurB Accommodates Two Distinct Substrates. *PLoS ONE*, **2013**, 8, e66936	3.7	3
3	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. *European Journal of Medicinal Chemistry*, **2021**, 113976	6.8	1
2	N-Thio-β-lactams targeting L,D-transpeptidase-2, with activity against drug-resistant strains of Mycobacterium tuberculosis. *Cell Chemical Biology*, **2021**, 28, 1321-1332.e5	8.2	1
1	Crystal structure of the flavoenzyme PA4991 from Pseudomonas aeruginosa. *Acta Crystallographica Section F, Structural Biology Communications*, **2016**, 72, 105-11	1.1	