

# Robert Schnell

## List of Publications by Year in Descending Order

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**Version:** 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	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> , <b>2021</b> , 113976	6.8	1
30	A FabG inhibitor targeting an allosteric binding site inhibits several orthologs from Gram-negative ESKAPE pathogens. <i>Bioorganic and Medicinal Chemistry</i> , <b>2021</b> , 30, 115898	3.4	7
29	Engineering of Ancestors as a Tool to Elucidate Structure, Mechanism, and Specificity of Extant Terpene Cyclase. <i>Journal of the American Chemical Society</i> , <b>2021</b> , 143, 3794-3807	16.4	8
28	N-Thio- $\beta$ -lactams targeting L,D-transpeptidase-2, with activity against drug-resistant strains of Mycobacterium tuberculosis. <i>Cell Chemical Biology</i> , <b>2021</b> , 28, 1321-1332.e5	8.2	1
27	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> , <b>2018</b> , 86, 912-923	4.2	16
26	Structural and Functional Characterization of the BcsG Subunit of the Cellulose Synthase in Salmonella typhimurium. <i>Journal of Molecular Biology</i> , <b>2018</b> , 430, 3170-3189	6.5	19
25	Secretagogin protects Pdx1 from proteasomal degradation to control a transcriptional program required for $\beta$ cell specification. <i>Molecular Metabolism</i> , <b>2018</b> , 14, 108-120	8.8	10
24	Binding and processing of $\beta$ -lactam antibiotics by the transpeptidase Ldt from Mycobacterium tuberculosis. <i>FEBS Journal</i> , <b>2017</b> , 284, 725-741	5.7	22
23	A TRPV1-to-secretagogin regulatory axis controls pancreatic $\beta$ cell survival by modulating protein turnover. <i>EMBO Journal</i> , <b>2017</b> , 36, 2107-2125	13	31
22	Profiling of in vitro activities of urea-based inhibitors against cysteine synthases from Mycobacterium tuberculosis. <i>Bioorganic and Medicinal Chemistry Letters</i> , <b>2017</b> , 27, 4582-4587	2.9	10
21	Crystal structure of the flavoenzyme PA4991 from Pseudomonas aeruginosa. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2016</b> , 72, 105-11	1.1	
20	Inhibitors of the Cysteine Synthase CysM with Antibacterial Potency against Dormant Mycobacterium tuberculosis. <i>Journal of Medicinal Chemistry</i> , <b>2016</b> , 59, 6848-59	8.3	33
19	Structural characterization of substrate and inhibitor binding to farnesyl pyrophosphate synthase from Pseudomonas aeruginosa. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 721-31		11
18	Pyridoxal-phosphate dependent mycobacterial cysteine synthases: Structure, mechanism and potential as drug targets. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2015</b> , 1854, 1175-83	4	14
17	A secretagogin locus of the mammalian hypothalamus controls stress hormone release. <i>EMBO Journal</i> , <b>2015</b> , 34, 36-54	13	46
16	Structures of Pseudomonas aeruginosa $\beta$ -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> , <b>2015</b> , 71, 1020-6	1.1	3
15	Crystal structures of the kinase domain of the sulfate-activating complex in Mycobacterium tuberculosis. <i>PLoS ONE</i> , <b>2015</b> , 10, e0121494	3.7	4

14	RipD (Rv1566c) from <i>Mycobacterium tuberculosis</i> : adaptation of an NlpC/p60 domain to a non-catalytic peptidoglycan-binding function. <i>Biochemical Journal</i> , <b>2014</b> , 457, 33-41	3.8	16
13	CysK2 from <i>Mycobacterium tuberculosis</i> is an O-phospho-L-serine-dependent S-sulfocysteine synthase. <i>Journal of Bacteriology</i> , <b>2014</b> , 196, 3410-20	3.5	16
12	GABAergic terminals are a source of galanin to modulate cholinergic neuron development in the neonatal forebrain. <i>Cerebral Cortex</i> , <b>2014</b> , 24, 3277-88	5.1	8
11	The AEROPATH project targeting <i>Pseudomonas aeruginosa</i> : crystallographic studies for assessment of potential targets in early-stage drug discovery. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2013</b> , 69, 25-34		28
10	Structure of LdtMt2, an L,D-transpeptidase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 432-41		26
9	Discovery of an allosteric inhibitor binding site in 3-Oxo-acyl-ACP reductase from <i>Pseudomonas aeruginosa</i> . <i>ACS Chemical Biology</i> , <b>2013</b> , 8, 2518-27	4.9	26
8	Substrate Channel Flexibility in <i>Pseudomonas aeruginosa</i> MurB Accommodates Two Distinct Substrates. <i>PLoS ONE</i> , <b>2013</b> , 8, e66936	3.7	3
7	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> , <b>2012</b> , 80, 2799-803	4.2	7
6	Tetrahydrodipicolinate N-succinyltransferase and dihydrodipicolinate synthase from <i>Pseudomonas aeruginosa</i> : structure analysis and gene deletion. <i>PLoS ONE</i> , <b>2012</b> , 7, e31133	3.7	15
5	Peptidoglycan remodeling in <i>Mycobacterium tuberculosis</i> : comparison of structures and catalytic activities of RipA and RipB. <i>Journal of Molecular Biology</i> , <b>2011</b> , 413, 247-60	6.5	41
4	Structural enzymology of sulphur metabolism in <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2010</b> , 396, 33-8	3.4	21
3	1.9 Å structure of the signal receiver domain of the putative response regulator NarL from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2008</b> , 64, 1096-100		22
2	Structural insights into catalysis and inhibition of O-acetylserine sulfhydrylase from <i>Mycobacterium tuberculosis</i> . Crystal structures of the enzyme alpha-aminoacrylate intermediate and an enzyme-inhibitor complex. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 23473-81	5.4	77
1	Siroheme- and [Fe4-S4]-dependent NirA from <i>Mycobacterium tuberculosis</i> is a sulfite reductase with a covalent Cys-Tyr bond in the active site. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 27319-28	5.4	84