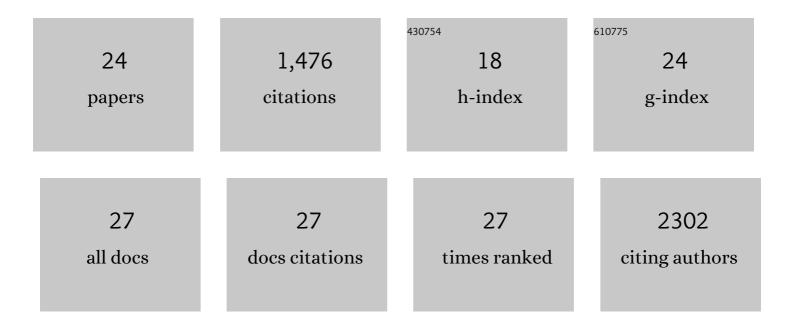
## **Ben Sidders**

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8489694/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Hypervirulent mutant of Mycobacterium tuberculosis resulting from disruption of the mce1 operon. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15918-15923.	3.3	205
2	A highly conserved transcriptional repressor controls a large regulon involved in lipid degradation in <i>Mycobacterium smegmatis</i> and <i>Mycobacterium tuberculosis</i> . Molecular Microbiology, 2007, 65, 684-699.	1.2	190
3	HDAC inhibitors attenuate the development of hypersensitivity in models of neuropathic pain. Pain, 2013, 154, 1668-1679.	2.0	135
4	Causal reasoning on biological networks: interpreting transcriptional changes. Bioinformatics, 2012, 28, 1114-1121.	1.8	126
5	5'-Adenosinephosphosulphate reductase (CysH) protects Mycobacterium tuberculosis against free radicals during chronic infection phase in mice. Molecular Microbiology, 2006, 59, 1744-1753.	1.2	102
6	Mycobacterium tuberculosis strains disrupted in mce3 and mce4 operons are attenuated in mice. Journal of Medical Microbiology, 2008, 57, 164-170.	0.7	98
7	Screening of Highly Expressed Mycobacterial Genes Identifies Rv3615c as a Useful Differential Diagnostic Antigen for the <i>Mycobacterium tuberculosis</i> Complex. Infection and Immunity, 2008, 76, 3932-3939.	1.0	95
8	The pain interactome: Connecting pain-specific protein interactions. Pain, 2014, 155, 2243-2252.	2.0	65
9	Drug mechanismâ€ofâ€action discovery through the integration of pharmacological and <scp>CRISPR</scp> screens. Molecular Systems Biology, 2020, 16, e9405.	3.2	63
10	Adenosine Signaling Is Prognostic for Cancer Outcome and Has Predictive Utility for Immunotherapeutic Response. Clinical Cancer Research, 2020, 26, 2176-2187.	3.2	54
11	Selection, Optimization, and Pharmacokinetic Properties of a Novel, Potent Antiviral Locked Nucleic Acid-Based Antisense Oligomer Targeting Hepatitis C Virus Internal Ribosome Entry Site. Antimicrobial Agents and Chemotherapy, 2011, 55, 3105-3114.	1.4	48
12	Molecular profiling of aged neural progenitors identifies <i>Dbx2</i> as a candidate regulator of ageâ€associated neurogenic decline. Aging Cell, 2018, 17, e12745.	3.0	46
13	Network-Based Drug Discovery: Coupling Network Pharmacology with Phenotypic Screening for Neuronal Excitability. Journal of Molecular Biology, 2018, 430, 3005-3015.	2.0	41
14	Quantification of global transcription patterns in prokaryotes using spotted microarrays. Genome Biology, 2007, 8, R265.	13.9	34
15	Knowledge graph-based recommendation framework identifies drivers of resistance in ECFR mutant non-small cell lung cancer. Nature Communications, 2022, 13, 1667.	5.8	33
16	Interpreting transcriptional changes using causal graphs: new methods and their practical utility on public networks. BMC Bioinformatics, 2016, 17, 318.	1.2	28
17	Enhanced mortality despite control of lung infection in mice aerogenically infected with a Mycobacterium tuberculosis mce1 operon mutant. Microbes and Infection, 2007, 9, 1285-1290.	1.0	26
18	An Integrated Transcriptomic and Meta-Analysis of Hepatoma Cells Reveals Factors That Influence Susceptibility to HCV Infection. PLoS ONE, 2011, 6, e25584.	1.1	18

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#	Article	IF	CITATIONS
19	Molecular causes of transcriptional response: a Bayesian prior knowledge approach. Bioinformatics, 2013, 29, 3167-3173.	1.8	15
20	Cataloging the biomedical world of pain through semi-automated curation of molecular interactions. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat033.	1.4	14
21	Precompetitive activity to address the biological data needs of drug discovery. Nature Reviews Drug Discovery, 2014, 13, 83-84.	21.5	14
22	A FOXM1 Dependent Mesenchymal-Epithelial Transition in Retinal Pigment Epithelium Cells. PLoS ONE, 2015, 10, e0130379.	1.1	14
23	Identification of Intrinsic Drug Resistance and Its Biomarkers in High-Throughput Pharmacogenomic and CRISPR Screens. Patterns, 2020, 1, 100065.	3.1	6
24	Transcriptome Analysis: Towards a Comprehensive Understanding of Global Transcription Activity. , 2006, , 21-41.		1