## Stefanie Widder

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7531920/publications.pdf

Version: 2024-02-01

24 papers 3,252 citations

16 h-index 610482 24 g-index

25 all docs

25 docs citations

25 times ranked

5654 citing authors

#	Article	IF	CITATIONS
1	Deciphering microbial interactions and detecting keystone species with co-occurrence networks. Frontiers in Microbiology, 2014, 5, 219.	1.5	1,109
2	The origin and evolution of cell types. Nature Reviews Genetics, 2016, 17, 744-757.	7.7	572
3	Challenges in microbial ecology: building predictive understanding of community function and dynamics. ISME Journal, 2016, 10, 2557-2568.	4.4	570
4	Fluvial network organization imprints on microbial co-occurrence networks. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12799-12804.	3.3	193
5	p59OASL, a 2'-5' oligoadenylate synthetase like protein: a novel human gene related to the 2'-5' oligoadenylate synthetase family. Nucleic Acids Research, 1998, 26, 4121-4128.	6.5	100
6	The SBML ODE Solver Library: a native API for symbolic and fast numerical analysis of reaction networks. Bioinformatics, 2006, 22, 1406-1407.	1.8	88
7	A generalized model of the repressilator. Journal of Mathematical Biology, 2006, 53, 905-937.	0.8	86
8	Signatures of ecological processes in microbial community time series. Microbiome, 2018, 6, 120.	4.9	81
9	Ecological networking of cystic fibrosis lung infections. Npj Biofilms and Microbiomes, 2016, 2, 4.	2.9	77
10	Using metabolic networks to resolve ecological properties of microbiomes. Current Opinion in Systems Biology, 2018, 8, 73-80.	1.3	61
11	Dynamic patterns of gene regulation I: Simple two-gene systems. Journal of Theoretical Biology, 2007, 246, 395-419.	0.8	48
12	Biogeographic variation in the microbiome of the ecologically important sponge, <i>Carteriospongia foliascens</i> . PeerJ, 2015, 3, e1435.	0.9	42
13	Why are cellular switches Boolean? General conditions for multistable genetic circuits. Journal of Theoretical Biology, 2009, 261, 126-135.	0.8	36
14	Specialized or flexible feed-forward loop motifs: a question of topology. BMC Systems Biology, 2009, 3, 84.	3.0	32
15	Ultra Deep Sequencing of Listeria monocytogenes sRNA Transcriptome Revealed New Antisense RNAs. PLoS ONE, 2014, 9, e83979.	1.1	31
16	Metagenomic Analysis Reveals Presence of Treponema denticola in a Tissue Biopsy of the Iceman. PLoS ONE, 2014, 9, e99994.	1.1	30
17	Association of bacterial community types, functional microbial processes and lung disease in cystic fibrosis airways. ISME Journal, 2022, 16, 905-914.	4.4	20
18	Evolvability of feed-forward loop architecture biases its abundance in transcription networks. BMC Systems Biology, 2012, 6, 7.	3.0	17

#	Article	IF	CITATION
19	Multi-omics profiling predicts allograft function after lung transplantation. European Respiratory Journal, 2022, 59, 2003292.	3.1	16
20	Wiring for independence: Positive feedback motifs facilitate individuation of traits in development and evolution. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2015, 324, 104-113.	0.6	13
21	Monomeric Bistability and the Role of Autoloops in Gene Regulation. PLoS ONE, 2009, 4, e5399.	1.1	13
22	A minimal and self-consistent in silico cell model based on macromolecular interactions. Philosophical Transactions of the Royal Society B: Biological Sciences, 2007, 362, 1831-1839.	1.8	7
23	Metagenomic sequencing reveals time, host, and body compartment-specific viral dynamics after lung transplantation. Microbiome, 2022, 10, 66.	4.9	7
24	Microbial Metabolites in Cystic Fibrosis: A Target for Future Therapy?. American Journal of Respiratory Cell and Molecular Biology, 2019, 61, 132-133.	1.4	3