

# Stefanie Widder

## List of Publications by Year in descending order

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Version: 2024-02-01

24  
papers

3,252  
citations

516710

16  
h-index

610901

24  
g-index

25  
all docs

25  
docs citations

25  
times ranked

5654  
citing authors

#	ARTICLE	IF	CITATIONS
1	Multi-omics profiling predicts allograft function after lung transplantation. <i>European Respiratory Journal</i> , 2022, 59, 2003292.	6.7	16
2	Association of bacterial community types, functional microbial processes and lung disease in cystic fibrosis airways. <i>ISME Journal</i> , 2022, 16, 905-914.	9.8	20
3	Metagenomic sequencing reveals time, host, and body compartment-specific viral dynamics after lung transplantation. <i>Microbiome</i> , 2022, 10, 66.	11.1	7
4	Microbial Metabolites in Cystic Fibrosis: A Target for Future Therapy?. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019, 61, 132-133.	2.9	3
5	Using metabolic networks to resolve ecological properties of microbiomes. <i>Current Opinion in Systems Biology</i> , 2018, 8, 73-80.	2.6	61
6	Signatures of ecological processes in microbial community time series. <i>Microbiome</i> , 2018, 6, 120.	11.1	81
7	Challenges in microbial ecology: building predictive understanding of community function and dynamics. <i>ISME Journal</i> , 2016, 10, 2557-2568.	9.8	570
8	The origin and evolution of cell types. <i>Nature Reviews Genetics</i> , 2016, 17, 744-757.	16.3	572
9	Ecological networking of cystic fibrosis lung infections. <i>Npj Biofilms and Microbiomes</i> , 2016, 2, 4.	6.4	77
10	Wiring for independence: Positive feedback motifs facilitate individuation of traits in development and evolution. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2015, 324, 104-113.	1.3	13
11	Biogeographic variation in the microbiome of the ecologically important sponge, <i>Carteriospongia foliascens</i> . <i>PeerJ</i> , 2015, 3, e1435.	2.0	42
12	Ultra Deep Sequencing of <i>Listeria monocytogenes</i> sRNA Transcriptome Revealed New Antisense RNAs. <i>PLoS ONE</i> , 2014, 9, e83979.	2.5	31
13	Fluvial network organization imprints on microbial co-occurrence networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12799-12804.	7.1	193
14	Deciphering microbial interactions and detecting keystone species with co-occurrence networks. <i>Frontiers in Microbiology</i> , 2014, 5, 219.	3.5	1,109
15	Metagenomic Analysis Reveals Presence of <i>Treponema denticola</i> in a Tissue Biopsy of the Iceman. <i>PLoS ONE</i> , 2014, 9, e99994.	2.5	30
16	Evolvability of feed-forward loop architecture biases its abundance in transcription networks. <i>BMC Systems Biology</i> , 2012, 6, 7.	3.0	17
17	Specialized or flexible feed-forward loop motifs: a question of topology. <i>BMC Systems Biology</i> , 2009, 3, 84.	3.0	32
18	Why are cellular switches Boolean? General conditions for multistable genetic circuits. <i>Journal of Theoretical Biology</i> , 2009, 261, 126-135.	1.7	36

#	ARTICLE	IF	CITATIONS
19	Monomeric Bistability and the Role of Autoloops in Gene Regulation. PLoS ONE, 2009, 4, e5399.	2.5	13
20	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.	4.0	7
21	Dynamic patterns of gene regulation I: Simple two-gene systems. Journal of Theoretical Biology, 2007, 246, 395-419.	1.7	48
22	A generalized model of the repressilator. Journal of Mathematical Biology, 2006, 53, 905-937.	1.9	86
23	The SBML ODE Solver Library: a native API for symbolic and fast numerical analysis of reaction networks. Bioinformatics, 2006, 22, 1406-1407.	4.1	88
24	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.	14.5	100