

# Amanda Birmingham

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4367141/publications.pdf>

Version: 2024-02-01

14  
papers

3,746  
citations

840119

11  
h-index

1058022

14  
g-index

15  
all docs

15  
docs citations

15  
times ranked

7420  
citing authors

#	ARTICLE	IF	CITATIONS
1	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017, 5, 27.	4.9	1,434
2	Adipose Tissue Macrophage-Derived Exosomal miRNAs Can Modulate In Vivo and In Vitro Insulin Sensitivity. <i>Cell</i> , 2017, 171, 372-384.e12.	13.5	858
3	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016, 10, 1669-1681.	4.4	593
4	Combinatorial CRISPR-Cas9 screens for de novo mapping of genetic interactions. <i>Nature Methods</i> , 2017, 14, 573-576.	9.0	287
5	QIIME 2 Enables Comprehensive End-to-End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e100.	25.8	212
6	Ten simple rules for writing and sharing computational analyses in Jupyter Notebooks. <i>PLoS Computational Biology</i> , 2019, 15, e1007007.	1.5	86
7	Context and the human microbiome. <i>Microbiome</i> , 2015, 3, 52.	4.9	81
8	Combinatorial CRISPR-Cas9 Metabolic Screens Reveal Critical Redox Control Points Dependent on the KEAP1-NRF2 Regulatory Axis. <i>Molecular Cell</i> , 2018, 69, 699-708.e7.	4.5	81
9	HIV-1 TAT protein enhances sensitization to methamphetamine by affecting dopaminergic function. <i>Brain, Behavior, and Immunity</i> , 2017, 65, 210-221.	2.0	47
10	Inflammation-driven deaminase deregulation fuels human pre-leukemia stem cell evolution. <i>Cell Reports</i> , 2021, 34, 108670.	2.9	22
11	Interactive network visualization in Jupyter notebooks: visJS2jupyter. <i>Bioinformatics</i> , 2018, 34, 126-128.	1.8	14
12	Interspecies transcriptomics identify genes that underlie disproportionate foot growth in jerboas. <i>Current Biology</i> , 2022, 32, 289-303.e6.	1.8	13
13	The ViReflow pipeline enables user friendly large scale viral consensus genome reconstruction. <i>Scientific Reports</i> , 2022, 12, 5077.	1.6	12
14	Efficient population-scale variant analysis and prioritization with VAPr. <i>Bioinformatics</i> , 2018, 34, 2843-2845.	1.8	1