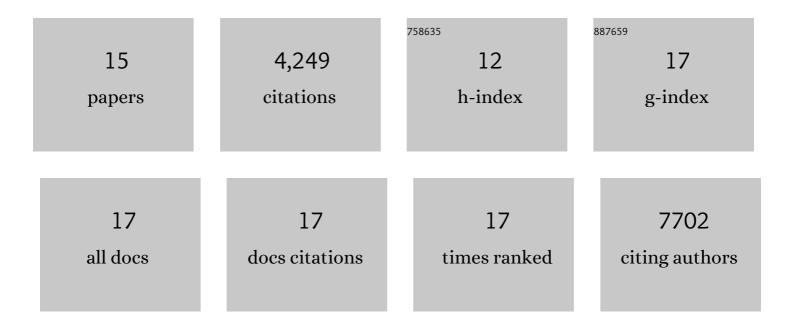
Amanda Birmingham

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10945340/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	QIIME 2 Enables Comprehensive Endâ€ŧoâ€End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. Current Protocols in Bioinformatics, 2020, 70, e100.	25.8	212
2	Combinatorial CRISPR-Cas9 Metabolic Screens Reveal Critical Redox Control Points Dependent on the KEAP1-NRF2 Regulatory Axis. Molecular Cell, 2018, 69, 699-708.e7.	4.5	81
3	Normalization and microbial differential abundance strategies depend upon data characteristics. Microbiome, 2017, 5, 27.	4.9	1,434
4	Combinatorial CRISPR–Cas9 screens for de novo mapping of genetic interactions. Nature Methods, 2017, 14, 573-576.	9.0	287
5	Advances in CRISPR-Cas9 genome engineering: lessons learned from RNA interference. Nucleic Acids Research, 2015, 43, 3407-3419.	6.5	124
6	The Power Decoder Simulator for the Evaluation of Pooled shRNA Screen Performance. Journal of Biomolecular Screening, 2015, 20, 965-975.	2.6	3
7	Meeting report of the RNA Ontology Consortium January 8-9, 2011. Standards in Genomic Sciences, 2011, 4, 252-256.	1.5	1
8	Sharing and archiving nucleic acid structure mapping data. Rna, 2011, 17, 1204-1212.	1.6	28
9	NoiseMaker: simulated screens for statistical assessment. Bioinformatics, 2010, 26, 2484-2485.	1.8	3
10	The RNA structure alignment ontology. Rna, 2009, 15, 1623-1631.	1.6	34
11	Statistical methods for analysis of high-throughput RNA interference screens. Nature Methods, 2009, 6, 569-575.	9.0	532
12	Experimental validation of the importance of seed complement frequency to siRNA specificity. Rna, 2008, 14, 853-861.	1.6	122
13	A protocol for designing siRNAs with high functionality and specificity. Nature Protocols, 2007, 2, 2068-2078.	5.5	197
14	3′ UTR seed matches, but not overall identity, are associated with RNAi off-targets. Nature Methods, 2006, 3, 199-204.	9.0	782
15	Off-target effects by siRNA can induce toxic phenotype. Rna, 2006, 12, 1188-1196.	1.6	407