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List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

4,249
citations

758635

12
h-index

887659

17
g-index

17
all docs

17
docs citations

17
times ranked

7702
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017, 5, 27.	4.9	1,434
4	Combinatorial CRISPR-Cas9 screens for de novo mapping of genetic interactions. <i>Nature Methods</i> , 2017, 14, 573-576.	9.0	287
5	Advances in CRISPR-Cas9 genome engineering: lessons learned from RNA interference. <i>Nucleic Acids Research</i> , 2015, 43, 3407-3419.	6.5	124
6	The Power Decoder Simulator for the Evaluation of Pooled shRNA Screen Performance. <i>Journal of Biomolecular Screening</i> , 2015, 20, 965-975.	2.6	3
7	Meeting report of the RNA Ontology Consortium January 8-9, 2011. <i>Standards in Genomic Sciences</i> , 2011, 4, 252-256.	1.5	1
8	Sharing and archiving nucleic acid structure mapping data. <i>Rna</i> , 2011, 17, 1204-1212.	1.6	28
9	NoiseMaker: simulated screens for statistical assessment. <i>Bioinformatics</i> , 2010, 26, 2484-2485.	1.8	3
10	The RNA structure alignment ontology. <i>Rna</i> , 2009, 15, 1623-1631.	1.6	34
11	Statistical methods for analysis of high-throughput RNA interference screens. <i>Nature Methods</i> , 2009, 6, 569-575.	9.0	532
12	Experimental validation of the importance of seed complement frequency to siRNA specificity. <i>Rna</i> , 2008, 14, 853-861.	1.6	122
13	A protocol for designing siRNAs with high functionality and specificity. <i>Nature Protocols</i> , 2007, 2, 2068-2078.	5.5	197
14	3' UTR seed matches, but not overall identity, are associated with RNAi off-targets. <i>Nature Methods</i> , 2006, 3, 199-204.	9.0	782
15	Off-target effects by siRNA can induce toxic phenotype. <i>Rna</i> , 2006, 12, 1188-1196.	1.6	407