

Anat Kreimer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3863951/publications.pdf>

Version: 2024-02-01

16
papers

1,148
citations

759233

12
h-index

996975

15
g-index

21
all docs

21
docs citations

21
times ranked

1960
citing authors

#	ARTICLE	IF	CITATIONS
1	The large-scale organization of the bacterial network of ecological co-occurrence interactions. <i>Nucleic Acids Research</i> , 2010, 38, 3857-3868.	14.5	259
2	The evolution of modularity in bacterial metabolic networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6976-6981.	7.1	197
3	Single-cell epigenomics reveals mechanisms of human cortical development. <i>Nature</i> , 2021, 598, 205-213.	27.8	154
4	Impact of pre-adapted HIV transmission. <i>Nature Medicine</i> , 2016, 22, 606-613.	30.7	87
5	NetCooperate: a network-based tool for inferring host-microbe and microbe-microbe cooperation. <i>BMC Bioinformatics</i> , 2015, 16, 164.	2.6	82
6	Identification and Massively Parallel Characterization of Regulatory Elements Driving Neural Induction. <i>Cell Stem Cell</i> , 2019, 25, 713-727.e10.	11.1	76
7	lentiMPRA and MPRAflow for high-throughput functional characterization of gene regulatory elements. <i>Nature Protocols</i> , 2020, 15, 2387-2412.	12.0	65
8	MPRAnalyze: statistical framework for massively parallel reporter assays. <i>Genome Biology</i> , 2019, 20, 183.	8.8	58
9	Integration of multiple epigenomic marks improves prediction of variant impact in saturation mutagenesis reporter assay. <i>Human Mutation</i> , 2019, 40, 1280-1291.	2.5	46
10	Predicting gene expression in massively parallel reporter assays: A comparative study. <i>Human Mutation</i> , 2017, 38, 1240-1250.	2.5	39
11	Decoupling Environment-Dependent and Independent Genetic Robustness across Bacterial Species. <i>PLoS Computational Biology</i> , 2010, 6, e1000690.	3.2	31
12	Massively parallel reporter perturbation assays uncover temporal regulatory architecture during neural differentiation. <i>Nature Communications</i> , 2022, 13, 1504.	12.8	16
13	Meta-analysis of massively parallel reporter assays enables prediction of regulatory function across cell types. <i>Human Mutation</i> , 2019, 40, 1299-1313.	2.5	15
14	Inference of modules associated to eQTLs. <i>Nucleic Acids Research</i> , 2012, 40, e98-e98.	14.5	12
15	Co-regulated Transcripts Associated to Cooperating eSNPs Define Bi-fan Motifs in Human Gene Networks. <i>PLoS Genetics</i> , 2014, 10, e1004587.	3.5	0
16	Evaluation of Davis et al.: Exploring Sequence of Determinants of Transcriptional Regulation – The Case of c-AMP Response Element. <i>Cell Systems</i> , 2020, 11, 2-4.	6.2	0