

Elior Rahmani

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6710437/publications.pdf>

Version: 2024-02-01

26
papers

1,008
citations

759233

12
h-index

839539

18
g-index

34
all docs

34
docs citations

34
times ranked

2004
citing authors

#	ARTICLE	IF	CITATIONS
1	Sparse PCA corrects for cell type heterogeneity in epigenome-wide association studies. <i>Nature Methods</i> , 2016, 13, 443-445.	19.0	205
2	Accurate estimation of cell composition in bulk expression through robust integration of single-cell information. <i>Nature Communications</i> , 2020, 11, 1971.	12.8	200
3	Genome-wide methylation data mirror ancestry information. <i>Epigenetics and Chromatin</i> , 2017, 10, 1.	3.9	120
4	Cell-type-specific resolution epigenetics without the need for cell sorting or single-cell biology. <i>Nature Communications</i> , 2019, 10, 3417.	12.8	92
5	Enhancing droplet-based single-nucleus RNA-seq resolution using the semi-supervised machine learning classifier DIEM. <i>Scientific Reports</i> , 2020, 10, 11019.	3.3	64
6	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. <i>PLoS ONE</i> , 2020, 15, e0239474.	2.5	53
7	Rheumatoid Arthritis Naive T Cells Share Hypermethylation Sites With Synoviocytes. <i>Arthritis and Rheumatology</i> , 2017, 69, 550-559.	5.6	50
8	GLINT: a user-friendly toolset for the analysis of high-throughput DNA-methylation array data. <i>Bioinformatics</i> , 2017, 33, 1870-1872.	4.1	48
9	BayesCCE: a Bayesian framework for estimating cell-type composition from DNA methylation without the need for methylation reference. <i>Genome Biology</i> , 2018, 19, 141.	8.8	40
10	Correcting for cell-type heterogeneity in DNA methylation: a comprehensive evaluation. <i>Nature Methods</i> , 2017, 14, 218-219.	19.0	33
11	The causal effect of obesity on prediabetes and insulin resistance reveals the important role of adipose tissue in insulin resistance. <i>PLoS Genetics</i> , 2020, 16, e1009018.	3.5	29
12	RL-SKAT: An Exact and Efficient Score Test for Heritability and Set Tests. <i>Genetics</i> , 2017, 207, 1275-1283.	2.9	19
13	EPIQâ€”efficient detection of SNPâ€”SNP epistatic interactions for quantitative traits. <i>Bioinformatics</i> , 2014, 30, i19-i25.	4.1	11
14	Using Stochastic Approximation Techniques to Efficiently Construct Confidence Intervals for Heritability. <i>Journal of Computational Biology</i> , 2018, 25, 794-808.	1.6	11
15	Association testing of bisulfite-sequencing methylation data via a Laplace approximation. <i>Bioinformatics</i> , 2017, 33, i325-i332.	4.1	9
16	Detecting heritable phenotypes without a model using fast permutation testing for heritability and set-tests. <i>Nature Communications</i> , 2018, 9, 4919.	12.8	6
17	CONFINED: distinguishing biological from technical sources of variation by leveraging multiple methylation datasets. <i>Genome Biology</i> , 2019, 20, 138.	8.8	6
18	The Effect of Model Directionality on Cell-Type-Specific Differential DNA Methylation Analysis. <i>Frontiers in Bioinformatics</i> , 2022, 1, .	2.1	1

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 16, e1009018.		0
20	Title is missing!. , 2020, 16, e1009018.		0
21	Title is missing!. , 2020, 16, e1009018.		0
22	Title is missing!. , 2020, 16, e1009018.		0
23	Title is missing!. , 2020, 16, e1009018.		0
24	Title is missing!. , 2020, 16, e1009018.		0
25	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. , 2020, 15, e0239474.		0
26	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. , 2020, 15, e0239474.		0