Elior Rahmani

List of Publications by Year
in descending order

26	1,008	759233	839539
papers	citations	12 h-index	18 g-index

34	34	34	2004
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Effect of Model Directionality on Cell-Type-Specific Differential DNA Methylation Analysis. Frontiers in Bioinformatics, 2022, 1, .	2.1	1
2	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. PLoS ONE, 2020, 15, e0239474.	2.5	53
3	The causal effect of obesity on prediabetes and insulin resistance reveals the important role of adipose tissue in insulin resistance. PLoS Genetics, 2020, 16, e1009018.	3.5	29
4	Enhancing droplet-based single-nucleus RNA-seq resolution using the semi-supervised machine learning classifier DIEM. Scientific Reports, 2020, 10, 11019.	3.3	64
5	Accurate estimation of cell composition in bulk expression through robust integration of single-cell information. Nature Communications, 2020, 11, 1971.	12.8	200
6	Title is missing!. , 2020, 16, e1009018.		0
7	Title is missing!. , 2020, 16, e1009018.		0
8	Title is missing!. , 2020, 16, e1009018.		0
9	Title is missing!. , 2020, 16, e1009018.		0
10	Title is missing!. , 2020, 16, e1009018.		0
11	Title is missing!. , 2020, 16, e1009018.		0
12	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. , 2020, 15, e0239474.		0
13	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. , 2020, 15, e0239474.		0
14	Cell-type-specific resolution epigenetics without the need for cell sorting or single-cell biology. Nature Communications, 2019, 10, 3417.	12.8	92
15	CONFINED: distinguishing biological from technical sources of variation by leveraging multiple methylation datasets. Genome Biology, 2019, 20, 138.	8.8	6
16	Detecting heritable phenotypes without a model using fast permutation testing for heritability and set-tests. Nature Communications, 2018, 9, 4919.	12.8	6
17	BayesCCE: a Bayesian framework for estimating cell-type composition from DNA methylation without the need for methylation reference. Genome Biology, 2018, 19, 141.	8.8	40
18	Using Stochastic Approximation Techniques to Efficiently Construct Confidence Intervals for Heritability. Journal of Computational Biology, 2018, 25, 794-808.	1.6	11

#	Article	IF	Citations
19	Correcting for cell-type heterogeneity in DNA methylation: a comprehensive evaluation. Nature Methods, 2017, 14, 218-219.	19.0	33
20	GLINT: a user-friendly toolset for the analysis of high-throughput DNA-methylation array data. Bioinformatics, 2017, 33, 1870-1872.	4.1	48
21	RL-SKAT: An Exact and Efficient Score Test for Heritability and Set Tests. Genetics, 2017, 207, 1275-1283.	2.9	19
22	Genome-wide methylation data mirror ancestry information. Epigenetics and Chromatin, 2017, 10, 1.	3.9	120
23	Rheumatoid Arthritis Naive T Cells Share Hypermethylation Sites With Synoviocytes. Arthritis and Rheumatology, 2017, 69, 550-559.	5.6	50
24	Association testing of bisulfite-sequencing methylation data via a Laplace approximation. Bioinformatics, 2017, 33, i325-i332.	4.1	9
25	Sparse PCA corrects for cell type heterogeneity in epigenome-wide association studies. Nature Methods, 2016, 13, 443-445.	19.0	205
26	EPIQâ€”efficient detection of SNPâ€“SNP epistatic interactions for quantitative traits. Bioinformatics, 2014, 30, i19-i25.	4.1	11