Alexis Battle

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4927216/publications.pdf

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51	20,686	117625	175258
papers	citations	34 h-index	52 g-index

71	71	71	38931
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	21.4	6,815
2	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	12.6	4,659
3	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	27.8	3,500
4	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	21.4	590
5	Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. Genome Research, 2014, 24, 14-24.	5.5	547
6	Impact of regulatory variation from RNA to protein. Science, 2015, 347, 664-667.	12.6	399
7	The impact of structural variation on human gene expression. Nature Genetics, 2017, 49, 692-699.	21.4	334
8	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	12.6	329
9	The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243.	27.8	229
10	Identification of rare-disease genes using blood transcriptome sequencing and large control cohorts. Nature Medicine, 2019, 25, 911-919.	30.7	221
11	Retinal transcriptome and eQTL analyses identify genes associated with age-related macular degeneration. Nature Genetics, 2019, 51, 606-610.	21.4	201
12	Where Are the Disease-Associated eQTLs?. Trends in Genetics, 2021, 37, 109-124.	6.7	163
13	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. PLoS Computational Biology, 2015, 11, e1004220.	3.2	158
14	Type I interferon signaling genes in recurrent major depression: increased expression detected by whole-blood RNA sequencing. Molecular Psychiatry, 2014, 19, 1267-1274.	7.9	151
15	Genetic variation in MHC proteins is associated with T cell receptor expression biases. Nature Genetics, 2016, 48, 995-1002.	21.4	151
16	Dynamic genetic regulation of gene expression during cellular differentiation. Science, 2019, 364, 1287-1290.	12.6	142
17	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. Genome Research, 2017, 27, 1843-1858.	5.5	139
18	Allele-specific expression reveals interactions between genetic variation and environment. Nature Methods, 2017, 14, 699-702.	19.0	135

#	Article	IF	Citations
19	InÂvivo CD8+ TÂcell CRISPR screening reveals control by Fli1 in infection and cancer. Cell, 2021, 184, 1262-1280.e22.	28.9	107
20	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
21	An Efficient Multiple-Testing Adjustment for eQTL Studies that Accounts for Linkage Disequilibrium between Variants. American Journal of Human Genetics, 2016, 98, 216-224.	6.2	91
22	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	12.6	89
23	Impact of the X Chromosome and sex on regulatory variation. Genome Research, 2016, 26, 768-777.	5.5	88
24	Linear and Nonlinear Mendelian Randomization Analyses of the Association Between Diastolic Blood Pressure and Cardiovascular Events. Circulation, 2021, 143, 895-906.	1.6	73
25	Transcriptome Analysis Reveals Differential Splicing Events in IPF Lung Tissue. PLoS ONE, 2014, 9, e92111.	2.5	73
26	Automated identification of pathways from quantitative genetic interaction data. Molecular Systems Biology, 2010, 6, 379.	7.2	70
27	Normalizing RNA-Sequencing Data by Modeling Hidden Covariates with Prior Knowledge. PLoS ONE, 2013, 8, e68141.	2.5	68
28	Addressing confounding artifacts in reconstruction of gene co-expression networks. Genome Biology, 2019, 20, 94.	8.8	68
29	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
30	Transcriptome Sequencing of a Large Human Family Identifies the Impact of Rare Noncoding Variants. American Journal of Human Genetics, 2014, 95, 245-256.	6.2	63
31	Determining causality and consequence of expression quantitative trait loci. Human Genetics, 2014, 133, 727-735.	3.8	58
32	Genome-wide association and multi-omic analyses reveal ACTN2 as a gene linked to heart failure. Nature Communications, 2020, 11, 1122.	12.8	57
33	False positives in trans-eQTL and co-expression analyses arising from RNA-sequencing alignment errors. F1000Research, 2018, 7, 1860.	1.6	51
34	High-Resolution Transcriptome Analysis with Long-Read RNA Sequencing. PLoS ONE, 2014, 9, e108095.	2.5	47
35	False positives in trans-eQTL and co-expression analyses arising from RNA-sequencing alignment errors. F1000Research, 2018, 7, 1860.	1.6	45
36	Coexpression network architecture reveals the brain-wide and multiregional basis of disease susceptibility. Nature Neuroscience, 2021, 24, 1313-1323.	14.8	44

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37	Population- and individual-specific regulatory variation in Sardinia. Nature Genetics, 2017, 49, 700-707.	21.4	38
38	DNA methylation signatures reveal that distinct combinations of transcription factors specify human immune cell epigenetic identity. Immunity, 2021, 54, 2465-2480.e5.	14.3	31
39	FIRE: functional inference of genetic variants that regulate gene expression. Bioinformatics, 2017, 33, 3895-3901.	4.1	30
40	Single-cell sequencing reveals lineage-specific dynamic genetic regulation of gene expression during human cardiomyocyte differentiation. PLoS Genetics, 2022, 18, e1009666.	3.5	28
41	Identifying global expression patterns and key regulators in epithelial to mesenchymal transition through multi-study integration. BMC Cancer, 2017, 17, 447.	2.6	26
42	Redefining tissue specificity of genetic regulation of gene expression in the presence of allelic heterogeneity. American Journal of Human Genetics, 2022, 109, 223-239.	6.2	26
43	Probabilistic Discovery of Overlapping Cellular Processes and Their Regulation. Journal of Computational Biology, 2005, 12, 909-927.	1.6	24
44	Incorporation of Biological Knowledge Into the Study of Gene-Environment Interactions. American Journal of Epidemiology, 2017, 186, 771-777.	3.4	23
45	EIF3G is associated with narcolepsy across ethnicities. European Journal of Human Genetics, 2015, 23, 1573-1580.	2.8	21
46	Transcriptional profile of platelets and iPSC-derived megakaryocytes from whole-genome and RNA sequencing. Blood, 2021, 137, 959-968.	1.4	21
47	Imputed gene associations identify replicable transâ€acting genes enriched in transcription pathways and complex traits. Genetic Epidemiology, 2019, 43, 596-608.	1.3	19
48	sn-spMF: matrix factorization informs tissue-specific genetic regulation of gene expression. Genome Biology, 2020, 21, 235.	8.8	18
49	GBAT: a gene-based association test for robust detection of trans-gene regulation. Genome Biology, 2020, 21, 211.	8.8	12
50	ACE inhibition and cardiometabolic risk factors, lungACE2andTMPRSS2gene expression, and plasma ACE2 levels: a Mendelian randomization study. Royal Society Open Science, 2020, 7, 200958.	2.4	12
51	Human embryoid bodies as a novel system for genomic studies of functionally diverse cell types. ELife, 2022, 11, .	6.0	7