# 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 | 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 |
| 2 | Single-cell sequencing reveals lineage-specific dynamic genetic regulation of gene expression during human cardiomyocyte differentiation. PLoS Genetics, 2022, 18, e1009666. | 3.5 | 28 |
| 3 | Human embryoid bodies as a novel system for genomic studies of functionally diverse cell types. ELife, 2022, 11, . | 6.0 | 7 |
| 4 | Where Are the Disease-Associated eQTLs?. Trends in Genetics, 2021, 37, 109-124. | 6.7 | 163 |
| 5 | Transcriptional profile of platelets and iPSC-derived megakaryocytes from whole-genome and RNA sequencing. Blood, 2021, 137, 959-968. | 1.4 | 21 |
| 6 | Linear and Nonlinear Mendelian Randomization Analyses of the Association Between Diastolic Blood Pressure and Cardiovascular Events. Circulation, 2021, 143, 895-906. | 1.6 | 73 |
| 7 | InÂvivo CD8+ TÂcell CRISPR screening reveals control by Fli1 in infection and cancer. Cell, 2021, 184, 1262-1280.e22. | 28.9 | 107 |
| 8 | Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19. | 28.9 | 94 |
| 9 | Coexpression network architecture reveals the brain-wide and multiregional basis of disease susceptibility. Nature Neuroscience, 2021, 24, 1313-1323. | 14.8 | 44 |
| 10 | 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 |
| 11 | 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 |
| 12 | GBAT: a gene-based association test for robust detection of trans-gene regulation. Genome Biology, 2020, 21, 211. | 8.8 | 12 |
| 13 | Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, . | 12.6 | 89 |
| 14 | The impact of sex on gene expression across human tissues. Science, 2020, 369, . | 12.6 | 329 |
| 15 | A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234. | 8.8 | 68 |
| 16 | sn-spMF: matrix factorization informs tissue-specific genetic regulation of gene expression. Genome Biology, 2020, 21, 235. | 8.8 | 18 |
| 17 | Genome-wide association and multi-omic analyses reveal ACTN2 as a gene linked to heart failure. Nature Communications, 2020, 11, 1122. | 12.8 | 57 |
| 18 | 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Dynamic genetic regulation of gene expression during cellular differentiation. Science, 2019, 364, 1287-1290. | 12.6 | 142 |
| 20 | Identification of rare-disease genes using blood transcriptome sequencing and large control cohorts. Nature Medicine, 2019, 25, 911-919. | 30.7 | 221 |
| 21 | Addressing confounding artifacts in reconstruction of gene co-expression networks. Genome Biology, 2019, 20, 94. | 8.8 | 68 |
| 22 | Imputed gene associations identify replicable transâ€acting genes enriched in transcription pathways and complex traits. Genetic Epidemiology, 2019, 43, 596-608. | 1.3 | 19 |
| 23 | Retinal transcriptome and eQTL analyses identify genes associated with age-related macular degeneration. Nature Genetics, 2019, 51, 606-610. | 21.4 | 201 |
| 24 | False positives in trans-eQTL and co-expression analyses arising from RNA-sequencing alignment errors. F1000Research, 2018, 7, 1860. | 1.6 | 51 |
| 25 | False positives in trans-eQTL and co-expression analyses arising from RNA-sequencing alignment errors. F1000Research, 2018, 7, 1860. | 1.6 | 45 |
| 26 | Population- and individual-specific regulatory variation in Sardinia. Nature Genetics, 2017, 49, 700-707. | 21.4 | 38 |
| 27 | Allele-specific expression reveals interactions between genetic variation and environment. Nature Methods, 2017, 14, 699-702. | 19.0 | 135 |
| 28 | The impact of structural variation on human gene expression. Nature Genetics, 2017, 49, 692-699. | 21.4 | 334 |
| 29 | The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243. | 27.8 | 229 |
| 30 | Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213. | 27.8 | 3,500 |
| 31 | Co-expression networks reveal the tissue-specific regulation of transcription and splicing. Genome Research, 2017, 27, 1843-1858. | 5.5 | 139 |
| 32 | FIRE: functional inference of genetic variants that regulate gene expression. Bioinformatics, 2017, 33, 3895-3901. | 4.1 | 30 |
| 33 | Incorporation of Biological Knowledge Into the Study of Gene-Environment Interactions. American Journal of Epidemiology, 2017, 186, 771-777. | 3.4 | 23 |
| 34 | Identifying global expression patterns and key regulators in epithelial to mesenchymal transition through multi-study integration. BMC Cancer, 2017, 17, 447. | 2.6 | 26 |
| 35 | Impact of the X Chromosome and sex on regulatory variation. Genome Research, 2016, 26, 768-777. | 5.5 | 88 |
| 36 | Genetic variation in MHC proteins is associated with T cell receptor expression biases. Nature Genetics, 2016, 48, 995-1002. | 21.4 | 151 |

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|---|---|---|---|
| 37 | 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 |
| 38 | EIF3G is associated with narcolepsy across ethnicities. European Journal of Human Genetics, 2015, 23, 1573-1580. | 2.8 | 21 |
| 39 | Sharing and Specificity of Co-expression Networks across 35 Human Tissues. PLoS Computational Biology, 2015, 11, e1004220. | 3.2 | 158 |
| 40 | The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660. | 12.6 | 4,659 |
| 41 | Impact of regulatory variation from RNA to protein. Science, 2015, 347, 664-667. | 12.6 | 399 |
| 42 | High-Resolution Transcriptome Analysis with Long-Read RNA Sequencing. PLoS ONE, 2014, 9, e108095. | 2.5 | 47 |
| 43 | 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 |
| 44 | 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 |
| 45 | Determining causality and consequence of expression quantitative trait loci. Human Genetics, 2014, 133, 727-735. | 3.8 | 58 |
| 46 | Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. Genome Research, 2014, 24, 14-24. | 5.5 | 547 |
| 47 | Transcriptome Analysis Reveals Differential Splicing Events in IPF Lung Tissue. PLoS ONE, 2014, 9, e92111. | 2.5 | 73 |
| 48 | The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585. | 21.4 | 6,815 |
| 49 | Normalizing RNA-Sequencing Data by Modeling Hidden Covariates with Prior Knowledge. PLoS ONE, 2013, 8, e68141. | 2.5 | 68 |
| 50 | Automated identification of pathways from quantitative genetic interaction data. Molecular Systems Biology, 2010, 6, 379. | 7.2 | 70 |
| 51 | Probabilistic Discovery of Overlapping Cellular Processes and Their Regulation. Journal of Computational Biology, 2005, 12, 909-927. | 1.6 | 24 |