

Daniel J Gaffney

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

9,286
citations

117571

34
h-index

206029

48
g-index

63
all docs

63
docs citations

63
times ranked

19215
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , 2016, 17, 13. | 3.8 | 1,898 |
| 2 | DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. <i>Genome Biology</i> , 2011, 12, R10. | 3.8 | 754 |
| 3 | DNase-seq sensitivity QTLs are a major determinant of human expression variation. <i>Nature</i> , 2012, 482, 390-394. | 13.7 | 608 |
| 4 | Accurate inference of transcription factor binding from DNA sequence and chromatin accessibility data. <i>Genome Research</i> , 2011, 21, 447-455. | 2.4 | 501 |
| 5 | Common genetic variation drives molecular heterogeneity in human iPSCs. <i>Nature</i> , 2017, 546, 370-375. | 13.7 | 491 |
| 6 | DNA Sequence-Dependent Compartmentalization and Silencing of Chromatin at the Nuclear Lamina. <i>Cell</i> , 2012, 149, 1474-1487. | 13.5 | 405 |
| 7 | Genetic Background Drives Transcriptional Variation in Human Induced Pluripotent Stem Cells. <i>PLoS Genetics</i> , 2014, 10, e1004432. | 1.5 | 260 |
| 8 | Genome-wide meta-analysis, fine-mapping and integrative prioritization implicate new Alzheimer's disease risk genes. <i>Nature Genetics</i> , 2021, 53, 392-402. | 9.4 | 258 |
| 9 | Controls of Nucleosome Positioning in the Human Genome. <i>PLoS Genetics</i> , 2012, 8, e1003036. | 1.5 | 255 |
| 10 | Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response. <i>Nature Genetics</i> , 2018, 50, 424-431. | 9.4 | 253 |
| 11 | Dense fine-mapping study identifies new susceptibility loci for primary biliary cirrhosis. <i>Nature Genetics</i> , 2012, 44, 1137-1141. | 9.4 | 251 |
| 12 | Epithelial IL-22RA1-Mediated Fucosylation Promotes Intestinal Colonization Resistance to an Opportunistic Pathogen. <i>Cell Host and Microbe</i> , 2014, 16, 504-516. | 5.1 | 237 |
| 13 | Souporcell: robust clustering of single-cell RNA-seq data by genotype without reference genotypes. <i>Nature Methods</i> , 2020, 17, 615-620. | 9.0 | 232 |
| 14 | Genome-wide association study of primary sclerosing cholangitis identifies new risk loci and quantifies the genetic relationship with inflammatory bowel disease. <i>Nature Genetics</i> , 2017, 49, 269-273. | 9.4 | 230 |
| 15 | Fine-mapping cellular QTLs with RASQUAL and ATAC-seq. <i>Nature Genetics</i> , 2016, 48, 206-213. | 9.4 | 199 |
| 16 | Quantifying the Slightly Deleterious Mutation Model of Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2002, 19, 2142-2149. | 3.5 | 191 |
| 17 | Molecular and functional variation in iPSC-derived sensory neurons. <i>Nature Genetics</i> , 2018, 50, 54-61. | 9.4 | 191 |
| 18 | Dissecting the regulatory architecture of gene expression QTLs. <i>Genome Biology</i> , 2012, 13, R7. | 13.9 | 188 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | N6-methyladenosine regulates the stability of RNA:DNA hybrids in human cells. <i>Nature Genetics</i> , 2020, 52, 48-55. | 9.4 | 147 |
| 20 | Population-scale single-cell RNA-seq profiling across dopaminergic neuron differentiation. <i>Nature Genetics</i> , 2021, 53, 304-312. | 9.4 | 146 |
| 21 | Functional constraints and frequency of deleterious mutations in noncoding DNA of rodents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13402-13406. | 3.3 | 120 |
| 22 | Early maturation and distinct tau pathology in induced pluripotent stem cell-derived neurons from patients with <i>MAPT</i> mutations. <i>Brain</i> , 2015, 138, 3345-3359. | 3.7 | 116 |
| 23 | Activin/Nodal signaling and NANOG orchestrate human embryonic stem cell fate decisions by controlling the H3K4me3 chromatin mark. <i>Genes and Development</i> , 2015, 29, 702-717. | 2.7 | 115 |
| 24 | A map of transcriptional heterogeneity and regulatory variation in human microglia. <i>Nature Genetics</i> , 2021, 53, 861-868. | 9.4 | 115 |
| 25 | The Contribution of RNA Decay Quantitative Trait Loci to Inter-Individual Variation in Steady-State Gene Expression Levels. <i>PLoS Genetics</i> , 2012, 8, e1003000. | 1.5 | 104 |
| 26 | Transcriptional profiling of macrophages derived from monocytes and iPS cells identifies a conserved response to LPS and novel alternative transcription. <i>Scientific Reports</i> , 2015, 5, 12524. | 1.6 | 94 |
| 27 | High-resolution genetic mapping of putative causal interactions between regions of open chromatin. <i>Nature Genetics</i> , 2019, 51, 128-137. | 9.4 | 80 |
| 28 | The scale of mutational variation in the murid genome. <i>Genome Research</i> , 2005, 15, 1086-1094. | 2.4 | 75 |
| 29 | False positive peaks in ChIP-seq and other sequencing-based functional assays caused by unannotated high copy number regions. <i>Bioinformatics</i> , 2011, 27, 2144-2146. | 1.8 | 74 |
| 30 | Genomic Selective Constraints in Murid Noncoding DNA. <i>PLoS Genetics</i> , 2006, 2, e204. | 1.5 | 60 |
| 31 | Global Properties and Functional Complexity of Human Gene Regulatory Variation. <i>PLoS Genetics</i> , 2013, 9, e1003501. | 1.5 | 55 |
| 32 | Genetic effects on promoter usage are highly context-specific and contribute to complex traits. <i>ELife</i> , 2019, 8, . | 2.8 | 53 |
| 33 | Loss of IL-10 signaling in macrophages limits bacterial killing driven by prostaglandin E2. <i>Journal of Experimental Medicine</i> , 2020, 217, . | 4.2 | 51 |
| 34 | Evolutionary constraints in conserved nongenic sequences of mammals. <i>Genome Research</i> , 2005, 15, 1373-1378. | 2.4 | 50 |
| 35 | Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes. <i>Nature Methods</i> , 2020, 17, 414-421. | 9.0 | 48 |
| 36 | Population-scale proteome variation in human induced pluripotent stem cells. <i>ELife</i> , 2020, 9, . | 2.8 | 40 |

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|----|--|-----|-----------|
| 37 | Locus-specific expression of transposable elements in single cells with CELLO-seq. <i>Nature Biotechnology</i> , 2022, 40, 546-554. | 9.4 | 38 |
| 38 | DNA Sequence Error Rates in Genbank Records Estimated using the Mouse Genome as a Reference. <i>DNA Sequence</i> , 2004, 15, 362-364. | 0.7 | 37 |
| 39 | Unexpected conserved non-coding DNA blocks in mammals. <i>Trends in Genetics</i> , 2004, 20, 332-337. | 2.9 | 22 |
| 40 | Cell reprogramming shapes the mitochondrial DNA landscape. <i>Nature Communications</i> , 2021, 12, 5241. | 5.8 | 21 |
| 41 | Selective Constraints in Experimentally Defined Primate Regulatory Regions. <i>PLoS Genetics</i> , 2008, 4, e1000157. | 1.5 | 20 |
| 42 | Exon-Specific QTLs Skew the Inferred Distribution of Expression QTLs Detected Using Gene Expression Array Data. <i>PLoS ONE</i> , 2012, 7, e30629. | 1.1 | 18 |
| 43 | Effect of the assignment of ancestral CpG state on the estimation of nucleotide substitution rates in mammals. <i>BMC Evolutionary Biology</i> , 2008, 8, 265. | 3.2 | 15 |
| 44 | Robust temporal map of human in vitro myelopoiesis using single-cell genomics. <i>Nature Communications</i> , 2022, 13, . | 5.8 | 13 |
| 45 | Mapping and predicting gene-enhancer interactions. <i>Nature Genetics</i> , 2019, 51, 1662-1663. | 9.4 | 11 |