

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	Locus-specific expression of transposable elements in single cells with CELLO-seq. <i>Nature Biotechnology</i> , 2022, 40, 546-554.	9.4	38
2	Robust temporal map of human in vitro myelopoiesis using single-cell genomics. <i>Nature Communications</i> , 2022, 13, .	5.8	13
3	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
4	Population-scale single-cell RNA-seq profiling across dopaminergic neuron differentiation. <i>Nature Genetics</i> , 2021, 53, 304-312.	9.4	146
5	A map of transcriptional heterogeneity and regulatory variation in human microglia. <i>Nature Genetics</i> , 2021, 53, 861-868.	9.4	115
6	Cell reprogramming shapes the mitochondrial DNA landscape. <i>Nature Communications</i> , 2021, 12, 5241.	5.8	21
7	N6-methyladenosine regulates the stability of RNA:DNA hybrids in human cells. <i>Nature Genetics</i> , 2020, 52, 48-55.	9.4	147
8	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
9	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
10	Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes. <i>Nature Methods</i> , 2020, 17, 414-421.	9.0	48
11	Population-scale proteome variation in human induced pluripotent stem cells. <i>ELife</i> , 2020, 9, .	2.8	40
12	Mapping and predicting gene-enhancer interactions. <i>Nature Genetics</i> , 2019, 51, 1662-1663.	9.4	11
13	High-resolution genetic mapping of putative causal interactions between regions of open chromatin. <i>Nature Genetics</i> , 2019, 51, 128-137.	9.4	80
14	Genetic effects on promoter usage are highly context-specific and contribute to complex traits. <i>ELife</i> , 2019, 8, .	2.8	53
15	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
16	Molecular and functional variation in iPSC-derived sensory neurons. <i>Nature Genetics</i> , 2018, 50, 54-61.	9.4	191
17	Common genetic variation drives molecular heterogeneity in human iPSCs. <i>Nature</i> , 2017, 546, 370-375.	13.7	491
18	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

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19	Fine-mapping cellular QTLs with RASQUAL and ATAC-seq. <i>Nature Genetics</i> , 2016, 48, 206-213.	9.4	199
20	A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , 2016, 17, 13.	3.8	1,898
21	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
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	Genetic Background Drives Transcriptional Variation in Human Induced Pluripotent Stem Cells. <i>PLoS Genetics</i> , 2014, 10, e1004432.	1.5	260
25	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
26	Global Properties and Functional Complexity of Human Gene Regulatory Variation. <i>PLoS Genetics</i> , 2013, 9, e1003501.	1.5	55
27	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
28	Controls of Nucleosome Positioning in the Human Genome. <i>PLoS Genetics</i> , 2012, 8, e1003036.	1.5	255
29	Dissecting the regulatory architecture of gene expression QTLs. <i>Genome Biology</i> , 2012, 13, R7.	13.9	188
30	DNase-seq sensitivity QTLs are a major determinant of human expression variation. <i>Nature</i> , 2012, 482, 390-394.	13.7	608
31	Dense fine-mapping study identifies new susceptibility loci for primary biliary cirrhosis. <i>Nature Genetics</i> , 2012, 44, 1137-1141.	9.4	251
32	DNA Sequence-Dependent Compartmentalization and Silencing of Chromatin at the Nuclear Lamina. <i>Cell</i> , 2012, 149, 1474-1487.	13.5	405
33	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
34	DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. <i>Genome Biology</i> , 2011, 12, R10.	3.8	754
35	Accurate inference of transcription factor binding from DNA sequence and chromatin accessibility data. <i>Genome Research</i> , 2011, 21, 447-455.	2.4	501
36	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

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37	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
38	Selective Constraints in Experimentally Defined Primate Regulatory Regions. <i>PLoS Genetics</i> , 2008, 4, e1000157.	1.5	20
39	Genomic Selective Constraints in Murid Noncoding DNA. <i>PLoS Genetics</i> , 2006, 2, e204.	1.5	60
40	Evolutionary constraints in conserved nongenic sequences of mammals. <i>Genome Research</i> , 2005, 15, 1373-1378.	2.4	50
41	The scale of mutational variation in the murid genome. <i>Genome Research</i> , 2005, 15, 1086-1094.	2.4	75
42	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
43	Unexpected conserved non-coding DNA blocks in mammals. <i>Trends in Genetics</i> , 2004, 20, 332-337.	2.9	22
44	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
45	Quantifying the Slightly Deleterious Mutation Model of Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2002, 19, 2142-2149.	3.5	191