Daniel J Gaffney

List of Publications by Year
in descending order

45	9,286	117453	205818
papers	citations	34 h-index	48 g-index

63	63	63	19215
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Locus-specific expression of transposable elements in single cells with CELLO-seq. Nature Biotechnology, 2022, 40, 546-554.	9.4	38
2	Robust temporal map of human in vitro myelopoiesis using single-cell genomics. Nature Communications, 2022, 13, .	5.8	13
3	Genome-wide meta-analysis, fine-mapping and integrative prioritization implicate new Alzheimerâ€™s disease risk genes. Nature Genetics, 2021, 53, 392-402.	9.4	258
4	Population-scale single-cell RNA-seq profiling across dopaminergic neuron differentiation. Nature Genetics, 2021, 53, 304-312.	9.4	146
5	A map of transcriptional heterogeneity and regulatory variation in human microglia. Nature Genetics, 2021, 53, 861-868.	9.4	115
6	Cell reprogramming shapes the mitochondrial DNA landscape. Nature Communications, 2021, 12, 5241.	5.8	21
7	N6-methyladenosine regulates the stability of RNA:DNA hybrids in human cells. Nature Genetics, 2020, 52, 48-55.	9.4	147
8	Loss of IL-10 signaling in macrophages limits bacterial killing driven by prostaglandin E2. Journal of Experimental Medicine, 2020, 217, .	4.2	51
9	Souporcell: robust clustering of single-cell RNA-seq data by genotype without reference genotypes. Nature Methods, 2020, 17, 615-620.	9.0	232
10	Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes. Nature Methods, 2020, 17, 414-421.	9.0	48
11	Population-scale proteome variation in human induced pluripotent stem cells. ELife, 2020, 9, .	2.8	40
12	Mapping and predicting geneâ€“enhancer interactions. Nature Genetics, 2019, 51, 1662-1663.	9.4	11
13	High-resolution genetic mapping of putative causal interactions between regions of open chromatin. Nature Genetics, 2019, 51, 128-137.	9.4	80
14	Genetic effects on promoter usage are highly context-specific and contribute to complex traits. ELife, 2019, 8, .	2.8	53
15	Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response. Nature Genetics, 2018, 50, 424-431.	9.4	253
16	Molecular and functional variation in iPSC-derived sensory neurons. Nature Genetics, 2018, 50, 54-61.	9.4	191
17	Common genetic variation drives molecular heterogeneity in human iPSCs. Nature, 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. Nature Genetics, 2017, 49, 269-273.	9.4	230

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19	Fine-mapping cellular QTLs with RASQUAL and ATAC-seq. Nature Genetics, 2016, 48, 206-213.	9.4	199
20	A survey of best practices for RNA-seq data analysis. Genome Biology, 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. Scientific Reports, 2015, 5, 12524.	1.6	94
22	Early maturation and distinct tau pathology in induced pluripotent stem cell-derived neurons from patients withMAPTmutations. Brain, 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. Genes and Development, 2015, 29, 702-717.	2.7	115
24	Genetic Background Drives Transcriptional Variation in Human Induced Pluripotent Stem Cells. PLoS Genetics, 2014, 10, e1004432.	1.5	260
25	Epithelial IL-22RA1-Mediated Fucosylation Promotes Intestinal Colonization Resistance to an Opportunistic Pathogen. Cell Host and Microbe, 2014, 16, 504-516.	5.1	237
26	Global Properties and Functional Complexity of Human Gene Regulatory Variation. PLoS Genetics, 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. PLoS Genetics, 2012, 8, e1003000.	1.5	104
28	Controls of Nucleosome Positioning in the Human Genome. PLoS Genetics, 2012, 8, e1003036.	1.5	255
29	Dissecting the regulatory architecture of gene expression QTLs. Genome Biology, 2012, 13, R7.	13.9	188
30	DNaseâ€‰I sensitivity QTLs are a major determinant of human expression variation. Nature, 2012, 482, 390-394.	13.7	608
31	Dense fine-mapping study identifies new susceptibility loci for primary biliary cirrhosis. Nature Genetics, 2012, 44, 1137-1141.	9.4	251
32	DNA Sequence-Dependent Compartmentalization and Silencing of Chromatin at the Nuclear Lamina. Cell, 2012, 149, 1474-1487.	13.5	405
33	Exon-Specific QTLs Skew the Inferred Distribution of Expression QTLs Detected Using Gene Expression Array Data. PLoS ONE, 2012, 7, e30629.	1.1	18
34	DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. Genome Biology, 2011, 12, R10.	3.8	754
35	Accurate inference of transcription factor binding from DNA sequence and chromatin accessibility data. Genome Research, 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. Bioinformatics, 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. BMC Evolutionary Biology, 2008, 8, 265.	3.2	15
38	Selective Constraints in Experimentally Defined Primate Regulatory Regions. PLoS Genetics, 2008, 4, e1000157.	1.5	20
39	Genomic Selective Constraints in Murid Noncoding DNA. PLoS Genetics, 2006, 2, e204.	1.5	60
40	Evolutionary constraints in conserved nongenic sequences of mammals. Genome Research, 2005, 15, 1373-1378.	2.4	50
41	The scale of mutational variation in the murid genome. Genome Research, 2005, 15, 1086-1094.	2.4	75
42	DNA Sequence Error Rates in Genbank Records Estimated using the Mouse Genome as a Reference. DNA Sequence, 2004, 15, 362-364.	0.7	37
43	Unexpected conserved non-coding DNA blocks in mammals. Trends in Genetics, 2004, 20, 332-337.	2.9	22
44	Functional constraints and frequency of deleterious mutations in noncoding DNA of rodents. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13402-13406.	3.3	120
45	Quantifying the Slightly Deleterious Mutation Model of Molecular Evolution. Molecular Biology and Evolution, 2002, 19, 2142-2149.	3.5	191