Joseph E Powell

List of Publications by Year
in descending order

90 papers	**11,603** citations	66343 **42** h-index	43889 **91** g-index
109 all docs	**109** docs citations	**109** times ranked	**21694** citing authors

#	Article	IF	Citations
1	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. Nature Genetics, 2016, 48, 481-487.	21.4	1,757
2	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	21.4	1,544
3	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
4	A single-cell and spatially resolved atlas of human breast cancers. Nature Genetics, 2021, 53, 1334-1347.	21.4	535
5	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	27.8	383
6	Signatures of negative selection in the genetic architecture of human complex traits. Nature Genetics, 2018, 50, 746-753.	21.4	304
7	Reconciling the analysis of IBD and IBS in complex trait studies. Nature Reviews Genetics, 2010, 11, 800-805.	16.3	295
8	scPred: accurate supervised method for cell-type classification from single-cell RNA-seq data. Genome Biology, 2019, 20, 264.	8.8	263
9	Neonatal DNA methylation profile in human twins is specified by a complex interplay between intrauterine environmental and genetic factors, subject to tissue-specific influence. Genome Research, 2012, 22, 1395-1406.	5.5	246
10	Contribution of genetic variation to transgenerational inheritance of DNA methylation. Genome Biology, 2014, 15, R73.	9.6	231
11	Population genetic differentiation of height and body mass index across Europe. Nature Genetics, 2015, 47, 1357-1362.	21.4	227
12	Stromal cell diversity associated with immune evasion in human triple‐negative breast cancer. EMBO Journal, 2020, 39, e104063.	7.8	224
13	Single-Cell Transcriptomic Analysis of Cardiac Differentiation from Human PSCs Reveals HOPX-Dependent Cardiomyocyte Maturation. Cell Stem Cell, 2018, 23, 586-598.e8.	11.1	215
14	Benchmarking of cell type deconvolution pipelines for transcriptomics data. Nature Communications, 2020, 11, 5650.	12.8	207
15	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	12.8	192
16	A single‐cell transcriptome atlas of the adult human retina. EMBO Journal, 2019, 38, e100811.	7.8	185
17	The Genetic Architecture of Gene Expression in Peripheral Blood. American Journal of Human Genetics, 2017, 100, 228-237.	6.2	178
18	Single-cell eQTL mapping identifies cell type–specific genetic control of autoimmune disease. Science, 2022, 376, eabf3041.	12.6	171

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19	Identification of 55,000 Replicated DNA Methylation QTL. Scientific Reports, 2018, 8, 17605.	3.3	157
20	Genome-wide association study of intraocular pressure uncovers new pathways to glaucoma. Nature Genetics, 2018, 50, 1067-1071.	21.4	152
21	Human population dispersal â€œOut of Africaâ€•estimated from linkage disequilibrium and allele frequencies of SNPs. Genome Research, 2011, 21, 821-829.	5.5	137
22	<i>Nebulosa</i> recovers single-cell gene expression signals by kernel density estimation. Bioinformatics, 2021, 37, 2485-2487.	4.1	133
23	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. Science Advances, 2019, 5, eaaw3538.	10.3	123
24	Genetic Dissection of Acute Anterior Uveitis Reveals Similarities and Differences in Associations Observed With Ankylosing Spondylitis. Arthritis and Rheumatology, 2015, 67, 140-151.	5.6	114
25	Dynamics of human monocytes and airway macrophages during healthy aging and after transplant. Journal of Experimental Medicine, 2020, 217, .	8.5	113
26	Inference of the Genetic Architecture Underlying BMI and Height with the Use of 20,240 Sibling Pairs. American Journal of Human Genetics, 2013, 93, 865-875.	6.2	104
27	Single-cell RNA-seq of human induced pluripotent stem cells reveals cellular heterogeneity and cell state transitions between subpopulations. Genome Research, 2018, 28, 1053-1066.	5.5	102
28	Genetic parameters of production traits in Atlantic salmon (Salmo salar). Aquaculture, 2008, 274, 225-231.	3.5	98
29	Single-Cell Transcriptional Profiling of Aortic Endothelium Identifies a Hierarchy from Endovascular Progenitors to Differentiated Cells. Cell Reports, 2019, 27, 2748-2758.e3.	6.4	96
30	Distinct Brainstem and Forebrain Circuits Receiving Tracheal Sensory Neuron Inputs Revealed Using a Novel Conditional Anterograde Transsynaptic Viral Tracing System. Journal of Neuroscience, 2015, 35, 7041-7055.	3.6	94
31	A single-cell tumor immune atlas for precision oncology. Genome Research, 2021, 31, 1913-1926.	5.5	87
32	The Brisbane Systems Genetics Study: Genetical Genomics Meets Complex Trait Genetics. PLoS ONE, 2012, 7, e35430.	2.5	83
33	Congruence of Additive and Non-Additive Effects on Gene Expression Estimated from Pedigree and SNP Data. PLoS Genetics, 2013, 9, e1003502.	3.5	79
34	Transcriptomics and singleâ€cell RNAâ€sequencing. Respirology, 2019, 24, 29-36.	2.3	77
35	Genetic control of gene expression in whole blood and lymphoblastoid cell lines is largely independent. Genome Research, 2012, 22, 456-466.	5.5	75
36	Itaconate controls the severity of pulmonary fibrosis. Science Immunology, 2020, 5, .	11.9	73

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37	Expression quantitative trait locus analysis for translational medicine. Genome Medicine, 2015, 7, 60.	8.2	69
38	Single cell eQTL analysis identifies cell type-specific genetic control of gene expression in fibroblasts and reprogrammed induced pluripotent stem cells. Genome Biology, 2021, 22, 76.	8.8	58
39	Endometriosis risk alleles at 1p36.12 act through inverse regulation ofCDC42andLINC00339. Human Molecular Genetics, 2016, 25, ddw320.	2.9	56
40	Single cell RNA sequencing of stem cell-derived retinal ganglion cells. Scientific Data, 2018, 5, 180013.	5.3	55
41	Genotype-free demultiplexing of pooled single-cell RNA-seq. Genome Biology, 2019, 20, 290.	8.8	55
42	Overlap of expression Quantitative Trait Loci (eQTL) in human brain and blood. BMC Medical Genomics, 2014, 7, 31.	1.5	53
43	Genetic variation affects morphological retinal phenotypes extracted from UK Biobank optical coherence tomography images. PLoS Genetics, 2021, 17, e1009497.	3.5	50
44	Genetic regulation of disease risk and endometrial gene expression highlights potential target genes for endometriosis and polycystic ovarian syndrome. Scientific Reports, 2018, 8, 11424.	3.3	49
45	Seasonal Effects on Gene Expression. PLoS ONE, 2015, 10, e0126995.	2.5	48
46	The Medical Genome Reference Bank contains whole genome and phenotype data of 2570 healthy elderly. Nature Communications, 2020, 11, 435.	12.8	47
47	DNA methylation is required to maintain both DNA replication timing precision and 3D genome organization integrity. Cell Reports, 2021, 36, 109722.	6.4	39
48	Comparative performance of the BGI and Illumina sequencing technology for single-cell RNA-sequencing. NAR Genomics and Bioinformatics, 2020, 2, lqaa034.	3.2	37
49	ascend: R package for analysis of single-cell RNA-seq data. GigaScience, 2019, 8, .	6.4	36
50	Genome-wide analysis of blood gene expression in migraine implicates immune-inflammatory pathways. Cephalalgia, 2018, 38, 292-303.	3.9	34
51	The genetic regulation of transcription in human endometrial tissue. Human Reproduction, 2017, 32, 893-904.	0.9	32
52	Single-Cell Profiling Identifies Key Pathways Expressed by iPSCs Cultured in Different Commercial Media. IScience, 2018, 7, 30-39.	4.1	28
53	A new regulatory variant in the interleukin-6 receptor gene associates with asthma risk. Genes and Immunity, 2013, 14, 441-446.	4.1	27
54	DropletQC: improved identification of empty droplets and damaged cells in single-cell RNA-seq data. Genome Biology, 2021, 22, 329.	8.8	27

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55	Endometrial vezatin and its association with endometriosis risk. Human Reproduction, 2016, 31, 999-1013.	0.9	25
56	Transcriptomic Profiling of Human Pluripotent Stem Cell-derived Retinal Pigment Epithelium over Time. Genomics, Proteomics and Bioinformatics, 2021, 19, 223-242.	6.9	25
57	Cryopreservation of human cancers conserves tumour heterogeneity for single-cell multi-omics analysis. Genome Medicine, 2021, 13, 81.	8.2	25
58	Genetic and Nongenetic Variation Revealed for the Principal Components of Human Gene Expression. Genetics, 2013, 195, 1117-1128.	2.9	23
59	Ribosomal protein S6 mRNA is a biomarker upregulated in multiple sclerosis, downregulated by interferon treatment, and affected by season. Multiple Sclerosis Journal, 2014, 20, 675-685.	3.0	23
60	Constraints on eQTL Fine Mapping in the Presence of Multisite Local Regulation of Gene Expression. G3: Genes, Genomes, Genetics, 2017, 7, 2533-2544.	1.8	23
61	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. Genetics, 2019, 212, 905-918.	2.9	23
62	DevKidCC allows for robust classification and direct comparisons of kidney organoid datasets. Genome Medicine, 2022, 14, 19.	8.2	23
63	The low EOMES/TBX21 molecular phenotype in multiple sclerosis reflects CD56+ cell dysregulation and is affected by immunomodulatory therapies. Clinical Immunology, 2016, 163, 96-107.	3.2	22
64	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. Nature Communications, 2017, 8, 483.	12.8	22
65	Human iPSC-Derived Cerebellar Neurons from a Patient with Ataxia-Telangiectasia Reveal Disrupted Gene Regulatory Networks. Frontiers in Cellular Neuroscience, 2017, 11, 321.	3.7	22
66	*LPAR1* and *ITGA4* regulate peripheral blood monocyte counts. Human Mutation, 2011, 32, 873-876.	2.5	20
67	Blood gene expression studies in migraine: Potential and caveats. Cephalalgia, 2016, 36, 669-678.	3.9	19
68	Detection of HPV E7 Transcription atÂSingle-Cell Resolution in Epidermis. Journal of Investigative Dermatology, 2018, 138, 2558-2567.	0.7	19
69	Singleâ€Cell Immune Profiling in Coronary Artery Disease: The Role of Stateâ€ofâ€theâ€Art Immunophenotyping With Mass Cytometry in the Diagnosis of Atherosclerosis. Journal of the American Heart Association, 2020, 9, e017759.	3.7	19
70	Phantom epistasis between unlinked loci. Nature, 2021, 596, E1-E3.	27.8	16
71	Autosomal genetic control of human gene expression does not differ across the sexes. Genome Biology, 2016, 17, 248.	8.8	15
72	Refining Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder Genetic Loci by Integrating Summary Data From Genome-wide Association, Gene Expression, and DNA Methylation Studies. Biological Psychiatry, 2020, 88, 470-479.	1.3	14

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73	Hemani et al. reply. Nature, 2014, 514, E5-E6.	27.8	12
74	Testing Two Evolutionary Theories of Human Aging with DNA Methylation Data. Genetics, 2017, 207, 1547-1560.	2.9	12
75	The relationship between adrenocortical candidate gene expression and clinical response to hydrocortisone in patients with septic shock. Intensive Care Medicine, 2021, 47, 974-983.	8.2	12
76	Single-cell transcriptomics of alloreactive CD4+ T cells over time reveals divergent fates during gut graft-versus-host disease. JCI Insight, 2020, 5, .	5.0	12
77	A combined strategy for quantitative trait loci detection by genome-wide association. BMC Proceedings, 2009, 3, S6.	1.6	10
78	Predicting Sensation Seeking From Dopamine Genes. Psychological Science, 2011, 22, 413-415.	3.3	10
79	Shared genetic control of expression and methylation in peripheral blood. BMC Genomics, 2016, 17, 278.	2.8	10
80	No evidence that plasmablasts transdifferentiate into developing neutrophils in severe COVIDâ€19 disease. Clinical and Translational Immunology, 2021, 10, e1308.	3.8	10
81	Retinal ganglion cell-specific genetic regulation in primary open-angle glaucoma. Cell Genomics, 2022, 2, 100142.	6.5	9
82	Optimal use of regression models in genomeâ€wide association studies. Animal Genetics, 2012, 43, 133-143.	1.7	8
83	MHC-Dependent Mate Selection within 872 Spousal Pairs of European Ancestry from the Health and Retirement Study. Genes, 2018, 9, 53.	2.4	8
84	Integrating single-cell genomics pipelines to discover mechanisms of stem cell differentiation. Trends in Molecular Medicine, 2021, 27, 1135-1158.	6.7	8
85	A model of impaired Langerhans cell maturation associated with HPV induced epithelial hyperplasia. IScience, 2021, 24, 103326.	4.1	7
86	Evidence for mitochondrial genetic control of autosomal gene expression. Human Molecular Genetics, 2016, 25, ddw347.	2.9	6
87	Trans-eQTLs identified in whole blood have limited influence on complex disease biology. European Journal of Human Genetics, 2018, 26, 1361-1368.	2.8	3
88	scGPS: Determining Cell States and Global Fate Potential of Subpopulations. Frontiers in Genetics, 2021, 12, 666771.	2.3	2
89	TNFAIP3 Reduction-of-Function Drives Female Infertility and CNS Inflammation. Frontiers in Immunology, 2022, 13, 811525.	4.8	2
90	Using single cell genomics to change the treatment of lung cancer.. Journal of Clinical Oncology, 2019, 37, e20563-e20563.	1.6	0