Peter F Hickey

List of Publications by Year in descending order

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39 papers	6,785 citations	304602 22 h-index	395590 33 g-index
51 all docs	51 docs citations	51 times ranked	17631 citing authors

#	Article	IF	Citations
1	BAF complex-mediated chromatin relaxation is required for establishment of X chromosome inactivation. Nature Communications, 2022, 13, 1658.	5.8	7
2	Early introduction of high-intensity eccentric loading into hamstring strain injury rehabilitation. Journal of Science and Medicine in Sport, 2022, , .	0.6	2
3	Epigenetic modifier SMCHD1 maintains a normal pool of long-term hematopoietic stem cells. IScience, 2022, 25, 104684.	1.9	1
4	Human brain region-specific variably methylated regions are enriched for heritability of distinct neuropsychiatric traits. Genome Biology, 2021, 22, 116.	3.8	22
5	Genetic demultiplexing of pooled single-cell RNA-sequencing samples in cancer facilitates effective experimental design. GigaScience, 2021, 10, .	3.3	17
6	Zinc Supplementation with or without Additional Micronutrients Does Not Affect Peripheral Blood Gene Expression or Serum Cytokine Level in Bangladeshi Children. Nutrients, 2021, 13, 3516.	1.7	2
7	NanoMethViz: An R/Bioconductor package for visualizing long-read methylation data. PLoS Computational Biology, 2021, 17, e1009524.	1.5	11
8	Benchmarking UMI-based single-cell RNA-seq preprocessing workflows. Genome Biology, 2021, 22, 339.	3.8	25
9	The neuropeptide VIP confers anticipatory mucosal immunity by regulating ILC3 activity. Nature Immunology, 2020, 21, 168-177.	7.0	133
10	CellBench: R/Bioconductor software for comparing single-cell RNA-seq analysis methods. Bioinformatics, 2020, 36, 2288-2290.	1.8	20
11	Gene expression profiling of epithelium-associated FcRL4+ B cells in primary SjÃ¶gren's syndrome reveals a pathogenic signature. Journal of Autoimmunity, 2020, 109, 102439.	3.0	35
12	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. PLoS Computational Biology, 2020, 16, e1007664.	1.5	165
13	Pain-Free Versus Pain-Threshold Rehabilitation Following Acute Hamstring Strain Injury: A Randomized Controlled Trial. Journal of Orthopaedic and Sports Physical Therapy, 2020, 50, 91-103.	1.7	34
14	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
15	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
16	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
17	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
18	Pain-Free Versus Pain-Threshold Rehabilitation Following Acute Hamstring Strain Injury: A Randomized Controlled Trial. Journal of Orthopaedic and Sports Physical Therapy, 2019, , 1-35.	1.7	7

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19	Coexpression patterns define epigenetic regulators associated with neurological dysfunction. Genome Research, 2019, 29, 532-542.	2.4	42
20	A divergent transcriptional landscape underpins the development and functional branching of MAIT cells. Science Immunology, 2019, 4, .	5.6	75
21	Neuronal brain-region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric trait heritability. Nature Neuroscience, 2019, 22, 307-316.	7.1	120
22	A Novel Apparatus to Measure Knee Flexor Strength During Various Hamstring Exercises: A Reliability and Retrospective Injury Study. Journal of Orthopaedic and Sports Physical Therapy, 2018, 48, 72-80.	1.7	23
23	Smchd1 Targeting to the Inactive X Is Dependent on the Xist-HnrnpK-PRC1 Pathway. Cell Reports, 2018, 25, 1912-1923.e9.	2.9	56
24	Smchd1 regulates long-range chromatin interactions on the inactive X chromosome and at Hox clusters. Nature Structural and Molecular Biology, 2018, 25, 766-777.	3.6	84
25	Dynamic landscape and regulation of RNA editing in mammals. Nature, 2017, 550, 249-254.	13.7	495
26	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	13.7	764
27	The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243.	13.7	229
28	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	13.7	3,500
29	Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease. Nature Genetics, 2017, 49, 1664-1670.	9.4	179
30	Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis. Genome Research, 2017, 27, 1859-1871.	2.4	72
31	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. Genome Research, 2017, 27, 1843-1858.	2.4	139
32	ALPK3-deficient cardiomyocytes generated from patient-derived induced pluripotent stem cells and mutant human embryonic stem cells display abnormal calcium handling and establish that ALPK3 deficiency underlies familial cardiomyopathy. European Heart Journal, 2016, 37, 2586-2590.	1.0	49
33	Setdb1-mediated H3K9 methylation is enriched on the inactive X and plays a role in its epigenetic silencing. Epigenetics and Chromatin, 2016, 9, 16.	1.8	63
34	Representation and Manipulation of Genomic Tuples in R. Journal of Open Source Software, 2016, 1, 20.	2.0	0
35	Genetic and epigenetic variation among inbred mouse littermates: identification of inter-individual differentially methylated regions. Epigenetics and Chromatin, 2015, 8, 54.	1.8	60
36	Spontaneous retrotransposon insertion into TNF 3â€²UTR causes heart valve disease and chronic polyarthritis. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9698-9703.	3.3	29

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37	X chromosome association testing in genome wide association studies. Genetic Epidemiology, 2011, 35, 664-670.	0.6	43
38	Mutation of the Mitochondrial Tyrosyl-tRNA Synthetase Gene, YARS2, Causes Myopathy, Lactic Acidosis, and Sideroblastic Anemiaâ€"MLASA Syndrome. American Journal of Human Genetics, 2010, 87, 52-59.	2.6	211
39	Saliva-Derived DNA Performs Well in Large-Scale, High-Density Single-Nucleotide Polymorphism Microarray Studies. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 794-798.	1.1	52