

Peter F Hickey

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6297257/publications.pdf>

Version: 2024-02-01

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	Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017, 550, 204-213.	13.7	3,500
2	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , 2017, 550, 244-248.	13.7	764
3	Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , 2017, 550, 249-254.	13.7	495
4	The impact of rare variation on gene expression across tissues. <i>Nature</i> , 2017, 550, 239-243.	13.7	229
5	Mutation of the Mitochondrial Tyrosyl-tRNA Synthetase Gene, YARS2, Causes Myopathy, Lactic Acidosis, and Sideroblastic Anemia—MLASA Syndrome. <i>American Journal of Human Genetics</i> , 2010, 87, 52-59.	2.6	211
6	Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease. <i>Nature Genetics</i> , 2017, 49, 1664-1670.	9.4	179
7	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. <i>PLoS Computational Biology</i> , 2020, 16, e1007664.	1.5	165
8	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. <i>Genome Research</i> , 2017, 27, 1843-1858.	2.4	139
9	The neuropeptide VIP confers anticipatory mucosal immunity by regulating ILC3 activity. <i>Nature Immunology</i> , 2020, 21, 168-177.	7.0	133
10	Neuronal brain-region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric trait heritability. <i>Nature Neuroscience</i> , 2019, 22, 307-316.	7.1	120
11	Smchd1 regulates long-range chromatin interactions on the inactive X chromosome and at Hox clusters. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 766-777.	3.6	84
12	A divergent transcriptional landscape underpins the development and functional branching of MAIT cells. <i>Science Immunology</i> , 2019, 4, .	5.6	75
13	Identifying <i>cis</i> -mediators for <i>trans</i> -eQTLs across many human tissues using genomic mediation analysis. <i>Genome Research</i> , 2017, 27, 1859-1871.	2.4	72
14	Setdb1-mediated H3K9 methylation is enriched on the inactive X and plays a role in its epigenetic silencing. <i>Epigenetics and Chromatin</i> , 2016, 9, 16.	1.8	63
15	Genetic and epigenetic variation among inbred mouse littermates: identification of inter-individual differentially methylated regions. <i>Epigenetics and Chromatin</i> , 2015, 8, 54.	1.8	60
16	Smchd1 Targeting to the Inactive X Is Dependent on the Xist-HnrnpK-PRC1 Pathway. <i>Cell Reports</i> , 2018, 25, 1912-1923.e9.	2.9	56
17	Saliva-Derived DNA Performs Well in Large-Scale, High-Density Single-Nucleotide Polymorphism Microarray Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 794-798.	1.1	52
18	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. <i>European Heart Journal</i> , 2016, 37, 2586-2590.	1.0	49

#	ARTICLE	IF	CITATIONS
19	X chromosome association testing in genome wide association studies. <i>Genetic Epidemiology</i> , 2011, 35, 664-670.	0.6	43
20	Coexpression patterns define epigenetic regulators associated with neurological dysfunction. <i>Genome Research</i> , 2019, 29, 532-542.	2.4	42
21	Gene expression profiling of epithelium-associated FcRL4+ B cells in primary Sjögren's syndrome reveals a pathogenic signature. <i>Journal of Autoimmunity</i> , 2020, 109, 102439.	3.0	35
22	Pain-Free Versus Pain-Threshold Rehabilitation Following Acute Hamstring Strain Injury: A Randomized Controlled Trial. <i>Journal of Orthopaedic and Sports Physical Therapy</i> , 2020, 50, 91-103.	1.7	34
23	Spontaneous retrotransposon insertion into <i>TNF</i> 3'UTR causes heart valve disease and chronic polyarthritis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9698-9703.	3.3	29
24	Benchmarking UMI-based single-cell RNA-seq preprocessing workflows. <i>Genome Biology</i> , 2021, 22, 339.	3.8	25
25	A Novel Apparatus to Measure Knee Flexor Strength During Various Hamstring Exercises: A Reliability and Retrospective Injury Study. <i>Journal of Orthopaedic and Sports Physical Therapy</i> , 2018, 48, 72-80.	1.7	23
26	Human brain region-specific variably methylated regions are enriched for heritability of distinct neuropsychiatric traits. <i>Genome Biology</i> , 2021, 22, 116.	3.8	22
27	<i>CellBench</i> : <i>R/Bioconductor</i> software for comparing single-cell RNA-seq analysis methods. <i>Bioinformatics</i> , 2020, 36, 2288-2290.	1.8	20
28	Genetic demultiplexing of pooled single-cell RNA-sequencing samples in cancer facilitates effective experimental design. <i>GigaScience</i> , 2021, 10, .	3.3	17
29	<i>NanoMethViz</i> : An <i>R/Bioconductor</i> package for visualizing long-read methylation data. <i>PLoS Computational Biology</i> , 2021, 17, e1009524.	1.5	11
30	Pain-Free Versus Pain-Threshold Rehabilitation Following Acute Hamstring Strain Injury: A Randomized Controlled Trial. <i>Journal of Orthopaedic and Sports Physical Therapy</i> , 2019, , 1-35.	1.7	7
31	BAF complex-mediated chromatin relaxation is required for establishment of X chromosome inactivation. <i>Nature Communications</i> , 2022, 13, 1658.	5.8	7
32	Zinc Supplementation with or without Additional Micronutrients Does Not Affect Peripheral Blood Gene Expression or Serum Cytokine Level in Bangladeshi Children. <i>Nutrients</i> , 2021, 13, 3516.	1.7	2
33	Early introduction of high-intensity eccentric loading into hamstring strain injury rehabilitation. <i>Journal of Science and Medicine in Sport</i> , 2022, , .	0.6	2
34	Epigenetic modifier SMCHD1 maintains a normal pool of long-term hematopoietic stem cells. <i>IScience</i> , 2022, 25, 104684.	1.9	1
35	Representation and Manipulation of Genomic Tuples in R. <i>Journal of Open Source Software</i> , 2016, 1, 20.	2.0	0
36	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0

#	ARTICLE	IF	CITATIONS
37	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
38	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
39	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0