Jason Ernst

List of Publications by Year
in descending order

45 papers	20,479 citations	196777 29 h-index	242451 47 g-index
61 all docs	61 docs citations	61 times ranked	38139 citing authors

#	Article	IF	Citations
1	Epigenetic clock and methylation studies in vervet monkeys. GeroScience, 2022, 44, 699-717.	2.1	18
2	Universal annotation of the human genome through integration of over a thousand epigenomic datasets. Genome Biology, 2022, 23, 9.	3.8	39
3	A mammalian methylation array for profiling methylation levels at conserved sequences. Nature Communications, 2022, 13, 783.	5.8	93
4	Transcriptional analysis of cystic fibrosis airways at single-cell resolution reveals altered epithelial cell states and composition. Nature Medicine, 2021, 27, 806-814.	15.2	101
5	Learning a genome-wide score of human–mouse conservation at the functional genomics level. Nature Communications, 2021, 12, 2495.	5.8	12
6	Integration of evidence across human and model organism studies: A meeting report. Genes, Brain and Behavior, 2021, 20, e12738.	1.1	12
7	Single-nucleotide conservation state annotation of the SARS-CoV-2 genome. Communications Biology, 2021, 4, 698.	2.0	2
8	Epigenetic clock and methylation studies in the rhesus macaque. GeroScience, 2021, 43, 2441-2453.	2.1	28
9	Marginal Contribution Feature Importance - an Axiomatic Approach for Explaining Data. Proceedings of Machine Learning Research, 2021, 139, 1324-1335.	0.3	1
10	Identification and characterization of constrained non-exonic bases lacking predictive epigenomic and transcription factor binding annotations. Nature Communications, 2020, 11, 6168.	5.8	1
11	ConsHMM Atlas: conservation state annotations for major genomes and human genetic variation. NAR Genomics and Bioinformatics, 2020, 2, lqaa104.	1.5	4
12	Systematic discovery of conservation states for single-nucleotide annotation of the human genome. Communications Biology, 2019, 2, 248.	2.0	15
13	Analysis of cardiomyocyte clonal expansion during mouse heart development and injury. Nature Communications, 2018, 9, 754.	5.8	94
14	Investigating enhancer evolution with massively parallel reporter assays. Genome Biology, 2018, 19, 114.	3.8	2
15	Mapping molecular landmarks of human skeletal ontogeny and pluripotent stem cell-derived articular chondrocytes. Nature Communications, 2018, 9, 3634.	5.8	49
16	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. Nature Communications, 2018, 9, 2606.	5.8	79
17	ChromTime: modeling spatio-temporal dynamics of chromatin marks. Genome Biology, 2018, 19, 109.	3.8	10
18	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	5.8	140

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19	Cooperative Binding of Transcription Factors Orchestrates Reprogramming. Cell, 2017, 168, 442-459.e20.	13.5	432
20	Systematic Epigenomic Analysis Reveals Chromatin States Associated with Melanoma Progression. Cell Reports, 2017, 19, 875-889.	2.9	78
21	Chromatin-state discovery and genome annotation with ChromHMM. Nature Protocols, 2017, 12, 2478-2492.	5.5	613
22	Evidence of reduced recombination rate in human regulatory domains. Genome Biology, 2017, 18, 193.	3.8	38
23	Circadian variation of the pancreatic islet transcriptome. Physiological Genomics, 2016, 48, 677-687.	1.0	28
24	Genome-scale high-resolution mapping of activating and repressive nucleotides in regulatory regions. Nature Biotechnology, 2016, 34, 1180-1190.	9.4	132
25	Large-scale imputation of epigenomic datasets for systematic annotation of diverse human tissues. Nature Biotechnology, 2015, 33, 364-376.	9.4	354
26	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
27	Dual Roles of RNF2 in Melanoma Progression. Cancer Discovery, 2015, 5, 1314-1327.	7.7	57
28	Distinct and Predictive Histone Lysine Acetylation Patterns at Promoters, Enhancers, and Gene Bodies. G3: Genes, Genomes, Genetics, 2014, 4, 2051-2063.	0.8	39
29	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. Nature Neuroscience, 2014, 17, 1156-1163.	7.1	800
30	Long-Range Chromatin Contacts in Embryonic Stem Cells Reveal a Role for Pluripotency Factors and Polycomb Proteins in Genome Organization. Cell Stem Cell, 2013, 13, 602-616.	5.2	246
31	Integrative annotation of chromatin elements from ENCODE data. Nucleic Acids Research, 2013, 41, 827-841.	6.5	490
32	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. Genome Research, 2013, 23, 2136-2148.	2.4	51
33	Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay. Genome Research, 2013, 23, 800-811.	2.4	298
34	Interplay between chromatin state, regulator binding, and regulatory motifs in six human cell types. Genome Research, 2013, 23, 1142-1154.	2.4	84
35	Mapping enhancer and promoter interactions. Cell Research, 2012, 22, 789-790.	5.7	7
36	ChromHMM: automating chromatin-state discovery and characterization. Nature Methods, 2012, 9, 215-216.	9.0	2,127

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37	Comprehensive analysis of the chromatin landscape in Drosophila melanogaster. Nature, 2011, 471, 480-485.	13.7	781
38	Mapping and analysis of chromatin state dynamics in nine human cell types. Nature, 2011, 473, 43-49.	13.7	2,630
39	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	13.7	1,016
40	Discovery and characterization of chromatin states for systematic annotation of the human genome. Nature Biotechnology, 2010, 28, 817-825.	9.4	947
41	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. Science, 2010, 330, 1787-1797.	6.0	1,124
42	IL-3 and Oncogenic Abl Regulate the Myeloblast Transcriptome by Altering mRNA Stability. PLoS ONE, 2009, 4, e7469.	1.1	9
43	A Semi-Supervised Method for Predicting Transcription Factorâ€"Gene Interactions in Escherichia coli. PLoS Computational Biology, 2008, 4, e1000044.	1.5	85
44	Reconstructing dynamic regulatory maps. Molecular Systems Biology, 2007, 3, 74.	3.2	183
45	STEM: a tool for the analysis of short time series gene expression data. BMC Bioinformatics, 2006, 7, 191.	1.2	1,309