

# Jason Ernst

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9108975/publications.pdf>

Version: 2024-02-01

45  
papers

20,479  
citations

172457

29  
h-index

214800

47  
g-index

61  
all docs

61  
docs citations

61  
times ranked

34102  
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
2	Mapping and analysis of chromatin state dynamics in nine human cell types. <i>Nature</i> , 2011, 473, 43-49.	27.8	2,630
3	ChromHMM: automating chromatin-state discovery and characterization. <i>Nature Methods</i> , 2012, 9, 215-216.	19.0	2,127
4	STEM: a tool for the analysis of short time series gene expression data. <i>BMC Bioinformatics</i> , 2006, 7, 191.	2.6	1,309
5	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	12.6	1,124
6	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	27.8	1,016
7	Discovery and characterization of chromatin states for systematic annotation of the human genome. <i>Nature Biotechnology</i> , 2010, 28, 817-825.	17.5	947
8	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. <i>Nature Neuroscience</i> , 2014, 17, 1156-1163.	14.8	800
9	Comprehensive analysis of the chromatin landscape in <i>Drosophila melanogaster</i> . <i>Nature</i> , 2011, 471, 480-485.	27.8	781
10	Chromatin-state discovery and genome annotation with ChromHMM. <i>Nature Protocols</i> , 2017, 12, 2478-2492.	12.0	613
11	Integrative annotation of chromatin elements from ENCODE data. <i>Nucleic Acids Research</i> , 2013, 41, 827-841.	14.5	490
12	Cooperative Binding of Transcription Factors Orchestrates Reprogramming. <i>Cell</i> , 2017, 168, 442-459.e20.	28.9	432
13	Large-scale imputation of epigenomic datasets for systematic annotation of diverse human tissues. <i>Nature Biotechnology</i> , 2015, 33, 364-376.	17.5	354
14	Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay. <i>Genome Research</i> , 2013, 23, 800-811.	5.5	298
15	Long-Range Chromatin Contacts in Embryonic Stem Cells Reveal a Role for Pluripotency Factors and Polycomb Proteins in Genome Organization. <i>Cell Stem Cell</i> , 2013, 13, 602-616.	11.1	246
16	Reconstructing dynamic regulatory maps. <i>Molecular Systems Biology</i> , 2007, 3, 74.	7.2	183
17	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. <i>Nature Communications</i> , 2018, 9, 3391.	12.8	140
18	Genome-scale high-resolution mapping of activating and repressive nucleotides in regulatory regions. <i>Nature Biotechnology</i> , 2016, 34, 1180-1190.	17.5	132

#	ARTICLE	IF	CITATIONS
19	Transcriptional analysis of cystic fibrosis airways at single-cell resolution reveals altered epithelial cell states and composition. <i>Nature Medicine</i> , 2021, 27, 806-814.	30.7	101
20	Analysis of cardiomyocyte clonal expansion during mouse heart development and injury. <i>Nature Communications</i> , 2018, 9, 754.	12.8	94
21	A mammalian methylation array for profiling methylation levels at conserved sequences. <i>Nature Communications</i> , 2022, 13, 783.	12.8	93
22	A Semi-Supervised Method for Predicting Transcription Factor-Gene Interactions in <i>Escherichia coli</i> . <i>PLoS Computational Biology</i> , 2008, 4, e1000044.	3.2	85
23	Interplay between chromatin state, regulator binding, and regulatory motifs in six human cell types. <i>Genome Research</i> , 2013, 23, 1142-1154.	5.5	84
24	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. <i>Nature Communications</i> , 2018, 9, 2606.	12.8	79
25	Systematic Epigenomic Analysis Reveals Chromatin States Associated with Melanoma Progression. <i>Cell Reports</i> , 2017, 19, 875-889.	6.4	78
26	Dual Roles of RNF2 in Melanoma Progression. <i>Cancer Discovery</i> , 2015, 5, 1314-1327.	9.4	57
27	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. <i>Genome Research</i> , 2013, 23, 2136-2148.	5.5	51
28	Mapping molecular landmarks of human skeletal ontogeny and pluripotent stem cell-derived articular chondrocytes. <i>Nature Communications</i> , 2018, 9, 3634.	12.8	49
29	Distinct and Predictive Histone Lysine Acetylation Patterns at Promoters, Enhancers, and Gene Bodies. <i>C3: Genes, Genomes, Genetics</i> , 2014, 4, 2051-2063.	1.8	39
30	Universal annotation of the human genome through integration of over a thousand epigenomic datasets. <i>Genome Biology</i> , 2022, 23, 9.	8.8	39
31	Evidence of reduced recombination rate in human regulatory domains. <i>Genome Biology</i> , 2017, 18, 193.	8.8	38
32	Circadian variation of the pancreatic islet transcriptome. <i>Physiological Genomics</i> , 2016, 48, 677-687.	2.3	28
33	Epigenetic clock and methylation studies in the rhesus macaque. <i>GeroScience</i> , 2021, 43, 2441-2453.	4.6	28
34	Epigenetic clock and methylation studies in vervet monkeys. <i>GeroScience</i> , 2022, 44, 699-717.	4.6	18
35	Systematic discovery of conservation states for single-nucleotide annotation of the human genome. <i>Communications Biology</i> , 2019, 2, 248.	4.4	15
36	Learning a genome-wide score of human-mouse conservation at the functional genomics level. <i>Nature Communications</i> , 2021, 12, 2495.	12.8	12

#	ARTICLE	IF	CITATIONS
37	Integration of evidence across human and model organism studies: A meeting report. <i>Genes, Brain and Behavior</i> , 2021, 20, e12738.	2.2	12
38	ChromTime: modeling spatio-temporal dynamics of chromatin marks. <i>Genome Biology</i> , 2018, 19, 109.	8.8	10
39	IL-3 and Oncogenic Abl Regulate the Myeloblast Transcriptome by Altering mRNA Stability. <i>PLoS ONE</i> , 2009, 4, e7469.	2.5	9
40	Mapping enhancer and promoter interactions. <i>Cell Research</i> , 2012, 22, 789-790.	12.0	7
41	ConsHMM Atlas: conservation state annotations for major genomes and human genetic variation. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa104.	3.2	4
42	Investigating enhancer evolution with massively parallel reporter assays. <i>Genome Biology</i> , 2018, 19, 114.	8.8	2
43	Single-nucleotide conservation state annotation of the SARS-CoV-2 genome. <i>Communications Biology</i> , 2021, 4, 698.	4.4	2
44	Identification and characterization of constrained non-exonic bases lacking predictive epigenomic and transcription factor binding annotations. <i>Nature Communications</i> , 2020, 11, 6168.	12.8	1
45	Marginal Contribution Feature Importance - an Axiomatic Approach for Explaining Data. <i>Proceedings of Machine Learning Research</i> , 2021, 139, 1324-1335.	0.3	1