

# Jason Ernst

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

53  
papers

14,457  
citations

28  
h-index

61  
g-index

61  
ext. papers

18,488  
ext. citations

20  
avg, IF

6.44  
L-index

| #  | Paper   | IF   | Citations |
|----|---|------|-----------|
| 53 | Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , <b>2015</b> , 518, 317-30   | 50.4 | 3849      |
| 52 | Mapping and analysis of chromatin state dynamics in nine human cell types. <i>Nature</i> , <b>2011</b> , 473, 43-9  | 50.4 | 2153      |
| 51 | ChromHMM: automating chromatin-state discovery and characterization. <i>Nature Methods</i> , <b>2012</b> , 9, 215-216   | 21.6 | 1413      |
| 50 | Identification of functional elements and regulatory circuits by Drosophila modENCODE. <i>Science</i> , <b>2010</b> , 330, 1787-97  | 33.3 | 892       |
| 49 | STEM: a tool for the analysis of short time series gene expression data. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 191   | 3.6  | 810       |
| 48 | A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , <b>2011</b> , 478, 476-82  | 50.4 | 802       |
| 47 | Discovery and characterization of chromatin states for systematic annotation of the human genome. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 817-25                                    | 44.5 | 757       |
| 46 | Comprehensive analysis of the chromatin landscape in <i>Drosophila melanogaster</i> . <i>Nature</i> , <b>2011</b> , 471, 480-5  | 50.4 | 641       |
| 45 | Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. <i>Nature Neuroscience</i> , <b>2014</b> , 17, 1156-63                                | 25.5 | 579       |
| 44 | Integrative annotation of chromatin elements from ENCODE data. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 827-40   | 11.1 | 383       |
| 43 | Cooperative Binding of Transcription Factors Orchestrates Reprogramming. <i>Cell</i> , <b>2017</b> , 168, 442-459.e20   | 56.2 | 274       |
| 42 | Chromatin-state discovery and genome annotation with ChromHMM. <i>Nature Protocols</i> , <b>2017</b> , 12, 2478-2492  | 24.8 | 257       |
| 41 | Large-scale imputation of epigenomic datasets for systematic annotation of diverse human tissues. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 364-76                                    | 44.5 | 252       |
| 40 | 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> , <b>2013</b> , 13, 602-16 | 18   | 197       |
| 39 | Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay. <i>Genome Research</i> , <b>2013</b> , 23, 800-11                   | 9.7  | 191       |
| 38 | Reconstructing dynamic regulatory maps. <i>Molecular Systems Biology</i> , <b>2007</b> , 3, 74  | 12.2 | 139       |
| 37 | Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. <i>Nature Communications</i> , <b>2018</b> , 9, 3391  | 17.4 | 90        |

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| 36 | Genome-scale high-resolution mapping of activating and repressive nucleotides in regulatory regions. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 1180-1190                           | 44.5 | 85 |
| 35 | Interplay between chromatin state, regulator binding, and regulatory motifs in six human cell types. <i>Genome Research</i> , <b>2013</b> , 23, 1142-54                                  | 9.7  | 72 |
| 34 | A semi-supervised method for predicting transcription factor-gene interactions in Escherichia coli. <i>PLoS Computational Biology</i> , <b>2008</b> , 4, e1000044                        | 5    | 67 |
| 33 | Analysis of cardiomyocyte clonal expansion during mouse heart development and injury. <i>Nature Communications</i> , <b>2018</b> , 9, 754  | 17.4 | 65 |
| 32 | Systematic Epigenomic Analysis Reveals Chromatin States Associated with Melanoma Progression. <i>Cell Reports</i> , <b>2017</b> , 19, 875-889  | 10.6 | 53 |
| 31 | Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. <i>Nature Communications</i> , <b>2018</b> , 9, 2606                   | 17.4 | 53 |
| 30 | Dual Roles of RNF2 in Melanoma Progression. <i>Cancer Discovery</i> , <b>2015</b> , 5, 1314-27   | 24.4 | 47 |
| 29 | Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. <i>Genome Research</i> , <b>2013</b> , 23, 2136-48                                   | 9.7  | 39 |
| 28 | A mammalian methylation array for profiling methylation levels at conserved sequences  |      | 31 |
| 27 | Universal DNA methylation age across mammalian tissues   |      | 31 |
| 26 | Transcriptional analysis of cystic fibrosis airways at single-cell resolution reveals altered epithelial cell states and composition. <i>Nature Medicine</i> , <b>2021</b> , 27, 806-814 | 50.5 | 29 |
| 25 | Distinct and predictive histone lysine acetylation patterns at promoters, enhancers, and gene bodies. <i>G3: Genes, Genomes, Genetics</i> , <b>2014</b> , 4, 2051-63                     | 3.2  | 27 |
| 24 | Mapping molecular landmarks of human skeletal ontogeny and pluripotent stem cell-derived articular chondrocytes. <i>Nature Communications</i> , <b>2018</b> , 9, 3634                    | 17.4 | 27 |
| 23 | Evidence of reduced recombination rate in human regulatory domains. <i>Genome Biology</i> , <b>2017</b> , 18, 193  | 18.3 | 23 |
| 22 | Circadian variation of the pancreatic islet transcriptome. <i>Physiological Genomics</i> , <b>2016</b> , 48, 677-87  | 3.6  | 22 |
| 21 | A mammalian methylation array for profiling methylation levels at conserved sequences.. <i>Nature Communications</i> , <b>2022</b> , 13, 783   | 17.4 | 15 |
| 20 | Systematic discovery of conservation states for single-nucleotide annotation of the human genome. <i>Communications Biology</i> , <b>2019</b> , 2, 248                                   | 6.7  | 11 |
| 19 | Epigenetic clock and methylation studies in the rhesus macaque   |      | 10 |

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|----|---|------|----|
| 18 | Epigenetic clock and methylation studies in the rhesus macaque. <i>GeroScience</i> , <b>2021</b> , 43, 2441-2453  | 8.9  | 10 |
| 17 | IL-3 and oncogenic Abl regulate the myeloblast transcriptome by altering mRNA stability. <i>PLoS ONE</i> , <b>2009</b> , 4, e7469   | 3.7  | 9  |
| 16 | ChromTime: modeling spatio-temporal dynamics of chromatin marks. <i>Genome Biology</i> , <b>2018</b> , 19, 109  | 18.3 | 7  |
| 15 | Epigenetic clock and methylation studies in vervet monkeys  |      | 7  |
| 14 | DNA methylation study of age and sex in baboons and four other primates   |      | 7  |
| 13 | Mapping enhancer and promoter interactions. <i>Cell Research</i> , <b>2012</b> , 22, 789-90   | 24.7 | 5  |
| 12 | Universal annotation of the human genome through integration of over a thousand epigenomic datasets.. <i>Genome Biology</i> , <b>2022</b> , 23, 9   | 18.3 | 5  |
| 11 | Epigenetic predictors of maximum lifespan and other life history traits in mammals  |      | 5  |
| 10 | Epigenetic clock and methylation studies in vervet monkeys. <i>GeroScience</i> , <b>2021</b> , 1  | 8.9  | 5  |
| 9  | Universal annotation of the human genome through integration of over a thousand epigenomic datasets   |      | 3  |
| 8  | Learning a genome-wide score of human-mouse conservation at the functional genomics level. <i>Nature Communications</i> , <b>2021</b> , 12, 2495  | 17.4 | 2  |
| 7  | ConsHMM Atlas: conservation state annotations for major genomes and human genetic variation. <i>NAR Genomics and Bioinformatics</i> , <b>2020</b> , 2, lqaa104  | 3.7  | 1  |
| 6  | Single-nucleotide conservation state annotation of the SARS-CoV-2 genome <b>2020</b> ,  |      | 1  |
| 5  | Identification and characterization of constrained non-exonic bases lacking predictive epigenomic and transcription factor binding annotations. <i>Nature Communications</i> , <b>2020</b> , 11, 6168 | 17.4 | 1  |
| 4  | Integration of evidence across human and model organism studies: A meeting report. <i>Genes, Brain and Behavior</i> , <b>2021</b> , 20, e12738  | 3.6  | 1  |
| 3  | Investigating enhancer evolution with massively parallel reporter assays. <i>Genome Biology</i> , <b>2018</b> , 19, 114   | 18.3 | 1  |
| 2  | Marginal Contribution Feature Importance - an Axiomatic Approach for Explaining Data. <i>Proceedings of Machine Learning Research</i> , <b>2021</b> , 139, 1324-1335                                  | 0.4  |    |
| 1  | Single-nucleotide conservation state annotation of the SARS-CoV-2 genome. <i>Communications Biology</i> , <b>2021</b> , 4, 698  | 6.7  |    |

