Joel Rozowsky

List of Publications by Year
in descending order

36 papers	19,301 citations	136950 32 h-index	345221 36 g-index
37 all docs	37 docs citations	37 times ranked	29305 citing authors

#	Article	IF	Citations
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
2	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	27.8	4,484
3	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 2012, 22, 1813-1831.	5.5	1,708
4	Architecture of the human regulatory network derived from ENCODE data. Nature, 2012, 489, 91-100.	27.8	1,384
5	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	27.8	1,252
6	Integrative Analysis of the *Caenorhabditis elegans* Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	12.6	912
7	Variation in Transcription Factor Binding Among Humans. Science, 2010, 328, 232-235.	12.6	521
8	PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls. Nature Biotechnology, 2009, 27, 66-75.	17.5	514
9	Annotating non-coding regions of the genome. Nature Reviews Genetics, 2010, 11, 559-571.	16.3	398
10	A myelopoiesis-associated regulatory intergenic noncoding RNA transcript within the human HOXA cluster. Blood, 2009, 113, 2526-2534.	1.4	330
11	Divergence of Transcription Factor Binding Sites Across Related Yeast Species. Science, 2007, 317, 815-819.	12.6	320
12	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	27.8	289
13	AlleleSeq: analysis of allele‑specific expression and binding in a network framework. Molecular Systems Biology, 2011, 7, 522.	7.2	284
14	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. Genome Biology, 2012, 13, R48.	9.6	233
15	Mapping accessible chromatin regions using Sono-Seq. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14926-14931.	7.1	186
16	Diverse Roles and Interactions of the SWI/SNF Chromatin Remodeling Complex Revealed Using Global Approaches. PLoS Genetics, 2011, 7, e1002008.	3.5	185
17	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	27.8	184
18	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Genome Research, 2012, 22, 1658-1667.	5.5	166

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19	Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing. BMC Genomics, 2009, 10, 37.	2.8	137
20	A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. Genome Biology, 2011, 12, R15.	9.6	118
21	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. Genome Research, 2008, 18, 393-403.	5.5	117
22	Comparison and calibration of transcriptome data from RNA-Seq and tiling arrays. BMC Genomics, 2010, 11, 383.	2.8	97
23	An integrative ENCODE resource for cancer genomics. Nature Communications, 2020, 11, 3696.	12.8	95
24	Construction and Analysis of an Integrated Regulatory Network Derived from High-Throughput Sequencing Data. PLoS Computational Biology, 2011, 7, e1002190.	3.2	92
25	MUSIC: identification of enriched regions in ChIP-Seq experiments using a mappability-corrected multiscale signal processing framework. Genome Biology, 2014, 15, 474.	8.8	81
26	A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals. Nature Communications, 2016, 7, 11101.	12.8	78
27	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. Nature Methods, 2020, 17, 807-814.	19.0	71
28	Modeling ChIP Sequencing In Silico with Applications. PLoS Computational Biology, 2008, 4, e1000158.	3.2	70
29	Prediction and characterization of noncoding RNAs in C. elegans by integrating conservation, secondary structure, and high-throughput sequencing and array data. Genome Research, 2011, 21, 276-285.	5.5	60
30	Systematic analysis of transcribed loci in ENCODE regions using RACE sequencing reveals extensive transcription in the human genome. Genome Biology, 2008, 9, R3.	9.6	53
31	OrthoClust: an orthology-based network framework for clustering data across multiple species. Genome Biology, 2014, 15, R100.	9.6	46
32	Tilescope: online analysis pipeline for high-density tiling microarray data. Genome Biology, 2007, 8, R81.	9.6	39
33	ACT: aggregation and correlation toolbox for analyses of genome tracks. Bioinformatics, 2011, 27, 1152-1154.	4.1	35
34	Transcription factor binding site identification in yeast: a comparison of high-density oligonucleotide and PCR-based microarray platforms. Functional and Integrative Genomics, 2007, 7, 335-345.	3.5	22
35	Loregic: A Method to Characterize the Cooperative Logic of Regulatory Factors. PLoS Computational Biology, 2015, 11, e1004132.	3.2	18
36	Tiling array data analysis: a multiscale approach using wavelets. BMC Bioinformatics, 2011, 12, 57.	2.6	7