

Joel Rozowsky

List of Publications by Year in descending order

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Version: 2024-02-01

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	An integrative ENCODE resource for cancer genomics. <i>Nature Communications</i> , 2020, 11, 3696.	12.8	95
2	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	1,252
3	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. <i>Nature Methods</i> , 2020, 17, 807-814.	19.0	71
4	A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals. <i>Nature Communications</i> , 2016, 7, 11101.	12.8	78
5	Loregic: A Method to Characterize the Cooperative Logic of Regulatory Factors. <i>PLoS Computational Biology</i> , 2015, 11, e1004132.	3.2	18
6	OrthoClust: an orthology-based network framework for clustering data across multiple species. <i>Genome Biology</i> , 2014, 15, R100.	9.6	46
7	MUSIC: identification of enriched regions in ChIP-Seq experiments using a mappability-corrected multiscale signal processing framework. <i>Genome Biology</i> , 2014, 15, 474.	8.8	81
8	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014, 512, 445-448.	27.8	289
9	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014, 512, 453-456.	27.8	184
10	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. <i>Genome Biology</i> , 2012, 13, R48.	9.6	233
11	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831.	5.5	1,708
12	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012, 489, 91-100.	27.8	1,384
13	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667.	5.5	166
14	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	27.8	4,484
15	AlleleSeq: analysis of allele-specific expression and binding in a network framework. <i>Molecular Systems Biology</i> , 2011, 7, 522.	7.2	284
16	A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. <i>Genome Biology</i> , 2011, 12, R15.	9.6	118
17	Diverse Roles and Interactions of the SWI/SNF Chromatin Remodeling Complex Revealed Using Global Approaches. <i>PLoS Genetics</i> , 2011, 7, e1002008.	3.5	185
18	Tiling array data analysis: a multiscale approach using wavelets. <i>BMC Bioinformatics</i> , 2011, 12, 57.	2.6	7

#	ARTICLE	IF	CITATIONS
19	ACT: aggregation and correlation toolbox for analyses of genome tracks. <i>Bioinformatics</i> , 2011, 27, 1152-1154.	4.1	35
20	Prediction and characterization of noncoding RNAs in <i>C. elegans</i> by integrating conservation, secondary structure, and high-throughput sequencing and array data. <i>Genome Research</i> , 2011, 21, 276-285.	5.5	60
21	Construction and Analysis of an Integrated Regulatory Network Derived from High-Throughput Sequencing Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002190.	3.2	92
22	Comparison and calibration of transcriptome data from RNA-Seq and tiling arrays. <i>BMC Genomics</i> , 2010, 11, 383.	2.8	97
23	Annotating non-coding regions of the genome. <i>Nature Reviews Genetics</i> , 2010, 11, 559-571.	16.3	398
24	Variation in Transcription Factor Binding Among Humans. <i>Science</i> , 2010, 328, 232-235.	12.6	521
25	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	12.6	912
26	Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing. <i>BMC Genomics</i> , 2009, 10, 37.	2.8	137
27	PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls. <i>Nature Biotechnology</i> , 2009, 27, 66-75.	17.5	514
28	Mapping accessible chromatin regions using Sono-Seq. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14926-14931.	7.1	186
29	A myelopoiesis-associated regulatory intergenic noncoding RNA transcript within the human HOXA cluster. <i>Blood</i> , 2009, 113, 2526-2534.	1.4	330
30	Systematic analysis of transcribed loci in ENCODE regions using RACE sequencing reveals extensive transcription in the human genome. <i>Genome Biology</i> , 2008, 9, R3.	9.6	53
31	Modeling ChIP Sequencing In Silico with Applications. <i>PLoS Computational Biology</i> , 2008, 4, e1000158.	3.2	70
32	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. <i>Genome Research</i> , 2008, 18, 393-403.	5.5	117
33	Divergence of Transcription Factor Binding Sites Across Related Yeast Species. <i>Science</i> , 2007, 317, 815-819.	12.6	320
34	TileScope: online analysis pipeline for high-density tiling microarray data. <i>Genome Biology</i> , 2007, 8, R81.	9.6	39
35	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
36	Transcription factor binding site identification in yeast: a comparison of high-density oligonucleotide and PCR-based microarray platforms. <i>Functional and Integrative Genomics</i> , 2007, 7, 335-345.	3.5	22