

Joel H Graber

List of Publications by Year in descending order

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37
papers

2,966
citations

304743

22
h-index

330143

37
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39
docs citations

39
times ranked

4685
citing authors

#	ARTICLE	IF	CITATIONS
1	Retrotransposons Regulate Host Genes in Mouse Oocytes and Preimplantation Embryos. <i>Developmental Cell</i> , 2004, 7, 597-606.	7.0	610
2	A customized and versatile high-density genotyping array for the mouse. <i>Nature Methods</i> , 2009, 6, 663-666.	19.0	236
3	Gene-specific RNA polymerase II phosphorylation and the CTD code. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1279-1286.	8.2	200
4	Signals for pre-mRNA cleavage and polyadenylation. <i>Wiley Interdisciplinary Reviews RNA</i> , 2012, 3, 385-396.	6.4	192
5	A Ubiquitous and Conserved Signal for RNA Localization in Chordates. <i>Current Biology</i> , 2002, 12, 1756-1761.	3.9	148
6	Cracking the egg: molecular dynamics and evolutionary aspects of the transition from the fully grown oocyte to embryo. <i>Genes and Development</i> , 2006, 20, 2713-2727.	5.9	147
7	Position-dependent motif characterization using non-negative matrix factorization. <i>Bioinformatics</i> , 2008, 24, 2684-2690.	4.1	140
8	Global Changes in Processing of mRNA 3' Untranslated Regions Characterize Clinically Distinct Cancer Subtypes. <i>Cancer Research</i> , 2009, 69, 9422-9430.	0.9	136
9	The Recombinational Anatomy of a Mouse Chromosome. <i>PLoS Genetics</i> , 2008, 4, e1000119.	3.5	135
10	Genomic detection of new yeast pre-mRNA 3'-end-processing signals. <i>Nucleic Acids Research</i> , 1999, 27, 888-894.	14.5	118
11	Systematic variation in mRNA 3'-processing signals during mouse spermatogenesis. <i>Nucleic Acids Research</i> , 2007, 35, 234-246.	14.5	114
12	Probabilistic prediction of <i>Saccharomyces cerevisiae</i> mRNA 3'-processing sites. <i>Nucleic Acids Research</i> , 2002, 30, 1851-1858.	14.5	101
13	Evidence of a Large-Scale Functional Organization of Mammalian Chromosomes. <i>PLoS Genetics</i> , 2005, 1, e33.	3.5	88
14	RNA-Seq Alignment to Individualized Genomes Improves Transcript Abundance Estimates in Multiparent Populations. <i>Genetics</i> , 2014, 198, 59-73.	2.9	82
15	PACdb: PolyA Cleavage Site and 3'-UTR Database. <i>Bioinformatics</i> , 2005, 21, 3691-3693.	4.1	53
16	DNA damage induces targeted, genome-wide variation of poly(A) sites in budding yeast. <i>Genome Research</i> , 2013, 23, 1690-1703.	5.5	50
17	Temporal dynamics of the developing lung transcriptome in three common inbred strains of laboratory mice reveals multiple stages of postnatal alveolar development. <i>PeerJ</i> , 2016, 4, e2318.	2.0	47
18	A multispecies comparison of the metazoan 3'-processing downstream elements and the CstF-64 RNA recognition motif. <i>BMC Genomics</i> , 2006, 7, 55.	2.8	44

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19	<i>C. elegans</i> sequences that control trans-splicing and operon pre-mRNA processing. <i>Rna</i> , 2007, 13, 1409-1426.	3.5	37
20	Quantitative comparison of EST libraries requires compensation for systematic biases in cDNA generation. <i>BMC Bioinformatics</i> , 2006, 7, 77.	2.6	31
21	Advances in DNA diagnostics. <i>Current Opinion in Biotechnology</i> , 1998, 9, 14-18.	6.6	29
22	Probe-Level Analysis of Expression Microarrays Characterizes Isoform-Specific Degradation during Mouse Oocyte Maturation. <i>PLoS ONE</i> , 2009, 4, e7479.	2.5	27
23	Patterns of Recombination Activity on Mouse Chromosome 11 Revealed by High Resolution Mapping. <i>PLoS ONE</i> , 2010, 5, e15340.	2.5	27
24	Reprogramming and Differentiation in Mammals: Motifs and Mechanisms. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2008, 73, 33-38.	1.1	21
25	Variations in yeast 3' processing cis-elements correlate with transcript stability. <i>Trends in Genetics</i> , 2003, 19, 473-476.	6.7	19
26	Differential sequencing with mass spectrometry. <i>Genetic Analysis, Techniques and Applications</i> , 1999, 14, 215-219.	1.5	16
27	Evidence of a Large-Scale Functional Organization of Mammalian Chromosomes. <i>PLoS Biology</i> , 2007, 5, e127.	5.6	16
28	TauCstF-64 Mediates Correct mRNA Polyadenylation and Splicing of Activator and Repressor Isoforms of the Cyclic AMP-Responsive Element Modulator (CREM) in Mouse Testis1. <i>Biology of Reproduction</i> , 2016, 94, 34.	2.7	16
29	PCR based targeted genomic and cDNA differential display. <i>Genetic Analysis, Techniques and Applications</i> , 1999, 15, 51-63.	1.5	15
30	Patterns and mechanisms of genome organization in the mouse. <i>Journal of Experimental Zoology Part A, Comparative Experimental Biology</i> , 2006, 305A, 683-688.	1.3	15
31	Mutant KLF1 in Adult Anemic Nan Mice Leads to Profound Transcriptome Changes and Disordered Erythropoiesis. <i>Scientific Reports</i> , 2018, 8, 12793.	3.3	14
32	Reference Trait Analysis Reveals Correlations Between Gene Expression and Quantitative Traits in Disjoint Samples. <i>Genetics</i> , 2019, 212, 919-929.	2.9	12
33	CGDSNPdb: a database resource for error-checked and imputed mouse SNPs. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq008.	3.0	8
34	Ipa1 Is an RNA Polymerase II Elongation Factor that Facilitates Termination by Maintaining Levels of the Poly(A) Site Endonuclease Ysh1. <i>Cell Reports</i> , 2019, 26, 1919-1933.e5.	6.4	8
35	Regulation of the Ysh1 endonuclease of the mRNA cleavage/polyadenylation complex by ubiquitin-mediated degradation. <i>RNA Biology</i> , 2020, 17, 689-702.	3.1	7
36	Interrogating the Transcriptome of Oocytes and Preimplantation Embryos. <i>Methods in Enzymology</i> , 2010, 477, 481-510.	1.0	3

#	ARTICLE	IF	CITATIONS
37	Differential effects of RASA3 mutations on hematopoiesis are profoundly influenced by genetic background and molecular variant. PLoS Genetics, 2020, 16, e1008857.	3.5	3