

Karl Kornacker

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

2,085
citations

759233

12
h-index

1058476

14
g-index

15
all docs

15
docs citations

15
times ranked

3348
citing authors

#	ARTICLE	IF	CITATIONS
1	Guidelines for Genome-Scale Analysis of Biological Rhythms. <i>Journal of Biological Rhythms</i> , 2017, 32, 380-393.	2.6	237
2	MetaCycle: an integrated R package to evaluate periodicity in large scale data. <i>Bioinformatics</i> , 2016, 32, 3351-3353.	4.1	413
3	The Triform algorithm: improved sensitivity and specificity in ChIP-Seq peak finding. <i>BMC Bioinformatics</i> , 2012, 13, 176.	2.6	8
4	Age-Associated Disruption of Molecular Clock Expression in Skeletal Muscle of the Spontaneously Hypertensive Rat. <i>PLoS ONE</i> , 2011, 6, e27168.	2.5	44
5	Accurate Expression Profiling of Very Small Cell Populations. <i>PLoS ONE</i> , 2010, 5, e14418.	2.5	60
6	JTK_CYCLE: An Efficient Nonparametric Algorithm for Detecting Rhythmic Components in Genome-Scale Data Sets. <i>Journal of Biological Rhythms</i> , 2010, 25, 372-380.	2.6	919
7	Expression Profiling Using Affymetrix GeneChip Microarrays. <i>Methods in Molecular Biology</i> , 2009, 509, 35-46.	0.9	30
8	Transcriptional profiling of the megabladder mouse: A unique model of bladder dysmorphogenesis. <i>Developmental Dynamics</i> , 2008, 237, 170-186.	1.8	11
9	Identification of a Unique Transgenic Mouse Line That Develops Megabladder, Obstructive Uropathy, and Renal Dysfunction. <i>Journal of the American Society of Nephrology: JASN</i> , 2007, 18, 461-471.	6.1	36
10	Gene-resolution analysis of DNA copy number variation using oligonucleotide expression microarrays. <i>BMC Genomics</i> , 2007, 8, 111.	2.8	19
11	Big results from small samples: evaluation of amplification protocols for gene expression profiling. <i>Journal of Biomolecular Techniques</i> , 2007, 18, 150-61.	1.5	22
12	Quantification of DNA methylation in electrofluidics chips (Bio-COBRA). <i>Nature Protocols</i> , 2006, 1, 52-58.	12.0	39
13	Accurate quantification of DNA methylation using combined bisulfite restriction analysis coupled with the Agilent 2100 Bioanalyzer platform. <i>Nucleic Acids Research</i> , 2006, 34, e17-e17.	14.5	62
14	Chipping away at the chip bias: RNA degradation in microarray analysis. <i>Nature Genetics</i> , 2003, 35, 292-293.	21.4	185
15	Discrete finite nilpotent Lie algebras: New models for unified gauge field theory. <i>Journal of Mathematical Physics</i> , 1978, 19, 1584-1586.	1.1	0