

Steffen Heber

List of Publications by Year in descending order

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43
papers

2,171
citations

471061

17
h-index

414034

32
g-index

44
all docs

44
docs citations

44
times ranked

4034
citing authors

#	ARTICLE	IF	CITATIONS
1	A New Discrete Whale Optimization Algorithm with a Spiral 3-opt Local Search for Solving the Traveling Salesperson Problem. , 2022, , .		0
2	PeakPass: Automating ChIP-Seq Blacklist Creation. Journal of Computational Biology, 2020, 27, 259-268.	0.8	11
3	RiboSimR: A Tool for Simulation and Power Analysis of Ribo-seq Data. Lecture Notes in Computer Science, 2020, , 121-133.	1.0	1
4	Using a Novel Negative Selection Inspired Anomaly Detection Algorithm to Identify Corrupted Ribo-seq and RNA-seq Samples. , 2019, , .		1
5	RiboStreamR: a web application for quality control, analysis, and visualization of Ribo-seq data. BMC Genomics, 2019, 20, 422.	1.2	16
6	PeakPass: Automating ChIP-Seq Blacklist Creation. Lecture Notes in Computer Science, 2019, , 232-243.	1.0	0
7	Identification of Ribosome Pause Sites Using a Z-Score Based Peak Detection Algorithm. , 2018, , .		9
8	Identifying the Signatures of Missing Transcripts. , 2018, , .		0
9	Disruption of Trim9 function abrogates macrophage motility in vivo. Journal of Leukocyte Biology, 2017, 102, 1371-1380.	1.5	8
10	riboStreamR: A web application for quality control, analysis, and visualization of Ribo-seq data. , 2017, , .		0
11	Transcriptomic Signature of the <i>SHATTERPROOF2</i> Expression Domain Reveals the Meristematic Nature of Arabidopsis Cynoecial Medial Domain. Plant Physiology, 2016, 171, 42-61.	2.3	32
12	Genome-Wide Search for Translated Upstream Open Reading Frames in Arabidopsis Thaliana. IEEE Transactions on Nanobioscience, 2016, 15, 148-157.	2.2	16
13	Mining transcript features related to translation in Arabidopsis using LASSO and random forest. , 2015, , .		0
14	Gene-Specific Translation Regulation Mediated by the Hormone-Signaling Molecule EIN2. Cell, 2015, 163, 684-697.	13.5	306
15	Targeted Combinatorial Alternative Splicing Generates Brain Region-Specific Repertoires of Neurexins. Neuron, 2014, 84, 386-398.	3.8	165
16	High-Throughput RNA Sequencing of Pseudomonas-Infected Arabidopsis Reveals Hidden Transcriptome Complexity and Novel Splice Variants. PLoS ONE, 2013, 8, e74183.	1.1	82
17	Improved RNA-Seq Partitions in Linear Models for Isoform Quantification. , 2011, , .		0
18	Workshop: Using a transcript catalog and paired-end RNA-Seq data to identify differential alternative splicing. , 2011, , .		0

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19	Common Intervals of Multiple Permutations. <i>Algorithmica</i> , 2011, 60, 175-206.	1.0	11
20	Towards reliable isoform quantification using RNA-SEQ data. <i>BMC Bioinformatics</i> , 2010, 11, S6.	1.2	32
21	Towards a Systems Approach for Lignin Biosynthesis in <i>Populus trichocarpa</i> : Transcript Abundance and Specificity of the Monoglignol Biosynthetic Genes. <i>Plant and Cell Physiology</i> , 2010, 51, 144-163.	1.5	280
22	Detection of Alternative Splice Variants at the Proteome Level in <i>Aspergillus flavus</i> . <i>Journal of Proteome Research</i> , 2010, 9, 1209-1217.	1.8	29
23	Unsupervised assessment of microarray data quality using a Gaussian mixture model. <i>BMC Bioinformatics</i> , 2009, 10, 191.	1.2	3
24	The deep evolution of metazoan microRNAs. <i>Evolution & Development</i> , 2009, 11, 50-68.	1.1	491
25	Mining of cis-Regulatory Motifs Associated with Tissue-Specific Alternative Splicing. <i>Lecture Notes in Computer Science</i> , 2009, , 260-271.	1.0	3
26	Analysis of Cis-Regulatory Motifs in Cassette Exons by Incorporating Exon Skipping Rates. <i>Lecture Notes in Computer Science</i> , 2009, , 272-283.	1.0	1
27	Practical Quality Assessment of Microarray Data by Simulation of Differential Gene Expression. <i>Lecture Notes in Computer Science</i> , 2009, , 18-27.	1.0	0
28	Non-monotonic dose-response relationship in steroid hormone receptor-mediated gene expression. <i>Journal of Molecular Endocrinology</i> , 2007, 38, 569-585.	1.1	65
29	Correcting Base-Assignment Errors in Repeat Regions of Shotgun Assembly. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 54-64.	1.9	9
30	Quality Assessment of Affymetrix GeneChip Data using the EM Algorithm and a Naive Bayes Classifier. , 2007, , .		1
31	Accessible proteomics space and its implications for peak capacity for zero-, one- and two-dimensional separations coupled with FT-ICR and TOF mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2006, 41, 281-288.	0.7	55
32	Quality Assessment of Affymetrix GeneChip Data. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 358-368.	1.0	88
33	In silico prediction of yeast deletion phenotypes. <i>Genetics and Molecular Research</i> , 2006, 5, 224-32.	0.3	27
34	Common intervals of trees. <i>Information Processing Letters</i> , 2005, 93, 69-74.	0.4	1
35	RACE: Remote Analysis Computation for gene Expression data. <i>Nucleic Acids Research</i> , 2005, 33, W638-W643.	6.5	53
36	The Alternative Splicing Gallery (ASG): bridging the gap between genome and transcriptome. <i>Nucleic Acids Research</i> , 2004, 32, 3977-3983.	6.5	77

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37	Splicing graphs and EST assembly problem. <i>Bioinformatics</i> , 2002, 18, S181-S188.	1.8	172
38	Algorithms for Finding Gene Clusters. <i>Lecture Notes in Computer Science</i> , 2001, , 252-263.	1.0	26
39	Finding All Common Intervals of k Permutations. <i>Lecture Notes in Computer Science</i> , 2001, , 207-218.	1.0	65
40	Contig Selection in Physical Mapping. <i>Journal of Computational Biology</i> , 2000, 7, 395-408.	0.8	2
41	Mapping analysis of the <i>Xylella fastidiosa</i> genome. <i>Nucleic Acids Research</i> , 2000, 28, 3100-3104.	6.5	18
42	Application of Bootstrap Techniques to Physical Mapping. <i>Genomics</i> , 2000, 69, 235-241.	1.3	5
43	Optimization and automation of fluorescence-based DNA hybridization for high-throughput clone mapping. <i>Electrophoresis</i> , 1998, 19, 504-508.	1.3	10