

# Steffen Heber

## List of Publications by Year in descending order

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Version: 2024-02-01

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	The deep evolution of metazoan microRNAs. <i>Evolution &amp; Development</i> , 2009, 11, 50-68.	1.1	491
2	Gene-Specific Translation Regulation Mediated by the Hormone-Signaling Molecule EIN2. <i>Cell</i> , 2015, 163, 684-697.	13.5	306
3	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
4	Splicing graphs and EST assembly problem. <i>Bioinformatics</i> , 2002, 18, S181-S188.	1.8	172
5	Targeted Combinatorial Alternative Splicing Generates Brain Region-Specific Repertoires of Neurexins. <i>Neuron</i> , 2014, 84, 386-398.	3.8	165
6	Quality Assessment of Affymetrix GeneChip Data. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 358-368.	1.0	88
7	High-Throughput RNA Sequencing of <i>Pseudomonas</i> -Infected <i>Arabidopsis</i> Reveals Hidden Transcriptome Complexity and Novel Splice Variants. <i>PLoS ONE</i> , 2013, 8, e74183.	1.1	82
8	The Alternative Splicing Gallery (ASG): bridging the gap between genome and transcriptome. <i>Nucleic Acids Research</i> , 2004, 32, 3977-3983.	6.5	77
9	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
10	Finding All Common Intervals of $k$ Permutations. <i>Lecture Notes in Computer Science</i> , 2001, , 207-218.	1.0	65
11	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
12	RACE: Remote Analysis Computation for gene Expression data. <i>Nucleic Acids Research</i> , 2005, 33, W638-W643.	6.5	53
13	Towards reliable isoform quantification using RNA-SEQ data. <i>BMC Bioinformatics</i> , 2010, 11, S6.	1.2	32
14	Transcriptomic Signature of the <i>SHATTERPROOF2</i> Expression Domain Reveals the Meristematic Nature of <i>Arabidopsis</i> Gynoecial Medial Domain. <i>Plant Physiology</i> , 2016, 171, 42-61.	2.3	32
15	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
16	In silico prediction of yeast deletion phenotypes. <i>Genetics and Molecular Research</i> , 2006, 5, 224-32.	0.3	27
17	Algorithms for Finding Gene Clusters. <i>Lecture Notes in Computer Science</i> , 2001, , 252-263.	1.0	26
18	Mapping analysis of the <i>Xylella fastidiosa</i> genome. <i>Nucleic Acids Research</i> , 2000, 28, 3100-3104.	6.5	18

#	ARTICLE	IF	CITATIONS
19	Genome-Wide Search for Translated Upstream Open Reading Frames in Arabidopsis Thaliana. IEEE Transactions on Nanobioscience, 2016, 15, 148-157.	2.2	16
20	RiboStreamR: a web application for quality control, analysis, and visualization of Ribo-seq data. BMC Genomics, 2019, 20, 422.	1.2	16
21	Common Intervals of Multiple Permutations. Algorithmica, 2011, 60, 175-206.	1.0	11
22	PeakPass: Automating CHIP-Seq Blacklist Creation. Journal of Computational Biology, 2020, 27, 259-268.	0.8	11
23	Optimization and automation of fluorescence-based DNA hybridization for high-throughput clone mapping. Electrophoresis, 1998, 19, 504-508.	1.3	10
24	Correcting Base-Assignment Errors in Repeat Regions of Shotgun Assembly. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 54-64.	1.9	9
25	Identification of Ribosome Pause Sites Using a Z-Score Based Peak Detection Algorithm. , 2018, , .		9
26	Disruption of Trim9 function abrogates macrophage motility in vivo. Journal of Leukocyte Biology, 2017, 102, 1371-1380.	1.5	8
27	Application of Bootstrap Techniques to Physical Mapping. Genomics, 2000, 69, 235-241.	1.3	5
28	Unsupervised assessment of microarray data quality using a Gaussian mixture model. BMC Bioinformatics, 2009, 10, 191.	1.2	3
29	Mining of cis-Regulatory Motifs Associated with Tissue-Specific Alternative Splicing. Lecture Notes in Computer Science, 2009, , 260-271.	1.0	3
30	Contig Selection in Physical Mapping. Journal of Computational Biology, 2000, 7, 395-408.	0.8	2
31	Common intervals of trees. Information Processing Letters, 2005, 93, 69-74.	0.4	1
32	Quality Assessment of Affymetrix GeneChip Data using the EM Algorithm and a Naive Bayes Classifier. , 2007, , .		1
33	Using a Novel Negative Selection Inspired Anomaly Detection Algorithm to Identify Corrupted Ribo-seq and RNA-seq Samples. , 2019, , .		1
34	RiboSimR: A Tool for Simulation and Power Analysis of Ribo-seq Data. Lecture Notes in Computer Science, 2020, , 121-133.	1.0	1
35	Analysis of Cis-Regulatory Motifs in Cassette Exons by Incorporating Exon Skipping Rates. Lecture Notes in Computer Science, 2009, , 272-283.	1.0	1
36	Improved RNA-Seq Partitions in Linear Models for Isoform Quantification. , 2011, , .		0

#	ARTICLE	IF	CITATIONS
37	Workshop: Using a transcript catalog and paired-end RNA-Seq data to identify differential alternative splicing. , 2011, , .		0
38	Mining transcript features related to translation in Arabidopsis using LASSO and random forest. , 2015, , .		0
39	riboStreamR: A web application for quality control, analysis, and visualization of Ribo-seq data. , 2017, , .		0
40	Identifying the Signatures of Missing Transcripts. , 2018, , .		0
41	PeakPass: Automating ChIP-Seq Blacklist Creation. Lecture Notes in Computer Science, 2019, , 232-243.	1.0	0
42	Practical Quality Assessment of Microarray Data by Simulation of Differential Gene Expression. Lecture Notes in Computer Science, 2009, , 18-27.	1.0	0
43	A New Discrete Whale Optimization Algorithm with a Spiral 3-opt Local Search for Solving the Traveling Salesperson Problem. , 2022, , .		0