Jens Allmer

List of Publications by Year
in descending order

75 papers	3,679 citations	394421 19 h-index	138484 58 g-index
80 all docs	80 docs citations	80 times ranked	5308 citing authors

#	Article	IF	Citations
1	Noncoding RNA Databases. Current Pharmaceutical Biotechnology, 2023, 24, 825-831.	1.6	3
2	Ensemble Classifiers for Multiclass MicroRNA Classification. Methods in Molecular Biology, 2022, 2257, 235-254.	0.9	0
3	44 Current Challenges in miRNomics. Methods in Molecular Biology, 2022, 2257, 423-438.	0.9	6
4	Special issue on COVID-19 data integration opportunities and vaccine development strategies. Journal of Integrative Bioinformatics, 2021, 18, 1-2.	1.5	2
5	Novel perspectives for SARS-CoV-2 genome browsing. Journal of Integrative Bioinformatics, 2021, 18, 19-26.	1.5	2
6	Classification of Precursor MicroRNAs from Different Species Based on K-mer Distance Features. Algorithms, 2021, 14, 132.	2.1	0
7	Systems analysis of miRNA biomarkers to inform drug safety. Archives of Toxicology, 2021, 95, 3475-3495.	4.2	14
8	Special Issue of the 1st International Applied Bioinformatics Conference (iABC'21). Journal of Integrative Bioinformatics, 2021, 18, .	1.5	2
9	A Machine Learning-based Approach for the Categorization of MicroRNAs to Their Species of Origin. , 2020, , .		0
10	DNMSO; an ontology for representing de novo sequencing results from Tandem-MS data. PeerJ, 2020, 8, e10216.	2.0	1
11	Classification of Pre-cursor microRNAs from Different Species Using a New Set of Features. Communications in Computer and Information Science, 2019, , 15-20.	0.5	0
12	Towards an Internet of Science. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	3
13	maTE: discovering expressed interactions between microRNAs and their targets. Bioinformatics, 2019, 35, 4020-4028.	4.1	26
14	Computational Prediction of Functional MicroRNA–mRNA Interactions. Methods in Molecular Biology, 2019, 1912, 175-196.	0.9	21
15	Transcriptomic analysis of boron hyperaccumulation mechanisms in Puccinellia distans. Chemosphere, 2018, 199, 390-401.	8.2	17
16	Development of Simple Sequence Repeat Markers in Hazelnut (Corylus avellana L.) by Next-Generation Sequencing and Discrimination of Turkish Hazelnut Cultivars. Plant Molecular Biology Reporter, 2018, 36, 800-811.	1.8	8
17	Visualization and Analysis of miRNAs Implicated in Amyotrophic Lateral Sclerosis Within Gene Regulatory Pathways. Studies in Health Technology and Informatics, 2018, 253, 183-187.	0.3	8
18	AltORFev facilitates the prediction of alternative open reading frames in eukaryotic mRNAs. Bioinformatics, 2017, 33, 923-925.	4.1	9

#	ARTICLE	IF	CITATIONS
19	Newly developed SSR markers reveal genetic diversity and geographical clustering in spinach (Spinacia) Tj ETQq1 1 0.784314 rgBT /Ov	2.1	24
20	Computational miRNomics â€" Integrative Approaches. Journal of Integrative Bioinformatics, 2017, 14, .	1.5	1
21	Visualization and Analysis of MicroRNAs within KEGG Pathways using VANESA. Journal of Integrative Bioinformatics, 2017, 14, .	1.5	11
22	MicroRNA categorization using sequence motifs and k-mers. BMC Bioinformatics, 2017, 18, 170.	2.6	25
23	On the performance of pre-microRNA detection algorithms. Nature Communications, 2017, 8, 330.	12.8	47
24	Improving the Quality of Positive Datasets for the Establishment of Machine Learning Models for pre-microRNA Detection. Journal of Integrative Bioinformatics, 2017, 14, .	1.5	2
25	PGMiner: Complete proteogenomics workflow; from data acquisition to result visualization. Information Sciences, 2017, 384, 126-134.	6.9	3
26	Development of genomic simple sequence repeat markers in faba bean by next-generation sequencing. Plant Molecular Biology Reporter, 2017, 35, 61-71.	1.8	5
27	Categorization of species based on their microRNAs employing sequence motifs, information-theoretic sequence feature extraction, and k-mers. Eurasip Journal on Advances in Signal Processing, 2017, 2017, .	1.7	11
28	The Expressed MicroRNAâ€"mRNA Interactions of Toxoplasma gondii. Frontiers in Microbiology, 2017, 8, 2630.	3.5	10
29	Distinguishing between MicroRNA Targets from Diverse Species using Sequence Motifs and K-mers. , 2017, , .		4
30	Delineating the impact of machine learning elements in pre-microRNA detection. PeerJ, 2017, 5, e3131.	2.0	13
31	PGMiner reloaded, fully automated proteogenomic annotation tool linking genomes to proteomes. Journal of Integrative Bioinformatics, 2016, 13, 16-23.	1.5	3
32	Feature Selection Has a Large Impact on One-Class Classification Accuracy for MicroRNAs in Plants. Advances in Bioinformatics, 2016, 2016, 1-6.	5.7	17
33	One Step Forward, Two Steps Back; Xeno-MicroRNAs Reported in Breast Milk Are Artifacts. PLoS ONE, 2016, 11, e0145065.	2.5	26
34	Computational miRNomics. Journal of Integrative Bioinformatics, 2016, 13, 1-2.	1.5	5
35	A Machine Learning Approach for MicroRNA Precursor Prediction in Retro-transcribing Virus Genomes. Journal of Integrative Bioinformatics, 2016, 13, .	1.5	3
36	Accurate Plant MicroRNA Prediction Can Be Achieved Using Sequence Motif Features. Journal of Intelligent Learning Systems and Applications, 2016, 08, 9-22.	0.5	8

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37	Feature Selection for MicroRNA Target Prediction - Comparison of One-Class Feature Selection Methodologies. , 2016, , .		5
38	The impact of feature selection on one and two-class classification performance for plant microRNAs. PeerJ, 2016, 4, e2135.	2.0	12
39	A Machine Learning Approach for MicroRNA Precursor Prediction in Retro-transcribing Virus Genomes. Journal of Integrative Bioinformatics, 2016, 13, 303.	1.5	5
40	PGMiner reloaded, fully automated proteogenomic annotation tool linking genomes to proteomes. Journal of Integrative Bioinformatics, 2016, 13, 293.	1.5	4
41	Genomic Simple Sequence Repeat Markers Reveal Patterns of Genetic Relatedness and Diversity in Sesame. Plant Genome, 2015, 8, eplantgenome2014.11.0087.	2.8	29
42	Lithium protects against paraquat neurotoxicity by NRF2 activation and miR-34a inhibition in SH-SY5Y cells. Frontiers in Cellular Neuroscience, 2015, 9, 209.	3.7	58
43	Sequence Motif-Based One-Class Classifiers Can Achieve Comparable Accuracy to Two-Class Learners for Plant microRNA Detection. Journal of Biomedical Science and Engineering, 2015, 08, 684-694.	0.4	13
44	Mass Spectrometry Based Proteomics. Acta Endocrinologica, 2015, 11, 139-142.	0.3	0
45	EPO Mediates Neurotrophic, Neuroprotective, Anti-Oxidant, and Anti-Apoptotic Effects via Downregulation of miR-451 and miR-885-5p in SH-SY5Y Neuron-Like Cells. Frontiers in Immunology, 2014, 5, 475.	4.8	46
46	Development of genomic simple sequence repeat markers in opium poppy by next-generation sequencing. Molecular Breeding, 2014, 34, 323-334.	2.1	30
47	Computational Methods for MicroRNA Target Prediction. Methods in Molecular Biology, 2014, 1107, 207-221.	0.9	41
48	miRNomics: MicroRNA Biology and Computational Analysis. Methods in Molecular Biology, 2014, , .	0.9	15
49	Computational Prediction of MicroRNAs from Toxoplasma gondii Potentially Regulating the Hostsâ€™ Gene Expression. Genomics, Proteomics and Bioinformatics, 2014, 12, 228-238.	6.9	38
50	Computational Methods for MicroRNA Target Prediction. Genes, 2014, 5, 671-683.	2.4	92
51	Machine Learning Methods for MicroRNA Gene Prediction. Methods in Molecular Biology, 2014, 1107, 177-187.	0.9	28
52	Computational and Bioinformatics Methods for MicroRNA Gene Prediction. Methods in Molecular Biology, 2014, 1107, 157-175.	0.9	13
53	Intersection of MicroRNA and Gene Regulatory Networks and their Implication in Cancer. Current Pharmaceutical Biotechnology, 2014, 15, 445-454.	1.6	12
54	Development of <scp>EST</scp>â€‹<scp>SSR</scp> markers for diversity and breeding studies in opium poppy. Plant Breeding, 2013, 132, 344-351.	1.9	24

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55	Ranking tandem mass spectra: And the impact of database size and scoring function on peptide spectrum matches. , 2013, , .		1
56	Data mining for microrna gene prediction: On the impact of class imbalance and feature number for microrna gene prediction. , 2013, , .		12
57	Can MiRBase Provide Positive Data for Machine Learning for the Detection of MiRNA Hairpins?. Journal of Integrative Bioinformatics, 2013, 10, 1-11.	1.5	18
58	Determining the C-Terminal Amino Acid of a Peptide from MS/MS Data. Journal of Integrated OMICS, 2013, 3, .	0.5	0
59	Can MiRBase provide positive data for machine learning for the detection of MiRNA hairpins?. Journal of Integrative Bioinformatics, 2013, 10, 215.	1.5	19
60	Comparison of Four Ab Initio MicroRNA Prediction Tools. , 2013, , .		3
61	Computational methods for ab initio detection of microRNAs. Frontiers in Genetics, 2012, 3, 209.	2.3	32
62	Removing contamination from genomic sequences based on vector reference libraries. , 2012, , .		1
63	De novo markup language, a standard to represent de novo sequencing results from MS/MS data. , 2012, , .		0
64	Existing bioinformatics tools for the quantitation of post-translational modifications. Amino Acids, 2012, 42, 129-138.	2.7	13
65	A Call for Benchmark Data in Mass Spectrometry-Based Proteomics. Journal of Integrated OMICS, 2012, 2, .	0.5	9
66	Algorithms for the *de novo* sequencing of peptides from tandem mass spectra. Expert Review of Proteomics, 2011, 8, 645-657.	3.0	100
67	Label-free quantitation, an extension to 2DB. Amino Acids, 2010, 38, 1075-1087.	2.7	4
68	Relative protein quantitation with post translational modifications in mass spectrometry based proteomics. , 2010, , .		0
69	Systematic computational analysis of potential RNAi regulation in Toxoplasma gondii. , 2010, , .		20
70	Computational Systems Biology. Methods in Molecular Biology, 2009, , .	0.9	5
71	2DB: a Proteomics database for storage, analysis, presentation, and retrieval of information from mass spectrometric experiments. BMC Bioinformatics, 2008, 9, 302.	2.6	8
72	Comparative quantitative proteomics to investigate the remodeling of bioenergetic pathways under iron deficiency in *Chlamydomonas reinhardtii*. Proteomics, 2007, 7, 3964-3979.	2.2	168

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73	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. Science, 2007, 318, 245-250.	12.6	2,354
74	Mass spectrometric genomic data mining: Novel insights into bioenergetic pathways inChlamydomonas reinhardtii. Proteomics, 2006, 6, 6207-6220.	2.2	70
75	A new approach that allows identification of intron-split peptides from mass spectrometric data in genomic databases. FEBS Letters, 2004, 562, 202-206.	2.8	20