

# Jens Allmer

## List of Publications by Year in descending order

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Version: 2024-02-01

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	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. <i>Science</i> , 2007, 318, 245-250.	12.6	2,354
2	Comparative quantitative proteomics to investigate the remodeling of bioenergetic pathways under iron deficiency in <i>Chlamydomonas reinhardtii</i> . <i>Proteomics</i> , 2007, 7, 3964-3979.	2.2	168
3	Algorithms for the <i>de novo</i> sequencing of peptides from tandem mass spectra. <i>Expert Review of Proteomics</i> , 2011, 8, 645-657.	3.0	100
4	Computational Methods for MicroRNA Target Prediction. <i>Genes</i> , 2014, 5, 671-683.	2.4	92
5	Mass spectrometric genomic data mining: Novel insights into bioenergetic pathways in <i>Chlamydomonas reinhardtii</i> . <i>Proteomics</i> , 2006, 6, 6207-6220.	2.2	70
6	Lithium protects against paraquat neurotoxicity by NRF2 activation and miR-34a inhibition in SH-SY5Y cells. <i>Frontiers in Cellular Neuroscience</i> , 2015, 9, 209.	3.7	58
7	On the performance of pre-microRNA detection algorithms. <i>Nature Communications</i> , 2017, 8, 330.	12.8	47
8	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. <i>Frontiers in Immunology</i> , 2014, 5, 475.	4.8	46
9	Computational Methods for MicroRNA Target Prediction. <i>Methods in Molecular Biology</i> , 2014, 1107, 207-221.	0.9	41
10	Computational Prediction of MicroRNAs from <i>Toxoplasma gondii</i> Potentially Regulating the Hosts' Gene Expression. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 228-238.	6.9	38
11	Computational methods for ab initio detection of microRNAs. <i>Frontiers in Genetics</i> , 2012, 3, 209.	2.3	32
12	Development of genomic simple sequence repeat markers in opium poppy by next-generation sequencing. <i>Molecular Breeding</i> , 2014, 34, 323-334.	2.1	30
13	Genomic Simple Sequence Repeat Markers Reveal Patterns of Genetic Relatedness and Diversity in Sesame. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.11.0087.	2.8	29
14	Machine Learning Methods for MicroRNA Gene Prediction. <i>Methods in Molecular Biology</i> , 2014, 1107, 177-187.	0.9	28
15	One Step Forward, Two Steps Back; Xeno-MicroRNAs Reported in Breast Milk Are Artifacts. <i>PLoS ONE</i> , 2016, 11, e0145065.	2.5	26
16	maTE: discovering expressed interactions between microRNAs and their targets. <i>Bioinformatics</i> , 2019, 35, 4020-4028.	4.1	26
17	MicroRNA categorization using sequence motifs and k-mers. <i>BMC Bioinformatics</i> , 2017, 18, 170.	2.6	25
18	Development of EST-SSR markers for diversity and breeding studies in opium poppy. <i>Plant Breeding</i> , 2013, 132, 344-351.	1.9	24

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19	Newly developed SSR markers reveal genetic diversity and geographical clustering in spinach ( <i>Spinacia</i> ) Tj ETQq1 1,0,784314,rgBT /Ower	2.1	24
20	Computational Prediction of Functional MicroRNA-mRNA Interactions. <i>Methods in Molecular Biology</i> , 2019, 1912, 175-196.	0.9	21
21	A new approach that allows identification of intron-split peptides from mass spectrometric data in genomic databases. <i>FEBS Letters</i> , 2004, 562, 202-206.	2.8	20
22	Systematic computational analysis of potential RNAi regulation in <i>Toxoplasma gondii</i> . , 2010, , .		20
23	Can MiRBase provide positive data for machine learning for the detection of MiRNA hairpins?. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 215.	1.5	19
24	Can MiRBase Provide Positive Data for Machine Learning for the Detection of MiRNA Hairpins?. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 1-11.	1.5	18
25	Feature Selection Has a Large Impact on One-Class Classification Accuracy for MicroRNAs in Plants. <i>Advances in Bioinformatics</i> , 2016, 2016, 1-6.	5.7	17
26	Transcriptomic analysis of boron hyperaccumulation mechanisms in <i>Puccinellia distans</i> . <i>Chemosphere</i> , 2018, 199, 390-401.	8.2	17
27	miRNomics: MicroRNA Biology and Computational Analysis. <i>Methods in Molecular Biology</i> , 2014, , .	0.9	15
28	Systems analysis of miRNA biomarkers to inform drug safety. <i>Archives of Toxicology</i> , 2021, 95, 3475-3495.	4.2	14
29	Existing bioinformatics tools for the quantitation of post-translational modifications. <i>Amino Acids</i> , 2012, 42, 129-138.	2.7	13
30	Computational and Bioinformatics Methods for MicroRNA Gene Prediction. <i>Methods in Molecular Biology</i> , 2014, 1107, 157-175.	0.9	13
31	Sequence Motif-Based One-Class Classifiers Can Achieve Comparable Accuracy to Two-Class Learners for Plant microRNA Detection. <i>Journal of Biomedical Science and Engineering</i> , 2015, 08, 684-694.	0.4	13
32	Delineating the impact of machine learning elements in pre-microRNA detection. <i>PeerJ</i> , 2017, 5, e3131.	2.0	13
33	Data mining for microrna gene prediction: On the impact of class imbalance and feature number for microrna gene prediction. , 2013, , .		12
34	Intersection of MicroRNA and Gene Regulatory Networks and their Implication in Cancer. <i>Current Pharmaceutical Biotechnology</i> , 2014, 15, 445-454.	1.6	12
35	The impact of feature selection on one and two-class classification performance for plant microRNAs. <i>PeerJ</i> , 2016, 4, e2135.	2.0	12
36	Visualization and Analysis of MicroRNAs within KEGG Pathways using VANESA. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.5	11

#	ARTICLE	IF	CITATIONS
37	Categorization of species based on their microRNAs employing sequence motifs, information-theoretic sequence feature extraction, and k-mers. <i>Eurasip Journal on Advances in Signal Processing</i> , 2017, 2017, .	1.7	11
38	The Expressed MicroRNA-mRNA Interactions of <i>Toxoplasma gondii</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2630.	3.5	10
39	AltORFev facilitates the prediction of alternative open reading frames in eukaryotic mRNAs. <i>Bioinformatics</i> , 2017, 33, 923-925.	4.1	9
40	A Call for Benchmark Data in Mass Spectrometry-Based Proteomics. <i>Journal of Integrated OMICS</i> , 2012, 2, .	0.5	9
41	2DB: a Proteomics database for storage, analysis, presentation, and retrieval of information from mass spectrometric experiments. <i>BMC Bioinformatics</i> , 2008, 9, 302.	2.6	8
42	Development of Simple Sequence Repeat Markers in Hazelnut ( <i>Corylus avellana</i> L.) by Next-Generation Sequencing and Discrimination of Turkish Hazelnut Cultivars. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 800-811.	1.8	8
43	Accurate Plant MicroRNA Prediction Can Be Achieved Using Sequence Motif Features. <i>Journal of Intelligent Learning Systems and Applications</i> , 2016, 08, 9-22.	0.5	8
44	Visualization and Analysis of miRNAs Implicated in Amyotrophic Lateral Sclerosis Within Gene Regulatory Pathways. <i>Studies in Health Technology and Informatics</i> , 2018, 253, 183-187.	0.3	8
45	44 Current Challenges in miRNomics. <i>Methods in Molecular Biology</i> , 2022, 2257, 423-438.	0.9	6
46	Computational Systems Biology. <i>Methods in Molecular Biology</i> , 2009, .	0.9	5
47	Computational miRNomics. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 1-2.	1.5	5
48	Development of genomic simple sequence repeat markers in faba bean by next-generation sequencing. <i>Plant Molecular Biology Reporter</i> , 2017, 35, 61-71.	1.8	5
49	Feature Selection for MicroRNA Target Prediction - Comparison of One-Class Feature Selection Methodologies. , 2016, , .		5
50	A Machine Learning Approach for MicroRNA Precursor Prediction in Retro-transcribing Virus Genomes. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 303.	1.5	5
51	Label-free quantitation, an extension to 2DB. <i>Amino Acids</i> , 2010, 38, 1075-1087.	2.7	4
52	Distinguishing between MicroRNA Targets from Diverse Species using Sequence Motifs and K-mers. , 2017, , .		4
53	PGMiner reloaded, fully automated proteogenomic annotation tool linking genomes to proteomes. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 293.	1.5	4
54	PGMiner reloaded, fully automated proteogenomic annotation tool linking genomes to proteomes. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 16-23.	1.5	3

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55	A Machine Learning Approach for MicroRNA Precursor Prediction in Retro-transcribing Virus Genomes. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, .	1.5	3
56	PGMiner: Complete proteogenomics workflow; from data acquisition to result visualization. <i>Information Sciences</i> , 2017, 384, 126-134.	6.9	3
57	Towards an Internet of Science. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.5	3
58	Comparison of Four Ab Initio MicroRNA Prediction Tools. , 2013, , .		3
59	Noncoding RNA Databases. <i>Current Pharmaceutical Biotechnology</i> , 2023, 24, 825-831.	1.6	3
60	Improving the Quality of Positive Datasets for the Establishment of Machine Learning Models for pre-microRNA Detection. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.5	2
61	Special issue on COVID-19 data integration opportunities and vaccine development strategies. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, 1-2.	1.5	2
62	Novel perspectives for SARS-CoV-2 genome browsing. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, 19-26.	1.5	2
63	Special Issue of the 1st International Applied Bioinformatics Conference (iABC'21). <i>Journal of Integrative Bioinformatics</i> , 2021, 18, .	1.5	2
64	Removing contamination from genomic sequences based on vector reference libraries. , 2012, , .		1
65	Ranking tandem mass spectra: And the impact of database size and scoring function on peptide spectrum matches. , 2013, , .		1
66	Computational miRNomics – Integrative Approaches. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.5	1
67	DNMSO; an ontology for representing de novo sequencing results from Tandem-MS data. <i>PeerJ</i> , 2020, 8, e10216.	2.0	1
68	Relative protein quantitation with post translational modifications in mass spectrometry based proteomics. , 2010, , .		0
69	De novo markup language, a standard to represent de novo sequencing results from MS/MS data. , 2012, , .		0
70	Determining the C-Terminal Amino Acid of a Peptide from MS/MS Data. <i>Journal of Integrated OMICS</i> , 2013, 3, .	0.5	0
71	Classification of Pre-cursor microRNAs from Different Species Using a New Set of Features. <i>Communications in Computer and Information Science</i> , 2019, , 15-20.	0.5	0
72	Classification of Precursor MicroRNAs from Different Species Based on K-mer Distance Features. <i>Algorithms</i> , 2021, 14, 132.	2.1	0

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73	Ensemble Classifiers for Multiclass MicroRNA Classification. <i>Methods in Molecular Biology</i> , 2022, 2257, 235-254.	0.9	0
74	Mass Spectrometry Based Proteomics. <i>Acta Endocrinologica</i> , 2015, 11, 139-142.	0.3	0
75	A Machine Learning-based Approach for the Categorization of MicroRNAs to Their Species of Origin. , 2020, , .		0