

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Rapid protein evolution, organellar reductions, and invasive intronic elements in the marine aerobic parasite dinoflagellate <i>Amoebophrya</i> spp. <i>BMC Biology</i> , 2021, 19, 1.	3.8	135
2	Complex Evolutionary Dynamics of Massively Expanded Chemosensory Receptor Families in an Extreme Generalist Chelicerate Herbivore. <i>Genome Biology and Evolution</i> , 2016, 8, 3323-3339.	2.5	42
3	The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. <i>Nature</i> , 2016, 530, 331-335.	27.8	460
4	The Complex Intron Landscape and Massive Intron Invasion in a Picoeukaryote Provides Insights into Intron Evolution. <i>Genome Biology and Evolution</i> , 2013, 5, 2393-2401.	2.5	28
5	Orthology-guided assembly in highly heterozygous crops: creating a reference transcriptome to uncover genetic diversity in <i>Lotus perenne</i> . <i>Plant Biotechnology Journal</i> , 2013, 11, 605-617.	8.3	23
6	A Comprehensive Analysis of Genes Encoding Small Secreted Proteins Identifies Candidate Effectors in <i>Melampsora larici-populina</i> (Poplar Leaf Rust). <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 279-293.	2.6	150
7	Gene functionalities and genome structure in <i>Bathycoccus prasinos</i> reflect cellular specializations at the base of the green lineage. <i>Genome Biology</i> , 2012, 13, R74.	9.6	143
8	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. <i>New Phytologist</i> , 2012, 194, 1001-1013.	7.3	210
9	The <i>Ectocarpus</i> Genome and Brown Algal Genomics. <i>Advances in Botanical Research</i> , 2012, 64, 141-184.	1.1	18
10	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9166-9171.	7.1	640
11	The genome of <i>Tetranychus urticae</i> reveals herbivorous pest adaptations. <i>Nature</i> , 2011, 479, 487-492.	27.8	897
12	The <i>Ectocarpus</i> genome and the independent evolution of multicellularity in brown algae. <i>Nature</i> , 2010, 465, 617-621.	27.8	774
13	The genome of the domesticated apple (<i>Malus domestica</i> Borkh.). <i>Nature Genetics</i> , 2010, 42, 833-839.	21.4	1,891
14	Genome sequence of the recombinant protein production host <i>Pichia pastoris</i> . <i>Nature Biotechnology</i> , 2009, 27, 561-566.	17.5	422
15	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 2009, 324, 268-272.	12.6	591
16	Open access to sequence: Browsing the <i>Pichia pastoris</i> genome. <i>Microbial Cell Factories</i> , 2009, 8, 53.	4.0	55
17	Global expression analysis of the brown alga <i>Ectocarpus siliculosus</i> (Phaeophyceae) reveals large-scale reprogramming of the transcriptome in response to abiotic stress. <i>Genome Biology</i> , 2009, 10, R66.	9.6	138
18	Generic eukaryotic core promoter prediction using structural features of DNA. <i>Genome Research</i> , 2008, 18, 310-323.	5.5	181

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19	Genome Annotation in Plants and Fungi: EuGene as a Model Platform. <i>Current Bioinformatics</i> , 2008, 3, 87-97.	1.5	102
20	The tiny eukaryote <i>Ostreococcus</i> provides genomic insights into the paradox of plankton speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7705-7710.	7.1	563
21	In search of the small ones: improved prediction of short exons in vertebrates, plants, fungi and protists. <i>Bioinformatics</i> , 2007, 23, 414-420.	4.1	40
22	Unique Regulation of the Calvin Cycle in the Ultrasmall Green Alga <i>Ostreococcus</i> . <i>Journal of Molecular Evolution</i> , 2007, 64, 601-604.	1.8	21
23	Genome analysis of the smallest free-living eukaryote <i>Ostreococcus tauri</i> unveils many unique features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11647-11652.	7.1	809
24	The small RNA world of plants. <i>New Phytologist</i> , 2006, 171, 451-468.	7.3	136
25	SpliceMachine: predicting splice sites from high-dimensional local context representations. <i>Bioinformatics</i> , 2005, 21, 1332-1338.	4.1	92
26	GeneFarm, structural and functional annotation of <i>Arabidopsis</i> gene and protein families by a network of experts. <i>Nucleic Acids Research</i> , 2004, 33, D641-D646.	14.5	16
27	Versatile Gene-Specific Sequence Tags for <i>Arabidopsis</i> Functional Genomics: Transcript Profiling and Reverse Genetics Applications. <i>Genome Research</i> , 2004, 14, 2176-2189.	5.5	282
28	Feature selection for splice site prediction: a new method using EDA-based feature ranking. <i>BMC Bioinformatics</i> , 2004, 5, 64.	2.6	49
29	Detection of 91 potential conserved plant microRNAs in <i>Arabidopsis thaliana</i> and <i>Oryza sativa</i> identifies important target genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11511-11516.	7.1	427
30	Automatic design of gene-specific sequence tags for genome-wide functional studies. <i>Bioinformatics</i> , 2003, 19, 2191-2198.	4.1	44
31	CATMA: a complete <i>Arabidopsis</i> GST database. <i>Nucleic Acids Research</i> , 2003, 31, 156-158.	14.5	133
32	Computational Approaches to Identify Promoters and cis-Regulatory Elements in Plant Genomes. <i>Plant Physiology</i> , 2003, 132, 1162-1176.	4.8	158
33	Current methods of gene prediction, their strengths and weaknesses. <i>Nucleic Acids Research</i> , 2002, 30, 4103-4117.	14.5	374
34	Genome-Wide Analysis of Core Cell Cycle Genes in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2002, 14, 903-916.	6.6	523
35	INCLUSive: INtegrated Clustering, Upstream sequence retrieval and motif Sampling. <i>Bioinformatics</i> , 2002, 18, 331-332.	4.1	78
36	PlantCARE, a database of plant cis-acting regulatory elements and a portal to tools for in silico analysis of promoter sequences. <i>Nucleic Acids Research</i> , 2002, 30, 325-327.	14.5	4,875

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37	A Gibbs Sampling Method to Detect Overrepresented Motifs in the Upstream Regions of Coexpressed Genes. <i>Journal of Computational Biology</i> , 2002, 9, 447-464.	1.6	301
38	Eugène: An Eukaryotic Gene Finder That Combines Several Sources of Evidence. <i>Lecture Notes in Computer Science</i> , 2001, , 111-125.	1.3	55
39	Gene prediction and gene classes in <i>Arabidopsis thaliana</i> . <i>Journal of Biotechnology</i> , 2000, 78, 293-299.	3.8	13
40	Genome annotation: which tools do we have for it?. <i>Current Opinion in Plant Biology</i> , 1999, 2, 90-95.	7.1	45
41	Classification of <i>Arabidopsis thaliana</i> gene sequences: clustering of coding sequences into two groups according to codon usage improves gene prediction 1 Edited by G. Von Heijne. <i>Journal of Molecular Biology</i> , 1999, 285, 1977-1991.	4.2	36
42	Plant cyclins: a unified nomenclature for plant A-, B- and D-type cyclins based on sequence organization. <i>Plant Molecular Biology</i> , 1996, 32, 1003-1018.	3.9	232