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List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

4,135
citations

218677

26
h-index

345221

36
g-index

38
all docs

38
docs citations

38
times ranked

4891
citing authors

#	ARTICLE	IF	CITATIONS
1	Towards a deeper haplotype mining of complex traits in rice with <sc>RFGB</sc> v2.0. Plant Biotechnology Journal, 2020, 18, 14-16.	8.3	78
2	Predicting rice phenotypes with meta and multi-target learning. Machine Learning, 2020, 109, 2195-2212.	5.4	3
3	A platinum standard pan-genome resource that represents the population structure of Asian rice. Scientific Data, 2020, 7, 113.	5.3	86
4	Rice Galaxy: an open resource for plant science. GigaScience, 2019, 8, .	6.4	11
5	Structural variants in 3000 rice genomes. Genome Research, 2019, 29, 870-880.	5.5	112
6	Shared cis-regulatory architecture identified across defense response genes is associated with broad-spectrum quantitative resistance in rice. Scientific Reports, 2019, 9, 1536.	3.3	6
7	Progress in single-access information systems for wheat and rice crop improvement. Briefings in Bioinformatics, 2019, 20, 565-571.	6.5	4
8	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. Nature, 2018, 557, 43-49.	27.8	1,091
9	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus Oryza. Nature Genetics, 2018, 50, 285-296.	21.4	413
10	Predicting Rice Phenotypes with Meta-learning. Lecture Notes in Computer Science, 2018, , 144-158.	1.3	2
11	An imputation platform to enhance integration of rice genetic resources. Nature Communications, 2018, 9, 3519.	12.8	65
12	Whole genome sequencing-based association study to unravel genetic architecture of cooked grain width and length traits in rice. Scientific Reports, 2017, 7, 12478.	3.3	69
13	Rice SNP-seek database update: new SNPs, indels, and queries. Nucleic Acids Research, 2017, 45, D1075-D1081.	14.5	290
14	SNP-Seek II: A resource for allele mining and analysis of big genomic data in Oryza sativa. Current Plant Biology, 2016, 7-8, 16-25.	4.7	48
15	Nucleotide diversity analysis highlights functionally important genomic regions. Scientific Reports, 2016, 6, 35730.	3.3	48
16	SNP-Seek database of SNPs derived from 3000 rice genomes. Nucleic Acids Research, 2015, 43, D1023-D1027.	14.5	357
17	Allele mining and enhanced genetic recombination for rice breeding. Rice, 2015, 8, 34.	4.0	57
18	High Resolution Genetic Mapping by Genome Sequencing Reveals Genome Duplication and Tetraploid Genetic Structure of the Diploid Miscanthus sinensis. PLoS ONE, 2012, 7, e33821.	2.5	103

#	ARTICLE	IF	CITATIONS
19	GC3 biology in corn, rice, sorghum and other grasses. BMC Genomics, 2010, 11, 308.	2.8	116
20	Genome-Wide Discovery of <i>cis</i> -Elements in Promoter Sequences Using Gene Expression. OMICS A Journal of Integrative Biology, 2009, 13, 139-151.	2.0	32
21	Insights into corn genes derived from large-scale cDNA sequencing. Plant Molecular Biology, 2009, 69, 179-194.	3.9	212
22	Features of Arabidopsis Genes and Genome Discovered using Full-length cDNAs. Plant Molecular Biology, 2006, 60, 69-85.	3.9	145
23	Toward Consistent Assignment of Structural Domains in Proteins. Journal of Molecular Biology, 2004, 339, 647-678.	4.2	63
24	A comparative proteomics resource: proteins of Arabidopsis thaliana. Genome Biology, 2003, 4, R51.	9.6	25
25	Skew in CG content near the transcription start site in Arabidopsis thaliana. Bioinformatics, 2003, 19, i313-i314.	4.1	32
26	PDP: protein domain parser. Bioinformatics, 2003, 19, 429-430.	4.1	152
27	Full-length messenger RNA sequences greatly improve genome annotation. Genome Biology, 2002, 3, research0029.1.	9.6	147
28	Analysis of topological and nontopological structural similarities in the PDB: New examples with old structures. Proteins: Structure, Function and Bioinformatics, 1996, 25, 354-365.	2.6	49
29	SARFing the PDB. Protein Engineering, Design and Selection, 1996, 9, 727-732.	2.1	76
30	Biological meaning, statistical significance, and classification of local spatial similarities in nonhomologous proteins. Protein Science, 1994, 3, 866-875.	7.6	68
31	Nucleotide binding in β -sheet topologies. Nature Structural and Molecular Biology, 1994, 1, 677-678.	8.2	4
32	Structural argument for N-terminal initiation of protein folding. Protein Science, 1993, 2, 1989-1991.	7.6	27
33	Local multiple alignment by consensus matrix. Bioinformatics, 1992, 8, 339-345.	4.1	1
34	Common spatial arrangements of backbone fragments in homologous and non-homologous proteins. Journal of Molecular Biology, 1992, 225, 5-9.	4.2	102
35	Application of a new method of pattern recognition in DNA sequence analysis: a study of E.coli promoters. Nucleic Acids Research, 1990, 18, 1847-1852.	14.5	22
36	Statistical method for rapid homology search. Nucleic Acids Research, 1988, 16, 5169-5173.	14.5	17