

Changhui Yan

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

360
citations

1040056

9
h-index

888059

17
g-index

27
all docs

27
docs citations

27
times ranked

602
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluation of a <i>Pyrenophora teres</i> f. <i>teres</i> mapping population reveals multiple independent interactions with a region of barley chromosome 6H. <i>Fungal Genetics and Biology</i> , 2014, 70, 104-112.	2.1	53
2	Dbf4 recruitment by forkhead transcription factors defines an upstream rate-limiting step in determining origin firing timing. <i>Genes and Development</i> , 2017, 31, 2405-2415.	5.9	53
3	RNA-seq reveals weed-induced PIF-like as a candidate target to manipulate weed stress response in soybean. <i>New Phytologist</i> , 2015, 207, 196-210.	7.3	40
4	Genotype-by-sequencing of the plant-pathogenic fungi <i>Pyrenophora teres</i> and <i>Sphaerulina musiva</i> utilizing long-read sequencing technology. <i>Molecular Plant Pathology</i> , 2015, 16, 623-632.	4.2	36
5	Deep BBN Learning for Health Assessment toward Decision-Making on Structures under Uncertainties. <i>KSCE Journal of Civil Engineering</i> , 2018, 22, 928-940.	1.9	28
6	Molecular cytogenetic and genomic analyses reveal new insights into the origin of the wheat B genome. <i>Theoretical and Applied Genetics</i> , 2018, 131, 365-375.	3.6	28
7	An Analysis of Reentrant Loops. <i>Protein Journal</i> , 2010, 29, 350-354.	1.6	26
8	Knockdown of delta-5-desaturase promotes the anti-cancer activity of dihomo- γ -linolenic acid and enhances the efficacy of chemotherapy in colon cancer cells expressing COX-2. <i>Free Radical Biology and Medicine</i> , 2016, 96, 67-77.	2.9	26
9	RNA-Seq Revealed Differences in Transcriptomes between 3ADON and 15ADON Populations of <i>Fusarium graminearum</i> In Vitro and In Planta. <i>PLoS ONE</i> , 2016, 11, e0163803.	2.5	25
10	Gene Space and Transcriptome Assemblies of Leafy Spurge (<i>Euphorbia esula</i>) Identify Promoter Sequences, Repetitive Elements, High-Quality Markers, and a Full-Length Chloroplast Genome. <i>Weed Science</i> , 2018, 66, 355-367.	1.5	11
11	A genome-wide genetic linkage map and reference quality genome sequence for a new race in the wheat pathogen <i>Pyrenophora tritici-repentis</i> . <i>Fungal Genetics and Biology</i> , 2021, 152, 103571.	2.1	8
12	Dissection and physical mapping of wheat chromosome 7B by inducing meiotic recombination with its homoeologues in <i>Aegilops speltoides</i> and <i>Thinopyrum elongatum</i> . <i>Theoretical and Applied Genetics</i> , 2020, 133, 3455-3467.	3.6	6
13	A Graph Approach to Mining Biological Patterns in the Binding Interfaces. <i>Journal of Computational Biology</i> , 2017, 24, 31-39.	1.6	4
14	Partitioning and physical mapping of wheat chromosome 3B and its homoeologue 3E in <i>Thinopyrum elongatum</i> by inducing homoeologous recombination. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1277-1289.	3.6	4
15	Mining graph patterns in the protein-RNA interfaces. , 2015, , .		3
16	Genome sequence and analysis of <i>Mycobacterium tuberculosis</i> strain SWLPK. <i>Journal of Global Antimicrobial Resistance</i> , 2018, 13, 211-213.	2.2	3
17	An enrichment method for mapping ambiguous reads to the reference genome for NGS analysis. <i>Journal of Bioinformatics and Computational Biology</i> , 2019, 17, 1940012.	0.8	2
18	Exploring structural modeling of proteins for kernel-based enzyme discrimination. , 2010, , .		1

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19	Prediction of enzyme catalytic sites on protein using a graph kernel method. , 2013, , .		1
20	Graph methods for predicting the function of chemical compounds. , 2014, , .		1
21	Impacts of reference selection on the assembly of suspicious coronavirus genome. Journal of Bioinformatics and Computational Biology, 2021, 19, 2140005.	0.8	1
22	A Comparison between Transmembrane Helices and Reentrant Loops. , 2010, , .		0
23	A nearest neighbor method for predicting solenoid proteins. , 2012, , .		0
24	A method for discriminating native protein-DNA complexes from decoys using spatial specific scoring matrices. , 2013, , .		0
25	Mining structure patterns on the protein-DNA interfaces. , 2016, , .		0
26	An Efficient Method for Discovering Functionally Important Motifs in a Group of Protein Structures. , 2018, , .		0
27	A Concurrent Neural Network (CNN) Method for RNA-binding Site Prediction. , 2019, , .		0