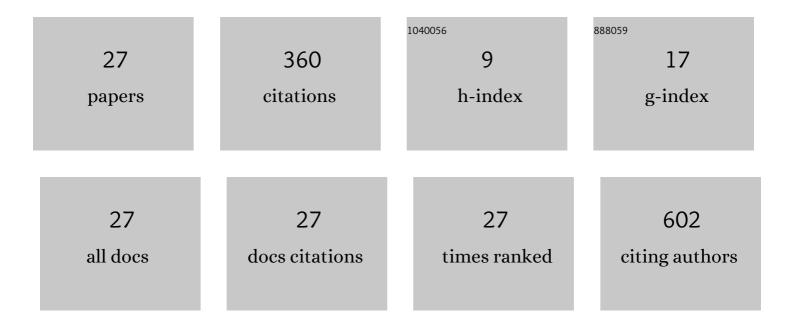
Changhui Yan

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8640535/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Impacts of reference selection on the assembly of suspicious coronavirus genome. Journal of Bioinformatics and Computational Biology, 2021, 19, 2140005.	0.8	1
2	A genome-wide genetic linkage map and reference quality genome sequence for a new race in the wheat pathogen Pyrenophora tritici-repentis. Fungal Genetics and Biology, 2021, 152, 103571.	2.1	8
3	Dissection and physical mapping of wheat chromosome 7B by inducing meiotic recombination with its homoeologues in Aegilops speltoides and Thinopyrum elongatum. Theoretical and Applied Genetics, 2020, 133, 3455-3467.	3.6	6
4	Partitioning and physical mapping of wheat chromosome 3B and its homoeologue 3E in Thinopyrum elongatum by inducing homoeologous recombination. Theoretical and Applied Genetics, 2020, 133, 1277-1289.	3.6	4
5	A Concurrent Neural Network (CNN) Method for RNA-binding Site Prediction. , 2019, , .		0
6	An enrichment method for mapping ambiguous reads to the reference genome for NGS analysis. Journal of Bioinformatics and Computational Biology, 2019, 17, 1940012.	0.8	2
7	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. Weed Science, 2018, 66, 355-367.	1.5	11
8	Deep BBN Learning for Health Assessment toward Decision-Making on Structures under Uncertainties. KSCE Journal of Civil Engineering, 2018, 22, 928-940.	1.9	28
9	Molecular cytogenetic and genomic analyses reveal new insights into the origin of the wheat B genome. Theoretical and Applied Genetics, 2018, 131, 365-375.	3.6	28
10	An Efficient Method for Discovering Functionally Important Motifs in a Group of Protein Structures. , 2018, , .		0
11	Genome sequence and analysis of Mycobacterium tuberculosis strain SWLPK. Journal of Global Antimicrobial Resistance, 2018, 13, 211-213.	2.2	3
12	A Graph Approach to Mining Biological Patterns in the Binding Interfaces. Journal of Computational Biology, 2017, 24, 31-39.	1.6	4
13	Dbf4 recruitment by forkhead transcription factors defines an upstream rate-limiting step in determining origin firing timing. Genes and Development, 2017, 31, 2405-2415.	5.9	53
14	Mining structure patterns on the protein-DNA interfaces. , 2016, , .		0
15	Knockdown of delta-5-desaturase promotes the anti-cancer activity of dihomo-Î ³ -linolenic acid and enhances the efficacy of chemotherapy in colon cancer cells expressing COX-2. Free Radical Biology and Medicine, 2016, 96, 67-77.	2.9	26
16	RNA-Seq Revealed Differences in Transcriptomes between 3ADON and 15ADON Populations of Fusarium graminearum In Vitro and In Planta. PLoS ONE, 2016, 11, e0163803.	2.5	25
17	Mining graph patterns in the protein-RNA interfaces. , 2015, , .		3
18	Genotypeâ€byâ€sequencing of the plantâ€pathogenic fungi <i><scp>P</scp>yrenophora teres</i> and <i><scp>S</scp>phaerulina musiva</i> utilizing <scp>I</scp> on <scp>T</scp> orrent sequence technology. Molecular Plant Pathology, 2015, 16, 623-632.	4.2	36

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#	Article	IF	CITATIONS
19	<scp>RNA</scp> seq reveals weedâ€induced <scp>PIF</scp> 3â€like as a candidate target to manipulate weed stress response in soybean. New Phytologist, 2015, 207, 196-210.	7.3	40
20	Graph methods for predicting the function of chemical compounds. , 2014, , .		1
21	Evaluation of a Pyrenophora teres f. teres mapping population reveals multiple independent interactions with a region of barley chromosome 6H. Fungal Genetics and Biology, 2014, 70, 104-112.	2.1	53
22	Prediction of enzyme catalytic sites on protein using a graph kernel method. , 2013, , .		1
23	A method for discriminating native protein-DNA complexes from decoys using spatial specific scoring matrices. , 2013, , .		0
24	A nearest neighbor method for predicting solenoid proteins. , 2012, , .		0
25	An Analysis of Reentrant Loops. Protein Journal, 2010, 29, 350-354.	1.6	26
26	A Comparison between Transmembrane Helices and Reentrant Loops. , 2010, , .		0
27	Exploring structural modeling of proteins for kernel-based enzyme discrimination. , 2010, , .		1