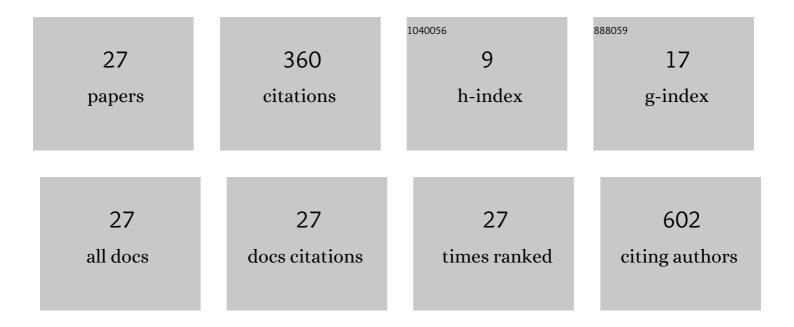
Changhui Yan

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 |

Changhui Yan

| # | 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 |