

Likun Wang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2841905/publications.pdf>

Version: 2024-02-01

13
papers

4,111
citations

933447

10
h-index

1125743

13
g-index

13
all docs

13
docs citations

13
times ranked

6805
citing authors

#	ARTICLE	IF	CITATIONS
1	SGII: Systematic Identification of Essential lncRNAs in Mouse and Human Genome With lncRNA-Protein-Protein Heterogeneous Interaction Network. <i>Frontiers in Genetics</i> , 2022, 13, 864564.	2.3	4
2	XGEM: Predicting Essential miRNAs by the Ensembles of Various Sequence-Based Classifiers With XGBoost Algorithm. <i>Frontiers in Genetics</i> , 2022, 13, 877409.	2.3	6
3	Application of Whole Exome and Targeted Panel Sequencing in the Clinical Molecular Diagnosis of 319 Chinese Families with Inherited Retinal Dystrophy and Comparison Study. <i>Genes</i> , 2018, 9, 360.	2.4	47
4	A Brief Review on Software Tools in Generating Chou's Pseudo-factor Representations for All Types of Biological Sequences. <i>Protein and Peptide Letters</i> , 2018, 25, 822-829.	0.9	33
5	Systematic analysis of gene expression patterns associated with postmortem interval in human tissues. <i>Scientific Reports</i> , 2017, 7, 5435.	3.3	80
6	UltraPse: A Universal and Extensible Software Platform for Representing Biological Sequences. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2400.	4.1	16
7	SoftPanel: a website for grouping diseases and related disorders for generation of customized panels. <i>BMC Bioinformatics</i> , 2016, 17, 153.	2.6	4
8	A mutation in ADIPOR1 causes nonsyndromic autosomal dominant retinitis pigmentosa. <i>Human Genetics</i> , 2016, 135, 1375-1387.	3.8	44
9	cisPath: an R/Bioconductor package for cloud users for visualization and management of functional protein interaction networks. <i>BMC Systems Biology</i> , 2015, 9, S1.	3.0	12
10	Characterization and Prediction of Lysine (K)-Acetyl-Transferase Specific Acetylation Sites. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.011080.	3.8	49
11	ASEB: a web server for KAT-specific acetylation site prediction. <i>Nucleic Acids Research</i> , 2012, 40, W376-W379.	14.5	72
12	Observations on novel splice junctions from RNA sequencing data. <i>Biochemical and Biophysical Research Communications</i> , 2011, 409, 299-303.	2.1	16
13	DEGseq: an R package for identifying differentially expressed genes from RNA-seq data. <i>Bioinformatics</i> , 2010, 26, 136-138.	4.1	3,728