

Chih-Hao Lu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6397656/publications.pdf>

Version: 2024-02-01

14
papers

2,105
citations

1039406

9
h-index

1058022

14
g-index

14
all docs

14
docs citations

14
times ranked

3219
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting Anticancer Drug Resistance Mediated by Mutations. <i>Pharmaceuticals</i> , 2022, 15, 136.	1.7	4
2	Recognition of a Novel Gene Signature for Human Glioblastoma. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4157.	1.8	8
3	The structure-based cancer-related single amino acid variation prediction. <i>Scientific Reports</i> , 2021, 11, 13599.	1.6	10
4	Impact Assessment of heavy metal cations to the characteristics of photosynthetic phycocyanin. <i>Journal of Hazardous Materials</i> , 2020, 391, 122225.	6.5	20
5	Understanding the functional properties of bio-inorganic nanoflowers as biocatalysts by deciphering the metal-binding sites of enzymes. <i>Journal of Materials Chemistry B</i> , 2017, 5, 4478-4486.	2.9	55
6	MIB: Metal Ion-Binding Site Prediction and Docking Server. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 2287-2291.	2.5	185
7	Predicting Flavin and Nicotinamide Adenine Dinucleotide-Binding Sites in Proteins Using the Fragment Transformation Method. <i>BioMed Research International</i> , 2015, 2015, 1-13.	0.9	4
8	EXIA2: Web Server of Accurate and Rapid Protein Catalytic Residue Prediction. <i>BioMed Research International</i> , 2014, 2014, 1-12.	0.9	6
9	CELLO2GO: A Web Server for Protein subCELLular LOcalization Prediction with Functional Gene Ontology Annotation. <i>PLoS ONE</i> , 2014, 9, e99368.	1.1	357
10	Identification of Antifreeze Proteins and Their Functional Residues by Support Vector Machine and Genetic Algorithms based on n-Peptide Compositions. <i>PLoS ONE</i> , 2011, 6, e20445.	1.1	30
11	Deriving protein dynamical properties from weighted protein contact number. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 929-935.	1.5	72
12	Predicting disulfide connectivity patterns. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 262-270.	1.5	23
13	The fragment transformation method to detect the protein structural motifs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 636-643.	1.5	17
14	Prediction of protein subcellular localization. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 643-651.	1.5	1,314