

Yanrui Ding

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1621033/publications.pdf>

Version: 2024-02-01

25
papers

206
citations

1040056

9
h-index

1058476

14
g-index

25
all docs

25
docs citations

25
times ranked

316
citing authors

#	ARTICLE	IF	CITATIONS
1	Human skeleton representation for 3D action recognition based on complex network coding and LSTM. <i>Journal of Visual Communication and Image Representation</i> , 2022, 82, 103386.	2.8	13
2	Identification of Anticancer and Anti-inflammatory Drugs from Drugtarget Interaction Descriptors by Machine Learning. <i>Letters in Drug Design and Discovery</i> , 2022, 19, 800-810.	0.7	0
3	Teaching Model Design of Computer Programming Courses for Digital Media Technology Students. <i>Wireless Communications and Mobile Computing</i> , 2022, 2022, 1-5.	1.2	0
4	A 70â€œRNA model based on SVR and RFE for predicting the pancreatic cancer clinical prognosis. <i>Methods</i> , 2022, 204, 278-285.	3.8	4
5	Probing the Relation Between Community Evolution in Dynamic Residue Interaction Networks and Xylanase Thermostability. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 686-696.	3.0	1
6	Identification of Key Features of CNS Drugs Based on SVM and Greedy Algorithm. <i>Current Computer-Aided Drug Design</i> , 2021, 16, 725-733.	1.2	4
7	ACHP: A Web Server for Predicting Anti-Cancer Peptide and Anti-Hypertensive Peptide. <i>International Journal of Peptide Research and Therapeutics</i> , 2021, 27, 1933-1944.	1.9	9
8	Community evolution and frequent subgraph patterns affect the thermostability of B. subtilis lipase A. <i>Food Bioscience</i> , 2021, 41, 100984.	4.4	0
9	Identification of subtype specific biomarkers of clear cell renal cell carcinoma using random forest and greedy algorithm. <i>BioSystems</i> , 2021, 204, 104372.	2.0	5
10	Dissecting the critical pathway crosstalk mechanisms of thyroid cancer based on drug-target genes and disease genes. <i>Biologia (Poland)</i> , 2021, 76, 3489-3499.	1.5	1
11	Determination of the key ccRCC-related molecules from monolayer network to three-layer network. <i>Cancer Genetics</i> , 2021, 256-257, 40-47.	0.4	2
12	The Quantitative Structure-Activity Relationships between GABAA Receptor and Ligands based on Binding Interface Characteristic. <i>Current Computer-Aided Drug Design</i> , 2021, 17, 785-796.	1.2	1
13	Identification of the complex regulatory relationships related to gastric cancer from lncRNAâ€œmiRNAâ€œmRNA network. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 876-887.	2.6	32
14	T-DYNMOGA-Qw: Detecting Community From Dynamic Residue Interaction Energy Network and Its Application in Analyzing Lipase Thermostability. <i>IEEE Access</i> , 2020, 8, 89439-89447.	4.2	0
15	Polygala tenuifolia-Acori tatarinowii herbal pair as an inspiration for substituted cinnamic Î±-asaronol esters: Design, synthesis, anticonvulsant activity, and inhibition of lactate dehydrogenase study. <i>European Journal of Medicinal Chemistry</i> , 2019, 183, 111650.	5.5	17
16	Thermostability of Lipase A and Dynamic Communication Based on Residue Interaction Network. <i>Protein and Peptide Letters</i> , 2019, 26, 702-716.	0.9	4
17	Identification of the Key Factors Related to Bladder Cancer by lncRNA-miRNA-mRNA Three-Layer Network. <i>Frontiers in Genetics</i> , 2019, 10, 1398.	2.3	15
18	The Thermo Stability of Lipase: Salt Bridge and Salt Bridge Network Perspective Based on Long Time Molecular Dynamics Simulation. , 2017, , .		0

#	ARTICLE	IF	CITATIONS
19	The Relation Between Lipase Thermostability and Dynamics of Hydrogen Bond and Hydrogen Bond Network Based on Long Time Molecular Dynamics Simulation. <i>Protein and Peptide Letters</i> , 2017, 24, 643-648.	0.9	7
20	Communities in the iron superoxide dismutase amino acid network. <i>Journal of Theoretical Biology</i> , 2015, 367, 278-285.	1.7	0
21	Comparison of Protein-water Interactions in Psychrophilic, Mesophilic, and Thermophilic Fe-SOD. <i>Protein and Peptide Letters</i> , 2014, 21, 578-583.	0.9	10
22	Conformational dynamics of xylanase a from <i>Streptomyces lividans</i> : Implications for TIM β -barrel enzyme thermostability. <i>Biopolymers</i> , 2013, 99, 594-604.	2.4	13
23	Application of principal component analysis to determine the key structural features contributing to iron superoxide dismutase thermostability. <i>Biopolymers</i> , 2012, 97, 864-872.	2.4	11
24	Comparison of the structural basis for thermal stability between archaeal and bacterial proteins. <i>Extremophiles</i> , 2012, 16, 67-78.	2.3	12
25	The influence of dipeptide composition on protein thermostability. <i>FEBS Letters</i> , 2004, 569, 284-288.	2.8	45