

Anisah W Ghoorah

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

755
citations

1307594

7
h-index

1125743

13
g-index

16
all docs

16
docs citations

16
times ranked

1488
citing authors

#	ARTICLE	IF	CITATIONS
1	African Genomic Medicine Portal: A Web Portal for Biomedical Applications. <i>Journal of Personalized Medicine</i> , 2022, 12, 265.	2.5	0
2	TAGOPSIN: collating taxa-specific gene and protein functional and structural information. <i>BMC Bioinformatics</i> , 2021, 22, 517.	2.6	0
3	Population Structure of the South West Indian Ocean Islands: Implications for Precision Medicine. <i>Frontiers in Genetics</i> , 2021, 12, 758563.	2.3	1
4	High-depth African genomes inform human migration and health. <i>Nature</i> , 2020, 586, 741-748.	27.8	197
5	Discovering novel driver mutations from pan-cancer analysis of mutational and gene expression profiles. <i>PLoS ONE</i> , 2020, 15, e0242780.	2.5	6
6	Modeling and minimizing CAPRI round 30 symmetrical protein complexes from CASPâ€11 structural models. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 463-469.	2.6	2
7	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 323-348.	2.6	148
8	Classification and Exploration of 3D Protein Domain Interactions Using Kbdock. <i>Methods in Molecular Biology</i> , 2016, 1415, 91-105.	0.9	4
9	A Structure-Based Classification and Analysis of Protein Domain Family Binding Sites and Their Interactions. <i>Biology</i> , 2015, 4, 327-343.	2.8	5
10	KBDOCK 2013: a spatial classification of 3D protein domain family interactions. <i>Nucleic Acids Research</i> , 2014, 42, D389-D395.	14.5	31
11	Protein docking using caseâ€based reasoning. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2150-2158.	2.6	98
12	Fast protein structure alignment using Gaussian overlap scoring of backbone peptide fragment similarity. <i>Bioinformatics</i> , 2012, 28, 3274-3281.	4.1	38
13	Representing and comparing protein folds and fold families using threeâ€dimensional shapeâ€density representations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 530-545.	2.6	6
14	Spatial clustering of protein binding sites for template based protein docking. <i>Bioinformatics</i> , 2011, 27, 2820-2827.	4.1	36
15	jMOTU and Taxonator: Turning DNA Barcode Sequences into Annotated Operational Taxonomic Units. <i>PLoS ONE</i> , 2011, 6, e19259.	2.5	180