

Gaston K Mazandu

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

49
papers

669
citations

15
h-index

24
g-index

60
ext. papers

939
ext. citations

7.1
avg, IF

4.36
L-index

#	Paper	IF	Citations
49	High-depth African genomes inform human migration and health. <i>Nature</i> , 2020 , 586, 741-748	50.4	75
48	Function prediction and analysis of mycobacterium tuberculosis hypothetical proteins. <i>International Journal of Molecular Sciences</i> , 2012 , 13, 7283-302	6.3	69
47	Gene Ontology semantic similarity tools: survey on features and challenges for biological knowledge discovery. <i>Briefings in Bioinformatics</i> , 2017 , 18, 886-901	13.4	41
46	Computational/in silico methods in drug target and lead prediction. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1663-1675	13.4	40
45	A topology-based metric for measuring term similarity in the gene ontology. <i>Advances in Bioinformatics</i> , 2012 , 2012, 975783	5.5	37
44	Information content-based gene ontology semantic similarity approaches: toward a unified framework theory. <i>BioMed Research International</i> , 2013 , 2013, 292063	3	34
43	Using biological networks to improve our understanding of infectious diseases. <i>Computational and Structural Biotechnology Journal</i> , 2014 , 11, 1-10	6.8	31
42	Information content-based Gene Ontology functional similarity measures: which one to use for a given biological data type?. <i>PLoS ONE</i> , 2014 , 9, e113859	3.7	30
41	DaGO-Fun: tool for Gene Ontology-based functional analysis using term information content measures. <i>BMC Bioinformatics</i> , 2013 , 14, 284	3.6	28
40	Predicting and analyzing interactions between Mycobacterium tuberculosis and its human host. <i>PLoS ONE</i> , 2013 , 8, e67472	3.7	28
39	Generation and Analysis of Large-Scale Data-Driven Mycobacterium tuberculosis Functional Networks for Drug Target Identification. <i>Advances in Bioinformatics</i> , 2011 , 2011, 801478	5.5	21
38	A-DaGO-Fun: an adaptable Gene Ontology semantic similarity-based functional analysis tool. <i>Bioinformatics</i> , 2016 , 32, 477-9	7.2	20
37	A web-based protein interaction network visualizer. <i>BMC Bioinformatics</i> , 2014 , 15, 129	3.6	19
36	Scoring protein relationships in functional interaction networks predicted from sequence data. <i>PLoS ONE</i> , 2011 , 6, e18607	3.7	19
35	Using the underlying biological organization of the Mycobacterium tuberculosis functional network for protein function prediction. <i>Infection, Genetics and Evolution</i> , 2012 , 12, 922-32	4.5	18
34	ancGWAS: a post genome-wide association study method for interaction, pathway and ancestry analysis in homogeneous and admixed populations. <i>Bioinformatics</i> , 2016 , 32, 549-56	7.2	15
33	Implementing Artificial Intelligence and Digital Health in Resource-Limited Settings? Top 10 Lessons We Learned in Congenital Heart Defects and Cardiology. <i>OMICS A Journal of Integrative Biology</i> , 2020 , 24, 264-277	3.8	14

32	A comprehensive survey of models for dissecting local ancestry deconvolution in human genome. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1709-1724	13.4	13
31	Dissecting Mutation Prediction of Variants in African Genomes: Challenges and Perspectives. <i>Frontiers in Genetics</i> , 2019 , 10, 601	4.5	10
30	Contribution of microarray data to the advancement of knowledge on the Mycobacterium tuberculosis interactome: use of the random partial least squares approach. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 725-33	4.5	10
29	Hydroxyurea-Induced miRNA Expression in Sickle Cell Disease Patients in Africa. <i>Frontiers in Genetics</i> , 2019 , 10, 509	4.5	9
28	SickleInAfrica. <i>Lancet Haematology</i> , 2020 , 7, e98-e99	14.6	9
27	A Quantitative Approach to Analyzing Genome Reductive Evolution Using Protein-Protein Interaction Networks: A Case Study of Mycobacterium leprae. <i>Frontiers in Genetics</i> , 2016 , 7, 39	4.5	8
26	Large-scale data-driven integrative framework for extracting essential targets and processes from disease-associated gene data sets. <i>Briefings in Bioinformatics</i> , 2018 , 19, 1141-1152	13.4	7
25	Dating admixture events is unsolved problem in multi-way admixed populations. <i>Briefings in Bioinformatics</i> , 2018 ,	13.4	7
24	Contribution of microarray data to the advancement of knowledge on the Mycobacterium tuberculosis interactome: use of the random partial least squares approach. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 181-9	4.5	6
23	A broad survey of DNA sequence data simulation tools. <i>Briefings in Functional Genomics</i> , 2020 , 19, 49-59	4.9	6
22	The Sickle Cell Disease Ontology: enabling universal sickle cell-based knowledge representation. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	6
21	A systems-level analysis of drug-target-disease associations for drug repositioning. <i>Briefings in Functional Genomics</i> , 2018 , 17, 34-41	4.9	5
20	Identifying genetic variants and pathways associated with extreme levels of fetal hemoglobin in sickle cell disease in Tanzania. <i>BMC Medical Genetics</i> , 2020 , 21, 125	2.1	4
19	The use of semantic similarity measures for optimally integrating heterogeneous Gene Ontology data from large scale annotation pipelines. <i>Frontiers in Genetics</i> , 2014 , 5, 264	4.5	4
18	Establishing a Multi-Country Sickle Cell Disease Registry in Africa: Ethical Considerations. <i>Frontiers in Genetics</i> , 2019 , 10, 943	4.5	4
17	Post genome-wide association analysis: dissecting computational pathway/network-based approaches. <i>Briefings in Bioinformatics</i> , 2019 , 20, 690-700	13.4	4
16	Orienting Future Trends in Local Ancestry Deconvolution Models to Optimally Decipher Admixed Individual Genome Variations 2019 ,		3
15	A post-gene silencing bioinformatics protocol for plant-defence gene validation and underlying process identification: case study of the Arabidopsis thaliana NPR1. <i>BMC Plant Biology</i> , 2017 , 17, 218	5.3	2

14	A multi-scenario genome-wide medical population genetics simulation framework. <i>Bioinformatics</i> , 2017 , 33, 2995-3002	7.2	2
13	Simulation of African and non-African low and high coverage whole genome sequence data to assess variant calling approaches. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
12	The Hearing Impairment Ontology: A Tool for Unifying Hearing Impairment Knowledge to Enhance Collaborative Research. <i>Genes</i> , 2019 , 10,	4.2	2
11	Establishing a Sickle Cell Disease Registry in Africa: Experience From the Sickle Pan-African Research Consortium, Kumasi-Ghana.. <i>Frontiers in Genetics</i> , 2022 , 13, 802355	4.5	2
10	A potential roadmap to overcome the current eastern DRC Ebola virus disease outbreak: From a computational perspective. <i>Scientific African</i> , 2020 , 7, e00282	1.7	1
9	Impairment Aware Multi-path Routing in GMPLS-based Networks 2008 ,		1
8	Network-driven analysis of human-Plasmodium falciparum interactome: processes for malaria drug discovery and extracting in silico targets. <i>Malaria Journal</i> , 2021 , 20, 421	3.6	1
7	IHP-PING-generating integrated human protein-protein interaction networks on-the-fly. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	1
6	Investigations of Kidney Dysfunction-Related Gene Variants in Sickle Cell Disease Patients in Cameroon (Sub-Saharan Africa). <i>Frontiers in Genetics</i> , 2021 , 12, 595702	4.5	0
5	Factors associated with blood pressure variation in sickle cell disease patients: a systematic review and meta-analyses.. <i>Expert Review of Hematology</i> , 2022 , 1-10	2.8	0
4	Genetic Analysis of TB Susceptibility Variants in Ghana Reveals Candidate Protective Loci in and Genes.. <i>Frontiers in Genetics</i> , 2021 , 12, 729737	4.5	0
3	MSclassifier: median-supplement model-based classification tool for automated knowledge discovery. <i>F1000Research</i> , 2020 , 9, 1114	3.6	
2	FRANC: a unified framework for multi-way local ancestry deconvolution with high density SNP data. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1837-1845	13.4	
1	Modelling the human immune response dynamics during progression from Mycobacterium latent infection to disease. <i>Applied Mathematical Modelling</i> , 2020 , 80, 217-237	4.5	