

Gaston K Mazandu

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

1,180
citations

430874

18
h-index

434195

31
g-index

60
all docs

60
docs citations

60
times ranked

1661
citing authors

#	ARTICLE	IF	CITATIONS
1	High-depth African genomes inform human migration and health. <i>Nature</i> , 2020, 586, 741-748.	27.8	197
2	Computational/in silico methods in drug target and lead prediction. <i>Briefings in Bioinformatics</i> , 2020, 21, 1663-1675.	6.5	107
3	Function Prediction and Analysis of <i>Mycobacterium tuberculosis</i> Hypothetical Proteins. <i>International Journal of Molecular Sciences</i> , 2012, 13, 7283-7302.	4.1	88
4	Gene Ontology semantic similarity tools: survey on features and challenges for biological knowledge discovery. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw067.	6.5	63
5	A Topology-Based Metric for Measuring Term Similarity in the Gene Ontology. <i>Advances in Bioinformatics</i> , 2012, 2012, 1-17.	5.7	44
6	Information Content-Based Gene Ontology Semantic Similarity Approaches: Toward a Unified Framework Theory. <i>BioMed Research International</i> , 2013, 2013, 1-11.	1.9	43
7	Using biological networks to improve our understanding of infectious diseases. <i>Computational and Structural Biotechnology Journal</i> , 2014, 11, 1-10.	4.1	43
8	Predicting and Analyzing Interactions between <i>Mycobacterium tuberculosis</i> and Its Human Host. <i>PLoS ONE</i> , 2013, 8, e67472.	2.5	34
9	DaGO-Fun: tool for Gene Ontology-based functional analysis using term information content measures. <i>BMC Bioinformatics</i> , 2013, 14, 284.	2.6	33
10	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.	2.5	33
11	A comprehensive survey of models for dissecting local ancestry deconvolution in human genome. <i>Briefings in Bioinformatics</i> , 2019, 20, 1709-1724.	6.5	29
12	Generation and Analysis of Large-Scale Data-Driven <i>Mycobacterium tuberculosis</i> Functional Networks for Drug Target Identification. <i>Advances in Bioinformatics</i> , 2011, 2011, 1-14.	5.7	28
13	A-DaGO-Fun: an adaptable Gene Ontology semantic similarity-based functional analysis tool. <i>Bioinformatics</i> , 2016, 32, 477-479.	4.1	28
14	SickleInAfrica. <i>Lancet Haematology</i> , the, 2020, 7, e98-e99.	4.6	28
15	Dissecting in silico Mutation Prediction of Variants in African Genomes: Challenges and Perspectives. <i>Frontiers in Genetics</i> , 2019, 10, 601.	2.3	25
16	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.	2.0	24
17	Scoring Protein Relationships in Functional Interaction Networks Predicted from Sequence Data. <i>PLoS ONE</i> , 2011, 6, e18607.	2.5	24
18	A web-based protein interaction network visualizer. <i>BMC Bioinformatics</i> , 2014, 15, 129.	2.6	21

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19	ancGWAS: a post genome-wide association study method for interaction, pathway and ancestry analysis in homogeneous and admixed populations. <i>Bioinformatics</i> , 2016, 32, 549-556.	4.1	21
20	Hydroxyurea-Induced miRNA Expression in Sickle Cell Disease Patients in Africa. <i>Frontiers in Genetics</i> , 2019, 10, 509.	2.3	20
21	A broad survey of DNA sequence data simulation tools. <i>Briefings in Functional Genomics</i> , 2020, 19, 49-59.	2.7	20
22	Using the underlying biological organization of the Mycobacterium tuberculosis functional network for protein function prediction. <i>Infection, Genetics and Evolution</i> , 2012, 12, 922-932.	2.3	19
23	Dating admixture events is unsolved problem in multi-way admixed populations. <i>Briefings in Bioinformatics</i> , 2020, 21, 144-155.	6.5	15
24	The Sickle Cell Disease Ontology: enabling universal sickle cell-based knowledge representation. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	14
25	Establishing a Multi-Country Sickle Cell Disease Registry in Africa: Ethical Considerations. <i>Frontiers in Genetics</i> , 2019, 10, 943.	2.3	14
26	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, 181-189.	2.3	13
27	Post genome-wide association analysis: dissecting computational pathway/network-based approaches. <i>Briefings in Bioinformatics</i> , 2019, 20, 690-700.	6.5	13
28	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.	2.3	12
29	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, 725-733.	2.3	11
30	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.	2.3	11
31	A systems-level analysis of drug-target-disease associations for drug repositioning. <i>Briefings in Functional Genomics</i> , 2018, 17, 34-41.	2.7	10
32	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	9
33	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.	6.5	8
34	IHP-PING-generating integrated human protein-protein interaction networks on-the-fly. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	7
35	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.	2.3	7
36	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.	2.3	6

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37	The Hearing Impairment Ontology: A Tool for Unifying Hearing Impairment Knowledge to Enhance Collaborative Research. <i>Genes</i> , 2019, 10, 960.	2.4	6
38	A multi-scenario genome-wide medical population genetics simulation framework. <i>Bioinformatics</i> , 2017, 33, 2995-3002.	4.1	5
39	A post-gene silencing bioinformatics protocol for plant-defence gene validation and underlying process identification: case study of the <i>Arabidopsis thaliana</i> NPR1. <i>BMC Plant Biology</i> , 2017, 17, 218.	3.6	5
40	The Sickle Cell Disease Ontology: recent development and expansion of the universal sickle cell knowledge representation. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	5
41	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.	2.3	4
42	Reviewing and assessing existing meta-analysis models and tools. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	4
43	Orienting Future Trends in Local Ancestry Deconvolution Models to Optimally Decipher Admixed Individual Genome Variations. , 2019, , .		3
44	FRANC: a unified framework for multi-way local ancestry deconvolution with high density SNP data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1837-1845.	6.5	3
45	Simulation of African and non-African low and high coverage whole genome sequence data to assess variant calling approaches. <i>Briefings in Bioinformatics</i> , 2020, 22, .	6.5	3
46	A potential roadmap to overcome the current eastern DRC Ebola virus disease outbreak: From a computational perspective. <i>Scientific African</i> , 2020, 7, e00282.	1.5	3
47	Genetic Analysis of TB Susceptibility Variants in Ghana Reveals Candidate Protective Loci in <i>SORBS2</i> and <i>SCL11A1</i> Genes. <i>Frontiers in Genetics</i> , 2021, 12, 729737.	2.3	3
48	Skills Capacity Building For Health Care Services and Research Through the Sickle Pan African Research Consortium. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	3
49	Factors associated with blood pressure variation in sickle cell disease patients: a systematic review and meta-analyses. <i>Expert Review of Hematology</i> , 2022, 15, 359-368.	2.2	2
50	Impairment Aware Multi-path Routing in GMPLS-based Networks. , 2008, , .		1
51	Designing Data-Driven Learning Algorithms: A Necessity to Ensure Effective Post-Genomic Medicine and Biomedical Research. , 0, , .		0
52	Modelling the human immune response dynamics during progression from <i>Mycobacterium</i> latent infection to disease. <i>Applied Mathematical Modelling</i> , 2020, 80, 217-237.	4.2	0
53	MSclassifier: median-supplement model-based classification tool for automated knowledge discovery. <i>F1000Research</i> , 2020, 9, 1114.	1.6	0