Gaston K Mazandu

List of Publications by Year
in descending order

53	1,180	430754 18	434063 31
papers	citations	h-index	g-index

60	60	60	1661
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	High-depth African genomes inform human migration and health. Nature, 2020, 586, 741-748.	13.7	197
2	Computational/in silico methods in drug target and lead prediction. Briefings in Bioinformatics, 2020, 21, 1663-1675.	3.2	107
3	Function Prediction and Analysis of Mycobacterium tuberculosis Hypothetical Proteins. International Journal of Molecular Sciences, 2012, 13, 7283-7302.	1.8	88
4	Gene Ontology semantic similarity tools: survey on features and challenges for biological knowledge discovery. Briefings in Bioinformatics, 2017, 18, bbw067.	3.2	63
5	A Topology-Based Metric for Measuring Term Similarity in the Gene Ontology. Advances in Bioinformatics, 2012, 2012, 1-17.	5.7	44
6	Information Content-Based Gene Ontology Semantic Similarity Approaches: Toward a Unified Framework Theory. BioMed Research International, 2013, 2013, 1-11.	0.9	43
7	Using biological networks to improve our understanding of infectious diseases. Computational and Structural Biotechnology Journal, 2014, 11, 1-10.	1.9	43
8	Predicting and Analyzing Interactions between Mycobacterium tuberculosis and Its Human Host. PLoS ONE, 2013, 8, e67472.	1.1	34
9	DaGO-Fun: tool for Gene Ontology-based functional analysis using term information content measures. BMC Bioinformatics, 2013, 14, 284.	1.2	33
10	Information Content-Based Gene Ontology Functional Similarity Measures: Which One to Use for a Given Biological Data Type?. PLoS ONE, 2014, 9, e113859.	1.1	33
11	A comprehensive survey of models for dissecting local ancestry deconvolution in human genome. Briefings in Bioinformatics, 2019, 20, 1709-1724.	3.2	29
12	Generation and Analysis of Large-Scale Data-Driven Mycobacterium tuberculosis Functional Networks for Drug Target Identification. Advances in Bioinformatics, 2011, 2011, 1-14.	5.7	28
13	A-DaGO-Fun: an adaptable Gene Ontology semantic similarity-based functional analysis tool. Bioinformatics, 2016, 32, 477-479.	1.8	28
14	SickleInAfrica. Lancet Haematology,the, 2020, 7, e98-e99.	2.2	28
15	Dissecting in silico Mutation Prediction of Variants in African Genomes: Challenges and Perspectives. Frontiers in Genetics, 2019, 10, 601.	1.1	25
16	Implementing Artificial Intelligence and Digital Health in Resource-Limited Settings? Top 10 Lessons We Learned in Congenital Heart Defects and Cardiology. OMICS A Journal of Integrative Biology, 2020, 24, 264-277.	1.0	24
17	Scoring Protein Relationships in Functional Interaction Networks Predicted from Sequence Data. PLoS ONE, 2011, 6, e18607.	1.1	24
18	A web-based protein interaction network visualizer. BMC Bioinformatics, 2014, 15, 129.	1.2	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. Bioinformatics, 2016, 32, 549-556.	1.8	21
20	Hydroxyurea-Induced miRNA Expression in Sickle Cell Disease Patients in Africa. Frontiers in Genetics, 2019, 10, 509.	1.1	20
21	A broad survey of DNA sequence data simulation tools. Briefings in Functional Genomics, 2020, 19, 49-59.	1.3	20
22	Using the underlying biological organization of the Mycobacterium tuberculosis functional network for protein function prediction. Infection, Genetics and Evolution, 2012, 12, 922-932.	1.0	19
23	Dating admixture events is unsolved problem in multi-way admixed populations. Briefings in Bioinformatics, 2020, 21, 144-155.	3.2	15
24	The Sickle Cell Disease Ontology: enabling universal sickle cell-based knowledge representation. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	14
25	Establishing a Multi-Country Sickle Cell Disease Registry in Africa: Ethical Considerations. Frontiers in Genetics, 2019, 10, 943.	1.1	14
26	Contribution of microarray data to the advancement of knowledge on the Mycobacterium tuberculosis interactome: Use of the random partial least squares approach. Infection, Genetics and Evolution, 2011, 11, 181-189.	1.0	13
27	Post genome-wide association analysis: dissecting computational pathway/network-based approaches. Briefings in Bioinformatics, 2019, 20, 690-700.	3.2	13
28	Establishing a Sickle Cell Disease Registry in Africa: Experience From the Sickle Pan-African Research Consortium, Kumasi-Ghana. Frontiers in Genetics, 2022, 13, 802355.	1.1	12
29	Contribution of microarray data to the advancement of knowledge on the Mycobacterium tuberculosis interactome: Use of the random partial least squares approach. Infection, Genetics and Evolution, 2011, 11, 725-733.	1.0	11
30	A Quantitative Approach to Analyzing Genome Reductive Evolution Using Proteinâ€“Protein Interaction Networks: A Case Study of Mycobacterium leprae. Frontiers in Genetics, 2016, 7, 39.	1.1	11
31	A systems-level analysis of drugâ€“targetâ€“disease associations for drug repositioning. Briefings in Functional Genomics, 2018, 17, 34-41.	1.3	10
32	Identifying genetic variants and pathways associated with extreme levels of fetal hemoglobin in sickle cell disease in Tanzania. BMC Medical Genetics, 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. Briefings in Bioinformatics, 2018, 19, 1141-1152.	3.2	8
34	IHP-PINGâ€”generating integrated human proteinâ€“protein interaction networks on-the-fly. Briefings in Bioinformatics, 2021, 22, .	3.2	7
35	Network-driven analysis of humanâ€“Plasmodium falciparum interactome: processes for malaria drug discovery and extracting in silico targets. Malaria Journal, 2021, 20, 421.	0.8	7
36	The use of semantic similarity measures for optimally integrating heterogeneous Gene Ontology data from large scale annotation pipelines. Frontiers in Genetics, 2014, 5, 264.	1.1	6

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37	The Hearing Impairment Ontology: A Tool for Unifying Hearing Impairment Knowledge to Enhance Collaborative Research. Genes, 2019, 10, 960.	1.0	6
38	A multi-scenario genome-wide medical population genetics simulation framework. Bioinformatics, 2017, 33, 2995-3002.	1.8	5
39	A post-gene silencing bioinformatics protocol for plant-defence gene validation and underlying process identification: case study of the Arabidopsis thaliana NPR1. BMC Plant Biology, 2017, 17, 218.	1.6	5
40	The Sickle Cell Disease Ontology: recent development and expansion of the universal sickle cell knowledge representation. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	5
41	Investigations of Kidney Dysfunction-Related Gene Variants in Sickle Cell Disease Patients in Cameroon (Sub-Saharan Africa). Frontiers in Genetics, 2021, 12, 595702.	1.1	4
42	Reviewing and assessing existing meta-analysis models and tools. Briefings in Bioinformatics, 2021, 22, .	3.2	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. Briefings in Bioinformatics, 2020, 21, 1837-1845.	3.2	3
45	Simulation of African and non-African low and high coverage whole genome sequence data to assess variant calling approaches. Briefings in Bioinformatics, 2020, 22, .	3.2	3
46	A potential roadmap to overcome the current eastern DRC Ebola virus disease outbreak: From a computational perspective. Scientific African, 2020, 7, e00282.	0.7	3
47	Genetic Analysis of TB Susceptibility Variants in Ghana Reveals Candidate Protective Loci in SORBS2 and SCL11A1 Genes. Frontiers in Genetics, 2021, 12, 729737.	1.1	3
48	Skills Capacity Building For Health Care Services and Research Through the Sickle Pan African Research Consortium. Frontiers in Genetics, 0, 13, .	1.1	3
49	Factors associated with blood pressure variation in sickle cell disease patients: a systematic review and meta-analyses. Expert Review of Hematology, 2022, 15, 359-368.	1.0	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 Mycobacterium latent infection to disease. Applied Mathematical Modelling, 2020, 80, 217-237.	2.2	0
53	MSclassifier: median-supplement model-based classification tool for automated knowledge discovery. F1000Research, 2020, 9, 1114.	0.8	0