

Emile Chimusa

List of Publications by Year in descending order

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Version: 2024-02-01

79
papers

1,836
citations

430442

18
h-index

329751

37
g-index

97
all docs

97
docs citations

97
times ranked

3016
citing authors

#	ARTICLE	IF	CITATIONS
1	Investigation of multiple populations highlight <i>VEGFA</i> polymorphisms to modulate anterior cruciate ligament injury. <i>Journal of Orthopaedic Research</i> , 2022, 40, 1604-1612.	1.2	3
2	Warfarin Pharmacogenomics for Precision Medicine in Real-Life Clinical Practice in Southern Africa: Harnessing 73 Variants in 29 Pharmacogenes. <i>OMICS A Journal of Integrative Biology</i> , 2022, 26, 35-50.	1.0	9
3	Dissecting Meta-Analysis in GWAS Era: Bayesian Framework for Gene/Subnetwork-Specific Meta-Analysis. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	6
4	IHP-PINGâ€”generating integrated human proteinâ€”protein interaction networks on-the-fly. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
5	Whole exome sequencing identifies rare coding variants in novel human-mouse ortholog genes in African individuals diagnosed with non-syndromic hearing impairment. <i>Experimental Biology and Medicine</i> , 2021, 246, 197-206.	1.1	6
6	Whole exome sequencing reveals pathogenic variants in MYO3A, MYO15A and COL9A3 and differential frequencies in ancestral alleles in hearing impairment genes among individuals from Cameroon. <i>Human Molecular Genetics</i> , 2021, 29, 3729-3743.	1.4	9
7	Heritability jointly explained by host genotype and microbiome: will improve traits prediction?. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
8	Fine scale human genetic structure in three regions of Cameroon reveals episodic diversifying selection. <i>Scientific Reports</i> , 2021, 11, 1039.	1.6	3
9	Utilization of Pneumococcal Vaccine and Penicillin Prophylaxis in Sickle Cell Disease in Three African Countries: Assessment among Healthcare Providers in SickleInAfrica. <i>Hemoglobin</i> , 2021, 45, 163-170.	0.4	6
10	Reviewing and assessing existing meta-analysis models and tools. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
11	Profiling of warfarin pharmacokineticsâ€”associated genetic variants: Black Africans portray unique genetic markers important for an African specific warfarin pharmacogeneticsâ€”dosing algorithm. <i>Journal of Thrombosis and Haemostasis</i> , 2021, 19, 2957-2973.	1.9	14
12	Drug response in association with pharmacogenomics and pharmacomicrobiomics: towards a better personalized medicine. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	14
13	Network-driven analysis of humanâ€”Plasmodium falciparum interactome: processes for malaria drug discovery and extracting in silico targets. <i>Malaria Journal</i> , 2021, 20, 421.	0.8	7
14	Editorial: Immunotherapy as an Evolving Approach for the Treatment of Breast Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 752689.	1.3	2
15	In silico Functional Analysis of Genome-Wide Dataset From 17,000 Individuals Identifies Candidate Malaria Resistance Genes Enriched in Malaria Pathogenic Pathways. <i>Frontiers in Genetics</i> , 2021, 12, 676960.	1.1	1
16	Relating Global and Local Connectome Changes to Dementia and Targeted Gene Expression in Alzheimer's Disease. <i>Frontiers in Human Neuroscience</i> , 2021, 15, 761424.	1.0	6
17	Dating admixture events is unsolved problem in multi-way admixed populations. <i>Briefings in Bioinformatics</i> , 2020, 21, 144-155.	3.2	15
18	Genome-wide heritability analysis of severe malaria resistance reveals evidence of polygenic inheritance. <i>Human Molecular Genetics</i> , 2020, 29, 168-176.	1.4	8

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19	Computational/in silico methods in drug target and lead prediction. Briefings in Bioinformatics, 2020, 21, 1663-1675.	3.2	107
20	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
21	A broad survey of DNA sequence data simulation tools. Briefings in Functional Genomics, 2020, 19, 49-59.	1.3	20
22	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
23	High-depth African genomes inform human migration and health. Nature, 2020, 586, 741-748.	13.7	197
24	Genetic modifiers of long-term survival in sickle cell anemia. Clinical and Translational Medicine, 2020, 10, e152.	1.7	21
25	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
26	Dissecting genome-wide studies for microbiome-related metabolic diseases. Human Molecular Genetics, 2020, 29, R73-R80.	1.4	1
27	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
28	Hearing Impairment Overview in Africa: the Case of Cameroon. Genes, 2020, 11, 233.	1.0	14
29	Genome-Wide Association Study of Brain Connectivity Changes for Alzheimer's Disease. Scientific Reports, 2020, 10, 1433.	1.6	24
30	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
31	Corrigendum to: Genome-wide heritability analysis of severe malaria resistance reveals evidence of polygenic inheritance. Human Molecular Genetics, 2020, 29, 3464-3464.	1.4	0
32	An African-specific profile of pharmacogene variants for rosuvastatin plasma variability: limited role for SLCO1B1 c.521T>C and ABCG2 c.421A>C. Pharmacogenomics Journal, 2019, 19, 240-248.	0.9	12
33	A comprehensive survey of models for dissecting local ancestry deconvolution in human genome. Briefings in Bioinformatics, 2019, 20, 1709-1724.	3.2	29
34	Genome-wide association studies of severe P. falciparum malaria susceptibility: progress, pitfalls and prospects. BMC Medical Genomics, 2019, 12, 120.	0.7	28
35	Dissecting in silico Mutation Prediction of Variants in African Genomes: Challenges and Perspectives. Frontiers in Genetics, 2019, 10, 601.	1.1	25
36	Seroprevalence of Cytomegalovirus Infection Among HIV-Infected and HIV-Uninfected Pregnant Women Attending Antenatal Clinic in Harare, Zimbabwe. Viral Immunology, 2019, 32, 289-295.	0.6	9

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37	Genetic diversity and drug susceptibility profiles of Mycobacterium tuberculosis obtained from Saint Peter's TB specialized Hospital, Ethiopia. PLoS ONE, 2019, 14, e0218545.	1.1	18
38	Population Structure and Implications on the Genetic Architecture of HIV-1 Phenotypes Within Southern Africa. Frontiers in Genetics, 2019, 10, 905.	1.1	15
39	Tantalizing dilemma in risk prediction from disease scoring statistics. Briefings in Functional Genomics, 2019, 18, 211-219.	1.3	1
40	Hydroxyurea-Induced miRNA Expression in Sickle Cell Disease Patients in Africa. Frontiers in Genetics, 2019, 10, 509.	1.1	20
41	Multi-stage Association Analysis of Glioblastoma Gene Expressions with Texture and Spatial Patterns. Lecture Notes in Computer Science, 2019, 11383, 239-250.	1.0	9
42	Polygenic Adaptation Underlies Evolution of Brain Structures and Behavioral Traits. European Neuropsychopharmacology, 2019, 29, S755-S756.	0.3	1
43	Concordance of genetic variation that increases risk for Tourette Syndrome and that influences its underlying neurocircuitry. Translational Psychiatry, 2019, 9, 120.	2.4	24
44	Orienting Future Trends in Local Ancestry Deconvolution Models to Optimally Decipher Admixed Individual Genome Variations. , 2019, . .		3
45	GJB2 and GJB6 Mutations in Hereditary Recessive Non-Syndromic Hearing Impairment in Cameroon. Genes, 2019, 10, 844.	1.0	17
46	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
47	Warfarin Dose and CYP2C Gene Cluster: An African Ancestral-Specific Variant Is a Strong Predictor of Dose in Black South African Patients. OMICS A Journal of Integrative Biology, 2019, 23, 36-44.	1.0	11
48	Detecting genetic modifiers of spondyloepimetaphyseal dysplasia with joint laxity in the Caucasian Afrikaner community. Human Molecular Genetics, 2019, 28, 1053-1063.	1.4	1
49	Post genome-wide association analysis: dissecting computational pathway/network-based approaches. Briefings in Bioinformatics, 2019, 20, 690-700.	3.2	13
50	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
51	Clinical and genetic factors are associated with pain and hospitalisation rates in sickle cell anaemia in Cameroon. British Journal of Haematology, 2018, 180, 134-146.	1.2	31
52	Relating connectivity changes in brain networks to genetic information in Alzheimer patients. , 2018, . .		5
53	Genomics and Epigenomics of Congenital Heart Defects: Expert Review and Lessons Learned in Africa. OMICS A Journal of Integrative Biology, 2018, 22, 301-321.	1.0	18
54	Personalized Herbal Medicine? A Roadmap for Convergence of Herbal and Precision Medicine Biomarker Innovations. OMICS A Journal of Integrative Biology, 2018, 22, 375-391.	1.0	17

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55	Minimum Information Required for Pharmacogenomics Experiments. , 2018, , 179-193.		0
56	Host and Microbiome Genome-Wide Association Studies: Current State and Challenges. <i>Frontiers in Genetics</i> , 2018, 9, 637.	1.1	71
57	Gene Ontology semantic similarity tools: survey on features and challenges for biological knowledge discovery. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw067.	3.2	63
58	A Genomic and Proteinâ€“Protein Interaction Analyses of Nonsyndromic Hearing Impairment in Cameroon Using Targeted Genomic Enrichment and Massively Parallel Sequencing. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 90-99.	1.0	16
59	Clinical and genetic predictors of renal dysfunctions in sickle cell anaemia in Cameroon. <i>British Journal of Haematology</i> , 2017, 178, 629-639.	1.2	48
60	A multi-scenario genome-wide medical population genetics simulation framework. <i>Bioinformatics</i> , 2017, 33, 2995-3002.	1.8	5
61	Beta-globin gene haplotypes and selected Malaria-associated variants among black Southern African populations. <i>Global Health, Epidemiology and Genomics</i> , 2017, 2, e17.	0.2	7
62	Whole-genome sequencing for an enhanced understanding of genetic variation among South Africans. <i>Nature Communications</i> , 2017, 8, 2062.	5.8	88
63	Assessing computational genomics skills: Our experience in the H3ABioNet African bioinformatics network. <i>PLoS Computational Biology</i> , 2017, 13, e1005419.	1.5	9
64	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.	1.6	5
65	South African student protests, 2015Ã– 2016: The aftermath viewed through Medical Science Honours students at the University of Cape Town. <i>South African Medical Journal</i> , 2017, 107, 723.	0.2	3
66	Development of Bioinformatics Infrastructure for Genomics Research. <i>Global Heart</i> , 2017, 12, 91.	0.9	47
67	Minimum information required for a DMET experiment reporting. <i>Pharmacogenomics</i> , 2016, 17, 1533-1545.	0.6	6
68	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.	1.8	21
69	A-DaGO-Fun: an adaptable Gene Ontology semantic similarity-based functional analysis tool. <i>Bioinformatics</i> , 2016, 32, 477-479.	1.8	28
70	â€œBroadbandâ€•Bioinformatics Skills Transfer with the Knowledge Transfer Programme (KTP): Educational Model for Upliftment and Sustainable Development. <i>PLoS Computational Biology</i> , 2015, 11, e1004512.	1.5	9
71	A Genomic Portrait of Haplotype Diversity and Signatures of Selection in Indigenous Southern African Populations. <i>PLoS Genetics</i> , 2015, 11, e1005052.	1.5	42
72	Genome-wide association study of ancestry-specific TB risk in the South African Coloured population. <i>Human Molecular Genetics</i> , 2014, 23, 796-809.	1.4	162

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73	Bioinformatics Knowledge Transfer Programme (KTP) for Human and Capital Development in South Africa. EMBnet Journal, 2014, 20, 791.	0.2	0
74	Determining Ancestry Proportions in Complex Admixture Scenarios in South Africa Using a Novel Proxy Ancestry Selection Method. PLoS ONE, 2013, 8, e73971.	1.1	42
75	A Panel of Ancestry Informative Markers for the Complex Five-Way Admixed South African Coloured Population. PLoS ONE, 2013, 8, e82224.	1.1	74
76	Genome-wide analysis of the structure of the South African Coloured Population in the Western Cape. Human Genetics, 2010, 128, 145-153.	1.8	177
77	Designing Data-Driven Learning Algorithms: A Necessity to Ensure Effective Post-Genomic Medicine and Biomedical Research. , 0, , .		0
78	Computational Generalization of Mixed Models on Large-Scale Data with Applications to Genetic Studies. Asian Journal of Probability and Statistics, 0, , 1-31.	0.0	0
79	Dissecting Generalizability and Actionability of Disease-Associated Genes From 20 Worldwide Ethnolinguistic Cultural Groups. Frontiers in Genetics, 0, 13, .	1.1	3