

# 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	High-depth African genomes inform human migration and health. <i>Nature</i> , 2020, 586, 741-748.	13.7	197
2	Genome-wide analysis of the structure of the South African Coloured Population in the Western Cape. <i>Human Genetics</i> , 2010, 128, 145-153.	1.8	177
3	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
4	Computational/in silico methods in drug target and lead prediction. <i>Briefings in Bioinformatics</i> , 2020, 21, 1663-1675.	3.2	107
5	Whole-genome sequencing for an enhanced understanding of genetic variation among South Africans. <i>Nature Communications</i> , 2017, 8, 2062.	5.8	88
6	A Panel of Ancestry Informative Markers for the Complex Five-Way Admixed South African Coloured Population. <i>PLoS ONE</i> , 2013, 8, e82224.	1.1	74
7	Host and Microbiome Genome-Wide Association Studies: Current State and Challenges. <i>Frontiers in Genetics</i> , 2018, 9, 637.	1.1	71
8	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
9	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
10	Development of Bioinformatics Infrastructure for Genomics Research. <i>Global Heart</i> , 2017, 12, 91.	0.9	47
11	Determining Ancestry Proportions in Complex Admixture Scenarios in South Africa Using a Novel Proxy Ancestry Selection Method. <i>PLoS ONE</i> , 2013, 8, e73971.	1.1	42
12	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
13	Clinical and genetic factors are associated with pain and hospitalisation rates in sickle cell anaemia in Cameroon. <i>British Journal of Haematology</i> , 2018, 180, 134-146.	1.2	31
14	A comprehensive survey of models for dissecting local ancestry deconvolution in human genome. <i>Briefings in Bioinformatics</i> , 2019, 20, 1709-1724.	3.2	29
15	A-DaGO-Fun: an adaptable Gene Ontology semantic similarity-based functional analysis tool. <i>Bioinformatics</i> , 2016, 32, 477-479.	1.8	28
16	Genome-wide association studies of severe <i>P. falciparum</i> malaria susceptibility: progress, pitfalls and prospects. <i>BMC Medical Genomics</i> , 2019, 12, 120.	0.7	28
17	Dissecting in silico Mutation Prediction of Variants in African Genomes: Challenges and Perspectives. <i>Frontiers in Genetics</i> , 2019, 10, 601.	1.1	25
18	Concordance of genetic variation that increases risk for Tourette Syndrome and that influences its underlying neurocircuitry. <i>Translational Psychiatry</i> , 2019, 9, 120.	2.4	24

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19	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
20	Genome-Wide Association Study of Brain Connectivity Changes for Alzheimer's Disease. Scientific Reports, 2020, 10, 1433.	1.6	24
21	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
22	Genetic modifiers of long-term survival in sickle cell anemia. Clinical and Translational Medicine, 2020, 10, e152.	1.7	21
23	Hydroxyurea-Induced miRNA Expression in Sickle Cell Disease Patients in Africa. Frontiers in Genetics, 2019, 10, 509.	1.1	20
24	A broad survey of DNA sequence data simulation tools. Briefings in Functional Genomics, 2020, 19, 49-59.	1.3	20
25	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
26	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
27	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
28	GJB2 and GJB6 Mutations in Hereditary Recessive Non-Syndromic Hearing Impairment in Cameroon. Genes, 2019, 10, 844.	1.0	17
29	A Genomic and Protein-Protein Interaction Analyses of Nonsyndromic Hearing Impairment in Cameroon Using Targeted Genomic Enrichment and Massively Parallel Sequencing. OMICS A Journal of Integrative Biology, 2017, 21, 90-99.	1.0	16
30	Dating admixture events is unsolved problem in multi-way admixed populations. Briefings in Bioinformatics, 2020, 21, 144-155.	3.2	15
31	Population Structure and Implications on the Genetic Architecture of HIV-1 Phenotypes Within Southern Africa. Frontiers in Genetics, 2019, 10, 905.	1.1	15
32	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
33	Hearing Impairment Overview in Africa: the Case of Cameroon. Genes, 2020, 11, 233.	1.0	14
34	Profiling of warfarin pharmacokinetics-associated genetic variants: Black Africans portray unique genetic markers important for an African specific warfarin pharmacogenetics dosing algorithm. Journal of Thrombosis and Haemostasis, 2021, 19, 2957-2973.	1.9	14
35	Drug response in association with pharmacogenomics and pharmacomicrobiomics: towards a better personalized medicine. Briefings in Bioinformatics, 2021, 22, .	3.2	14
36	Post genome-wide association analysis: dissecting computational pathway/network-based approaches. Briefings in Bioinformatics, 2019, 20, 690-700.	3.2	13

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37	An African-specific profile of pharmacogene variants for rosuvastatin plasma variability: limited role for SLCO1B1 c.521T>C and ABCG2 c.421A>C. <i>Pharmacogenomics Journal</i> , 2019, 19, 240-248.	0.9	12
38	Warfarin Dose and CYP2C Gene Cluster: An African Ancestral-Specific Variant Is a Strong Predictor of Dose in Black South African Patients. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 36-44.	1.0	11
39	“Broadband” 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
40	Assessing computational genomics skills: Our experience in the H3ABioNet African bioinformatics network. <i>PLoS Computational Biology</i> , 2017, 13, e1005419.	1.5	9
41	Seroprevalence of Cytomegalovirus Infection Among HIV-Infected and HIV-Uninfected Pregnant Women Attending Antenatal Clinic in Harare, Zimbabwe. <i>Viral Immunology</i> , 2019, 32, 289-295.	0.6	9
42	Multi-stage Association Analysis of Glioblastoma Gene Expressions with Texture and Spatial Patterns. <i>Lecture Notes in Computer Science</i> , 2019, 11383, 239-250.	1.0	9
43	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
44	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
45	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
46	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.	3.2	8
47	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
48	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
49	IHP-PING “generating integrated human protein-protein interaction networks on-the-fly. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
50	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.	0.8	7
51	Minimum information required for a DMET experiment reporting. <i>Pharmacogenomics</i> , 2016, 17, 1533-1545.	0.6	6
52	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
53	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
54	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

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55	Dissecting Meta-Analysis in GWAS Era: Bayesian Framework for Gene/Subnetwork-Specific Meta-Analysis. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	6
56	A multi-scenario genome-wide medical population genetics simulation framework. <i>Bioinformatics</i> , 2017, 33, 2995-3002.	1.8	5
57	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
58	Relating connectivity changes in brain networks to genetic information in Alzheimer patients. , 2018, , .		5
59	Reviewing and assessing existing meta-analysis models and tools. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
60	South African student protests, 2015-2016: 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
61	Orienting Future Trends in Local Ancestry Deconvolution Models to Optimally Decipher Admixed Individual Genome Variations. , 2019, , .		3
62	FRANC: a unified framework for multi-way local ancestry deconvolution with high density SNP data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1837-1845.	3.2	3
63	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, .	3.2	3
64	A potential roadmap to overcome the current eastern DRC Ebola virus disease outbreak: From a computational perspective. <i>Scientific African</i> , 2020, 7, e00282.	0.7	3
65	Heritability jointly explained by host genotype and microbiome: will improve traits prediction?. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
66	Fine scale human genetic structure in three regions of Cameroon reveals episodic diversifying selection. <i>Scientific Reports</i> , 2021, 11, 1039.	1.6	3
67	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
68	Dissecting Generalizability and Actionability of Disease-Associated Genes From 20 Worldwide Ethnolinguistic Cultural Groups. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
69	Editorial: Immunotherapy as an Evolving Approach for the Treatment of Breast Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 752689.	1.3	2
70	Tantalizing dilemma in risk prediction from disease scoring statistics. <i>Briefings in Functional Genomics</i> , 2019, 18, 211-219.	1.3	1
71	Polygenic Adaptation Underlies Evolution of Brain Structures and Behavioral Traits. <i>European Neuropsychopharmacology</i> , 2019, 29, S755-S756.	0.3	1
72	Detecting genetic modifiers of spondyloepimetaphyseal dysplasia with joint laxity in the Caucasian Afrikaner community. <i>Human Molecular Genetics</i> , 2019, 28, 1053-1063.	1.4	1

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73	Dissecting genome-wide studies for microbiome-related metabolic diseases. Human Molecular Genetics, 2020, 29, R73-R80.	1.4	1
74	Insilico Functional Analysis of Genome-Wide Dataset From 17,000 Individuals Identifies Candidate Malaria Resistance Genes Enriched in Malaria Pathogenic Pathways. Frontiers in Genetics, 2021, 12, 676960.	1.1	1
75	Minimum Information Required for Pharmacogenomics Experiments. , 2018, , 179-193.		0
76	Designing Data-Driven Learning Algorithms: A Necessity to Ensure Effective Post-Genomic Medicine and Biomedical Research. , 0, , .		0
77	Bioinformatics Knowledge Transfer Programme (KTP) for Human and Capital Development in South Africa. EMBnet Journal, 2014, 20, 791.	0.2	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	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