

Muntaser E Ibrahim

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

6,046
citations

257450

24
h-index

110387

64
g-index

73
all docs

73
docs citations

73
times ranked

9204
citing authors

#	ARTICLE	IF	CITATIONS
1	Individualized Medicine in Africa: Bringing the Practice Into the Realms of Population Heterogeneity. <i>Frontiers in Genetics</i> , 2022, 13, 853969.	2.3	0
2	CMMRD caused by PMS1 mutation in a sudanese consanguineous family. <i>Hereditary Cancer in Clinical Practice</i> , 2022, 20, 16.	1.5	0
3	Mitochondrial HVRI and whole mitogenome sequence variations portray similar scenarios on the genetic structure and ancestry of northeast Africans. <i>Meta Gene</i> , 2021, 27, 100837.	0.6	2
4	The Y chromosome ancestry marker R1b1b2: a surrogate of the SARS-CoV-2 population affinity. <i>Human Genome Variation</i> , 2021, 8, 11.	0.7	6
5	Genetic diversity of the Sudanese: insights on origin and implications for health. <i>Human Molecular Genetics</i> , 2021, 30, R37-R41.	2.9	3
6	Pathogenesis and Management of COVID-19. <i>Journal of Xenobiotics</i> , 2021, 11, 77-93.	6.7	10
7	Pathogenic Variants in ABHD16A Cause a Novel Psychomotor Developmental Disorder With Spastic Paraplegia. <i>Frontiers in Neurology</i> , 2021, 12, 720201.	2.4	5
8	Novel Homozygous Missense Mutation in the ARG1 Gene in a Large Sudanese Family. <i>Frontiers in Neurology</i> , 2020, 11, 569996.	2.4	6
9	The Duffy T-33C is an insightful marker of human history and admixture. <i>Meta Gene</i> , 2020, 26, 100782.	0.6	3
10	Host genetic susceptibility to mycetoma. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008053.	3.0	11
11	Distribution of Duffy Phenotypes among Plasmodium vivax Infections in Sudan. <i>Genes</i> , 2019, 10, 437.	2.4	13
12	The Possible Role of Helicobacter pylori in Gastric Cancer and Its Management. <i>Frontiers in Oncology</i> , 2019, 9, 75.	2.8	64
13	Genomic evidence for shared common ancestry of East African hunting-gathering populations and insights into local adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4166-4175.	7.1	40
14	Neurogenetic Disorders in Africa: Hereditary Spastic Paraplegia. , 2019, , 311-319.		2
15	Reflections on Conceptualizing Africa for Biological Studies with a Historical Component. , 2019, , 1-25.		1
16	History and Genetics in Africa. , 2019, , 26-49.		0
17	Sociobiological Transition and Cancer. , 2019, , 217-232.		0
18	Disease, Selection, and Evolution in the African Landscape. , 2019, , 50-70.		2

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19	Understanding the Evolutionary Biology of CVD From Analysis of Ancestral Population Genomes. <i>Global Heart</i> , 2019, 12, 73.	2.3	2
20	Rare variant in gene causing congenital muscular dystrophy in a Sudanese family. A case report. <i>Acta Myologica</i> , 2019, 38, 21-24.	1.5	3
21	EBV Associated Breast Cancer Whole Methylome Analysis Reveals Viral and Developmental Enriched Pathways. <i>Frontiers in Oncology</i> , 2018, 8, 316.	2.8	12
22	Challenges imposed by minor reference alleles on the identification and reporting of clinical variants from exome data. <i>BMC Genomics</i> , 2018, 19, 46.	2.8	14
23	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. <i>Lancet Haematology</i> , 2018, 5, e333-e345.	4.6	90
24	Case report of a novel homozygous splice site mutation in PLA2G6 gene causing infantile neuroaxonal dystrophy in a Sudanese family. <i>BMC Medical Genetics</i> , 2018, 19, 72.	2.1	12
25	High altitude and pre-eclampsia: Adaptation or protection. <i>Medical Hypotheses</i> , 2017, 104, 128-132.	1.5	18
26	Hereditary spastic paraplegias: identification of a novel SPG57 variant affecting TFG oligomerization and description of HSP subtypes in Sudan. <i>European Journal of Human Genetics</i> , 2017, 25, 100-110.	2.8	28
27	Association of Epstein - Barr virus and breast cancer in Eritrea. <i>Infectious Agents and Cancer</i> , 2017, 12, 62.	2.6	21
28	Genetic determinants of anti-malarial acquired immunity in a large multi-centre study. <i>Malaria Journal</i> , 2015, 14, 333.	2.3	26
29	Candidate gene analysis supports a role for polymorphisms at TCF7L2 as risk factors for type 2 diabetes in Sudan. <i>Journal of Diabetes and Metabolic Disorders</i> , 2015, 15, 4.	1.9	10
30	Exome sequencing of a colorectal cancer family reveals shared mutation pattern and predisposition circuitry along tumor pathways. <i>Frontiers in Genetics</i> , 2015, 6, 288.	2.3	11
31	Part I: cancer in Sudan—burden, distribution, and trends breast, gynecological, and prostate cancers. <i>Cancer Medicine</i> , 2015, 4, 447-456.	2.8	52
32	The Episode of Genetic Drift Defining the Migration of Humans out of Africa Is Derived from a Large East African Population Size. <i>PLoS ONE</i> , 2014, 9, e97674.	2.5	21
33	Insights into the possible role of IFNG and IFNGR1 in Kala-azar and Post Kala-azar Dermal Leishmaniasis in Sudanese patients. <i>BMC Infectious Diseases</i> , 2014, 14, 662.	2.9	4
34	Y-chromosome E haplogroups: their distribution and implication to the origin of Afro-Asiatic languages and pastoralism. <i>European Journal of Human Genetics</i> , 2014, 22, 1387-1392.	2.8	13
35	Genetic Origins of Lactase Persistence and the Spread of Pastoralism in Africa. <i>American Journal of Human Genetics</i> , 2014, 94, 496-510.	6.2	174
36	Epstein Barr virus: a prime candidate of breast cancer aetiology in Sudanese patients. <i>Infectious Agents and Cancer</i> , 2014, 9, 9.	2.6	59

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37	Glycolysis, tumor metabolism, cancer growth and dissemination. A new pH-based etiopathogenic perspective and therapeutic approach to an old cancer question. <i>Oncoscience</i> , 2014, 1, 777-802.	2.2	198
38	Patterns of nucleotide and haplotype diversity at ICAM-1 across global human populations with varying levels of malaria exposure. <i>Human Genetics</i> , 2013, 132, 987-999.	3.8	5
39	Contribution of retinoblastoma LOH and the p53 Arg/Pro polymorphism to cervical cancer. <i>Molecular Medicine Reports</i> , 2012, 6, 473-6.	2.4	18
40	p53 Codon 72 arginine/proline polymorphism and cancer in Sudan. <i>Molecular Biology Reports</i> , 2012, 39, 10833-10836.	2.3	20
41	Structural diversity and African origin of the 17q21.31 inversion polymorphism. <i>Nature Genetics</i> , 2012, 44, 872-880.	21.4	129
42	Effects of Natural Selection and Gene Conversion on the Evolution of Human Glycophorins Coding for MNS Blood Polymorphisms in Malaria-Endemic African Populations. <i>American Journal of Human Genetics</i> , 2011, 88, 741-754.	6.2	52
43	Haplotype variation and genotype imputation in African populations. <i>Genetic Epidemiology</i> , 2011, 35, 766-780.	1.3	39
44	Characterization of genetic variation and natural selection at the arylamine <i>N</i> -acetyltransferase genes in global human populations. <i>Pharmacogenomics</i> , 2011, 12, 1545-1558.	1.3	38
45	Genetic and Functional Evidence Implicating DLL1 as the Gene That Influences Susceptibility to Visceral Leishmaniasis at Chromosome 6q27. <i>Journal of Infectious Diseases</i> , 2011, 204, 467-477.	4.0	15
46	Candidate malaria susceptibility/protective SNPs in hospital and population-based studies: the effect of sub-structuring. <i>Malaria Journal</i> , 2010, 9, 119.	2.3	28
47	Loss of balancing selection in the β S globin locus. <i>BMC Medical Genetics</i> , 2010, 11, 21.	2.1	11
48	The emergence of Y-chromosome haplogroup J1e among Arabic-speaking populations. <i>European Journal of Human Genetics</i> , 2010, 18, 348-353.	2.8	71
49	Molecular Cloning, Characterization and Overexpression of a Novel Cyclin from <i>Leishmania mexicana</i> . <i>Pakistan Journal of Biological Sciences</i> , 2010, 13, 775-784.	0.5	9
50	Genome-wide and fine-resolution association analysis of malaria in West Africa. <i>Nature Genetics</i> , 2009, 41, 657-665.	21.4	345
51	The Genetic Structure and History of Africans and African Americans. <i>Science</i> , 2009, 324, 1035-1044.	12.6	1,267
52	Genetic studies of African populations: an overview on disease susceptibility and response to vaccines and therapeutics. <i>Human Genetics</i> , 2008, 123, 557-598.	3.8	79
53	Y-chromosome variation among Sudanese: Restricted gene flow, concordance with language, geography, and history. <i>American Journal of Physical Anthropology</i> , 2008, 137, 316-323.	2.1	71
54	Evolutionary conservation of RNA editing in the genus <i>Leishmania</i> . <i>Infection, Genetics and Evolution</i> , 2008, 8, 378-380.	2.3	6

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55	Y Chromosome Lineage- and Village-Specific Genes on Chromosomes 1p22 and 6q27 Control Visceral Leishmaniasis in Sudan. <i>PLoS Genetics</i> , 2007, 3, e71.	3.5	64
56	Convergent adaptation of human lactase persistence in Africa and Europe. <i>Nature Genetics</i> , 2007, 39, 31-40.	21.4	1,375
57	Co-introgression of Y-chromosome haplogroups and the sickle cell gene across Africa's Sahel. <i>European Journal of Human Genetics</i> , 2007, 15, 1183-1185.	2.8	18
58	Relationship of the Sickle Cell Gene to the Ethnic and Geographic Groups Populating the Sudan. <i>Public Health Genomics</i> , 2006, 9, 113-120.	1.0	20
59	High frequency of <i>Plasmodium falciparum</i> PfCRT K76T and PfpgH86Y in patients clearing infection after chloroquine treatment in the Sudan. <i>Acta Tropica</i> , 2006, 97, 19-25.	2.0	13
60	Sudanese mucosal leishmaniasis: isolation of a parasite within the <i>Leishmania donovani</i> complex that differs genotypically from <i>L. donovani</i> causing classical visceral leishmaniasis. <i>Infection, Genetics and Evolution</i> , 2005, 5, 29-33.	2.3	26
61	Genetics and visceral leishmaniasis in the Sudan: seeking a link. <i>Trends in Parasitology</i> , 2004, 20, 268-274.	3.3	36
62	Allele frequency and genotype distribution of polymorphisms within disease-related genes is influenced by ethnic population sub-structuring in Sudan. <i>Genetica</i> , 2003, 119, 57-63.	1.1	16
63	The epidemiology of visceral leishmaniasis in East Africa: hints and molecular revelations. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2002, 96, S25-S29.	1.8	7
64	SLC11A1 (formerly NRAMP1) and disease resistance. Microreview. <i>Cellular Microbiology</i> , 2001, 3, 773-784.	2.1	231
65	The origin and evolution of the <i>Leishmania donovani</i> complex as inferred from a mitochondrial cytochrome oxidase II gene sequence. <i>Infection, Genetics and Evolution</i> , 2001, 1, 61-68.	2.3	39
66	Y chromosome sequence variation and the history of human populations. <i>Nature Genetics</i> , 2000, 26, 358-361.	21.4	935
67	A View of Modern Human Origins from Y Chromosome Microsatellite Variation. <i>Genome Research</i> , 1999, 9, 558-567.	5.5	91
68	Oronasal Leishmaniasis Caused by a Parasite with an Unusual Isoenzyme Profile. <i>American Journal of Tropical Medicine and Hygiene</i> , 1997, 56, 96-98.	1.4	9