Muntaser E Ibrahim

List of Publications by Year
in descending order

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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	Convergent adaptation of human lactase persistence in Africa and Europe. Nature Genetics, 2007, 39, 31-40.	21.4	1,375
2	The Genetic Structure and History of Africans and African Americans. Science, 2009, 324, 1035-1044.	12.6	1,267
3	Y chromosome sequence variation and the history of human populations. Nature Genetics, 2000, 26, 358-361.	21.4	935
4	Genome-wide and fine-resolution association analysis of malaria in West Africa. Nature Genetics, 2009, 41, 657-665.	21.4	345
5	SLC11A1 (formerly NRAMP1) and disease resistance. Microreview. Cellular Microbiology, 2001, 3, 773-784.	2.1	231
6	Glycolysis, tumor metabolism, cancer growth and dissemination. A new pH-based etiopathogenic perspective and therapeutic approach to an old cancer question. Oncoscience, 2014, 1, 777-802.	2.2	198
7	Genetic Origins of Lactase Persistence and the Spread of Pastoralism in Africa. American Journal of Human Genetics, 2014, 94, 496-510.	6.2	174
8	Structural diversity and African origin of the 17q21.31 inversion polymorphism. Nature Genetics, 2012, 44, 872-880.	21.4	129
9	A View of Modern Human Origins from Y Chromosome Microsatellite Variation. Genome Research, 1999, 9, 558-567.	5.5	91
10	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. Lancet Haematology,the, 2018, 5, e333-e345.	4.6	90
11	Genetic studies of African populations: an overview on disease susceptibility and response to vaccines and therapeutics. Human Genetics, 2008, 123, 557-598.	3.8	79
12	Yâ€¢chromosome variation among Sudanese: Restricted gene flow, concordance with language, geography, and history. American Journal of Physical Anthropology, 2008, 137, 316-323.	2.1	71
13	The emergence of Y-chromosome haplogroup J1e among Arabic-speaking populations. European Journal of Human Genetics, 2010, 18, 348-353.	2.8	71
14	Y Chromosome Lineage- and Village-Specific Genes on Chromosomes 1p22 and 6q27 Control Visceral Leishmaniasis in Sudan. PLoS Genetics, 2007, 3, e71.	3.5	64
15	The Possible Role of Helicobacter pylori in Gastric Cancer and Its Management. Frontiers in Oncology, 2019, 9, 75.	2.8	64
16	Epstein Barr virus: a prime candidate of breast cancer aetiology in Sudanese patients. Infectious Agents and Cancer, 2014, 9, 9.	2.6	59
17	Effects of Natural Selection and Gene Conversion on the Evolution of Human Glycophorins Coding for MNS Blood Polymorphisms in Malaria-Endemic African Populations. American Journal of Human Genetics, 2011, 88, 741-754.	6.2	52
18	Part I: cancer in Sudanâ€"burden, distribution, and trends breast, gynecological, and prostate cancers. Cancer Medicine, 2015, 4, 447-456.	2.8	52

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19	Genomic evidence for shared common ancestry of East African hunting-gathering populations and insights into local adaptation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 4166-4175.	7.1	40
20	The origin and evolution of the Leishmania donovani complex as inferred from a mitochondrial cytochrome oxidase II gene sequence. Infection, Genetics and Evolution, 2001, 1, 61-68.	2.3	39
21	Haplotype variation and genotype imputation in African populations. Genetic Epidemiology, 2011, 35, 766-780.	1.3	39
22	Characterization of genetic variation and natural selection at the arylamine N-acetyltransferase genes in global human populations. Pharmacogenomics, 2011, 12, 1545-1558.	1.3	38
23	Genetics and visceral leishmaniasis in the Sudan: seeking a link. Trends in Parasitology, 2004, 20, 268-274.	3.3	36
24	Candidate malaria susceptibility/protective SNPs in hospital and population-based studies: the effect of sub-structuring. Malaria Journal, 2010, 9, 119.	2.3	28
25	Hereditary spastic paraplegias: identification of a novel SPG57 variant affecting TFG oligomerization and description of HSP subtypes in Sudan. European Journal of Human Genetics, 2017, 25, 100-110.	2.8	28
26	Sudanese mucosal leishmaniasis: isolation of a parasite within the Leishmania donovani complex that differs genotypically from L. donovani causing classical visceral leishmaniasis. Infection, Genetics and Evolution, 2005, 5, 29-33.	2.3	26
27	Genetic determinants of anti-malarial acquired immunity in a large multi-centre study. Malaria Journal, 2015, 14, 333.	2.3	26
28	The Episode of Genetic Drift Defining the Migration of Humans out of Africa Is Derived from a Large East African Population Size. PLoS ONE, 2014, 9, e97674.	2.5	21
29	Association of Epstein - Barr virus and breast cancer in Eritrea. Infectious Agents and Cancer, 2017, 12, 62.	2.6	21
30	Relationship of the Sickle Cell Gene to the Ethnic and Geographic Groups Populating the Sudan. Public Health Genomics, 2006, 9, 113-120.	1.0	20
31	p53 Codon 72 arginine/proline polymorphism and cancer in Sudan. Molecular Biology Reports, 2012, 39, 10833-10836.	2.3	20
32	Co-introgression of Y-chromosome haplogroups and the sickle cell gene across Africa's Sahel. European Journal of Human Genetics, 2007, 15, 1183-1185.	2.8	18
33	Contribution of retinoblastoma LOH and the p53 Arg/Pro polymorphism to cervical cancer. Molecular Medicine Reports, 2012, 6, 473-6.	2.4	18
34	High altitude and pre-eclampsia: Adaptation or protection. Medical Hypotheses, 2017, 104, 128-132.	1.5	18
35	Allele frequency and genotype distribution of polymorphisms within disease-related genes is influenced by ethnic population sub-structuring in Sudan. Genetica, 2003, 119, 57-63.	1.1	16
36	Genetic and Functional Evidence Implicating DLL1 as the Gene That Influences Susceptibility to Visceral Leishmaniasis at Chromosome 6q27. Journal of Infectious Diseases, 2011, 204, 467-477.	4.0	15

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37	Challenges imposed by minor reference alleles on the identification and reporting of clinical variants from exome data. BMC Genomics, 2018, 19, 46.	2.8	14
38	High frequency of Plasmodium falciparum PfCRT K76T and PfpghN86Y in patients clearing infection after chloroquine treatment in the Sudan. Acta Tropica, 2006, 97, 19-25.	2.0	13
39	Y-chromosome E haplogroups: their distribution and implication to the origin of Afro-Asiatic languages and pastoralism. European Journal of Human Genetics, 2014, 22, 1387-1392.	2.8	13
40	Distribution of Duffy Phenotypes among Plasmodium vivax Infections in Sudan. Genes, 2019, 10, 437.	2.4	13
41	EBV Associated Breast Cancer Whole Methylome Analysis Reveals Viral and Developmental Enriched Pathways. Frontiers in Oncology, 2018, 8, 316.	2.8	12
42	Case report of a novel homozygous splice site mutation in PLA2G6 gene causing infantile neuroaxonal dystrophy in a Sudanese family. BMC Medical Genetics, 2018, 19, 72.	2.1	12
43	Loss of balancing selection in the Î²S globin locus. BMC Medical Genetics, 2010, 11, 21.	2.1	11
44	Exome sequencing of a colorectal cancer family reveals shared mutation pattern and predisposition circuitry along tumor pathways. Frontiers in Genetics, 2015, 6, 288.	2.3	11
45	Host genetic susceptibility to mycetoma. PLoS Neglected Tropical Diseases, 2020, 14, e0008053.	3.0	11
46	Candidate gene analysis supports a role for polymorphisms at TCF7L2 as risk factors for type 2 diabetes in Sudan. Journal of Diabetes and Metabolic Disorders, 2015, 15, 4.	1.9	10
47	Pathogenesis and Management of COVID-19. Journal of Xenobiotics, 2021, 11, 77-93.	6.7	10
48	Molecular Cloning, Characterization and Overexpression of a Novel Cyclin from Leishmania mexicana. Pakistan Journal of Biological Sciences, 2010, 13, 775-784.	0.5	9
49	Oronasal Leishmaniasis Caused by a Parasite with an Unusual Isoenzyme Profile. American Journal of Tropical Medicine and Hygiene, 1997, 56, 96-98.	1.4	9
50	The epidemiology of visceral leishmaniasis in East Africa: hints and molecular revelations. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2002, 96, S25-S29.	1.8	7
51	Evolutionary conservation of RNA editing in the genus Leishmania. Infection, Genetics and Evolution, 2008, 8, 378-380.	2.3	6
52	Novel Homozygous Missense Mutation in the ARG1 Gene in a Large Sudanese Family. Frontiers in Neurology, 2020, 11, 569996.	2.4	6
53	The Y chromosome ancestry marker R1b1b2: a surrogate of the SARS-CoV-2 population affinity. Human Genome Variation, 2021, 8, 11.	0.7	6
54	Patterns of nucleotide and haplotype diversity at ICAM-1 across global human populations with varying levels of malaria exposure. Human Genetics, 2013, 132, 987-999.	3.8	5

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55	Pathogenic Variants in ABHD16A Cause a Novel Psychomotor Developmental Disorder With Spastic Paraplegia. Frontiers in Neurology, 2021, 12, 720201.	2.4	5
56	Insights into the possible role of IFNG and IFNGR1 in Kala-azar and Post Kala-azar Dermal Leishmaniasis in Sudanese patients. BMC Infectious Diseases, 2014, 14, 662.	2.9	4
57	The Duffy T-33C is an insightful marker of human history and admixture. Meta Gene, 2020, 26, 100782.	0.6	3
58	Genetic diversity of the Sudanese: insights on origin and implications for health. Human Molecular Genetics, 2021, 30, R37-R41.	2.9	3
59	Rare variant in gene causing congenital muscular dystrophy in a Sudanese family. A case report. Acta Myologica, 2019, 38, 21-24.	1.5	3
60	Neurogenetic Disorders in Africa: Hereditary Spastic Paraplegia. , 2019, , 311-319.		2
61	Disease, Selection, and Evolution in the African Landscape. , 2019, , 50-70.		2
62	Understanding the Evolutionary Biology of CVD From Analysis of Ancestral Population Genomes. Global Heart, 2019, 12, 73.	2.3	2
63	Mitochondrial HVRI and whole mitogenome sequence variations portray similar scenarios on the genetic structure and ancestry of northeast Africans. Meta Gene, 2021, 27, 100837.	0.6	2
64	Reflections on Conceptualizing Africa for Biological Studies with a Historical Component. , 2019, , 1-25.		1
65	History and Genetics in Africa. , 2019, , 26-49.		0
66	Sociobiological Transition and Cancer. , 2019, , 217-232.		0
67	Individualized Medicine in Africa: Bringing the Practice Into the Realms of Population Heterogeneity. Frontiers in Genetics, 2022, 13, 853969.	2.3	0
68	CMMRD caused by PMS1 mutation in a sudanese consanguineous family. Hereditary Cancer in Clinical Practice, 2022, 20, 16.	1.5	0