

Massimo Mezzavilla

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

5,559
citations

236612

25
h-index

149479

56
g-index

70
all docs

70
docs citations

70
times ranked

16429
citing authors

#	ARTICLE	IF	CITATIONS
1	Runs of homozygosity are associated with staging of periodontitis in isolated populations. <i>Human Molecular Genetics</i> , 2021, 30, 1154-1159.	1.4	3
2	Natural human knockouts and Mendelian disorders: deep phenotyping in Italian isolates. <i>European Journal of Human Genetics</i> , 2021, 29, 1272-1281.	1.4	6
3	The landscape of autosomal-recessive pathogenic variants in European populations reveals phenotype-specific effects. <i>American Journal of Human Genetics</i> , 2021, 108, 608-619.	2.6	36
4	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
5	Poking COVID-19: Insights on Genomic Constraints among Immune-Related Genes between Qatari and Italian Populations. <i>Genes</i> , 2021, 12, 1842.	1.0	1
6	Fine-scale population structure and demographic history of British Pakistanis. <i>Nature Communications</i> , 2021, 12, 7189.	5.8	21
7	A bird's-eye view of Italian genomic variation through whole-genome sequencing. <i>European Journal of Human Genetics</i> , 2020, 28, 435-444.	1.4	29
8	Glucagon-like peptide-1 receptor and sarcoglycan delta genetic variants can affect cardiovascular risk in chronic kidney disease patients under hemodialysis. <i>CKJ: Clinical Kidney Journal</i> , 2020, 13, 666-673.	1.4	3
9	Deleterious variants in genes associated with bone mineral density are linked to susceptibility to periodontitis development. <i>Meta Gene</i> , 2020, 24, 100670.	0.3	2
10	A population-based approach for gene prioritization in understanding complex traits. <i>Human Genetics</i> , 2020, 139, 647-655.	1.8	7
11	Mutations in <i>PLS1</i> , encoding fimbrin, cause autosomal dominant nonsyndromic hearing loss. <i>Human Mutation</i> , 2019, 40, 2286-2295.	1.1	23
12	A transcriptomic atlas of mammalian olfactory mucosae reveals an evolutionary influence on food odor detection in humans. <i>Science Advances</i> , 2019, 5, eaax0396.	4.7	59
13	Next generation sequencing study in a cohort of Italian patients with syndromic hearing loss. <i>Hearing Research</i> , 2019, 381, 107769.	0.9	7
14	Establishment and equilibrium levels of deleterious mutations in large populations. <i>Scientific Reports</i> , 2019, 9, 10384.	1.6	2
15	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	5.8	84
16	Investigation of the link between PROP taste perception and vegetables consumption using FAOSTAT data. <i>International Journal of Food Sciences and Nutrition</i> , 2019, 70, 484-490.	1.3	6
17	Response to Giem. <i>American Journal of Human Genetics</i> , 2018, 102, 331.	2.6	1
18	MMAB, a novel candidate gene to be screened in the molecular diagnosis of Mevalonate Kinase Deficiency. <i>Rheumatology International</i> , 2018, 38, 121-127.	1.5	1

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19	Genetic Landscape of Slovenians: Past Admixture and Natural Selection Pattern. <i>Frontiers in Genetics</i> , 2018, 9, 551.	1.1	8
20	Demographic History and Genetic Adaptation in the Himalayan Region Inferred from Genome-Wide SNP Genotypes of 49 Populations. <i>Molecular Biology and Evolution</i> , 2018, 35, 1916-1933.	3.5	36
21	Mutations in L-type amino acid transporter-2 support SLC7A8 as a novel gene involved in age-related hearing loss. <i>ELife</i> , 2018, 7, .	2.8	38
22	Investigation of genetic variation and lifestyle determinants in vitamin D levels in Arab individuals. <i>Journal of Translational Medicine</i> , 2018, 16, 20.	1.8	9
23	FineMAV: prioritizing candidate genetic variants driving local adaptations in human populations. <i>Genome Biology</i> , 2018, 19, 5.	3.8	20
24	Whole-genome sequencing reveals new insights into age-related hearing loss: cumulative effects, pleiotropy and the role of selection. <i>European Journal of Human Genetics</i> , 2018, 26, 1167-1179.	1.4	22
25	Continuity and Admixture in the Last Five Millennia of Levantine History from Ancient Canaanite and Present-Day Lebanese Genome Sequences. <i>American Journal of Human Genetics</i> , 2017, 101, 274-282.	2.6	102
26	“Like sugar in milk” reconstructing the genetic history of the Parsi population. <i>Genome Biology</i> , 2017, 18, 110.	3.8	29
27	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. <i>Nature Communications</i> , 2017, 8, 15927.	5.8	64
28	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	9.4	2,421
29	Global diversity in the TAS2R38 bitter taste receptor: revisiting a classic evolutionary PROposal. <i>Scientific Reports</i> , 2016, 6, 25506.	1.6	69
30	Chad Genetic Diversity Reveals an African History Marked by Multiple Holocene Eurasian Migrations. <i>American Journal of Human Genetics</i> , 2016, 99, 1316-1324.	2.6	37
31	Wide distribution and altitude correlation of an archaic high-altitude-adaptive EPAS1 haplotype in the Himalayas. <i>Human Genetics</i> , 2016, 135, 393-402.	1.8	41
32	Genetic evidence for an origin of the Armenians from Bronze Age mixing of multiple populations. <i>European Journal of Human Genetics</i> , 2016, 24, 931-936.	1.4	44
33	Response to Hellenthal et al.:. <i>American Journal of Human Genetics</i> , 2016, 98, 398.	2.6	1
34	Understanding the role of personality and alexithymia in food preferences and PROP taste perception. <i>Physiology and Behavior</i> , 2016, 157, 72-78.	1.0	37
35	Tracking of the origin of recurrent mutations of the BRCA1 and BRCA2 genes in the North-East of Italy and improved mutation analysis strategy. <i>BMC Medical Genetics</i> , 2016, 17, 11.	2.1	16
36	Ancient DNA and the rewriting of human history: be sparing with Occam’s razor. <i>Genome Biology</i> , 2016, 17, 1.	3.8	1,335

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37	Early modern human dispersal from Africa: genomic evidence for multiple waves of migration. <i>Investigative Genetics</i> , 2015, 6, 13.	3.3	34
38	Neon: An R Package to Estimate Human Effective Population Size and Divergence Time from Patterns of Linkage Disequilibrium between SNPs. <i>Journal of Computer Science and Systems Biology</i> , 2015, 8, .	0.0	28
39	Increased Rate of Deleterious Variants in Long Runs of Homozygosity of an Inbred Population from Qatar. <i>Human Heredity</i> , 2015, 79, 14-19.	0.4	28
40	Analysis of functional variants reveals new candidate genes associated with alexithymia. <i>Psychiatry Research</i> , 2015, 227, 363-365.	1.7	12
41	The Kalash Genetic Isolate: Ancient Divergence, Drift, and Selection. <i>American Journal of Human Genetics</i> , 2015, 96, 775-783.	2.6	46
42	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , 2015, 47, 1357-1362.	9.4	227
43	Insights into the origin of rare haplogroup C3* Y chromosomes in South America from high-density autosomal SNP genotyping. <i>Forensic Science International: Genetics</i> , 2015, 15, 115-120.	1.6	10
44	Assessment of the Olfactory Function in Italian Patients with Type 3 von Willebrand Disease Caused by a Homozygous 253 Kb Deletion Involving VWF and TMEM16B/ANO2. <i>PLoS ONE</i> , 2015, 10, e0116483.	1.1	7
45	A Population-Based Approach to Study the Impact of PROP Perception on Food Liking in Populations along the Silk Road. <i>PLoS ONE</i> , 2014, 9, e91716.	1.1	34
46	Genetic characterization of Greek population isolates reveals strong genetic drift at missense and trait-associated variants. <i>Nature Communications</i> , 2014, 5, 5345.	5.8	60
47	Consanguinity and Hereditary Hearing Loss in Qatar. <i>Human Heredity</i> , 2014, 77, 175-182.	0.4	15
48	Genetic landscape of populations along the Silk Road: admixture and migration patterns. <i>BMC Genetics</i> , 2014, 15, 131.	2.7	24
49	Insight into genetic determinants of resting heart rate. <i>Gene</i> , 2014, 545, 170-174.	1.0	7
50	Evidence for past and present hybridization in three Antarctic icefish species provides new perspectives on an evolutionary radiation. <i>Molecular Ecology</i> , 2013, 22, 5148-5161.	2.0	29
51	Genetic characterization of northeastern Italian population isolates in the context of broader European genetic diversity. <i>European Journal of Human Genetics</i> , 2013, 21, 659-665.	1.4	64
52	High variance in reproductive success generates a false signature of a genetic bottleneck in populations of constant size: a simulation study. <i>BMC Bioinformatics</i> , 2013, 14, 309.	1.2	29
53	Genetics of eye colours in different rural populations on the Silk Road. <i>European Journal of Human Genetics</i> , 2013, 21, 1320-1323.	1.4	11
54	Population genetic structure and gene flow patterns between populations of the Antarctic icefish <i>Chionodraco rastrospinosus</i> . <i>Journal of Biogeography</i> , 2012, 39, 1361-1372.	1.4	27

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55	Gone with the currents: lack of genetic differentiation at the circum-continental scale in the Antarctic krill <i>Euphausia superba</i> . <i>BMC Genetics</i> , 2011, 12, 32.	2.7	51