Massimo Mezzavilla

List of Publications by Year in descending order

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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	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
2	Ancient DNA and the rewriting of human history: be sparing with Occamâ€™s razor. Genome Biology, 2016, 17, 1.	3.8	1,335
3	Population genetic differentiation of height and body mass index across Europe. Nature Genetics, 2015, 47, 1357-1362.	9.4	227
4	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
5	Continuity and Admixture in the Last Five Millennia of Levantine History from Ancient Canaanite and Present-Day Lebanese Genome Sequences. American Journal of Human Genetics, 2017, 101, 274-282.	2.6	102
6	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
7	Global diversity in the TAS2R38 bitter taste receptor: revisiting a classic evolutionary PROPosal. Scientific Reports, 2016, 6, 25506.	1.6	69
8	Genetic characterization of northeastern Italian population isolates in the context of broader European genetic diversity. European Journal of Human Genetics, 2013, 21, 659-665.	1.4	64
9	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. Nature Communications, 2017, 8, 15927.	5.8	64
10	Genetic characterization of Greek population isolates reveals strong genetic drift at missense and trait-associated variants. Nature Communications, 2014, 5, 5345.	5.8	60
11	A transcriptomic atlas of mammalian olfactory mucosae reveals an evolutionary influence on food odor detection in humans. Science Advances, 2019, 5, eaax0396.	4.7	59
12	Gone with the currents: lack of genetic differentiation at the circum-continental scale in the Antarctic krill Euphausia superba. BMC Genetics, 2011, 12, 32.	2.7	51
13	The Kalash Genetic Isolate: Ancient Divergence, Drift, and Selection. American Journal of Human Genetics, 2015, 96, 775-783.	2.6	46
14	Genetic evidence for an origin of the Armenians from Bronze Age mixing of multiple populations. European Journal of Human Genetics, 2016, 24, 931-936.	1.4	44
15	Wide distribution and altitude correlation of an archaic high-altitude-adaptive EPAS1 haplotype in the Himalayas. Human Genetics, 2016, 135, 393-402.	1.8	41
16	Mutations in L-type amino acid transporter-2 support SLC7A8 as a novel gene involved in age-related hearing loss. ELife, 2018, 7, .	2.8	38
17	Chad Genetic Diversity Reveals an African History Marked by Multiple Holocene Eurasian Migrations. American Journal of Human Genetics, 2016, 99, 1316-1324.	2.6	37
18	Understanding the role of personality and alexithymia in food preferences and PROP taste perception. Physiology and Behavior, 2016, 157, 72-78.	1.0	37

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19	Demographic History and Genetic Adaptation in the Himalayan Region Inferred from Genome-Wide SNP Genotypes of 49 Populations. Molecular Biology and Evolution, 2018, 35, 1916-1933.	3.5	36
20	The landscape of autosomal-recessive pathogenic variants in European populations reveals phenotype-specific effects. American Journal of Human Genetics, 2021, 108, 608-619.	2.6	36
21	A Population-Based Approach to Study the Impact of PROP Perception on Food Liking in Populations along the Silk Road. PLoS ONE, 2014, 9, e91716.	1.1	34
22	Early modern human dispersal from Africa: genomic evidence for multiple waves of migration. Investigative Genetics, 2015, 6, 13.	3.3	34
23	Evidence for past and present hybridization in three <scp>A</scp>ntarctic icefish species provides new perspectives on an evolutionary radiation. Molecular Ecology, 2013, 22, 5148-5161.	2.0	29
24	High variance in reproductive success generates a false signature of a genetic bottleneck in populations of constant size: a simulation study. BMC Bioinformatics, 2013, 14, 309.	1.2	29
25	â€œLike sugar in milkâ€• reconstructing the genetic history of the Parsi population. Genome Biology, 2017, 18, 110.	3.8	29
26	A birdâ€™s-eye view of Italian genomic variation through whole-genome sequencing. European Journal of Human Genetics, 2020, 28, 435-444.	1.4	29
27	Neon: An R Package to Estimate Human Effective Population Size and Divergence Time from Patterns of Linkage Disequilibrium between SNPS. Journal of Computer Science and Systems Biology, 2015, 8, .	0.0	28
28	Increased Rate of Deleterious Variants in Long Runs of Homozygosity of an Inbred Population from Qatar. Human Heredity, 2015, 79, 14-19.	0.4	28
29	Population genetic structure and gene flow patterns between populations of the Antarctic icefish Chionodraco rastrospinosus. Journal of Biogeography, 2012, 39, 1361-1372.	1.4	27
30	Genetic landscape of populations along the Silk Road: admixture and migration patterns. BMC Genetics, 2014, 15, 131.	2.7	24
31	Mutations in PLS1 , encoding fimbrin, cause autosomal dominant nonsyndromic hearing loss. Human Mutation, 2019, 40, 2286-2295.	1.1	23
32	Whole-genome sequencing reveals new insights into age-related hearing loss: cumulative effects, pleiotropy and the role of selection. European Journal of Human Genetics, 2018, 26, 1167-1179.	1.4	22
33	Fine-scale population structure and demographic history of British Pakistanis. Nature Communications, 2021, 12, 7189.	5.8	21
34	FineMAV: prioritizing candidate genetic variants driving local adaptations in human populations. Genome Biology, 2018, 19, 5.	3.8	20
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. BMC Medical Genetics, 2016, 17, 11.	2.1	16
36	Consanguinity and Hereditary Hearing Loss in Qatar. Human Heredity, 2014, 77, 175-182.	0.4	15

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37	Analysis of functional variants reveals new candidate genes associated with alexithymia. Psychiatry Research, 2015, 227, 363-365.	1.7	12
38	Genetics of eye colours in different rural populations on the Silk Road. European Journal of Human Genetics, 2013, 21, 1320-1323.	1.4	11
39	Insights into the origin of rare haplogroup C3* Y chromosomes in South America from high-density autosomal SNP genotyping. Forensic Science International: Genetics, 2015, 15, 115-120.	1.6	10
40	Investigation of genetic variation and lifestyle determinants in vitamin D levels in Arab individuals. Journal of Translational Medicine, 2018, 16, 20.	1.8	9
41	Genetic Landscape of Slovenians: Past Admixture and Natural Selection Pattern. Frontiers in Genetics, 2018, 9, 551.	1.1	8
42	Insight into genetic determinants of resting heart rate. Gene, 2014, 545, 170-174.	1.0	7
43	Next generation sequencing study in a cohort of Italian patients with syndromic hearing loss. Hearing Research, 2019, 381, 107769.	0.9	7
44	A population-based approach for gene prioritization in understanding complex traits. Human Genetics, 2020, 139, 647-655.	1.8	7
45	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. PLoS ONE, 2015, 10, e0116483.	1.1	7
46	Investigation of the link between PROP taste perception and vegetables consumption using FAOSTAT data. International Journal of Food Sciences and Nutrition, 2019, 70, 484-490.	1.3	6
47	Natural human knockouts and Mendelian disorders: deep phenotyping in Italian isolates. European Journal of Human Genetics, 2021, 29, 1272-1281.	1.4	6
48	Glucagon-like peptide-1 receptor and sarcoglycan delta genetic variants can affect cardiovascular risk in chronic kidney disease patients under hemodialysis. CKJ: Clinical Kidney Journal, 2020, 13, 666-673.	1.4	3
49	Runs of homozygosity are associated with staging of periodontitis in isolated populations. Human Molecular Genetics, 2021, 30, 1154-1159.	1.4	3
50	Establishment and equilibrium levels of deleterious mutations in large populations. Scientific Reports, 2019, 9, 10384.	1.6	2
51	Deleterious variants in genes associated with bone mineral density are linked to susceptibility to periodontitis development. Meta Gene, 2020, 24, 100670.	0.3	2
52	Response to Hellenthal etÂal.:. American Journal of Human Genetics, 2016, 98, 398.	2.6	1
53	Response to Giem. American Journal of Human Genetics, 2018, 102, 331.	2.6	1
54	MMAB, a novel candidate gene to be screened in the molecular diagnosis of Mevalonate Kinase Deficiency. Rheumatology International, 2018, 38, 121-127.	1.5	1

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55	Poking COVID-19: Insights on Genomic Constraints among Immune-Related Genes between Qatari and Italian Populations. Genes, 2021, 12, 1842.	1.0	1