

Large-Scale Whole-Genome Sequencing of Three Divers

Cell

179, 736-749.e15

DOI: [10.1016/j.cell.2019.09.019](https://doi.org/10.1016/j.cell.2019.09.019)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Hemoglobin E, malaria and natural selection. <i>Evolution, Medicine and Public Health</i> , 2019, 2019, 232-241.	1.1	13
2	PGG.Han: the Han Chinese genome database and analysis platform. <i>Nucleic Acids Research</i> , 2020, 48, D971-D976.	6.5	51
3	“Who is watching the watchdog?” ethical perspectives of sharing health-related data for precision medicine in Singapore. <i>BMC Medical Ethics</i> , 2020, 21, 118.	1.0	16
4	Understanding the genetic history of Malay populations in Peninsular Malaysia via KIR genes diversity. <i>American Journal of Human Biology</i> , 2021, 33, e23545.	0.8	2
5	Genetic profiling of Vietnamese population from large-scale genomic analysis of non-invasive prenatal testing data. <i>Scientific Reports</i> , 2020, 10, 19142.	1.6	8
6	Ethnicity, Neighborhood and Individual Socioeconomic Status, and Obesity: The Singapore Multiethnic Cohort. <i>Obesity</i> , 2020, 28, 2405-2413.	1.5	18
7	Evolutionary Genomics of High Fecundity. <i>Annual Review of Genetics</i> , 2020, 54, 213-236.	3.2	14
8	YAP is essential for TGF β -induced retinal fibrosis in diabetic rats via promoting the fibrogenic activity of Müller cells. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 12390-12400.	1.6	21
9	Genome-Wide Meta-Analysis Identifies Three Novel Susceptibility Loci and Reveals Ethnic Heterogeneity of Genetic Susceptibility for IgA Nephropathy. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 2949-2963.	3.0	42
10	Genetic Association of Age-Related Macular Degeneration and Polypoidal Choroidal Vasculopathy. <i>Asia-Pacific Journal of Ophthalmology</i> , 2020, 9, 104-109.	1.3	16
11	Whole-Exome Sequencing in Czech Patients with Neurogenetic Diseases. <i>Genetic Testing and Molecular Biomarkers</i> , 2020, 24, 264-273.	0.3	0
12	Prevalence of <i>BRCA1</i> / <i>BRCA2</i> pathogenic variation in Chinese Han population. <i>Journal of Medical Genetics</i> , 2021, 58, 565-569.	1.5	27
13	Evaluating individual genome similarity with a topic model. <i>Bioinformatics</i> , 2020, 36, 4757-4764.	1.8	1
14	Risk factors for insulin resistance in midlife Singaporean women. <i>Maturitas</i> , 2020, 137, 50-56.	1.0	6
15	The ChinaMAP analytics of deep whole genome sequences in 10,588 individuals. <i>Cell Research</i> , 2020, 30, 717-731.	5.7	165
16	Using off-target data from whole-exome sequencing to improve genotyping accuracy, association analysis and polygenic risk prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	8
17	Cohort Profile: The Singapore Epidemiology of Eye Diseases study (SEED). <i>International Journal of Epidemiology</i> , 2021, 50, 41-52.	0.9	49
19	The indigenous populations as the model by nature to understand human genomic-environmental interactions. <i>Quantitative Biology</i> , 2022, 10, 35-43.	0.3	0

#	ARTICLE	IF	CITATIONS
21	Genome-wide identification of cis DNA methylation quantitative trait loci in three Southeast Asian Populations. <i>Human Molecular Genetics</i> , 2021, 30, 603-618.	1.4	5
23	A data set of variants derived from 1455 clinical and research exomes is efficient in variant prioritization for early-onset monogenic disorders in Indians. <i>Human Mutation</i> , 2021, 42, e15-e61.	1.1	25
24	How to design a national genomic project—a systematic review of active projects. <i>Human Genomics</i> , 2021, 15, 20.	1.4	12
25	Perceptions of “Precision” and “Personalised” Medicine in Singapore and Associated Ethical Issues. <i>Asian Bioethics Review</i> , 2021, 13, 179-194.	0.9	16
26	GenomeAsia100K: Singapore Builds National Science with Asian DNA. <i>East Asian Science, Technology and Society</i> , 2021, 15, 238-259.	0.2	5
27	Low frequency variants associated with leukocyte telomere length in the Singapore Chinese population. <i>Communications Biology</i> , 2021, 4, 519.	2.0	15
28	Prevalence and spectrum of DNA mismatch repair gene variation in the general Chinese population. <i>Journal of Medical Genetics</i> , 2022, 59, 652-661.	1.5	9
29	Genetic Admixture in the Culturally Unique Peranakan Chinese Population in Southeast Asia. <i>Molecular Biology and Evolution</i> , 2021, 38, 4463-4474.	3.5	8
30	Generational Medicine in Singapore: A National Biobank for a Greying Nation. <i>East Asian Science, Technology and Society</i> , 2023, 17, 71-87.	0.2	3
32	Psi-Caller: A Lightweight Short Read-Based Variant Caller With High Speed and Accuracy. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 731424.	1.8	5
33	The Thai reference exome (Tâ€REx) variant database. <i>Clinical Genetics</i> , 2021, 100, 703-712.	1.0	24
35	Spectrum of Germline Mutations Within Fanconi Anemia—Associated Genes Across Populations of Varying Ancestry. <i>JNCI Cancer Spectrum</i> , 2021, 5, .	1.4	3
37	Pharmacogenomics and Rheumatological Practice. <i>Journal of Clinical Rheumatology and Immunology</i> , 0, , 1-12.	0.4	0
39	Beyond sequencing: machine learning algorithms extract biology hidden in Nanopore signal data. <i>Trends in Genetics</i> , 2022, 38, 246-257.	2.9	42
40	Yes—associated protein is essential for proliferative vitreoretinopathy development via the epithelial—mesenchymal transition in retinal pigment epithelial fibrosis. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 10213-10223.	1.6	9
42	Mapping “bio geo-body” of Southeast Asia: strategic differentiation and identification of ethnic identity in Vietnam and Singapore. <i>BioSocieties</i> , 2021, 16, 530.	0.8	0
43	Mid-pass whole genome sequencing enables biomedical genetic studies of diverse populations. <i>BMC Genomics</i> , 2021, 22, 666.	1.2	5
44	Reconstruction of the Austronesian Diaspora in the Era of Genomics. <i>Human Biology</i> , 2020, 92, 247.	0.4	6

#	ARTICLE	IF	CITATIONS
45	NyuWa Genome resource: A deep whole-genome sequencing-based variation profile and reference panel for the Chinese population. <i>Cell Reports</i> , 2021, 37, 110017.	2.9	49
46	Rare variant association tests for ancestry-matched case-control data based on conditional logistic regression. <i>Briefings in Bioinformatics</i> , 2022, . .	3.2	2
48	The Peopling and Migration History of the Natives in Peninsular Malaysia and Borneo: A Glimpse on the Studies Over the Past 100 years. <i>Frontiers in Genetics</i> , 2022, 13, 767018.	1.1	1
49	Genome-Wide Association Analyses Identify <i>CATSPERE</i> as a Mediator of Colorectal Cancer Susceptibility and Progression. <i>Cancer Research</i> , 2022, 82, 986-997.	0.4	3
50	A meta-analysis of clinical manifestations in asian systemic lupus erythematosus: The effects of ancestry, ethnicity and gender. <i>Seminars in Arthritis and Rheumatism</i> , 2022, 52, 151932.	1.6	8
51	Qatar genome: Insights on genomics from the Middle East. <i>Human Mutation</i> , 2022, 43, 499-510.	1.1	29
52	Multicenter study on the genetics of glomerular diseases among southeast and south Asians: Deciphering Diversities –Renal Asian Genetics Network (DRAGoN). <i>Clinical Genetics</i> , 2022, 101, 541-551.	1.0	6
53	Effects of interracial experience on the race preferences of infants. <i>Journal of Experimental Child Psychology</i> , 2022, 216, 105352.	0.7	2
54	Causative Variants for Inherited Cardiac Conditions in a Southeast Asian Population Cohort. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, CIRCGEN121003536.	1.6	1
55	Etiological roles of core promoter variation in triple-negative breast cancer. <i>Genes and Diseases</i> , 2023, 10, 228-238.	1.5	1
56	Compound Heterozygous Factor VII Deficiency c.1025G>A p.(Arg342Gln) With Novel Missense Variant c.194C>G p.(Ala65Gly). <i>Journal of Hematology (Brossard, Quebec)</i> , 2022, 11, 29-33.	0.4	1
57	A homozygous hypomorphic <i>BNIP1</i> variant causes an increase in autophagosomes and reduced autophagic flux and results in a spondyloepiphyseal dysplasia. <i>Human Mutation</i> , 2022, 43, 625-642.	1.1	3
58	Variant landscape of the RYR1 gene based on whole genome sequencing of the Singaporean population. <i>Scientific Reports</i> , 2022, 12, 5429.	1.6	1
59	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. <i>Communications Biology</i> , 2022, 5, 329.	2.0	21
60	Forensic genetic genealogy using microarrays for the identification of human remains: The need for good quality samples – A pilot study. <i>Forensic Science International</i> , 2022, 334, 111242.	1.3	16
61	Deviation from baseline mutation burden provides powerful and robust rare-variants association test for complex diseases. <i>Nucleic Acids Research</i> , 2022, 50, e34-e34.	6.5	3
62	Prioritising positively selected variants in whole-genome sequencing data using FineMAV. <i>BMC Bioinformatics</i> , 2021, 22, 604.	1.2	0
64	Evaluating the Coronary Artery Disease Consortium Model and the Coronary Artery Calcium Score in Predicting Obstructive Coronary Artery Disease in a Symptomatic Mixed Asian Cohort. <i>Journal of the American Heart Association</i> , 2022, 11, e022697.	1.6	3

#	ARTICLE	IF	CITATIONS
65	Integrative Multi-Omics database (iMOMdb) of Asian Pregnant Women. Human Molecular Genetics, 2022, , .	1.4	2
66	Genetic associations with healthy ageing among Chinese adults. , 2022, 8, .		1
67	An Eigenvalue Ratio Approach to Inferring Population Structure from Whole Genome Sequencing Data. Biometrics, 2023, 79, 891-902.	0.8	2
68	Genomic analyses of 10,376 individuals in the Westlake BioBank for Chinese (WBBC) pilot project. Nature Communications, 2022, 13, .	5.8	41
69	Identification of genomic regions distorting population structure inference in diverse continental groups. Quantitative Biology, 2022, 10, 287-298.	0.3	2
71	An efficient ancestry informative SNPs panel for further discriminating East Asian populations. Electrophoresis, 2022, 43, 1774-1783.	1.3	2
72	Sharing precision medicine data with private industry: Outcomes of a citizensâ€™ jury in Singapore. Big Data and Society, 2022, 9, 205395172211089.	2.6	3
73	Is blockchain the breakthrough we are looking for to facilitate genomic data sharing? The European Union perspective. Digital Health, 2022, 8, 205520762211142.	0.9	0
75	Analyses of rare predisposing variants of lung cancer in 6,004 whole genomes in Chinese. Cancer Cell, 2022, 40, 1223-1239.e6.	7.7	23
78	Use of race, ethnicity, and ancestry data in health research. PLOS Global Public Health, 2022, 2, e0001060.	0.5	32
80	Construction of a trio-based structural variation panel utilizing activated T lymphocytes and long-read sequencing technology. Communications Biology, 2022, 5, .	2.0	4
82	Taiwan Biobank: A rich biomedical research database of the Taiwanese population. Cell Genomics, 2022, 2, 100197.	3.0	21
83	Identification of genomic regions associated with total and progressive sperm motility in Italian Holstein bulls. Journal of Dairy Science, 2023, 106, 407-420.	1.4	10
84	Analysis of clinically relevant variants from ancestrally diverse Asian genomes. Nature Communications, 2022, 13, .	5.8	16
85	Mutant MESD links cellular stress to type I collagen aggregation in osteogenesis imperfecta type XX. Matrix Biology, 2023, 115, 81-106.	1.5	5
88	A robust pipeline for ranking carrier frequencies of autosomal recessive and X-linked Mendelian disorders. Npj Genomic Medicine, 2022, 7, .	1.7	3
89	Comparison of calling pipelines for whole genome sequencing: an empirical study demonstrating the importance of mapping and alignment. Scientific Reports, 2022, 12, .	1.6	9
91	Demographic model and biological adaptation inferred from the genome-wide single nucleotide polymorphism data reveal tripartite origins of southernmost Chinese. American Journal of Biological Anthropology, 2023, 180, 488-505.	0.6	1

#	ARTICLE	IF	CITATIONS
92	Comparing the pooled cohort equations and coronary artery calcium scores in a symptomatic mixed Asian cohort. <i>Frontiers in Cardiovascular Medicine</i> , 0, 10, .	1.1	0
93	Understanding cancer predisposition in Singapore: What's next. <i>Singapore Medical Journal</i> , 2023, 64, 37.	0.3	2
94	Genome-wide allele and haplotype-sharing patterns suggested one unique Hmong-related lineage and biological adaptation history in Southwest China. <i>Human Genomics</i> , 2023, 17, .	1.4	6
95	Robust SNP-based prediction of rheumatoid arthritis through machine-learning-optimized polygenic risk score. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	5
97	No evidence for a common blood microbiome based on a population study of 9,770 healthy humans. <i>Nature Microbiology</i> , 2023, 8, 973-985.	5.9	18
98	GBC: a parallel toolkit based on highly addressable byte-encoding blocks for extremely large-scale genotypes of species. <i>Genome Biology</i> , 2023, 24, .	3.8	0
106	Somatic mutations in facial skin from countries of contrasting skin cancer risk. <i>Nature Genetics</i> , 2023, 55, 1440-1447.	9.4	5
113	Implementation of Exome Sequencing to Identify Rare Genetic Diseases. <i>Methods in Molecular Biology</i> , 2024, , 79-98.	0.4	0