

Large-Scale Whole-Genome Sequencing of Three Divers

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Hemoglobin E, malaria and natural selection. <i>Evolution, Medicine and Public Health</i> , 2019, 2019, 232-241.	2.5	13
2	PGC.Han: the Han Chinese genome database and analysis platform. <i>Nucleic Acids Research</i> , 2020, 48, D971-D976.	14.5	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.	2.4	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.	1.6	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.	3.3	8
6	Ethnicity, Neighborhood and Individual Socioeconomic Status, and Obesity: The Singapore Multiethnic Cohort. <i>Obesity</i> , 2020, 28, 2405-2413.	3.0	18
7	Evolutionary Genomics of High Fecundity. <i>Annual Review of Genetics</i> , 2020, 54, 213-236.	7.6	14
8	YAP is essential for TGF β 2-induced retinal fibrosis in diabetic rats via promoting the fibrogenic activity of M α ller cells. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 12390-12400.	3.6	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.	6.1	42
10	Genetic Association of Age-Related Macular Degeneration and Polypoidal Choroidal Vasculopathy. <i>Asia-Pacific Journal of Ophthalmology</i> , 2020, 9, 104-109.	2.5	16
11	Whole-Exome Sequencing in Czech Patients with Neurogenetic Diseases. <i>Genetic Testing and Molecular Biomarkers</i> , 2020, 24, 264-273.	0.7	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.	3.2	27
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14	Risk factors for insulin resistance in midlife Singaporean women. <i>Maturitas</i> , 2020, 137, 50-56.	2.4	6
15	The ChinaMAP analytics of deep whole genome sequences in 10,588 individuals. <i>Cell Research</i> , 2020, 30, 717-731.	12.0	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, .	6.5	8
17	Cohort Profile: The Singapore Epidemiology of Eye Diseases study (SEED). <i>International Journal of Epidemiology</i> , 2021, 50, 41-52.	1.9	49
19	The indigenous populations as the model by nature to understand human genomic-phenomics interactions. <i>Quantitative Biology</i> , 2022, 10, 35-43.	0.5	0

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21	Genome-wide identification of cis DNA methylation quantitative trait loci in three Southeast Asian Populations. Human Molecular Genetics, 2021, 30, 603-618.	2.9	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. Human Mutation, 2021, 42, e15-e61.	2.5	25
24	How to design a national genomic project—a systematic review of active projects. Human Genomics, 2021, 15, 20.	2.9	12
25	Perceptions of “Precision” and “Personalised” Medicine in Singapore and Associated Ethical Issues. Asian Bioethics Review, 2021, 13, 179-194.	1.3	16
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37	Pharmacogenomics and Rheumatological Practice. Journal of Clinical Rheumatology and Immunology, 0, , 1-12.	0.4	0
39	Beyond sequencing: machine learning algorithms extract biology hidden in Nanopore signal data. Trends in Genetics, 2022, 38, 246-257.	6.7	42
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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.	3.4	8
51	Qatar genome: Insights on genomics from the Middle East. <i>Human Mutation</i> , 2022, 43, 499-510.	2.5	29
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59	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. <i>Communications Biology</i> , 2022, 5, 329.	4.4	21
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