

Sungwon Jeon

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

689
citations

840776

11
h-index

642732

23
g-index

31
all docs

31
docs citations

31
times ranked

1429
citing authors

#	ARTICLE	IF	CITATIONS
1	The <i>Galleria mellonella</i> Hologenome Supports Microbiota-Independent Metabolism of Long-Chain Hydrocarbon Beeswax. <i>Cell Reports</i> , 2019, 26, 2451-2464.e5.	6.4	103
2	Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. <i>Genome Biology</i> , 2016, 17, 211.	8.8	101
3	Genome-wide data from two early Neolithic East Asian individuals dating to 7700 years ago. <i>Science Advances</i> , 2017, 3, e1601877.	10.3	100
4	Korean Genome Project: 1094 Korean personal genomes with clinical information. <i>Science Advances</i> , 2020, 6, eaaz7835.	10.3	75
5	The Draft Genome of an Octocoral, <i>Dendronephthya gigantea</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 949-953.	2.5	44
6	Depression and suicide risk prediction models using blood-derived multi-omics data. <i>Translational Psychiatry</i> , 2019, 9, 262.	4.8	38
7	The genome of the giant <i>Nomura</i> 's jellyfish sheds light on the early evolution of active predation. <i>BMC Biology</i> , 2019, 17, 28.	3.8	38
8	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, <i>Homotherium latidens</i> . <i>Current Biology</i> , 2020, 30, 5018-5025.e5.	3.9	34
9	The whale shark genome reveals how genomic and physiological properties scale with body size. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20662-20671.	7.1	32
10	Chromosome-scale assembly comparison of the Korean Reference Genome KOREF from PromethION and PacBio with Hi-C mapping information. <i>GigaScience</i> , 2019, 8, .	6.4	18
11	The Origin and Composition of Korean Ethnicity Analyzed by Ancient and Present-Day Genome Sequences. <i>Genome Biology and Evolution</i> , 2020, 12, 553-565.	2.5	17
12	Regional TMPRSS2 V197M Allele Frequencies Are Correlated with COVID-19 Case Fatality Rates. <i>Molecules and Cells</i> , 2021, 44, 680-687.	2.6	12
13	<i>Myotis rufoniger</i> genome sequence and analyses: <i>M. rufoniger</i> 's genomic feature and the decreasing effective population size of <i>Myotis</i> bats. <i>PLoS ONE</i> , 2017, 12, e0180418.	2.5	10
14	Whole genome sequencing and bioinformatics analysis of two Egyptian genomes. <i>Gene</i> , 2018, 668, 129-134.	2.2	9
15	Sequencing and analysis of the whole genome of Indian Gujarati male. <i>Genomics</i> , 2019, 111, 196-204.	2.9	9
16	Multiple types of genomic variation contribute to adaptive traits in the mustelid subfamily Guloninae. <i>Molecular Ecology</i> , 2022, 31, 2898-2919.	3.9	8
17	Polygenic risk score validation using Korean genomes of 265 early-onset acute myocardial infarction patients and 636 healthy controls. <i>PLoS ONE</i> , 2021, 16, e0246538.	2.5	7
18	Welfare Genome Project: A Participatory Korean Personal Genome Project With Free Health Check-Up and Genetic Report Followed by Counseling. <i>Frontiers in Genetics</i> , 2021, 12, 633731.	2.3	6

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19	Whole Genome Analysis of the Red-Crowned Crane Provides Insight into Avian Longevity. <i>Molecules and Cells</i> , 2020, 43, 86-95.	2.6	6
20	Northeastern Asian and Jomon-related genetic structure in the Three Kingdoms period of Gimhae, Korea. <i>Current Biology</i> , 2022, 32, 3232-3244.e6.	3.9	6
21	Complete genome sequence and bioinformatics analysis of nine Egyptian females with clinical information from different geographic regions in Egypt. <i>Gene</i> , 2021, 769, 145237.	2.2	5
22	Decoding a highly mixed Kazakh genome. <i>Human Genetics</i> , 2020, 139, 557-568.	3.8	4
23	KOREF_S1: phased, parental trio-binned Korean reference genome using long reads and Hi-C sequencing methods. <i>GigaScience</i> , 2022, 11, .	6.4	3
24	LT1, an ONT long-read-based assembly scaffolded with Hi-C data and polished with short reads. <i>GigaByte</i> , 0, 2022, 1-16.	0.0	0