

Hak-Min Kim

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/510104/publications.pdf>

Version: 2024-02-01

22
papers

1,225
citations

567281

15
h-index

713466

21
g-index

23
all docs

23
docs citations

23
times ranked

3040
citing authors

#	ARTICLE	IF	CITATIONS
1	Minke whale genome and aquatic adaptation in cetaceans. <i>Nature Genetics</i> , 2014, 46, 88-92.	21.4	227
2	The tiger genome and comparative analysis with lion and snow leopard genomes. <i>Nature Communications</i> , 2013, 4, 2433.	12.8	217
3	Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. <i>Genome Biology</i> , 2016, 17, 211.	8.8	101
4	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
5	Korean Genome Project: 1094 Korean personal genomes with clinical information. <i>Science Advances</i> , 2020, 6, eaaz7835.	10.3	75
6	Whole transcriptome analyses of six thoroughbred horses before and after exercise using RNA-Seq. <i>BMC Genomics</i> , 2012, 13, 473.	2.8	73
7	Genomic profile analysis of diffuse-type gastric cancers. <i>Genome Biology</i> , 2014, 15, R55.	9.6	58
8	An ethnically relevant consensus Korean reference genome is a step towards personal reference genomes. <i>Nature Communications</i> , 2016, 7, 13637.	12.8	58
9	Comprehensive genome- and transcriptome-wide analyses of mutations associated with microsatellite instability in Korean gastric cancers. <i>Genome Research</i> , 2013, 23, 1109-1117.	5.5	56
10	The first whole genome and transcriptome of the cinereous vulture reveals adaptation in the gastric and immune defense systems and possible convergent evolution between the Old and New World vultures. <i>Genome Biology</i> , 2015, 16, 215.	8.8	41
11	KoVariome: Korean National Standard Reference Variome database of whole genomes with comprehensive SNV, indel, CNV, and SV analyses. <i>Scientific Reports</i> , 2018, 8, 5677.	3.3	39
12	Depression and suicide risk prediction models using blood-derived multi-omics data. <i>Translational Psychiatry</i> , 2019, 9, 262.	4.8	38
13	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
14	Whole genome sequence and analysis of the Marwari horse breed and its genetic origin. <i>BMC Genomics</i> , 2014, 15, S4.	2.8	30
15	Peeling Back the Evolutionary Layers of Molecular Mechanisms Responsive to Exercise-Stress in the Skeletal Muscle of the Racing Horse. <i>DNA Research</i> , 2013, 20, 287-298.	3.4	20
16	Whole genome sequencing of an ethnic Pathan (Pakhtun) from the north-west of Pakistan. <i>BMC Genomics</i> , 2015, 16, 172.	2.8	16
17	Homozygous deletions at 3p22, 5p14, 6q15, and 9p21 result in aberrant expression of tumor suppressor genes in gastric cancer. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 142-155.	2.8	13
18	Whole genome comparison of donor and cloned dogs. <i>Scientific Reports</i> , 2013, 3, 2998.	3.3	11

#	ARTICLE	IF	CITATIONS
19	Myotis rufoniger genome sequence and analyses: M. rufoniger's genomic feature and the decreasing effective population size of Myotis bats. PLoS ONE, 2017, 12, e0180418.	2.5	10
20	Whole-genome analysis of a patient with early-stage small-cell lung cancer. Pharmacogenomics Journal, 2014, 14, 503-508.	2.0	7
21	COMUS: Clinician-Oriented locus-specific MUtation detection and deposition System. BMC Genomics, 2009, 10, S35.	2.8	2
22	Abstract 2024: Identification of novel oncogenes in a stage I small cell lung cancer through whole-genome sequencing.. , 2013, , .		0