

Arang Rhie

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

9,853
citations

186209

28
h-index

360920

35
g-index

72
all docs

72
docs citations

72
times ranked

8317
citing authors

#	ARTICLE	IF	CITATIONS
1	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	33
2	Merfin: improved variant filtering, assembly evaluation and polishing via k-mer validation. Nature Methods, 2022, 19, 696-704.	9.0	30
3	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. Nature Methods, 2022, 19, 687-695.	9.0	42
4	Epigenetic patterns in a complete human genome. Science, 2022, 376, eabj5089.	6.0	118
5	Complete genomic and epigenetic maps of human centromeres. Science, 2022, 376, eabl4178.	6.0	204
6	From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. Science, 2022, 376, eabk3112.	6.0	146
7	A complete reference genome improves analysis of human genetic variation. Science, 2022, 376, eabl3533.	6.0	144
8	The complete sequence of a human genome. Science, 2022, 376, 44-53.	6.0	1,222
9	Long-read mapping to repetitive reference sequences using Winnowmap2. Nature Methods, 2022, 19, 705-710.	9.0	80
10	Reference genome and demographic history of the most endangered marine mammal, the vaquita. Molecular Ecology Resources, 2021, 21, 1008-1020.	2.2	54
11	The structure, function and evolution of a complete human chromosome 8. Nature, 2021, 593, 101-107.	13.7	221
12	Evolutionary and biomedical insights from a marmoset diploid genome assembly. Nature, 2021, 594, 227-233.	13.7	42
13	Extended haplotype-phasing of long-read de novo genome assemblies using Hi-C. Nature Communications, 2021, 12, 1935.	5.8	64
14	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. Genome Biology, 2021, 22, 120.	3.8	69
15	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	13.7	1,139
16	Hi-C scaffolded short- and long-read genome assemblies of the California sea lion are broadly consistent for syntenic inference across 45 million years of evolution. Molecular Ecology Resources, 2021, 21, 2455-2470.	2.2	7
17	Population genomics of the critically endangered kakapo. Cell Genomics, 2021, 1, 100002.	3.0	106
18	Platypus and echidna genomes reveal mammalian biology and evolution. Nature, 2021, 592, 756-762.	13.7	85

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19	Weighted minimizer sampling improves long read mapping. <i>Bioinformatics</i> , 2020, 36, i111-i118.	1.8	116
20	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	13.7	549
21	Improved reference genome of the arboviral vector <i>Aedes albopictus</i> . <i>Genome Biology</i> , 2020, 21, 215.	3.8	65
22	Mercury: reference-free quality, completeness, and phasing assessment for genome assemblies. <i>Genome Biology</i> , 2020, 21, 245.	3.8	975
23	HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. <i>Genome Research</i> , 2020, 30, 1291-1305.	2.4	440
24	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. <i>Nature Communications</i> , 2020, 11, 2071.	5.8	84
25	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	3.3	46
26	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	3.3	380
27	Genetic variations associated with response to dutasteride in the treatment of male subjects with androgenetic alopecia. <i>PLoS ONE</i> , 2019, 14, e0222533.	1.1	4
28	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. <i>PLoS Computational Biology</i> , 2019, 15, e1007273.	1.5	509
29	HLA*LA€”HLA typing from linearly projected graph alignments. <i>Bioinformatics</i> , 2019, 35, 4394-4396.	1.8	88
30	New insights into mammalian sex chromosome structure and evolution using high-quality sequences from bovine X and Y chromosomes. <i>BMC Genomics</i> , 2019, 20, 1000.	1.2	21
31	Nanopore sequencing and assembly of a human genome with ultra-long reads. <i>Nature Biotechnology</i> , 2018, 36, 338-345.	9.4	1,443
32	De novo assembly of haplotype-resolved genomes with trio binning. <i>Nature Biotechnology</i> , 2018, 36, 1174-1182.	9.4	352
33	De novo assembly and phasing of a Korean human genome. <i>Nature</i> , 2016, 538, 243-247.	13.7	310
34	Genomic Copy Number Variations Characterize the Prognosis of Both P16-Positive and P16-Negative Oropharyngeal Squamous Cell Carcinoma After Curative Resection. <i>Medicine (United States)</i> , 2015, 94, e2187.	0.4	14
35	Abstract 4802: Transcriptional landscape of lung squamous cell carcinoma in Northeast Asian patients. , 2015, , .		0
36	Abstract 4574: Genomic copy number variations characterize prognosis of oropharyngeal squamous cell carcinoma, including p16 positive subset, after surgery-based treatment. , 2015, , .		0

#	ARTICLE	IF	CITATIONS
37	FX: an RNA-Seq analysis tool on the cloud. <i>Bioinformatics</i> , 2012, 28, 721-723.	1.8	66
38	Toward automatically drawn metabolic pathway atlas with peripheral node abstraction algorithm. , 2010, , .		0
39	Trace of evolutionary evidence by analyzing clustering information of metabolic pathways in eukaryotes. , 2010, , .		0
40	A genomic datawarehouse model for fast manipulation using repeat region. , 2010, , .		0