

Kai Ye

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

15,170
citations

186254

28
h-index

149686

56
g-index

72
all docs

72
docs citations

72
times ranked

30299
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutational landscape and significance across 12 major cancer types. <i>Nature</i> , 2013, 502, 333-339.	27.8	3,695
2	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015, 526, 75-81.	27.8	1,994
3	Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. <i>Bioinformatics</i> , 2009, 25, 2865-2871.	4.1	1,811
4	A comprehensive catalogue of somatic mutations from a human cancer genome. <i>Nature</i> , 2010, 463, 191-196.	27.8	1,519
5	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. <i>Science</i> , 2012, 335, 823-828.	12.6	1,095
6	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011, 470, 59-65.	27.8	991
7	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784.	12.8	636
8	MSIsensor: microsatellite instability detection using paired tumor-normal sequence data. <i>Bioinformatics</i> , 2014, 30, 1015-1016.	4.1	599
9	Genome-wide patterns and properties of de novo mutations in humans. <i>Nature Genetics</i> , 2015, 47, 822-826.	21.4	384
10	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. <i>Science</i> , 2021, 372, .	12.6	358
11	The Genome of the Netherlands: design, and project goals. <i>European Journal of Human Genetics</i> , 2014, 22, 221-227.	2.8	246
12	Patterns and functional implications of rare germline variants across 12 cancer types. <i>Nature Communications</i> , 2015, 6, 10086.	12.8	243
13	The opium poppy genome and morphinan production. <i>Science</i> , 2018, 362, 343-347.	12.6	225
14	Characteristics of de novo structural changes in the human genome. <i>Genome Research</i> , 2015, 25, 792-801.	5.5	115
15	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. <i>Nature Communications</i> , 2016, 7, 12989.	12.8	99
16	Systematic discovery of complex insertions and deletions in human cancers. <i>Nature Medicine</i> , 2016, 22, 97-104.	30.7	93
17	High-quality <i>Arabidopsis thaliana</i> Genome Assembly with Nanopore and HiFi Long Reads. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 4-13.	6.9	80
18	Application of Metagenomic Next-Generation Sequencing in the Diagnosis of Pulmonary Infectious Pathogens From Bronchoalveolar Lavage Samples. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 541092.	3.9	72

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19	Divergent viral presentation among human tumors and adjacent normal tissues. <i>Scientific Reports</i> , 2016, 6, 28294.	3.3	60
20	One reference genome is not enough. <i>Genome Biology</i> , 2019, 20, 104.	8.8	58
21	An exploration strategy improves the diversity of de novo ligands using deep reinforcement learning: a case for the adenosine A2A receptor. <i>Journal of Cheminformatics</i> , 2019, 11, 35.	6.1	58
22	MSIsensor-pro: Fast, Accurate, and Matched-normal-sample-free Detection of Microsatellite Instability. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 65-71.	6.9	53
23	Three chromosome-scale Papaver genomes reveal punctuated patchwork evolution of the morphinan and noscapine biosynthesis pathway. <i>Nature Communications</i> , 2021, 12, 6030.	12.8	51
24	A gain of function mutation in <i>TNFRSF11B</i> encoding osteoprotegerin causes osteoarthritis with chondrocalcinosis. <i>Annals of the Rheumatic Diseases</i> , 2015, 74, 1756-1762.	0.9	44
25	Aging as Accelerated Accumulation of Somatic Variants: Whole-Genome Sequencing of Centenarian and Middle-Aged Monozygotic Twin Pairs. <i>Twin Research and Human Genetics</i> , 2013, 16, 1026-1032.	0.6	40
26	A novel CD4+ CTL subtype characterized by chemotaxis and inflammation is involved in the pathogenesis of Graves' orbitopathy. <i>Cellular and Molecular Immunology</i> , 2021, 18, 735-745.	10.5	37
27	A two-entropies analysis to identify functional positions in the transmembrane region of class A G protein-coupled receptors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 1018-1030.	2.6	35
28	Tracing evolutionary pressure. <i>Bioinformatics</i> , 2008, 24, 908-915.	4.1	35
29	What Is Required to Prevent a Second Major Outbreak of SARS-CoV-2 upon Lifting Quarantine in Wuhan City, China. <i>Innovation(China)</i> , 2020, 1, 100006.	9.1	32
30	Multifactorial Deep Learning Reveals Pan-Cancer Genomic Tumor Clusters with Distinct Immunogenomic Landscape and Response to Immunotherapy. <i>Clinical Cancer Research</i> , 2020, 26, 2908-2920.	7.0	30
31	DrugEx v2: de novo design of drug molecules by Pareto-based multi-objective reinforcement learning in polypharmacology. <i>Journal of Cheminformatics</i> , 2021, 13, 85.	6.1	30
32	Chromosome-Scale Genome Assembly of <i>Fusarium oxysporum</i> Strain Fo47, a Fungal Endophyte and Biocontrol Agent. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1108-1111.	2.6	29
33	A Chromosome-Scale Genome Assembly for the <i>Fusarium oxysporum</i> Strain Fo5176 To Establish a Model <i>Arabidopsis</i> -Fungal Pathosystem. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3549-3555.	1.8	28
34	Cold atmospheric plasma as a potential tool for multiple myeloma treatment. <i>Oncotarget</i> , 2018, 9, 18002-18017.	1.8	28
35	An efficient, versatile and scalable pattern growth approach to mine frequent patterns in unaligned protein sequences. <i>Bioinformatics</i> , 2007, 23, 687-693.	4.1	23
36	Split-Read Indel and Structural Variant Calling Using PINDEL. <i>Methods in Molecular Biology</i> , 2018, 1833, 95-105.	0.9	20

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37	Integrating bulk and single-cell RNA sequencing reveals cellular heterogeneity and immune infiltration in hepatocellular carcinoma. <i>Molecular Oncology</i> , 2022, 16, 2195-2213.	4.6	16
38	Precision Medicine: What Challenges Are We Facing?. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 253-261.	6.9	15
39	Cellular heterogeneity and transcriptomic profiles during intrahepatic cholangiocarcinoma initiation and progression. <i>Hepatology</i> , 2022, 76, 1302-1317.	7.3	13
40	An improved burden-test pipeline for identifying associations from rare germline and somatic variants. <i>BMC Genomics</i> , 2017, 18, 753.	2.8	11
41	Haplotype-resolved Chinese male genome assembly based on high-fidelity sequencing. <i>Fundamental Research</i> , 2022, 2, 946-953.	3.3	11
42	MEpurity: estimating tumor purity using DNA methylation data. <i>Bioinformatics</i> , 2019, 35, 5298-5300.	4.1	8
43	Dynamic network inference and association computation discover gene modules regulating virulence, mycotoxin and sexual reproduction in <i>Fusarium graminearum</i> . <i>BMC Genomics</i> , 2020, 21, 179.	2.8	8
44	Homotopic Convex Transformation: A New Landscape Smoothing Method for the Traveling Salesman Problem. <i>IEEE Transactions on Cybernetics</i> , 2022, 52, 495-507.	9.5	7
45	PVTree: A Sequential Pattern Mining Method for Alignment Independent Phylogeny Reconstruction. <i>Genes</i> , 2019, 10, 73.	2.4	6
46	PRESM: personalized reference editor for somatic mutation discovery in cancer genomics. <i>Bioinformatics</i> , 2019, 35, 1445-1452.	4.1	6
47	Mako: A Graph-based Pattern Growth Approach to Detect Complex Structural Variants. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 205-218.	6.9	6
48	A global survey of the transcriptome of the opium poppy (<i>Papaver somniferum</i>) based on single-molecule long-read isoform sequencing. <i>Plant Journal</i> , 2022, 110, 607-620.	5.7	5
49	IAGS: Inferring Ancestor Genome Structure under a Wide Range of Evolutionary Scenarios. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	5
50	Cerebrospinal Fluid from Healthy Pregnant Women Does Not Harbor a Detectable Microbial Community. <i>Microbiology Spectrum</i> , 2021, 9, e0076921.	3.0	5
51	Chromosome-Scale Genome Assembly of <i>Talaromyces rugulosus</i> W13939, a Mycoparasitic Fungus and Promising Biocontrol Agent. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1446-1450.	2.6	4
52	Transportation, germs, culture: a dynamic graph model of COVID-19 outbreak. <i>Quantitative Biology</i> , 2020, 8, 238-244.	0.5	4
53	Mining Unique-m Substrings from Genomes. <i>Journal of Proteomics and Bioinformatics</i> , 2010, 03, 099-103.	0.4	4
54	From Innovations to Prospects. , 2020, , .		3

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55	JAX-CNV: A Whole-genome Sequencing-based Algorithm for Copy Number Detection at Clinical Grade Level. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1197-1206.	6.9	3
56	Predicting the early risk of ophthalmopathy in Graves's disease patients using TCR repertoire. <i>Clinical and Translational Medicine</i> , 2020, 10, e218.	4.0	2
57	Mapping Genome Variants Sheds Light on Genetic and Phenotypic Differentiation in Chinese. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 226-228.	6.9	1
58	gCAnno: a graph-based single cell type annotation method. <i>BMC Genomics</i> , 2020, 21, 823.	2.8	0