

Kai Wang

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

18,037
citations

212478

28
h-index

175968

55
g-index

67
all docs

67
docs citations

67
times ranked

46459
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell multiomics reveals increased plasticity, resistant populations, and stem-cell-like blasts in <i>KMT2A</i> -rearranged leukemia. <i>Blood</i> , 2022, 139, 2198-2211.	0.6	37
2	DeepRepeat: direct quantification of short tandem repeats on signal data from nanopore sequencing. <i>Genome Biology</i> , 2022, 23, 108.	3.8	16
3	CancerVar: An artificial intelligence-empowered platform for clinical interpretation of somatic mutations in cancer. <i>Science Advances</i> , 2022, 8, eabj1624.	4.7	14
4	Expediting knowledge acquisition by a web framework for Knowledge Graph Exploration and Visualization (KGEV): case studies on COVID-19 and Human Phenotype Ontology. <i>BMC Medical Informatics and Decision Making</i> , 2022, 22, .	1.5	3
5	Multiplex gene and phenotype network to characterize shared genetic pathways of epilepsy and autism. <i>Scientific Reports</i> , 2021, 11, 952.	1.6	27
6	A computational method for direct imputation of cell type-specific expression profiles and cellular compositions from bulk-tissue RNA-Seq in brain disorders. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab056.	1.5	5
7	PhenCards: a data resource linking human phenotype information to biomedical knowledge. <i>Genome Medicine</i> , 2021, 13, 91.	3.6	6
8	LIQA: long-read isoform quantification and analysis. <i>Genome Biology</i> , 2021, 22, 182.	3.8	49
9	Clinical Phenotypic Spectrum of 4095 Individuals with Down Syndrome from Text Mining of Electronic Health Records. <i>Genes</i> , 2021, 12, 1159.	1.0	6
10	NanoCaller for accurate detection of SNPs and indels in difficult-to-map regions from long-read sequencing by haplotype-aware deep neural networks. <i>Genome Biology</i> , 2021, 22, 261.	3.8	33
11	The proteome and its dynamics: A missing piece for integrative multi-omics in schizophrenia. <i>Schizophrenia Research</i> , 2020, 217, 148-161.	1.1	16
12	Single-molecule optical mapping enables quantitative measurement of D4Z4 repeats in facioscapulohumeral muscular dystrophy (FSHD). <i>Journal of Medical Genetics</i> , 2020, 57, 109-120.	1.5	43
13	Ultrafast and scalable variant annotation and prioritization with big functional genomics data. <i>Genome Research</i> , 2020, 30, 1789-1801.	2.4	14
14	Cell-Type-Specific Proteogenomic Signal Diffusion for Integrating Multi-Omics Data Predicts Novel Schizophrenia Risk Genes. <i>Patterns</i> , 2020, 1, 100091.	3.1	5
15	Detection of base analogs incorporated during DNA replication by nanopore sequencing. <i>Nucleic Acids Research</i> , 2020, 48, e88-e88.	6.5	31
16	Cell Type-Specific Annotation and Fine Mapping of Variants Associated With Brain Disorders. <i>Frontiers in Genetics</i> , 2020, 11, 575928.	1.1	2
17	Detecting differential alternative splicing events in scRNA-seq with or without Unique Molecular Identifiers. <i>PLoS Computational Biology</i> , 2020, 16, e1007925.	1.5	20
18	Phen2Gene: rapid phenotype-driven gene prioritization for rare diseases. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa032.	1.5	45

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19	Gene Expression in Patient-Derived Neural Progenitors Implicates WNT5A Signaling in the Etiology of Schizophrenia. <i>Biological Psychiatry</i> , 2020, 88, 236-247.	0.7	28
20	Innovating Computational Biology and Intelligent Medicine: ICIBM 2019 Special Issue. <i>Genes</i> , 2020, 11, 437.	1.0	0
21	Genome-wide detection of short tandem repeat expansions by long-read sequencing. <i>BMC Bioinformatics</i> , 2020, 21, 542.	1.2	11
22	LongGF: computational algorithm and software tool for fast and accurate detection of gene fusions by long-read transcriptome sequencing. <i>BMC Genomics</i> , 2020, 21, 793.	1.2	22
23	Accelerating bioinformatics research with International Conference on Intelligent Biology and Medicine 2020. <i>BMC Bioinformatics</i> , 2020, 21, 563.	1.2	2
24	Variant Interpretation for Cancer (VIC): a computational tool for assessing clinical impacts of somatic variants. <i>Genome Medicine</i> , 2019, 11, 53.	3.6	36
25	Deconvolution of transcriptional networks identifies TCF4 as a master regulator in schizophrenia. <i>Science Advances</i> , 2019, 5, eaau4139.	4.7	59
26	NanoMod: a computational tool to detect DNA modifications using Nanopore long-read sequencing data. <i>BMC Genomics</i> , 2019, 20, 78.	1.2	50
27	Detection of DNA base modifications by deep recurrent neural network on Oxford Nanopore sequencing data. <i>Nature Communications</i> , 2019, 10, 2449.	5.8	237
28	Doc2Hpo: a web application for efficient and accurate HPO concept curation. <i>Nucleic Acids Research</i> , 2019, 47, W566-W570.	6.5	47
29	Group Lasso Regularized Deep Learning for Cancer Prognosis from Multi-Omics and Clinical Features. <i>Genes</i> , 2019, 10, 240.	1.0	59
30	LinkedSV for detection of mosaic structural variants from linked-read exome and genome sequencing data. <i>Nature Communications</i> , 2019, 10, 5585.	5.8	24
31	Long-read sequencing identified intronic repeat expansions in <i>SAMD12</i> from Chinese pedigrees affected with familial cortical myoclonic tremor with epilepsy. <i>Journal of Medical Genetics</i> , 2019, 56, 265-270.	1.5	82
32	Evaluation of biological and technical variations in low-input RNA-Seq and single-cell RNA-Seq. <i>International Journal of Computational Biology and Drug Design</i> , 2018, 11, 5.	0.3	2
33	A semi-supervised approach for predicting cell-type specific functional consequences of non-coding variation using MPRAs. <i>Nature Communications</i> , 2018, 9, 5199.	5.8	34
34	Deep Phenotyping on Electronic Health Records Facilitates Genetic Diagnosis by Clinical Exomes. <i>American Journal of Human Genetics</i> , 2018, 103, 58-73.	2.6	99
35	NextSV: a meta-caller for structural variants from low-coverage long-read sequencing data. <i>BMC Bioinformatics</i> , 2018, 19, 180.	1.2	29
36	Identification of Copy Number Variants from SNP Arrays Using PennCNV. <i>Methods in Molecular Biology</i> , 2018, 1833, 1-28.	0.4	8

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37	Evaluation of biological and technical variations in low-input RNA-Seq and single-cell RNA-Seq. <i>International Journal of Computational Biology and Drug Design</i> , 2018, 11, 5.	0.3	1
38	InterVar: Clinical Interpretation of Genetic Variants by the 2015 ACMG-AMP Guidelines. <i>American Journal of Human Genetics</i> , 2017, 100, 267-280.	2.6	717
39	Interrogating the "unsequenceable" genomic trinucleotide repeat disorders by long-read sequencing. <i>Genome Medicine</i> , 2017, 9, 65.	3.6	79
40	<i>SCN8A</i> mutation in a child presenting with seizures and developmental delays. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a001073.	0.5	12
41	iCAGES: integrated CANcer GENome Score for comprehensively prioritizing driver genes in personal cancer genomes. <i>Genome Medicine</i> , 2016, 8, 135.	3.6	45
42	Long-read sequencing and de novo assembly of a Chinese genome. <i>Nature Communications</i> , 2016, 7, 12065.	5.8	242
43	KBC syndrome involving a single-nucleotide duplication in <i>ANKRD11</i> . <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a001131.	0.5	15
44	TAF1 Variants Are Associated with Dysmorphic Features, Intellectual Disability, and Neurological Manifestations. <i>American Journal of Human Genetics</i> , 2015, 97, 922-932.	2.6	101
45	Phenolyzer: phenotype-based prioritization of candidate genes for human diseases. <i>Nature Methods</i> , 2015, 12, 841-843.	9.0	327
46	Improved exome prioritization of disease genes through cross-species phenotype comparison. <i>Genome Research</i> , 2014, 24, 340-348.	2.4	300
47	Jannovar: A Java Library for Exome Annotation. <i>Human Mutation</i> , 2014, 35, 548-555.	1.1	63
48	Genome-Wide Association Study of Multiplex Schizophrenia Pedigrees. <i>American Journal of Psychiatry</i> , 2012, 169, 963-973.	4.0	61
49	wANNOVAR: annotating genetic variants for personal genomes via the web. <i>Journal of Medical Genetics</i> , 2012, 49, 433-436.	1.5	366
50	Genomic characteristics of cattle copy number variations. <i>BMC Genomics</i> , 2011, 12, 127.	1.2	201
51	A human B cell interactome identifies MYB and FOXM1 as master regulators of proliferation in germinal centers. <i>Molecular Systems Biology</i> , 2010, 6, 377.	3.2	336
52	MapSplice: Accurate mapping of RNA-seq reads for splice junction discovery. <i>Nucleic Acids Research</i> , 2010, 38, e178-e178.	6.5	946
53	ANNOVAR: functional annotation of genetic variants from high-throughput sequencing data. <i>Nucleic Acids Research</i> , 2010, 38, e164-e164.	6.5	10,960
54	Modeling genetic inheritance of copy number variations. <i>Nucleic Acids Research</i> , 2008, 36, e138-e138.	6.5	77

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55	PennCNV: An integrated hidden Markov model designed for high-resolution copy number variation detection in whole-genome SNP genotyping data. <i>Genome Research</i> , 2007, 17, 1665-1674.	2.4	1,586
56	Reverse engineering cellular networks. <i>Nature Protocols</i> , 2006, 1, 662-671.	5.5	345
57	Polishing high-quality genome assemblies. <i>Nature Methods</i> , 0, , .	9.0	1
58	Epigenetic Dysregulation in Meningiomas. <i>Neuro-Oncology Advances</i> , 0, , .	0.4	0