# Kai Ye

List of Publications by Year
in descending order



| 58 | 15,170 | 212478 28 | 169272 56 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 72 | 72 | 72 | 33452 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Homotopic Convex Transformation: A New Landscape Smoothing Method for the Traveling Salesman Problem. IEEE Transactions on Cybernetics, 2022, 52, 495-507. | 6.2 | 7 |
| 2 | Mako: A Graph-based Pattern Growth Approach to Detect Complex Structural Variants. Genomics, Proteomics and Bioinformatics, 2022, 20, 205-218. | 3.0 | 6 |
| 3 | High-quality Arabidopsis thaliana Genome Assembly with Nanopore and HiFi Long Reads. Genomics, Proteomics and Bioinformatics, 2022, 20, 4-13. | 3.0 | 80 |
| 4 | A global survey of the transcriptome of the opium poppy (Papaver somniferum) based on singleâ€molecule longâ€read isoform sequencing. Plant Journal, 2022, 110, 607-620. | 2.8 | 5 |
| 5 | JAX-CNV: A Whole-genome Sequencing-based Algorithm for Copy Number Detection at Clinical Grade Level. Genomics, Proteomics and Bioinformatics, 2022, 20, 1197-1206. | 3.0 | 3 |
| 6 | Integrating bulk and singleâ€cell RNA sequencing reveals cellular heterogeneity and immune infiltration in hepatocellular carcinoma. Molecular Oncology, 2022, 16, 2195-2213. | 2.1 | 16 |
| 7 | IAGS: Inferring Ancestor Genome Structure under a Wide Range of Evolutionary Scenarios. Molecular Biology and Evolution, 2022, 39, . | 3.5 | 5 |
| 8 | Cellular heterogeneity and transcriptomic profiles during intrahepatic cholangiocarcinoma initiation and progression. Hepatology, 2022, 76, 1302-1317. | 3.6 | 13 |
| 9 | Haplotype-resolved Chinese male genome assembly based on high-fidelity sequencing. Fundamental Research, 2022, 2, 946-953. | 1.6 | 11 |
| 10 | A novel CD4+ CTL subtype characterized by chemotaxis and inflammation is involved in the pathogenesis of Gravesâ€™ orbitopathy. Cellular and Molecular Immunology, 2021, 18, 735-745. | 4.8 | 37 |
| 11 | Application of Metagenomic Next-Generation Sequencing in the Diagnosis of Pulmonary Infectious Pathogens From Bronchoalveolar Lavage Samples. Frontiers in Cellular and Infection Microbiology, 2021, 11, 541092. | 1.8 | 72 |
| 12 | Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, . | 6.0 | 358 |
| 13 | Three chromosome-scale Papaver genomes reveal punctuated patchwork evolution of the morphinan and noscapine biosynthesis pathway. Nature Communications, 2021, 12, 6030. | 5.8 | 51 |
| 14 | DrugEx v2: de novo design of drug molecules by Pareto-based multi-objective reinforcement learning in polypharmacology. Journal of Cheminformatics, 2021, 13, 85. | 2.8 | 30 |
| 15 | Cerebrospinal Fluid from Healthy Pregnant Women Does Not Harbor a Detectable Microbial Community. Microbiology Spectrum, 2021, 9, e0076921. | 1.2 | 5 |
| 16 | Multifactorial Deep Learning Reveals Pan-Cancer Genomic Tumor Clusters with Distinct Immunogenomic Landscape and Response to Immunotherapy. Clinical Cancer Research, 2020, 26, 2908-2920. | 3.2 | 30 |
| 17 | Chromosome-Scale Genome Assembly of Talaromyces rugulosus W13939, a Mycoparasitic Fungus and Promising Biocontrol Agent. Molecular Plant-Microbe Interactions, 2020, 33, 1446-1450. | 1.4 | 4 |
| 18 | Predicting the early risk of ophthalmopathy in Gravesâ€™ disease patients using TCR repertoire. Clinical and Translational Medicine, 2020, 10, e218. | 1.7 | 2 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | gCAnno: a graph-based single cell type annotation method. BMC Genomics, 2020, 21, 823. | 1.2 | 0 |
| 20 | A Chromosome-Scale Genome Assembly for the Fusarium oxysporum Strain Fo5176 To Establish a Model Arabidopsis-Fungal Pathosystem. G3: Genes, Genomes, Genetics, 2020, 10, 3549-3555. | 0.8 | 28 |
| 21 | Transportation, germs, culture: a dynamic graph model of COVIDâ€19 outbreak. Quantitative Biology, 2020, 8, 238-244. | 0.3 | 4 |
| 22 | MSIsensor-pro: Fast, Accurate, and Matched-normal-sample-free Detection of Microsatellite Instability. Genomics, Proteomics and Bioinformatics, 2020, 18, 65-71. | 3.0 | 53 |
| 23 | Chromosome-Scale Genome Assembly of Fusarium oxysporum Strain Fo47, a Fungal Endophyte and Biocontrol Agent. Molecular Plant-Microbe Interactions, 2020, 33, 1108-1111. | 1.4 | 29 |
| 24 | Dynamic network inference and association computation discover gene modules regulating virulence, mycotoxin and sexual reproduction in Fusarium graminearum. BMC Genomics, 2020, 21, 179. | 1.2 | 8 |
| 25 | What Is Required to Prevent a Second Major Outbreak of SARS-CoV-2 upon Lifting Quarantine in Wuhan City, China. Innovation(China), 2020, 1, 100006. | 5.2 | 32 |
| 26 | From Innovations to Prospects. , 2020, , . | | 3 |
| 27 | MEpurity: estimating tumor purity using DNA methylation data. Bioinformatics, 2019, 35, 5298-5300. | 1.8 | 8 |
| 28 | Mapping Genome Variants Sheds Light on Genetic and Phenotypic Differentiation in Chinese. Genomics, Proteomics and Bioinformatics, 2019, 17, 226-228. | 3.0 | 1 |
| 29 | One reference genome is not enough. Genome Biology, 2019, 20, 104. | 3.8 | 58 |
| 30 | An exploration strategy improves the diversity of de novo ligands using deep reinforcement learning: a case for the adenosine A2A receptor. Journal of Cheminformatics, 2019, 11, 35. | 2.8 | 58 |
| 31 | Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784. | 5.8 | 636 |
| 32 | PVTree: A Sequential Pattern Mining Method for Alignment Independent Phylogeny Reconstruction. Genes, 2019, 10, 73. | 1.0 | 6 |
| 33 | PRESM: personalized reference editor for somatic mutation discovery in cancer genomics. Bioinformatics, 2019, 35, 1445-1452. | 1.8 | 6 |
| 34 | The opium poppy genome and morphinan production. Science, 2018, 362, 343-347. | 6.0 | 225 |
| 35 | Split-Read Indel and Structural Variant Calling Using PINDEL. Methods in Molecular Biology, 2018, 1833, 95-105. | 0.4 | 20 |
| 36 | Cold atmospheric plasma as a potential tool for multiple myeloma treatment. Oncotarget, 2018, 9, 18002-18017. | 0.8 | 28 |

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|---|---|---|---|
| 37 | An improved burden-test pipeline for identifying associations from rare germline and somatic variants. BMC Genomics, 2017, 18, 753. | 1.2 | 11 |
| 38 | Divergent viral presentation among human tumors and adjacent normal tissues. Scientific Reports, 2016, 6, 28294. | 1.6 | 60 |
| 39 | Precision Medicine: What Challenges Are We Facing?. Genomics, Proteomics and Bioinformatics, 2016, 14, 253-261. | 3.0 | 15 |
| 40 | A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989. | 5.8 | 99 |
| 41 | Systematic discovery of complex insertions and deletions in human cancers. Nature Medicine, 2016, 22, 97-104. | 15.2 | 93 |
| 42 | Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications, 2015, 6, 10086. | 5.8 | 243 |
| 43 | Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801. | 2.4 | 115 |
| 44 | Genome-wide patterns and properties of de novo mutations in humans. Nature Genetics, 2015, 47, 822-826. | 9.4 | 384 |
| 45 | An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81. | 13.7 | 1,994 |
| 46 | A gain of function mutation inTNFRSF11Bencoding osteoprotegerin causes osteoarthritis with chondrocalcinosis. Annals of the Rheumatic Diseases, 2015, 74, 1756-1762. | 0.5 | 44 |
| 47 | The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227. | 1.4 | 246 |
| 48 | MSIsensor: microsatellite instability detection using paired tumor-normal sequence data. Bioinformatics, 2014, 30, 1015-1016. | 1.8 | 599 |
| 49 | Mutational landscape and significance across 12 major cancer types. Nature, 2013, 502, 333-339. | 13.7 | 3,695 |
| 50 | Aging as Accelerated Accumulation of Somatic Variants: Whole-Genome Sequencing of Centenarian and Middle-Aged Monozygotic Twin Pairs. Twin Research and Human Genetics, 2013, 16, 1026-1032. | 0.3 | 40 |
| 51 | A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828. | 6.0 | 1,095 |
| 52 | Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65. | 13.7 | 991 |
| 53 | A comprehensive catalogue of somatic mutations from a human cancer genome. Nature, 2010, 463, 191-196. | 13.7 | 1,519 |
| 54 | Mining Unique-m Substrings from Genomes. Journal of Proteomics and Bioinformatics, 2010, 03, 099-103. | 0.4 | 4 |

| # | Article | IF | Citations |
|---|---|---|---|
| 55 | Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. Bioinformatics, 2009, 25, 2865-2871. | 1.8 | 1,811 |
| 56 | Tracing evolutionary pressure. Bioinformatics, 2008, 24, 908-915. | 1.8 | 35 |
| 57 | An efficient, versatile and scalable pattern growth approach to mine frequent patterns in unaligned protein sequences. Bioinformatics, 2007, 23, 687-693. | 1.8 | 23 |
| 58 | A two-entropies analysis to identify functional positions in the transmembrane region of class A G protein-coupled receptors. Proteins: Structure, Function and Bioinformatics, 2006, 63, 1018-1030. | 1.5 | 35 |