

# Kin Fai Au

## List of Publications by Year in descending order

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Version: 2024-02-01

28  
papers

4,996  
citations

430442

18  
h-index

500791

28  
g-index

31  
all docs

31  
docs citations

31  
times ranked

7120  
citing authors

#	ARTICLE	IF	CITATIONS
1	The blooming of long-read sequencing reforms biomedical research. <i>Genome Biology</i> , 2022, 23, 21.	3.8	8
2	A network-based computational framework to predict and differentiate functions for gene isoforms using exon-level expression data. <i>Methods</i> , 2021, 189, 54-64.	1.9	2
3	Single-molecule long-read sequencing reveals a conserved intact long RNA profile in sperm. <i>Nature Communications</i> , 2021, 12, 1361.	5.8	43
4	Real-time mapping of nanopore raw signals. <i>Bioinformatics</i> , 2021, 37, i477-i483.	1.8	41
5	Nanopore sequencing technology, bioinformatics and applications. <i>Nature Biotechnology</i> , 2021, 39, 1348-1365.	9.4	521
6	Performance difference of graph-based and alignment-based hybrid error correction methods for error-prone long reads. <i>Genome Biology</i> , 2020, 21, 14.	3.8	8
7	Single-molecule long-read sequencing reveals the chromatin basis of gene expression. <i>Genome Research</i> , 2019, 29, 1329-1342.	2.4	46
8	A comparative evaluation of hybrid error correction methods for error-prone long reads. <i>Genome Biology</i> , 2019, 20, 26.	3.8	86
9	Revealing tumor heterogeneity of breast cancer by utilizing the linkage between somatic and germline mutations. <i>Briefings in Bioinformatics</i> , 2019, 20, 2306-2315.	3.2	4
10	iASPP mediates p53 selectivity through a modular mechanism fine-tuning DNA recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17470-17479.	3.3	20
11	IDP-denovo: <i>de novo</i> transcriptome assembly and isoform annotation by hybrid sequencing. <i>Bioinformatics</i> , 2018, 34, 2168-2176.	1.8	41
12	E-C coupling structural protein junctophilin-2 encodes a stress-adaptive transcription regulator. <i>Science</i> , 2018, 362, .	6.0	78
13	A Statistical Method for Observing Personal Diploid Methylomes and Transcriptomes with Single-Molecule Real-Time Sequencing. <i>Genes</i> , 2018, 9, 460.	1.0	2
14	Single cell expression analysis of primate-specific retroviruses-derived HPAT lincRNAs in viable human blastocysts identifies embryonic cells co-expressing genetic markers of multiple lineages. <i>Heliyon</i> , 2018, 4, e00667.	1.4	23
15	IDP-ASE: haplotyping and quantifying allele-specific expression at the gene and gene isoform level by hybrid sequencing. <i>Nucleic Acids Research</i> , 2017, 45, e32-e32.	6.5	42
16	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. <i>Nature Communications</i> , 2017, 8, 59.	5.8	225
17	Hybrid Sequencing of Full-Length cDNA Transcripts of Stems and Leaves in <i>Dendrobium officinale</i> . <i>Genes</i> , 2017, 8, 257.	1.0	20
18	Comprehensive comparison of Pacific Biosciences and Oxford Nanopore Technologies and their applications to transcriptome analysis. <i>F1000Research</i> , 2017, 6, 100.	0.8	366

#	ARTICLE	IF	CITATIONS
19	Comprehensive comparison of Pacific Biosciences and Oxford Nanopore Technologies and their applications to transcriptome analysis. F1000Research, 2017, 6, 100.	0.8	203
20	The primate-specific noncoding RNA HPAT5 regulates pluripotency during human preimplantation development and nuclear reprogramming. Nature Genetics, 2016, 48, 44-52.	9.4	153
21	PacBio Sequencing and Its Applications. Genomics, Proteomics and Bioinformatics, 2015, 13, 278-289.	3.0	1,669
22	Full-length transcriptome sequences and splice variants obtained by a combination of sequencing platforms applied to different root tissues of <i>Salvia miltiorrhiza</i> and tanshinone biosynthesis. Plant Journal, 2015, 82, 951-961.	2.8	337
23	Characterization of fusion genes and the significantly expressed fusion isoforms in breast cancer by hybrid sequencing. Nucleic Acids Research, 2015, 43, e116-e116.	6.5	104
24	Accurate Mapping of RNA-Seq Data. Methods in Molecular Biology, 2015, 1269, 147-161.	0.4	2
25	The transcriptome of human pluripotent stem cells. Current Opinion in Genetics and Development, 2014, 28, 71-77.	1.5	14
26	Characterization of the human ESC transcriptome by hybrid sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4821-30.	3.3	316
27	Improving PacBio Long Read Accuracy by Short Read Alignment. PLoS ONE, 2012, 7, e46679.	1.1	289
28	Detection of splice junctions from paired-end RNA-seq data by SpliceMap. Nucleic Acids Research, 2010, 38, 4570-4578.	6.5	300