Kin Fai Au

List of Publications by Year
in descending order

28 papers	4,996 citations	430874 18 h-index	501196 28 g-index
31 all docs	31 docs citations	31 times ranked	7120 citing authors

#	Article	IF	Citations
1	PacBio Sequencing and Its Applications. Genomics, Proteomics and Bioinformatics, 2015, 13, 278-289.	6.9	1,669
2	Nanopore sequencing technology, bioinformatics and applications. Nature Biotechnology, 2021, 39, 1348-1365.	17.5	521
3	Comprehensive comparison of Pacific Biosciences and Oxford Nanopore Technologies and their applications to transcriptome analysis. F1000Research, 2017, 6, 100.	1.6	366
4	Fullâ€length transcriptome sequences and splice variants obtained by a combination of sequencing platforms applied to different root tissues of <scp>S</scp>alvia miltiorrhiza and tanshinone biosynthesis. Plant Journal, 2015, 82, 951-961.	5.7	337
5	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.	7.1	316
6	Detection of splice junctions from paired-end RNA-seq data by SpliceMap. Nucleic Acids Research, 2010, 38, 4570-4578.	14.5	300
7	Improving PacBio Long Read Accuracy by Short Read Alignment. PLoS ONE, 2012, 7, e46679.	2.5	289
8	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. Nature Communications, 2017, 8, 59.	12.8	225
9	Comprehensive comparison of Pacific Biosciences and Oxford Nanopore Technologies and their applications to transcriptome analysis. F1000Research, 2017, 6, 100.	1.6	203
10	The primate-specific noncoding RNA HPAT5 regulates pluripotency during human preimplantation development and nuclear reprogramming. Nature Genetics, 2016, 48, 44-52.	21.4	153
11	Characterization of fusion genes and the significantly expressed fusion isoforms in breast cancer by hybrid sequencing. Nucleic Acids Research, 2015, 43, e116-e116.	14.5	104
12	A comparative evaluation of hybrid error correction methods for error-prone long reads. Genome Biology, 2019, 20, 26.	8.8	86
13	E-C coupling structural protein junctophilin-2 encodes a stress-adaptive transcription regulator. Science, 2018, 362, .	12.6	78
14	Single-molecule long-read sequencing reveals the chromatin basis of gene expression. Genome Research, 2019, 29, 1329-1342.	5.5	46
15	Single-molecule long-read sequencing reveals a conserved intact long RNA profile in sperm. Nature Communications, 2021, 12, 1361.	12.8	43
16	IDP-ASE: haplotyping and quantifying allele-specific expression at the gene and gene isoform level by hybrid sequencing. Nucleic Acids Research, 2017, 45, e32-e32.	14.5	42
17	IDP-denovo: de novo transcriptome assembly and isoform annotation by hybrid sequencing. Bioinformatics, 2018, 34, 2168-2176.	4.1	41
18	Real-time mapping of nanopore raw signals. Bioinformatics, 2021, 37, i477-i483.	4.1	41

#	Article	IF	Citations
19	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. Heliyon, 2018, 4, e00667.	3.2	23
20	Hybrid Sequencing of Full-Length cDNA Transcripts of Stems and Leaves in Dendrobium officinale. Genes, 2017, 8, 257.	2.4	20
21	iASPP mediates p53 selectivity through a modular mechanism fine-tuning DNA recognition. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17470-17479.	7.1	20
22	The transcriptome of human pluripotent stem cells. Current Opinion in Genetics and Development, 2014, 28, 71-77.	3.3	14
23	Performance difference of graph-based and alignment-based hybrid error correction methods for error-prone long reads. Genome Biology, 2020, 21, 14.	8.8	8
24	The blooming of long-read sequencing reforms biomedical research. Genome Biology, 2022, 23, 21.	8.8	8
25	Revealing tumor heterogeneity of breast cancer by utilizing the linkage between somatic and germline mutations. Briefings in Bioinformatics, 2019, 20, 2306-2315.	6.5	4
26	A Statistical Method for Observing Personal Diploid Methylomes and Transcriptomes with Single-Molecule Real-Time Sequencing. Genes, 2018, 9, 460.	2.4	2
27	A network-based computational framework to predict and differentiate functions for gene isoforms using exon-level expression data. Methods, 2021, 189, 54-64.	3.8	2
28	Accurate Mapping of RNA-Seq Data. Methods in Molecular Biology, 2015, 1269, 147-161.	0.9	2