Kin Fai Au

List of Publications by Year
in descending order

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

#	Article	IF	Citations
1	The blooming of long-read sequencing reforms biomedical research. Genome Biology, 2022, 23, 21.	8.8	8
2	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
3	Single-molecule long-read sequencing reveals a conserved intact long RNA profile in sperm. Nature Communications, 2021, 12, 1361.	12.8	43
4	Real-time mapping of nanopore raw signals. Bioinformatics, 2021, 37, i477-i483.	4.1	41
5	Nanopore sequencing technology, bioinformatics and applications. Nature Biotechnology, 2021, 39, 1348-1365.	17.5	521
6	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
7	Single-molecule long-read sequencing reveals the chromatin basis of gene expression. Genome Research, 2019, 29, 1329-1342.	5.5	46
8	A comparative evaluation of hybrid error correction methods for error-prone long reads. Genome Biology, 2019, 20, 26.	8.8	86
9	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
10	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
11	IDP-denovo: *de novo* transcriptome assembly and isoform annotation by hybrid sequencing. Bioinformatics, 2018, 34, 2168-2176.	4.1	41
12	E-C coupling structural protein junctophilin-2 encodes a stress-adaptive transcription regulator. Science, 2018, 362, .	12.6	78
13	A Statistical Method for Observing Personal Diploid Methylomes and Transcriptomes with Single-Molecule Real-Time Sequencing. Genes, 2018, 9, 460.	2.4	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. Heliyon, 2018, 4, e00667.	3.2	23
15	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
16	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. Nature Communications, 2017, 8, 59.	12.8	225
17	Hybrid Sequencing of Full-Length cDNA Transcripts of Stems and Leaves in Dendrobium officinale. Genes, 2017, 8, 257.	2.4	20
18	Comprehensive comparison of Pacific Biosciences and Oxford Nanopore Technologies and their applications to transcriptome analysis. F1000Research, 2017, 6, 100.	1.6	366

#	Article	IF	Citations
19	Comprehensive comparison of Pacific Biosciences and Oxford Nanopore Technologies and their applications to transcriptome analysis. F1000Research, 2017, 6, 100.	1.6	203
20	The primate-specific noncoding RNA HPAT5 regulates pluripotency during human preimplantation development and nuclear reprogramming. Nature Genetics, 2016, 48, 44-52.	21.4	153
21	PacBio Sequencing and Its Applications. Genomics, Proteomics and Bioinformatics, 2015, 13, 278-289.	6.9	1,669
22	Full‐length transcriptome sequences and splice variants obtained by a combination of sequencing platforms applied to different root tissues of *Salvia miltiorrhiza* and tanshinone biosynthesis. Plant Journal, 2015, 82, 951-961.	5.7	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.	14.5	104
24	Accurate Mapping of RNA-Seq Data. Methods in Molecular Biology, 2015, 1269, 147-161.	0.9	2
25	The transcriptome of human pluripotent stem cells. Current Opinion in Genetics and Development, 2014, 28, 71-77.	3.3	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.	7.1	316
27	Improving PacBio Long Read Accuracy by Short Read Alignment. PLoS ONE, 2012, 7, e46679.	2.5	289
28	Detection of splice junctions from paired-end RNA-seq data by SpliceMap. Nucleic Acids Research, 2010, 38, 4570-4578.	14.5	300