

Minh Duc Cao

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

671
citations

840119

11
h-index

676716

22
g-index

39
all docs

39
docs citations

39
times ranked

1162
citing authors

#	ARTICLE	IF	CITATIONS
1	Chiron: translating nanopore raw signal directly into nucleotide sequence using deep learning. <i>GigaScience</i> , 2018, 7, .	3.3	123
2	Scaffolding and completing genome assemblies in real-time with nanopore sequencing. <i>Nature Communications</i> , 2017, 8, 14515.	5.8	104
3	Streaming algorithms for identification of pathogens and antibiotic resistance potential from real-time MinIONTM sequencing. <i>GigaScience</i> , 2016, 5, 32.	3.3	79
4	Inferring short tandem repeat variation from paired-end short reads. <i>Nucleic Acids Research</i> , 2014, 42, e16-e16.	6.5	54
5	Complete Genome Sequence of <i>Klebsiella quasipneumoniae</i> subsp. <i>similipneumoniae</i> Strain ATCC 700603. <i>Genome Announcements</i> , 2016, 4, .	0.8	44
6	A Simple Statistical Algorithm for Biological Sequence Compression. , 2007, , .		43
7	Multifactorial chromosomal variants regulate polymyxin resistance in extensively drug-resistant <i>Klebsiella pneumoniae</i> . <i>Microbial Genomics</i> , 2018, 4, .	1.0	39
8	Sequencing technologies and tools for short tandem repeat variation detection. <i>Briefings in Bioinformatics</i> , 2015, 16, 193-204.	3.2	32
9	Realtime analysis and visualization of MinION sequencing data with npReader. <i>Bioinformatics</i> , 2016, 32, 764-766.	1.8	25
10	Octapeptin C4 and polymyxin resistance occur via distinct pathways in an epidemic XDR <i>Klebsiella pneumoniae</i> ST258 isolate. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 582-593.	1.3	16
11	Combining Contents and Citations for Scientific Document Classification. <i>Lecture Notes in Computer Science</i> , 2005, , 143-152.	1.0	14
12	Assembly of whole-chromosome pseudomolecules for polyploid plant genomes using outbred mapping populations. <i>Nature Genetics</i> , 2020, 52, 1256-1264.	9.4	13
13	A genome alignment algorithm based on compression. <i>BMC Bioinformatics</i> , 2010, 11, 599.	1.2	10
14	Repeat-encoded poly-Q tracts show statistical commonalities across species. <i>BMC Genomics</i> , 2013, 14, 76.	1.2	6
15	Real-time demultiplexing Nanopore barcoded sequencing data with npBarcode. <i>Bioinformatics</i> , 2017, 33, 3988-3990.	1.8	6
16	Computing Substitution Matrices for Genomic Comparative Analysis. <i>Lecture Notes in Computer Science</i> , 2009, , 647-655.	1.0	5
17	Neural Networks for Scientific Paper Classification. , 0, , .		4
18	Statistical Enrichment of Epigenetic States Around Triplet Repeats that Can Undergo Expansions. <i>Frontiers in Neuroscience</i> , 2016, 10, 92.	1.4	4

#	ARTICLE	IF	CITATIONS
19	Real-time resolution of short-read assembly graph using ONT long reads. PLoS Computational Biology, 2021, 17, e1008586.	1.5	4
20	A Biological Compression Model and Its Applications. Advances in Experimental Medicine and Biology, 2011, 696, 657-666.	0.8	3
21	Modelling Citation Networks for Improving Scientific Paper Classification Performance. Lecture Notes in Computer Science, 2006, , 413-422.	1.0	3
22	Robust Estimation of Evolutionary Distances with Information Theory. Molecular Biology and Evolution, 2016, 33, 1349-1357.	3.5	2
23	GtTR: Bayesian estimation of absolute tandem repeat copy number using sequence capture and high throughput sequencing. BMC Bioinformatics, 2018, 19, 267.	1.2	2
24	TreeWrapper: Automatic Data Extraction Based on Tree Representation. Lecture Notes in Computer Science, 2006, , 566-576.	1.0	0
25	High-throughput multiplexed tandem repeat genotyping using targeted long-read sequencing. F1000Research, 0, 9, 1084.	0.8	0