Minh Duc Cao

List of Publications by Year
in descending order

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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	Real-time resolution of short-read assembly graph using ONT long reads. PLoS Computational Biology, 2021, 17, e1008586.	1.5	4
2	Assembly of whole-chromosome pseudomolecules for polyploid plant genomes using outbred mapping populations. Nature Genetics, 2020, 52, 1256-1264.	9.4	13
3	Octapeptin C4 and polymyxin resistance occur via distinct pathways in an epidemic XDRKlebsiella pneumoniaeST258 isolate. Journal of Antimicrobial Chemotherapy, 2019, 74, 582-593.	1.3	16
4	Chiron: translating nanopore raw signal directly into nucleotide sequence using deep learning. GigaScience, 2018, 7, .	3.3	123
5	Multifactorial chromosomal variants regulate polymyxin resistance in extensively drug-resistant Klebsiella pneumoniae. Microbial Genomics, 2018, 4, .	1.0	39
6	GtTR: Bayesian estimation of absolute tandem repeat copy number using sequence capture and high throughput sequencing. BMC Bioinformatics, 2018, 19, 267.	1.2	2
7	Scaffolding and completing genome assemblies in real-time with nanopore sequencing. Nature Communications, 2017, 8, 14515.	5.8	104
8	Real-time demultiplexing Nanopore barcoded sequencing data with npBarcode. Bioinformatics, 2017, 33, 3988-3990.	1.8	6
9	Statistical Enrichment of Epigenetic States Around Triplet Repeats that Can Undergo Expansions. Frontiers in Neuroscience, 2016, 10, 92.	1.4	4
10	Complete Genome Sequence of Klebsiella quasipneumoniae subsp. similipneumoniae Strain ATCC 700603. Genome Announcements, 2016, 4, .	0.8	44
11	Streaming algorithms for identification of pathogens and antibiotic resistance potential from real-time MinIONTM sequencing. GigaScience, 2016, 5, 32.	3.3	79
12	Realtime analysis and visualization of MinION sequencing data with npReader. Bioinformatics, 2016, 32, 764-766.	1.8	25
13	Robust Estimation of Evolutionary Distances with Information Theory. Molecular Biology and Evolution, 2016, 33, 1349-1357.	3.5	2
14	Sequencing technologies and tools for short tandem repeat variation detection. Briefings in Bioinformatics, 2015, 16, 193-204.	3.2	32
15	Inferring short tandem repeat variation from paired-end short reads. Nucleic Acids Research, 2014, 42, e16-e16.	6.5	54
16	Repeat-encoded poly-Q tracts show statistical commonalities across species. BMC Genomics, 2013, 14, 76.	1.2	6
17	A Biological Compression Model and Its Applications. Advances in Experimental Medicine and Biology, 2011, 696, 657-666.	0.8	3
18	A genome alignment algorithm based on compression. BMC Bioinformatics, 2010, 11, 599.	1.2	10

#	Article	IF	Citations
19	Computing Substitution Matrices for Genomic Comparative Analysis. Lecture Notes in Computer Science, 2009, , 647-655.	1.0	5
20	A Simple Statistical Algorithm for Biological Sequence Compression. , 2007, , .		43
21	TreeWrapper: Automatic Data Extraction Based on Tree Representation. Lecture Notes in Computer Science, 2006, , 566-576.	1.0	0
22	Modelling Citation Networks for Improving Scientific Paper Classification Performance. Lecture Notes in Computer Science, 2006, , 413-422.	1.0	3
23	Combining Contents and Citations for Scientific Document Classification. Lecture Notes in Computer Science, 2005, , 143-152.	1.0	14
24	Neural Networks for Scientific Paper Classification. , 0, , .		4
25	High-throughput multiplexed tandem repeat genotyping using targeted long-read sequencing. F1000Research, 0, 9, 1084.	0.8	0