

Minh Duc Cao

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

35
papers

445
citations

11
h-index

20
g-index

39
ext. papers

582
ext. citations

7
avg, IF

3.64
L-index

#	Paper	IF	Citations
35	Chiron: translating nanopore raw signal directly into nucleotide sequence using deep learning. <i>GigaScience</i> , 2018 , 7,	7.6	80
34	Scaffolding and completing genome assemblies in real-time with nanopore sequencing. <i>Nature Communications</i> , 2017 , 8, 14515	17.4	72
33	Streaming algorithms for identification of pathogens and antibiotic resistance potential from real-time MinION(TM) sequencing. <i>GigaScience</i> , 2016 , 5, 32	7.6	58
32	Inferring short tandem repeat variation from paired-end short reads. <i>Nucleic Acids Research</i> , 2014 , 42, e16	20.1	42
31	Multifactorial chromosomal variants regulate polymyxin resistance in extensively drug-resistant <i>Klebsiella pneumoniae</i> . <i>Microbial Genomics</i> , 2018 , 4,	4.4	28
30	Realtime analysis and visualization of MinION sequencing data with npReader. <i>Bioinformatics</i> , 2016 , 32, 764-6	7.2	22
29	Complete Genome Sequence of <i>Klebsiella quasipneumoniae</i> subsp. <i>similipneumoniae</i> Strain ATCC 700603. <i>Genome Announcements</i> , 2016 , 4,		19
28	Sequencing technologies and tools for short tandem repeat variation detection. <i>Briefings in Bioinformatics</i> , 2015 , 16, 193-204	13.4	18
27	A Simple Statistical Algorithm for Biological Sequence Compression 2007 ,		14
26	Combining Contents and Citations for Scientific Document Classification. <i>Lecture Notes in Computer Science</i> , 2005 , 143-152	0.9	12
25	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	5.1	11
24	A genome alignment algorithm based on compression. <i>BMC Bioinformatics</i> , 2010 , 11, 599	3.6	10
23	Assembly of whole-chromosome pseudomolecules for polyploid plant genomes using outbred mapping populations. <i>Nature Genetics</i> , 2020 , 52, 1256-1264	36.3	7
22	Repeat-encoded poly-Q tracts show statistical commonalities across species. <i>BMC Genomics</i> , 2013 , 14, 76	4.5	6
21	Streaming algorithms for identification of pathogens and antibiotic resistance potential from real-time MinION™ sequencing		5
20	Real-time demultiplexing Nanopore barcoded sequencing data with npBarcode. <i>Bioinformatics</i> , 2017 , 33, 3988-3990	7.2	4
19	Computing Substitution Matrices for Genomic Comparative Analysis. <i>Lecture Notes in Computer Science</i> , 2009 , 647-655	0.9	4

18	Chiron: Translating nanopore raw signal directly into nucleotide sequence using deep learning		4
17	Statistical Enrichment of Epigenetic States Around Triplet Repeats that Can Undergo Expansions. <i>Frontiers in Neuroscience</i> , 2016 , 10, 92	5.1	4
16	A biological compression model and its applications. <i>Advances in Experimental Medicine and Biology</i> , 2011 , 696, 657-66	3.6	3
15	Neural Networks for Scientific Paper Classification		3
14	Robust Estimation of Evolutionary Distances with Information Theory. <i>Molecular Biology and Evolution</i> , 2016 , 33, 1349-57	8.3	2
13	GtTR: Bayesian estimation of absolute tandem repeat copy number using sequence capture and high throughput sequencing. <i>BMC Bioinformatics</i> , 2018 , 19, 267	3.6	2
12	Modelling Citation Networks for Improving Scientific Paper Classification Performance. <i>Lecture Notes in Computer Science</i> , 2006 , 413-422	0.9	2
11	A Distance Measure for Genome Phylogenetic Analysis. <i>Lecture Notes in Computer Science</i> , 2009 , 71-80	0.9	2
10	Real-time resolution of short-read assembly graph using ONT long reads. <i>PLoS Computational Biology</i> , 2021 , 17, e1008586	5	2
9	GtTR: Bayesian estimation of absolute tandem repeat copy number using sequence capture and high throughput sequencing		1
8	Assembly of whole-chromosome pseudomolecules for polyploid plant genomes using outcrossed mapping populations		1
7	npInv: accurate detection and genotyping of inversions mediated by non-allelic homologous recombination using long read sub-alignment		1
6	Octapeptin C4 Induces Less Resistance and Novel Mutations in an Epidemic Carbapenemase-producing <i>Klebsiella pneumoniae</i> ST258 Clinical Isolate Compared to Polymyxins		1
5	High-throughput multiplexed tandem repeat genotyping using targeted long-read sequencing		1
4	Real-time demultiplexing Nanopore barcoded sequencing data with npBarcode		1
3	Simulating the Dynamics of Targeted Capture Sequencing with CapSim		1
2	TreeWrapper: Automatic Data Extraction Based on Tree Representation. <i>Lecture Notes in Computer Science</i> , 2006 , 566-576	0.9	
1	High-throughput multiplexed tandem repeat genotyping using targeted long-read sequencing. <i>F1000Research</i> , 9 , 1084	3.6	

