

Nam-phuong Nguyen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4278299/publications.pdf>

Version: 2024-02-01

19
papers

4,033
citations

623734

14
h-index

752698

20
g-index

22
all docs

22
docs citations

22
times ranked

6375
citing authors

#	ARTICLE	IF	CITATIONS
1	One thousand plant transcriptomes and the phylogenomics of green plants. <i>Nature</i> , 2019, 574, 679-685.	27.8	1,162
2	Phylotranscriptomic analysis of the origin and early diversification of land plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4859-68.	7.1	1,123
3	PASTA: Ultra-Large Multiple Sequence Alignment for Nucleotide and Amino-Acid Sequences. <i>Journal of Computational Biology</i> , 2015, 22, 377-386.	1.6	360
4	Circular ecDNA promotes accessible chromatin and high oncogene expression. <i>Nature</i> , 2019, 575, 699-703.	27.8	343
5	Extrachromosomal DNA is associated with oncogene amplification and poor outcome across multiple cancers. <i>Nature Genetics</i> , 2020, 52, 891-897.	21.4	273
6	A perspective on 16S rRNA operational taxonomic unit clustering using sequence similarity. <i>Npj Biofilms and Microbiomes</i> , 2016, 2, 16004.	6.4	208
7	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	13.3	184
8	TIPP: taxonomic identification and phylogenetic profiling. <i>Bioinformatics</i> , 2014, 30, 3548-3555.	4.1	93
9	Primates, Lice and Bacteria: Speciation and Genome Evolution in the Symbionts of Hominid Lice. <i>Molecular Biology and Evolution</i> , 2017, 34, 1743-1757.	8.9	51
10	Phylogenomics from Whole Genome Sequences Using aTRAM. <i>Systematic Biology</i> , 2017, 66, syw105.	5.6	47
11	ViFi: accurate detection of viral integration and mRNA fusion reveals indiscriminate and unregulated transcription in proximal genomic regions in cervical cancer. <i>Nucleic Acids Research</i> , 2018, 46, 3309-3325.	14.5	47
12	Simultaneous radiation of bird and mammal lice following the K-Pg boundary. <i>Biology Letters</i> , 2018, 14, 20180141.	2.3	33
13	Phylogenomics using Target-restricted Assembly Resolves Intra-generic Relationships of Parasitic Lice (Phthiraptera: <i>Columbicola</i>). <i>Systematic Biology</i> , 2017, 66, syx027.	5.6	22
14	Extrachromosomal DNA in HPV-Mediated Oropharyngeal Cancer Drives Diverse Oncogene Transcription. <i>Clinical Cancer Research</i> , 2021, 27, 6772-6786.	7.0	20
15	HIPPI: highly accurate protein family classification with ensembles of HMMs. <i>BMC Genomics</i> , 2016, 17, 765.	2.8	17
16	High diversity of picornaviruses in rats from different continents revealed by deep sequencing. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-8.	6.5	14
17	Long-distance dispersal of pigeons and doves generated new ecological opportunities for host-switching and adaptive radiation by their parasites. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20220042.	2.6	13
18	Design and analysis of a robust genetic Muller C-element. <i>Journal of Theoretical Biology</i> , 2010, 264, 174-187.	1.7	12

#	ARTICLE	IF	CITATIONS
19	Fully automated sequence alignment methods are comparable to, and much faster than, traditional methods in large data sets: an example with hepatitis B virus. PeerJ, 2019, 7, e6142.	2.0	3