

Evan W. Floden

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4996034/publications.pdf>

Version: 2024-02-01

18
papers

4,719
citations

623734

14
h-index

794594

19
g-index

21
all docs

21
docs citations

21
times ranked

8368
citing authors

#	ARTICLE	IF	CITATIONS
1	Nextflow enables reproducible computational workflows. <i>Nature Biotechnology</i> , 2017, 35, 316-319.	17.5	1,867
2	Rfam 12.0: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2015, 43, D130-D137.	14.5	1,000
3	The nf-core framework for community-curated bioinformatics pipelines. <i>Nature Biotechnology</i> , 2020, 38, 276-278.	17.5	963
4	TCS: A New Multiple Sequence Alignment Reliability Measure to Estimate Alignment Accuracy and Improve Phylogenetic Tree Reconstruction. <i>Molecular Biology and Evolution</i> , 2014, 31, 1625-1637.	8.9	183
5	Accurate multiple sequence alignment of transmembrane proteins with PSI-Coffee. <i>BMC Bioinformatics</i> , 2012, 13, S1.	2.6	148
6	The impact of Docker containers on the performance of genomic pipelines. <i>PeerJ</i> , 2015, 3, e1273.	2.0	101
7	Using the T-Coffee package to build multiple sequence alignments of protein, RNA, DNA sequences and 3D structures. <i>Nature Protocols</i> , 2011, 6, 1669-1682.	12.0	87
8	A functional extracellular matrix biomaterial derived from ovine forestomach. <i>Biomaterials</i> , 2010, 31, 4517-4529.	11.4	69
9	PSI/TM-Coffee: a web server for fast and accurate multiple sequence alignments of regular and transmembrane proteins using homology extension on reduced databases. <i>Nucleic Acids Research</i> , 2016, 44, W339-W343.	14.5	55
10	Quantification of inÂvitro and inÂvivo angiogenesis stimulated by ovine forestomach matrix biomaterial. <i>Biomaterials</i> , 2011, 32, 6351-6361.	11.4	47
11	TCS: a web server for multiple sequence alignment evaluation and phylogenetic reconstruction: Figure 1.. <i>Nucleic Acids Research</i> , 2015, 43, W3-W6.	14.5	44
12	Biophysical characterization of ovine forestomach extracellular matrix biomaterials. <i>Journal of Biomedical Materials Research - Part B Applied Biomaterials</i> , 2011, 96B, 67-75.	3.4	29
13	Scalable Workflows and Reproducible Data Analysis for Genomics. <i>Methods in Molecular Biology</i> , 2019, 1910, 723-745.	0.9	25
14	Large multiple sequence alignments with a root-to-leaf regressive method. <i>Nature Biotechnology</i> , 2019, 37, 1466-1470.	17.5	25
15	Generalized Bootstrap Supports for Phylogenetic Analyses of Protein Sequences Incorporating Alignment Uncertainty. <i>Systematic Biology</i> , 2018, 67, 997-1009.	5.6	12
16	Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. <i>Bioinformatics</i> , 2021, 37, 1506-1514.	4.1	7
17	HCIVdb: The hepatitis-C IRES variation database. <i>BMC Microbiology</i> , 2016, 16, 187.	3.3	6
18	Multiple Sequence Alignment Computation Using the T-Coffee Regressive Algorithm Implementation. <i>Methods in Molecular Biology</i> , 2021, 2231, 89-97.	0.9	6