Evan W. Floden

List of Publications by Year
in descending order

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