

Paolo Di Tommaso

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

3,549
citations

1040056

9
h-index

1199594

12
g-index

14
all docs

14
docs citations

14
times ranked

6941
citing authors

#	ARTICLE	IF	CITATIONS
1	Nextflow enables reproducible computational workflows. <i>Nature Biotechnology</i> , 2017, 35, 316-319.	17.5	1,867
2	T-Coffee: a web server for the multiple sequence alignment of protein and RNA sequences using structural information and homology extension. <i>Nucleic Acids Research</i> , 2011, 39, W13-W17.	14.5	982
3	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
4	Accurate multiple sequence alignment of transmembrane proteins with PSI-Coffee. <i>BMC Bioinformatics</i> , 2012, 13, S1.	2.6	148
5	AMPA: an automated web server for prediction of protein antimicrobial regions. <i>Bioinformatics</i> , 2012, 28, 130-131.	4.1	140
6	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
7	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
8	Cloud-Coffee: implementation of a parallel consistency-based multiple alignment algorithm in the T-Coffee package and its benchmarking on the Amazon Elastic-Cloud. <i>Bioinformatics</i> , 2010, 26, 1903-1904.	4.1	30
9	Generalized Bootstrap Supports for Phylogenetic Analyses of Protein Sequences Incorporating Alignment Uncertainty. <i>Systematic Biology</i> , 2018, 67, 997-1009.	5.6	12
10	Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. <i>Bioinformatics</i> , 2021, 37, 1506-1514.	4.1	7
11	Definition of visual processes in a language for expressing transitions. <i>Journal of Visual Languages and Computing</i> , 2004, 15, 211-242.	1.8	5
12	T-RMSD: a web server for automated fine-grained protein structural classification. <i>Nucleic Acids Research</i> , 2013, 41, W358-W362.	14.5	3