

Shiran Abadi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4278575/publications.pdf>

Version: 2024-02-01

9
papers

3,481
citations

1039406

9
h-index

1473754

9
g-index

11
all docs

11
docs citations

11
times ranked

7010
citing authors

#	ARTICLE	IF	CITATIONS
1	ConSurf 2016: an improved methodology to estimate and visualize evolutionary conservation in macromolecules. <i>Nucleic Acids Research</i> , 2016, 44, W344-W350.	6.5	2,395
2	The Chromosome Counts Database (<scp>CCDB</scp>) â€“ a community resource of plant chromosome numbers. <i>New Phytologist</i> , 2015, 206, 19-26.	3.5	561
3	Model selection may not be a mandatory step for phylogeny reconstruction. <i>Nature Communications</i> , 2019, 10, 934.	5.8	266
4	A machine learning approach for predicting CRISPR-Cas9 cleavage efficiencies and patterns underlying its mechanism of action. <i>PLoS Computational Biology</i> , 2017, 13, e1005807.	1.5	147
5	<scp>COVID</scp> â€“19 pandemicâ€“related lockdown: response time is more important than its strictness. <i>EMBO Molecular Medicine</i> , 2020, 12, e13171.	3.3	31
6	ModelTeller: Model Selection for Optimal Phylogenetic Reconstruction Using Machine Learning. <i>Molecular Biology and Evolution</i> , 2020, 37, 3338-3352.	3.5	30
7	Harnessing machine learning to guide phylogenetic-tree search algorithms. <i>Nature Communications</i> , 2021, 12, 1983.	5.8	20
8	CRISPys: Optimal sgRNA Design for Editing Multiple Members of a Gene Family Using the CRISPR System. <i>Journal of Molecular Biology</i> , 2018, 430, 2184-2195.	2.0	18
9	Prediction of synonymous corrections by the BE-FF computational tool expands the targeting scope of base editing. <i>Nucleic Acids Research</i> , 2020, 48, W340-W347.	6.5	13