

Asif U Tamuri

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/781621/publications.pdf>

Version: 2024-02-01

17
papers

1,265
citations

759233

12
h-index

940533

16
g-index

23
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23
docs citations

23
times ranked

3612
citing authors

#	ARTICLE	IF	CITATIONS
1	A Mutation-Selection Model of Protein Evolution under Persistent Positive Selection. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	10
2	A phylogenetic approach for weighting genetic sequences. <i>BMC Bioinformatics</i> , 2021, 22, 285.	2.6	3
3	chaste_codegen: automatic CellML to C++ code generation with fixes for singularities and automatically generated Jacobians. <i>Wellcome Open Research</i> , 2021, 6, 261.	1.8	1
4	Rapid morphological evolution in placental mammals post-dates the origin of the crown group. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182418.	2.6	29
5	Human cytomegalovirus haplotype reconstruction reveals high diversity due to superinfection and evidence of within-host recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5693-5698.	7.1	94
6	Alignment Modulates Ancestral Sequence Reconstruction Accuracy. <i>Molecular Biology and Evolution</i> , 2018, 35, 1783-1797.	8.9	70
7	ALVIS: interactive non-aggregative visualization and explorative analysis of multiple sequence alignments. <i>Nucleic Acids Research</i> , 2016, 44, e77-e77.	14.5	9
8	A Penalized-Likelihood Method to Estimate the Distribution of Selection Coefficients from Phylogenetic Data. <i>Genetics</i> , 2014, 197, 257-271.	2.9	55
9	Transcriptional diversity during lineage commitment of human blood progenitors. <i>Science</i> , 2014, 345, 1251033.	12.6	253
10	Genome sequencing of normal cells reveals developmental lineages and mutational processes. <i>Nature</i> , 2014, 513, 422-425.	27.8	315
11	SMIM1 underlies the Vel blood group and influences red blood cell traits. <i>Nature Genetics</i> , 2013, 45, 542-545.	21.4	96
12	Estimating the Distribution of Selection Coefficients from Phylogenetic Data Using Site-wise Mutation-Selection Models. <i>Genetics</i> , 2012, 190, 1101-1115.	2.9	114
13	Charting the Host Adaptation of Influenza Viruses. <i>Molecular Biology and Evolution</i> , 2011, 28, 1755-1767.	8.9	28
14	PCR Master Mixes Harbour Murine DNA Sequences. Caveat Emptor!. <i>PLoS ONE</i> , 2011, 6, e19953.	2.5	48
15	ArchSchema: a tool for interactive graphing of related Pfam domain architectures. <i>Bioinformatics</i> , 2010, 26, 1260-1261.	4.1	21
16	Identifying Changes in Selective Constraints: Host Shifts in Influenza. <i>PLoS Computational Biology</i> , 2009, 5, e1000564.	3.2	106
17	cellmlmanip and chaste_codegen: automatic CellML to C++ code generation with fixes for singularities and automatically generated Jacobians. <i>Wellcome Open Research</i> , 0, 6, 261.	1.8	2