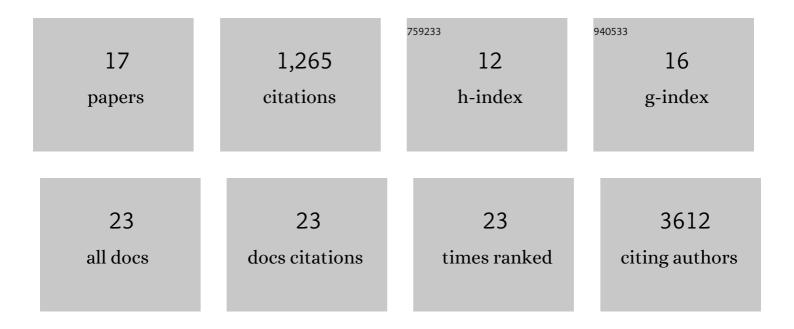
Asif U Tamuri

List of Publications by Year in descending order

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Asie II Tamiidi

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