Asif U Tamuri

List of Publications by Year
in descending order

17 papers	1,265 citations	759233 12 h-index	940533 16 g-index
23 all docs	23 docs citations	23 times ranked	3612 citing authors

#	Article	IF	Citations
1	Genome sequencing of normal cells reveals developmental lineages and mutational processes. Nature, 2014, 513, 422-425.	27.8	315
2	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	12.6	253
3	Estimating the Distribution of Selection Coefficients from Phylogenetic Data Using Sitewise Mutation-Selection Models. Genetics, 2012, 190, 1101-1115.	2.9	114
4	Identifying Changes in Selective Constraints: Host Shifts in Influenza. PLoS Computational Biology, 2009, 5, e1000564.	3.2	106
5	SMIM1 underlies the Vel blood group and influences red blood cell traits. Nature Genetics, 2013, 45, 542-545.	21.4	96
6	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
7	Alignment Modulates Ancestral Sequence Reconstruction Accuracy. Molecular Biology and Evolution, 2018, 35, 1783-1797.	8.9	70
8	A Penalized-Likelihood Method to Estimate the Distribution of Selection Coefficients from Phylogenetic Data. Genetics, 2014, 197, 257-271.	2.9	55
9	PCR Master Mixes Harbour Murine DNA Sequences. Caveat Emptor!. PLoS ONE, 2011, 6, e19953.	2.5	48
10	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
11	Charting the Host Adaptation of Influenza Viruses. Molecular Biology and Evolution, 2011, 28, 1755-1767.	8.9	28
12	ArchSchema: a tool for interactive graphing of related Pfam domain architectures. Bioinformatics, 2010, 26, 1260-1261.	4.1	21
13	A Mutationâ€"Selection Model of Protein Evolution under Persistent Positive Selection. Molecular Biology and Evolution, 2022, 39, .	8.9	10
14	ALVIS: interactive non-aggregative visualization and explorative analysis of multiple sequence alignments. Nucleic Acids Research, 2016, 44, e77-e77.	14.5	9
15	A phylogenetic approach for weighting genetic sequences. BMC Bioinformatics, 2021, 22, 285.	2.6	3
16	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
17	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