Stefanie MÃ¼hlhausen

List of Publications by Year
in descending order

17 papers	574 citations	759233 12 h-index	940533 16 g-index
19 all docs	19 docs citations	19 times ranked	893 citing authors

#	Article	IF	Citations
1	Six Subgroups and Extensive Recent Duplications Characterize the Evolution of the Eukaryotic Tubulin Protein Family. Genome Biology and Evolution, 2014, 6, 2274-2288.	2.5	110
2	Evidence for Strong Mutation Bias toward, and Selection against, U Content in SARS-CoV-2: Implications for Vaccine Design. Molecular Biology and Evolution, 2021, 38, 67-83.	8.9	68
3	A novel nuclear genetic code alteration in yeasts and the evolution of codon reassignment in eukaryotes. Genome Research, 2016, 26, 945-955.	5.5	61
4	Whole genome duplication events in plant evolution reconstructed and predicted using myosin motor proteins. BMC Evolutionary Biology, 2013, 13, 202.	3.2	51
5	Myosin repertoire expansion coincides with eukaryotic diversification in the Mesoproterozoic era. BMC Evolutionary Biology, 2017, 17, 211.	3.2	50
6	Causes and Consequences of Purifying Selection on SARS-CoV-2. Genome Biology and Evolution, 2021, 13, .	2.5	37
7	Nuclear codon reassignments in the genomics era and mechanisms behind their evolution. BioEssays, 2017, 39, 1600221.	2.5	35
8	Molecular Phylogeny of Sequenced Saccharomycetes Reveals Polyphyly of the Alternative Yeast Codon Usage. Genome Biology and Evolution, 2014, 6, 3222-3237.	2.5	34
9	GenePainter: a fast tool for aligning gene structures of eukaryotic protein families, visualizing the alignments and mapping gene structures onto protein structures. BMC Bioinformatics, 2013, 14, 77.	2.6	24
10	Endogenous Stochastic Decoding of the CUG Codon by Competing Ser- and Leu-tRNAs in Ascoidea asiatica. Current Biology, 2018, 28, 2046-2057.e5.	3.9	22
11	Predicting the fungal CUG codon translation with Bagheera. BMC Genomics, 2014, 15, 411.	2.8	18
12	The Protein‐Coding Human Genome: Annotating High‐Hanging Fruits. BioEssays, 2019, 41, e1900066.	2.5	17
13	Predicting phenotypic traits of prokaryotes from protein domain frequencies. BMC Bioinformatics, 2010, 11, 481.	2.6	14
14	How tRNAs dictate nuclear codon reassignments: Only a few can capture non-cognate codons. RNA Biology, 2017, 14, 293-299.	3.1	13
15	GenePainter v. 2.0 resolves the taxonomic distribution of intron positions. Bioinformatics, 2015, 31, 1302-1304.	4.1	9
16	Proteogenomics analysis of CUG codon translation in the human pathogen Candida albicans. BMC Biology, 2021, 19, 258.	3.8	2
17	Transgene-design: a web application for the design of mammalian transgenes. Bioinformatics, 2022, 38, 2626-2627.	4.1	1