

Stefanie MÃ¼hlhausen

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

574
citations

759233

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940533

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g-index

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all docs

19
docs citations

19
times ranked

893
citing authors

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