

Steven E Massey

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

976
citations

516561

16
h-index

501076

28
g-index

43
all docs

43
docs citations

43
times ranked

1965
citing authors

#	ARTICLE	IF	CITATIONS
1	Host Manipulation Mechanisms of SARS-CoV-2. <i>Acta Biotheoretica</i> , 2022, 70, 4.	0.7	0
2	How signalling games explain mimicry at many levels: from viral epidemiology to human sociology. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20200689.	1.5	9
3	Form and relationship of the social networks of the New Testament. <i>Social Network Analysis and Mining</i> , 2019, 9, 1.	1.9	4
4	On the Origin of Biomolecular Networks. <i>Frontiers in Genetics</i> , 2019, 10, 240.	1.1	17
5	Functional Metagenomics Characterization of an Anaerobic Saltwater Bioreactor. <i>Journal of Renewable Energy</i> , 2019, 2019, 1-15.	2.1	3
6	Mycobiome of Brevipalpus Mite Strains and Insights on Metabolic Function in the Bacteriome of the Tetranychidae Mites. , 2019, , 79-91.		1
7	Genetic Code Error Minimization as a Non-Adaptive But Beneficial Trait. <i>Journal of Molecular Evolution</i> , 2019, 87, 4-6.	0.8	9
8	How to find an error minimized genetic code: neutral emergence as an alternative to direct Darwinian selection for evolutionary optimization. <i>Natural Computing</i> , 2019, 18, 203-212.	1.8	6
9	Machine Learning Algorithm for Predicting Warfarin Dose in Caribbean Hispanics Using Pharmacogenetic Data. <i>Frontiers in Pharmacology</i> , 2019, 10, 1550.	1.6	26
10	Mapping Base Modifications in DNA by Transverse-Current Sequencing. <i>Physical Review Applied</i> , 2018, 9, .	1.5	2
11	Origin of biomolecular games: deception and molecular evolution. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180429.	1.5	20
12	Strong Amerindian Mitonuclear Discordance in Puerto Rican Genomes Suggests Amerindian Mitochondrial Benefit. <i>Annals of Human Genetics</i> , 2017, 81, 59-77.	0.3	1
13	The identities of stop codon reassignments support ancestral tRNA stop codon decoding activity as a facilitator of gene duplication and evolution of novel function. <i>Gene</i> , 2017, 619, 37-43.	1.0	7
14	Reduced Diversity in the Bacteriome of the Phytophagous Mite <i>Brevipalpus yothersi</i> (Acari: Tj ETQq0 0 0 rgBT /Overlock 10 Tj 50 222 T	1.0	3
15	Comparative Microbial Genomics and Forensics. <i>Microbiology Spectrum</i> , 2016, 4, .	1.2	4
16	Social network analysis of the biblical Moses. <i>Applied Network Science</i> , 2016, 1, 13.	0.8	3
17	The neutral emergence of error minimized genetic codes superior to the standard genetic code. <i>Journal of Theoretical Biology</i> , 2016, 408, 237-242.	0.8	41
18	DNA/RNA transverse current sequencing: intrinsic structural noise from neighboring bases. <i>Frontiers in Genetics</i> , 2015, 6, 213.	1.1	8

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19	SmileFinder: a resampling-based approach to evaluate signatures of selection from genome-wide sets of matching allele frequency data in two or more diploid populations. <i>GigaScience</i> , 2015, 4, 1.	3.3	241
20	Genetic Code Evolution Reveals the Neutral Emergence of Mutational Robustness, and Information as an Evolutionary Constraint. <i>Life</i> , 2015, 5, 1301-1332.	1.1	32
21	DNA Repair Is Associated with Information Content in Bacteria, Archaea, and DNA Viruses. <i>Journal of Heredity</i> , 2015, 106, 644-659.	1.0	15
22	Paleomicrobiology: Revealing Fecal Microbiomes of Ancient Indigenous Cultures. <i>PLoS ONE</i> , 2014, 9, e106833.	1.1	60
23	Intrinsic Noise from Neighboring Bases in the DNA Transverse Tunneling Current. <i>Physical Review Applied</i> , 2014, 1, .	1.5	8
24	A Nonadaptive Origin of a Beneficial Trait: In Silico Selection for Free Energy of Folding Leads to the Neutral Emergence of Mutational Robustness in Single Domain Proteins. <i>Journal of Molecular Evolution</i> , 2014, 78, 130-139.	0.8	4
25	What can information-asymmetric games tell us about the context of Crick's "frozen accident"? <i>Journal of the Royal Society Interface</i> , 2013, 10, 20130614.	1.5	13
26	Proteome size as the major factor determining mutation rates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E858-E859.	3.3	6
27	The Presence of the DNA Repair Genes <i>mutM</i> , <i>mutY</i> , <i>mutL</i> , and <i>mutS</i> is Related to Proteome Size in Bacterial Genomes. <i>Frontiers in Genetics</i> , 2012, 3, 3.	1.1	26
28	Positive selection on a bacterial oncoprotein associated with gastric cancer. <i>Gut Pathogens</i> , 2011, 3, 18.	1.6	7
29	Searching of Code Space for an Error-Minimized Genetic Code Via Codon Capture Leads to Failure, or Requires At Least 20 Improving Codon Reassignments Via the Ambiguous Intermediate Mechanism. <i>Journal of Molecular Evolution</i> , 2010, 70, 106-115.	0.8	12
30	Lineage-Specific Differences in the Amino Acid Substitution Process. <i>Journal of Molecular Biology</i> , 2010, 396, 1410-1421.	2.0	12
31	Pseudadaptations and the Emergence of Beneficial Traits. , 2010, , 81-98.		2
32	ScanMoment: a web server for combinatorial analysis of basic residues in nucleic acid binding sites. <i>Bioinformatics</i> , 2009, 3, 293-295.	0.2	1
33	A Neutral Origin for Error Minimization in the Genetic Code. <i>Journal of Molecular Evolution</i> , 2008, 67, 510-516.	0.8	70
34	Characterizing positive and negative selection and their phylogenetic effects. <i>Gene</i> , 2008, 418, 22-26.	1.0	26
35	The Proteomic Constraint and Its Role in Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2008, 25, 2557-2565.	3.5	18
36	Newly metamorphosed <i>Elysia clarki</i> juveniles feed on and sequester chloroplasts from algal species different from those utilized by adult slugs. <i>Marine Biology</i> , 2007, 150, 797-806.	0.7	30

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37	A Comparative Genomics Analysis of Codon Reassignments Reveals a Link with Mitochondrial Proteome Size and a Mechanism of Genetic Code Change Via Suppressor tRNAs. <i>Journal of Molecular Evolution</i> , 2007, 64, 399-410.	0.8	32
38	The symbiotic chloroplasts in the sacoglossan <i>Elysia clarki</i> are from several algal species. <i>Invertebrate Biology</i> , 2006, 125, 336-345.	0.3	53
39	A Sequential 2-1-3 Model of Genetic Code Evolution That Explains Codon Constraints. <i>Journal of Molecular Evolution</i> , 2006, 62, 809-810.	0.8	30
40	Basic faced alpha-helices are widespread in the peptide extensions of the eukaryotic aminoacyl-tRNA synthetases. <i>In Silico Biology</i> , 2006, 6, 259-73.	0.4	2
41	Comparative Evolutionary Genomics Unveils the Molecular Mechanism of Reassignment of the CTG Codon in <i>Candida</i> spp.. <i>Genome Research</i> , 2003, 13, 544-557.	2.4	111
42	Comparative Microbial Genomics and Forensics. , 0, , 237-276.		0