Steven E Massey

List of Publications by Year
in descending order

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	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. GigaScience, 2015, 4, 1.	3.3	241
2	Comparative Evolutionary Genomics Unveils the Molecular Mechanism of Reassignment of the CTG Codon in Candida spp.. Genome Research, 2003, 13, 544-557.	2.4	111
3	A Neutral Origin for Error Minimization in the Genetic Code. Journal of Molecular Evolution, 2008, 67, 510-516.	0.8	70
4	Paleomicrobiology: Revealing Fecal Microbiomes of Ancient Indigenous Cultures. PLoS ONE, 2014, 9, e106833.	1.1	60
5	The symbiotic chloroplasts in the sacoglossan Elysia clarki are from several algal species. Invertebrate Biology, 2006, 125, 336-345.	0.3	53
6	The neutral emergence of error minimized genetic codes superior to the standard genetic code. Journal of Theoretical Biology, 2016, 408, 237-242.	0.8	41
7	A Comparative Genomics Analysis of Codon Reassignments Reveals a Link with Mitochondrial Proteome Size and a Mechanism of Genetic Code Change Via Suppressor tRNAs. Journal of Molecular Evolution, 2007, 64, 399-410.	0.8	32
8	Genetic Code Evolution Reveals the Neutral Emergence of Mutational Robustness, and Information as an Evolutionary Constraint. Life, 2015, 5, 1301-1332.	1.1	32
9	A Sequential â€œ2-1-3â€•Model of Genetic Code Evolution That Explains Codon Constraints. Journal of Molecular Evolution, 2006, 62, 809-810.	0.8	30
10	Newly metamorphosed Elysia clarki juveniles feed on and sequester chloroplasts from algal species different from those utilized by adult slugs. Marine Biology, 2007, 150, 797-806.	0.7	30
11	Characterizing positive and negative selection and their phylogenetic effects. Gene, 2008, 418, 22-26.	1.0	26
12	The Presence of the DNA Repair Genes mutM, mutY, mutL, and mutS is Related to Proteome Size in Bacterial Genomes. Frontiers in Genetics, 2012, 3, 3.	1.1	26
13	Machine Learning Algorithm for Predicting Warfarin Dose in Caribbean Hispanics Using Pharmacogenetic Data. Frontiers in Pharmacology, 2019, 10, 1550.	1.6	26
14	Origin of biomolecular games: deception and molecular evolution. Journal of the Royal Society Interface, 2018, 15, 20180429.	1.5	20
15	The Proteomic Constraint and Its Role in Molecular Evolution. Molecular Biology and Evolution, 2008, 25, 2557-2565.	3.5	18
16	On the Origin of Biomolecular Networks. Frontiers in Genetics, 2019, 10, 240.	1.1	17
17	DNA Repair Is Associated with Information Content in Bacteria, Archaea, and DNA Viruses. Journal of Heredity, 2015, 106, 644-659.	1.0	15
18	What can information-asymmetric games tell us about the context of Crick's â€˜frozen accidentâ€™?. Journal of the Royal Society Interface, 2013, 10, 20130614.	1.5	13

#	Article	IF	Citations
19	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. Journal of Molecular Evolution, 2010, 70, 106-115.	0.8	12
20	Lineage-Specific Differences in the Amino Acid Substitution Process. Journal of Molecular Biology, 2010, 396, 1410-1421.	2.0	12
21	Genetic Code Error Minimization as a Non-Adaptive But Beneficial Trait. Journal of Molecular Evolution, 2019, 87, 4-6.	0.8	9
22	How signalling games explain mimicry at many levels: from viral epidemiology to human sociology. Journal of the Royal Society Interface, 2021, 18, 20200689.	1.5	9
23	Intrinsic Noise from Neighboring Bases in the DNA Transverse Tunneling Current. Physical Review Applied, 2014, 1, .	1.5	8
24	DNA/RNA transverse current sequencing: intrinsic structural noise from neighboring bases. Frontiers in Genetics, 2015, 6, 213.	1.1	8
25	Positive selection on a bacterial oncoprotein associated with gastric cancer. Gut Pathogens, 2011, 3, 18.	1.6	7
26	The identities of stop codon reassignments support ancestral tRNA stop codon decoding activity as a facilitator of gene duplication and evolution of novel function. Gene, 2017, 619, 37-43.	1.0	7
27	Proteome size as the major factor determining mutation rates. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E858-E859.	3.3	6
28	How to 'find' an error minimized genetic code: neutral emergence as an alternative to direct Darwinian selection for evolutionary optimization. Natural Computing, 2019, 18, 203-212.	1.8	6
29	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. Journal of Molecular Evolution, 2014, 78, 130-139.	0.8	4
30	Comparative Microbial Genomics and Forensics. Microbiology Spectrum, 2016, 4, .	1.2	4
31	Form and relationship of the social networks of the New Testament. Social Network Analysis and Mining, 2019, 9, 1.	1.9	4
32	Reduced Diversity in the Bacteriome of the Phytophagous Mite Brevipalpus yothersi (Acari:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 Td	1.0	3
33	Social network analysis of the biblical Moses. Applied Network Science, 2016, 1, 13.	0.8	3
34	Functional Metagenomics Characterization of an Anaerobic Saltwater Bioreactor. Journal of Renewable Energy, 2019, 2019, 1-15.	2.1	3
35	Mapping Base Modifications in DNA by Transverse-Current Sequencing. Physical Review Applied, 2018, 9, .	1.5	2
36	Pseudaptations and the Emergence of Beneficial Traits. , 2010, , 81-98.		2

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37	Basic faced alpha-helices are widespread in the peptide extensions of the eukaryotic aminoacyl-tRNA synthetases. In Silico Biology, 2006, 6, 259-73.	0.4	2
38	Strong Amerindian Mitonuclear Discordance in Puerto Rican Genomes Suggests Amerindian Mitochondrial Benefit. Annals of Human Genetics, 2017, 81, 59-77.	0.3	1
39	Mycobiome of Brevipalpus Mite Strains and Insights on Metabolic Function in the Bacteriome of the Tetranychoidea Mites. , 2019, , 79-91.		1
40	ScanMoment: a web server for combinatorial analysis of basic residues in nucleic acid binding sites. Bioinformation, 2009, 3, 293-295.	0.2	1
41	Comparative Microbial Genomics and Forensics. , 0, , 237-276.		0
42	Host Manipulation Mechanisms of SARS-CoV-2. Acta Biotheoretica, 2022, 70, 4.	0.7	0