

Arlin Stoltzfus

List of Publications by Year in descending order

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43
papers

2,575
citations

236925

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39
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54
all docs

54
docs citations

54
times ranked

2447
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutation bias shapes the spectrum of adaptive substitutions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	34
2	Phylotastic: Improving Access to Tree-of-Life Knowledge With Flexible, on-the-Fly Delivery of Trees. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693431989938.	1.2	2
3	Avoidance of Self during CRISPR Immunization. <i>Trends in Microbiology</i> , 2020, 28, 543-553.	7.7	19
4	The role of mutation bias in adaptive molecular evolution: insights from convergent changes in protein function. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180238.	4.0	43
5	Hacking and Making at Time-Bounded Events. , 2017, , .		14
6	Mutational Biases Influence Parallel Adaptation. <i>Molecular Biology and Evolution</i> , 2017, 34, 2163-2172.	8.9	93
7	Why we don't want another "Synthesis" <i>Biology Direct</i> , 2017, 12, 23.	4.6	49
8	On the Causes of Evolutionary Transition: Transversion Bias. <i>Molecular Biology and Evolution</i> , 2016, 33, 595-602.	8.9	91
9	Mutation-biased adaptation in Andean house wrens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13753-13754.	7.1	6
10	Modeling Evolution Using the Probability of Fixation: History and Implications. <i>Quarterly Review of Biology</i> , 2014, 89, 225-252.	0.1	150
11	Mendelian-Mutationism: The Forgotten Evolutionary Synthesis. <i>Journal of the History of Biology</i> , 2014, 47, 501-546.	0.5	40
12	Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. <i>BMC Bioinformatics</i> , 2013, 14, 158.	2.6	33
13	NeXML: Rich, Extensible, and Verifiable Representation of Comparative Data and Metadata. <i>Systematic Biology</i> , 2012, 61, 675-689.	5.6	90
14	Population Diversity of ORFan Genes in <i>Escherichia coli</i> . <i>Genome Biology and Evolution</i> , 2012, 4, 1176-1187.	2.5	24
15	PhylOnt: A domain-specific ontology for phylogeny analysis. , 2012, , .		2
16	Constructive neutral evolution: exploring evolutionary theory's curious disconnect. <i>Biology Direct</i> , 2012, 7, 35.	4.6	70
17	Sharing and re-use of phylogenetic trees (and associated data) to facilitate synthesis. <i>BMC Research Notes</i> , 2012, 5, 574.	1.4	42
18	Gene identification in black cohosh (<i>Actaea racemosa</i> L.): expressed sequence tag profiling and genetic screening yields candidate genes for production of bioactive secondary metabolites. <i>Plant Cell Reports</i> , 2011, 30, 613-629.	5.6	13

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19	Climbing Mount Probable: Mutation as a Cause of Nonrandomness in Evolution. <i>Journal of Heredity</i> , 2009, 100, 637-647.	2.4	78
20	Knowledge Standardization in Evolutionary Biology: The Comparative Data Analysis Ontology. , 2009, , 195-214.		2
21	Initial Implementation of a Comparative Data Analysis Ontology. <i>Evolutionary Bioinformatics</i> , 2009, 5, EBO.S2320.	1.2	30
22	Evidence for a predominant role of oxidative damage in germline mutation in mammals. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2008, 644, 71-73.	1.0	13
23	A Sequence-Based Model Accounts Largely for the Relationship of Intron Positions to Protein Structural Features. <i>Molecular Biology and Evolution</i> , 2007, 24, 2158-2168.	8.9	8
24	Bio::NEXUS: a Perl API for the NEXUS format for comparative biological data. <i>BMC Bioinformatics</i> , 2007, 8, 191.	2.6	8
25	Amino Acid Exchangeability and the Adaptive Code Hypothesis. <i>Journal of Molecular Evolution</i> , 2007, 65, 456-462.	1.8	28
26	Mutationism and the dual causation of evolutionary change. <i>Evolution & Development</i> , 2006, 8, 304-317.	2.0	58
27	Nexplorer: phylogeny-based exploration of sequence family data. <i>Bioinformatics</i> , 2006, 22, 120-121.	4.1	8
28	Mutation-Biased Adaptation in a Protein NK Model. <i>Molecular Biology and Evolution</i> , 2006, 23, 1852-1862.	8.9	34
29	The Exchangeability of Amino Acids in Proteins. <i>Genetics</i> , 2005, 170, 1459-1472.	2.9	119
30	The Evolutionary Gain of Spliceosomal Introns: Sequence and Phase Preferences. <i>Molecular Biology and Evolution</i> , 2004, 21, 1252-1263.	8.9	115
31	Molecular Evolution: Introns Fall into Place. <i>Current Biology</i> , 2004, 14, R351-R352.	3.9	28
32	Bias in the introduction of variation as an orienting factor in evolution. <i>Evolution & Development</i> , 2001, 3, 73-83.	2.0	151
33	On the Possibility of Constructive Neutral Evolution. <i>Journal of Molecular Evolution</i> , 1999, 49, 169-181.	1.8	418
34	Molecular evolution: Recent cases of spliceosomal intron gain?. <i>Current Biology</i> , 1998, 8, R560-R563.	3.9	98
35	Intron "sliding" and the diversity of intron positions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 10739-10744.	7.1	156
36	Methods for evaluating exon-protein correspondences. <i>Bioinformatics</i> , 1995, 11, 509-515.	4.1	4

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37	<i>Response</i> : Introns and the Origin of Protein-Coding Genes. Science, 1995, 268, 1367-1369.	12.6	0
38	<i>Response</i> : Introns and the Origin of Protein-Coding Genes. Science, 1995, 268, 1367-1369.	12.6	0
39	Testing the exon theory of genes: the evidence from protein structure. Science, 1994, 265, 202-207.	12.6	224
40	Origin of introns—early or late?. Nature, 1994, 369, 526-527.	27.8	43
41	Genes-in-pieces revisited. Nature, 1993, 361, 403-403.	27.8	26
42	Slippery introns and globin gene evolution. Current Biology, 1993, 3, 215-217.	3.9	30
43	Community and Code: Nine Lessons from Nine NESCent Hackathons. F1000Research, 0, 6, 786.	1.6	18