Simon Whelan

List of Publications by Year in descending order

33 papers	15,434 citations	361413 20 h-index	434195 31 g-index
34 all docs	34 docs citations	34 times ranked	22025 citing authors

#	Article	IF	Citations
1	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
2	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
3	A General Empirical Model of Protein Evolution Derived from Multiple Protein Families Using a Maximum-Likelihood Approach. Molecular Biology and Evolution, 2001, 18, 691-699.	8.9	2,599
4	Molecular phylogenetics: state-of-the-art methods for looking into the past. Trends in Genetics, 2001, 17, 262-272.	6.7	376
5	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. Genome Research, 2003, 13, 13-26.	5.5	263
6	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	5.5	184
7	Identifying Clusters of High Confidence Homologies in Multiple Sequence Alignments. Molecular Biology and Evolution, 2019, 36, 2340-2351.	8.9	108
8	PREQUAL: detecting non-homologous characters in sets of unaligned homologous sequences. Bioinformatics, 2018, 34, 3929-3930.	4.1	96
9	Measuring the distance between multiple sequence alignments. Bioinformatics, 2012, 28, 495-502.	4.1	86
10	Estimating the Frequency of Events That Cause Multiple-Nucleotide Changes. Genetics, 2004, 167, 2027-2043.	2.9	81
11	ModelOMatic: Fast and Automated Model Selection between RY, Nucleotide, Amino Acid, and Codon Substitution Models. Systematic Biology, 2015, 64, 42-55.	5.6	68
12	Class of Multiple Sequence Alignment Algorithm Affects Genomic Analysis. Molecular Biology and Evolution, 2013, 30, 642-653.	8.9	61
13	PANDIT: an evolution-centric database of protein and associated nucleotide domains with inferred trees. Nucleic Acids Research, 2006, 34, D327-D331.	14.5	59
14	Covariation Is a Poor Measure of Molecular Coevolution. Molecular Biology and Evolution, 2015, 32, 2456-2468.	8.9	49
15	A Novel Use of Equilibrium Frequencies in Models of Sequence Evolution. Molecular Biology and Evolution, 2002, 19, 1821-1831.	8.9	46
16	Pandit: a database of protein and associated nucleotide domains with inferred trees. Bioinformatics, 2003, 19, 1556-1563.	4.1	44
17	Spatial and Temporal Heterogeneity in Nucleotide Sequence Evolution. Molecular Biology and Evolution, 2008, 25, 1683-1694.	8.9	36
18	New Approaches to Phylogenetic Tree Search and Their Application to Large Numbers of Protein Alignments. Systematic Biology, 2007, 56, 727-740.	5.6	30

#	Article	IF	Citations
19	Phylogenetics by likelihood: Evolutionary modeling as a tool for understanding the genome. Journal of Biomedical Informatics, 2006, 39, 51-61.	4.3	27
20	Statistical Methods in Molecular Evolution. Systematic Biology, 2006, 55, 698-700.	5.6	26
21	Determination and validation of principal gene products. Bioinformatics, 2008, 24, 11-17.	4.1	23
22	Characterizing the Phylogenetic Tree-Search Problem. Systematic Biology, 2012, 61, 228.	5.6	23
23	Physicochemical Amino Acid Properties Better Describe Substitution Rates in Large Populations. Molecular Biology and Evolution, 2019, 36, 679-690.	8.9	20
24	Assessing the State of Substitution Models Describing Noncoding RNA Evolution. Genome Biology and Evolution, 2014, 6, 65-75.	2.5	18
25	Phylogenetic Substitution Models for Detecting Heterotachy during Plastid Evolution. Molecular Biology and Evolution, 2011, 28, 449-458.	8.9	17
26	Evidence of Statistical Inconsistency of Phylogenetic Methods in the Presence of Multiple Sequence Alignment Uncertainty. Genome Biology and Evolution, 2015, 7, 2102-2116.	2.5	17
27	Phylogenetic Tree Estimation With and Without Alignment: New Distance Methods and Benchmarking. Systematic Biology, 2016, 66, syw074.	5.6	17
28	Inferring Trees. Methods in Molecular Biology, 2008, 452, 287-309.	0.9	13
29	The genetic code can cause systematic bias in simple phylogenetic models. Philosophical Transactions of the Royal Society B: Biological Sciences, 2008, 363, 4003-4011.	4.0	11
30	Inferring Trees. Methods in Molecular Biology, 2017, 1525, 349-377.	0.9	5
31	Impact of deep coalescence and recombination on the estimation of phylogenetic relationships among species using AFLP markers. Molecular Phylogenetics and Evolution, 2014, 76, 102-109.	2.7	3
32	GeLL: a generalized likelihood library for phylogenetic models: Fig. 1.. Bioinformatics, 2015, 31, 2391-2393.	4.1	0
33	Automated Removal of Non-homologous Sequence Stretches with PREQUAL. Methods in Molecular Biology, 2021, 2231, 147-162.	0.9	0