

# A Case for Evolutionary Genomics and the Comprehensive Biodiversity

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Evolutionary biology meets genomics. <i>Trends in Ecology and Evolution</i> , 2001, 16, 15-16.	4.2	3
2	Evolution in Health and Disease: Work in Progress. <i>Quarterly Review of Biology</i> , 2001, 76, 417-432.	0.0	101
3	Current Awareness on Comparative and Functional Genomics. <i>Comparative and Functional Genomics</i> , 2001, 2, 265-272.	2.0	0
4	Mitogenomic Exploration of Higher Teleostean Phylogenies: A Case Study for Moderate-Scale Evolutionary Genomics with 38 Newly Determined Complete Mitochondrial DNA Sequences. <i>Molecular Biology and Evolution</i> , 2001, 18, 1993-2009.	3.5	360
5	Evaluation of Methods for Determination of a Reconstructed History of Gene Sequence Evolution. <i>Molecular Biology and Evolution</i> , 2001, 18, 2040-2047.	3.5	61
6	A Comprehensive Vertebrate Phylogeny Using Vector Representations of Protein Sequences from Whole Genomes. <i>Molecular Biology and Evolution</i> , 2002, 19, 554-562.	3.5	95
7	Phylogeny Reconstruction and Functional Constraints in Organellar Genomes: Plastid <i>atpB</i> and <i>rbcl</i> Sequences Versus Animal Mitochondrion. <i>Systematic Biology</i> , 2002, 51, 638-647.	2.7	16
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14	Palaeoecology of Triassic stem turtles sheds new light on turtle origins. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2004, 271, 1-5.	1.2	177
15	Genome-scale data, angiosperm relationships, and "ending incongruence": a cautionary tale in phylogenetics. <i>Trends in Plant Science</i> , 2004, 9, 477-483.	4.3	176
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18	Divergence, recombination and retention of functionality during protein evolution. <i>Human Genomics</i> , 2005, 2, 158.	1.4	5
19	Ecological perspectives on the sequenced genome collection. <i>Ecology Letters</i> , 2005, 8, 1334-1345.	3.0	28
20	Magic bullets and golden rules: Data sampling in molecular phylogenetics. <i>Zoology</i> , 2005, 108, 329-336.	0.6	43

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21	Complete Genome Sequence of the Grouper Iridovirus and Comparison of Genomic Organization with Those of Other Iridoviruses. <i>Journal of Virology</i> , 2005, 79, 2010-2023.	1.5	101
22	Phylogenetics of modern birds in the era of genomics. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005, 272, 979-992.	1.2	83
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31	Log-correlation Distance And Fourier Transform With Kullback-Leibler Divergence Distance For Construction Of Vertebrate Phylogeny Using Complete Mitochondrial Genomes. , 2007, , .		9
32	Bio-STEER: A Semantic Web workflow tool for Grid computing in the life sciences. <i>Future Generation Computer Systems</i> , 2007, 23, 497-509.	4.9	34
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39	Rapid Likelihood Analysis on Large Phylogenies Using Partial Sampling of Substitution Histories. <i>Molecular Biology and Evolution</i> , 2010, 27, 249-265.	3.5	23
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41	Prospects for the Use of Next-Generation Sequencing Methods in Ornithology. <i>Auk</i> , 2010, 127, 4-15.	0.7	49
42	Temporal Bone Arrangements in Turtles: An Overview. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2012, 318, 235-249.	0.6	29
43	The complete mitochondrial genome sequences of <i>Chelodina rugosa</i> and <i>Chelus fimbriata</i> (Pleurodira: Testudines). <i>Biology Reports</i> , 2012, 39, 2097-2107.	1.0	13
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51	On nonepistemic values in conservation biology. <i>Conservation Biology</i> , 2017, 31, 48-55.	2.4	17
52	Genomics-based plant germplasm research (GPGR). <i>Crop Journal</i> , 2017, 5, 166-174.	2.3	28
53	Insights into the phylogeny of Hemiptera from increased mitogenomic taxon sampling. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 236-249.	1.2	59
54	Gene-wise resampling outperforms site-wise resampling in phylogenetic coalescence analyses. <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 80-92.	1.2	33
55	Alignment-free inference of hierarchical and reticulate phylogenomic relationships. <i>Briefings in Bioinformatics</i> , 2019, 20, 426-435.	3.2	74
56	Bayesian Phylogeny on Grid. <i>Communications in Computer and Information Science</i> , 2008, , 404-416.	0.4	9
57	Likelihood Analysis of Asymmetrical Mutation Bias Gradients in Vertebrate Mitochondrial Genomes. <i>Genetics</i> , 2003, 165, 735-745.	1.2	91
58	Chaos Game Representation of Mitochondrial Genomes. <i>Advances in Bioinformatics and Biomedical Engineering Book Series</i> , 0, , 28-38.	0.2	0

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61	Increasing Taxa Sampling Provides New Insights on the Phylogenetic Relationship Between <i>Eriobotrya</i> and <i>Rhaphiolepis</i> . <i>Frontiers in Genetics</i> , 2022, 13, 831206.	1.1	7