

Phylogenomic analyses data of the avian phylogenomic

GigaScience

4, 4

DOI: [10.1186/s13742-014-0038-1](https://doi.org/10.1186/s13742-014-0038-1)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Divergence and gene flow among Darwin's finches: A genome-wide view of adaptive radiation driven by interspecies allele sharing. <i>BioEssays</i> , 2015, 37, 968-974.	1.2	16
2	Avianbase: a community resource for bird genomics. <i>Genome Biology</i> , 2015, 16, 21.	3.8	28
3	Temporal Dynamics of Avian Populations during Pleistocene Revealed by Whole-Genome Sequences. <i>Current Biology</i> , 2015, 25, 1375-1380.	1.8	243
4	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015, 4, 4.	3.3	72
5	A new look at the LTR retrotransposon content of the chicken genome. <i>BMC Genomics</i> , 2016, 17, 688.	1.2	35
6	The phylogenomic forest of bird trees contains a hard polytomy at the root of Neoaves. <i>Zoologica Scripta</i> , 2016, 45, 50-62.	0.7	122
7	Ancient horizontal transfers of retrotransposons between birds and ancestors of human pathogenic nematodes. <i>Nature Communications</i> , 2016, 7, 11396.	5.8	76
8	Computing the Internode Certainty and Related Measures from Partial Gene Trees. <i>Molecular Biology and Evolution</i> , 2016, 33, 1606-1617.	3.5	73
9	Conserved Nonexonic Elements: A Novel Class of Marker for Phylogenomics. <i>Systematic Biology</i> , 2017, 66, 1028-1044.	2.7	46
10	Purifying selection and concerted evolution of RNA-sensing toll-like receptors in migratory waders. <i>Infection, Genetics and Evolution</i> , 2017, 53, 135-145.	1.0	15
11	Why Do Phylogenomic Data Sets Yield Conflicting Trees? Data Type Influences the Avian Tree of Life more than Taxon Sampling. <i>Systematic Biology</i> , 2017, 66, 857-879.	2.7	242
12	Evolution of ribosomal internal transcribed spacers in Deuterostomia. <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 87-96.	1.2	5
13	Experiences in integrated data and research object publishing using GigaDB. <i>International Journal on Digital Libraries</i> , 2017, 18, 99-111.	1.1	14
14	Uncovering missing pieces: duplication and deletion history of arrestins in deuterostomes. <i>BMC Evolutionary Biology</i> , 2017, 17, 163.	3.2	39
15	Phylogenomic Insights into Mouse Evolution Using a Pseudoreference Approach. <i>Genome Biology and Evolution</i> , 2017, 9, 726-739.	1.1	47
16	Single-molecule, full-length transcript sequencing provides insight into the extreme metabolism of the ruby-throated hummingbird <i>Archilochus colubris</i> . <i>GigaScience</i> , 2018, 7, 1-12.	3.3	67
17	Few mitochondrial <i>scn</i> DNA sequences are inserted into the turkey (<i>Meleagris</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td</i> <i>Animal Genetics</i> , 2018, 49, 259-264.	0.6	5
18	Filtering nucleotide sites by phylogenetic signal to noise ratio increases confidence in the Neoaves phylogeny generated from ultraconserved elements. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 116-128.	1.2	19

#	ARTICLE	IF	CITATIONS
19	So many genes, so little time: A practical approach to divergence-time estimation in the genomic era. <i>PLoS ONE</i> , 2018, 13, e0197433.	1.1	167
20	An evolutionary model motivated by physicochemical properties of amino acids reveals variation among proteins. <i>Bioinformatics</i> , 2018, 34, i350-i356.	1.8	12
21	Phylogenetic Signal of Indels and the Neoavian Radiation. <i>Diversity</i> , 2019, 11, 108.	0.7	33
22	A Multireference-Based Whole Genome Assembly for the Obligate Ant-Following Antbird, <i>Rhegmatorhina melanosticta</i> (Thamnophilidae). <i>Diversity</i> , 2019, 11, 144.	0.7	13
23	Supergene validation: A model-based protocol for assessing the accuracy of non-model-based supergene methods. <i>MethodsX</i> , 2019, 6, 2181-2188.	0.7	1
24	A stem anseriform from the early Palaeocene of Antarctica provides new key evidence in the early evolution of waterfowl. <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 673-700.	1.0	25
25	De novo assembly of the Indian blue peacock (<i>Pavo cristatus</i>) genome using Oxford Nanopore technology and Illumina sequencing. <i>GigaScience</i> , 2019, 8, .	3.3	25
26	Whole-Genome Analyses Resolve the Phylogeny of Flightless Birds (Palaeognathae) in the Presence of an Empirical Anomaly Zone. <i>Systematic Biology</i> , 2019, 68, 937-955.	2.7	88
27	Statistical binning leads to profound model violation due to gene tree error incurred by trying to avoid gene tree error. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 164-171.	1.2	20
28	Skmer: assembly-free and alignment-free sample identification using genome skims. <i>Genome Biology</i> , 2019, 20, 34.	3.8	70
29	Physicochemical Amino Acid Properties Better Describe Substitution Rates in Large Populations. <i>Molecular Biology and Evolution</i> , 2019, 36, 679-690.	3.5	20
30	A new zygodactylid species indicates the persistence of stem passerines into the early Oligocene in North America. <i>BMC Evolutionary Biology</i> , 2019, 19, 3.	3.2	8
31	Understanding the Evolution of Reptile Chromosomes through Applications of Combined Cytogenetics and Genomics Approaches. <i>Cytogenetic and Genome Research</i> , 2019, 157, 7-20.	0.6	56
32	SMRT long reads and Direct Label and Stain optical maps allow the generation of a high-quality genome assembly for the European barn swallow (<i>Hirundo rustica rustica</i>). <i>GigaScience</i> , 2019, 8, .	3.3	23
33	The lacrimal/ectethmoid region of waterfowl (Aves, Anseriformes): Phylogenetic signal and major evolutionary patterns. <i>Journal of Morphology</i> , 2020, 281, 1486-1500.	0.6	3
34	Introducing the Bird Chromosome Database: An Overview of Cytogenetic Studies in Birds. <i>Cytogenetic and Genome Research</i> , 2020, 160, 199-205.	0.6	45
35	New Methods to Calculate Concordance Factors for Phylogenomic Datasets. <i>Molecular Biology and Evolution</i> , 2020, 37, 2727-2733.	3.5	354
36	Variations of Mesozoic feathers: Insights from the morphogenesis of extant feather rachises. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 2121-2133.	1.1	4

#	ARTICLE	IF	CITATIONS
37	Deep-Time Demographic Inference Suggests Ecological Release as Driver of Neoavian Adaptive Radiation. <i>Diversity</i> , 2020, 12, 164.	0.7	11
38	Integrating Sequence Capture and Restriction Site-Associated DNA Sequencing to Resolve Recent Radiations of Pelagic Seabirds. <i>Systematic Biology</i> , 2021, 70, 976-996.	2.7	12
39	Chromosome-Level Genome Assembly of the Common Chaffinch (<i>Aves: <i>Fringilla coelebs</i></i>): A Valuable Resource for Evolutionary Biology. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	12
40	Transcriptomic analysis to infer key molecular players involved during host response to NDV challenge in <i>Gallus gallus</i> (Leghorn & Fayoumi). <i>Scientific Reports</i> , 2021, 11, 8486.	1.6	4
47	Protein evolution is structure dependent and non-homogeneous across the tree of life. , 2020, , .		4
48	The Dynamics of Incomplete Lineage Sorting across the Ancient Adaptive Radiation of Neoavian Birds. <i>PLoS Biology</i> , 2015, 13, e1002224.	2.6	223
49	AMAS: a fast tool for alignment manipulation and computing of summary statistics. <i>PeerJ</i> , 2016, 4, e1660.	0.9	535
51	Genetic diversity and population history of eight Italian beef cattle breeds using measures of autozygosity. <i>PLoS ONE</i> , 2021, 16, e0248087.	1.1	10
57	Whole Genome Analysis of the Red-Crowned Crane Provides Insight into Avian Longevity. <i>Molecules and Cells</i> , 2020, 43, 86-95.	1.0	6
58	nQMaker: Estimating Time Nonreversible Amino Acid Substitution Models. <i>Systematic Biology</i> , 2022, 71, 1110-1123.	2.7	9
60	Evaluation of four methods to identify the homozygotic sex chromosome in small populations. <i>BMC Genomics</i> , 2022, 23, 160.	1.2	2
61	Olfactory receptor subgenome and expression in a highly olfactory procellariiform seabird. <i>Genetics</i> , 2022, 220, .	1.2	8
63	CHAPAO: Likelihood and hierarchical reference-based representation of biomolecular sequences and applications to compressing multiple sequence alignments. <i>PLoS ONE</i> , 2022, 17, e0265360.	1.1	0
64	Genome Assembly and Evolutionary Analysis of the Mandarin Duck <i>Aix galericulata</i> Reveal Strong Genome Conservation among Ducks. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	1
65	Categorical edge-based analyses of phylogenomic data reveal conflicting signals for difficult relationships in the avian tree. <i>Molecular Phylogenetics and Evolution</i> , 2022, 174, 107550.	1.2	1
66	Species delimitation using genomic data to resolve taxonomic uncertainties in a speciation continuum of pelagic seabirds. <i>Molecular Phylogenetics and Evolution</i> , 2023, 179, 107671.	1.2	7
67	Estimating phylogenies from genomes: A beginners review of commonly used genomic data in vertebrate phylogenomics. <i>Journal of Heredity</i> , 2023, 114, 1-13.	1.0	2
70	Phylogenomics using Compression Distances: Incorporating Rate Heterogeneity and Amino Acid Properties. , 2023, , .		0

#	ARTICLE	IF	CITATIONS
---	---------	----	-----------