

HyPhy: hypothesis testing using phylogenies

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Broad-Scale Analysis Contradicts the Theory That Generation Time Affects Molecular Evolutionary Rates in Plants. <i>Journal of Molecular Evolution</i> , 2003, 56, 223-233.	0.8	61
3	Duplication and Diversifying Selection Among Termite Antifungal Peptides. <i>Molecular Biology and Evolution</i> , 2004, 21, 2256-2264.	3.5	124
4	Estimation of Phylogeny Using a General Markov Model. <i>Evolutionary Bioinformatics</i> , 2005, 1, 117693430500100.	0.6	39
5	Identification of a positively evolving putative binding region with increased variability in posttranslational motifs in zonadhesin MAM domain 2. <i>Molecular Phylogenetics and Evolution</i> , 2005, 37, 62-72.	1.2	12
6	Processes of diversification and dispersion of Rice yellow mottle virus inferred from large-scale and high-resolution phylogeographical studies. <i>Molecular Ecology</i> , 2005, 14, 2097-2110.	2.0	59
7	POPULATION STRUCTURE AT TWO GEOGRAPHIC SCALES IN THE BURROWING CRUSTACEAN CALLICHIRUS ISLAGRANDE (DECAPODA, THALASSINIDEA): HISTORICAL AND CONTEMPORARY BARRIERS TO PLANKTONIC DISPERSAL. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2125-2138.	1.1	26
8	Codon volatility does not reflect selective pressure on the HIV-1 genome. <i>Virology</i> , 2005, 336, 137-143.	1.1	14
9	Current Awareness on Comparative and Functional Genomics. <i>Comparative and Functional Genomics</i> , 2005, 6, 412-430.	2.0	0
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11	Directed Mutagenesis Confirms the Functional Importance of Positively Selected Sites in Polygalacturonase Inhibitor Protein. <i>Molecular Biology and Evolution</i> , 2005, 22, 1531-1534.	3.5	53
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17	POPULATION STRUCTURE AT TWO GEOGRAPHIC SCALES IN THE BURROWING CRUSTACEAN CALLICHIRUS ISLAGRANDE (DECAPODA, THALASSINIDEA): HISTORICAL AND CONTEMPORARY BARRIERS TO PLANKTONIC DISPERSAL. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2125.	1.1	8
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1300	Mutation signature in neuraminidase gene of avian influenza H9N2/G1 in Egypt. <i>VirusDisease</i> , 2017, 28, 164-173.	1.0	4
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1304	HIV Trafficking Between Blood and Semen During Early Untreated HIV Infection. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2017, 74, 95-102.	0.9	19
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1313	Phylodynamics of foot-and-mouth disease virus O/PanAsia in Vietnam 2010–2014. <i>Veterinary Research</i> , 2017, 48, 24.	1.1	24
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1323	Comparative analysis of protein evolution in the genome of pre-epidemic and epidemic Zika virus. <i>Infection, Genetics and Evolution</i> , 2017, 51, 74-85.	1.0	23
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1327	Genotypes of IFIH1 and IFIT5 in seven chicken breeds indicated artificial selection for commercial traits influenced antiviral genes. <i>Infection, Genetics and Evolution</i> , 2017, 56, 54-61.	1.0	5

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1349	Host association and selection on salivary protein genes in bed bugs and related blood-feeding ectoparasites. <i>Royal Society Open Science</i> , 2017, 4, 170446.	1.1	7
1350	Genetic diversity and population structure of Watermelon mosaic virus. <i>Journal of Plant Diseases and Protection</i> , 2017, 124, 601-610.	1.6	8
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1363	<scp>ggtree</scp>: an <scp>r</scp> package for visualization and annotation of phylogenetic trees with their covariates and other associated data. <i>Methods in Ecology and Evolution</i> , 2017, 8, 28-36.	2.2	2,998

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1368	Genetic differentiation and adaptive evolution at reproductive loci in incipient <i>Drosophila</i> species. <i>Journal of Evolutionary Biology</i> , 2017, 30, 524-537.	0.8	4
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1371	Causes and Consequences of Rapidly Evolving mtDNA in a Plant Lineage. <i>Genome Biology and Evolution</i> , 2017, 9, 323-336.	1.1	64
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1391	Haplotype Structure and Phylogeographic Evolution of West African Populations of <i>Sitophilus zeamais</i> (Coleoptera, Curculionidae). Journal of Phylogenetics & Evolutionary Biology, 2017, 05, .	0.2	1
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1395	Ancient Evolution of Mammarenaviruses: Adaptation via Changes in the L Protein and No Evidence for Host-Virus Codivergence. Genome Biology and Evolution, 2018, 10, 863-874.	1.1	22
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1421	Phylogeny and molecular evolution of the DMC1 gene in the polyploid genus <i>Roegneria</i> and its affinitive genera (Poaceae: Triticeae). <i>Botanical Journal of the Linnean Society</i> , 2018, 186, 129-142.	0.8	4
1422	Datamonkey 2.0: A Modern Web Application for Characterizing Selective and Other Evolutionary Processes. <i>Molecular Biology and Evolution</i> , 2018, 35, 773-777.	3.5	643
1423	Functional domain analysis of SOX18 transcription factor using a single-chain variable fragment-based approach. <i>MAbs</i> , 2018, 10, 596-606.	2.6	7
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1427	Phenomenological Load on Model Parameters Can Lead to False Biological Conclusions. <i>Molecular Biology and Evolution</i> , 2018, 35, 1473-1488.	3.5	23
1428	Evolutionary origins and diversification of testis-specific short histone H2A variants in mammals. <i>Genome Research</i> , 2018, 28, 460-473.	2.4	46
1429	Genomic Insights into Evolution of AdpA Family Master Regulators of Morphological Differentiation and Secondary Metabolism in <i>Streptomyces</i> . <i>Journal of Molecular Evolution</i> , 2018, 86, 204-215.	0.8	20
1430	Small-scale intraspecific patterns of adaptive immunogenetic polymorphisms and neutral variation in Lake Superior lake trout. <i>Immunogenetics</i> , 2018, 70, 53-66.	1.2	7
1431	Phylogenetic analysis of Human papillomavirus 16 variants isolated from Indian Breast cancer patients showed difference in genetic diversity with that of cervical cancer isolates. <i>Virus Research</i> , 2018, 243, 1-9.	1.1	6
1432	Mutation and recombination in pathogen evolution: Relevance, methods and controversies. <i>Infection, Genetics and Evolution</i> , 2018, 63, 295-306.	1.0	32
1433	The systematics and biogeography of African tailorbirds (Cisticolidae: Artisornis) with comment on the choice of Bayesian branch-length prior when analyzing heterogeneous data. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 172-183.	1.2	5
1434	Evolution of lacewings and allied orders using anchored phylogenomics (N europtera,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.7	183
1435	Mitogenomics supports an unexpected taxonomic relationship for the extinct diving duck <i>Chendytes lawi</i> and definitively places the extinct Labrador Duck. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 102-109.	1.2	14

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1437	Weaker HLA Footprints on HIV in the Unique and Highly Genetically Admixed Host Population of Mexico. <i>Journal of Virology</i> , 2018, 92, .	1.5	5
1438	Light sensing by opsins and fungal ecology: <i>NOP</i> modulates entry into sexual reproduction in response to environmental cues. <i>Molecular Ecology</i> , 2018, 27, 216-232.	2.0	43
1439	Size, Composition, and Evolution of HIV DNA Populations during Early Antiretroviral Therapy and Intensification with Maraviroc. <i>Journal of Virology</i> , 2018, 92, .	1.5	17
1440	Lost but not forgotten: MHC genotypes predict overwinter survival despite depauperate MHC diversity in a declining frog. <i>Conservation Genetics</i> , 2018, 19, 309-322.	0.8	24
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1588	Duplicated Myosin V Genes in Teleosts Show Evolutionary Rate Variations among the Motor and Cargo-Binding Domains. <i>Genome Biology and Evolution</i> , 2019, 11, 415-430.	1.1	0
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1655	Large Scale Ecological Modeling With Viruses: A Review. , 2019, , 9-16.		0
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1658	Analysis of natural recombination and host-related evolutionary dynamics of avian avulavirus 1 isolates based on positive and negative selection from 1948 to 2017. <i>Archives of Virology</i> , 2019, 164, 717-724.	0.9	2
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1665	Evidence for intra-mitochondrial variation in population genetic structure of<i>Platycephalus</i>sp.1 In the Northwestern Pacific. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 281-288.	0.7	9
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1672	Two New <i>Kremastochrysopsis</i> species, <i>K. Austriaca</i> sp. nov. and <i>K. Americana</i> sp. nov. (Chrysophyceae) 1. <i>Journal of Phycology</i> , 2020, 56, 135-145.	1.0	14
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1685	DGINN, an automated and highly-flexible pipeline for the detection of genetic innovations on protein-coding genes. <i>Nucleic Acids Research</i> , 2020, 48, e103-e103.	6.5	19
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1691	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	6.0	508
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1693	Six reference-quality genomes reveal evolution of bat adaptations. <i>Nature</i> , 2020, 583, 578-584.	13.7	210
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1704	Comparative Genomic Analysis of Rapidly Evolving SARS-CoV-2 Reveals Mosaic Pattern of Phylogeographical Distribution. <i>MSystems</i> , 2020, 5, .	1.7	60
1705	Phylogenomic proof of Recurrent Demipolyploidization and Evolutionary Stalling of the "Triplod Bridge" in <i>Arundo</i> (Poaceae). <i>International Journal of Molecular Sciences</i> , 2020, 21, 5247.	1.8	5
1706	Molecular Evolution and Developmental Expression of Melanin Pathway Genes in Lepidoptera. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	10

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1708	Phylogenetic relationships and the maternal donor of <i>Roegneria</i> (Triticeae: Poaceae) based on three nuclear DNA sequences (ITS, Acc1, and Pgi1) and one chloroplast region (trnL). <i>Journal of Systematics and Evolution</i> , 2020, .	1.6	4
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1710	Reconstructing plastome evolution across the phylogenetic backbone of the parasitic plant genus <i>Cuscuta</i> (Convolvulaceae). <i>Botanical Journal of the Linnean Society</i> , 2020, 194, 423-438.	0.8	9
1711	In silico functional and evolutionary analyses of rubber oxygenases (RoxA and RoxB). <i>3 Biotech</i> , 2020, 10, 376.	1.1	2
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1714	Studying Natural Selection in the Era of Ubiquitous Genomes. <i>Trends in Genetics</i> , 2020, 36, 792-803.	2.9	7
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1718	Formation and diversification of a paradigm biosynthetic gene cluster in plants. <i>Nature Communications</i> , 2020, 11, 5354.	5.8	50
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1722	Molecular evolution of tomato black ring virus and de novo generation of a new type of defective RNAs during long-term passaging in different hosts. <i>Plant Pathology</i> , 2020, 69, 1767-1776.	1.2	6
1723	DELLA family duplication events lead to different selective constraints in angiosperms. <i>Genetica</i> , 2020, 148, 243-251.	0.5	2
1724	Variation in HIV-1 Nef function within and among viral subtypes reveals genetically separable antagonism of SERINC3 and SERINC5. <i>PLoS Pathogens</i> , 2020, 16, e1008813.	2.1	20

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1726	Population genomics of louping ill virus provide new insights into the evolution of tick-borne flaviviruses. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008133.	1.3	11
1727	Distinct evolutionary trajectories of V1R clades across mouse species. <i>BMC Evolutionary Biology</i> , 2020, 20, 99.	3.2	8
1728	Amalgamated cross-species transcriptomes reveal organ-specific propensity in gene expression evolution. <i>Nature Communications</i> , 2020, 11, 4459.	5.8	46
1729	Impaired ability of Nef to counteract SERINC5 is associated with reduced plasma viremia in HIV-infected individuals. <i>Scientific Reports</i> , 2020, 10, 19416.	1.6	8
1730	Rapid Evolution of HERC6 and Duplication of a Chimeric HERC5/6 Gene in Rodents and Bats Suggest an Overlooked Role of HERCs in Mammalian Immunity. <i>Frontiers in Immunology</i> , 2020, 11, 605270.	2.2	16
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1732	Identifying Candidate Genetic Markers of CDV Cross-Species Pathogenicity in African Lions. <i>Pathogens</i> , 2020, 9, 872.	1.2	9
1733	Trends of mutation accumulation across global SARS-CoV-2 genomes: Implications for the evolution of the novel coronavirus. <i>Genomics</i> , 2020, 112, 5331-5342.	1.3	32
1734	The cognitive and speech genes are jointly shaped by both positive and relaxed selection in the human lineage. <i>Genomics</i> , 2020, 112, 2922-2927.	1.3	4
1735	Under-the-Radar Dengue Virus Infections in Natural Populations of <i>Aedes aegypti</i> Mosquitoes. <i>MSphere</i> , 2020, 5, .	1.3	19
1736	Adaptation of the master antioxidant response connects metabolism, lifespan and feather development pathways in birds. <i>Nature Communications</i> , 2020, 11, 2476.	5.8	34
1737	Drug Resistance Prediction Using Deep Learning Techniques on HIV-1 Sequence Data. <i>Viruses</i> , 2020, 12, 560.	1.5	32
1738	Phylogenomics unravels Quaternary vicariance and allopatric speciation patterns in temperate-montane plant species: A case study on the <i>Ranunculus auricomus</i> species complex. <i>Molecular Ecology</i> , 2020, 29, 2031-2049.	2.0	41
1739	Phyloanatomic characterization of the distinct T cell and monocyte contributions to the peripheral blood HIV population within the host. <i>Virus Evolution</i> , 2020, 6, veaa005.	2.2	6
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1741	Identifying branch-specific positive selection throughout the regulatory genome using an appropriate proxy neutral. <i>BMC Genomics</i> , 2020, 21, 359.	1.2	10
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1744	Evolutionary genetic analysis of unassigned peptidase clan-associated microbial virulence and pathogenesis. <i>Biologia (Poland)</i> , 2020, 75, 2083-2092.	0.8	7
1745	Conserved exons of FLAGELLIN-SENSING 2 (FLS2) across dicot plants and their functions. <i>Plant Science</i> , 2020, 296, 110507.	1.7	7
1746	Comparative Genomic Analysis Reveals the Metabolism and Evolution of the Thermophilic Archaeal Genus <i>Metallosphaera</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1192.	1.5	8
1747	Episodic and guanine-rich cytosine-biased bursts of intragenomic and interspecific synonymous divergence in <i>Ajugoideae</i> (Lamiaceae) mitogenomes. <i>New Phytologist</i> , 2020, 228, 1107-1114.	3.5	13
1748	Genomic consequences of dietary diversification and parallel evolution due to nectarivory in leaf-nosed bats. <i>GigaScience</i> , 2020, 9, .	3.3	18
1749	Replication of Influenza D Viruses of Bovine and Swine Origin in Ovine Respiratory Explants and Their Attachment to the Respiratory Tract of Bovine, Sheep, Goat, Horse, and Swine. <i>Frontiers in Microbiology</i> , 2020, 11, 1136.	1.5	15
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1751	Plastome Evolution in <i>Dolomiaea</i> (Asteraceae, Cardueae) Using Phylogenomic and Comparative Analyses. <i>Frontiers in Plant Science</i> , 2020, 11, 376.	1.7	18
1752	The evolution of metabolism: How to test evolutionary hypotheses at the genomic level. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 482-500.	1.9	36
1753	Into the Deep (Sequence) of the Foot-and-Mouth Disease Virus Gene Pool: Bottlenecks and Adaptation during Infection in Naïve and Vaccinated Cattle. <i>Pathogens</i> , 2020, 9, 208.	1.2	7
1754	Genomic Signature of Shifts in Selection in a Subalpine Ant and Its Physiological Adaptations. <i>Molecular Biology and Evolution</i> , 2020, 37, 2211-2227.	3.5	14
1755	Analyzing drivers of speciation in the Southern Ocean using the sea spider species complex <i>Colossendeis megalonyx</i> as a test case. <i>Polar Biology</i> , 2020, 43, 319-342.	0.5	5
1756	Equiprobable discrete models of site-specific substitution rates underestimate the extent of rate variability. <i>PLoS ONE</i> , 2020, 15, e0229493.	1.1	2
1757	Genotyping Porcine Circovirus 3 (PCV-3) Nowadays: Does It Make Sense?. <i>Viruses</i> , 2020, 12, 265.	1.5	47
1758	Mitochondrial genome diversity and population mitogenomics of polar cod (<i>Boreogadus saida</i>) and Arctic dwelling gadoids. <i>Polar Biology</i> , 2020, 43, 979-994.	0.5	7
1759	Ecological fitting is the forerunner to diversification in a plant virus with broad host range. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1917-1931.	0.8	9
1760	No evidence for accumulation of deleterious mutations and fitness degradation in clonal fish hybrids: Abandoning sex without regrets. <i>Molecular Ecology</i> , 2020, 29, 3038-3055.	2.0	18

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1762	Mandarin fish (<i>Siniperca</i>) genomes provide insights into innate predatory feeding. <i>Communications Biology</i> , 2020, 3, 361.	2.0	33
1763	Complete Chloroplast Genomes of <i>Anthurium huixtlense</i> and <i>Pothos scandens</i> (Pothoideae, Araceae): Unique Inverted Repeat Expansion and Contraction Affect Rate of Evolution. <i>Journal of Molecular Evolution</i> , 2020, 88, 562-574.	0.8	33
1764	Molecular Epidemiology of B3 and D8 Measles Viruses through Hemagglutinin Phylogenetic History. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4435.	1.8	12
1765	Avian Metapneumovirus subtype B around Europe: a phylodynamic reconstruction. <i>Veterinary Research</i> , 2020, 51, 88.	1.1	22
1766	Adaptive evolution of peptidoglycan recognition protein family regulates the innate signaling against microbial pathogens in vertebrates. <i>Microbial Pathogenesis</i> , 2020, 147, 104361.	1.3	13
1767	A cross-sectional study to characterize local HIV-1 dynamics in Washington, DC using next-generation sequencing. <i>Scientific Reports</i> , 2020, 10, 1989.	1.6	9
1768	Phylogenetic Systematics of the Water Toad (<i>Bufo stejnegeri</i>) Elucidates the Evolution of Semi-aquatic Toad Ecology and Pleistocene Glacial Refugia. <i>Frontiers in Ecology and Evolution</i> , 2020, 7, .	1.1	13
1769	The first complete mitochondrial genome sequence of the endangered mountain anoa (<i>Bubalus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4 13, 123-133.	0.2	5
1770	Standardized phylogenetic and molecular evolutionary analysis applied to species across the microbial tree of life. <i>Scientific Reports</i> , 2020, 10, 1723.	1.6	65
1771	Target Nuclear and Off-Target Plastid Hybrid Enrichment Data Inform a Range of Evolutionary Depths in the Orchid Genus <i>Epidendrum</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1761.	1.7	42
1772	Signature of adaptive evolution in olfactory receptor genes in <i>Coryâ€™s</i> Shearwater supports molecular basis for smell in procellariiform seabirds. <i>Scientific Reports</i> , 2020, 10, 543.	1.6	13
1773	Intraâ€™strain biological and epidemiological characterization of plum pox virus. <i>Molecular Plant Pathology</i> , 2020, 21, 475-488.	2.0	11
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1775	Evolutionary rates of and selective constraints on the mitochondrial genomes of Orthoptera insects with different wing types. <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106734.	1.2	47
1776	Phylogenetic informativeness analyses to clarify past diversification processes in Cucurbitaceae. <i>Scientific Reports</i> , 2020, 10, 488.	1.6	17
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1778	Inter-Versus Intra-Host Sequence Diversity of pH1N1 and Associated Clinical Outcomes. <i>Microorganisms</i> , 2020, 8, 133.	1.6	2

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1780	Statistical Modelling and Machine Learning Principles for Bioinformatics Techniques, Tools, and Applications. <i>Algorithms for Intelligent Systems</i> , 2020, , .	0.5	5
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1783	Evolution of NLR resistance genes with noncanonical N-terminal domains in wild tomato species. <i>New Phytologist</i> , 2020, 227, 1530-1543.	3.5	60
1784	Directional auxin fluxes in plants by intramolecular domain domain coevolution of PIN auxin transporters. <i>New Phytologist</i> , 2020, 227, 1406-1416.	3.5	20
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1787	Deep Sequencing Reveals Compartmentalized HIV-1 in the Semen of Men with and without Sexually Transmitted Infection-Associated Urethritis. <i>Journal of Virology</i> , 2020, 94, .	1.5	6
1788	Genetic Variability of Long Terminal Repeat Region between HIV-2 Groups Impacts Transcriptional Activity. <i>Journal of Virology</i> , 2020, 94, .	1.5	5
1789	LysM Proteins Regulate Fungal Development and Contribute to Hyphal Protection and Biocontrol Traits in <i>Clonostachys rosea</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 679.	1.5	32
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1793	Integrating structural and evolutionary data to interpret variation and pathogenicity in adapter protein complex 4. <i>Protein Science</i> , 2020, 29, 1535-1549.	3.1	10
1794	Relaxed constraint and functional divergence of the progesterone receptor (PGR) in the human stem-lineage. <i>PLoS Genetics</i> , 2020, 16, e1008666.	1.5	9
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1799	PoSeiDon: a Nextflow pipeline for the detection of evolutionary recombination events and positive selection. <i>Bioinformatics</i> , 2021, 37, 1018-1020.	1.8	8
1800	A Codon Model for Associating Phenotypic Traits with Altered Selective Patterns of Sequence Evolution. <i>Systematic Biology</i> , 2021, 70, 608-622.	2.7	5
1801	Next generation sequencing of SARS-CoV-2 genomes: challenges, applications and opportunities. <i>Briefings in Bioinformatics</i> , 2021, 22, 616-630.	3.2	143
1802	Convergent Cortistatin losses parallel modifications in circadian rhythmicity and energy homeostasis in Cetacea and other mammalian lineages. <i>Genomics</i> , 2021, 113, 1064-1070.	1.3	7
1803	Disruption of duplicated yellow genes in <i>Bactrocera tryoni</i> modifies pigmentation colouration and impacts behaviour. <i>Journal of Pest Science</i> , 2021, 94, 917-932.	1.9	5
1804	Flourishing in water: the early evolution and diversification of plant receptor-like kinases. <i>Plant Journal</i> , 2021, 106, 174-184.	2.8	22
1805	Using molecular transmission networks to understand the epidemic characteristics of HIV-1 CRF08_BC across China. <i>Emerging Microbes and Infections</i> , 2021, 10, 497-506.	3.0	10
1806	Using longitudinal genetic-network study to understand HIV treatment-as-prevention. <i>Aids</i> , 2021, 35, 947-955.	1.0	16
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1808	HIV-2 diversity displays two clades within group A with distinct geographical distribution and evolution. <i>Virus Evolution</i> , 2021, 7, veab024.	2.2	5
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1818	Electric Blue: Molecular Evolution of Three-Finger Toxins in the Long-Glanded Coral Snake Species <i>Calliophis bivirgatus</i> . <i>Toxins</i> , 2021, 13, 124.	1.5	9
1820	Kinetochores and microtubule-destabilizing factors are fast evolving in eutherian mammals. <i>Molecular Ecology</i> , 2021, 30, 1505-1515.	2.0	8
1821	Relationships between fox populations and rabies virus spread in northern Canada. <i>PLoS ONE</i> , 2021, 16, e0246508.	1.1	18
1822	Lineage-specific plastid degradation in subtribe <i>Gentianinae</i> (<i>Gentianaceae</i>). <i>Ecology and Evolution</i> , 2021, 11, 3286-3299.	0.8	21
1824	Antigenic cartography reveals complexities of genetic determinants that lead to antigenic differences among pandemic GII.4 noroviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	28
1825	Phylogenetic prospecting for cryptic species of the genus <i>Merluccius</i> (<i>Actinopterygii</i> : <i>Merlucciidae</i>). <i>Scientific Reports</i> , 2021, 11, 5929.	1.6	1
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1828	Genomes of 12 fig wasps provide insights into the adaptation of pollinators to fig syconia. <i>Journal of Genetics and Genomics</i> , 2021, 48, 225-236.	1.7	6
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1831	Evidence of gene nucleotide composition favoring replication and growth in a fastidious plant pathogen. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
1832	The highly conserved <i>rps12</i> gene in ferns provides strong evidence for decreased substitution rates in the inverted repeat region. <i>Plant Systematics and Evolution</i> , 2021, 307, 1.	0.3	4
1834	Initial Insights Into the Genetic Epidemiology of SARS-CoV-2 Isolates From Kerala Suggest Local Spread From Limited Introductions. <i>Frontiers in Genetics</i> , 2021, 12, 630542.	1.1	11
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1836	Evolution, inactivation and loss of short wavelength-sensitive opsin genes during the diversification of Neotropical cichlids. <i>Molecular Ecology</i> , 2021, 30, 1688-1703.	2.0	12
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1843	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021, 372, 815-821.	6.0	1,125
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1853	Molecular population genetics of <i>Sex-lethal</i> (<i>Sxl</i>) in the <i>Drosophila melanogaster</i> species group: a locus that genetically interacts with <i>Wolbachia pipientis</i> in <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	2
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1856	Niche adaptation promoted the evolutionary diversification of tiny ocean predators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	12
1858	Genome of the pincer wasp <i>Gonatopus flavifemur</i> reveals unique venom evolution and a dual adaptation to parasitism and predation. <i>BMC Biology</i> , 2021, 19, 145.	1.7	15
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1861	Gene Loss, Pseudogenization in Plastomes of Genus <i>Allium</i> (Amaryllidaceae), and Putative Selection for Adaptation to Environmental Conditions. <i>Frontiers in Genetics</i> , 2021, 12, 674783.	1.1	16
1862	Full Genome Evolutionary Studies of Wheat Streak Mosaic-Associated Viruses Using High-Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 699078.	1.5	13

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1864	An Update on <i>Trichoderma</i> Mitogenomes: Complete De Novo Mitochondrial Genome of the Fungal Biocontrol Agent <i>Trichoderma harzianum</i> (Hypocreales, Sordariomycetes), an Ex-Neotype Strain CBS 226.95, and Tracing the Evolutionary Divergences of Mitogenomes in <i>Trichoderma</i> . <i>Microorganisms</i> , 2021, 9, 1564.	1.6	8
1865	Early origin of sweet perception in the songbird radiation. <i>Science</i> , 2021, 373, 226-231.	6.0	34
1866	Molecular evolutionary insights from PRLR in mammals. <i>General and Comparative Endocrinology</i> , 2021, 309, 113791.	0.8	4
1867	Genome Evolution in Bacteria Isolated from Million-Year-Old Subseafloor Sediment. <i>MBio</i> , 2021, 12, e0115021.	1.8	9
1868	Elucidation of the speciation history of three sister species of crown-of-thorns starfish (<i>Acanthaster</i> spp.) based on genomic analysis. <i>DNA Research</i> , 2021, 28, .	1.5	6
1870	Metagenomic analysis reveals <i>Culex</i> mosquito virome diversity and Japanese encephalitis genotype V in the Republic of Korea. <i>Molecular Ecology</i> , 2021, 30, 5470-5487.	2.0	19
1871	Plastome Evolution in the Hyperdiverse Genus <i>Euphorbia</i> (Euphorbiaceae) Using Phylogenomic and Comparative Analyses: Large-Scale Expansion and Contraction of the Inverted Repeat Region. <i>Frontiers in Plant Science</i> , 2021, 12, 712064.	1.7	16
1874	A drastic shift in the energetic landscape of toothed whale sperm cells. <i>Current Biology</i> , 2021, 31, 3648-3655.e9.	1.8	8
1875	Impact of viral features, host jumps and phylogeography on the rapid evolution of Aleutian mink disease virus (AMDV). <i>Scientific Reports</i> , 2021, 11, 16464.	1.6	3
1877	Isolation and Genetic Characterization of Canine Parvovirus in a Malayan Tiger. <i>Frontiers in Veterinary Science</i> , 2021, 8, 660046.	0.9	5
1878	BASE: A novel workflow to integrate nonubiquitous genes in comparative genomics analyses for selection. <i>Ecology and Evolution</i> , 2021, 11, 13029-13035.	0.8	5
1879	Increased hepatitis B virus quasispecies diversity is correlated with liver fibrosis progression. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104938.	1.0	2
1881	Relaxed selection on male mitochondrial genes in DUI bivalves eases the need for mitonuclear coevolution. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1722-1736.	0.8	10
1882	Selection on genes associated with the evolution of divergent life histories: Gamete recognition or something else?. <i>Evolution & Development</i> , 2021, 23, 423-438.	1.1	1
1885	E484K as an innovative phylogenetic event for viral evolution: Genomic analysis of the E484K spike mutation in SARS-CoV-2 lineages from Brazil. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104941.	1.0	58
1887	Stepwise Evolution and Exceptional Conservation of ORF1a/b Overlap in Coronaviruses. <i>Molecular Biology and Evolution</i> , 2021, 38, 5678-5684.	3.5	6
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