

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.	1.8	61
3	Duplication and Diversifying Selection Among Termite Antifungal Peptides. <i>Molecular Biology and Evolution</i> , 2004, 21, 2256-2264.	8.9	124
4	Estimation of Phylogeny Using a General Markov Model. <i>Evolutionary Bioinformatics</i> , 2005, 1, 117693430500100.	1.2	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.	2.7	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.	3.9	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.	2.3	26
8	Codon volatility does not reflect selective pressure on the HIV-1 genome. <i>Virology</i> , 2005, 336, 137-143.	2.4	14
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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.	2.3	8
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1325	Characterization of founder viruses in very early SIV rectal transmission. <i>Virology</i> , 2017, 502, 97-105.	2.4	18
1326	Virulence in Newcastle disease virus: A genotyping and molecular evolution spectrum perspective. <i>Research in Veterinary Science</i> , 2017, 111, 49-54.	1.9	13
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1473	Molecular epidemiology of coxsackievirus A6 circulating in Hong Kong reveals common neurological manifestations and emergence of novel recombinant groups. <i>Journal of Clinical Virology</i> , 2018, 108, 43-49.	3.1	13
1474	First Genome Sequence of <i>Pasteurella multocida</i> Type B Strain BAUTB2, a Major Pathogen Responsible for Mortality of Bovines in Bangladesh. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	1
1475	Full-Genome Characterization and Genetic Evolution of West African Isolates of Bagaza Virus. <i>Viruses</i> , 2018, 10, 193.	3.3	5
1476	Three-Finger Toxin Diversification in the Venoms of Cat-Eye Snakes (Colubridae: Boiga). <i>Journal of Molecular Evolution</i> , 2018, 86, 531-545.	1.8	14
1477	Comparative Genomics Approaches Accurately Predict Deleterious Variants in Plants. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3321-3329.	1.8	36
1478	High and Variable Rates of Repeat-Mediated Mitochondrial Genome Rearrangement in a Genus of Plants. <i>Molecular Biology and Evolution</i> , 2018, 35, 2773-2785.	8.9	60
1479	Testing the sensory trade-off hypothesis in New World bats. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181523.	2.6	50
1480	Software for Characterizing the Antigenic and Genetic Evolution of Human Influenza Viruses. <i>Methods in Molecular Biology</i> , 2018, 1836, 551-565.	0.9	1
1481	Characterization of Papaya ringspot virus isolates infecting transgenic papaya ‘Huanong No.1’™ in South China. <i>Scientific Reports</i> , 2018, 8, 8206.	3.3	16
1482	A tangle of forms and phylogeny: Extensive morphological homoplasy and molecular clock heterogeneity in <i>Bonnetina</i> and related tarantulas. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 55-73.	2.7	25
1483	Repeated Cis-Regulatory Tuning of a Metabolic Bottleneck Gene during Evolution. <i>Molecular Biology and Evolution</i> , 2018, 35, 1968-1981.	8.9	30
1484	Phototransduction Gene Expression and Evolution in Cave and Surface Crayfishes. <i>Integrative and Comparative Biology</i> , 2018, 58, 398-410.	2.0	17
1485	Changes in selection intensity on the mitogenome of subterranean and fossorial rodents respective to aboveground species. <i>Mammalian Genome</i> , 2018, 29, 353-363.	2.2	10
1486	Smc5/6 Antagonism by HBx Is an Evolutionarily Conserved Function of Hepatitis B Virus Infection in Mammals. <i>Journal of Virology</i> , 2018, 92, .	3.4	34
1487	Parallel evolution of site-specific changes in divergent caribou lineages. <i>Ecology and Evolution</i> , 2018, 8, 6053-6064.	1.9	9
1488	Multinucleotide mutations cause false inferences of lineage-specific positive selection. <i>Nature Ecology and Evolution</i> , 2018, 2, 1280-1288.	7.8	121
1489	Serotonin, behavior, and natural selection in New World monkeys. <i>Journal of Evolutionary Biology</i> , 2018, 31, 1180-1192.	1.7	7

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1491	Evaluation of global HIV/SIV envelope gp120 RNA structure and evolution within and among infected hosts. <i>Virus Evolution</i> , 2018, 4, vey018.	4.9	2
1492	Electrostatic Tuning of a Potassium Channel in Electric Fish. <i>Current Biology</i> , 2018, 28, 2094-2102.e5.	3.9	26
1493	Analysis of Reptarenavirus genomes indicates different selective forces acting on the S and L segments and recent expansion of common genotypes. <i>Infection, Genetics and Evolution</i> , 2018, 64, 212-218.	2.3	6
1494	Relative Evolutionary Rates in Proteins Are Largely Insensitive to the Substitution Model. <i>Molecular Biology and Evolution</i> , 2018, 35, 2307-2317.	8.9	19
1495	An evolutionary transcriptomics approach links CD36 to membrane remodeling in replicative senescence. <i>Molecular Omics</i> , 2018, 14, 237-246.	2.8	12
1496	Evolution and dynamics of the pandemic H1N1 influenza hemagglutinin protein from 2009 to 2017. <i>Archives of Virology</i> , 2018, 163, 3035-3049.	2.1	18
1497	Within-Genome Shineâ€Dalgarno Sequences Are Not Selected for Function. <i>Molecular Biology and Evolution</i> , 2018, 35, 2487-2498.	8.9	16
1498	Association genetics studies on frost tolerance in wheat (<i>Triticum aestivum</i> L.) reveal new highly conserved amino acid substitutions in CBF-A3, CBF-A15, VRN3 and PPD1 genes. <i>BMC Genomics</i> , 2018, 19, 409.	2.8	31
1499	Landscape genomics: natural selection drives the evolution of mitogenome in penguins. <i>BMC Genomics</i> , 2018, 19, 53.	2.8	27
1500	Adding Complexity to Complexity: Gene Family Evolution in Polyploids. <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	2.2	13
1501	Distribution and characterization of Shiga toxin converting temperate phages carried by <i>Shigella flexneri</i> in Hispaniola. <i>Infection, Genetics and Evolution</i> , 2018, 65, 321-328.	2.3	13
1502	Identifying Potential <i>Plasmodium vivax</i> Sporozoite Stage Vaccine Candidates: An Analysis of Genetic Diversity and Natural Selection. <i>Frontiers in Genetics</i> , 2018, 9, 10.	2.3	15
1503	Multi-drug resistant <i>Pseudomonas aeruginosa</i> nosocomial strains: Molecular epidemiology and evolution. <i>Microbial Pathogenesis</i> , 2018, 123, 233-241.	2.9	19
1504	Molecular footprints of selective pressure in the neuraminidase gene of currently circulating human influenza subtypes and lineages. <i>Virology</i> , 2018, 522, 122-130.	2.4	7
1505	Exploring data processing strategies in NGS target enrichment to disentangle radiations in the tribe Cardueae (Compositae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 69-87.	2.7	38
1506	Anchored hybrid enrichment generated nuclear, plastid and mitochondrial markers resolve the <i>Lepanthes horrida</i> (Orchidaceae: Pleurothallidinae) species complex. <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 27-47.	2.7	42
1507	Genetic variation analysis of PCV1 strains isolated from Guangxi Province of China in 2015. <i>BMC Veterinary Research</i> , 2018, 14, 43.	1.9	15

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1509	Emergence of the Asian lineage dengue virus type 3 genotype III in Malaysia. <i>BMC Evolutionary Biology</i> , 2018, 18, 58.	3.2	11
1510	Nearly neutral evolution in IFNL3 gene retains the immune function to detect and clear the viral infection in HCV. <i>Progress in Biophysics and Molecular Biology</i> , 2018, 140, 107-116.	2.9	0
1511	Assembly and comparative analysis of the complete mitochondrial genome sequence of <i>Sophora japonica</i> “Jinhua”™. <i>PLoS ONE</i> , 2018, 13, e0202485.	2.5	21
1512	Molecular evolution and functional divergence of IspD homologs in malarial parasites. <i>Infection, Genetics and Evolution</i> , 2018, 65, 340-349.	2.3	7
1513	Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in <i>Agave</i> . <i>BMC Genomics</i> , 2018, 19, 588.	2.8	64
1514	Dissecting the phyloepidemiology of <i>Trypanosoma cruzi</i> I (Tcl) in Brazil by the use of high resolution genetic markers. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006466.	3.0	15
1515	NS1 codon usage adaptation to humans in pandemic Zika virus. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2018, 113, e170385.	1.6	11
1516	Diversity and natural selection on the thrombospondin-related adhesive protein (TRAP) gene of <i>Plasmodium knowlesi</i> in Malaysia. <i>Malaria Journal</i> , 2018, 17, 274.	2.3	12
1517	Proteomic and evolutionary analyses of sperm activation identify uncharacterized genes in <i>Caenorhabditis nematodes</i> . <i>BMC Genomics</i> , 2018, 19, 593.	2.8	3
1518	Evolutionary rates of mammalian telomere-stability genes correlate with karyotype features and female germline expression. <i>Nucleic Acids Research</i> , 2018, 46, 7153-7168.	14.5	8
1519	Positive selection and climatic effects on MHC class II gene diversity in hares (<i>Lepus capensis</i>) from a steep ecological gradient. <i>Scientific Reports</i> , 2018, 8, 11514.	3.3	18
1520	Seminal Simian Immunodeficiency Virus in Chronically Infected <i>Cynomolgus</i> Macaques Is Dominated by Virus Originating from Multiple Genital Organs. <i>Journal of Virology</i> , 2018, 92, .	3.4	20
1521	Evolution for extreme living: variation in mitochondrial cytochrome <i>c</i> oxidase genes correlated with elevation in pikas (genus <i>Ochotona</i>). <i>Integrative Zoology</i> , 2018, 13, 517-535.	2.6	8
1522	Multiple Class I and Class II <i>Haemophilus ducreyi</i> Strains Cause Cutaneous Ulcers in Children on an Endemic Island. <i>Clinical Infectious Diseases</i> , 2018, 67, 1768-1774.	5.8	3
1523	Genetic and antigenic relationship of foot-and-mouth disease virus serotype O isolates with the vaccine strain O1/BFS. <i>Vaccine</i> , 2018, 36, 3802-3808.	3.8	6
1524	Purifying Selection in the Toll-Like Receptors of Song Sparrows <i>Melospiza melodia</i> . <i>Journal of Heredity</i> , 2018, 109, 501-509.	2.4	17
1525	Insights into the phylogenetic and molecular evolutionary histories of <i>Fad</i> and <i>Elovl</i> gene families in Actiniaria. <i>Ecology and Evolution</i> , 2018, 8, 5323-5335.	1.9	17

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1527	HIV-2/SIV viral protein X counteracts HUSH repressor complex. <i>Nature Microbiology</i> , 2018, 3, 891-897.	13.3	99
1528	The full-length genome characterization, genetic diversity and evolutionary analyses of Senecavirus A isolated in Thailand in 2016. <i>Infection, Genetics and Evolution</i> , 2018, 64, 32-45.	2.3	25
1529	Hyperendemic dengue transmission and identification of a locally evolved DENV-3 lineage, Papua New Guinea 2007-2010. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006254.	3.0	4
1530	An evaluation of alternative explanations for widespread cytonuclear discordance in annual sunflowers (<i>Helianthus</i>). <i>New Phytologist</i> , 2019, 221, 515-526.	7.3	118
1531	The Sub-Chromosomal Macronuclear Pheromone Genes of the Ciliate <i>Euplotes raikovi</i> : Comparative Structural Analysis and Insights into the Mechanism of Expression. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 376-384.	1.7	10
1532	Evolutionary dynamics of the H7N9 avian influenza virus based on large-scale sequence analysis. <i>PLoS ONE</i> , 2019, 14, e0220249.	2.5	0
1533	Identification and assessment of variable single-copy orthologous (SCO) nuclear loci for low-level phylogenomics: a case study in the genus <i>Rosa</i> (Rosaceae). <i>BMC Evolutionary Biology</i> , 2019, 19, 152.	3.2	16
1534	Contrasting selective patterns across the segmented genome of bluetongue virus in a global reassortment hotspot. <i>Virus Evolution</i> , 2019, 5, vez027.	4.9	17
1535	A Species-Wide Inventory of NLR Genes and Alleles in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2019, 178, 1260-1272.e14.	28.9	265
1536	Signatures of Relaxed Selection in the CYP8B1 Gene of Birds and Mammals. <i>Journal of Molecular Evolution</i> , 2019, 87, 209-220.	1.8	13
1537	Population Gene Introgression and High Genome Plasticity for the Zoonotic Pathogen <i>Streptococcus agalactiae</i> . <i>Molecular Biology and Evolution</i> , 2019, 36, 2572-2590.	8.9	36
1538	TRIM69 Inhibits Vesicular Stomatitis Indiana Virus. <i>Journal of Virology</i> , 2019, 93, .	3.4	35
1539	The biosynthetic origin of psychoactive kavalactones in kava. <i>Nature Plants</i> , 2019, 5, 867-878.	9.3	58
1540	Genomic Characterization of Jumbo Salmonella Phages That Effectively Target United Kingdom Pig-Associated Salmonella Serotypes. <i>Frontiers in Microbiology</i> , 2019, 10, 1491.	3.5	28
1541	To see or not to see: molecular evolution of the rhodopsin visual pigment in neotropical electric fishes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191182.	2.6	3
1542	A Homeostasis Hypothesis of Avian Influenza Resistance in Chickens. <i>Genes</i> , 2019, 10, 543.	2.4	6
1543	Indication of ongoing amphipod speciation in Lake Baikal by genetic structures within endemic species. <i>BMC Evolutionary Biology</i> , 2019, 19, 138.	3.2	12

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1545	Chromosome-Level Alpaca Reference Genome VicPac3.1 Improves Genomic Insight Into the Biology of New World Camelids. <i>Frontiers in Genetics</i> , 2019, 10, 586.	2.3	19
1546	Cosmopolitan A1 lineage of dengue virus serotype 2 is circulating in Pakistan: A study from 2017 dengue viral outbreak. <i>Journal of Medical Virology</i> , 2019, 91, 1909-1917.	5.0	12
1547	Convergent vomeronasal system reduction in mammals coincides with convergent losses of calcium signalling and odorant-degrading genes. <i>Molecular Ecology</i> , 2019, 28, 3656-3668.	3.9	18
1548	The lichen symbiosis re-viewed through the genomes of <i>Cladonia grayi</i> and its algal partner <i>Asterochloris glomerata</i> . <i>BMC Genomics</i> , 2019, 20, 605.	2.8	98
1549	Mycoheterotrophic <i>Epirixanthes</i> (Polygalaceae) has a typical angiosperm mitogenome but unorthodox plastid genomes. <i>Annals of Botany</i> , 2019, 124, 791-807.	2.9	14
1550	Viral Long-Term Evolutionary Strategies Favor Stability over Proliferation. <i>Viruses</i> , 2019, 11, 677.	3.3	4
1551	Genome of the Komodo dragon reveals adaptations in the cardiovascular and chemosensory systems of monitor lizards. <i>Nature Ecology and Evolution</i> , 2019, 3, 1241-1252.	7.8	67
1552	Evolutionary dynamics and molecular epidemiology of West Nile virus in New York State: 1999–2015. <i>Virus Evolution</i> , 2019, 5, vez020.	4.9	14
1553	Chance and predictability in evolution: The genomic basis of convergent dietary specializations in an adaptive radiation. <i>Molecular Ecology</i> , 2019, 28, 4028-4045.	3.9	21
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1555	Long-Term Intrahost Evolution of Methicillin Resistant <i>Staphylococcus aureus</i> Among Cystic Fibrosis Patients With Respiratory Carriage. <i>Frontiers in Genetics</i> , 2019, 10, 546.	2.3	24
1556	The Genetic Variability and Demographic History of a Population of the Even-Year Broodline Pink Salmon <i>Oncorhynchus gorbuscha</i> (Walbaum, 1792) (Bakhura River, Sakhalin Island) Inferred from the Polymorphism of Two Mitochondrial Genes. <i>Russian Journal of Marine Biology</i> , 2019, 45, 47-55.	0.6	1
1557	On estimating evolutionary probabilities of population variants. <i>BMC Evolutionary Biology</i> , 2019, 19, 133.	3.2	5
1558	Relaxed Selection Limits Lifespan by Increasing Mutation Load. <i>Cell</i> , 2019, 178, 385-399.e20.	28.9	94
1559	Widespread nocturnality of living birds stemming from their common ancestor. <i>BMC Evolutionary Biology</i> , 2019, 19, 189.	3.2	8
1560	Molecular evolution in immune genes across the avian tree of life. <i>Parasitology Open</i> , 2019, 5, .	0.9	3
1561	The range of sampling times affects Zika virus evolutionary rates and divergence times. <i>Archives of Virology</i> , 2019, 164, 3027-3034.	2.1	3

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1563	Highly Divergent Genetic Variants of Soricid-Borne Altai Virus (Hantaviridae) in Eurasia Suggest Ancient Host-Switching Events. <i>Viruses</i> , 2019, 11, 857.	3.3	12
1564	The Vertebrate TLR Supergene Family Evolved Dynamically by Gene Gain/Loss and Positive Selection Revealing a Host-Pathogen Arms Race in Birds. <i>Diversity</i> , 2019, 11, 131.	1.7	25
1565	Natural HIV-1 Nef Polymorphisms Impair SERINC5 Downregulation Activity. <i>Cell Reports</i> , 2019, 29, 1449-1457.e5.	6.4	18
1566	Evidence for Adaptive Selection in the Mitogenome of a Mesoparasitic Monogenean Flatworm <i>Enterogyrus malmbergi</i> . <i>Genes</i> , 2019, 10, 863.	2.4	4
1567	Evolution of infectious bronchitis virus in the field after homologous vaccination introduction. <i>Veterinary Research</i> , 2019, 50, 92.	3.0	40
1568	191 Early weaning in pigs induces long-term alterations in intestinal nutrient transporter function and expression partially via beta adrenergic enteric neural receptors. <i>Journal of Animal Science</i> , 2019, 97, 112-113.	0.5	0
1569	Combining morphological and genomic evidence to resolve species diversity and study speciation processes of the <i>Pallenopsis patagonica</i> (Pycnogonida) species complex. <i>Frontiers in Zoology</i> , 2019, 16, 36.	2.0	12
1570	Noda-Like RNA Viruses Infecting <i>Caenorhabditis</i> Nematodes: Sympatry, Diversity, and Reassortment. <i>Journal of Virology</i> , 2019, 93, .	3.4	17
1571	Clinical implications of convergent procoagulant toxicity and differential antivenom efficacy in Australian elapid snake venoms. <i>Toxicology Letters</i> , 2019, 316, 171-182.	0.8	20
1572	Phylogenomic analysis of UDP-dependent glycosyltransferases provides insights into the evolutionary landscape of glycosylation in plant metabolism. <i>Plant Journal</i> , 2019, 100, 1273-1288.	5.7	75
1573	Plastome Reduction in the Only Parasitic Gymnosperm <i>Parasitaxus</i> Is Due to Losses of Photosynthesis but Not Housekeeping Genes and Apparently Involves the Secondary Gain of a Large Inverted Repeat. <i>Genome Biology and Evolution</i> , 2019, 11, 2789-2796.	2.5	31
1574	Influence of directional positive Darwinian selection-driven evolution on arboviruses Dengue and Zika virulence and pathogenesis. <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106607.	2.7	1
1575	Divergence dating using mixed effects clock modelling: An application to HIV-1. <i>Virus Evolution</i> , 2019, 5, vez036.	4.9	24
1576	Can extreme MHC class I diversity be a feature of a wide geographic range? The example of <i>Seba's</i> short-tailed bat (<i>Carollia perspicillata</i>). <i>Immunogenetics</i> , 2019, 71, 575-587.	2.4	15
1577	Distinct evolution of toll-like receptor signaling pathway genes in cetaceans. <i>Genes and Genomics</i> , 2019, 41, 1417-1430.	1.4	6
1578	Data for positive selection test and co-evolutionary analysis on mammalian cereblon. <i>Data in Brief</i> , 2019, 26, 104499.	1.0	1
1579	Evolutionary Dissection of the Dot/Icm System Based on Comparative Genomics of 58 <i>Legionella</i> Species. <i>Genome Biology and Evolution</i> , 2019, 11, 2619-2632.	2.5	12

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1581	Genome editing retraces the evolution of toxin resistance in the monarch butterfly. <i>Nature</i> , 2019, 574, 409-412.	27.8	120
1582	Comparative Transcriptomics Provides Insights into Reticulate and Adaptive Evolution of a Butterfly Radiation. <i>Genome Biology and Evolution</i> , 2019, 11, 2963-2975.	2.5	7
1583	Duplication history and molecular evolution of the rbcS multigene family in angiosperms. <i>Journal of Experimental Botany</i> , 2019, 70, 6127-6139.	4.8	16
1584	Allele-specific nonstationarity in evolution of influenza A virus surface proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21104-21112.	7.1	10
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1586	Genome-wide association analyses of invasive pneumococcal isolates identify a missense bacterial mutation associated with meningitis. <i>Nature Communications</i> , 2019, 10, 178.	12.8	33
1587	Evolution of sex determination and heterogamety changes in section <i>Otites</i> of the genus <i>Silene</i> . <i>Scientific Reports</i> , 2019, 9, 1045.	3.3	29
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.	2.5	0
1589	Allelic diversity and selection at the MHC class I and class II in a bottlenecked bird of prey, the White-tailed Eagle. <i>BMC Evolutionary Biology</i> , 2019, 19, 2.	3.2	22
1590	Evolution of salivary glue genes in <i>Drosophila</i> species. <i>BMC Evolutionary Biology</i> , 2019, 19, 36.	3.2	14
1591	Ensembles from Ordered and Disordered Proteins Reveal Similar Structural Constraints during Evolution. <i>Journal of Molecular Biology</i> , 2019, 431, 1298-1307.	4.2	8
1592	Combination of surveillance tools reveals that Yellow Fever virus can remain in the same Atlantic Forest area at least for three transmission seasons. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2019, 114, e190076.	1.6	38
1593	Comparative analysis of peripheral blood reveals transcriptomic adaptations to extreme environments on the Qinghai-Tibetan Plateau in the gray wolf (<i>Canis lupus chanco</i>). <i>Organisms Diversity and Evolution</i> , 2019, 19, 543-556.	1.6	5
1594	Comparative Analyses of Chromatin Landscape in White Adipose Tissue Suggest Humans May Have Less Beigeing Potential than Other Primates. <i>Genome Biology and Evolution</i> , 2019, 11, 1997-2008.	2.5	23
1595	Historical contingency shapes adaptive radiation in Antarctic fishes. <i>Nature Ecology and Evolution</i> , 2019, 3, 1102-1109.	7.8	50
1596	Integrating natural history collections and comparative genomics to study the genetic architecture of convergent evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180248.	4.0	32
1597	Evidence for long-term prevalence of cucumber vein yellowing virus in Sudan and genetic variation of the virus in Sudan and the Mediterranean Basin. <i>Plant Pathology</i> , 2019, 68, 1268-1275.	2.4	15

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1599	Characterization of the complete mitochondrial genome of Chinese Triops granarius and implications for species delimitation. <i>International Journal of Biological Macromolecules</i> , 2019, 135, 734-744.	7.5	7
1600	Caught in action: fine-scale plastome evolution in the parasitic plants of Cuscuta section Ceratophorae (Convolvulaceae). <i>Plant Molecular Biology</i> , 2019, 100, 621-634.	3.9	17
1601	Evolution and functional differentiation of recently diverged phytochelatin synthase genes from Arundo donax L.. <i>Journal of Experimental Botany</i> , 2019, 70, 5391-5405.	4.8	15
1602	Phylogenomic analyses and distribution of terpene synthases among Streptomyces. <i>Beilstein Journal of Organic Chemistry</i> , 2019, 15, 1181-1193.	2.2	28
1603	Genomic determinants of speciation and spread of the <i>Mycobacterium tuberculosis</i> complex. <i>Science Advances</i> , 2019, 5, eaaw3307.	10.3	61
1604	HIV Diversity and Genetic Compartmentalization in Blood and Testes during Suppressive Antiretroviral Therapy. <i>Journal of Virology</i> , 2019, 93, .	3.4	35
1605	Genetic Diversity of atp6 and cox3 Gene in Wild Drosophila melanogaster. <i>Russian Journal of Genetics</i> , 2019, 55, 360-367.	0.6	0
1606	M1CROB1AL1Z3Râ€”a user-friendly web server for the analysis of large-scale microbial genomics data. <i>Nucleic Acids Research</i> , 2019, 47, W88-W92.	14.5	86
1607	Redondoviridae, a Family of Small, Circular DNA Viruses of the Human Oro-Respiratory Tract Associated with Periodontitis and Critical Illness. <i>Cell Host and Microbe</i> , 2019, 25, 719-729.e4.	11.0	83
1608	Convergent Co-option of the Retroviral <i>gag</i> Gene during the Early Evolution of Mammals. <i>Journal of Virology</i> , 2019, 93, .	3.4	5
1609	Reptile enamel matrix proteins: Selection, divergence, and functional constraint. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2019, 332, 136-148.	1.3	4
1610	Evolution and Genetic Diversity of the <i>k13</i> Gene Associated with Artemisinin Delayed Parasite Clearance in Plasmodium falciparum. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	15
1611	Genetic architecture and sex-specific selection govern modular, male-biased evolution of <i>doublesex</i> . <i>Science Advances</i> , 2019, 5, eaau3753.	10.3	32
1612	Structures and functions linked to genome-wide adaptation of human influenza A viruses. <i>Scientific Reports</i> , 2019, 9, 6267.	3.3	4
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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.	1.7	9
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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.	1.8	33
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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, .	2.2	13
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1773	Intraâ€™strain biological and epidemiological characterization of plum pox virus. <i>Molecular Plant Pathology</i> , 2020, 21, 475-488.	4.2	11
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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.	2.9	7
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1822	Lineageâ€specific plastid degradation in subtribe Gentianinae (Gentianaceae). <i>Ecology and Evolution</i> , 2021, 11, 3286-3299.	1.9	21
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1825	Phylogenetic prospecting for cryptic species of the genus <i>Merluccius</i> (Actinopterygii: Merlucciidae). <i>Scientific Reports</i> , 2021, 11, 5929.	3.3	1
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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, .	7.1	12
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1897	Ultradeep HIV-1 Proviral Envelope Sequencing Reveals Complex Population Structure within and between Brain and Splenic Tissues. <i>Journal of Virology</i> , 2021, 95, e0120221.	3.4	5
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1907	Molecular evolutionary analysis reveals Arctic-like rabies viruses evolved and dispersed independently in North and South Asia. <i>Journal of Veterinary Science</i> , 2021, 22, e5.	1.3	4
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1917	DNA Barcoding for Diagnosis and Monitoring of Fungal Plant Pathogens. <i>Fungal Biology</i> , 2017, , 87-122.	0.6	23
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1924	Selection analyses of paired HIV-1 gag and gp41 sequences obtained before and after antiretroviral therapy. <i>Scientific Data</i> , 2018, 5, 180147.	5.3	1
1925	Direct whole-genome deep-sequencing of human respiratory syncytial virus A and B from Vietnamese children identifies distinct patterns of inter- and intra-host evolution. <i>Journal of General Virology</i> , 2015, 96, 3470-3483.	2.9	30
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1928	Increase in human immunodeficiency virus 1 diversity and detection of various subtypes and recombinants in north-eastern Brazil. <i>Journal of Medical Microbiology</i> , 2017, 66, 526-535.	1.8	11
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