

PAML 4: Phylogenetic Analysis by Maximum Likelihood

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Citation Report

#	ARTICLE	IF	CITATIONS
1	MORPH: Probabilistic Alignment Combined with Hidden Markov Models of cis-Regulatory Modules. PLoS Computational Biology, 2007, 3, e216.	1.5	36
2	Evolutionary Dynamics of Introns in Plastid-Derived Genes in Plants: Saturation Nearly Reached but Slow Intron Gain Continues. Molecular Biology and Evolution, 2007, 25, 111-119.	3.5	27
3	Detecting groups of co-evolving positions in a molecule: a clustering approach. BMC Evolutionary Biology, 2007, 7, 242.	3.2	46
4	Diversifying and Purifying Selection in the Peptide Binding Region of DRB in Mammals. Journal of Molecular Evolution, 2008, 66, 384-394.	0.8	46
5	Positive Selection on HIV Accessory Proteins and the Analysis of Molecular Adaptation After Interspecies Transmission. Journal of Molecular Evolution, 2008, 66, 598-604.	0.8	6
6	The Evolutionary Dynamics of Human Influenza B Virus. Journal of Molecular Evolution, 2008, 66, 655-663.	0.8	194
7	Molecular Evolution of the CPP-like Gene Family in Plants: Insights from Comparative Genomics of Arabidopsis and Rice. Journal of Molecular Evolution, 2008, 67, 266-277.	0.8	78
8	Adaptive Evolution of Gamete-Recognition Proteins in Birds. Journal of Molecular Evolution, 2008, 67, 488-496.	0.8	18
9	Selection on an Antimicrobial Peptide Defensin in Ants. Journal of Molecular Evolution, 2008, 67, 643-652.	0.8	43
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11	Species-specific evolution of class I MHC genes in iguanas (Order: Squamata; Subfamily: Iguaninae). Immunogenetics, 2008, 60, 371-382.	1.2	18
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14	DNA evidence for a Paleocene origin of the Alcidae (Aves: Charadriiformes) in the Pacific and multiple dispersals across northern oceans. Molecular Phylogenetics and Evolution, 2008, 46, 430-445.	1.2	47
15	Relative rates of synonymous substitutions in the mitochondrial, chloroplast and nuclear genomes of seed plants. Molecular Phylogenetics and Evolution, 2008, 49, 827-831.	1.2	354
16	â€œREVERSE ECOLOGYâ€ AND THE POWER OF POPULATION GENOMICS. Evolution; International Journal of Organic Evolution, 2008, 62, 2984-2994.	1.1	121
17	AN EVOLUTIONARY EXPRESSED SEQUENCE TAG ANALYSIS OF DROSOPHILA SPERMATHECA GENES. Evolution; International Journal of Organic Evolution, 2008, 62, 2936-2947.	1.1	67
18	The evolution of animal chemosensory receptor gene repertoires: roles of chance and necessity. Nature Reviews Genetics, 2008, 9, 951-963.	7.7	533

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19	Evolutionary history of the ancient cutinase family in five filamentous Ascomycetes reveals differential gene duplications and losses and in <i>Magnaporthe grisea</i> shows evidence of sub- and neo-functionalization. <i>New Phytologist</i> , 2008, 180, 711-721.	3.5	41
20	Comparative genomics and the study of evolution by natural selection. <i>Molecular Ecology</i> , 2008, 17, 4586-4596.	2.0	133
21	Polymorphic MHC loci in an asexual fish, the amazon molly (<i>Poecilia formosa</i> ; Poeciliidae). <i>Molecular Ecology</i> , 2008, 17, 5220-5230.	2.0	24
22	IDEA: Interactive Display for Evolutionary Analyses. <i>BMC Bioinformatics</i> , 2008, 9, 524.	1.2	23
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129	Learning to Count: Robust Estimates for Labeled Distances between Molecular Sequences. <i>Molecular Biology and Evolution</i> , 2009, 26, 801-814.	3.5	102
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1456	Evolution of MHC class I genes in the European badger (<i>Meles meles</i>). <i>Ecology and Evolution</i> , 2012, 2, 1644-1662.	0.8	14
1457	Genome-wide and molecular evolution analysis of the <i>KTP/HAK/KUP</i> potassium transporter gene family. <i>Ecology and Evolution</i> , 2012, 2, 1996-2004.	0.8	48
1458	Incorrect handling of calibration information in divergence time inference: an example from volcanic islands. <i>Ecology and Evolution</i> , 2012, 2, 493-500.	0.8	10
1459	The origins and evolution of ubiquitination sites. <i>Molecular BioSystems</i> , 2012, 8, 1865.	2.9	23
1460	Altered Patterns of Fractionation and Exon Deletions in <i>Brassica rapa</i> Support a Two-Step Model of Paleohexaploidy. <i>Genetics</i> , 2012, 190, 1563-1574.	1.2	163
1461	Deleterious Mutation Accumulation in Asexual <i>Timema</i> Stick Insects. <i>Molecular Biology and Evolution</i> , 2012, 29, 401-408.	3.5	65
1462	Gene transfer agents: phage-like elements of genetic exchange. <i>Nature Reviews Microbiology</i> , 2012, 10, 472-482.	13.6	336
1463	A Reassessment of the Human Mitochondrial DNA Tree from its Root. <i>American Journal of Human Genetics</i> , 2012, 90, 675-684.	2.6	416
1464	Phylogenomic analyses support the position of turtles as the sister group of birds and crocodiles (Archosauria). <i>BMC Biology</i> , 2012, 10, 65.	1.7	296
1465	Fitness conferred by replaced amino acids declines with time. <i>Biology Letters</i> , 2012, 8, 825-828.	1.0	27
1466	Quantifying the Elevation of Mitochondrial DNA Evolutionary Substitution Rates Over Nuclear Rates in the Intertidal Copepod <i>Tigriopus californicus</i> . <i>Journal of Molecular Evolution</i> , 2012, 74, 310-318.	0.8	28
1467	Evolutionary Dynamics and Functional Specialization of Plant Paralogs Formed by Whole and Small-Scale Genome Duplications. <i>Molecular Biology and Evolution</i> , 2012, 29, 3541-3551.	3.5	86
1468	Relaxed Genetic Constraint is Ancestral to the Evolution of Phenotypic Plasticity. <i>Integrative and Comparative Biology</i> , 2012, 52, 16-30.	0.9	46
1469	Phylogenetic Analysis of Ancient DNA using BEAST. <i>Methods in Molecular Biology</i> , 2012, 840, 229-241.	0.4	0
1470	The yak genome and adaptation to life at high altitude. <i>Nature Genetics</i> , 2012, 44, 946-949.	9.4	708
1471	Major taste loss in carnivorous mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4956-4961.	3.3	237
1472	Phylogenomic analysis of transcriptome data elucidates occurrence of a paleopolyploid event and the origin of bimodal karyotypes in Agavoideae (Asparagaceae). <i>American Journal of Botany</i> , 2012, 99, 397-406.	0.8	94

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1473	Cloning and expression analysis of an anti-lipopolysaccharide factor from giant freshwater prawn, <i>Macrobrachium rosenbergii</i> . <i>Molecular Biology Reports</i> , 2012, 39, 7673-7680.	1.0	16
1474	Positive selection pressure within teleost toll-like receptors tlr21 and tlr22 subfamilies and their response to temperature stress and microbial components in zebrafish. <i>Molecular Biology Reports</i> , 2012, 39, 8965-8975.	1.0	54
1475	Positive selection sites in the surface genes of dengue virus: phylogenetic analysis of the interserotypic branches of the four serotypes. <i>Virus Genes</i> , 2012, 44, 408-414.	0.7	7
1476	Timing of butterfly parasitization of a plant-ant scale symbiosis. <i>Ecological Research</i> , 2012, 27, 437-443.	0.7	6
1477	Phylogenetic relationships and estimation of divergence times among Sisoridae catfishes. <i>Science China Life Sciences</i> , 2012, 55, 312-320.	2.3	14
1478	Gene Duplication and Positive Selection Explains Unusual Physiological Roles of the Relaxin Gene in the European Rabbit. <i>Journal of Molecular Evolution</i> , 2012, 74, 52-60.	0.8	7
1479	Recombination, Diversity and Allele Sharing of Infectivity Proteins Between <i>Bartonella</i> Species from Rodents. <i>Microbial Ecology</i> , 2012, 64, 525-536.	1.4	10
1480	Molecular evolution of a malaria resistance gene (DARC) in primates. <i>Immunogenetics</i> , 2012, 64, 497-505.	1.2	11
1481	Independent evolution of functional MHC class II DRB genes in New World bat species. <i>Immunogenetics</i> , 2012, 64, 535-547.	1.2	18
1482	The chimpanzee GH locus: composition, organization, and evolution. <i>Mammalian Genome</i> , 2012, 23, 387-398.	1.0	6
1483	Population dynamics and ORF3 gene evolution of porcine circovirus type 2 circulating in Korea. <i>Archives of Virology</i> , 2012, 157, 799-810.	0.9	8
1484	Genetic variability and potential recombination events in the HC-Pro gene of sugarcane streak mosaic virus. <i>Archives of Virology</i> , 2012, 157, 1371-1375.	0.9	20
1485	Molecular Cloning and Evolutionary Analysis of GJB6 in Mammals. <i>Biochemical Genetics</i> , 2012, 50, 213-226.	0.8	2
1486	Positive Selection and Functional Divergence After Melanopsin Gene Duplication. <i>Biochemical Genetics</i> , 2012, 50, 235-248.	0.8	9
1487	Evolutionary History of Copy-Number-Variable Locus for the Low-Affinity Fc γ 3 Receptor: Mutation Rate, Autoimmune Disease, and the Legacy of Helminth Infection. <i>American Journal of Human Genetics</i> , 2012, 90, 973-985.	2.6	38
1488	Divergent evolution of oxidosqualene cyclases in plants. <i>New Phytologist</i> , 2012, 193, 1022-1038.	3.5	122
1489	Metagenomic analysis of a complex marine planktonic thaumarchaeal community from the Gulf of Maine. <i>Environmental Microbiology</i> , 2012, 14, 254-267.	1.8	56
1490	Phylogeography and binding evolution in <i>Arbacia</i> , a sea urchin genus with an unusual distribution. <i>Molecular Ecology</i> , 2012, 21, 130-144.	2.0	49

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1492	Analysis of polymorphism and transcription of the effector gene <i>Avr1b</i> in <i>Phytophthora sojae</i> isolates from China virulent to <i>Rps1b</i> . <i>Molecular Plant Pathology</i> , 2012, 13, 114-122.	2.0	23
1493	Tunisian <i>Potato virus Y</i> isolates with unnecessary pathogenicity towards pepper: support for the matching allele model in eIF4E resistance-potyvirus interactions. <i>Plant Pathology</i> , 2012, 61, 441-447.	1.2	14
1494	Striking coat colour variation in tuco-tucos (Rodentia: Ctenomyidae): a role for the melanocortin-1 receptor?. <i>Biological Journal of the Linnean Society</i> , 2012, 105, 665-680.	0.7	7
1495	EVOLUTION OF <i>ASPM</i> , IS ASSOCIATED WITH BOTH INCREASES AND DECREASES IN BRAIN SIZE IN PRIMATES. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 927-932.	1.1	40
1496	Adaptive evolution of the <i>rbcL</i> gene in Brassicaceae. <i>Biochemical Systematics and Ecology</i> , 2012, 44, 13-19.	0.6	9
1497	Adaptive diversity of innate immune receptor family short pentraxins in Murinae. <i>FEBS Letters</i> , 2012, 586, 798-803.	1.3	3
1498	Novel HBsAg markers tightly correlate with occult HBV infection and strongly affect HBsAg detection. <i>Antiviral Research</i> , 2012, 93, 86-93.	1.9	71
1499	Computational model for analyzing the evolutionary patterns of the neuraminidase gene of influenza A/H1N1. <i>Computational Biology and Chemistry</i> , 2012, 36, 23-30.	1.1	3
1500	MOLECULAR PHYLOGENY AND TAXONOMY OF THE <i>AEGAGROPILA</i> CLADE (CLADOPHORALES), Tj ETQq1 1 0.784314 rgBT /Overl <i>PSEUDOCLADOPHORA</i> GEN. NOV. ¹ . <i>Journal of Phycology</i> , 2012, 48, 808-825.	1.0	38
1501	No recent adaptive selection on the apyrase of Mediterranean <i>Phlebotomus</i> : implications for using salivary peptides to vaccinate against canine leishmaniasis. <i>Evolutionary Applications</i> , 2012, 5, 293-305.	1.5	11
1502	Gene flow networks among American <i>Aedes aegypti</i> populations. <i>Evolutionary Applications</i> , 2012, 5, 664-676.	1.5	38
1503	THE TEGULA TANGO: A COEVOLUTIONARY DANCE OF INTERACTING, POSITIVELY SELECTED SPERM AND EGG PROTEINS. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1681-1694.	1.1	21
1504	LINEAGE-SPECIFIC VARIATION IN SLOW- AND FAST-X EVOLUTION IN PRIMATES. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1751-1761.	1.1	18
1505	PHYLOGENY OF LEAVENWORTHIA S-ALLELES SUGGESTS UNIDIRECTIONAL MATING SYSTEM EVOLUTION AND ENHANCED POSITIVE SELECTION FOLLOWING AN ANCIENT POPULATION BOTTLENECK. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1849-1861.	1.1	19
1506	PROTEOMIC AND UTR ANALYSES OF A RAPIDLY EVOLVING HYPERVARIABLE FAMILY OF VERTEBRATE PHEROMONES. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 2227-2239.	1.1	26
1507	LOW RATES OF BINDIN CODON EVOLUTION IN LECITHOTROPHIC HELIOCIDARIS SEA URCHINS. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1709-1721.	1.1	7
1508	Evolution of the 4-coumarate:coenzyme A ligase (<i>4CL</i>) gene family: Conserved evolutionary pattern and two new gene classes in gymnosperms. <i>Journal of Systematics and Evolution</i> , 2012, 50, 195-205.	1.6	6

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1509	Evolutionary divergence of the APETALA1 and CAULIFLOWER proteins. <i>Journal of Systematics and Evolution</i> , 2012, 50, 502-511.	1.6	14
1510	Epidemiologic and Phylogenetic Characteristics of Porcine Reproductive and Respiratory Syndrome Viruses in Conventional Swine Farms of Jeju Island as a Candidate Region for PRRSV Eradication. <i>Transboundary and Emerging Diseases</i> , 2012, 59, 62-71.	1.3	9
1511	Comparative evolutionary epidemiology of dengue virus serotypes. <i>Infection, Genetics and Evolution</i> , 2012, 12, 309-314.	1.0	69
1512	Genes under positive selection in a model plant pathogenic fungus, <i>Botrytis</i> . <i>Infection, Genetics and Evolution</i> , 2012, 12, 987-996.	1.0	40
1513	The SLC4A1 gene is under differential selective pressure in primates infected by <i>Plasmodium falciparum</i> and related parasites. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1037-1045.	1.0	7
1514	Porcine reproductive and respiratory syndrome virus diversity of Eastern Canada swine herds in a large sequence dataset reveals two hypervariable regions under positive selection. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1111-1119.	1.0	51
1515	Phylogeny and evolutionary genetics of porcine parvovirus in wild boars. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1163-1171.	1.0	40
1516	Positive selection pressure on the B/C domains of the E2-gene of classical swine fever virus in endemic areas under C-strain vaccination. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1405-1412.	1.0	63
1517	Molecular evolution of $\alpha 4$ integrin binding site to lentiviral envelope proteins in new world primates. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1501-1507.	1.0	14
1518	Emergent properties of gene evolution: Species as attractors in phenotypic space. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2012, 391, 1172-1178.	1.2	6
1519	Monitoring of wild birds for Newcastle disease virus in north Queensland, Australia. <i>Preventive Veterinary Medicine</i> , 2012, 103, 49-62.	0.7	31
1520	Similar Relative Mutation Rates in the Three Genetic Compartments of <i>Mesostigma</i> and <i>Chlamydomonas</i> . <i>Protist</i> , 2012, 163, 105-115.	0.6	32
1521	Rates of molecular evolution vary in vertebrates for insulin-like growth factor-1 (IGF-1), a pleiotropic locus that regulates life history traits. <i>General and Comparative Endocrinology</i> , 2012, 178, 164-173.	0.8	29
1522	Interspecific hybridization increases MHC class II diversity in two sister species of newts. <i>Molecular Ecology</i> , 2012, 21, 887-906.	2.0	69
1523	MHC diversity, malaria and lifetime reproductive success in collared flycatchers. <i>Molecular Ecology</i> , 2012, 21, 2469-2479.	2.0	82
1524	Mitochondrial genomes reveal the global phylogeography and dispersal routes of the migratory locust. <i>Molecular Ecology</i> , 2012, 21, 4344-4358.	2.0	171
1525	Comparative transcriptomics of three Poaceae species reveals patterns of gene expression evolution. <i>Plant Journal</i> , 2012, 71, 492-502.	2.8	209
1526	Transcriptome sequencing of wild chickpea as a rich resource for marker development. <i>Plant Biotechnology Journal</i> , 2012, 10, 690-702.	4.1	111

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1527	Molecular phylogenetics reveals a pattern of biome conservatism in New World anchovies (family) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	0.8	58
1528	Contrasting patterns of selection acting on MHC class I and class II DRB genes in the Alpine marmot (<i>Marmota marmota</i>). <i>Journal of Evolutionary Biology</i> , 2012, 25, 1686-1693.	0.8	14
1529	Adaptive molecular evolution of a defence gene in sexual but not functionally asexual evening primroses. <i>Journal of Evolutionary Biology</i> , 2012, 25, 1576-1586.	0.8	21
1530	Analysis of the mitochondrial DNA variation in pond smelt <i>Hypomesus olidus</i> (Osmeridae). <i>Russian Journal of Genetics</i> , 2012, 48, 713-722.	0.2	8
1531	Gene duplication and an accelerated evolutionary rate in 11S globulin genes are associated with higher protein synthesis in dicots as compared to monocots. <i>BMC Evolutionary Biology</i> , 2012, 12, 15.	3.2	13
1532	Molecular evolution of <i>Drosophila</i> Sex-lethal and related sex determining genes. <i>BMC Evolutionary Biology</i> , 2012, 12, 5.	3.2	16
1533	Rates of evolution in stress-related genes are associated with habitat preference in two Cardamine lineages. <i>BMC Evolutionary Biology</i> , 2012, 12, 7.	3.2	24
1534	Rate and breadth of protein evolution are only weakly correlated. <i>Biology Direct</i> , 2012, 7, 8.	1.9	1
1535	Duplication and diversification of the LEAFY HULL STERILE1 and <i>Oryza sativa</i> MADS5 SEPALLATA lineages in graminoid Poales. <i>EvoDevo</i> , 2012, 3, 4.	1.3	17
1536	Adrenal androgen production in catarrhine primates and the evolution of adrenarche. <i>American Journal of Physical Anthropology</i> , 2012, 147, 389-400.	2.1	44
1537	Positive selection of Toll-like receptor 2 polymorphisms in two closely related old world monkey species, rhesus and Japanese macaques. <i>Immunogenetics</i> , 2012, 64, 15-29.	1.2	6
1538	MHC class II genes in the European badger (<i>Meles meles</i>): characterization, patterns of variation, and transcription analysis. <i>Immunogenetics</i> , 2012, 64, 313-327.	1.2	32
1539	Molecular analyses of ostracod flocks from Lake Baikal and Lake Tanganyika. <i>Hydrobiologia</i> , 2012, 682, 91-110.	1.0	36
1540	Cloning and characterization of boron transporters in <i>Brassica napus</i> . <i>Molecular Biology Reports</i> , 2012, 39, 1963-1973.	1.0	37
1541	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. <i>Genome Biology</i> , 2013, 14, R28.	13.9	276
1542	Analysis of a rare functional truncating mutation rs61757459 in vaspin (SERPINA12) on circulating vaspin levels. <i>Journal of Molecular Medicine</i> , 2013, 91, 1285-1292.	1.7	6
1543	Evolutionary analysis of TLR9 genes reveals the positive selection of extant teleosts in Perciformes. <i>Fish and Shellfish Immunology</i> , 2013, 35, 448-457.	1.6	21
1544	Evolution of plant Ash1 SET genes: structural divergence and functional differentiation. <i>Genes and Genomics</i> , 2013, 35, 463-473.	0.5	1

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1545	Novel algorithm for phylogenetic analysis of proteins: application to analysis of the evolution of H5N1 influenza viruses. <i>Journal of Mathematical Chemistry</i> , 2013, 51, 2238-2255.	0.7	10
1546	Evolution of the ABPA Subunit of Androgen-Binding Protein Expressed in the Submaxillary Glands in New and Old World Rodent Taxa. <i>Journal of Molecular Evolution</i> , 2013, 76, 324-331.	0.8	7
1547	Molecular Phylogeny and Evolution of the Proteins Encoded by Coleoid (Cuttlefish, Octopus, and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	62
1548	Mosaic Evolution of Silk Genes in <i>Aliatypus</i> Trapdoor Spiders (Mygalomorphae, Antrodiaetidae). <i>Journal of Molecular Evolution</i> , 2013, 76, 216-227.	0.8	1
1549	Evolution of General Transcription Factors. <i>Journal of Molecular Evolution</i> , 2013, 76, 28-47.	0.8	7
1550	A divergence dating analysis of turtles using fossil calibrations: an example of best practices. <i>Journal of Paleontology</i> , 2013, 87, 612-634.	0.5	128
1551	Enzyme Engineering. <i>Methods in Molecular Biology</i> , 2013, , .	0.4	4
1552	Adaptive evolution of Mediterranean pines. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 555-566.	1.2	46
1553	Accelerated Evolutionary Rate of the Myoglobin Gene in Long-Diving Whales. <i>Journal of Molecular Evolution</i> , 2013, 76, 380-387.	0.8	23
1554	Transcriptome analysis of female reproductive tissues of <i>A. nastrepha obliqua</i> and molecular evolution of eggshell proteins in the <i>fraterculus</i> group. <i>Insect Molecular Biology</i> , 2013, 22, 551-561.	1.0	8
1555	Molecular evolution of the moonlighting protein SMN in metazoans. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2013, 8, 220-230.	0.4	3
1556	The evolution and pathogenic mechanisms of the rice sheath blight pathogen. <i>Nature Communications</i> , 2013, 4, 1424.	5.8	268
1557	Clustering evolving proteins into homologous families. <i>BMC Bioinformatics</i> , 2013, 14, 120.	1.2	9
1558	Sequence analyses of the distal-less homeobox gene family in East African cichlid fishes reveal signatures of positive selection. <i>BMC Evolutionary Biology</i> , 2013, 13, 153.	3.2	9
1559	Parasitic plants have increased rates of molecular evolution across all three genomes. <i>BMC Evolutionary Biology</i> , 2013, 13, 126.	3.2	120
1560	Evolution and divergence of the mammalian SAMD9/SAMD9L gene family. <i>BMC Evolutionary Biology</i> , 2013, 13, 121.	3.2	43
1561	Evolution by selection, recombination, and gene duplication in MHC class I genes of two Rhacophoridae species. <i>BMC Evolutionary Biology</i> , 2013, 13, 113.	3.2	35
1562	Phylogenomics of stronglycentrotid sea urchins. <i>BMC Evolutionary Biology</i> , 2013, 13, 88.	3.2	42

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1563	Rapid birth-and-death evolution of the xenobiotic metabolizing NAT gene family in vertebrates with evidence of adaptive selection. <i>BMC Evolutionary Biology</i> , 2013, 13, 62.	3.2	39
1564	A system-level, molecular evolutionary analysis of mammalian phototransduction. <i>BMC Evolutionary Biology</i> , 2013, 13, 52.	3.2	21
1565	Characterization of hairless (Hr) and FGF5 genes provides insights into the molecular basis of hair loss in cetaceans. <i>BMC Evolutionary Biology</i> , 2013, 13, 34.	3.2	51
1566	Molecular decay of enamel matrix protein genes in turtles and other edentulous amniotes. <i>BMC Evolutionary Biology</i> , 2013, 13, 20.	3.2	53
1567	Evolutionary history of black grouse major histocompatibility complex class IIB genes revealed through single locus sequence-based genotyping. <i>BMC Genetics</i> , 2013, 14, 29.	2.7	16
1568	The genesis of an exceptionally lethal venom in the timber rattlesnake (<i>Crotalus horridus</i>) revealed through comparative venom-gland transcriptomics. <i>BMC Genomics</i> , 2013, 14, 394.	1.2	95
1569	Genomic basis of ecological niche divergence among cryptic sister species of non-biting midges. <i>BMC Genomics</i> , 2013, 14, 384.	1.2	25
1570	Structural and functional annotation of the porcine immunome. <i>BMC Genomics</i> , 2013, 14, 332.	1.2	203
1571	Comparative transcriptome analysis and marker development of two closely related Primrose species (<i>Primula poissonii</i> and <i>Primula wilsonii</i>). <i>BMC Genomics</i> , 2013, 14, 329.	1.2	62
1572	Haplotype analysis of sucrose synthase gene family in three <i>Saccharum</i> species. <i>BMC Genomics</i> , 2013, 14, 314.	1.2	47
1573	Genome analyses of the wheat yellow (stripe) rust pathogen <i>Puccinia striiformis</i> f. sp. <i>tritici</i> reveal polymorphic and haustorial expressed secreted proteins as candidate effectors. <i>BMC Genomics</i> , 2013, 14, 270.	1.2	235
1574	Transcriptome characterisation of <i>Pinus tabulaeformis</i> and evolution of genes in the <i>Pinus</i> phylogeny. <i>BMC Genomics</i> , 2013, 14, 263.	1.2	56
1575	Ancient orphan crop joins modern era: gene-based SNP discovery and mapping in lentil. <i>BMC Genomics</i> , 2013, 14, 192.	1.2	115
1576	Comparative genomics of parasitic silkworm microsporidia reveal an association between genome expansion and host adaptation. <i>BMC Genomics</i> , 2013, 14, 186.	1.2	127
1577	Insights into the evolution of Darwin's finches from comparative analysis of the <i>Geospiza magnirostris</i> genome sequence. <i>BMC Genomics</i> , 2013, 14, 95.	1.2	38
1578	Evolution of land plant genes encoding L-Ala-D/L-Glu epimerases (AEs) via horizontal gene transfer and positive selection. <i>BMC Plant Biology</i> , 2013, 13, 34.	1.6	16
1579	Codon pairs of the HIV-1 <i>vif</i> gene correlate with CD4+ T cell count. <i>BMC Infectious Diseases</i> , 2013, 13, 173.	1.3	8
1580	EVALUATING PATTERNS OF CONVERGENT EVOLUTION AND TRANS-SPECIES POLYMORPHISM AT MHC IMMUNOGENES IN TWO SYMPATRIC STICKLEBACK SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2400-2412.	1.1	43

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1581	Positive selection signals of hepatitis B virus and their association with disease stages and viral genotypes. <i>Infection, Genetics and Evolution</i> , 2013, 19, 176-187.	1.0	7
1582	High altitude adaptation of the schizothoracine fishes (Cyprinidae) revealed by the mitochondrial genome analyses. <i>Gene</i> , 2013, 517, 169-178.	1.0	55
1583	The evolution of lineage-specific clusters of single nucleotide substitutions in the human genome. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 276-285.	1.2	3
1584	Haplotype variability and identification of new functional alleles at the Rdg2a leaf stripe resistance gene locus. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1575-1586.	1.8	9
1585	Neurexophilin 1 Gene Polymorphism in Chickens and Its Variation Among Species. <i>Biochemical Genetics</i> , 2013, 51, 618-625.	0.8	1
1586	Transcriptional abundance is not the single force driving the evolution of bacterial proteins. <i>BMC Evolutionary Biology</i> , 2013, 13, 162.	3.2	5
1587	Utility of the phylotoxigenic relationships among trichothecene-producing <i>Fusarium</i> species for predicting their mycotoxin-producing potential. <i>Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment</i> , 2013, 30, 1370-1381.	1.1	9
1588	Birth, death and horizontal transfer of the fumonisin biosynthetic gene cluster during the evolutionary diversification of <i>Fusarium</i> . <i>Molecular Microbiology</i> , 2013, 90, 290-306.	1.2	118
1589	The sacred lotus genome provides insights into the evolution of flowering plants. <i>Plant Journal</i> , 2013, 76, 557-567.	2.8	75
1590	Characterization of MHC class II B polymorphism in bottlenecked New Zealand saddlebacks reveals low levels of genetic diversity. <i>Immunogenetics</i> , 2013, 65, 619-633.	1.2	21
1591	In silico peptide-binding predictions of passerine MHC class I reveal similarities across distantly related species, suggesting convergence on the level of protein function. <i>Immunogenetics</i> , 2013, 65, 299-311.	1.2	14
1592	Characterization of MHC class I in a long-distance migrant shorebird suggests multiple transcribed genes and intergenic recombination. <i>Immunogenetics</i> , 2013, 65, 211-225.	1.2	19
1593	Phylogeny of Microcystins: Evidence of a Biogeographical Trend?. <i>Current Microbiology</i> , 2013, 66, 214-221.	1.0	15
1594	EVOLUTION OF SEX DETERMINATION SYSTEMS WITH HETEROGAMETIC MALES AND FEMALES IN <i>SILENE</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 3669-3677.	1.1	44
1595	MHC II DRB variation and trans-species polymorphism in the golden snub-nosed monkey (<i>Rhinopithecus</i>). <i>Trends in Ecology and Evolution</i> , 2013, 24, 117-119.	1.7	9
1596	Characterization of major histocompatibility complex DRA and DRB genes of the forest musk deer (<i>Moschus berezovskii</i>). <i>Science Bulletin</i> , 2013, 58, 2191-2197.	1.7	6
1597	Genome-wide signatures of convergent evolution in echolocating mammals. <i>Nature</i> , 2013, 502, 228-231.	13.7	321
1598	Repeated loss of an anciently horizontally transferred gene cluster in <i>Botrytis</i> . <i>Mycologia</i> , 2013, 105, 1126-1134.	0.8	39

#	ARTICLE	IF	CITATIONS
1599	The wheat powdery mildew genome shows the unique evolution of an obligate biotroph. <i>Nature Genetics</i> , 2013, 45, 1092-1096.	9.4	236
1600	Residue mutations and their impact on protein structure and function: detecting beneficial and pathogenic changes. <i>Biochemical Journal</i> , 2013, 449, 581-594.	1.7	172
1601	A draft genome sequence of the pulse crop chickpea (<i>Cicer arietinum</i>). <i>Plant Journal</i> , 2013, 74, 715-729.	2.8	382
1602	Evolution of Functional Genes in Cetaceans Driven by Natural Selection on a Phylogenetic and Population Level. <i>Evolutionary Biology</i> , 2013, 40, 341-354.	0.5	2
1603	Episodic positive selection during the evolution of naphthalene dioxygenase to nitroarene dioxygenase. <i>Biochemical and Biophysical Research Communications</i> , 2013, 440, 68-75.	1.0	0
1604	MicroRNA or NMD: Why Have Two RNA Silencing Systems?. <i>Journal of Genetics and Genomics</i> , 2013, 40, 497-513.	1.7	6
1605	The evolutionary analysis on complement genes reveals that fishes C3 and C9 experience different evolutionary patterns. <i>Fish and Shellfish Immunology</i> , 2013, 35, 2040-2045.	1.6	17
1606	Distinct quasispecies characteristics and positive selection within precore/core gene in hepatitis B virus associated acute-chronic liver failure. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2013, 28, 1040-1046.	1.4	15
1607	Analysis of mitochondrial genome diversity identifies new and ancient maternal lineages in Cambodian aborigines. <i>Nature Communications</i> , 2013, 4, 2599.	5.8	37
1608	<i>Pseudoplusia includens</i> single nucleopolyhedrovirus: Genetic diversity, phylogeny and hypervariability of the pif-2 gene. <i>Journal of Invertebrate Pathology</i> , 2013, 114, 258-267.	1.5	19
1609	Expression and Sequence Evolution of Aromatase cyp19a1 and Other Sexual Development Genes in East African Cichlid Fishes. <i>Molecular Biology and Evolution</i> , 2013, 30, 2268-2285.	3.5	62
1610	Flight loss linked to faster molecular evolution in insects. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20131128.	1.2	60
1611	Patterns of Transcriptome Divergence in the Male Accessory Gland of Two Closely Related Species of Field Crickets. <i>Genetics</i> , 2013, 193, 501-513.	1.2	49
1612	Adaptive evolution of Hoxc13 genes in the origin and diversification of the vertebrate integument. , 2013, 320, n/a-n/a.		5
1613	Why Do More Divergent Sequences Produce Smaller Nonsynonymous/Synonymous Rate Ratios in Pairwise Sequence Comparisons?. <i>Genetics</i> , 2013, 195, 195-204.	1.2	44
1614	Phylogeny and genetic diversity of foot and mouth disease virus serotype Asia1 in India during 1964-2012. <i>Veterinary Microbiology</i> , 2013, 167, 280-288.	0.8	14
1615	Analysis of selective constraints on mitochondrial DNA, Flight ability and physiological index on avian. , 2013, 2013, 1498-501.		1
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1618	Complete mitochondrial genomes from four subspecies of common chaffinch (<i>Fringilla coelebs</i>): New inferences about mitochondrial rate heterogeneity, neutral theory, and phylogenetic relationships within the order Passeriformes. <i>Gene</i> , 2013, 517, 37-45.	1.0	13
1619	Phylogenomic Analyses Elucidate the Evolutionary Relationships of Bats. <i>Current Biology</i> , 2013, 23, 2262-2267.	1.8	139
1620	Comparative genomics of two <i>Candidatus</i> <i>Accumulibacter</i> ™ clades performing biological phosphorus removal. <i>ISME Journal</i> , 2013, 7, 2301-2314.	4.4	101
1621	Hybridization and long-distance colonization at different time scales: towards resolution of long-term controversies in the sweet vernal grasses (<i>Anthoxanthum</i>). <i>Annals of Botany</i> , 2013, 112, 1015-1030.	1.4	28
1622	Searching for efficient Markov chain Monte Carlo proposal kernels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19307-19312.	3.3	64
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1624	<i>Polynucleobacter necessarius</i> , a model for genome reduction in both free-living and symbiotic bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18590-18595.	3.3	80
1625	Spatial Distribution of Selection Pressure on a Protein Based on the Hierarchical Bayesian Model. <i>Molecular Biology and Evolution</i> , 2013, 30, 2714-2722.	3.5	1
1626	Evolutionary perspective on hepatitis B virus with an expanded sampling strategy. <i>Virus Research</i> , 2013, 178, 525-529.	1.1	0
1627	Genomic insights into salt adaptation in a desert poplar. <i>Nature Communications</i> , 2013, 4, 2797.	5.8	286
1628	The evolution of evolvability in microRNA target sites in vertebrates. <i>Genome Research</i> , 2013, 23, 1810-1816.	2.4	53
1629	Protein Conformational Diversity Correlates with Evolutionary Rate. <i>Molecular Biology and Evolution</i> , 2013, 30, 1500-1503.	3.5	36
1630	Dating Phylogenies with Sequentially Sampled Tips. <i>Systematic Biology</i> , 2013, 62, 674-688.	2.7	79
1631	PAMLX: A Graphical User Interface for PAML. <i>Molecular Biology and Evolution</i> , 2013, 30, 2723-2724.	3.5	304
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1636	A heterozygous moth genome provides insights into herbivory and detoxification. <i>Nature Genetics</i> , 2013, 45, 220-225.	9.4	472
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1638	Stepwise Evolution of Essential Centromere Function in a <i>Drosophila</i> Neogene. <i>Science</i> , 2013, 340, 1211-1214.	6.0	94
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1640	ConSurf: Using Evolutionary Data to Raise Testable Hypotheses about Protein Function. <i>Israel Journal of Chemistry</i> , 2013, 53, 199-206.	1.0	459
1641	Models and Algorithms for Genome Evolution. <i>Computational Biology</i> , 2013, , .	0.1	7
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1644	Patterns of evolutionary selection pressure in the immune signaling protein TRAF3IP2 in mammals. <i>Gene</i> , 2013, 531, 403-410.	1.0	5
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1647	Comprehensive analysis of expressed sequence tags from cultivated and wild radish (<i>Raphanus</i> spp.). <i>BMC Genomics</i> , 2013, 14, 721.	1.2	16
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1652	Directional Darwinian Selection in proteins. <i>BMC Bioinformatics</i> , 2013, 14, S6.	1.2	21

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1657	4273€: Bioinformatics education on low cost ARM hardware. <i>BMC Bioinformatics</i> , 2013, 14, 243.	1.2	19
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1659	MHC genes and parasitism in <i>Carassius gibelio</i> , a diploid-triploid fish species with dual reproduction strategies. <i>BMC Evolutionary Biology</i> , 2013, 13, 122.	3.2	12
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1661	Comparative inner ear transcriptome analysis between the Rickettsia™s big-footed bats (<i>Myotis ricketti</i>) and the greater short-nosed fruit bats (<i>Cynopterus sphinx</i>). <i>BMC Genomics</i> , 2013, 14, 916.	1.2	25
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1663	Single-cell genomics reveal low recombination frequencies in freshwater bacteria of the SAR11 clade. <i>Genome Biology</i> , 2013, 14, R130.	13.9	74
1664	Genetic analyses of bone morphogenetic protein 2, 4 and 7 in congenital combined pituitary hormone deficiency. <i>BMC Endocrine Disorders</i> , 2013, 13, 56.	0.9	9
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1668	Two Rapidly Evolving Genes Contribute to Male Fitness in <i>Drosophila</i> . <i>Journal of Molecular Evolution</i> , 2013, 77, 246-259.	0.8	6
1669	Molecular Evolutionary Analysis of Vertebrate Transducins: A Role for Amino Acid Variation in Photoreceptor Deactivation. <i>Journal of Molecular Evolution</i> , 2013, 77, 231-245.	0.8	11
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1673	Expression of heat shock protein 90 genes during early development and infection in <i>Megalobrama amblycephala</i> and evidence for adaptive evolution in teleost. <i>Developmental and Comparative Immunology</i> , 2013, 41, 683-693.	1.0	17
1674	Combining fossil and molecular data to date the diversification of New World Primates. <i>Journal of Evolutionary Biology</i> , 2013, 26, 2438-2446.	0.8	35
1675	Population Genomics of Human Adaptation. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2013, 44, 123-143.	3.8	81
1676	Evolution of optimal codon choices in the family Enterobacteriaceae. <i>Microbiology (United Kingdom)</i> , 2013, 159, 555-564.	0.7	8
1677	A practical guide to molecular dating. <i>Comptes Rendus - Palevol</i> , 2013, 12, 355-367.	0.1	93
1678	Rapid Evolution of Beta-Keratin Genes Contribute to Phenotypic Differences That Distinguish Turtles and Birds from Other Reptiles. <i>Genome Biology and Evolution</i> , 2013, 5, 923-933.	1.1	43
1679	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	2.4	832
1680	Genome of the Chinese tree shrew. <i>Nature Communications</i> , 2013, 4, 1426.	5.8	284
1681	Pairwise Comparison of Orthologous Olfactory Receptor Genes Between Two Sympatric Sibling Sea Kraits of the Genus <i>Laticauda</i> in Vanuatu. <i>Zoological Science</i> , 2013, 30, 425.	0.3	1
1682	Association of Intron Loss with High Mutation Rate in <i>Arabidopsis</i> : Implications for Genome Size Evolution. <i>Genome Biology and Evolution</i> , 2013, 5, 723-733.	1.1	39
1683	Functional Annotation and Comparative Analysis of a Zygoteran Transcriptome. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 763-770.	0.8	5
1684	Prevalence of Multinucleotide Replacements in Evolution of Primates and <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2013, 30, 1315-1325.	3.5	28
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1686	Characterization and comprehensive analysis of the miiuy croaker TLR2 reveals a direct evidence for intron insert and loss. <i>Fish and Shellfish Immunology</i> , 2013, 34, 119-128.	1.6	19
1687	gKaKs: the pipeline for genome-level Ka/Ks calculation. <i>Bioinformatics</i> , 2013, 29, 645-646.	1.8	47
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1690	Phylogeny and biogeography of highly diverged freshwater fish species (Leuciscinae, Cyprinidae.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 662</i>	1.0	91
1691	Molecular phylogeny and historical biogeography of the Anatolian lizard <i>Apathya</i> (Squamata.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662</i>	1.2	56
1692	Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 2013, 493, 526-531.	13.7	564
1693	The evolutionary landscape of the <i>Mycobacterium tuberculosis</i> genome. <i>Gene</i> , 2013, 518, 187-193.	1.0	8
1694	Detecting the Signatures of Adaptive Evolution in Protein-coding Genes. <i>Current Protocols in Molecular Biology</i> , 2013, 101, Unit 19.1..	2.9	12
1695	Mitochondrial DNA of <i>Clathrina clathrus</i> (Calcarea, Calcinea): Six Linear Chromosomes, Fragmented rRNAs, tRNA Editing, and a Novel Genetic Code. <i>Molecular Biology and Evolution</i> , 2013, 30, 865-880.	3.5	78
1696	From Trajectories to Averages: An Improved Description of the Heterogeneity of Substitution Rates Along Lineages. <i>Systematic Biology</i> , 2013, 62, 22-34.	2.7	43
1697	Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity. <i>Science</i> , 2013, 339, 456-460.	6.0	522
1698	Estimating Empirical Codon Hidden Markov Models. <i>Molecular Biology and Evolution</i> , 2013, 30, 725-736.	3.5	51
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1700	Gene Flow, Recombination, and Selection in Cyanobacteria: Population Structure of Geographically Related <i>Planktothrix</i> Freshwater Strains. <i>Applied and Environmental Microbiology</i> , 2013, 79, 508-515.	1.4	16
1701	Greater prairie chickens have a compact MHC-B with a single class IA locus. <i>Immunogenetics</i> , 2013, 65, 133-144.	1.2	20
1702	Cloning and Molecular Evolution of the Aldehyde Dehydrogenase 2 Gene (<i>Aldh2</i>) in Bats (Chiroptera). <i>Biochemical Genetics</i> , 2013, 51, 7-19.	0.8	2
1703	Estimating Speciation and Extinction Rates for Phylogenies of Higher Taxa. <i>Systematic Biology</i> , 2013, 62, 220-230.	2.7	40
1704	Functional consequences of sequence variation in the pheromone biosynthetic gene <i>pgFAR</i> for <i>Ostrinia</i> moths. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3967-3972.	3.3	90
1705	Small open reading frames associated with morphogenesis are hidden in plant genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2395-2400.	3.3	178
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1708	Evolutionary genetic analyses of MEF2C gene: Implications for learning and memory in Homo sapiens. <i>Asian Journal of Psychiatry</i> , 2013, 6, 56-59.	0.9	2
1709	A heat shock protein 90 α isoform involved in immune response to bacteria challenge and heat shock from <i>Miichthys miiuy</i> . <i>Fish and Shellfish Immunology</i> , 2013, 35, 429-437.	1.6	28
1710	Functional and evolutionary analysis of DXL1, a non-essential gene encoding a 1-deoxy-D-xylulose 5-phosphate synthase like protein in <i>Arabidopsis thaliana</i> . <i>Gene</i> , 2013, 524, 40-53.	1.0	32
1711	The complete mitochondrial genomes of deep-sea squid (<i>Bathyteuthis abyssicola</i>), bob-tail squid (<i>Semirossia patagonica</i>) and four giant cuttlefish (<i>Sepia apama</i> , <i>S. latimanus</i> , <i>S. lycidas</i> and <i>S. pharansis</i>), and their application to the phylogenetic analysis of Decapodiformes. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 980-993.	1.2	29
1712	Vertebrate extracellular calcium-sensing receptor evolution: Selection in relation to life history and habitat. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2013, 8, 86-94.	0.4	25
1713	Genomic organization and transcription of the medaka and zebrafish cellular retinol-binding protein (rbp) genes. <i>Marine Genomics</i> , 2013, 11, 1-10.	0.4	9
1714	Identification and evolution of an NFAT gene involving <i>Branchiostoma belcheri</i> innate immunity. <i>Genomics</i> , 2013, 102, 355-362.	1.3	12
1715	Structural and phylogenetic comparison of napsin genes: The duplication, loss of function and human-specific pseudogenization of napsin B. <i>Gene</i> , 2013, 517, 147-157.	1.0	3
1716	Characterization of cys-loop receptor genes involved in inhibitory amine neurotransmission in parasitic and free living nematodes. <i>Parasitology International</i> , 2013, 62, 599-605.	0.6	18
1717	Following Gene Duplication, Paralog Interference Constrains Transcriptional Circuit Evolution. <i>Science</i> , 2013, 342, 104-108.	6.0	103
1718	Correlated Evolution of Gonadotropin-Releasing Hormone and Gonadotropin-Inhibitory Hormone and Their Receptors in Mammals. <i>Neuroendocrinology</i> , 2013, 97, 242-251.	1.2	6
1719	Early vertebrate origin of melanocortin 2 receptor accessory proteins (MRAPs). <i>General and Comparative Endocrinology</i> , 2013, 188, 123-132.	0.8	14
1720	Evolution of the ONSEN retrotransposon family activated upon heat stress in Brassicaceae. <i>Gene</i> , 2013, 518, 256-261.	1.0	59
1721	The first evidence of positive selection in peptidoglycan recognition protein (PGRP) genes of <i>Crassostrea gigas</i> . <i>Fish and Shellfish Immunology</i> , 2013, 34, 1352-1355.	1.6	22
1722	Genome-wide identification and divergent transcriptional expression of StAR-related lipid transfer (START) genes in teleosts. <i>Gene</i> , 2013, 519, 18-25.	1.0	4
1723	Evolution of infectious bronchitis virus in Taiwan: Positively selected sites in the nucleocapsid protein and their effects on RNA-binding activity. <i>Veterinary Microbiology</i> , 2013, 162, 408-418.	0.8	19
1724	Multiple bursts of pancreatic ribonuclease gene duplication in insect-eating bats. <i>Gene</i> , 2013, 526, 112-117.	1.0	27

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1725	Phylogenetic investigation of <i>Edwardsiella tarda</i> with multilocus sequence typing (MLST) and pulsed field gel electrophoresis (PFGE) typing methods. <i>Aquaculture</i> , 2013, 410-411, 79-85.	1.7	18
1726	Resurrection of an Urbilaterian U1A/U2B ³ /SNF Protein. <i>Journal of Molecular Biology</i> , 2013, 425, 3846-3862.	2.0	17
1727	Variations and evolution of polyubiquitin genes from ciliates. <i>European Journal of Protistology</i> , 2013, 49, 40-49.	0.5	1
1728	Gene conversions are under purifying selection in the carcinoembryonic antigen immunoglobulin gene families of primates. <i>Genomics</i> , 2013, 102, 301-309.	1.3	15
1729	From PPRM to caul: The evolution of membrane rupture in mammals. <i>Applied & Translational Genomics</i> , 2013, 2, 70-77.	2.1	3
1730	Different evolutionary patterns of hypoxia-inducible factor 1 \pm (HIF1 \pm) isoforms in the basal branches of Actinopterygii and Sarcopterygii. <i>FEBS Open Bio</i> , 2013, 3, 479-483.	1.0	18
1731	Cloning and identification of four Mu-type glutathione S-transferases from the giant freshwater prawn <i>Macrobrachium rosenbergii</i> . <i>Fish and Shellfish Immunology</i> , 2013, 35, 546-552.	1.6	15
1732	Class of Multiple Sequence Alignment Algorithm Affects Genomic Analysis. <i>Molecular Biology and Evolution</i> , 2013, 30, 642-653.	3.5	61
1733	First evidence for functional vomeronasal 2 receptor genes in primates. <i>Biology Letters</i> , 2013, 9, 20121006.	1.0	79
1734	Sea star populations diverge by positive selection at a sperm-egg compatibility locus. <i>Ecology and Evolution</i> , 2013, 3, 640-654.	0.8	17
1735	Differential requirements for mRNA folding partially explain why highly expressed proteins evolve slowly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E678-86.	3.3	110
1736	Molecular dating of phylogenies by likelihood methods: A comparison of models and a new information criterion. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 436-444.	1.2	157
1737	Multiple ancient horizontal gene transfers and duplications in lepidopteran species. <i>Insect Molecular Biology</i> , 2013, 22, 72-87.	1.0	43
1738	Extensive polymorphism and evidence of selection pressure on major histocompatibility complex <sc>DLA α DRB1</sc>, <sc>DQA1</sc> and <sc>DQB1</sc> class <sc>II</sc> genes in Croatian grey wolves. <i>Tissue Antigens</i> , 2013, 81, 19-27.	1.0	19
1739	The fate of duplicated genes in a polyploid plant genome. <i>Plant Journal</i> , 2013, 73, 143-153.	2.8	243
1740	Sequencing and annotation of the <i>Ophiostoma</i> ulmigenome. <i>BMC Genomics</i> , 2013, 14, 162.	1.2	40
1741	Natural selection and functional diversification of the epidermal growth factor receptor EGFR family in vertebrates. <i>Genomics</i> , 2013, 101, 318-325.	1.3	6
1742	Asymmetric Functional Divergence of Young, Dispersed Gene Duplicates in <i>Arabidopsis thaliana</i> . <i>Journal of Molecular Evolution</i> , 2013, 76, 13-27.	0.8	5

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1743	The unbearable uncertainty of Bayesian divergence time estimation. <i>Journal of Systematics and Evolution</i> , 2013, 51, 30-43.	1.6	130
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1888	Spatiotemporal Phylogenetic Analysis and Molecular Characterisation of Infectious Bursal Disease Viruses Based on the VP2 Hyper-Variable Region. <i>PLoS ONE</i> , 2013, 8, e65999.	1.1	26
1889	Reconstructing the Phylogenetic History of Long-Term Effective Population Size and Life-History Traits Using Patterns of Amino Acid Replacement in Mitochondrial Genomes of Mammals and Birds. <i>Genome Biology and Evolution</i> , 2013, 5, 1273-1290.	1.1	62
1890	Differential Genomic Variation between Short- and Long-Term Bacterial Evolution Revealed by Ultradeep Sequencing. <i>Genome Biology and Evolution</i> , 2013, 5, 572-577.	1.1	3
1891	The Complete Maternally and Paternally Inherited Mitochondrial Genomes of the Endangered Freshwater Mussel <i>Solenia carinatus</i> (Bivalvia: Unionidae) and Implications for Unionidae Taxonomy. <i>PLoS ONE</i> , 2013, 8, e84352.	1.1	66
1892	Selection Is No More Efficient in Haploid than in Diploid Life Stages of an Angiosperm and a Moss. <i>Molecular Biology and Evolution</i> , 2013, 30, 1929-1939.	3.5	41
1893	Mitochondrial Phylogenomics of Modern and Ancient Equids. <i>PLoS ONE</i> , 2013, 8, e55950.	1.1	123
1894	The Twin-Arginine Subunit C in <i>Oscarella</i> : Origin, Evolution, and Potential Functional Significance. <i>Integrative and Comparative Biology</i> , 2013, 53, 495-502.	0.9	15
1895	Evolutionary Rate Covariation in Meiotic Proteins Results from Fluctuating Evolutionary Pressure in Yeasts and Mammals. <i>Genetics</i> , 2013, 193, 529-538.	1.2	34
1896	Genome sequence of ground tit <i>Pseudopodoces humilis</i> and its adaptation to high altitude. <i>Genome Biology</i> , 2013, 14, R29.	13.9	81
1897	Genome sequencing reveals fine scale diversification and reticulation history during speciation in <i>Sus</i> . <i>Genome Biology</i> , 2013, 14, R107.	13.9	137
1898	Evolution of Three Parent Genes and Their Retrogene Copies in <i>Drosophila</i> Species. <i>International Journal of Evolutionary Biology</i> , 2013, 2013, 1-12.	1.0	2
1899	Inference of Genome Duplications from Age Distributions Revisited. <i>Molecular Biology and Evolution</i> , 2013, 30, 177-190.	3.5	145
1900	High Levels of Gene Expression Explain the Strong Evolutionary Constraint of Mitochondrial Protein-Coding Genes. <i>Molecular Biology and Evolution</i> , 2013, 30, 272-284.	3.5	67
1901	Extensive Trans-Specific Polymorphism at the Mating Type Locus of the Root Decay Fungus <i>Heterobasidion</i> . <i>Molecular Biology and Evolution</i> , 2013, 30, 2286-2301.	3.5	29
1902	Problems With Estimation of Ancestral Frequencies Under Stationary Models. <i>Systematic Biology</i> , 2013, 62, 330-338.	2.7	10
1903	A Branch-Heterogeneous Model of Protein Evolution for Efficient Inference of Ancestral Sequences. <i>Systematic Biology</i> , 2013, 62, 523-538.	2.7	47
1904	Genome Evolution and Phylogenomic Analysis of Candidatus <i>Kinetoplastibacterium</i> , the Betaproteobacterial Endosymbionts of <i>Strigomonas</i> and <i>Angomonas</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 338-350.	1.1	47

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1906	Pollen-Specific, but Not Sperm-Specific, Genes Show Stronger Purifying Selection and Higher Rates of Positive Selection Than Sporophytic Genes in <i>Capsella grandiflora</i> . <i>Molecular Biology and Evolution</i> , 2013, 30, 2475-2486.	3.5	90
1907	The Molecular Evolutionary Patterns of the Insulin/FOXO Signaling Pathway. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S10539.	0.6	10
1908	Comment on "The Molecular Evolutionary Patterns of the Insulin/FOXO Signaling Pathway". <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S11915.	0.6	2
1909	Molecular Evolution and Functional Divergence of Soluble Starch Synthase Genes in Cassava (<i>Manihot Esculenta</i> Crantz). <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S11991.	0.6	13
1910	Identification of Differentially Evolved Genes: An Alternative Approach to Detection of Accelerated Molecular Evolution from Genome-Wide Comparative Data. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S12166.	0.6	2
1911	Turning gold into "junk": transposable elements utilize central proteins of cellular networks. <i>Nucleic Acids Research</i> , 2013, 41, 3190-3200.	6.5	22
1912	Genetic and physiological data suggest demographic and adaptive responses in complex interactions between populations of figs (<i>Ficus pumila</i>) and their pollinating wasps (<i>Wespa pumilae</i>). <i>Molecular Ecology</i> , 2013, 22, 3814-3832.	2.0	7
1913	Evolution Along the Mutation Gradient in the Dynamic Mitochondrial Genome of Salamanders. <i>Genome Biology and Evolution</i> , 2013, 5, 1652-1660.	1.1	10
1914	Population-genomic insights into the evolutionary origin and fate of obligately asexual <i>Daphnia pulex</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15740-15745.	3.3	159
1915	Carving out turf in a biodiversity hotspot: multiple, previously unrecognized shrew species occur on Java Island, Indonesia. <i>Molecular Ecology</i> , 2013, 22, 4972-4987.	2.0	37
1916	RECURRENT AND RECENT SELECTIVE SWEEPS IN THE piRNA PATHWAY. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 1081-1090.	1.1	63
1917	Molecular cloning and characterisation of the tissue inhibitor of metalloproteinase-3 gene from canine mammary tumour. <i>Journal of Applied Animal Research</i> , 2013, 41, 294-299.	0.4	0
1918	Linking Genomics and Ecology to Investigate the Complex Evolution of an Invasive <i>Drosophila</i> Pest. <i>Genome Biology and Evolution</i> , 2013, 5, 745-757.	1.1	138
1919	Draft genome sequence of the Tibetan antelope. <i>Nature Communications</i> , 2013, 4, 1858.	5.8	229
1920	A phylomedicine approach to understanding the evolution of auditory sensory perception and disease in mammals. <i>Evolutionary Applications</i> , 2013, 6, 412-422.	1.5	14
1921	Nonagricultural reservoirs contribute to emergence and evolution of <i>Pseudomonas syringae</i> crop pathogens. <i>New Phytologist</i> , 2013, 199, 800-811.	3.5	84
1922	Evolutionary divergence of the PISTILLATA-like proteins in <i>Hedyosmum orientale</i> (<i>Celastraceae</i>) after gene duplication. <i>Journal of Systematics and Evolution</i> , 2013, 51, 681-692.	1.6	0

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1924	Extensive polymorphism of the major histocompatibility complex <i>DRA</i> gene in Balkan donkeys: perspectives on selection and genealogy. <i>Animal Genetics</i> , 2013, 44, 711-716.	0.6	6
1925	Identification and characterization of the major histocompatibility complex class II <i>DQB</i> (<i>MhcMATH1</i>) alleles in Tibetan macaques (<i>Macaca thibetana</i>). <i>Tissue Antigens</i> , 2013, 82, 113-121.	1.0	6
1926	Subfunctionalization of Duplicated Genes in the Evolution of Nine-spined Stickleback Hatching Enzyme. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2013, 320, 140-150.	0.6	9
1927	Molecular Dating of Evolutionary Events. , 2013, , 1-4.		0
1928	SUBFUNCTIONALIZATION OF CYPRINID HYPOXIA-INDUCIBLE FACTORS FOR ROLES IN DEVELOPMENT AND OXYGEN SENSING. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 873-882.	1.1	64
1929	Shifts in the evolutionary rate and intensity of purifying selection between two <i>Brassica</i> genomes revealed by analyses of orthologous transposons and relics of a whole genome triplication. <i>Plant Journal</i> , 2013, 76, 211-222.	2.8	38
1930	One Hundred Twenty Years of Koala Retrovirus Evolution Determined from Museum Skins. <i>Molecular Biology and Evolution</i> , 2013, 30, 299-304.	3.5	85
1931	Sequence Diversity of Pan troglodytes Subspecies and the Impact of WFDC6 Selective Constraints in Reproductive Immunity. <i>Genome Biology and Evolution</i> , 2013, 5, 2512-2523.	1.1	1
1932	Mitochondrial-Nuclear Interactions: Compensatory Evolution or Variable Functional Constraint among Vertebrate Oxidative Phosphorylation Genes?. <i>Genome Biology and Evolution</i> , 2013, 5, 1781-1791.	1.1	56
1933	Evolutionary Analysis of the Contact System Indicates that Kininogen Evolved Adaptively in Mammals and in Human Populations. <i>Molecular Biology and Evolution</i> , 2013, 30, 1397-1408.	3.5	21
1934	Mutational effects on stability are largely conserved during protein evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 21071-21076.	3.3	125
1935	Codon 104 variation of <i>p53</i> gene provides adaptive apoptotic responses to extreme environments in mammals of the Tibet plateau. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20639-20644.	3.3	37
1936	Plastome Sequences of <i>Lygodium japonicum</i> and <i>Marsilea crenata</i> Reveal the Genome Organization Transformation from Basal Ferns to Core Leptosporangiates. <i>Genome Biology and Evolution</i> , 2013, 5, 1403-1407.	1.1	36
1937	MHC Variability in an Isolated Wolf Population in Italy. <i>Journal of Heredity</i> , 2013, 104, 601-612.	1.0	18
1938	Draft genome sequence of the mulberry tree <i>Morus notabilis</i> . <i>Nature Communications</i> , 2013, 4, 2445.	5.8	277
1939	Evolution of Coding Microsatellites in Primate Genomes. <i>Genome Biology and Evolution</i> , 2013, 5, 283-295.	1.1	22
1940	Draft genome of the kiwifruit <i>Actinidia chinensis</i> . <i>Nature Communications</i> , 2013, 4, 2640.	5.8	423

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1942	The Complex Evolutionary Dynamics of Hsp70s: A Genomic and Functional Perspective. <i>Genome Biology and Evolution</i> , 2013, 5, 2460-2477.	1.1	44
1943	Molecular Adaptation during a Rapid Adaptive Radiation. <i>Molecular Biology and Evolution</i> , 2013, 30, 1051-1059.	3.5	23
1944	Function Relaxation Followed by Diversifying Selection after Whole-Genome Duplication in Flowering Plants. <i>Plant Physiology</i> , 2013, 162, 769-778.	2.3	44
1945	The euAP1 Protein MPF3 Represses MPF2 to Specify Floral Calyx Identity and Displays Crucial Roles in Chinese Lantern Development in <i>Physalis</i> . <i>Plant Cell</i> , 2013, 25, 2002-2021.	3.1	26
1946	Genomic Organization and Differential Signature of Positive Selection in the Alpha and Beta Globin Gene Clusters in Two Cetacean Species. <i>Genome Biology and Evolution</i> , 2013, 5, 2359-2367.	1.1	13
1947	The Developmental Brain Gene NPAS3 Contains the Largest Number of Accelerated Regulatory Sequences in the Human Genome. <i>Molecular Biology and Evolution</i> , 2013, 30, 1088-1102.	3.5	93
1948	Improving Genome-Wide Scans of Positive Selection by Using Protein Isoforms of Similar Length. <i>Genome Biology and Evolution</i> , 2013, 5, 457-467.	1.1	43
1949	The Evolution and Functional Significance of Nested Gene Structures in <i>Drosophila melanogaster</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 1978-1985.	1.1	22
1950	Neofunctionalization of young duplicate genes in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17409-17414.	3.3	172
1951	Identification of an overprinting gene in Merkel cell polyomavirus provides evolutionary insight into the birth of viral genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12744-12749.	3.3	132
1952	Fematin-1 Is Involved in Fetomaternal Cell-to-Cell Fusion in Bovinae Placenta and Has Contributed to Diversity of Ruminant Placentation. <i>Journal of Virology</i> , 2013, 87, 10563-10572.	1.5	58
1953	The Perennial Ryegrass GenomeZipper: Targeted Use of Genome Resources for Comparative Grass Genomics. <i>Plant Physiology</i> , 2013, 161, 571-582.	2.3	75
1954	Unequal Recombination and Evolution of the Mating-Type (MAT) Loci in the Pathogenic Fungus <i>Grosmannia claviger</i> and Relatives. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 465-480.	0.8	49
1955	Evidence for Diversifying Selection in a Set of <i>Mycobacterium tuberculosis</i> Genes in Response to Antibiotic- and Nonantibiotic-Related Pressure. <i>Molecular Biology and Evolution</i> , 2013, 30, 1326-1336.	3.5	43
1956	Statistical Evaluation of the Rodinâ€œOhno Hypothesis: Sense/Antisense Coding of Ancestral Class I and II Aminoacyl-tRNA Synthetases. <i>Molecular Biology and Evolution</i> , 2013, 30, 1588-1604.	3.5	47
1957	Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population. <i>Genome Research</i> , 2013, 23, 1663-1674.	2.4	227
1958	Selection Pressure and Founder Effects Constrain Genetic Variation in Differentiated Populations of Soilborne Bymovirus <i>Wheat yellow mosaic virus</i> (<i>Potyviridae</i>) in China. <i>Phytopathology</i> , 2013, 103, 949-959.	1.1	44

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1961	The draft genome of a socially polymorphic halictid bee, <i>Lasioglossum albipes</i> . <i>Genome Biology</i> , 2013, 14, R142.	13.9	72
1962	Not so pseudo: the evolutionary history of protein phosphatase 1 regulatory subunit 2 and related pseudogenes. <i>BMC Evolutionary Biology</i> , 2013, 13, 242.	3.2	14
1963	Afrobatrachian mitochondrial genomes: genome reorganization, gene rearrangement mechanisms, and evolutionary trends of duplicated and rearranged genes. <i>BMC Genomics</i> , 2013, 14, 633.	1.2	47
1964	Inter- and intra-specific pan-genomes of <i>Borrelia burgdorferi</i> sensu lato: genome stability and adaptive radiation. <i>BMC Genomics</i> , 2013, 14, 693.	1.2	74
1965	Characterization of the heart transcriptome of the white shark (<i>Carcharodon carcharias</i>). <i>BMC Genomics</i> , 2013, 14, 697.	1.2	25
1966	The large soybean (<i>Glycine max</i>) WRKY TF family expanded by segmental duplication events and subsequent divergent selection among subgroups. <i>BMC Plant Biology</i> , 2013, 13, 148.	1.6	121
1967	Does HIV evolve towards a more adaptive state similar to that of simian immunodeficiency virus?. <i>Aids</i> , 2013, 27, 2965-2967.	1.0	0
1968	Antennal transcriptome profiles of anopheline mosquitoes reveal human host olfactory specialization in <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , 2013, 14, 749.	1.2	94
1969	<scp>MHC</scp> class <scp>II</scp> B diversity in blue tits: a preliminary study. <i>Ecology and Evolution</i> , 2013, 3, 1878-1889.	0.8	3
1970	Combining molecular evolution and environmental genomics to unravel adaptive processes of <scp>MHC</scp> class <scp>IIB</scp> diversity in European minnows (<i>Phoxinus phoxinus</i>). <i>Ecology and Evolution</i> , 2013, 3, 2568-2585.	0.8	12
1971	<i>NEUROSPORA</i> AND THE DEAD-END HYPOTHESIS: GENOMIC CONSEQUENCES OF SELFING IN THE MODEL GENUS. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 3600-3616.	1.1	30
1972	Positive Evolutionary Selection On the RIG-I-Like Receptor Genes in Mammals. <i>PLoS ONE</i> , 2013, 8, e81864.	1.1	28
1973	Evolutionary and phylogeographic views on <i>Mclr</i> and <i>Asip</i> variation in mammals. <i>Genes and Genetic Systems</i> , 2013, 88, 155-164.	0.2	42
1974	Experimental Molecular Archeology: Reconstruction of Ancestral Mutants and Evolutionary History of Proteins as a New Approach in Protein Engineering. , 2013, , .		2
1975	The rise and fall of the <i>Phytophthora infestans</i> lineage that triggered the Irish potato famine. <i>ELife</i> , 2013, 2, e00731.	2.8	339
1976	Evolutionary analysis of the short-type peptidoglycan-recognition protein gene (PGLYRP1) in primates. <i>Genetics and Molecular Research</i> , 2013, 12, 453-462.	0.3	3

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1978	Conventional Simulation of Biological Sequences Leads to a Biased Assessment of Multi-Loci Phylogenetic Analysis. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S12483.	0.6	3
1979	A Conserved Mammalian Protein Interaction Network. <i>PLoS ONE</i> , 2013, 8, e52581.	1.1	10
1980	The Diversity and Evolution of Wolbachia Ankyrin Repeat Domain Genes. <i>PLoS ONE</i> , 2013, 8, e55390.	1.1	80
1981	Evolution of Red Algal Plastid Genomes: Ancient Architectures, Introns, Horizontal Gene Transfer, and Taxonomic Utility of Plastid Markers. <i>PLoS ONE</i> , 2013, 8, e59001.	1.1	112
1982	Characterization of an Ancient Lepidopteran Lateral Gene Transfer. <i>PLoS ONE</i> , 2013, 8, e59262.	1.1	52
1983	Genomic Comparison between <i>Salmonella Gallinarum</i> and <i>Pullorum</i> : Differential Pseudogene Formation under Common Host Restriction. <i>PLoS ONE</i> , 2013, 8, e59427.	1.1	29
1984	Multiple Interkingdom Horizontal Gene Transfers in <i>Pyrenophora</i> and Closely Related Species and Their Contributions to Phytopathogenic Lifestyles. <i>PLoS ONE</i> , 2013, 8, e60029.	1.1	30
1985	Computational Evolutionary Analysis of the Overlapped Surface (S) and Polymerase (P) Region in Hepatitis B Virus Indicates the Spacer Domain in P Is Crucial for Survival. <i>PLoS ONE</i> , 2013, 8, e60098.	1.1	18
1986	The Complete Sequence of the Mitochondrial Genome of <i>Butomus umbellatus</i> – A Member of an Early Branching Lineage of Monocotyledons. <i>PLoS ONE</i> , 2013, 8, e61552.	1.1	13
1987	Exploring the Molecular Epidemiology and Evolutionary Dynamics of Influenza A Virus in Taiwan. <i>PLoS ONE</i> , 2013, 8, e61957.	1.1	11
1988	Adaptive Evolution of the <i>Myo6</i> Gene in Old World Fruit Bats (Family: Pteropodidae). <i>PLoS ONE</i> , 2013, 8, e62307.	1.1	10
1989	ODoSE: A Webserver for Genome-Wide Calculation of Adaptive Divergence in Prokaryotes. <i>PLoS ONE</i> , 2013, 8, e62447.	1.1	9
1990	Phylogenomic Analyses of Nuclear Genes Reveal the Evolutionary Relationships within the BEP Clade and the Evidence of Positive Selection in Poaceae. <i>PLoS ONE</i> , 2013, 8, e64642.	1.1	37
1991	Genomic Porosity between Invasive <i>Chondrostoma nasus</i> and Endangered Endemic <i>Parachondrostoma toxostoma</i> (Cyprinidae): The Evolution of MHC IIB Genes. <i>PLoS ONE</i> , 2013, 8, e65883.	1.1	8
1992	Adaptive Evolution of the <i>Hox</i> Gene Family for Development in Bats and Dolphins. <i>PLoS ONE</i> , 2013, 8, e65944.	1.1	15
1993	Revealing Less Derived Nature of Cartilaginous Fish Genomes with Their Evolutionary Time Scale Inferred with Nuclear Genes. <i>PLoS ONE</i> , 2013, 8, e66400.	1.1	22
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1997	Transcriptome Characterisation of the Ant <i>Formica exsecta</i> with New Insights into the Evolution of Desaturase Genes in Social Hymenoptera. PLoS ONE, 2013, 8, e68200.	1.1	14
1998	Independent Losses of Visual Perception Genes <i>Cja10</i> and <i>Rbp3</i> in Echolocating Bats (Order: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.1	11
1999	MHC Class IIB Exon 2 Polymorphism in the Grey Partridge (<i>Perdix perdix</i>) Is Shaped by Selection, Recombination and Gene Conversion. PLoS ONE, 2013, 8, e69135.	1.1	22
2000	Beyond Reasonable Doubt: Evolution from DNA Sequences. PLoS ONE, 2013, 8, e69924.	1.1	6
2001	Patterns of Adaptive and Neutral Diversity Identify the Xiaoxiangling Mountains as a Refuge for the Giant Panda. PLoS ONE, 2013, 8, e70229.	1.1	45
2002	Genome-Wide Analysis of Selective Constraints on High Stability Regions of mRNA Reveals Multiple Compensatory Mutations in <i>Escherichia coli</i> . PLoS ONE, 2013, 8, e73299.	1.1	4
2003	Evolutionary Origin of the Scombridae (Tunas and Mackerels): Members of a Paleogene Adaptive Radiation with 14 Other Pelagic Fish Families. PLoS ONE, 2013, 8, e73535.	1.1	136
2004	Computational Analyses of an Evolutionary Arms Race between Mammalian Immunity Mediated by Immunoglobulin A and Its Subversion by Bacterial Pathogens. PLoS ONE, 2013, 8, e73934.	1.1	20
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2006	Transcriptome Sequences Resolve Deep Relationships of the Grape Family. PLoS ONE, 2013, 8, e74394.	1.1	104
2007	A Study on the Geophylogeny of Clinical and Environmental <i>Vibrio cholerae</i> in Kenya. PLoS ONE, 2013, 8, e74829.	1.1	33
2008	Evolutionary Reconstruction and Population Genetics Analysis of Aurora Kinases. PLoS ONE, 2013, 8, e75763.	1.1	3
2009	Complete Chloroplast Genome of <i>Sedum sarmentosum</i> and Chloroplast Genome Evolution in Saxifragales. PLoS ONE, 2013, 8, e77965.	1.1	105
2010	The Evolution and Expression of the Moth Visual Opsin Family. PLoS ONE, 2013, 8, e78140.	1.1	20
2011	Evolution of the bHLH Genes Involved in Stomatal Development: Implications for the Expansion of Developmental Complexity of Stomata in Land Plants. PLoS ONE, 2013, 8, e78997.	1.1	45
2012	Using Genes as Characters and a Parsimony Analysis to Explore the Phylogenetic Position of Turtles. PLoS ONE, 2013, 8, e79348.	1.1	26

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2014	A Distinct and Divergent Lineage of Genomic Island-Associated Type IV Secretion Systems in Legionella. PLoS ONE, 2013, 8, e82221.	1.1	19
2015	Phylogenetics of the Emergence of Influenza Viruses after Cross-Species Transmission. PLoS ONE, 2013, 8, e82486.	1.1	5
2016	Molecular Evolution and Diversity of Conus Peptide Toxins, as Revealed by Gene Structure and Intron Sequence Analyses. PLoS ONE, 2013, 8, e82495.	1.1	27
2017	Screening for candidate genes involved in the production of mouse subventricular zone proliferative cells and an estimation of their changes in evolutionary pressure during primate evolution. Frontiers in Neuroanatomy, 2013, 7, 24.	0.9	10
2018	Dynamic Evolution of Rht-1 Homologous Regions in Grass Genomes. PLoS ONE, 2013, 8, e75544.	1.1	3
2019	Evolutionary Genomics and Adaptive Evolution of the Hedgehog Gene Family (Shh, Ihh and Dhh) in Vertebrates. PLoS ONE, 2014, 9, e74132.	1.1	27
2020	Transcriptome Analysis of the Oil-Rich Tea Plant, Camellia oleifera, Reveals Candidate Genes Related to Lipid Metabolism. PLoS ONE, 2014, 9, e104150.	1.1	73
2021	The Relationship between the Structure of the Tick-Borne Encephalitis Virus Strains and Their Pathogenic Properties. PLoS ONE, 2014, 9, e94946.	1.1	57
2022	Diversity of Prdm9 Zinc Finger Array in Wild Mice Unravels New Facets of the Evolutionary Turnover of this Coding Minisatellite. PLoS ONE, 2014, 9, e85021.	1.1	64
2023	On the Origin and Evolutionary History of NANOG. PLoS ONE, 2014, 9, e85104.	1.1	21
2024	Genome-Wide Analysis of Soybean HD-Zip Gene Family and Expression Profiling under Salinity and Drought Treatments. PLoS ONE, 2014, 9, e87156.	1.1	104
2025	Molecular Phylogenetics and Temporal Diversification in the Genus Aeromonas Based on the Sequences of Five Housekeeping Genes. PLoS ONE, 2014, 9, e88805.	1.1	19
2026	Phylogeny and Molecular Evolution Analysis of PIN-FORMED 1 in Angiosperm. PLoS ONE, 2014, 9, e89289.	1.1	6
2027	Independent Expansion of Zincin Metalloproteinases in Onygenales Fungi May Be Associated with Their Pathogenicity. PLoS ONE, 2014, 9, e90225.	1.1	35
2028	Proteins Involved in Motility and Sperm-Egg Interaction Evolve More Rapidly in Mouse Spermatozoa. PLoS ONE, 2014, 9, e91302.	1.1	44
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2051	The evolution of embryo implantation. <i>International Journal of Developmental Biology</i> , 2014, 58, 155-161.	0.3	48
2052	Genomic Epidemiology of <i>Vibrio cholerae</i> O1 Associated with Floods, Pakistan, 2010. <i>Emerging Infectious Diseases</i> , 2014, 20, 13-20.	2.0	37
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2054	Sequence variation and molecular evolution of BMP4 genes. <i>Genetics and Molecular Research</i> , 2014, 13, 9196-9201.	0.3	2
2055	SWAMP: Sliding Window Alignment Masker for PAML. <i>Evolutionary Bioinformatics</i> , 2014, 10, EBO.S18193.	0.6	31
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2059	Markov-CA model using analytical hierarchy process and multiregression technique. <i>IOP Conference Series: Earth and Environmental Science</i> , 2014, 20, 012008.	0.2	19
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2108	Evolution of Protamine Genes and Changes in Sperm Head Phenotype in Rodents1. <i>Biology of Reproduction</i> , 2014, 90, 67.	1.2	41
2109	The Molecular Evolution of Cytochrome P450 Genes within and between <i>Drosophila</i> Species. <i>Genome Biology and Evolution</i> , 2014, 6, 1118-1134.	1.1	72
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2122	Climbing the vertebrate branch of U1A/U2B ϵ protein evolution. <i>Rna</i> , 2014, 20, 1035-1045.	1.6	10
2123	An Evolutionary Analysis of Antigen Processing and Presentation across Different Timescales Reveals Pervasive Selection. <i>PLoS Genetics</i> , 2014, 10, e1004189.	1.5	42
2124	The Transcriptomes of the Crucian Carp Complex (<i>Carassius auratus</i>) Provide Insights into the Distinction between Unisexual Triploids and Sexual Diploids. <i>International Journal of Molecular Sciences</i> , 2014, 15, 9386-9406.	1.8	12
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2151	Genome-Wide Analysis of Wild-Type Epstein-Barr Virus Genomes Derived from Healthy Individuals of the 1000 Genomes Project. <i>Genome Biology and Evolution</i> , 2014, 6, 846-860.	1.1	74
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2153	PhyloFlow: A fully customizable and automatic workflow for phylogenetic reconstruction. , 2014, , .		2
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2155	Phylogenetics of human Coxsackievirus B5. <i>Future Virology</i> , 2014, 9, 243-250.	0.9	0
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2324	Transcriptome resources for the frogs <i>Leptopelis thobates clamitans</i> and <i>Leptopelis pseudacris regilla</i> , emphasizing antimicrobial peptides and conserved loci for phylogenetics. <i>Molecular Ecology Resources</i> , 2014, 14, 178-183.	2.2	24
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3046	Comprehensive molecular evolution and gene expression analyses of the ABC1 atypical kinase family in rice and <i>Arabidopsis</i> . <i>Journal of Plant Biochemistry and Biotechnology</i> , 2015, 24, 210-217.	0.9	1
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3187	Co-expression network analysis of duplicate genes in maize (<i>Zea mays</i> L.) reveals no subgenome bias. <i>BMC Genomics</i> , 2016, 17, 875.	1.2	36
3188	Evolution of DNA Methylation across Insects. <i>Molecular Biology and Evolution</i> , 2017, 34, msw264.	3.5	246

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3626	The <i>Ectocarpus IMMEDIATE UPRIGHT</i> gene encodes a member of a novel family of cysteine-rich proteins that have an unusual distribution across the eukaryotes. <i>Development (Cambridge)</i> , 2017, 144, 409-418.	1.2	27
3627	Lineage-specific mutational clustering in protein structures predicts evolutionary shifts in function. <i>Bioinformatics</i> , 2017, 33, 1338-1345.	1.8	11
3628	Evolutionary interplay between structure, energy and epistasis in the coat protein of the <i>MS2</i> 174 phage family. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20160139.	1.5	2
3629	Phylogenetic Origin and Diversification of RNAi Pathway Genes in Insects. <i>Genome Biology and Evolution</i> , 2016, 8, evw281.	1.1	92
3630	ProtASR: An Evolutionary Framework for Ancestral Protein Reconstruction with Selection on Folding Stability. <i>Systematic Biology</i> , 2017, 66, syw121.	2.7	29
3631	Eggshell palaeogenomics: Palaeognath evolutionary history revealed through ancient nuclear and mitochondrial DNA from Madagascan elephant bird (<i>Aepyornis</i> sp.) eggshell. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 151-163.	1.2	65
3632	Prenatal development supports a single origin of laryngeal echolocation in bats. <i>Nature Ecology and Evolution</i> , 2017, 1, 21.	3.4	43
3633	Comparative transcriptomics of elasmobranchs and teleosts highlight important processes in adaptive immunity and regional endothermy. <i>BMC Genomics</i> , 2017, 18, 87.	1.2	31
3634	Transcriptome analysis of four poplars exposed to continuous salinity stress. <i>Biochemical Systematics and Ecology</i> , 2017, 70, 311-319.	0.6	4
3635	Missing something? Codon aversion as a new character system in phylogenetics. <i>Cladistics</i> , 2017, 33, 545-556.	1.5	14
3636	Transcriptome profiling of the floating-leaved aquatic plant <i>Nymphoides peltata</i> in response to flooding stress. <i>BMC Genomics</i> , 2017, 18, 119.	1.2	8
3637	Genome-Wide Convergence during Evolution of Mangroves from Woody Plants. <i>Molecular Biology and Evolution</i> , 2017, 34, msw277.	3.5	43
3638	Relative benefits of amino acid, codon, degeneracy, DNA, and purine-pyrimidine character coding for phylogenetic analyses of exons. <i>Journal of Systematics and Evolution</i> , 2017, 55, 85-109.	1.6	24
3639	BrRxLR11 – a new phylogenetic marker with high resolution in the downy mildew genus <i>Bremia</i> and related genera. <i>Mycological Progress</i> , 2017, 16, 185-190.	0.5	7
3640	Possible Roles of New Mutations Shared by Asian and American Zika Viruses. <i>Molecular Biology and Evolution</i> , 2017, 34, msw270.	3.5	19
3641	Functional mutations in spike glycoprotein of Zaire ebolavirus associated with an increase in infection efficiency. <i>Genes To Cells</i> , 2017, 22, 148-159.	0.5	29
3642	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	13.7	332

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3644	Proteome evolution of deep-sea hydrothermal vent alvinellid polychaetes supports the ancestry of thermophily and subsequent adaptation to cold in some lineages. <i>Genome Biology and Evolution</i> , 2017, 9, evw298.	1.1	39
3645	Positive selection on sperm ion channels in a brooding brittle star: consequence of life-history traits evolution. <i>Molecular Ecology</i> , 2017, 26, 3744-3759.	2.0	20
3646	<i>Trpc2</i> pseudogenization dynamics in bats reveal ancestral vomeronasal signaling, then pervasive loss. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 923-935.	1.1	32
3647	Plant Actin-Depolymerizing Factors Possess Opposing Biochemical Properties Arising from Key Amino Acid Changes throughout Evolution. <i>Plant Cell</i> , 2017, 29, 395-408.	3.1	52
3648	Both mechanism and age of duplications contribute to biased gene retention patterns in plants. <i>BMC Genomics</i> , 2017, 18, 46.	1.2	30
3649	Evolution of cancer suppression as revealed by mammalian comparative genomics. <i>Current Opinion in Genetics and Development</i> , 2017, 42, 40-47.	1.5	49
3650	The fire ant social chromosome supergene variant <i>Sb</i> shows low diversity but high divergence from <i>Sb</i> . <i>Molecular Ecology</i> , 2017, 26, 2864-2879.	2.0	65
3651	Genetic Adaptation of Schizothoracine Fish to the Phased Uplifting of the Qinghai-Tibetan Plateau. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1267-1276.	0.8	29
3652	Dissection of genomic features and variations of three pathotypes of <i>Puccinia striiformis</i> through whole genome sequencing. <i>Scientific Reports</i> , 2017, 7, 42419.	1.6	55
3653	Concomitant loss of <i>NDH</i> complex-related genes within chloroplast and nuclear genomes in some orchids. <i>Plant Journal</i> , 2017, 90, 994-1006.	2.8	99
3654	Mitogenome evolution in Cephini (Hymenoptera: Cephidae): Evidence for parallel adaptive evolution. <i>Biochemical Systematics and Ecology</i> , 2017, 71, 137-146.	0.6	14
3655	Comparative Analyses of Selection Operating on Nontranslated Intergenic Regions of Diverse Bacterial Species. <i>Genetics</i> , 2017, 206, 363-376.	1.2	65
3656	Experimental Evolution of <i>Escherichia coli</i> Harboring an Ancient Translation Protein. <i>Journal of Molecular Evolution</i> , 2017, 84, 69-84.	0.8	40
3657	Molecular Convergent Evolution of the MYBPC2 Gene Among Three High-Elevation Amphibian Species. <i>Journal of Molecular Evolution</i> , 2017, 84, 139-143.	0.8	2
3658	Genomic changes associated with the evolutionary transition of an insect gut symbiont into a blood-borne pathogen. <i>ISME Journal</i> , 2017, 11, 1232-1244.	4.4	84
3659	Plastome phylogeny and early diversification of Brassicaceae. <i>BMC Genomics</i> , 2017, 18, 176.	1.2	137
3660	Epistatic interactions influence terrestrial-marine functional shifts in cetacean rhodopsin. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162743.	1.2	26

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3662	Functional roles of <i>Aves</i> class-specific cis-regulatory elements on macroevolution of bird-specific features. <i>Nature Communications</i> , 2017, 8, 14229.	5.8	61
3663	Selection maintains signaling function of a highly diverged intrinsically disordered region. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1450-E1459.	3.3	65
3664	Unusual evolutionary mechanisms to escape effector-triggered immunity in the fungal phytopathogen <i>Leptosphaeria maculans</i> . <i>Molecular Ecology</i> , 2017, 26, 2183-2198.	2.0	30
3665	Candidate genes for adaptation to an aquatic habitat recovered from <i>Ranunculus bungei</i> and <i>Ranunculus sceleratus</i> . <i>Biochemical Systematics and Ecology</i> , 2017, 71, 16-25.	0.6	0
3666	Phylointeractomics reconstructs functional evolution of protein binding. <i>Nature Communications</i> , 2017, 8, 14334.	5.8	26
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3668	Inactivation of the olfactory marker protein (OMP) gene in river dolphins and other odontocete cetaceans. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 375-387.	1.2	19
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3670	Evidence of neofunctionalization after the duplication of the highly conserved Polycomb group gene <i>Caf1-55</i> in the <i>obscura</i> group of <i>Drosophila</i> . <i>Scientific Reports</i> , 2017, 7, 40536.	1.6	4
3671	Plastomes of <i>Mimosoideae</i> : structural and size variation, sequence divergence, and phylogenetic implication. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	56
3672	Genome sequencing of an Indian peste des petits ruminants virus isolate, Izatnagar/94, and its implications for virus diversity, divergence and phylogeography. <i>Archives of Virology</i> , 2017, 162, 1677-1693.	0.9	23
3673	Susceptibility to type 2 diabetes may be modulated by haplotypes in <i>G6PC2</i> , a target of positive selection. <i>BMC Evolutionary Biology</i> , 2017, 17, 43.	3.2	14
3674	Genomic signatures of adaptation to wine biological ageing conditions in biofilm-forming flor yeasts. <i>Molecular Ecology</i> , 2017, 26, 2150-2166.	2.0	68
3675	Origin and diversification of leucine-rich repeat receptor-like protein kinase (LRR-RLK) genes in plants. <i>BMC Evolutionary Biology</i> , 2017, 17, 47.	3.2	211
3676	Rapid transcriptional plasticity of duplicated gene clusters enables a clonally reproducing aphid to colonise diverse plant species. <i>Genome Biology</i> , 2017, 18, 27.	3.8	624
3677	A novel male-specific SET domain-containing gene <i>setdm</i> identified from extra microchromosomes of gibel carp males. <i>Science Bulletin</i> , 2017, 62, 528-536.	4.3	19
3678	Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. <i>Nature Genetics</i> , 2017, 49, 765-772.	9.4	316

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3680	PosiGene: automated and easy-to-use pipeline for genome-wide detection of positively selected genes. <i>Nucleic Acids Research</i> , 2017, 45, e100-e100.	6.5	50
3681	The genome sequence of the wisent (<i>Bison bonasus</i>). <i>GigaScience</i> , 2017, 6, 1-5.	3.3	22
3682	Genetic Stability and Evolution of the <i>clpX</i> Allele, Used for <i>Listeria Sensu Stricto</i> Subtyping and Phylogenetic Inference. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	36
3683	Molecular evolution of the plastid genome during diversification of the cotton genus. <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 268-276.	1.2	52
3684	Invasion of Ancestral Mammals into Dim-light Environments Inferred from Adaptive Evolution of the Phototransduction Genes. <i>Scientific Reports</i> , 2017, 7, 46542.	1.6	39
3685	Molecular adaptation in the world's deepest-living animal: Insights from transcriptome sequencing of the hadal amphipod <i>Hirondellea gigas</i> . <i>Molecular Ecology</i> , 2017, 26, 3732-3743.	2.0	69
3686	Molecular evolutionary mechanisms driving functional diversification of β -glucosidase in Lepidoptera. <i>Scientific Reports</i> , 2017, 7, 45787.	1.6	14
3687	Hybrid de novo genome assembly of the Chinese herbal fleabane <i>Erigeron breviscapus</i> . <i>GigaScience</i> , 2017, 6, 1-7.	3.3	22
3688	StarBEAST2 Brings Faster Species Tree Inference and Accurate Estimates of Substitution Rates. <i>Molecular Biology and Evolution</i> , 2017, 34, 2101-2114.	3.5	371
3689	Multiple strong postmating and intrinsic postzygotic reproductive barriers isolate florally diverse species of <i>Jaltomata</i> (Solanaceae). <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1556-1571.	1.1	26
3690	Cis-Regulatory Divergence in Gene Expression between Two Thermally Divergent Yeast Species. <i>Genome Biology and Evolution</i> , 2017, 9, 1120-1129.	1.1	57
3691	Genetic basis for soma is present in undifferentiated volvocine green algae. <i>Journal of Evolutionary Biology</i> , 2017, 30, 1205-1218.	0.8	26
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3693	Superoxide dismutase 1 is positively selected to minimize protein aggregation in great apes. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 3023-3037.	2.4	16
3694	Insights into evolution in Andean <i>Polystichum</i> (Dryopteridaceae) from expanded understanding of the cytosolic phosphoglucose isomerase gene. <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 36-46.	1.2	5
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3696	Signals of selection in conditionally expressed genes in the diversification of three horned beetle species. <i>Journal of Evolutionary Biology</i> , 2017, 30, 1644-1657.	0.8	10

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3698	The egg coat zona pellucida 3 glycoprotein " evolution of its putative sperm-binding region in Old World murine rodents (Rodentia: Muridae). <i>Reproduction, Fertility and Development</i> , 2017, 29, 2376.	0.1	3
3699	Introgression and repeated co-option facilitated the recurrent emergence of C ₄ photosynthesis among close relatives. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1541-1555.	1.1	51
3700	Contrasting evolutionary genome dynamics between domesticated and wild yeasts. <i>Nature Genetics</i> , 2017, 49, 913-924.	9.4	340
3701	Interspecific Plastome Recombination Reflects Ancient Reticulate Evolution in <i>Picea</i> (Pinaceae). <i>Molecular Biology and Evolution</i> , 2017, 34, 1689-1701.	3.5	69
3702	Ancestral Haloalkane Dehalogenases Show Robustness and Unique Substrate Specificity. <i>ChemBioChem</i> , 2017, 18, 1448-1456.	1.3	45
3703	Evolution of full-length genomes of HBV quasispecies in sera of patients with a coexistence of HBsAg and anti-HBs antibodies. <i>Scientific Reports</i> , 2017, 7, 661.	1.6	18
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3705	Less effective selection leads to larger genomes. <i>Genome Research</i> , 2017, 27, 1016-1028.	2.4	75
3706	Evolution and Antiviral Specificities of Interferon-Induced Mx Proteins of Bats against Ebola, Influenza, and Other RNA Viruses. <i>Journal of Virology</i> , 2017, 91, .	1.5	53
3707	Effective estimation of the minimum number of amino acid residues required for functional divergence between duplicate genes. <i>Molecular Phylogenetics and Evolution</i> , 2017, 113, 126-138.	1.2	7
3708	Evolution, expression analysis, and functional verification of <i>Catharanthus roseus</i> RLK1-like kinase (CrRLK1L) family proteins in pear (<i>Pyrus bretschneideri</i>). <i>Genomics</i> , 2017, 109, 290-301.	1.3	25
3709	Expansion of the redox-sensitive proteome coincides with the plastid endosymbiosis. <i>Nature Plants</i> , 2017, 3, 17066.	4.7	26
3710	Transposable Element Misregulation Is Linked to the Divergence between Parental piRNA Pathways in <i>Drosophila</i> Hybrids. <i>Genome Biology and Evolution</i> , 2017, 9, 1450-1470.	1.1	26
3711	Gene Duplication Leads to Altered Membrane Topology of a Cytochrome P450 Enzyme in Seed Plants. <i>Molecular Biology and Evolution</i> , 2017, 34, 2041-2056.	3.5	20
3712	Decipher the ancestry of the plant-specific LBD gene family. <i>BMC Genomics</i> , 2017, 18, 951.	1.2	27
3713	Diversity and evolution of sex determination systems in terrestrial isopods. <i>Scientific Reports</i> , 2017, 7, 1084.	1.6	35
3714	Origin of an ancient hormone/receptor couple revealed by resurrection of an ancestral estrogen. <i>Science Advances</i> , 2017, 3, e1601778.	4.7	49

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3716	Inferring the evolutionary mechanism of the chloroplast genome size by comparing whole-chloroplast genome sequences in seed plants. <i>Scientific Reports</i> , 2017, 7, 1555.	1.6	99
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3719	Genome Mutational and Transcriptional Hotspots Are Traps for Duplicated Genes and Sources of Adaptations. <i>Genome Biology and Evolution</i> , 2017, 9, 1229-1240.	1.1	17
3720	How do seemingly non-vagile clades accomplish trans-marine dispersal? Trait and dispersal evolution in the landfowl (Aves: Galliformes). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170210.	1.2	45
3721	Extinction vs. Rapid Radiation: The Juxtaposed Evolutionary Histories of Coelotine Spiders Support the Eocene–Oligocene Orogenesis of the Tibetan Plateau. <i>Systematic Biology</i> , 2017, 66, 988-1006.	2.7	39
3722	Antagonistic evolution of an antibiotic and its molecular chaperone: how to maintain a vital ectosymbiosis in a highly fluctuating habitat. <i>Scientific Reports</i> , 2017, 7, 1454.	1.6	10
3723	Effects of gene choice, base composition and rate heterogeneity on inference and estimates of divergence times in cypriniform fishes. <i>Biological Journal of the Linnean Society</i> , 2017, 121, 319-339.	0.7	16
3724	Comparative genomic analysis of SET domain family reveals the origin, expansion, and putative function of the arthropod-specific SmydA genes as histone modifiers in insects. <i>GigaScience</i> , 2017, 6, 1-16.	3.3	19
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3726	Concerted Divergence after Gene Duplication in Polycomb Repressive Complexes. <i>Plant Physiology</i> , 2017, 174, 1192-1204.	2.3	11
3727	Measuring Natural Selection. <i>Methods in Molecular Biology</i> , 2017, 1525, 315-347.	0.4	3
3728	High adaptive variability and virus-driven selection on major histocompatibility complex (MHC) genes in invasive wild rabbits in Australia. <i>Biological Invasions</i> , 2017, 19, 1255-1271.	1.2	15
3729	Resolving interspecific relationships within evolutionarily young lineages using RNA-seq data: An example from <i>Pedicularis</i> section <i>Cyathophora</i> (Orobanchaceae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 345-355.	1.2	21
3730	Mitochondrial DNA diversity of present-day Aboriginal Australians and implications for human evolution in Oceania. <i>Journal of Human Genetics</i> , 2017, 62, 343-353.	1.1	24
3731	Unparalleled replacement of native mitochondrial genes by foreign homologs in a holoparasitic plant. <i>New Phytologist</i> , 2017, 214, 376-387.	3.5	73
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3734	Pneumococcal Capsule Synthesis Locus <i>cps</i> as Evolutionary Hotspot with Potential to Generate Novel Serotypes by Recombination. <i>Molecular Biology and Evolution</i> , 2017, 34, 2537-2554.	3.5	65
3735	Long-read sequencing uncovers the adaptive topography of a carnivorous plant genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4435-E4441.	3.3	95
3736	Towards Navigating the Minotaur's Labyrinth: Cryptic Diversity and Taxonomic Revision within the Speciose Genus <i>Hipposideros</i> (Hipposideridae). <i>Acta Chiropterologica</i> , 2017, 19, 1-18.	0.2	34
3737	A null model for microbial diversification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5414-E5423.	3.3	9
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3739	COMPASS: the COMPLETELY Arbitrary Sequence Simulator. <i>Bioinformatics</i> , 2017, 33, 3101-3103.	1.8	3
3740	Rapid Evolution of Ovarian-Biased Genes in the Yellow Fever Mosquito (<i>Aedes aegypti</i>). <i>Genetics</i> , 2017, 206, 2119-2137.	1.2	22
3741	Transcriptome of <i>Pterospermum kingtungense</i> provides implications on the mechanism underlying its rapid vegetative growth and limestone adaptation. <i>Scientific Reports</i> , 2017, 7, 3198.	1.6	5
3742	Evolution of nonspectral rhodopsin function at high altitudes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7385-7390.	3.3	37
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3744	Testing the molecular clock using mechanistic models of fossil preservation and molecular evolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170227.	1.2	51
3745	Identification, polymorphism and expression of MHC class II α in golden pompano, <i>Trachinotus ovatus</i> . <i>Fish and Shellfish Immunology</i> , 2017, 67, 55-65.	1.6	16
3746	Causes and evolutionary consequences of primordial germ-cell specification mode in metazoans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5784-5791.	3.3	50
3747	History cleans up messes: The impact of time in driving divergence and introgression in a tropical suture zone. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1888-1899.	1.1	17
3748	Lateral Gene Transfer Dynamics in the Ancient Bacterial Genus <i>Streptomyces</i> . <i>MBio</i> , 2017, 8, .	1.8	110
3749	ARA-PEPs: a repository of putative sORF-encoded peptides in <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , 2017, 18, 37.	1.2	44
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3752	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
3753	Comparative genome analysis of <i>Lactobacillus plantarum</i> GB-LP3 provides candidates of survival-related genetic factors. <i>Infection, Genetics and Evolution</i> , 2017, 53, 218-226.	1.0	4
3754	The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. <i>Nature</i> , 2017, 546, 148-152.	13.7	579
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3756	The draft genome of blunt snout bream (<i>Megalobrama amblycephala</i>) reveals the development of intermuscular bone and adaptation to herbivorous diet. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	95
3757	Local adaptation shapes pattern of mitochondrial population structure in <i>Sebastiscus marmoratus</i> . <i>Environmental Biology of Fishes</i> , 2017, 100, 763-774.	0.4	15
3758	Bacterial colonization and succession in a newly opened hospital. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	248
3759	The Genome of Medicinal Plant <i>Macleaya cordata</i> Provides New Insights into Benzylisoquinoline Alkaloids Metabolism. <i>Molecular Plant</i> , 2017, 10, 975-989.	3.9	116
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3762	The phylogeny and biogeography of <i>Hakea</i> (<i>Proteaceae</i>) reveals the role of biome shifts in a continental plant radiation. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1928-1943.	1.1	60
3763	<i>Phylogenomics.</i> , 2017, , .		47
3764	<i>Phylogenetic Analyses.</i> , 2017, , 143-172.		1
3765	Phylogeny and biogeography of the genus <i>Stevia</i> (<i>Asteraceae: Eupatorieae</i>): an example of diversification in the <i>Asteraceae</i> in the new world. <i>Journal of Plant Research</i> , 2017, 130, 953-972.	1.2	12
3766	Correlated evolutionary rates across genomic compartments in <i>Annonaceae</i> . <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 63-72.	1.2	13
3767	Inferring Rates and Length-Distributions of Indels Using Approximate Bayesian Computation. <i>Genome Biology and Evolution</i> , 2017, 9, 1280-1294.	1.1	7
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3770	Multiple gene movements into and out of haploid sex chromosomes. <i>Genome Biology</i> , 2017, 18, 104.	3.8	63
3771	Plant Argonaute Proteins. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	1
3772	Extreme Mitogenomic Variation in Natural Populations of Chaetognaths. <i>Genome Biology and Evolution</i> , 2017, 9, 1374-1384.	1.1	21
3773	Evolutionary and Functional Mitogenomics Associated With the Genetic Restoration of the Florida Panther. <i>Journal of Heredity</i> , 2017, 108, 449-455.	1.0	9
3774	Signatures of adaptive molecular evolution in American pikas (<i>Ochotona princeps</i>). <i>Journal of Mammalogy</i> , 2017, 98, 1156-1167.	0.6	7
3775	Purifying and Positive Selection Influence Patterns of Gene Loss and Gene Expression in the Evolution of a Plant Sex Chromosome System. <i>Molecular Biology and Evolution</i> , 2017, 34, 1140-1154.	3.5	50
3776	Mitochondrial Retroprocessing Promoted Functional Transfers of <i>rpl5</i> to the Nucleus in Grasses. <i>Molecular Biology and Evolution</i> , 2017, 34, 2340-2354.	3.5	22
3777	Rapid and Recent Evolution of LTR Retrotransposons Drives Rice Genome Evolution During the Speciation of AA-Genome <i>Oryza</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1875-1885.	0.8	60
3778	Phylogenetic and Evolutionary Analysis of Plant ARGONAUTES. <i>Methods in Molecular Biology</i> , 2017, 1640, 267-294.	0.4	9
3779	Diversity and evolution of plastomes in Saharan mimosoids: potential use for phylogenetic and population genetic studies. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	10
3780	Lipidome determinants of maximal lifespan in mammals. <i>Scientific Reports</i> , 2017, 7, 5.	1.6	60
3781	Adaptive evolution of insect selective excitatory \hat{I}^2 -type sodium channel neurotoxins from scorpion venom. <i>Peptides</i> , 2017, 92, 31-37.	1.2	2
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3783	Diverse genome organization following 13 independent mesopolyploid events in Brassicaceae contrasts with convergent patterns of gene retention. <i>Plant Journal</i> , 2017, 91, 3-21.	2.8	95
3784	Scallop genome provides insights into evolution of bilaterian karyotype and development. <i>Nature Ecology and Evolution</i> , 2017, 1, 120.	3.4	353
3785	Adaptation to deep-sea chemosynthetic environments as revealed by mussel genomes. <i>Nature Ecology and Evolution</i> , 2017, 1, 121.	3.4	250
3786	Comparative Sperm Proteomics in Mouse Species with Divergent Mating Systems. <i>Molecular Biology and Evolution</i> , 2017, 34, 1403-1416.	3.5	29

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3788	Evolutionary History of the Hymenoptera. Current Biology, 2017, 27, 1013-1018.	1.8	611
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3790	The first complete mitogenome of the South China deep-sea giant isopod <i>Bathynomus</i> sp. (Crustacea: Isopoda: Cirolanidae) allows insights into the early mitogenomic evolution of isopods. Ecology and Evolution, 2017, 7, 1869-1881.	0.8	32
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3804	Molecular evolution of pancreatic ribonuclease gene (<i>RNase1</i>) in Rodentia. Journal of Genetics and Genomics, 2017, 44, 219-222.	1.7	7

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3807	Comparative transcriptome analyses of flower development in four species of <i>Achimenes</i> (Gesneriaceae). <i>BMC Genomics</i> , 2017, 18, 240.	1.2	41
3808	Phylogenomic proximity and metabolic discrepancy of <i>Methanosarcina mazei</i> Go1 across methanosarcinal genomes. <i>BioSystems</i> , 2017, 155, 20-28.	0.9	11
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3814	Identification of positive selection in genes is greatly improved by using experimentally informed site-specific models. <i>Biology Direct</i> , 2017, 12, 1.	1.9	88
3815	Genome-Wide Survey of Genes Under Positive Selection in Avian Pathogenic <i>Escherichia coli</i> Strains. <i>Foodborne Pathogens and Disease</i> , 2017, 14, 245-252.	0.8	8
3816	Selection and genetic drift in captive versus wild populations: an assessment of neutral and adaptive (MHC-linked) genetic variation in wild and hatchery brown trout (<i>Salmo trutta</i>) populations. <i>Conservation Genetics</i> , 2017, 18, 1011-1022.	0.8	14
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3821	Evolutionary drivers of thermoadaptation in enzyme catalysis. <i>Science</i> , 2017, 355, 289-294.	6.0	147
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3830	Evolutionary dynamic of antigenic residues on influenza B hemagglutinin. <i>Virology</i> , 2017, 502, 84-96.	1.1	16
3831	Atypical Protein Phosphatase 2A Gene Families Do Not Expand via Paleopolyploidization. <i>Plant Physiology</i> , 2017, 173, 1283-1300.	2.3	46
3832	Characterization of <i>CYCLOIDEA</i> -like genes in Proteaceae, a basal eudicot family with multiple shifts in floral symmetry. <i>Annals of Botany</i> , 2017, 119, 367-378.	1.4	37
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3835	Zinc Cluster Transcription Factors Alter Virulence in <i>Candida albicans</i> . <i>Genetics</i> , 2017, 205, 559-576.	1.2	31
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3840	The onâ€œagain, offâ€œagain relationship between mitochondrial genomes and species boundaries. <i>Molecular Ecology</i> , 2017, 26, 2212-2236.	2.0	206

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3842	The genome draft of coconut (<i>Cocos nucifera</i>). <i>GigaScience</i> , 2017, 6, 1-11.	3.3	96
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3844	Generalist species drive microbial dispersion and evolution. <i>Nature Communications</i> , 2017, 8, 1162.	5.8	139
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3846	Evolution and Spatiotemporal Dynamics of Enterovirus A71 Subgenogroups in Vietnam. <i>Journal of Infectious Diseases</i> , 2017, 216, 1371-1379.	1.9	19
3847	Legume isoflavone synthase genes have evolved by whole-genome and local duplications yielding transcriptionally active paralogs. <i>Plant Science</i> , 2017, 264, 149-167.	1.7	13
3848	Selection on start codons in prokaryotes and potential compensatory nucleotide substitutions. <i>Scientific Reports</i> , 2017, 7, 12422.	1.6	43
3849	Maximum-likelihood approaches reveal signatures of positive selection in BMP15 and GDF9 genes modulating ovarian function in mammalian female fertility. <i>Ecology and Evolution</i> , 2017, 7, 8895-8902.	0.8	23
3850	A new recent genus and species of three-toed jerboas (Rodentia: Dipodinae) from China: A living fossil?. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 356-368.	0.6	12
3851	Genetic variants affecting equivalent protein family positions reflect human diversity. <i>Scientific Reports</i> , 2017, 7, 12771.	1.6	8
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3854	Rates of Molecular Evolution Suggest Natural History of Life History Traits and a Post-K-Pg Nocturnal Bottleneck of Placentals. <i>Current Biology</i> , 2017, 27, 3025-3033.e5.	1.8	51
3855	Effective purifying selection in ancient asexual oribatid mites. <i>Nature Communications</i> , 2017, 8, 873.	5.8	32
3856	Genomic divergence within non-photosynthetic cyanobacterial endosymbionts in rhopalodiacean diatoms. <i>Scientific Reports</i> , 2017, 7, 13075.	1.6	17
3857	Universal Patterns of Selection in Cancer and Somatic Tissues. <i>Cell</i> , 2017, 171, 1029-1041.e21.	13.5	1,085
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3865	Reciprocally Retained Genes in the Angiosperm Lineage Show the Hallmarks of Dosage Balance Sensitivity. Plant Cell, 2017, 29, 2766-2785.	3.1	81
3866	DNA helix: the importance of being AT-rich. Mammalian Genome, 2017, 28, 455-464.	1.0	18
3867	Genetic wealth, population health: Major histocompatibility complex variation in captive and wild ring-tailed lemurs (<i>Lemur catta</i>). Ecology and Evolution, 2017, 7, 7638-7649.	0.8	17
3868	Characterization of major histocompatibility complex class I, and class II DRB loci of captive and wild Indian leopards (<i>Panthera pardus fusca</i>). Genetica, 2017, 145, 541-558.	0.5	5
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3873	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. Science Advances, 2017, 3, e1700299.	4.7	142
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3878	The Adaptive Evolution Database (TAED): A New Release of a Database of Phylogenetically Indexed Gene Families from Chordates. <i>Journal of Molecular Evolution</i> , 2017, 85, 46-56.	0.8	5
3879	The repertoire of bitter taste receptor genes in Ovalentaria fish. <i>Environmental Biology of Fishes</i> , 2017, 100, 1489-1496.	0.4	1
3880	The draft genome assembly of <i>Rhododendron delavayi</i> Franch. var. <i>delavayi</i> . <i>GigaScience</i> , 2017, 6, 1-11.	3.3	64
3881	Ancestral resurrection of anthropoid estrogen receptor $\hat{1}^2$ demonstrates functional consequences of positive selection. <i>Molecular Phylogenetics and Evolution</i> , 2017, 117, 2-9.	1.2	1
3882	Inactivation of thermogenic UCP1 as a historical contingency in multiple placental mammal clades. <i>Science Advances</i> , 2017, 3, e1602878.	4.7	78
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3889	The <i>Apostasia</i> genome and the evolution of orchids. <i>Nature</i> , 2017, 549, 379-383.	13.7	305
3890	A biologist's guide to Bayesian phylogenetic analysis. <i>Nature Ecology and Evolution</i> , 2017, 1, 1446-1454.	3.4	154
3891	Mitogenome Sequencing in the Genus <i>Camelus</i> Reveals Evidence for Purifying Selection and Long-term Divergence between Wild and Domestic Bactrian Camels. <i>Scientific Reports</i> , 2017, 7, 9970.	1.6	45
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3894	Differential evolutionary patterns and expression levels between sex-specific and somatic tissue-specific genes in peanut. <i>Scientific Reports</i> , 2017, 7, 9016.	1.6	9

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3896	Complete Chloroplast Genome Sequence of <i>Decaisnea insignis</i> : Genome Organization, Genomic Resources and Comparative Analysis. <i>Scientific Reports</i> , 2017, 7, 10073.	1.6	68
3897	Recurrent horizontal transfer of arsenite methyltransferase genes facilitated adaptation of life to arsenic. <i>Scientific Reports</i> , 2017, 7, 7741.	1.6	60
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3910	Genome-wide survey indicates diverse physiological roles of the barley (<i>Hordeum vulgare</i> L.) calcium-dependent protein kinase genes. <i>Scientific Reports</i> , 2017, 7, 5306.	1.6	32
3911	Accelerated Evolution and Functional Divergence of the Dim Light Visual Pigment Accompanies Cichlid Colonization of Central America. <i>Molecular Biology and Evolution</i> , 2017, 34, 2650-2664.	3.5	39
3912	Large Variation in the Ratio of Mitochondrial to Nuclear Mutation Rate across Animals: Implications for Genetic Diversity and the Use of Mitochondrial DNA as a Molecular Marker. <i>Molecular Biology and Evolution</i> , 2017, 34, 2762-2772.	3.5	240

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4065	Draft genome of the Marco Polo Sheep (<i>Ovis ammon polii</i>). <i>GigaScience</i> , 2017, 6, 1-7.	3.3	25
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4067	Genome-Wide Analysis of the Sucrose Synthase Gene Family in Grape (<i>Vitis vinifera</i>): Structure, Evolution, and Expression Profiles. <i>Genes</i> , 2017, 8, 111.	1.0	56
4068	Genome-Wide Characterization and Expression Profiling of Sugar Transporter Family in the Whitefly, <i>Bemisia tabaci</i> (Gennadius) (Hemiptera: Aleyrodidae). <i>Frontiers in Physiology</i> , 2017, 8, 322.	1.3	15
4069	Completion of the Chloroplast Genomes of Five Chinese <i>Juglans</i> and Their Contribution to Chloroplast Phylogeny. <i>Frontiers in Plant Science</i> , 2016, 7, 1955.	1.7	110
4070	Comparative Analysis of Six <i>Lagerstroemia</i> Complete Chloroplast Genomes. <i>Frontiers in Plant Science</i> , 2017, 8, 15.	1.7	138
4071	Genome-Wide Dissection of the Heat Shock Transcription Factor Family Genes in <i>Arachis</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 106.	1.7	55
4072	Computational Identification of Amino-Acid Mutations that Further Improve the Activity of a Chalcone-Flavonone Isomerase from <i>Glycine max</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 248.	1.7	6
4073	Genome-Wide Investigation of WRKY Transcription Factors Involved in Terminal Drought Stress Response in Common Bean. <i>Frontiers in Plant Science</i> , 2017, 8, 380.	1.7	60
4074	New Insights on Leucine-Rich Repeats Receptor-Like Kinase Orthologous Relationships in Angiosperms. <i>Frontiers in Plant Science</i> , 2017, 08, 381.	1.7	54

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4076	Transcriptome Comparison Reveals the Adaptive Evolution of Two Contrasting Ecotypes of Zn/Cd Hyperaccumulator <i>Sedum alfredii</i> Hance. <i>Frontiers in Plant Science</i> , 2017, 8, 425.	1.7	19
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4082	Genome-Wide Identification and Functional Analysis of the Calcineurin B-like Protein and Calcineurin B-like Protein-Interacting Protein Kinase Gene Families in Turnip (<i>Brassica rapa</i> var. <i>rapa</i>). <i>Frontiers in Plant Science</i> , 2017, 8, 1191.	1.7	39
4083	Identification of Genes under Positive Selection Reveals Differences in Evolutionary Adaptation between Brown-Algal Species. <i>Frontiers in Plant Science</i> , 2017, 8, 1429.	1.7	17
4084	Genome-Wide Identification and Characterization of BrrTCP Transcription Factors in <i>Brassica rapa</i> ssp. <i>rapa</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1588.	1.7	32
4085	Comparative Analysis of the Complete Plastomes of <i>Apostasia wallichii</i> and <i>Neuwiedia singaporeana</i> (Apostasioideae) Reveals Different Evolutionary Dynamics of IR/SSC Boundary among Photosynthetic Orchids. <i>Frontiers in Plant Science</i> , 2017, 8, 1713.	1.7	29
4086	Evolution and Expansion of the Prokaryote-Like Lipoyxygenase Family in the Brown Alga <i>Saccharina japonica</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 2018.	1.7	23
4087	Genomic signature of highland adaptation in fish: a case study in Tibetan Schizothoracinae species. <i>BMC Genomics</i> , 2017, 18, 948.	1.2	26
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4089	Bioinformatic Analyses of Whole-Genome Sequence Data in a Public Health Laboratory. <i>Emerging Infectious Diseases</i> , 2017, 23, 1441-1445.	2.0	40
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4091	Evaluation of Shear Strength of RC Beams with Multiple Interfaces Formed before Initial Setting Using 3D Printing Technology. <i>Materials</i> , 2017, 10, 1349.	1.3	26
4092	Contrasting patterns of evolutionary constraint and novelty revealed by comparative sperm proteomic analysis in Lepidoptera. <i>BMC Genomics</i> , 2017, 18, 931.	1.2	18

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4094	Evidence of a Conserved Molecular Response to Selection for Increased Brain Size in Primates. <i>Genome Biology and Evolution</i> , 2017, 9, 700-713.	1.1	31
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4099	The All-Rounder <i>Sodalis</i> : A New Bacteriome-Associated Endosymbiont of the Lygaeoid Bug <i>Henestaris halophilus</i> (Heteroptera: Henestarinae) and a Critical Examination of Its Evolution. <i>Genome Biology and Evolution</i> , 2017, 9, 2893-2910.	1.1	65
4100	Gene Duplication Analysis Reveals No Ancient Whole Genome Duplication but Extensive Small-Scale Duplications during Genome Evolution and Adaptation of <i>Schistosoma mansoni</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 412.	1.8	9
4101	RNA-Seq Analysis of the Distylous Plant <i>Nymphoides peltata</i> Identified Ortholog Genes between Long- and Short-Styled Flowers. <i>Frontiers in Ecology and Evolution</i> , 2017, 5, .	1.1	4
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4105	Adaptive Evolution of Energy Metabolism-Related Genes in Hypoxia-Tolerant Mammals. <i>Frontiers in Genetics</i> , 2017, 8, 205.	1.1	34
4106	Genome-Wide Analyses Reveal Genes Subject to Positive Selection in <i>Pasteurella multocida</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 961.	1.5	36
4107	HIV Progression Depends on Codon and Amino Acid Usage Profile of Envelope Protein and Associated Host-Genetic Influence. <i>Frontiers in Microbiology</i> , 2017, 8, 1083.	1.5	16
4108	Comprehensive Analysis of Codon Usage Bias in Seven <i>Epichloa</i> Species and Their Peramine-Coding Genes. <i>Frontiers in Microbiology</i> , 2017, 8, 1419.	1.5	29
4109	SMRT Sequencing Revealed Mitogenome Characteristics and Mitogenome-Wide DNA Modification Pattern in <i>Ophiocordyceps sinensis</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1422.	1.5	67
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4112	Genomic Comparisons Reveal Microevolutionary Differences in <i>Mycobacterium abscessus</i> Subspecies. <i>Frontiers in Microbiology</i> , 2017, 8, 2042.	1.5	16
4113	The FOXP2-Driven Network in Developmental Disorders and Neurodegeneration. <i>Frontiers in Cellular Neuroscience</i> , 2017, 11, 212.	1.8	38
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4115	Complete Chloroplast Genome Sequence of <i>Coptis chinensis</i> Franch. and Its Evolutionary History. <i>BioMed Research International</i> , 2017, 2017, 1-7.	0.9	6
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4118	The genome of the Antarctic-endemic copepod, <i>Tigriopus kingsejongensis</i> . <i>GigaScience</i> , 2017, 6, 1-9.	3.3	12
4119	Comparative analyses of plastid genomes from fourteen Cornales species: inferences for phylogenetic relationships and genome evolution. <i>BMC Genomics</i> , 2017, 18, 956.	1.2	40
4120	Modular Organization of Residue-Level Contacts Shapes the Selection Pressure on Individual Amino Acid Sites of Ribosomal Proteins. <i>Genome Biology and Evolution</i> , 2017, 9, 916-931.	1.1	4
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4123	Common and phylogenetically widespread coding for peptides by bacterial small RNAs. <i>BMC Genomics</i> , 2017, 18, 553.	1.2	32
4124	Network Centrality Analysis in Fungi Reveals Complex Regulation of Lost and Gained Genes. <i>PLoS ONE</i> , 2017, 12, e0169459.	1.1	12
4125	Whole-genome duplication and molecular evolution in <i>Cornus</i> L. (Cornaceae) – Insights from transcriptome sequences. <i>PLoS ONE</i> , 2017, 12, e0171361.	1.1	17
4126	Comparative transcriptomics of <i>Entelegyne</i> spiders (Araneae, Entelegynae), with emphasis on molecular evolution of orphan genes. <i>PLoS ONE</i> , 2017, 12, e0174102.	1.1	8
4127	Comprehensive bioinformatics analysis of <i>Mycoplasma pneumoniae</i> genomes to investigate underlying population structure and type-specific determinants. <i>PLoS ONE</i> , 2017, 12, e0174701.	1.1	27
4128	The emerging GII.P16-GII.4 Sydney 2012 norovirus lineage is circulating worldwide, arose by late-2014 and contains polymerase changes that may increase virus transmission. <i>PLoS ONE</i> , 2017, 12, e0179572.	1.1	63

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4141	Evidence of high-altitude adaptation in the glyptosternoid fish, Creteuchiloglanis macropterus from the Nujiang River obtained through transcriptome analysis. BMC Evolutionary Biology, 2017, 17, 229.	3.2	33
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4146	Negative correlation between rates of molecular evolution and flowering cycles in temperate woody bamboos revealed by plastid phylogenomics. BMC Plant Biology, 2017, 17, 260.	1.6	27

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4148	Genome sequencing of the staple food crop white Guinea yam enables the development of a molecular marker for sex determination. <i>BMC Biology</i> , 2017, 15, 86.	1.7	114
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4151	New reference genome sequences of hot pepper reveal the massive evolution of plant disease-resistance genes by retroduplication. <i>Genome Biology</i> , 2017, 18, 210.	3.8	255
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4155	Natural Selection Drives Rapid Functional Evolution of Young <i>Drosophila</i> Duplicate Genes. <i>Molecular Biology and Evolution</i> , 2017, 34, 3089-3098.	3.5	39
4156	Duplications and Positive Selection Drive the Evolution of Parasitism-Associated Gene Families in the Nematode <i>Strongyloides papillosus</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 790-801.	1.1	24
4157	Genetic diversity of the nucleocapsid protein gene of hippeastrum chlorotic ringspot virus from <i>Hymenocallis littoralis</i> in southern China. <i>Acta Virologica</i> , 2017, 61, 116-122.	0.3	3
4158	Genetics of Cerebellar and Neocortical Expansion in Anthropoid Primates: A Comparative Approach. <i>Brain, Behavior and Evolution</i> , 2017, 89, 274-285.	0.9	21
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4160	FOXP in Tetrapoda: Intrinsically Disordered Regions, Short Linear Motifs and their evolutionary significance. <i>Genetics and Molecular Biology</i> , 2017, 40, 181-190.	0.6	3
4161	Evolution of Vertebrate Ryanodine Receptors Family in Relation to Functional Divergence and Conservation. <i>International Heart Journal</i> , 2017, 58, 969-977.	0.5	4
4162	Mutational Biases and GC-Biased Gene Conversion Affect GC Content in the Plastomes of <i>Dendrobium</i> Genus. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2307.	1.8	52
4163	Genome-wide signals of positive selection in stronglylocentrotid sea urchins. <i>BMC Genomics</i> , 2017, 18, 555.	1.2	11
4164	Genome-wide Identification and Expression Analysis of Amino Acid Transporters in the Whitefly, <i>Bemisia tabaci</i> (Gennadius). <i>International Journal of Biological Sciences</i> , 2017, 13, 735-747.	2.6	11

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4165	Transcriptome Analysis for Non-Model Organism: Current Status and Best-Practices. , 0, , .		10
4166	Northern Spotted Owl (<i>Strix occidentalis caurina</i>) Genome: Divergence with the Barred Owl (<i>Strix</i>) Tj ETQq1 1 0.784314 rgBT /Overlo 2522-2545.	1.1	27
4167	The Small Noncoding RNA Processing Machinery of Two Living Fossil Species, Lungfish and Coelacanth, Gives New Insights into the Evolution of the Argonaute Protein Family. <i>Genome Biology and Evolution</i> , 2017, 9, 438-453.	1.1	11
4168	Identification of possible evolutionary pathways of Plum pox virus and predicting amino acid residues of importance to host adaptation. <i>Acta Horticulturae</i> , 2017, , 107-116.	0.1	4
4169	Variation in the intensity of selection on codon bias over time causes contrasting patterns of base composition evolution in <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2017, 9, eww291.	1.1	38
4170	Genome-wide analysis of the <i>Solanum tuberosum</i> (potato) trehalose-6-phosphate synthase (TPS) gene family: evolution and differential expression during development and stress. <i>BMC Genomics</i> , 2017, 18, 926.	1.2	38
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4173	Patterns of Spontaneous Nucleotide Substitutions in Grape Processed Pseudogenes. <i>Diversity</i> , 2017, 9, 45.	0.7	3
4174	Molecular epidemiology of influenza A(H1N1)PDM09 hemagglutinin gene circulating in SÃ£o Paulo State , Brazil: 2016 anticipated influenza season. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , 2017, 59, e9.	0.5	7
4175	Encoding Data Using Biological Principles: The Multisample Variant Format for Phylogenomics and Population Genomics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1231-1238.	1.9	23
4176	The timescale of early land plant evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2274-E2283.	3.3	654
4177	Analysis of <i>RPA190</i> revealed multiple positively selected mutations associated with metalaxyl resistance in <i>Phytophthora infestans</i> . <i>Pest Management Science</i> , 2018, 74, 1916-1924.	1.7	20
4178	SubRecon: ancestral reconstruction of amino acid substitutions along a branch in a phylogeny. <i>Bioinformatics</i> , 2018, 34, 2297-2299.	1.8	4
4179	Anisogamy evolved with a reduced sex-determining region in volvocine green algae. <i>Communications Biology</i> , 2018, 1, 17.	2.0	43
4180	The Rate of Evolution of Postmating-Prezygotic Reproductive Isolation in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2018, 35, 312-334.	3.5	82
4181	Whole genome diversity of inherited chromosomally integrated HHV-6 derived from healthy individuals of diverse geographic origin. <i>Scientific Reports</i> , 2018, 8, 3472.	1.6	26
4182	Shifts in Selective Pressures on Snake Phototransduction Genes Associated with Photoreceptor Transmutation and Dim-Light Ancestry. <i>Molecular Biology and Evolution</i> , 2018, 35, 1376-1389.	3.5	26

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4184	Habitat-driven diversification, hybridization and cryptic diversity in the Fork-tailed Drongo (Passeriformes: Dicruridae: <i>Dicrurus adsimilis</i>). <i>Zoologica Scripta</i> , 2018, 47, 266-284.	0.7	9
4185	Climate-driven range shifts of the king penguin in a fragmented ecosystem. <i>Nature Climate Change</i> , 2018, 8, 245-251.	8.1	95
4186	Whole-Genome Analysis Illustrates Global Clonal Population Structure of the Ubiquitous Dermatophyte Pathogen <i>Trichophyton rubrum</i>. <i>Genetics</i> , 2018, 208, 1657-1669.	1.2	48
4187	Functional divergence of duplicate genes several million years after gene duplication in Arabidopsis. <i>DNA Research</i> , 2018, 25, 327-339.	1.5	9
4188	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
4189	Substrate preferences of long-chain acyl-CoA synthetase and diacylglycerol acyltransferase contribute to enrichment of flax seed oil with Ω -3 linolenic acid. <i>Biochemical Journal</i> , 2018, 475, 1473-1489.	1.7	36
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4191	Isolation and characterization of the major histocompatibility complex DQA1 and DQA2 genes in gayal (<i>Bos frontalis</i>). <i>Journal of Genetics</i> , 2018, 97, 121-126.	0.4	5
4192	Large Scale Analyses and Visualization of Adaptive Amino Acid Changes Projects. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018, 10, 24-32.	2.2	14
4193	Cladogenesis and Genomic Streamlining in Extracellular Endosymbionts of Tropical Stink Bugs. <i>Genome Biology and Evolution</i> , 2018, 10, 680-693.	1.1	21
4194	Complete avian malaria parasite genomes reveal features associated with lineage-specific evolution in birds and mammals. <i>Genome Research</i> , 2018, 28, 547-560.	2.4	78
4195	Mitochondrial phylogeny, divergence history and high-altitude adaptation of grassland caterpillars (Lepidoptera: Lymantriinae: Gynaephora) inhabiting the Tibetan Plateau. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 116-124.	1.2	43
4196	Genetic signatures of microbial altruism and cheating in social amoebas in the wild. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3096-3101.	3.3	31
4197	FasParser2: a graphical platform for batch manipulation of tremendous amount of sequence data. <i>Bioinformatics</i> , 2018, 34, 2493-2495.	1.8	17
4198	Draft genome of the milu (<i>Elaphurus davidianus</i>). <i>GigaScience</i> , 2018, 7, .	3.3	22
4199	Draft genome sequence of <i>Camellia sinensis</i> var. <i>sinensis</i> provides insights into the evolution of the tea genome and tea quality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4151-E4158.	3.3	730
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4202	Population genetics, phylogenomics and hybrid speciation of <i>Juglans</i> in China determined from whole chloroplast genomes, transcriptomes, and genotyping-by-sequencing (GBS). <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 250-265.	1.2	78
4203	Selection outweighs drift at a fine scale: Lack of MHC differentiation within a family living lizard across geographically close but disconnected rocky outcrops. <i>Molecular Ecology</i> , 2018, 27, 2204-2214.	2.0	9
4204	Demography or selection on linked cultural traits or genes? Investigating the driver of low mtDNA diversity in the sperm whale using complementary mitochondrial and nuclear genome analyses. <i>Molecular Ecology</i> , 2018, 27, 2604-2619.	2.0	24
4205	Functional relevance of synonymous alleles reflected in allele rareness in the population. <i>Genomics</i> , 2018, 110, 347-354.	1.3	4
4206	Comparative chloroplast genomics between the invasive weed <i>Mikania micrantha</i> and its indigenous congener <i>Mikania cordata</i> : Structure variation, identification of highly divergent regions, divergence time estimation, and phylogenetic analysis. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 181-195.	1.2	19
4207	Evolution of cyclohexadienyl dehydratase from an ancestral solute-binding protein. <i>Nature Chemical Biology</i> , 2018, 14, 542-547.	3.9	79
4208	Time-calibrated phylogenomics of the porcine epidemic diarrhea virus: genome-wide insights into the spatio-temporal dynamics. <i>Genes and Genomics</i> , 2018, 40, 825-834.	0.5	4
4209	The <i>Gastrodia elata</i> genome provides insights into plant adaptation to heterotrophy. <i>Nature Communications</i> , 2018, 9, 1615.	5.8	170
4210	The ash dieback invasion of Europe was founded by two genetically divergent individuals. <i>Nature Ecology and Evolution</i> , 2018, 2, 1000-1008.	3.4	82
4211	Distinguishing Among Evolutionary Forces Acting on Genome-Wide Base Composition: Computer Simulation Analysis of Approximate Methods for Inferring Site Frequency Spectra of Derived Mutations. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1755-1769.	0.8	0
4212	Tracking the Rules of Transmission and Introgression with Networks. <i>Microbiology Spectrum</i> , 2018, 6, .	1.2	3
4213	Comparative genome and transcriptome analysis reveal the medicinal basis and environmental adaptation of artificially cultivated <i>Taiwanofungus camphoratus</i> . <i>Mycological Progress</i> , 2018, 17, 871-883.	0.5	9
4214	Consequences of Asexuality in Natural Populations: Insights from Stick Insects. <i>Molecular Biology and Evolution</i> , 2018, 35, 1668-1677.	3.5	63
4215	Introduction of Viral Hemorrhagic Septicemia Virus into Freshwater Cultured Rainbow Trout Is Followed by Bursts of Adaptive Evolution. <i>Journal of Virology</i> , 2018, 92, .	1.5	22
4216	Phylogeny, evolution and mitochondrial gene order rearrangement in scale worms (Aphroditiformia.) <i>Tj ETQq1 1 0.784314 rgBT /Over</i>	1.2	67
4217	Genetic Variation of <i>Candidatus</i> <i>Liberibacter solanacearum</i> ™ Haplotype C and Identification of a Novel Haplotype from <i>Trioza urticae</i> and Stinging Nettle. <i>Phytopathology</i> , 2018, 108, 925-934.	1.1	65
4218	Phylotranscriptomic analysis and genome evolution of the Cyripedioideae (Orchidaceae). <i>American Journal of Botany</i> , 2018, 105, 631-640.	0.8	25

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4221	Genome and evolution of the shade-requiring medicinal herb <i>Panax ginseng</i> . Plant Biotechnology Journal, 2018, 16, 1904-1917.	4.1	136
4222	Genetic footprints of adaptive divergence in the bracovirus of <i>Cotesia sesamiae</i> identified by targeted resequencing. Molecular Ecology, 2018, 27, 2109-2123.	2.0	23
4223	Retained duplications and deletions of CYP2C genes among primates. Molecular Phylogenetics and Evolution, 2018, 125, 204-212.	1.2	3
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4225	The evolution of immunity in relation to colonization and migration. Nature Ecology and Evolution, 2018, 2, 841-849.	3.4	56
4226	Recognition of the polycistronic nature of human genes is critical to understanding the genotype-phenotype relationship. Genome Research, 2018, 28, 609-624.	2.4	54
4227	Genome evolution across 1,011 <i>Saccharomyces cerevisiae</i> isolates. Nature, 2018, 556, 339-344.	13.7	952
4228	Genetic diversification of chemokine CXCL16 and its receptor CXCR6 in primates. Developmental and Comparative Immunology, 2018, 85, 86-94.	1.0	3
4229	Genome wide analysis of the transition to pathogenic lifestyles in Magnaporthales fungi. Scientific Reports, 2018, 8, 5862.	1.6	28
4230	New Methods for Inferring the Distribution of Fitness Effects for INDELs and SNPs. Molecular Biology and Evolution, 2018, 35, 1536-1546.	3.5	25
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4233	Draft genomes of two blister beetles <i>Hycleus cichorii</i> and <i>Hycleus phaleratus</i> . GigaScience, 2018, 7, 1-7.	3.3	30
4234	Divergent Selection of Pattern Recognition Receptors in Mammals with Different Ecological Characteristics. Journal of Molecular Evolution, 2018, 86, 138-149.	0.8	22
4235	Gene duplicates resolving sexual conflict rapidly evolved essential gametogenesis functions. Nature Ecology and Evolution, 2018, 2, 705-712.	3.4	68
4236	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. Nature Ecology and Evolution, 2018, 2, 659-668.	3.4	124

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4238	The genomes of two <i>Eutrema</i> species provide insight into plant adaptation to high altitudes. <i>DNA Research</i> , 2018, 25, 307-315.	1.5	38
4239	Constraining uncertainty in the timescale of angiosperm evolution and the veracity of a Cretaceous Terrestrial Revolution. <i>New Phytologist</i> , 2018, 218, 819-834.	3.5	149
4240	Divergent and parallel routes of biochemical adaptation in high-altitude passerine birds from the Qinghai-Tibet Plateau. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1865-1870.	3.3	74
4241	Codon usage variation of Zika virus: The potential roles of NS2B and NS4A in its global pandemic. <i>Virus Research</i> , 2018, 247, 71-83.	1.1	7
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4243	A Comprehensive and Dated Phylogenomic Analysis of Butterflies. <i>Current Biology</i> , 2018, 28, 770-778.e5.	1.8	249
4244	Salt and drought stress and ABA responses related to bZIP genes from <i>V. radiata</i> and <i>V. angularis</i> . <i>Gene</i> , 2018, 651, 152-160.	1.0	43
4245	Multiple losses of photosynthesis and convergent reductive genome evolution in the colourless green algae <i>Prototheca</i> . <i>Scientific Reports</i> , 2018, 8, 940.	1.6	46
4246	The State of Software for Evolutionary Biology. <i>Molecular Biology and Evolution</i> , 2018, 35, 1037-1046.	3.5	36
4247	Greenâ€shifting of <scp>SWS</scp>2A opsin sensitivity and loss of function of <scp>RH</scp>2â€A opsin in flounders, genus <i>Verasper</i>. <i>Ecology and Evolution</i> , 2018, 8, 1399-1410.	0.8	15
4248	Arms race of temporal partitioning between carnivorous and herbivorous mammals. <i>Scientific Reports</i> , 2018, 8, 1713.	1.6	35
4249	Comparative Genomics Reveals Accelerated Evolution in Conserved Pathways during the Diversification of Anole Lizards. <i>Genome Biology and Evolution</i> , 2018, 10, 489-506.	1.1	43
4250	Positively Selected Effector Genes and Their Contribution to Virulence in the Smut Fungus <i>Sporisorium reilianum</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 629-645.	1.1	48
4251	Does the Genetic Feature of the Chinese Tree Shrew (<i>Tupaia belangeri chinensis</i>) Support Its Potential as a Viable Model for Alzheimerâ€™s Disease Research?. <i>Journal of Alzheimer's Disease</i> , 2018, 61, 1015-1028.	1.2	25
4252	The mitochondrial genome of red-necked phalarope <i>Phalaropus lobatus</i> (Charadriiformes): Tj ETQq1 1 0.784314 rgBT _{0.5} /Overlock 10 Tf 50		
4253	The characterization of the circadian clock in the olive fly <i>Bactrocera oleae</i> (Diptera: Tephritidae) reveals a <i>Drosophila</i> -like organization. <i>Scientific Reports</i> , 2018, 8, 816.	1.6	13
4254	Evidence of Adaptive Evolution and Relaxed Constraints in Sex-Biased Genes of South American and West Indies Fruit Flies (Diptera: Tephritidae). <i>Genome Biology and Evolution</i> , 2018, 10, 380-395.	1.1	11

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4257	Human-Specific Mutations and Positively Selected Sites in MARCO Confer Functional Changes. <i>Molecular Biology and Evolution</i> , 2018, 35, 440-450.	3.5	11
4258	Evolutionary Epigenomics of Retrotransposon-Mediated Methylation Spreading in Rice. <i>Molecular Biology and Evolution</i> , 2018, 35, 365-382.	3.5	44
4259	Growing old, yet staying young: The role of telomeres in bats' exceptional longevity. <i>Science Advances</i> , 2018, 4, eaao0926.	4.7	120
4260	Evolution of methicillin-resistant <i>Staphylococcus aureus</i> : Evidence of positive selection in a penicillin-binding protein (PBP) 2a coding gene <i>mecA</i> . <i>Infection, Genetics and Evolution</i> , 2018, 59, 16-22.	1.0	20
4261	Draft genome sequence of ramie, <i>Boehmeria nivea</i> (L.) Gaudich. <i>Molecular Ecology Resources</i> , 2018, 18, 639-645.	2.2	46
4262	A novel chloroplast gene reported for flagellate plants. <i>American Journal of Botany</i> , 2018, 105, 117-121.	0.8	9
4263	De novo assembly and characterization of the <i>Hucho taimen</i> transcriptome. <i>Ecology and Evolution</i> , 2018, 8, 1271-1285.	0.8	8
4264	Genome and secretome analysis of <i>Pochonia chlamydosporia</i> provide new insight into egg-parasitic mechanisms. <i>Scientific Reports</i> , 2018, 8, 1123.	1.6	20
4265	Solution structure of sperm lysin yields novel insights into molecular dynamics of rapid protein evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1310-1315.	3.3	14
4266	DNA methylation changes and evolution of RNA-based duplication in <i>Sus scrofa</i> : based on a two-step strategy. <i>Epigenomics</i> , 2018, 10, 199-218.	1.0	6
4267	Phylogenetic Distribution of CMP-Neu5Ac Hydroxylase (CMAH), the Enzyme Synthetizing the Proinflammatory Human Xenoantigen Neu5Gc. <i>Genome Biology and Evolution</i> , 2018, 10, 207-219.	1.1	62
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4269	Unbiased Estimate of Synonymous and Nonsynonymous Substitution Rates with Nonstationary Base Composition. <i>Molecular Biology and Evolution</i> , 2018, 35, 734-742.	3.5	43
4270	Linkage between contextual factors, knowledge-sharing mediums, and behaviour: Moderating effect of knowledge-sharing intentions. <i>Knowledge and Process Management</i> , 2018, 25, 31-40.	2.9	9
4271	Lack of evidence for selection favouring MHC haplotypes that combine high functional diversity. <i>Heredity</i> , 2018, 120, 396-406.	1.2	14
4272	Evolutionary analyses of the avirulence effector <i>AvrStb6</i> in global populations of <i>Zymoseptoria tritici</i> identify candidate amino acids involved in recognition. <i>Molecular Plant Pathology</i> , 2018, 19, 1836-1846.	2.0	30

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4274	The pomegranate (<i>Punica granatum</i> L.) genome provides insights into fruit quality and ovule developmental biology. <i>Plant Biotechnology Journal</i> , 2018, 16, 1363-1374.	4.1	115
4275	Slow evolution of sex-biased genes in the reproductive tissue of the dioecious plant <i>Salix viminalis</i> . <i>Molecular Ecology</i> , 2018, 27, 694-708.	2.0	37
4276	Rapid Gene Family Evolution of a Nematode Sperm Protein Despite Sequence Hyper-conservation. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 353-362.	0.8	10
4277	Genome-wide searches and molecular analyses highlight the unique evolutionary path of flavone synthase I (FNSI) in Apiaceae. <i>Genome</i> , 2018, 61, 103-109.	0.9	7
4278	Comparative Genomics in <i>Drosophila</i> . <i>Methods in Molecular Biology</i> , 2018, 1704, 433-450.	0.4	1
4279	Selective pressure on the protein-coding genes of the pufferfish is correlated with phenotypic traits. <i>Marine Genomics</i> , 2018, 37, 182-186.	0.4	1
4280	Genomic evidence of gene duplication and adaptive evolution of Toll like receptors (TLR2 and TLR4) in reptiles. <i>International Journal of Biological Macromolecules</i> , 2018, 109, 698-703.	3.6	14
4281	The Long Intergenic Noncoding RNA (LincRNA) Landscape of the Soybean Genome. <i>Plant Physiology</i> , 2018, 176, 2133-2147.	2.3	88
4282	Molecular cloning and characterization of APOBEC3 family in tree shrew. <i>Gene</i> , 2018, 646, 143-152.	1.0	6
4283	Coelacanth-specific adaptive genes give insights into primitive evolution for water-to-land transition of tetrapods. <i>Marine Genomics</i> , 2018, 38, 89-95.	0.4	1
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4285	Speciation Generates Mosaic Genomes in Kangaroos. <i>Genome Biology and Evolution</i> , 2018, 10, 33-44.	1.1	26
4286	Comparative genomic analyses reveal the features for adaptation to nematodes in fungi. <i>DNA Research</i> , 2018, 25, 245-256.	1.5	28
4287	Phylogenomic Perspective on the Relationships and Evolutionary History of the Major Otocephalan Lineages. <i>Scientific Reports</i> , 2018, 8, 205.	1.6	21
4288	Phylogeographical study reveals high genetic diversity in a widespread desert rodent, <i>Dipus sagitta</i> (Dipodidae: Rodentia). <i>Biological Journal of the Linnean Society</i> , 2018, 123, 445-462.	0.7	18
4289	A Molecular Portrait of De Novo Genes in Yeasts. <i>Molecular Biology and Evolution</i> , 2018, 35, 631-645.	3.5	106
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4292	Positive selection on the mitochondrial <i>ATP synthase 6</i> and the <i>NADH dehydrogenase 2</i> genes across 22 hare species (genus <i>Lepus</i>). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 428-443.	0.6	8
4293	A Single Mutation Unlocks Cascading Exaptations in the Origin of a Potent Pitviper Neurotoxin. <i>Molecular Biology and Evolution</i> , 2018, 35, 887-898.	3.5	26
4294	Information Criteria for Comparing Partition Schemes. <i>Systematic Biology</i> , 2018, 67, 616-632.	2.7	17
4295	Sooty mangabey genome sequence provides insight into AIDS resistance in a natural SIV host. <i>Nature</i> , 2018, 553, 77-81.	13.7	81
4296	AMD1 mRNA employs ribosome stalling as a mechanism for molecular memory formation. <i>Nature</i> , 2018, 553, 356-360.	13.7	63
4297	Origin and Evolution of the Bartonella Gene Transfer Agent. <i>Molecular Biology and Evolution</i> , 2018, 35, 451-464.	3.5	24
4298	Evolution of Acidic Mammalian Chitinase Genes (CHIA) Is Related to Body Mass and Insectivory in Primates. <i>Molecular Biology and Evolution</i> , 2018, 35, 607-622.	3.5	51
4299	Transcriptome sequence-based phylogeny of chalcidoid wasps (Hymenoptera: Chalcidoidea) reveals a history of rapid radiations, convergence, and evolutionary success. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 286-296.	1.2	83
4300	Insufficient power of mitogenomic data in resolving the auchenorrhynchan monophyly. <i>Zoological Journal of the Linnean Society</i> , 2018, 183, 776-790.	1.0	22
4301	The complete mitochondrial genome of Huananpotamon lichuanense (Decapoda: Brachyura) with phylogenetic implications for freshwater crabs. <i>Gene</i> , 2018, 646, 217-226.	1.0	20
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4303	Extreme sensitivity to ultraviolet light in the fungal pathogen causing white-nose syndrome of bats. <i>Nature Communications</i> , 2018, 9, 35.	5.8	56
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4305	Recombinational DSBs-intersected genes converge on specific disease- and adaptability-related pathways. <i>Bioinformatics</i> , 2018, 34, 3421-3426.	1.8	1
4306	Influence of Effective Population Size on Genes under Varying Levels of Selection Pressure. <i>Genome Biology and Evolution</i> , 2018, 10, 756-762.	1.1	4
4307	Quantifying the Evolutionary Conservation of Genes Encoding Multidrug Efflux Pumps in the ESKAPE Pathogens To Identify Antimicrobial Drug Targets. <i>MSystems</i> , 2018, 3, .	1.7	20
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4310	Lineage-specific duplications of NBS-LRR genes occurring before the divergence of six <i>Fragaria</i> species. <i>BMC Genomics</i> , 2018, 19, 128.	1.2	27
4311	Evolutionary analysis of mitochondrially encoded proteins of toad-headed lizards, <i>Phrynocephalus</i> , along an altitudinal gradient. <i>BMC Genomics</i> , 2018, 19, 185.	1.2	19
4312	The unique evolutionary pattern of the Hydroxyproline-rich glycoproteins superfamily in Chinese white pear (<i>Pyrus bretschneideri</i>). <i>BMC Plant Biology</i> , 2018, 18, 36.	1.6	6
4313	The mining and evolutionary investigation of AP2/ERF genes in pear (<i>Pyrus</i>). <i>BMC Plant Biology</i> , 2018, 18, 46.	1.6	41
4314	The Antarctic sea ice alga <i>Chlamydomonas</i> sp. ICE-L provides insights into adaptive patterns of chloroplast evolution. <i>BMC Plant Biology</i> , 2018, 18, 53.	1.6	22
4315	Madagascar ground gecko genome analysis characterizes asymmetric fates of duplicated genes. <i>BMC Biology</i> , 2018, 16, 40.	1.7	49
4316	Comparative transcriptome reveal the potential adaptive evolutionary genes in <i>Andrias davidianus</i> . <i>Hereditas</i> , 2018, 155, 18.	0.5	4
4317	Signatures of historical selection on MHC reveal different selection patterns in the moor frog (<i>Rana</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.2	17
4318	Adaptive evolution of osmoregulatory-related genes provides insight into salinity adaptation in Chinese mitten crab, <i>Eriocheir sinensis</i> . <i>Genetica</i> , 2018, 146, 303-311.	0.5	14
4319	Evolutionary analysis of the carnitine- and choline acyltransferases suggests distinct evolution of CPT2 versus CPT1 and related variants. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2018, 1863, 909-918.	1.2	4
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4321	The prevalence of terraced treescapes in analyses of phylogenetic data sets. <i>BMC Evolutionary Biology</i> , 2018, 18, 46.	3.2	13
4322	Tissue-Specific Transcriptome for <i>Poeciliopsis prolifica</i> Reveals Evidence for Genetic Adaptation Related to the Evolution of a Placental Fish. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2181-2192.	0.8	10
4323	Failure to Recover Major Events of Gene Flux in Real Biological Data Due to Method Misapplication. <i>Genome Biology and Evolution</i> , 2018, 10, 1198-1209.	1.1	4
4324	Signature of positive selection in mitochondrial DNA in <i>Cetartiodactyla</i> . <i>Genes and Genetic Systems</i> , 2018, 93, 65-73.	0.2	21
4325	Hurdles in the evolutionary epidemiology of <i>Angiostrongylus cantonensis</i> : Pseudogenes, incongruence between taxonomy and DNA sequence variants, and cryptic lineages. <i>Evolutionary Applications</i> , 2018, 11, 1257-1269.	1.5	14
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4328	A fungal avirulence factor encoded in a highly plastic genomic region triggers partial resistance to septoria tritici blotch. <i>New Phytologist</i> , 2018, 219, 1048-1061.	3.5	103
4329	Comparative transcriptomics and genomic patterns of discordance in Capsiceae (Solanaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 293-302.	1.2	15
4330	H1N1 seasonal influenza virus evolutionary rate changed over time. <i>Virus Research</i> , 2018, 250, 43-50.	1.1	4
4331	DNA Conformation Induces Adaptable Binding by Tandem Zinc Finger Proteins. <i>Cell</i> , 2018, 173, 221-233.e12.	13.5	52
4332	Expansion of cap superfamily proteins in the genome of <i>Mesocestoides corti</i> : An extreme case of a general bilaterian trend. <i>Gene Reports</i> , 2018, 11, 110-120.	0.4	5
4333	Molecular Footprints of Aquatic Adaptation Including Bone Mass Changes in Cetaceans. <i>Genome Biology and Evolution</i> , 2018, 10, 967-975.	1.1	23
4334	Evolution of Melanoma Antigen-A11 (MAGEA11) During Primate Phylogeny. <i>Journal of Molecular Evolution</i> , 2018, 86, 240-253.	0.8	6
4335	Multiple Factors Confounding Phylogenetic Detection of Selection on Codon Usage. <i>Molecular Biology and Evolution</i> , 2018, 35, 1463-1472.	3.5	10
4336	Phenomenological Load on Model Parameters Can Lead to False Biological Conclusions. <i>Molecular Biology and Evolution</i> , 2018, 35, 1473-1488.	3.5	23
4337	Genome-wide organization, evolutionary diversification of the COMMD family genes of amphioxus (<i>Branchiostoma belcheri</i>) with the possible role in innate immunity. <i>Fish and Shellfish Immunology</i> , 2018, 77, 31-39.	1.6	3
4338	Rapid regulatory evolution of a nonrecombining autosome linked to divergent behavioral phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2794-2799.	3.3	28
4339	Theoretical Foundation of the RelTime Method for Estimating Divergence Times from Variable Evolutionary Rates. <i>Molecular Biology and Evolution</i> , 2018, 35, 1770-1782.	3.5	164
4340	Out of Water: The Origin and Early Diversification of Plant <i>R</i> -Genes. <i>Plant Physiology</i> , 2018, 177, 82-89.	2.3	117
4341	Genome-wide identification, putative functionality and interactions between lncRNAs and miRNAs in Brassica species. <i>Scientific Reports</i> , 2018, 8, 4960.	1.6	37
4342	Comparative genomic analysis of <i>Lactobacillus plantarum</i> GB-LP4 and identification of evolutionarily divergent genes in high-osmolarity environment. <i>Genes and Genomics</i> , 2018, 40, 217-223.	0.5	12
4343	Comparative Transcriptomics Among Four White Pine Species. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1461-1474.	0.8	35
4344	Genome-wide analysis indicates diverse physiological roles of the turnip (<i>Brassica rapa</i> var. <i>rapa</i>) oligopeptide transporters gene family. <i>Plant Diversity</i> , 2018, 40, 57-67.	1.8	9

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4351	Adaptive evolution to a high purine and fat diet of carnivorans revealed by gut microbiomes and host genomes. <i>Environmental Microbiology</i> , 2018, 20, 1711-1722.	1.8	61
4352	Identification of key amino acid residues determining product specificity of 2,3-oxidosqualene cyclase in <i>Oryza</i> species. <i>New Phytologist</i> , 2018, 218, 1076-1088.	3.5	39
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4376	Functional divergence and comparative in silico study of Cas4 proteins of DUF83 class. <i>Journal of Molecular Recognition</i> , 2018, 31, e2694.	1.1	0
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4488	Convergent Plastome Evolution and Gene Loss in Holoparasitic <i>Lennoaceae</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 2663-2670.	1.1	19
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4492	Evolution of olfactory functions on the fire ant social chromosome. <i>Genome Biology and Evolution</i> , 2018, 10, 2947-2960.	1.1	12
4493	Comparative Transcriptomic Analysis of Embryo Implantation in Mice and Rats. <i>Cellular Physiology and Biochemistry</i> , 2018, 50, 668-678.	1.1	3
4494	Genomic insights into host adaptation between the wheat stripe rust pathogen (<i>Puccinia striiformis</i> f. Tj ETQq1 1 0.784314 rgBT /Over) 19, 664.	1.2	31
4495	Positive selection in coding regions and motif duplication in regulatory regions of bottlenose dolphin MHC class II genes. <i>PLoS ONE</i> , 2018, 13, e0203450.	1.1	20
4496	Factors driving effective population size and pan-genome evolution in bacteria. <i>BMC Evolutionary Biology</i> , 2018, 18, 153.	3.2	107
4497	Early Diverging Insect-Pathogenic Fungi of the Order Entomophthorales Possess Diverse and Unique Subtilisin-Like Serine Proteases. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3311-3319.	0.8	20
4498	Evolutionary Genetics of Hypoxia and Cold Tolerance in Mammals. <i>Journal of Molecular Evolution</i> , 2018, 86, 618-634.	0.8	15
4499	Resurrected Protein Interaction Networks Reveal the Innovation Potential of Ancient Whole-Genome Duplication. <i>Plant Cell</i> , 2018, 30, 2741-2760.	3.1	13
4500	Genome Sequence of Peacock Reveals the Peculiar Case of a Glittering Bird. <i>Frontiers in Genetics</i> , 2018, 9, 392.	1.1	32
4501	The Roles of Introgression and Climate Change in the Rise to Dominance of <i>Acropora</i> Corals. <i>Current Biology</i> , 2018, 28, 3373-3382.e5.	1.8	65
4502	Positive Selection in the Evolution of Mammalian CRISPs. <i>Journal of Molecular Evolution</i> , 2018, 86, 635-645.	0.8	6
4503	Evidence of the Red-Queen Hypothesis from Accelerated Rates of Evolution of Genes Involved in Biotic Interactions in <i>Pneumocystis</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 1596-1606.	1.1	9
4504	Mitochondrial and Plastid Genomes from Coralline Red Algae Provide Insights into the Incongruent Evolutionary Histories of Organelles. <i>Genome Biology and Evolution</i> , 2018, 10, 2961-2972.	1.1	29
4505	Metabolic determinants of enzyme evolution in a genome-scale bacterial metabolic network. <i>Genome Biology and Evolution</i> , 2018, 10, 3076-3088.	1.1	19
4506	Urban land transformations and its implication on tree abundance distribution and richness in Kumasi, Ghana. <i>Journal of Urban Ecology</i> , 2018, 4, .	0.6	6
4507	Evolutionary conservation of Y Chromosome ampliconic gene families despite extensive structural variation. <i>Genome Research</i> , 2018, 28, 1841-1851.	2.4	33
4508	WRKY transcription factors in legumes. <i>BMC Plant Biology</i> , 2018, 18, 243.	1.6	66

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4509	Species groups distributed across elevational gradients reveal convergent and continuous genetic adaptation to high elevations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10634-E10641.	3.3	57
4510	Divergent subgenome evolution after allopolyploidization in African clawed frogs (<i>Xenopus</i>). <i>Journal of Evolutionary Biology</i> , 2018, 31, 1945-1958.	0.8	13
4511	Testing the validity of two putative sympatric species from <i>Sinocyclocheilus</i> (Cypriniformes:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 T</i>	0.2	9
4512	Origin and spread of Thoroughbred racehorses inferred from complete mitochondrial genome sequences: Phylogenomic and Bayesian coalescent perspectives. <i>PLoS ONE</i> , 2018, 13, e0203917.	1.1	5
4513	Influenza Virus. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	10
4514	Genome-Wide Identification and Characterization of Aquaporins and Their Role in the Flower Opening Processes in Carnation (<i>Dianthus caryophyllus</i>). <i>Molecules</i> , 2018, 23, 1895.	1.7	42
4515	A Gene-Based Positive Selection Detection Approach to Identify Vaccine Candidates Using <i>Toxoplasma gondii</i> as a Test Case Protozoan Pathogen. <i>Frontiers in Genetics</i> , 2018, 9, 332.	1.1	17
4516	Molecular evolution of prolactin in Chiroptera: Accelerated evolution and a large insertion in vespertilionid bats. <i>General and Comparative Endocrinology</i> , 2018, 269, 102-111.	0.8	2
4517	Phylogenomics, biogeography, and adaptive radiation of grapes. <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 258-267.	1.2	56
4518	Comprehensive exploration of the enzymes catalysing oxygen-involved reactions and COGs relevant to bacterial oxygen utilization. <i>Environmental Microbiology</i> , 2018, 20, 3836-3850.	1.8	1
4519	Draft genome sequence of wild <i>Prunus yedoensis</i> reveals massive inter-specific hybridization between sympatric flowering cherries. <i>Genome Biology</i> , 2018, 19, 127.	3.8	89
4520	Positive and balancing selection on <i>SLC18A1</i> gene associated with psychiatric disorders and human-unique personality traits. <i>Evolution Letters</i> , 2018, 2, 499-510.	1.6	16
4521	Transcriptome assembly of <i>Modiolus modiolus</i> and comparative analysis with <i>Bathymodiolus platifrons</i> . <i>Acta Oceanologica Sinica</i> , 2018, 37, 38-45.	0.4	1
4522	Whole Genome Sequencing of the Pirarucu (<i>Arapaima gigas</i>) Supports Independent Emergence of Major Teleost Clades. <i>Genome Biology and Evolution</i> , 2018, 10, 2366-2379.	1.1	33
4523	Transcriptional fates of human-specific segmental duplications in brain. <i>Genome Research</i> , 2018, 28, 1566-1576.	2.4	54
4524	Factors Influencing Gene Family Size Variation Among Related Species in a Plant Family, Solanaceae. <i>Genome Biology and Evolution</i> , 2018, 10, 2596-2613.	1.1	54
4525	Lineage-specific duplication and adaptive evolution of bitter taste receptor genes in bats. <i>Molecular Ecology</i> , 2018, 27, 4475-4488.	2.0	19
4526	Molecular genetic and biochemical evidence for adaptive evolution of leaf abaxial epicuticular wax crystals in the genus <i>Lithocarpus</i> (Fagaceae). <i>BMC Plant Biology</i> , 2018, 18, 196.	1.6	5

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4527	Characterization and Expression Patterns of Auxin Response Factors in Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 1395.	1.7	40
4528	Symbiodinium genomes reveal adaptive evolution of functions related to coral-dinoflagellate symbiosis. <i>Communications Biology</i> , 2018, 1, 95.	2.0	154
4529	Positive selection drives the evolution of endocrine regulatory bone morphogenetic protein system in mammals. <i>Oncotarget</i> , 2018, 9, 18435-18445.	0.8	15
4530	Molecular evolution and functional divergence of alcohol dehydrogenases in animals, fungi and plants. <i>Genetics and Molecular Biology</i> , 2018, 41, 341-354.	0.6	16
4531	Reconfiguration of the plastid genome in <i>Lamprocapnos spectabilis</i> : IR boundary shifting, inversion, and intraspecific variation. <i>Scientific Reports</i> , 2018, 8, 13568.	1.6	43
4532	Genome-Wide Analysis Elucidates the Role of CONSTANS-like Genes in Stress Responses of Cotton. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2658.	1.8	14
4533	Control of yeast retrotransposons mediated through nucleoporin evolution. <i>PLoS Genetics</i> , 2018, 14, e1007325.	1.5	12
4534	Deciphering evolutionary dynamics of SWEET genes in diverse plant lineages. <i>Scientific Reports</i> , 2018, 8, 13440.	1.6	20
4535	Comparative genomics and transcriptomics of <i>Chrysolophus</i> provide insights into the evolution of complex plumage colouration. <i>GigaScience</i> , 2018, 7, .	3.3	14
4536	Chromosome-level reference genome and alternative splicing atlas of moso bamboo (<i>Phyllostachys</i>) Tj ETQq1 1 0.784314 rgBT /Overlanc	3.3	98
4537	Natatanuran frogs used the Indian Plate to step-stone disperse and radiate across the Indian Ocean. <i>National Science Review</i> , 2018, 6, 10-14.	4.6	34
4538	Comparative Analyses of Chloroplast Genomes of Cucurbitaceae Species: Lights into Selective Pressures and Phylogenetic Relationships. <i>Molecules</i> , 2018, 23, 2165.	1.7	21
4539	Genome-wide analysis of purple acid phosphatase structure and expression in ten vegetable species. <i>BMC Genomics</i> , 2018, 19, 646.	1.2	16
4540	Global Rate Variation in Bony Vertebrates. <i>Genome Biology and Evolution</i> , 2018, 10, 1803-1815.	1.1	28
4541	Testing the sensory trade-off hypothesis in New World bats. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181523.	1.2	50
4542	Order-level fern plastome phylogenomics: new insights from Hymenophyllales. <i>American Journal of Botany</i> , 2018, 105, 1545-1555.	0.8	30
4543	Software for Characterizing the Antigenic and Genetic Evolution of Human Influenza Viruses. <i>Methods in Molecular Biology</i> , 2018, 1836, 551-565.	0.4	1
4544	Faster Evolving Primate Genes Are More Likely to Duplicate. <i>Molecular Biology and Evolution</i> , 2018, 35, 107-118.	3.5	38

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4545	Fast Evolution and Lineage-Specific Gene Family Expansions of Aphid Salivary Effectors Driven by Interactions with Host-Plants. <i>Genome Biology and Evolution</i> , 2018, 10, 1554-1572.	1.1	67
4546	Genetic Analyses of Elys Mutations in <i>Drosophila</i> Show Maternal-Effect Lethality and Interactions with Nucleoporin Genes. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2421-2431.	0.8	5
4547	Evolutionary divergence of mitochondrial genomes in two <i>Tetranychus</i> species distributed across different climates. <i>Insect Molecular Biology</i> , 2018, 27, 698-709.	1.0	40
4548	Adaptive genomic evolution of opsins reveals that early mammals flourished in nocturnal environments. <i>BMC Genomics</i> , 2018, 19, 121.	1.2	22
4549	Improving cytidine and adenine base editors by expression optimization and ancestral reconstruction. <i>Nature Biotechnology</i> , 2018, 36, 843-846.	9.4	644
4550	Identification and expression of forkhead box genes in the Chinese giant salamander <i>Andrias davidianus</i> . <i>Reproduction, Fertility and Development</i> , 2018, 30, 634.	0.1	5
4551	Constant conflict between <i>Gypsy</i> LTR retrotransposons and CHH methylation within a stress-adapted mangrove genome. <i>New Phytologist</i> , 2018, 220, 922-935.	3.5	31
4552	Chitinase genes (<i>CHIA</i> s) provide genomic footprints of a post-Cretaceous dietary radiation in placental mammals. <i>Science Advances</i> , 2018, 4, eaar6478.	4.7	55
4553	Inferring the Probability of the Derived vs. the Ancestral Allelic State at a Polymorphic Site. <i>Genetics</i> , 2018, 209, 897-906.	1.2	83
4554	Signatures of diversifying selection and convergence acting on passerine Toll-like receptor 4 in an evolutionary context. <i>Molecular Ecology</i> , 2018, 27, 2871-2883.	2.0	11
4555	Multiple convergent supergene evolution events in mating-type chromosomes. <i>Nature Communications</i> , 2018, 9, 2000.	5.8	81
4556	Genomes of all known members of a <i>Plasmodium</i> subgenus reveal paths to virulent human malaria. <i>Nature Microbiology</i> , 2018, 3, 687-697.	5.9	129
4557	Evolution of Gustatory Receptor Gene Family Provides Insights into Adaptation to Diverse Host Plants in Nymphalid Butterflies. <i>Genome Biology and Evolution</i> , 2018, 10, 1351-1362.	1.1	28
4558	Biological Processes Modulating Longevity across Primates: A Phylogenetic Genome-Phenome Analysis. <i>Molecular Biology and Evolution</i> , 2018, 35, 1990-2004.	3.5	58
4559	Simultaneous radiation of bird and mammal lice following the K-Pg boundary. <i>Biology Letters</i> , 2018, 14, 20180141.	1.0	33
4560	Pan-genomic approach shows insight of genetic divergence and pathogenic-adaptation of <i>Pasteurella multocida</i> . <i>Gene</i> , 2018, 670, 193-206.	1.0	31
4561	Plastome sequences and exploration of tree-space help to resolve the phylogeny of riceflowers (Thymelaeaceae: <i>Pimelea</i>). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 156-167.	1.2	23
4562	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018, 361, .	6.0	339

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4563	Genome-wide analysis of ionotropic receptor gene repertoire in Lepidoptera with an emphasis on its functions of <i>Helicoverpa armigera</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2018, 99, 37-53.	1.2	63
4564	A Multispecific Investigation of the Metal Effect in Mammalian Odorant Receptors for Sulfur-Containing Compounds. <i>Chemical Senses</i> , 2018, 43, 357-366.	1.1	7
4565	Remodeling of the juvenile hormone pathway through caste-biased gene expression and positive selection along a gradient of termite eusociality. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2018, 330, 296-304.	0.6	17
4566	Smc5/6 Antagonism by HBx Is an Evolutionarily Conserved Function of Hepatitis B Virus Infection in Mammals. <i>Journal of Virology</i> , 2018, 92, .	1.5	34
4567	Genetic diversity of Cahi DRB and DQB genes of caprine MHC class II in Sirohi goat. <i>Journal of Genetics</i> , 2018, 97, 483-492.	0.4	12
4568	Comprehensive phylogeny of ray-finned fishes (Actinopterygii) based on transcriptomic and genomic data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6249-6254.	3.3	445
4569	Population genomic data reveal genes related to important traits of quail. <i>GigaScience</i> , 2018, 7, .	3.3	38
4570	De novo genome assembly of the red silk cotton tree (<i>Bombax ceiba</i>). <i>GigaScience</i> , 2018, 7, .	3.3	27
4571	Convergent evolution of tertiary structure in rhodopsin visual proteins from vertebrates and box jellyfish. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6201-6206.	3.3	19
4572	Estimation of universal and taxon-specific parameters of prokaryotic genome evolution. <i>PLoS ONE</i> , 2018, 13, e0195571.	1.1	5
4573	Egg Coat Proteins Across Metazoan Evolution. <i>Current Topics in Developmental Biology</i> , 2018, 130, 443-488.	1.0	19
4574	Characterization of bi-domain drosomycin-type antifungal peptides in nematodes: An example of convergent evolution. <i>Developmental and Comparative Immunology</i> , 2018, 87, 90-97.	1.0	5
4575	The Genome Sequences of 90 Mushrooms. <i>Scientific Reports</i> , 2018, 8, 9982.	1.6	73
4576	Evolutionary history of the genus <i>Sorex</i> (Soricidae, Eulipotyphla) as inferred from multigene data. <i>Zoologica Scripta</i> , 2018, 47, 518-538.	0.7	18
4577	Ancient Evolutionary Origin and Positive Selection of the Retroviral Restriction Factor <i>Fv1</i> in Muroid Rodents. <i>Journal of Virology</i> , 2018, 92, .	1.5	23
4578	Molecular phylogenetics and taxonomy of dwarf hamsters <i>Cricetus</i> Milne-Edwards, 1867 (Cricetidae). <i>Tj ETQq1 1,0,784314,rgBT /Qv</i>	0.2	24
4579	Evolution of the Biosynthetic Pathway for Cyanogenic Glucosides in Lepidoptera. <i>Journal of Molecular Evolution</i> , 2018, 86, 379-394.	0.8	10
4580	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	4.7	391

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4581	Genomic Variability among Field Isolates and Laboratory-Adapted Strains of <i>Leptospira borgpetersenii</i> Serovar Hardjo. <i>International Journal of Microbiology</i> , 2018, 2018, 1-12.	0.9	2
4582	Genomic evidence for genes encoding leucine-rich repeat receptors linked to resistance against the eukaryotic extra- and intracellular <i>Brassica napus</i> pathogens <i>Leptosphaeria maculans</i> and <i>Plasmodiophora brassicae</i> . <i>PLoS ONE</i> , 2018, 13, e0198201.	1.1	13
4583	Phylogenetic analysis of DNA sequences based on fractional Fourier transform. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2018, 509, 795-808.	1.2	0
4584	Serotonin, behavior, and natural selection in New World monkeys. <i>Journal of Evolutionary Biology</i> , 2018, 31, 1180-1192.	0.8	7
4585	The genome of tapeworm <i>Taenia multiceps</i> sheds light on understanding parasitic mechanism and control of coenurosis disease. <i>DNA Research</i> , 2018, 25, 499-510.	1.5	36
4586	Transcriptional and Translational Landscape of Equine Torovirus. <i>Journal of Virology</i> , 2018, 92, .	1.5	24
4587	De novo genome assembly of <i>Oryza granulata</i> reveals rapid genome expansion and adaptive evolution. <i>Communications Biology</i> , 2018, 1, 84.	2.0	24
4588	Evolution of circadian genes <i>PER</i> and <i>CRY</i> in subterranean rodents. <i>International Journal of Biological Macromolecules</i> , 2018, 118, 1400-1405.	3.6	9
4589	Population Genomics Provide Insights into the Evolution and Adaptation of the Eastern Honey Bee (<i>Apis cerana</i>). <i>Molecular Biology and Evolution</i> , 2018, 35, 2260-2271.	3.5	61
4590	Dissecting the basis of novel trait evolution in a radiation with widespread phylogenetic discordance. <i>Molecular Ecology</i> , 2018, 27, 3301-3316.	2.0	59
4591	Footprints of parasitism in the genome of the parasitic flowering plant <i>Cuscuta campestris</i> . <i>Nature Communications</i> , 2018, 9, 2515.	5.8	141
4592	Inverted formin 2 regulates intracellular trafficking, placentation, and pregnancy outcome. <i>ELife</i> , 2018, 7, .	2.8	11
4593	Incomplete lineage sorting impacts the inference of macroevolutionary regimes from molecular phylogenies when concatenation is employed: An analysis based on Cetacea. <i>Ecology and Evolution</i> , 2018, 8, 6965-6971.	0.8	5
4594	Concurrent Duplication of <i>Drosophila</i> <i>Cid</i> and <i>Cenp-C</i> Genes Resulted in Accelerated Evolution and Male Germline-Biased Expression of the New Copies. <i>Journal of Molecular Evolution</i> , 2018, 86, 353-364.	0.8	7
4595	Mitogenome phylogeographic analysis of a planktonic crustacean. <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 138-148.	1.2	36
4596	Co-speciation in bedbug <i>Wolbachia</i> parallel the pattern in nematode hosts. <i>Scientific Reports</i> , 2018, 8, 8797.	1.6	43
4597	An evolutionary transcriptomics approach links CD36 to membrane remodeling in replicative senescence. <i>Molecular Omics</i> , 2018, 14, 237-246.	1.4	12
4598	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , 2018, 50, 1289-1295.	9.4	335

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4599	Comparative genomic investigation of high-elevation adaptation in ectothermic snakes. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8406-8411.	3.3	119
4600	Molecular Adaptations for Sensing and Securing Prey and Insight into Amniote Genome Diversity from the Garter Snake Genome. Genome Biology and Evolution, 2018, 10, 2110-2129.	1.1	72
4601	Draft Genome Sequence for the Tree Pathogen <i>Phytophthora plurivora</i> . Genome Biology and Evolution, 2018, 10, 2432-2442.	1.1	19
4602	Colour vision variation in leaf-nosed bats (Phyllostomidae): Links to cave roosting and dietary specialization. Molecular Ecology, 2018, 27, 3627-3640.	2.0	21
4603	The soft explosive model of placental mammal evolution. BMC Evolutionary Biology, 2018, 18, 104.	3.2	35
4604	Signatures of host specialization and a recent transposable element burst in the dynamic one-speed genome of the fungal barley powdery mildew pathogen. BMC Genomics, 2018, 19, 381.	1.2	138
4605	Insights into Avian Incomplete Dosage Compensation: Sex-Biased Gene Expression Coevolves with Sex Chromosome Degeneration in the Common Whitethroat. Genes, 2018, 9, 373.	1.0	13
4606	<i>Zygosaccharomyces pseudobailii</i> , another yeast interspecies hybrid that regained fertility by damaging one of its MAT loci. FEMS Yeast Research, 2018, 18, .	1.1	39
4607	Genome Plasticity of <i>agr</i> -Defective <i>Staphylococcus aureus</i> during Clinical Infection. Infection and Immunity, 2018, 86, .	1.0	50
4608	Multiple massive domestication and recent amplification of Kolobok superfamily transposons in the clawed frog <i>Xenopus</i> . Zoological Letters, 2018, 4, 17.	0.7	0
4609	Horizontal transfer and proliferation of <i>Tsu4</i> in <i>Saccharomyces paradoxus</i> . Mobile DNA, 2018, 9, 18.	1.3	18
4610	The Complete Mitogenome of <i>Falco amurensis</i> (Falconiformes, Falconidae), and a Comparative Analysis of Genus <i>Falco</i> . Zoological Science, 2018, 35, 367.	0.3	6
4611	Rapid evolutionary dynamics of pepper mild mottle virus. Virus Research, 2018, 256, 96-99.	1.1	7
4612	Genetic signatures of lipid metabolism evolution in Cetacea since the divergence from terrestrial ancestor. Journal of Evolutionary Biology, 2018, 31, 1655-1665.	0.8	18
4613	Extensive exchange of transposable elements in the <i>Drosophila pseudoobscura</i> group. Mobile DNA, 2018, 9, 20.	1.3	28
4614	Evolutionary Origin, Gradual Accumulation and Functional Divergence of Heat Shock Factor Gene Family with Plant Evolution. Frontiers in Plant Science, 2018, 9, 71.	1.7	41
4615	Positive Selection Driving Cytoplasmic Genome Evolution of the Medicinally Important Ginseng Plant Genus <i>Panax</i> . Frontiers in Plant Science, 2018, 9, 359.	1.7	34
4616	Genome Size, Molecular Phylogeny, and Evolutionary History of the Tribe Aquilarieae (Thymelaeaceae), the Natural Source of Agarwood. Frontiers in Plant Science, 2018, 9, 712.	1.7	19

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4618	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018, 2, 1468-1478.	3.4	156
4619	Tandem Duplicate Genes in Maize Are Abundant and Date to Two Distinct Periods of Time. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3049-3058.	0.8	13
4620	Evolution of DNMT2 in drosophilids: Evidence for positive and purifying selection and insights into new protein (pathways) interactions. <i>Genetics and Molecular Biology</i> , 2018, 41, 215-234.	0.6	14
4621	Evidence for a Unique DNA-Dependent RNA Polymerase in Cereal Crops. <i>Molecular Biology and Evolution</i> , 2018, 35, 2454-2462.	3.5	21
4622	A genome scan of diversifying selection in <i>Ophiocordyceps zombiae</i> fungi suggests a role for enterotoxins in co-evolution and host specificity. <i>Molecular Ecology</i> , 2018, 27, 3582-3598.	2.0	22
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4624	Pan-genome analyses of 24 <i>Shewanella</i> strains re-emphasize the diversification of their functions yet evolutionary dynamics of metal-reducing pathway. <i>Biotechnology for Biofuels</i> , 2018, 11, 193.	6.2	59
4625	Estimating the contribution of folding stability to nonspecific epistasis in protein evolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 1242-1250.	1.5	17
4626	Ecology can inform genetics: Disassortative mating contributes to MHC polymorphism in Leach's storm-petrels (<i>Oceanodroma leucorhoa</i>). <i>Molecular Ecology</i> , 2018, 27, 3371-3385.	2.0	37
4627	Comprehensive analysis of NAC transcription factors uncovers their roles during fiber development and stress response in cotton. <i>BMC Plant Biology</i> , 2018, 18, 150.	1.6	61
4628	Horse Y chromosome assembly displays unique evolutionary features and putative stallion fertility genes. <i>Nature Communications</i> , 2018, 9, 2945.	5.8	56
4629	Full-length transcriptome of <i>Misgurnus anguillicaudatus</i> provides insights into evolution of genus <i>Misgurnus</i> . <i>Scientific Reports</i> , 2018, 8, 11699.	1.6	44
4630	The first next-generation sequencing approach to the mitochondrial phylogeny of African monogenean parasites (Platyhelminthes: Gyrodactylidae and Dactylogyridae). <i>BMC Genomics</i> , 2018, 19, 520.	1.2	36
4631	Investigating the NAD-ME biochemical pathway within C4 grasses using transcript and amino acid variation in C4 photosynthetic genes. <i>Photosynthesis Research</i> , 2018, 138, 233-248.	1.6	13
4632	Evolution and diversification of the plant gibberellin receptor GID1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7844-E7853.	3.3	51
4633	Transcriptomic comparison reveals genetic variation potentially underlying seed developmental evolution of soybeans. <i>Journal of Experimental Botany</i> , 2018, 69, 5089-5104.	2.4	46
4634	The effects of repeated whole genome duplication events on the evolution of cytokinin signaling pathway. <i>BMC Evolutionary Biology</i> , 2018, 18, 76.	3.2	23

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4636	Genome-Wide Study of YABBY Genes in Upland Cotton and Their Expression Patterns under Different Stresses. <i>Frontiers in Genetics</i> , 2018, 9, 33.	1.1	71
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4706	The evolutionary dynamics of H1N1/pdm2009 in India. <i>Infection, Genetics and Evolution</i> , 2018, 65, 276-282.	1.0	13

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4708	Integrated genomic and fossil evidence illuminates life's early evolution and eukaryote origin. <i>Nature Ecology and Evolution</i> , 2018, 2, 1556-1562.	3.4	274
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4735	Trichoplax genomes reveal profound admixture and suggest stable wild populations without bisexual reproduction. <i>Scientific Reports</i> , 2018, 8, 11168.	1.6	36
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4737	Discovery of <i>Culex pipiens</i> associated tunisia virus: a new ssRNA(+) virus representing a new insect associated virus family. <i>Virus Evolution</i> , 2018, 4, vex040.	2.2	17
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4741	Toll-Like Receptor Evolution in Birds: Gene Duplication, Pseudogenization, and Diversifying Selection. <i>Molecular Biology and Evolution</i> , 2018, 35, 2170-2184.	3.5	107
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4762	Glutamine 89 is a key residue in the allosteric modulation of human serine racemase activity by ATP. <i>Scientific Reports</i> , 2018, 8, 9016.	1.6	12
4763	Recurrent Amplification of the Heterochromatin Protein 1 (HP1) Gene Family across Diptera. <i>Molecular Biology and Evolution</i> , 2018, 35, 2375-2389.	3.5	12
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4766	Recent polyploidization events in three <i>Saccharum</i> founding species. <i>Plant Biotechnology Journal</i> , 2019, 17, 264-274.	4.1	40
4767	Alternative Splicing of the Delta-Opioid Receptor Gene Suggests Existence of New Functional Isoforms. <i>Molecular Neurobiology</i> , 2019, 56, 2855-2869.	1.9	20
4768	The first draft genome of <i>Lophophorus</i> : A step forward for Phasianidae genomic diversity and conservation. <i>Genomics</i> , 2019, 111, 1209-1215.	1.3	9
4769	Genome sequence of <i>Jatropha curcas</i> L., a non-edible biodiesel plant, provides a resource to improve seed-related traits. <i>Plant Biotechnology Journal</i> , 2019, 17, 517-530.	4.1	56
4770	Molecular footprints of inshore aquatic adaptation in Indo-Pacific humpback dolphin (<i>Sousa</i>) Tj ETQq1 1 0.784314 13 / Overlock 10 TF	1.3	10
4771	Genome sequence and genetic transformation of a widely distributed and cultivated poplar. <i>Plant Biotechnology Journal</i> , 2019, 17, 451-460.	4.1	89
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4773	Gondwanan vicariance or trans-Atlantic dispersal of cichlid fishes: a review of the molecular evidence. <i>Hydrobiologia</i> , 2019, 832, 9-37.	1.0	23
4774	Genome-Wide Patterns of Sequence Divergence of Protein-Coding Genes Between <i>Drosophila buzzatii</i> and <i>D. mojavensis</i> . <i>Journal of Heredity</i> , 2019, 110, 92-101.	1.0	8
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4906	Identification and evolution of glucosinolate sulfatases in a specialist flea beetle. <i>Scientific Reports</i> , 2019, 9, 15725.	1.6	15

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4908	Nanopore Sequencing and De Novo Assembly of a Black-Shelled Pacific Oyster (<i>Crassostrea gigas</i>) Genome. <i>Frontiers in Genetics</i> , 2019, 10, 1211.	1.1	33
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4923	Modular nature of simian foamy virus genomes and their evolutionary history. <i>Virus Evolution</i> , 2019, 5, vez032.	2.2	14
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4936	Selective deployment of transcription factor paralogs with submaximal strength facilitates gene regulation in the immune system. <i>Nature Immunology</i> , 2019, 20, 1372-1380.	7.0	17
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4952	Can extreme MHC class I diversity be a feature of a wide geographic range? The example of <i>Seba's short-tailed bat</i> (<i>Carollia perspicillata</i>). <i>Immunogenetics</i> , 2019, 71, 575-587.	1.2	15
4953	Adaptive Evolution Is Common in Rapid Evolutionary Radiations. <i>Current Biology</i> , 2019, 29, 3081-3086.e5.	1.8	32
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4980	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.	3.3	10
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4986	Whole Genome Sequencing of Chinese White Dolphin (<i>Sousa chinensis</i>) for High-Throughput Screening of Antihypertensive Peptides. <i>Marine Drugs</i> , 2019, 17, 504.	2.2	12
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5019	Phylogenetic association of <i>Schizothorax esocinus</i> with other <i>Schizothoracinae</i> fishes based on protein coding genes. Mitochondrial DNA Part B: Resources, 2019, 4, 352-354.	0.2	4
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5030	Genomic signatures of heterokaryosis in the oomycete pathogen <i>Bremia lactucae</i> . Nature Communications, 2019, 10, 2645.	5.8	67
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5061	Rapid molecular evolution of pain insensitivity in multiple African rodents. <i>Science</i> , 2019, 364, 852-859.	6.0	57
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5064	Bursts of amino acid replacements in protein evolution. <i>Royal Society Open Science</i> , 2019, 6, 181095.	1.1	1
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5070	The role of mutation bias in adaptive molecular evolution: insights from convergent changes in protein function. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180238.	1.8	43
5071	Scotopic rod vision in tetrapods arose from multiple early adaptive shifts in the rate of retinal release. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12627-12628.	3.3	10
5072	Rapid Evolution of Gained Essential Developmental Functions of a Young Gene via Interactions with Other Essential Genes. <i>Molecular Biology and Evolution</i> , 2019, 36, 2212-2226.	3.5	28
5073	Evaluation of chloroplast genome annotation tools and application to analysis of the evolution of coffee species. <i>PLoS ONE</i> , 2019, 14, e0216347.	1.1	31
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5075	Global population genomics of the forest pathogen <i>Dothistroma septosporum</i> reveal chromosome duplications in high dothistromin-producing strains. <i>Molecular Plant Pathology</i> , 2019, 20, 784-799.	2.0	19
5076	Hidden genomic evolution in a morphospecies—The landscape of rapidly evolving genes in <i>Tetrahymena</i> . <i>PLoS Biology</i> , 2019, 17, e3000294.	2.6	31
5077	A metaanalysis of bat phylogenetics and positive selection based on genomes and transcriptomes from 18 species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11351-11360.	3.3	57
5078	Genome-wide identification of GhAAI genes reveals that GhAAI66 triggers a phase transition to induce early flowering. <i>Journal of Experimental Botany</i> , 2019, 70, 4721-4736.	2.4	43
5079	Genetic Diversity of atp6 and cox3 Gene in Wild <i>Drosophila melanogaster</i> . <i>Russian Journal of Genetics</i> , 2019, 55, 360-367.	0.2	0
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5081	Extensive loss of cell-cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. <i>PLoS Biology</i> , 2019, 17, e3000255.	2.6	116
5082	“Balancing-balancing selection? Assortative mating at the major histocompatibility complex despite molecular signatures of balancing selection. <i>Ecology and Evolution</i> , 2019, 9, 5146-5157.	0.8	8
5083	M1CROB1AL1Z3R—a user-friendly web server for the analysis of large-scale microbial genomics data. <i>Nucleic Acids Research</i> , 2019, 47, W88-W92.	6.5	86
5084	AutoMLST: an automated web server for generating multi-locus species trees highlighting natural product potential. <i>Nucleic Acids Research</i> , 2019, 47, W276-W282.	6.5	286
5085	Positive Selection Evidence in Xylose-Related Genes Suggests Methylglyoxal Reductase as a Target for the Improvement of Yeasts™ Fermentation in Industry. <i>Genome Biology and Evolution</i> , 2019, 11, 1923-1938.	1.1	11
5086	Return to the Sea, Get Huge, Beat Cancer: An Analysis of Cetacean Genomes Including an Assembly for the Humpback Whale (<i>Megaptera novaeangliae</i>). <i>Molecular Biology and Evolution</i> , 2019, 36, 1746-1763.	3.5	75

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5088	Origination and selection of ABCDE and AGL6 subfamily MADS-box genes in gymnosperms and angiosperms. <i>Biological Research</i> , 2019, 52, 25.	1.5	15
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5090	Tracing the evolution of novel features of human Toll-like receptor 4. <i>Protein Science</i> , 2019, 28, 1350-1358.	3.1	8
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5093	Chimeric dihydrofolate reductases display properties of modularity and biophysical diversity. <i>Protein Science</i> , 2019, 28, 1359-1367.	3.1	3
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5095	Bat adeno-associated viruses as gene therapy vectors with the potential to evade human neutralizing antibodies. <i>Gene Therapy</i> , 2019, 26, 264-276.	2.3	14
5096	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.	0.6	4
5097	Comparative studies on duplicated <i>tdrd7</i> paralogs in teleosts: Molecular evolution caused neo-functionalization. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 30, 347-357.	0.4	7
5098	Genome-wide Analysis of the MADS-Box Gene Family in Watermelon. <i>Computational Biology and Chemistry</i> , 2019, 80, 341-350.	1.1	25
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5100	A brief overview of the concepts, methods and computational tools used in phylogenetic tree construction and gene prediction. <i>Meta Gene</i> , 2019, 21, 100586.	0.3	8
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5103	Genome-wide comparison reveals divergence of cassava and rubber aquaporin family genes after the recent whole-genome duplication. <i>BMC Genomics</i> , 2019, 20, 380.	1.2	18
5104	Genetic basis of amphibian larval development along a latitudinal gradient: Gene diversity, selection and links with phenotypic variation in transcription factor <i>C/EBPβ</i> . <i>Molecular Ecology</i> , 2019, 28, 2786-2801.	2.0	5

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5108	Robust Method for Detecting Convergent Shifts in Evolutionary Rates. <i>Molecular Biology and Evolution</i> , 2019, 36, 1817-1830.	3.5	32
5109	The Complete Chloroplast Genome of <i>Euphrasia regelii</i> , Pseudogenization of <i>ndh</i> Genes and the Phylogenetic Relationships Within Orobanchaceae. <i>Frontiers in Genetics</i> , 2019, 10, 444.	1.1	31
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5111	Complete chloroplast genome of <i>Camellia japonica</i> genome structures, comparative and phylogenetic analysis. <i>PLoS ONE</i> , 2019, 14, e0216645.	1.1	53
5112	<i>De Novo</i> , Divergence, and Mixed Origin Contribute to the Emergence of Orphan Genes in <i>Pristionchus</i> Nematodes. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2277-2286.	0.8	34
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5116	Exploring the sequence, function, and evolutionary space of protein superfamilies using sequence similarity networks and phylogenetic reconstructions. <i>Methods in Enzymology</i> , 2019, 620, 315-347.	0.4	13
5117	Two new mitogenomes of Picidae (Aves, Piciformes): Sequence, structure and phylogenetic analyses. <i>International Journal of Biological Macromolecules</i> , 2019, 133, 683-692.	3.6	13
5118	Analyses of Livestock-Associated <i>Staphylococcus aureus</i> Pan-Genomes Suggest Virulence Is Not Primary Interest in Evolution of Its Genome. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 224-236.	1.0	5
5119	Systematic Identification and Evolution Analysis of Sox Genes in <i>Coturnix japonica</i> Based on Comparative Genomics. <i>Genes</i> , 2019, 10, 314.	1.0	10
5120	Evidence for relaxed selection of mitogenome in rapid-flow cyprinids. <i>Genes and Genomics</i> , 2019, 41, 863-869.	0.5	5
5121	Whole genomes and transcriptomes reveal adaptation and domestication of pistachio. <i>Genome Biology</i> , 2019, 20, 79.	3.8	81
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5124	Population genetic structure and selective pressure on the mitochondrial ATP6 gene of the Japanese sand lance <i>Ammodytes personatus</i> Girard. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2019, 99, 1409-1416.	0.4	6
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5129	Genomic analysis on pygmy hog reveals extensive interbreeding during wild boar expansion. <i>Nature Communications</i> , 2019, 10, 1992.	5.8	38
5130	The genomes of pecan and Chinese hickory provide insights into <i>Carya</i> evolution and nut nutrition. <i>GigaScience</i> , 2019, 8, .	3.3	88
5131	Genetic diversity of chemokine XCL1 and its receptor XCR1 in murine rodents. <i>Developmental and Comparative Immunology</i> , 2019, 98, 80-88.	1.0	3
5132	Genomic Diversity and Recombination among <i>Xylella fastidiosa</i> Subspecies. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	63
5133	Comparative transcriptome analysis of four co-occurring <i>Ulva</i> species for understanding the dominance of <i>Ulva prolifera</i> in the Yellow Sea green tides. <i>Journal of Applied Phycology</i> , 2019, 31, 3303-3316.	1.5	28
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5135	Convergent recombination cessation between mating-type genes and centromeres in selfing anther-smut fungi. <i>Genome Research</i> , 2019, 29, 944-953.	2.4	21
5136	Genomic analysis of Dof transcription factors in <i>Hevea brasiliensis</i> , a rubber-producing tree. <i>Industrial Crops and Products</i> , 2019, 134, 271-283.	2.5	15
5137	Light-Emitting Dehalogenases: Reconstruction of Multifunctional Biocatalysts. <i>ACS Catalysis</i> , 2019, 9, 4810-4823.	5.5	33
5138	Cardinalfishes (Apogonidae) show visual system adaptations typical of nocturnally and diurnally active fish. <i>Molecular Ecology</i> , 2019, 28, 3025-3041.	2.0	24
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5143	Variation in secondary metabolite production potential in the <i>Fusarium incarnatum-equiseti</i> species complex revealed by comparative analysis of 13 genomes. <i>BMC Genomics</i> , 2019, 20, 314.	1.2	68
5144	Dating Whole Genome Duplication in <i>Ceratopteris thalictroides</i> and Potential Adaptive Values of Retained Gene Duplicates. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1926.	1.8	11
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5148	Massive Changes of Genome Size Driven by Expansions of Non-autonomous Transposable Elements. <i>Current Biology</i> , 2019, 29, 1161-1168.e6.	1.8	71
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5152	Comparative mitogenomic and phylogenetic analysis of <i>Apalone spinifera</i> and <i>Apalone ferox</i> (Testudines: Trionychidae). <i>Genetica</i> , 2019, 147, 165-176.	0.5	5
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5160	Genomic analysis of <i>Leptospira interrogans</i> serovar Paidjan and Dadas isolates from carrier dogs and comparative genomic analysis to detect genes under positive selection. <i>BMC Genomics</i> , 2019, 20, 168.	1.2	8
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5170	Evolution of plastid genomes of <i>Holcoglossum</i> (Orchidaceae) with recent radiation. <i>BMC Evolutionary Biology</i> , 2019, 19, 63.	3.2	47
5171	Genome-Wide Identification of Papain-Like Cysteine Proteases in <i>Gossypium hirsutum</i> and Functional Characterization in Response to <i>Verticillium dahliae</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 134.	1.7	21
5172	Evolutionary dynamics of the chromatophore genome in three photosynthetic <i>Paulinella</i> species. <i>Scientific Reports</i> , 2019, 9, 2560.	1.6	30
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5175	Extreme mito-nuclear discordance in a peninsular lizard: the role of drift, selection, and climate. <i>Heredity</i> , 2019, 123, 359-370.	1.2	24
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5178	Evolutionary History of <i>Rhus chinensis</i> (Anacardiaceae) From the Temperate and Subtropical Zones of China Based on cpDNA and Nuclear DNA Sequences and Ecological Niche Model. <i>Frontiers in Genetics</i> , 2019, 10, 171.	1.1	4
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5185	Mitochondrial Genomics Reveals Shared Phylogeographic Patterns and Demographic History among Three Periodical Cicada Species Groups. <i>Molecular Biology and Evolution</i> , 2019, 36, 1187-1200.	3.5	92
5186	The genome-wide landscape of small insertion and deletion mutations in <i>Monopterus albus</i> . <i>Journal of Genetics and Genomics</i> , 2019, 46, 75-86.	1.7	2
5187	Evolution of the eyes of vipers with and without infrared-sensing pit organs. <i>Biological Journal of the Linnean Society</i> , 2019, 126, 796-823.	0.7	22
5188	Rapid evolution of protein diversity by de novo origination in <i>Oryza</i> . <i>Nature Ecology and Evolution</i> , 2019, 3, 679-690.	3.4	121
5189	Genome Sequencing Illustrates the Genetic Basis of the Pharmacological Properties of <i>Gloeostereum incarnatum</i> . <i>Genes</i> , 2019, 10, 188.	1.0	33
5190	Genome-wide analyses reveal genes subject to positive selection in <i>Toxoplasma gondii</i> . <i>Gene</i> , 2019, 699, 73-79.	1.0	1
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5192	Insights into the Genomics of Clownfish Adaptive Radiation: Genetic Basis of the Mutualism with Sea Anemones. <i>Genome Biology and Evolution</i> , 2019, 11, 869-882.	1.1	34
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5196	Whole-genome resequencing of 472 <i>Vitis</i> accessions for grapevine diversity and demographic history analyses. <i>Nature Communications</i> , 2019, 10, 1190.	5.8	155
5197	A High-Quality Grapevine Downy Mildew Genome Assembly Reveals Rapidly Evolving and Lineage-Specific Putative Host Adaptation Genes. <i>Genome Biology and Evolution</i> , 2019, 11, 954-969.	1.1	61
5198	Bayesian Detection of Convergent Rate Changes of Conserved Noncoding Elements on Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2019, 36, 1086-1100.	3.5	39
5199	The Genome of <i>Drosophila innubila</i> Reveals Lineage-Specific Patterns of Selection in Immune Genes. <i>Molecular Biology and Evolution</i> , 2019, 36, 1405-1417.	3.5	37
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5205	ProtParCon: A Framework for Processing Molecular Data and Identifying Parallel and Convergent Amino Acid Replacements. <i>Genes</i> , 2019, 10, 181.	1.0	4
5206	Molecular Evolution of Tryptophan Hydroxylases in Vertebrates: A Comparative Genomic Survey. <i>Genes</i> , 2019, 10, 203.	1.0	12
5207	Evolution of the Highly Repetitive PEVK Region of Titin Across Mammals. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1103-1115.	0.8	1
5208	Computational analysis of the evolutionarily conserved Missing In Metastasis/Metastasis Suppressor 1 gene predicts novel interactions, regulatory regions and transcriptional control. <i>Scientific Reports</i> , 2019, 9, 4155.	1.6	4
5209	Relative Mutation Rates in Nucleomorph-Bearing Algae. <i>Genome Biology and Evolution</i> , 2019, 11, 1045-1053.	1.1	8
5210	Paralogues From the Expanded Tlr11 Gene Family in Mudskipper (<i>Boleophthalmus pectinirostris</i>) Are Under Positive Selection and Respond Differently to LPS/Poly(I:C) Challenge. <i>Frontiers in Immunology</i> , 2019, 10, 343.	2.2	20
5211	Adaptive evolution of the ACSL gene family in Carnivora. <i>Genetica</i> , 2019, 147, 141-148.	0.5	6
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5215	Olfactory Proteins in <i>Timema</i> Stick Insects. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	1
5216	New Insights into Long Terminal Repeat Retrotransposons in Mulberry Species. <i>Genes</i> , 2019, 10, 285.	1.0	11
5217	Comparative Genomics Between <i>Saccharomyces kudriavzevii</i> and <i>S. cerevisiae</i> Applied to Identify Mechanisms Involved in Adaptation. <i>Frontiers in Genetics</i> , 2019, 10, 187.	1.1	27
5218	The First Transcriptome Assembly of Yenyuan Stream Salamander (<i>Batrachuperus yenyuanensis</i>) Provides Novel Insights into Its Molecular Evolution. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1529.	1.8	7
5219	Chromosomeâ€level genome assembly of <i>Triplophysa tibetana</i> , a fish adapted to the harsh highâ€altitude environment of the Tibetan Plateau. <i>Molecular Ecology Resources</i> , 2019, 19, 1027-1036.	2.2	39
5220	Developmental expression and evolution of hexamerin and haemocyanin from <i>Folsomia candida</i> (Collembola). <i>Insect Molecular Biology</i> , 2019, 28, 716-727.	1.0	5
5221	A global coexpression network of soybean genes gives insights into the evolution of nodulation in nonlegumes and legumes. <i>New Phytologist</i> , 2019, 223, 2104-2119.	3.5	21
5222	Analysis of the coding sequences of clownfish reveals molecular convergence in the evolution of lifespan. <i>BMC Evolutionary Biology</i> , 2019, 19, 89.	3.2	13
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5227	Morphology and genome of a snailfish from the Mariana Trench provide insights into deep-sea adaptation. <i>Nature Ecology and Evolution</i> , 2019, 3, 823-833.	3.4	99
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5230	Does the Presence of Transposable Elements Impact the Epigenetic Environment of Human Duplicated Genes?. <i>Genes</i> , 2019, 10, 249.	1.0	7
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5236	A widespread coral-infecting apicomplexan with chlorophyll biosynthesis genes. <i>Nature</i> , 2019, 568, 103-107.	13.7	102
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5239	Convergent regulatory evolution and loss of flight in paleognathous birds. <i>Science</i> , 2019, 364, 74-78.	6.0	189
5240	No signal of deleterious mutation accumulation in conserved gene sequences of extant asexual hexapods. <i>Scientific Reports</i> , 2019, 9, 5338.	1.6	17
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5252	A Chromosome-Scale Genome Assembly of Paper Mulberry (<i>Broussonetia papyrifera</i>) Provides New Insights into Its Forage and Papermaking Usage. <i>Molecular Plant</i> , 2019, 12, 661-677.	3.9	83
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5256	Resolving the backbone of the Brassicaceae phylogeny for investigating trait diversity. <i>New Phytologist</i> , 2019, 222, 1638-1651.	3.5	123
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5259	The first chromosome-level genome for a marine mammal as a resource to study ecology and evolution. <i>Molecular Ecology Resources</i> , 2019, 19, 944-956.	2.2	27
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5263	Genome-wide identification and characterization of sweet orange (<i>Citrus sinensis</i>) aquaporin genes and their expression in two citrus cultivars differing in drought tolerance. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	23
5264	Genomic and transcriptomic investigations of the evolutionary transition from oviparity to viviparity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3646-3655.	3.3	43
5265	Angiosperm-Wide and Family-Level Analyses of AP2/ERF Genes Reveal Differential Retention and Sequence Divergence After Whole-Genome Duplication. <i>Frontiers in Plant Science</i> , 2019, 10, 196.	1.7	42
5266	Simultaneous Bayesian inference of phylogeny and molecular coevolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5027-5036.	3.3	9
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5270	Antarctic blackfin icefish genome reveals adaptations to extreme environments. <i>Nature Ecology and Evolution</i> , 2019, 3, 469-478.	3.4	115
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5272	Draft genome of the river water buffalo. <i>Ecology and Evolution</i> , 2019, 9, 3378-3388.	0.8	32
5273	EasyCodeML: A visual tool for analysis of selection using CodeML. <i>Ecology and Evolution</i> , 2019, 9, 3891-3898.	0.8	291
5274	The <i>Galleria mellonella</i> Hologenome Supports Microbiota-Independent Metabolism of Long-Chain Hydrocarbon Beeswax. <i>Cell Reports</i> , 2019, 26, 2451-2464.e5.	2.9	103
5275	Molecular evolution of the plant ECERIFERUM1 and ECERIFERUM3 genes involved in aliphatic hydrocarbon production. <i>Computational Biology and Chemistry</i> , 2019, 80, 1-9.	1.1	26
5276	Genetic and expression differences between putative ecotypes of <i>Sphagnum denticulatum</i> Brid. (Sphagnaceae: Bryophyta) subjected to drought stress and rehydration. <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2019, 37, 39-52.	1.1	4
5277	Genome Sequencing of <i>Cladobotryum protrusum</i> Provides Insights into the Evolution and Pathogenic Mechanisms of the Cobweb Disease Pathogen on Cultivated Mushroom. <i>Genes</i> , 2019, 10, 124.	1.0	25
5278	The Old and the New: Discovery Proteomics Identifies Putative Novel Seminal Fluid Proteins in <i>Drosophila</i> . <i>Molecular and Cellular Proteomics</i> , 2019, 18, S23-S33.	2.5	20
5279	Divergent Evolution of E1A CR3 in Human Adenovirus Species D. <i>Viruses</i> , 2019, 11, 143.	1.5	3
5280	Analysis of mitochondrial and chloroplast genomes in two volvocine algae: <i>Eudorina elegans</i> and <i>Eudorina cylindrica</i> (Volvocaceae, Chlorophyta). <i>European Journal of Phycology</i> , 2019, 54, 193-205.	0.9	12
5281	Comparative Genome and Transcriptome Analysis Reveals Gene Selection Patterns Along with the Paleo-Climatic Change in the <i>Populus</i> Phylogeny. <i>Forests</i> , 2019, 10, 163.	0.9	1
5282	Characterization, evolution, and expression analysis of TLR7 gene subfamily members in <i>Mastacembelus armatus</i> (Synbranchiformes: Mastacembelidae). <i>Developmental and Comparative Immunology</i> , 2019, 95, 77-88.	1.0	12
5283	DNA Methylation Patterns in the Social Spider, <i>Stegodyphus dumicola</i> . <i>Genes</i> , 2019, 10, 137.	1.0	46
5284	Mechanistic insights into the evolution of DUF26-containing proteins in land plants. <i>Communications Biology</i> , 2019, 2, 56.	2.0	75
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5287	Tracking the Rules of Transmission and Introgression with Networks. , 2019, , 345-365.		0
5288	Disease Resistance Genetics and Genomics in Octoploid Strawberry. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3315-3332.	0.8	26
5289	Variation at an adhesin locus suggests sociality in natural populations of the yeast <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191948.	1.2	13
5290	Comprehensive Analysis Reveals the Evolution and Pathogenicity of <i>Aeromonas</i> , Viewed from Both Single Isolated Species and Microbial Communities. <i>MSystems</i> , 2019, 4, .	1.7	36
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5292	Parallel selection on ecologically relevant gene functions in the transcriptomes of highly diversifying salmonids. <i>BMC Genomics</i> , 2019, 20, 1010.	1.2	8
5293	Comparative Genomics Reveals Accelerated Evolution of Fright Reaction Genes in Ostariophysan Fishes. <i>Frontiers in Genetics</i> , 2019, 10, 1283.	1.1	3
5294	Greenlip Abalone (<i>Haliotis laevigata</i>) Genome and Protein Analysis Provides Insights into Maturation and Spawning. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3067-3078.	0.8	14
5295	New bobtail squid (Sepiolidae: Sepiolinae) from the Ryukyu islands revealed by molecular and morphological analysis. <i>Communications Biology</i> , 2019, 2, 465.	2.0	9
5296	Duplication and parallel evolution of the pancreatic ribonuclease gene (RNASE1) in folivorous non-colobine primates, the howler monkeys (<i>Alouatta</i> spp.). <i>Scientific Reports</i> , 2019, 9, 20366.	1.6	8
5297	Tung Tree (<i>Vernicia fordii</i>) Genome Provides A Resource for Understanding Genome Evolution and Improved Oil Production. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 558-575.	3.0	43
5298	A Coevolved EDS1-SAG101-NRG1 Module Mediates Cell Death Signaling by TIR-Domain Immune Receptors. <i>Plant Cell</i> , 2019, 31, 2430-2455.	3.1	198
5299	Characterization of the Complete Chloroplast Genome of <i>Acer truncatum</i> Bunge (Sapindales: Tj ETQq1 1 0.784314 rgBT /Ove 2019, 2019, 1-13.	0.9	12
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5301	<i>FAD2</i> Gene Radiation and Positive Selection Contributed to Polyacetylene Metabolism Evolution in Campanulids. <i>Plant Physiology</i> , 2019, 181, 714-728.	2.3	12
5302	Genome Sequencing of <i>Pleurozium schreberi</i> : The Assembled and Annotated Draft Genome of a Pleurocarpous Feather Moss. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2791-2797.	0.8	35
5303	<i>De Novo</i> Assembly and Annotation from Parental and F1 Puma Genomes of the Florida Panther Genetic Restoration Program. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3531-3536.	0.8	12

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5305	The genome of a subterrestrial nematode reveals adaptations to heat. <i>Nature Communications</i> , 2019, 10, 5268.	5.8	22
5306	Evolutionary balance between LRR domain loss and young NBS-LRR genes production governs disease resistance in <i>Arachis hypogaea</i> cv. Tifrunner. <i>BMC Genomics</i> , 2019, 20, 844.	1.2	30
5307	Evolutionary selection on MDA5 and LGP2 in the chicken preserves antiviral competence in the absence of RIG-I. <i>Journal of Genetics and Genomics</i> , 2019, 46, 499-503.	1.7	19
5308	The Mitochondrial Genome of <i>Eleusine indica</i> and Characterization of Gene Content Within Poaceae. <i>Genome Biology and Evolution</i> , 2019, 12, 3684-3697.	1.1	3
5309	A High-quality Draft Genome Assembly of the Black-necked Crane (<i>Grus nigricollis</i>) Based on Nanopore Sequencing. <i>Genome Biology and Evolution</i> , 2019, 11, 3332-3340.	1.1	5
5310	Mitogenomic diversity in Sacred Ibis Mummies sheds light on early Egyptian practices. <i>PLoS ONE</i> , 2019, 14, e0223964.	1.1	14
5311	Genome-wide analysis of Cushion willow provides insights into alpine plant divergence in a biodiversity hotspot. <i>Nature Communications</i> , 2019, 10, 5230.	5.8	75
5312	The persimmon (<i>Diospyros oleifera</i> Cheng) genome provides new insights into the inheritance of astringency and ancestral evolution. <i>Horticulture Research</i> , 2019, 6, 138.	2.9	39
5313	Comparative analysis of corrected tiger genome provides clues to its neuronal evolution. <i>Scientific Reports</i> , 2019, 9, 18459.	1.6	24
5314	Convergent degeneration of olfactory receptor gene repertoires in marine mammals. <i>BMC Genomics</i> , 2019, 20, 977.	1.2	31
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5316	Extensive host-switching of avian feather lice following the Cretaceous-Paleogene mass extinction event. <i>Communications Biology</i> , 2019, 2, 445.	2.0	20
5317	Repeated sex chromosome evolution in vertebrates supported by expanded avian sex chromosomes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20192051.	1.2	42
5318	Phylostratigraphic Analysis Shows the Earliest Origination of the Abiotic Stress Associated Genes in <i>A. thaliana</i> . <i>Genes</i> , 2019, 10, 963.	1.0	11
5319	The preponderance of nonsynonymous A-to-I RNA editing in coleoids is nonadaptive. <i>Nature Communications</i> , 2019, 10, 5411.	5.8	38
5320	The mitochondrial genomes of palaeopteran insects and insights into the early insect relationships. <i>Scientific Reports</i> , 2019, 9, 17765.	1.6	21
5321	Programmed DNA elimination of germline development genes in songbirds. <i>Nature Communications</i> , 2019, 10, 5468.	5.8	66

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5324	Polymorphism analyses and protein modelling inform on functional specialization of Piwi-clade genes in the arboviral vector <i>Aedes albopictus</i> . <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007919.	1.3	16
5325	<i>Trochodendron aralioides</i> , the first chromosome-level draft genome in Trochodendrales and a valuable resource for basal eudicot research. <i>GigaScience</i> , 2019, 8, .	3.3	20
5326	A Complete Transcriptional Landscape Analysis of <i>Pinus elliottii</i> Engelm. Using Third-Generation Sequencing and Comparative Analysis in the Pinus Phylogeny. <i>Forests</i> , 2019, 10, 942.	0.9	10
5327	Impact of a Live Attenuated Classical Swine Fever Virus Introduced to Jeju Island, a CSF-Free Area. <i>Pathogens</i> , 2019, 8, 251.	1.2	15
5328	Highly thermostable carboxylic acid reductases generated by ancestral sequence reconstruction. <i>Communications Biology</i> , 2019, 2, 429.	2.0	34
5329	Genomic insights from the first chromosome-scale assemblies of oat (<i>Avena</i> spp.) diploid species. <i>BMC Biology</i> , 2019, 17, 92.	1.7	58
5330	Evolutionary patterns of chimeric retrogenes in <i>Oryza</i> species. <i>Scientific Reports</i> , 2019, 9, 17733.	1.6	3
5331	Residual Variation Intolerance Score Detects Loci Under Selection in Neuroinvasive <i>Listeria monocytogenes</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2702.	1.5	1
5332	Contribution of Functional Divergence Through Copy Number Variations to the Inter-Species and Intra-Species Diversity in Specialized Metabolites. <i>Frontiers in Plant Science</i> , 2019, 10, 1567.	1.7	7
5333	Massive expansion and diversity of nicotinic acetylcholine receptors in lophotrochozoans. <i>BMC Genomics</i> , 2019, 20, 937.	1.2	32
5334	Host plant adaptation in the polyphagous whitefly, <i>Trialeurodes vaporariorum</i> , is associated with transcriptional plasticity and altered sensitivity to insecticides. <i>BMC Genomics</i> , 2019, 20, 996.	1.2	27
5335	Not so unique to Primates: The independent adaptive evolution of TRIM5 in Lagomorpha lineage. <i>PLoS ONE</i> , 2019, 14, e0226202.	1.1	7
5336	Genomic and transcriptomic insights into molecular basis of sexually dimorphic nuptial spines in <i>Leptobrachium leishanense</i> . <i>Nature Communications</i> , 2019, 10, 5551.	5.8	52
5337	Deciphering protein evolution and fitness landscapes with latent space models. <i>Nature Communications</i> , 2019, 10, 5644.	5.8	64
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5341	Higher-order epistasis shapes the fitness landscape of a xenobiotic-degrading enzyme. <i>Nature Chemical Biology</i> , 2019, 15, 1120-1128.	3.9	71
5342	Evolution and expression of genes encoding TCP transcription factors in <i>Solanum tuberosum</i> reveal the involvement of StTCP23 in plant defence. <i>BMC Genetics</i> , 2019, 20, 91.	2.7	20
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5355	One Hundred Mitochondrial Genomes of Cicadas. <i>Journal of Heredity</i> , 2019, 110, 247-256.	1.0	27
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5431	Comparative analysis of spleen transcriptome detects differences in evolutionary adaptation of immune defense functions in bighead carp and silver carp. <i>Fish and Shellfish Immunology</i> , 2019, 84, 148-157.	1.6	12
5432	Alignment-free inference of hierarchical and reticulate phylogenomic relationships. <i>Briefings in Bioinformatics</i> , 2019, 20, 426-435.	3.2	74
5433	The genetic divergence of <i>Oratosquilla oratoria</i> between the East China Sea and Yellow Sea: physical barrier and possible local adaptation. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2019, 99, 631-638.	0.4	0
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5462	Genomic evidence sheds light on the genetic mechanisms of musk secretion in muskrats. <i>International Journal of Biological Macromolecules</i> , 2020, 145, 1189-1198.	3.6	3
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5465	Diet and Adaptive Evolution of Alanine-Glyoxylate Aminotransferase Mitochondrial Targeting in Birds. <i>Molecular Biology and Evolution</i> , 2020, 37, 786-798.	3.5	11
5466	Distinct genotypes and phenotypes in European and American strains of <i>Drosophila suzukii</i> : implications for biology and management of an invasive organism. <i>Journal of Pest Science</i> , 2020, 93, 77-89.	1.9	29

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5468	Resolving the genetic paradox of invasions: Preadapted genomes and postintroduction hybridization of bigheaded carps in the Mississippi River Basin. <i>Evolutionary Applications</i> , 2020, 13, 263-277.	1.5	20
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5471	<i>Mesostigma viride</i> Genome and Transcriptome Provide Insights into the Origin and Evolution of Streptophyta. <i>Advanced Science</i> , 2020, 7, 1901850.	5.6	40
5472	Molecular evolution of autophagy rate-limiting factor LAMP2 in placental mammals. <i>Gene</i> , 2020, 727, 144231.	1.0	5
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5632	Avian phenotypic convergence is subject to low genetic constraints based on genomic evidence. <i>BMC Evolutionary Biology</i> , 2020, 20, 147.	3.2	2
5633	Genome-wide survey of sucrose non-fermenting 1-related protein kinase 2 in Rosaceae and expression analysis of PbrSnRK2 in response to ABA stress. <i>BMC Genomics</i> , 2020, 21, 781.	1.2	11
5634	Plastomes of eight <i>Ligusticum</i> species: characterization, genome evolution, and phylogenetic relationships. <i>BMC Plant Biology</i> , 2020, 20, 519.	1.6	42
5635	Genome-wide survey of soybean papain-like cysteine proteases and their expression analysis in root nodule symbiosis. <i>BMC Plant Biology</i> , 2020, 20, 517.	1.6	9
5636	Miocene Diversification and High-Altitude Adaptation of <i>Parnassius</i> Butterflies (Lepidoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 754.	1.0	10
5637	Comparative Analysis of the Circular and Highly Asymmetrical Marseilleviridae Genomes. <i>Viruses</i> , 2020, 12, 1270.	1.5	13
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5642	Genomic analyses of a livestock pest, the New World screwworm, find potential targets for genetic control programs. <i>Communications Biology</i> , 2020, 3, 424.	2.0	26
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5644	Link Your Sites (LYS) Scripts: Automated Search of Protein Structures and Mapping of Sites Under Positive Selection Detected by PAML. <i>Evolutionary Biology</i> , 2020, 47, 240-245.	0.5	0
5645	Increased Mutation Rate Is Linked to Genome Reduction in Prokaryotes. <i>Current Biology</i> , 2020, 30, 3848-3855.e4.	1.8	44
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5649	A high-contiguity <i>Brassica nigra</i> genome localizes active centromeres and defines the ancestral <i>Brassica</i> genome. <i>Nature Plants</i> , 2020, 6, 929-941.	4.7	94
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5651	The Genome of <i>Microthlaspi erraticum</i> (Brassicaceae) Provides Insights Into the Adaptation to Highly Calcareous Soils. <i>Frontiers in Plant Science</i> , 2020, 11, 943.	1.7	4
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5664	Diversity analysis at MHC class II DQA locus in buffalo (<i>Bubalus bubalis</i>) indicates extensive duplication and trans-species evolution. <i>Genomics</i> , 2020, 112, 4417-4426.	1.3	3

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5666	Genomic and transcriptomic evidence for descent from <i>Plasmodium</i> and loss of blood schizogony in <i>Hepaticystis</i> parasites from naturally infected red colobus monkeys. <i>PLoS Pathogens</i> , 2020, 16, e1008717.	2.1	18
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5672	A Genomewide Scan for Genetic Structure and Demographic History of Two Closely Related Species, <i>Rhododendron dauricum</i> and <i>R. mucronulatum</i> (<i>Rhododendron</i> , <i>Ericaceae</i>). <i>Frontiers in Plant Science</i> , 2020, 11, 1093.	1.7	7
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5687	African Arowana Genome Provides Insights on Ancient Teleost Evolution. <i>IScience</i> , 2020, 23, 101662.	1.9	3
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5692	Comparative ACE2 variation and primate COVID-19 risk. <i>Communications Biology</i> , 2020, 3, 641.	2.0	121
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5694	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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5706	Nucleotide substitution rates of diatom plastid encoded protein genes are positively correlated with genome architecture. <i>Scientific Reports</i> , 2020, 10, 14358.	1.6	7
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5724	Olfactory receptor gene evolution is unusually rapid across Tetrapoda and outpaces chemosensory phenotypic change. <i>Environmental Epigenetics</i> , 2020, 66, 505-514.	0.9	20
5725	Adaptive convergence at the genomic level—prevalent, uncommon or very rare?. <i>National Science Review</i> , 2020, 7, 947-951.	4.6	9
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5727	Comparative Analysis of Clinical and Environmental Strains of <i>Exophiala spinifera</i> by Long-Reads Sequencing and RNAseq Reveal Adaptive Strategies. <i>Frontiers in Microbiology</i> , 2020, 11, 1880.	1.5	6
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5736	A drift-barrier model drives the genomic landscape of a structured bacterial population. <i>Molecular Ecology</i> , 2020, 29, 4143-4156.	2.0	3

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5738	Variation Among Biosynthetic Gene Clusters, Secondary Metabolite Profiles, and Cards of Virulence Across <i>Aspergillus</i> Species. <i>Genetics</i> , 2020, 216, 481-497.	1.2	50
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5740	The chromosome-level draft genome of <i>Dalbergia odorifera</i> . <i>GigaScience</i> , 2020, 9, .	3.3	21
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5742	Divergent evolution and purifying selection of the Type 2 diabetes gene sequences in <i>Drosophila</i> : a phylogenomic study. <i>Genetica</i> , 2020, 148, 269-282.	0.5	4
5743	Cryptic variation in mole voles <i>Ellobius</i> (<i>Arvicolinae</i> , <i>Rodentia</i>) of Mongolia. <i>Zoologica Scripta</i> , 2020, 49, 535-548.	0.7	10
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5752	Unraveling the Molecular Evolution of Blood Coagulation Genes in Fishes and Cetaceans. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	2
5753	FireProtASR: A Web Server for Fully Automated Ancestral Sequence Reconstruction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	37
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5756	Identification of genes under positive selection reveals evolutionary adaptation of <i>Ulva mutabilis</i> . <i>Acta Oceanologica Sinica</i> , 2020, 39, 35-41.	0.4	0
5757	A chromosome-scale genome assembly of a diploid alfalfa, the progenitor of autotetraploid alfalfa. <i>Horticulture Research</i> , 2020, 7, 194.	2.9	25
5758	A chromosome-scale reference genome of <i>Lobularia maritima</i> , an ornamental plant with high stress tolerance. <i>Horticulture Research</i> , 2020, 7, 197.	2.9	6
5759	A hydrophobic ratchet entrenches molecular complexes. <i>Nature</i> , 2020, 588, 503-508.	13.7	75
5760	A phased <i>Vanilla planifolia</i> genome enables genetic improvement of flavour and production. <i>Nature Food</i> , 2020, 1, 811-819.	6.2	52
5761	Chromosome-level draft genome of a diploid plum (<i>Prunus salicina</i>). <i>GigaScience</i> , 2020, 9, .	3.3	39
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5763	Network and Evolutionary Analysis of Human Epigenetic Regulators to Unravel Disease Associations. <i>Genes</i> , 2020, 11, 1457.	1.0	4
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5766	The Draft Genome of Red Lechwe, <i>Kobus lechwe lechwe</i> . <i>Frontiers in Genetics</i> , 2020, 11, 582638.	1.1	0
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5768	Comparative Analyses of the Chloroplast Genomes of Patchouli Plants and Their Relatives in <i>Pogostemon</i> (Lamiaceae). <i>Plants</i> , 2020, 9, 1497.	1.6	6
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5770	Paleo-polyploidization in Lycophytes. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 333-340.	3.0	16
5771	Molecular evolution of GDP-L-galactose phosphorylase, a key regulatory gene in plant ascorbate biosynthesis. <i>AoB PLANTS</i> , 2020, 12, plaa055.	1.2	7
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5779	Noncoding regions underpin avian bill shape diversification at macroevolutionary scales. <i>Genome Research</i> , 2020, 30, 553-565.	2.4	24
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6059	Baby Genomics: Tracing the Evolutionary Changes That Gave Rise to Placentation. <i>Genome Biology and Evolution</i> , 2020, 12, 35-47.	1.1	11
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6064	Foraging shifts and visual preadaptation in ecologically diverse bats. <i>Molecular Ecology</i> , 2020, 29, 1839-1859.	2.0	19
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6068	Divergence of Peroxisome Membrane Gene Sequence and Expression Between Yeast Species. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2079-2085.	0.8	3
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6121	Higher level phylogeny of baleen whales. , 2021, , 3-10.		1
6122	Whole genome sequencing of silver carp (<i>Hypophthalmichthys molitrix</i>) and bighead carp (<i>Hypophthalmichthys nobilis</i>) provide novel insights into their evolution and speciation. <i>Molecular Ecology Resources</i> , 2021, 21, 912-923.	2.2	17
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6139	Inpatient Evolutionary Dynamics in an Individual Infected with HIV-1 CRF01_AE Who Experienced Periods of Treatment Failure. <i>AIDS Research and Human Retroviruses</i> , 2021, 37, 139-146.	0.5	2
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6168	Phylogenomic Resolution of Sea Spider Diversification through Integration of Multiple Data Classes. <i>Molecular Biology and Evolution</i> , 2021, 38, 686-701.	3.5	47

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6170	Chromosome-level de novo genome assembly of <i>Sarcophaga peregrina</i> provides insights into the evolutionary adaptation of flesh flies. <i>Molecular Ecology Resources</i> , 2021, 21, 251-262.	2.2	16
6171	Detection of genes positively selected in Cuban Anolis lizards that naturally inhabit hot and open areas and currently thrive in urban areas. <i>Ecology and Evolution</i> , 2021, 11, 1719-1728.	0.8	7
6174	Flourishing in water: the early evolution and diversification of plant receptor-like kinases. <i>Plant Journal</i> , 2021, 106, 174-184.	2.8	22
6175	New insights into the evolutionary characteristic between the New World and Old World <i>Lupinus</i> species using complete chloroplast genomes. <i>International Journal of Transgender Health</i> , 2021, 14, 414-427.	1.1	2
6176	Genome Assembly and Analyses of the Macrofungus <i>Macrocybe gigantea</i> . <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	4
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6179	Genomes reveal selective sweeps in kiang and donkey for high-altitude adaptation. <i>Zoological Research</i> , 2021, 42, 450-460.	0.9	9
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6184	De novo genome assembly of the potent medicinal plant <i>Rehmannia glutinosa</i> using nanopore technology. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3954-3963.	1.9	26
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6186	Complexity of the simplest species tree problem. <i>Molecular Biology and Evolution</i> , 2021, 38, 3993-4009.	3.5	22
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6192	Quasispecies of SARS-CoV-2 revealed by single nucleotide polymorphisms (SNPs) analysis. <i>Virulence</i> , 2021, 12, 1209-1226.	1.8	16
6193	The rise and fall of the ancient northern pike master sex-determining gene. <i>ELife</i> , 2021, 10, .	2.8	24
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6198	<i>Computational Evolutionary Biology</i> . , 2021, , 83-100.		0
6199	Genomic adaptation of <i>Pseudomonas</i> strains to acidity and antibiotics in hydrothermal vents at Kolumbo submarine volcano, Greece. <i>Scientific Reports</i> , 2021, 11, 1336.	1.6	9
6200	Comparative plastid genomics of four <i>Pilea</i> (Urticaceae) species: insight into interspecific plastid genome diversity in <i>Pilea</i> . <i>BMC Plant Biology</i> , 2021, 21, 25.	1.6	20
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6203	Computational Analysis of Recombination in Viral Nucleotide Sequences. , 2021, , 108-115.		2
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6209	Chromosome-scale genome assembly of brown-spotted flathead &Platycephalus& sp.1 provides insights into demersal adaptation in flathead fish. <i>Zoological Research</i> , 2021, 42, 660-665.	0.9	2
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6228	Evolution of regulatory networks associated with traits under selection in cichlids. <i>Genome Biology</i> , 2021, 22, 25.	3.8	17
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6258	Genome-wide analysis of pseudogenes reveals HBBP1's human-specific essentiality in erythropoiesis and implication in β -thalassemia. <i>Developmental Cell</i> , 2021, 56, 478-493.e11.	3.1	22

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6286	Comparative Analyses of <i>Euonymus</i> Chloroplast Genomes: Genetic Structure, Screening for Loci With Suitable Polymorphism, Positive Selection Genes, and Phylogenetic Relationships Within Celastrineae. <i>Frontiers in Plant Science</i> , 2020, 11, 593984.	1.7	25
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6307	Genomic Evidence for Convergent Molecular Adaptation in Electric Fishes. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	12
6308	Insights into triterpene synthesis and unsaturated fatty-acid accumulation provided by chromosomal-level genome analysis of <i>Akebia trifoliata</i> subsp. <i>australis</i> . <i>Horticulture Research</i> , 2021, 8, 33.	2.9	23
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6315	Phylostratigraphic analysis of gene networks of human diseases. <i>Vavilovskii Zhurnal Genetiki i Selektzii</i> , 2021, 25, 46-56.	0.4	1
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6368	Detection of subgenome bias using an anchored syntenic approach in <i>Eleusine coracana</i> (finger) Tj ETQq1 1 0.784314 rgBT /Qverlock	1.2	2
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6387	The Pan social brain: An evolutionary history of neurochemical receptor genes and their potential impact on sociocognitive differences. <i>Journal of Human Evolution</i> , 2021, 152, 102949.	1.3	12
6388	The genetic variation landscape of African swine fever virus reveals frequent positive selection and adaptive flexibility. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 2703-2721.	1.3	10
6389	Gene expression evolution in pattern-triggered immunity within <i>Arabidopsis thaliana</i> and across Brassicaceae species. <i>Plant Cell</i> , 2021, 33, 1863-1887.	3.1	27
6390	Comparative analysis of testis transcriptomes in laboratory cohorts of recently diverged allopatric <i>Drosophila nasuta nasuta</i> and <i>Drosophila nasuta albomicans</i> . <i>Journal of Asia-Pacific Entomology</i> , 2021, 24, 46-46.	0.4	0
6391	A gene that underwent adaptive evolution, LAC2 (LACCASE), in <i>Populus euphratica</i> improves drought tolerance by improving water transport capacity. <i>Horticulture Research</i> , 2021, 8, 88.	2.9	27
6393	Genome-scale analyses of polyketide synthases in banana: Phylogenetics and expression profiling forecast their candidacy in specialized metabolism. <i>Gene</i> , 2021, 778, 145472.	1.0	5
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6396	Local adaptation of <i>Mycobacterium tuberculosis</i> on the Tibetan Plateau. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	21
6397	The Evolution of Calcification in Reef-Building Corals. <i>Molecular Biology and Evolution</i> , 2021, 38, 3543-3555.	3.5	19
6398	The Transposable Element Environment of Human Genes Differs According to Their Duplication Status and Essentiality. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	1
6399	Signatures of optimal codon usage in metabolic genes inform budding yeast ecology. <i>PLoS Biology</i> , 2021, 19, e3001185.	2.6	18
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6401	Genomic assessment of the <i>Phyllodactylus tuberculosus</i> complex (Reptilia: Phyllodactylidae) in America. <i>Zoologica Scripta</i> , 2021, 50, 529-542.	0.7	5
6403	Reproductive Proteins Evolve Faster Than Non-reproductive Proteins Among Solanum Species. <i>Frontiers in Plant Science</i> , 2021, 12, 635990.	1.7	12
6404	The association of the heterogeneity of HBV reverse transcriptase quasispecies with antiviral efficacy after treatment with nucleos(t)ide analogues for 10 years. <i>Infection, Genetics and Evolution</i> , 2021, 89, 104706.	1.0	0
6405	The phylogenetic relationships within the Eastern Afromontane clade of <i>Crocidura</i> based on mitochondrial and nuclear data. <i>Mammalian Biology</i> , 2021, 101, 1005-1018.	0.8	6
6406	Quantifying evolutionary importance of protein sites: A Tale of two measures. <i>PLoS Genetics</i> , 2021, 17, e1009476.	1.5	8
6407	Evolutionary Analysis of Pre-S/S Mutations in HBeAg-Negative Chronic Hepatitis B With HBsAg ≤ 100 IU/ml. <i>Frontiers in Public Health</i> , 2021, 9, 633792.	1.3	4
6408	Shared evolutionary footprints suggest mitochondrial oxidative damage underlies multiple complex I losses in fungi. <i>Open Biology</i> , 2021, 11, 200362.	1.5	10
6409	Chromosome-level genome assembly of the Arctic fox (<i>Vulpes lagopus</i>) using PacBio sequencing and Hi-C technology. <i>Molecular Ecology Resources</i> , 2021, 21, 2093-2108.	2.2	15
6410	Evolutionary stasis of a deep subsurface microbial lineage. <i>ISME Journal</i> , 2021, 15, 2830-2842.	4.4	23
6411	Phylogeny of true ladybird beetles (Coccinellidae: Coccinellini) reveals pervasive convergent evolution and a rapid Cenozoic radiation. <i>Systematic Entomology</i> , 2021, 46, 611-631.	1.7	13
6415	The evolution of opsin genes in five species of mirid bugs: duplication of long-wavelength opsins and loss of blue-sensitive opsins. <i>Bmc Ecology and Evolution</i> , 2021, 21, 66.	0.7	6
6416	Molecular Evolutionary Analyses of <i>Euplotes</i> Species Living in Freshwater and Marine Habitats: A Mitogenomic Perspective. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	2

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6419	Divergent Gene Expression Following Duplication of Meiotic Genes in the Stick Insect <i>Clitarchus hookeri</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	1
6420	Large-Scale Phylogenomic Analyses Reveal the Monophyly of Bryophytes and Neoproterozoic Origin of Land Plants. <i>Molecular Biology and Evolution</i> , 2021, 38, 3332-3344.	3.5	56
6421	Chromosome-level genome assembly of burbot (<i>Lota lota</i>) provides insights into the evolutionary adaptations in freshwater. <i>Molecular Ecology Resources</i> , 2021, 21, 2022-2033.	2.2	8
6422	Evolutionary and biomedical insights from a marmoset diploid genome assembly. <i>Nature</i> , 2021, 594, 227-233.	13.7	42
6423	Phylotranscriptomics reveals the complex evolutionary and biogeographic history of the genus <i>Tsuga</i> with an East Asian-North American disjunct distribution. <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107066.	1.2	18
6425	Phylogenomics of <i>Brosimum</i> (Moraceae) and allied genera, including a revised subgeneric system. <i>Taxon</i> , 2021, 70, 778-792.	0.4	4
6426	New framework for recombination and adaptive evolution analysis with application to the novel coronavirus SARS-CoV-2. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
6428	Mutation Rates and Selection on Synonymous Mutations in SARS-CoV-2. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	83
6429	Construction of a chromosome-level genome and variation map for the Pacific oyster <i>Crassostrea gigas</i> . <i>Molecular Ecology Resources</i> , 2021, 21, 1670-1685.	2.2	45
6430	The reference genome and transcriptome of the limestone langur, <i>Trachypithecus leucocephalus</i> , reveal expansion of genes related to alkali tolerance. <i>BMC Biology</i> , 2021, 19, 67.	1.7	3
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6432	Patterns of Natural Selection on Mitochondrial Protein-Coding Genes in Lungless Salamanders: Relaxed Purifying Selection and Presence of Positively Selected Codon Sites in the Family Plethodontidae. <i>International Journal of Genomics</i> , 2021, 2021, 1-12.	0.8	0
6434	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , 2021, 31, 799-810.	2.4	21
6435	Phylogenomics and Historical Biogeography of Seahorses, Dragonets, Goatfishes, and Allies (Teleostei: Syngnatharia): Assessing Factors Driving Uncertainty in Biogeographic Inferences. <i>Systematic Biology</i> , 2021, 70, 1145-1162.	2.7	24
6436	Large-scale sequencing of flatfish genomes provides insights into the polyphyletic origin of their specialized body plan. <i>Nature Genetics</i> , 2021, 53, 742-751.	9.4	30
6438	Molecular Characterization of MHC Class I Genes in Four Species of the Turdidae Family to Assess Genetic Diversity and Selection. <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	0
6439	The Chinese mitten crab genome provides insights into adaptive plasticity and developmental regulation. <i>Nature Communications</i> , 2021, 12, 2395.	5.8	38

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6441	Predictive Models of Genetic Redundancy in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 3397-3414.	3.5	16
6442	The piggyBac-derived protein 5 (PGBD5) transposes both the closely and the distantly related piggyBac-like elements Tcr-pble and lfp2. <i>Journal of Molecular Biology</i> , 2021, 433, 166839.	2.0	5
6443	Genome-wide identification, evolution, and transcriptome-based expression profiling analysis of suppressors of cytokine signaling (SOCS) in grass carp (<i>Ctenopharyngodon idella</i>). <i>Aquaculture</i> , 2021, 536, 736484.	1.7	3
6445	Complete Chloroplast Genome of <i>Clethra fargesii</i> Franch., an Original Sympetalous Plant from Central China: Comparative Analysis, Adaptive Evolution, and Phylogenetic Relationships. <i>Forests</i> , 2021, 12, 441.	0.9	22
6446	Complex reticulate evolution of speckled brush-furred rats (<i>Lophuromys</i>) in the Ethiopian centre of endemism. <i>Molecular Ecology</i> , 2021, 30, 2349-2365.	2.0	21
6447	Cycad-Weevil Pollination Symbiosis Is Characterized by Rapidly Evolving and Highly Specific Plant-Insect Chemical Communication. <i>Frontiers in Plant Science</i> , 2021, 12, 639368.	1.7	8
6448	Population Genomics Reveals Molecular Determinants of Specialization to Tomato in the Polyphagous Fungal Pathogen <i>Botrytis cinerea</i> in France. <i>Phytopathology</i> , 2021, 111, 2355-2366.	1.1	11
6449	The complete mitochondrial genome of the intertidal spider (<i>Desis jiaxiangi</i>) provides novel insights into the adaptive evolution of the mitogenome and the evolution of spiders. <i>Bmc Ecology and Evolution</i> , 2021, 21, 72.	0.7	13
6451	Structural and Evolutionary Adaptation of NOD-Like Receptors in Birds. <i>BioMed Research International</i> , 2021, 2021, 1-11.	0.9	3
6453	A chromosome-level reference genome of the hazelnut, <i>Corylus heterophylla</i> Fisch. <i>GigaScience</i> , 2021, 10, .	3.3	13
6454	Pseudogenized Amelogenin Reveals Early Tooth Loss in True Toads (<i>Anura: Bufonidae</i>). <i>Integrative and Comparative Biology</i> , 2021, , .	0.9	2
6455	Unearthing LTR Retrotransposon <i>gag</i> Genes Co-opted in the Deep Evolution of Eukaryotes. <i>Molecular Biology and Evolution</i> , 2021, 38, 3267-3278.	3.5	11
6456	The genome of a new anemone species (<i>Actiniaria: Hormathiidae</i>) provides insights into deep-sea adaptation. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2021, 170, 103492.	0.6	11
6457	Comparative Gene Expression Analysis Reveals Mechanism of <i>Pinus contorta</i> Response to the Fungal Pathogen <i>Dothistroma septosporum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 397-409.	1.4	10
6458	Genome-wide investigation and expression analysis of membrane-bound fatty acid desaturase genes under different biotic and abiotic stresses in sunflower (<i>Helianthus annuus</i> L.). <i>International Journal of Biological Macromolecules</i> , 2021, 175, 188-198.	3.6	18
6459	Structural Insights into the Interaction of the Intrinsically Disordered Co-activator TIF2 with Retinoic Acid Receptor Heterodimer (RXR/RAR). <i>Journal of Molecular Biology</i> , 2021, 433, 166899.	2.0	14
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6463	Chloroplast genomes in <i>Populus</i> (Salicaceae): comparisons from an intensively sampled genus reveal dynamic patterns of evolution. <i>Scientific Reports</i> , 2021, 11, 9471.	1.6	15
6465	Evolutionary trade-offs between male secondary sexual traits revealed by a phylogeny of the hyperdiverse tribe Eumaeini (Lepidoptera: Lycaenidae). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20202512.	1.2	9
6466	Elevated phytohaemagglutinin-induced skin swelling response at an intermediate number of MHC class II alleles in bluethroat nestlings. <i>Journal of Avian Biology</i> , 2021, 52, .	0.6	3
6468	Chromosomal-Level Reference Genome of the Neotropical Tree <i>Jacaranda mimosifolia</i> D. Don. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
6469	Myoglobin primary structure reveals multiple convergent transitions to semi-aquatic life in the world's smallest mammalian divers. <i>ELife</i> , 2021, 10, .	2.8	8
6470	Adaptive Proteome Diversification by Nonsynonymous A-to-I RNA Editing in Coleoid Cephalopods. <i>Molecular Biology and Evolution</i> , 2021, 38, 3775-3788.	3.5	22
6471	Gene Duplication and Loss of <i>AANAT</i> in Mammals Driven by Rhythmic Adaptations. <i>Molecular Biology and Evolution</i> , 2021, 38, 3925-3937.	3.5	10
6472	Epidemiology and evolution of Middle East respiratory syndrome coronavirus, 2012–2020. <i>Infectious Diseases of Poverty</i> , 2021, 10, 66.	1.5	37
6473	Molecular phyloecology suggests a trophic shift concurrent with the evolution of the first birds. <i>Communications Biology</i> , 2021, 4, 547.	2.0	4
6474	The Evolution Pathway of Ammonia-Oxidizing Archaea Shaped by Major Geological Events. <i>Molecular Biology and Evolution</i> , 2021, 38, 3637-3648.	3.5	33
6475	Vulture Genomes Reveal Molecular Adaptations Underlying Obligate Scavenging and Low Levels of Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2021, 38, 3649-3663.	3.5	9
6476	Genome sequencing sheds light on the contribution of structural variants to <i>Brassica oleracea</i> diversification. <i>BMC Biology</i> , 2021, 19, 93.	1.7	41
6478	The genome of the warm-season turfgrass African bermudagrass (<i>Cynodon transvaalensis</i>). <i>Horticulture Research</i> , 2021, 8, 93.	2.9	19
6479	Diversification, selective sweep, and body size in the invasive Paelearctic alfalfa weevil infected with <i>Wolbachia</i> . <i>Scientific Reports</i> , 2021, 11, 9664.	1.6	3
6480	Spatial phylogenomics of acrobat ants in Madagascar's Mountains function as cradles for recent diversity and endemism. <i>Journal of Biogeography</i> , 2021, 48, 1706-1719.	1.4	6
6481	Three genomes in the algal genus <i>Volvox</i> reveal the fate of a haploid sex-determining region after a transition to homothallism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	18
6482	Rapid evolution of mammalian APLP1 as a synaptic adhesion molecule. <i>Scientific Reports</i> , 2021, 11, 11305.	1.6	6

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6484	The evolution of the placenta in poeciliid fishes. <i>Current Biology</i> , 2021, 31, 2004-2011.e5.	1.8	23
6485	An evolutionary genomic approach reveals both conserved and species-specific genetic elements related to human disease in closely related <i>Aspergillus</i> fungi. <i>Genetics</i> , 2021, 218, .	1.2	18
6486	Plastome structure and phylogenetic relationships of Styracaceae (Ericales). <i>Bmc Ecology and Evolution</i> , 2021, 21, 103.	0.7	13
6489	Molecular Evolution of Ecological Specialisation: Genomic Insights from the Diversification of Murine Rodents. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	11
6490	Contemporary and historical selection in Tasmanian devils (<i>Sarcophilus harrisii</i>) support novel, polygenic response to transmissible cancer. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20210577.	1.2	9
6491	Positive selection and intrinsic disorder are associated with multifunctional C4(AC4) proteins and geminivirus diversification. <i>Scientific Reports</i> , 2021, 11, 11150.	1.6	11
6492	Disruption of the odorant coreceptor Orco impairs foraging and host finding behaviors in the New World screwworm fly. <i>Scientific Reports</i> , 2021, 11, 11379.	1.6	7
6494	The chloroplast genome evolution of Venus slipper (<i>Paphiopedilum</i>): IR expansion, SSC contraction, and highly rearranged SSC regions. <i>BMC Plant Biology</i> , 2021, 21, 248.	1.6	49
6495	Evolution of the "world's only alpine parrot" Genomic adaptation or phenotypic plasticity, behaviour and ecology?. <i>Molecular Ecology</i> , 2021, 30, 6370-6386.	2.0	11
6496	Gene expression and alternative splicing dynamics are perturbed in female head transcriptomes following heterospecific copulation. <i>BMC Genomics</i> , 2021, 22, 359.	1.2	6
6497	Adaptive evolution of <i>Moniliophthora PR-1</i> proteins towards its pathogenic lifestyle. <i>Bmc Ecology and Evolution</i> , 2021, 21, 84.	0.7	1
6499	The virus-host interface: Molecular interactions of <i>Alphacoronavirus</i> variants from wild and domestic hosts with mammalian aminopeptidase N. <i>Molecular Ecology</i> , 2021, 30, 2607-2625.	2.0	8
6500	A phylogenetic approach for weighting genetic sequences. <i>BMC Bioinformatics</i> , 2021, 22, 285.	1.2	3
6501	Genome-wide identification, evolutionary estimation and functional characterization of two cotton CKI gene types. <i>BMC Plant Biology</i> , 2021, 21, 229.	1.6	1
6502	Morphological convergence and adaptation in cave and pelagic scale worms (Polynoidae, Annelida). <i>Scientific Reports</i> , 2021, 11, 10718.	1.6	9
6504	Molecular and morphological clocks for estimating evolutionary divergence times. <i>Bmc Ecology and Evolution</i> , 2021, 21, 83.	0.7	7
6505	Chromosome-scale assembly of the <i>Sparassia latifolia</i> genome obtained using long-read and Hi-C sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	4

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6508	The genome of <i>Nautilus pompilius</i> illuminates eye evolution and biomineralization. <i>Nature Ecology and Evolution</i> , 2021, 5, 927-938.	3.4	40
6509	Two repeated motifs enriched within some enhancers and origins of replication are bound by SETMAR isoforms in human colon cells. <i>Genomics</i> , 2021, 113, 1589-1604.	1.3	5
6511	Nuku, a family of primate retrocopies derived from <i>KU70</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	0
6512	Molecular mechanisms of mutualistic and antagonistic interactions in a plant-pollinator association. <i>Nature Ecology and Evolution</i> , 2021, 5, 974-986.	3.4	30
6513	Evolutionary, proteomic, and experimental investigations suggest the extracellular matrix of cumulus cells mediates fertilization outcomes. <i>Biology of Reproduction</i> , 2021, 105, 1043-1055.	1.2	7
6514	Extensive introgression and mosaic genomes of Mediterranean endemic lizards. <i>Nature Communications</i> , 2021, 12, 2762.	5.8	30
6515	Interleukins and Interleukin Receptors Evolutionary History and Origin in Relation to CD4+ T Cell Evolution. <i>Genes</i> , 2021, 12, 813.	1.0	21
6516	The tepary bean genome provides insight into evolution and domestication under heat stress. <i>Nature Communications</i> , 2021, 12, 2638.	5.8	43
6517	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	2.0	21
6518	Molecular evolutionary analysis of human primary microcephaly genes. <i>Bmc Ecology and Evolution</i> , 2021, 21, 76.	0.7	5
6519	The genome of a wild <i>Medicago</i> species provides insights into the tolerant mechanisms of legume forage to environmental stress. <i>BMC Biology</i> , 2021, 19, 96.	1.7	39
6520	Genome Sequencing and Assembly Strategies and a Comparative Analysis of the Genomic Characteristics in Penaeid Shrimp Species. <i>Frontiers in Genetics</i> , 2021, 12, 658619.	1.1	14
6521	Comparative Genomics Reveals Factors Associated with Phenotypic Expression of <i>Wolbachia</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	16
6522	The complete mitogenome of <i>Phymorhynchus</i> sp. (Neogastropoda, Conoidea, Raphitomidae) provides insights into the deep-sea adaptive evolution of Conoidea. <i>Ecology and Evolution</i> , 2021, 11, 7518-7531.	0.8	10
6523	Positive Selection in Gene Regulatory Factors Suggests Adaptive Pleiotropic Changes During Human Evolution. <i>Frontiers in Genetics</i> , 2021, 12, 662239.	1.1	8
6524	Searching for signatures of positive selection in cytochrome b gene associated with subterranean lifestyle in fast-evolving arviculines (Arvicolinae, Cricetidae, Rodentia). <i>Bmc Ecology and Evolution</i> , 2021, 21, 92.	0.7	7
6526	Divergence in red light responses associated with thermal reversion of phytochrome B between high- and low-latitude species. <i>New Phytologist</i> , 2021, 231, 75-84.	3.5	4

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6528	Enhanced Negative Regulation of the DHH Signaling Pathway as a Potential Mechanism of Ascrotal Testes in Laurasiatherians. <i>Evolutionary Biology</i> , 2021, 48, 335-345.	0.5	1
6529	A Chromosome-Level Genome Assembly of <i>Ephestia elutella</i> (Hübner, 1796) (Lepidoptera: Tortricidae). <i>Genome Biology and Evolution</i> , 2021, 13, 1-11.	0.784314	4
6530	A novel family of secreted insect proteins linked to plant gall development. <i>Current Biology</i> , 2021, 31, 1836-1849.e12.	1.8	37
6532	Polyploidy underlies co-option and diversification of biosynthetic triterpene pathways in the apple tribe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	37
6533	Expansion of C1Q Genes in Zhikong Scallop and Their Expression Profiling After Exposure to the Toxic Dinoflagellates. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	2
6534	Genomes of Anguillid Herpesvirus 1 Strains Reveal Evolutionary Disparities and Low Genetic Diversity in the Genus <i>Cyprinivirus</i> . <i>Microorganisms</i> , 2021, 9, 998.	1.6	10
6535	Positive selection of the long-wavelength opsin gene in South American cichlid fishes. <i>Hydrobiologia</i> , 2021, 848, 3805-3815.	1.0	2
6538	Positive selection on two mitochondrial coding genes and adaptation signals in hares (genus <i>Lepus</i>) from China. <i>Bmc Ecology and Evolution</i> , 2021, 21, 100.	0.7	4
6539	Phylogenomic and ecological analyses reveal the spatiotemporal evolution of global pines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	85
6540	Functional-genomic analysis reveals intraspecies diversification of antiviral receptor transporter proteins in <i>Xenopus laevis</i> . <i>PLoS Genetics</i> , 2021, 17, e1009578.	1.5	2
6541	Chromosome-level assembly of southern catfish (<i>Milostictus meridionalis</i>) provides insights into visual adaptation to nocturnal and benthic lifestyles. <i>Molecular Ecology Resources</i> , 2021, 21, 1575-1592.	2.2	20
6542	Genomic and anatomical comparisons of skin support independent adaptation to life in water by cetaceans and hippos. <i>Current Biology</i> , 2021, 31, 2124-2139.e3.	1.8	30
6543	Weak selection on synonymous codons substantially inflates <i>dN/dS</i> estimates in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	23
6544	Whole genome sequencing of a snailfish from the Yap Trench (~7,000 m) clarifies the molecular mechanisms underlying adaptation to the deep sea. <i>PLoS Genetics</i> , 2021, 17, e1009530.	1.5	26
6545	The Chromosome-Level Genome of <i>Triplophysa dalaica</i> (Cypriniformes: Cobitidae) Provides Insights into Its Survival in Extremely Alkaline Environment. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
6547	Population-scale peach genome analyses unravel selection patterns and biochemical basis underlying fruit flavor. <i>Nature Communications</i> , 2021, 12, 3604.	5.8	31
6548	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	4.7	53
6549	Distinctive genetic signatures of two fairy shrimp species with overlapping ranges in Iberian temporary ponds. <i>Freshwater Biology</i> , 2021, 66, 1680-1697.	1.2	1

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6550	Gapless indica rice genome reveals synergistic contributions of active transposable elements and segmental duplications to rice genome evolution. <i>Molecular Plant</i> , 2021, 14, 1745-1756.	3.9	50
6552	A chromosome-level <i>Camptotheca acuminata</i> genome assembly provides insights into the evolutionary origin of camptothecin biosynthesis. <i>Nature Communications</i> , 2021, 12, 3531.	5.8	66
6553	A Combined Morphological and Molecular Evolutionary Analysis of Karst-Environment Adaptation for the Genus <i>Urophysa</i> (Ranunculaceae). <i>Frontiers in Plant Science</i> , 2021, 12, 667988.	1.7	2
6555	Insight into the adaptive evolution of mitochondrial genomes in intertidal chitons. <i>Journal of Molluscan Studies</i> , 2021, 87, .	0.4	4
6556	Comparative analysis of the superoxide dismutase gene family in <i>Cetartiodactyla</i> . <i>Journal of Evolutionary Biology</i> , 2021, 34, 1046-1060.	0.8	2
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6560	Time-resolved comparative molecular evolution of oxygenic photosynthesis. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2021, 1862, 148400.	0.5	44
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6585	Identification and function analysis of fasciclin-like arabinogalactan protein family genes in pear (<i>Pyrus bretschneideri</i>). <i>Plant Systematics and Evolution</i> , 2021, 307, 1.	0.3	3
6586	Checklist of fossil liverworts suitable for calibrating phylogenetic reconstructions. <i>Bryophyte Diversity and Evolution</i> , 2021, 43, .	1.0	12
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6614	Chromosome-scale genome assembly of areca palm (<i>Areca catechu</i>). <i>Molecular Ecology Resources</i> , 2021, 21, 2504-2519.	2.2	20
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6621	Genome-wide investigation and transcriptional profiling of the oxidosqualene cyclase (<i>OSC</i>) genes in wheat (<i>Triticum aestivum</i>). <i>Journal of Systematics and Evolution</i> , 2022, 60, 1378-1392.	1.6	2
6623	A chromosome-level genome assembly of the blackspotted croaker (<i>Protonibea diacanthus</i>). <i>Aquaculture and Fisheries</i> , 2022, 7, 616-622.	1.2	1
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6629	Echolocation in soft-furred tree mice. <i>Science</i> , 2021, 372, .	6.0	28
6630	Dissecting the chromosome-level genome of the Asian Clam (<i>Corbicula fluminea</i>). <i>Scientific Reports</i> , 2021, 11, 15021.	1.6	5
6632	Whole-Genome Sequence Analysis of Pseudorabies Virus Clinical Isolates from Pigs in China between 2012 and 2017 in China. <i>Viruses</i> , 2021, 13, 1322.	1.5	9
6634	DNA transposons mediate duplications via transposition-independent and -dependent mechanisms in metazoans. <i>Nature Communications</i> , 2021, 12, 4280.	5.8	9
6635	High-Quality Genome Assembly and Comprehensive Transcriptome of the Painted Lady Butterfly <i>Vanessa cardui</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	10
6636	Prolonged norovirus infections correlate to quasispecies evolution resulting in structural changes of surface-exposed epitopes. <i>IScience</i> , 2021, 24, 102802.	1.9	3

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6641	Chromosome-level genome assembly of Sichuan pepper provides insights into apomixis, drought tolerance, and alkaloid biosynthesis. <i>Molecular Ecology Resources</i> , 2021, 21, 2533-2545.	2.2	30
6642	Evolutionary dynamics of sex-biased genes expressed in cricket brains and gonads. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1188-1211.	0.8	14
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6646	Genome-Wide Comparative Analysis of Flowering-Time Genes; Insights on the Gene Family Expansion and Evolutionary Perspective. <i>Frontiers in Plant Science</i> , 2021, 12, 702243.	1.7	8
6647	De novo chromosome-level assembly of the <i>Centella asiatica</i> genome. <i>Genomics</i> , 2021, 113, 2221-2228.	1.3	14
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6653	Differential insecticidal properties of <i>Spodoptera frugiperda</i> multiple nucleopolyhedrovirus isolates against corn-strain and rice-strain fall armyworm, and genomic analysis of three isolates. <i>Journal of Invertebrate Pathology</i> , 2021, 183, 107561.	1.5	10
6655	Characterization of Nucleotide Binding Site-Encoding Genes in Sweetpotato, <i>Ipomoea batatas</i> (L.) Lam., and Their Response to Biotic and Abiotic Stresses. <i>Cytogenetic and Genome Research</i> , 2021, 161, 257-271.	0.6	7
6657	The <i>Welwitschia</i> genome reveals a unique biology underpinning extreme longevity in deserts. <i>Nature Communications</i> , 2021, 12, 4247.	5.8	51
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6661	Genomic analysis of field pennycress (<i>Thlaspi arvense</i>) provides insights into mechanisms of adaptation to high elevation. <i>BMC Biology</i> , 2021, 19, 143.	1.7	23

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6663	Complete chloroplast genomes of <i>Leptodermis scabrada</i> complex: Comparative genomic analyses and phylogenetic relationships. <i>Gene</i> , 2021, 791, 145715.	1.0	16
6664	Chromosomal-scale genome assembly of <i>Eleutherococcus senticosus</i> provides insights into chromosome evolution in Araliaceae. <i>Molecular Ecology Resources</i> , 2021, 21, 2204-2220.	2.2	10
6665	RNA polymerases in strict endosymbiont bacteria with extreme genome reduction show distinct erosions that might result in limited and differential promoter recognition. <i>PLoS ONE</i> , 2021, 16, e0239350.	1.1	3
6666	Genome sequence of <i>Apostasia ramifera</i> provides insights into the adaptive evolution in orchids. <i>BMC Genomics</i> , 2021, 22, 536.	1.2	9
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6668	A chromosome-level genome assembly of the miiuy croaker (<i>Miichthys miiuy</i>) using nanopore sequencing and Hi-C. <i>Aquaculture and Fisheries</i> , 2024, 9, 218-225.	1.2	4
6669	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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6675	The complete mitochondrial genome of <i>Cycas debaoensis</i> revealed unexpected static evolution in gymnosperm species. <i>PLoS ONE</i> , 2021, 16, e0255091.	1.1	6
6676	Genomic insights into molecular adaptation to intertidal environments in the mangrove <i>Aegiceras corniculatum</i> . <i>New Phytologist</i> , 2021, 231, 2346-2358.	3.5	32
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6678	Nationwide genomic atlas of soil-dwelling <i>Listeria</i> reveals effects of selection and population ecology on pangeneome evolution. <i>Nature Microbiology</i> , 2021, 6, 1021-1030.	5.9	54
6679	Pedigree-based and phylogenetic methods support surprising patterns of mutation rate and spectrum in the gray mouse lemur. <i>Heredity</i> , 2021, 127, 233-244.	1.2	30

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6684	Draft genome of <i>Puya raimondii</i> (Bromeliaceae), the Queen of the Andes. <i>Genomics</i> , 2021, 113, 2537-2546.	1.3	4
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6686	Natural Selection Shapes Maintenance of Orthologous sRNAs in Divergent Host-Restricted Bacterial Genomes. <i>Molecular Biology and Evolution</i> , 2021, 38, 4778-4791.	3.5	2
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6688	An actin-related protein that is most highly expressed in <i>Drosophila</i> testes is critical for embryonic development. <i>ELife</i> , 2021, 10, .	2.8	4
6689	Whole-genome analysis of giraffe supports four distinct species. <i>Current Biology</i> , 2021, 31, 2929-2938.e5.	1.8	49
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6693	Evidence of Adaptive Evolution in Wolbachia-Regulated Gene DNMT2 and Its Role in the Dipteran Immune Response and Pathogen Blocking. <i>Viruses</i> , 2021, 13, 1464.	1.5	8
6695	Complete Chloroplast Genome Sequence of <i>Fortunella venosa</i> (Champ. ex Benth.) C.C.Huang (Rutaceae): Comparative Analysis, Phylogenetic Relationships, and Robust Support for Its Status as an Independent Species. <i>Forests</i> , 2021, 12, 996.	0.9	6
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6700	Ongoing global and regional adaptive evolution of SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	196
6701	Both Conifer II and Gnetales are characterized by a high frequency of ancient mitochondrial gene transfer to the nuclear genome. <i>BMC Biology</i> , 2021, 19, 146.	1.7	18
6702	Genomic regions associated with adaptation to predation in <i>Daphnia</i> often include members of expanded gene families. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20210803.	1.2	7

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6704	Characterizing chloroplast genomes and inferring maternal divergence of the Triticum–Aegilops complex. Scientific Reports, 2021, 11, 15363.	1.6	8
6706	Codon usage patterns and evolution of HSP60 in birds. International Journal of Biological Macromolecules, 2021, 183, 1002-1012.	3.6	12
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6709	Data-driven speciation tree prior for better species divergence times in calibration-poor molecular phylogenies. Bioinformatics, 2021, 37, i102-i110.	1.8	8
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6717	Molecular Evolution of clock Genes in Vertebrates. Journal of Molecular Evolution, 2021, 89, 494-512.	0.8	2
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6722	A shift to shorter cuticular hydrocarbons accompanies sexual isolation among <i>Drosophila americana</i> group populations. <i>Evolution Letters</i> , 2021, 5, 521-540.	1.6	4
6724	Genome-Wide Investigation of Spliceosomal SM/LSM Genes in Wheat (<i>Triticum aestivum</i> L.) and Its Progenitors. <i>Agronomy</i> , 2021, 11, 1429.	1.3	0
6726	Phylogeny and sex chromosome evolution of Palaeognathae. <i>Journal of Genetics and Genomics</i> , 2022, 49, 109-119.	1.7	10
6728	Draft Genome of the Mirrorwing Flyingfish (<i>Hirundichthys speculiger</i>). <i>Frontiers in Genetics</i> , 2021, 12, 695700.	1.1	1
6729	Comparative Genomics Provide Insights Into Function and Evolution of Odorant Binding Proteins in <i>Cydia pomonella</i> . <i>Frontiers in Physiology</i> , 2021, 12, 690185.	1.3	4
6730	Phylogenetic relationships and molecular evolution of woody forest tree family Aceraceae based on plastid phylogenomics and nuclear gene variations. <i>Genomics</i> , 2021, 113, 2365-2376.	1.3	5
6731	Commentary: Unbiasing Genome-Based Analyses of Selection: An Example Using Iconic Shark Species. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	0
6732	Early origin of sweet perception in the songbird radiation. <i>Science</i> , 2021, 373, 226-231.	6.0	34
6733	Rapid Radiation and Rampant Reticulation: Phylogenomics of South American <i>Liolaemus</i> Lizards. <i>Systematic Biology</i> , 2022, 71, 286-300.	2.7	20
6734	Genome assembly of primitive cultivated potato <i>Solanum stenotomum</i> provides insights into potato evolution. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
6735	Genomics and transcriptomics of epizoic Seisonidea (Rotifera, syn. Syndermata) reveal strain formation and gradual gene loss with growing ties to the host. <i>BMC Genomics</i> , 2021, 22, 604.	1.2	6
6737	Plastid genomes and phylogenomics of liverworts (Marchantiophyta): Conserved genome structure but highest relative plastid substitution rate in land plants. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107171.	1.2	12
6739	Exploring the evolutionary process of alkannin/shikonin <i>O</i> -acyltransferases by a reliable <i>Lithospermum erythrorhizon</i> genome. <i>DNA Research</i> , 2021, 28, .	1.5	5
6740	Evolution of the Insect PPK Gene Family. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	15
6741	Phylogenomics Based on Transcriptome Data Provides Evidence for the Internal Phylogenetic Relationships and Potential Terrestrial Evolutionary Genes of Lungfish. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	5
6742	Mitochondrial conflict in a macaque species exhibiting phylogenomic discordance. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1568-1579.	0.8	8
6743	Haplotype-resolved genome of diploid ginger (<i>Zingiber officinale</i>) and its unique gingerol biosynthetic pathway. <i>Horticulture Research</i> , 2021, 8, 189.	2.9	53
6744	Variables Influencing Differences in Sequence Conservation in the Fission Yeast <i>Schizosaccharomyces pombe</i> . <i>Journal of Molecular Evolution</i> , 2021, 89, 601-610.	0.8	0

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6745	Seadragon genome analysis provides insights into its phenotype and sex determination locus. <i>Science Advances</i> , 2021, 7, .	4.7	32
6746	Genome-wide Analysis of Basic Helix-Loop-Helix Family Genes and Expression Analysis in Response to Drought and Salt Stresses in <i>Hibiscus hamabo</i> Sieb. et Zucc. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8748.	1.8	14
6747	Chromosome-Level Genome Assembly of Chinese Sucker (<i>Myxocyprinus asiaticus</i>) Reveals Strongly Conserved Synteny Following a Catostomid-Specific Whole-Genome Duplication. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	12
6748	Molecular evolutionary insights from PRLR in mammals. <i>General and Comparative Endocrinology</i> , 2021, 309, 113791.	0.8	4
6749	The genome of the thin-necked bladder worm <i>Taenia hydatigena</i> reveals evolutionary strategies for helminth survival. <i>Communications Biology</i> , 2021, 4, 1004.	2.0	2
6750	Phylogenomics and evolutionary history of <i>Oreobates</i> (Anura: Craugastoridae) Neotropical frogs along elevational gradients. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107167.	1.2	1
6751	A transposon-mediated reciprocal translocation promotes environmental adaptation but compromises domesticability of wild soybeans. <i>New Phytologist</i> , 2021, 232, 1765-1777.	3.5	5
6752	Genomic comparison of non-photosynthetic plants from the family Balanophoraceae with their photosynthetic relatives. <i>PeerJ</i> , 2021, 9, e12106.	0.9	7
6753	Genome-Wide Analysis of Four Pathotypes of Wheat Rust Pathogen (<i>Puccinia graminis</i>) Reveals Structural Variations and Diversifying Selection. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 701.	1.5	2
6754	Comparative transcriptome provides insights into the selection adaptation between wild and farmed foxes. <i>Ecology and Evolution</i> , 2021, 11, 13475-13486.	0.8	2
6756	Haplotype-resolved genome assembly and allele-specific gene expression in cultivated ginger. <i>Horticulture Research</i> , 2021, 8, 188.	2.9	31
6757	Characterization and Comparative Analysis of Complete Chloroplast Genomes of Three Species From the Genus <i>Astragalus</i> (Leguminosae). <i>Frontiers in Genetics</i> , 2021, 12, 705482.	1.1	10
6759	Relaxation of Selective Constraint on the Ultra-Large Mitochondrial Genomes of Arcidae (Mollusca:). <i>Trends in Ecology and Evolution</i> , 2021, 36, 1073-1083.	0.6	3
6760	Microfossils from the Liuchapo Formation: Possible oldest radiolarians from deep-water chert and phylogenetic analysis. <i>Precambrian Research</i> , 2021, 362, 106312.	1.2	4
6761	Parallel Independent Losses of G-Type Lysozyme Genes in Hairless Aquatic Mammals. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	2
6763	Lycophyte transcriptomes reveal two whole-genome duplications in Lycopodiaceae: Insights into the polyploidization of <i>Phlegmariurus</i> . <i>Plant Diversity</i> , 2022, 44, 262-270.	1.8	6
6764	Hb adaptation to hypoxia in high-altitude fishes: Fresh evidence from schizothoracinae fishes in the Qinghai-Tibetan Plateau. <i>International Journal of Biological Macromolecules</i> , 2021, 185, 471-484.	3.6	8
6766	A derived ZW chromosome system in <i>Amborella trichopoda</i> , representing the sister lineage to all other extant flowering plants. <i>New Phytologist</i> , 2022, 233, 1636-1642.	3.5	10

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6767	The genome of a thorny species: comparative genomic analysis among South and North American Cactaceae. <i>Planta</i> , 2021, 254, 44.	1.6	8
6768	Differential patterns of diversity at neutral and adaptive loci in endangered <i>Rhodeus pseudosericeus</i> populations. <i>Scientific Reports</i> , 2021, 11, 15953.	1.6	3
6769	Common and unique strategies of myoglobin evolution for deep-sea adaptation of diving mammals. <i>IScience</i> , 2021, 24, 102920.	1.9	6
6770	Virulence effector Sidj evolution in <i>Legionella pneumophila</i> is driven by positive selection and intragenic recombination. <i>PeerJ</i> , 2021, 9, e12000.	0.9	1
6771	Plastome-based phylogenomics elucidate relationships in rare Isoetes species groups from the Neotropics. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107177.	1.2	15
6772	Genomic Variation Influences <i>Methanothermococcus</i> Fitness in Marine Hydrothermal Systems. <i>Frontiers in Microbiology</i> , 2021, 12, 714920.	1.5	3
6773	Transcriptomes of <i>Saussurea</i> (Asteraceae) Provide Insights into High-Altitude Adaptation. <i>Plants</i> , 2021, 10, 1715.	1.6	11
6775	Signals of Positive Selection in Sea Slug Transcriptomes. <i>Biological Bulletin</i> , 2021, 241, 55-64.	0.7	0
6776	Genome-wide identification, molecular evolution, and expression divergence of the hexokinase gene family in apple. <i>Journal of Integrative Agriculture</i> , 2021, 20, 2112-2125.	1.7	9
6779	Phylogenomic Analysis of Velvet Worms (Onychophora) Uncovers an Evolutionary Radiation in the Neotropics. <i>Molecular Biology and Evolution</i> , 2021, 38, 5391-5404.	3.5	10
6780	Evolutionary Profile for (Host and Viral) MLKL Indicates Its Activities as a Battlefield for Extensive Counteradaptation. <i>Molecular Biology and Evolution</i> , 2021, 38, 5405-5422.	3.5	13
6781	The <i>Cardamine ensiensis</i> genome reveals whole genome duplication and insight into selenium hyperaccumulation and tolerance. <i>Cell Discovery</i> , 2021, 7, 62.	3.1	15
6782	Convergent Phenotypic Evolution of Rhodopsin for Dim-Light Sensing across Deep-Diving Vertebrates. <i>Molecular Biology and Evolution</i> , 2021, 38, 5726-5734.	3.5	8
6783	VRILLE shows high divergence among Higher Diptera flies but may retain role as transcriptional repressor of Clock. <i>Journal of Insect Physiology</i> , 2021, 133, 104284.	0.9	3
6786	New high-quality peach (<i>Prunus persica</i> L. Batsch) genome assembly to analyze the molecular evolutionary mechanism of volatile compounds in peach fruits. <i>Plant Journal</i> , 2021, 108, 281-295.	2.8	31
6788	The chromosome-scale reference genome of <i>Rubus chingii</i> Hu provides insight into the biosynthetic pathway of hydrolyzable tannins. <i>Plant Journal</i> , 2021, 107, 1466-1477.	2.8	26
6789	Genomic bases underlying the adaptive radiation of core landbirds. <i>Bmc Ecology and Evolution</i> , 2021, 21, 162.	0.7	4
6790	Evolutionary patterns of nucleotide substitution rates in plastid genomes of <i>Quercus</i> . <i>Ecology and Evolution</i> , 2021, 11, 13401-13414.	0.8	9

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6791	Genomic investigation of colour polymorphism and phylogeographic variation among populations of black-headed bulbul (<i>Brachypodius atriceps</i>) in insular southeast Asia. <i>Molecular Ecology</i> , 2021, 30, 4757-4770.	2.0	4
6792	The coral symbiont <i>Candidatus Aquarickettsia</i> is variably abundant in threatened Caribbean acroporids and transmitted horizontally. <i>ISME Journal</i> , 2022, 16, 400-411.	4.4	21
6795	The coordination of major events in C4 photosynthesis evolution in the genus <i>Flaveria</i> . <i>Scientific Reports</i> , 2021, 11, 15618.	1.6	12
6796	Variation in selective constraints along the <i>Plasmodium</i> life cycle. <i>Infection, Genetics and Evolution</i> , 2021, 92, 104908.	1.0	1
6800	Ancient Gene Duplications, Rather Than Polyploidization, Facilitate Diversification of Petal Pigmentation Patterns in <i>Clarkia gracilis</i> (Onagraceae). <i>Molecular Biology and Evolution</i> , 2021, 38, 5528-5538.	3.5	4
6801	Venom of the Annulated Sea Snake <i>Hydrophis cyanocinctus</i> : A Biochemically Simple but Genetically Complex Weapon. <i>Toxins</i> , 2021, 13, 548.	1.5	4
6804	Detecting Selection on Segregating Gene Duplicates in a Population. <i>Journal of Molecular Evolution</i> , 2021, 89, 554-564.	0.8	2
6805	Genome-wide identification and evolutionary analysis of MLO gene family in Rosaceae plants. <i>Horticultural Plant Journal</i> , 2022, 8, 110-122.	2.3	8
6806	High-quality evergreen azalea genome reveals tandem duplication-facilitated low-altitude adaptability and floral scent evolution. <i>Plant Biotechnology Journal</i> , 2021, 19, 2544-2560.	4.1	35
6807	Analysis of the complete chloroplast genomes of <i>Scutellaria tsinyunensis</i> and <i>Scutellaria tubrifera</i> (Lamiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2672-2680.	0.2	4
6808	Whole-genome assembly and annotation of northern wild rice, <i>Zizania palustris</i> L., supports a whole-genome duplication in the <i>Zizania</i> genus. <i>Plant Journal</i> , 2021, 107, 1802-1818.	2.8	7
6809	Comparative Genomic Analysis Reveals Genetic Variation and Adaptive Evolution in the Pathogenicity-Related Genes of <i>Phytophthora capsici</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 694136.	1.5	4
6810	Congruence between oceanic dispersal modelling and phylogeography explains recent evolutionary history of <i>Cycas</i> species with buoyant seeds. <i>New Phytologist</i> , 2021, 232, 1863-1875.	3.5	15
6811	The Oldest Co-opted <i>gag</i> Gene of a Human Endogenous Retrovirus Shows Placenta-Specific Expression and Is Upregulated in Diffuse Large B-Cell Lymphomas. <i>Molecular Biology and Evolution</i> , 2021, 38, 5453-5471.	3.5	11
6814	Population Genomics Reveals Gene Flow and Adaptive Signature in Invasive Weed <i>Mikania micrantha</i> . <i>Genes</i> , 2021, 12, 1279.	1.0	2
6815	Diversity of MHC IIB genes and parasitism in hybrids of evolutionarily divergent cyprinoid species indicate heterosis advantage. <i>Scientific Reports</i> , 2021, 11, 16860.	1.6	5
6816	Taking flight: An ecological, evolutionary and genomic perspective on bat telomeres. <i>Molecular Ecology</i> , 2022, 31, 6053-6068.	2.0	4
6818	The whale shark genome reveals patterns of vertebrate gene family evolution. <i>ELife</i> , 2021, 10, .	2.8	19

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6819	The Interspecific Fungal Hybrid <i>Verticillium longisporum</i> Displays Subgenome-Specific Gene Expression. <i>MBio</i> , 2021, 12, e0149621.	1.8	8
6820	The genome of <i>Cymbidium sinense</i> revealed the evolution of orchid traits. <i>Plant Biotechnology Journal</i> , 2021, 19, 2501-2516.	4.1	46
6821	Comparative and Evolutionary Analyses on the Complete Plastomes of Five <i>Kalanchoe</i> Horticultural Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 705874.	1.7	6
6822	Positive selection as a key player for SARS-CoV-2 pathogenicity: Insights into ORF1ab, S and E genes. <i>Virus Research</i> , 2021, 302, 198472.	1.1	27
6823	Chromosome-scale assembly and evolution of the tetraploid <i>Salvia splendens</i> (Lamiaceae) genome. <i>Horticulture Research</i> , 2021, 8, 177.	2.9	27
6824	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
6825	Highly Diverse Shrub Willows (<i>Salix</i> L.) Share Highly Similar Plastomes. <i>Frontiers in Plant Science</i> , 2021, 12, 662715.	1.7	12
6826	Evidence of micro-evolution in <i>Crocidura russula</i> from two abandoned heavy metal mines: potential use of Cytb, CYP1A1, and p53 as gene biomarkers. <i>Ecotoxicology</i> , 2021, 30, 1969-1982.	1.1	2
6827	Chromosome-scale genome assembly and population genomics provide insights into the adaptation, domestication, and flavonoid metabolism of Chinese plum. <i>Plant Journal</i> , 2021, 108, 1174-1192.	2.8	16
6828	A chromosome-level genome of <i>Antechinus flavipes</i> provides a reference for an Australian marsupial genus with male death after mating. <i>Molecular Ecology Resources</i> , 2022, 22, 740-754.	2.2	12
6831	Examining Signatures of Natural Selection in Antifungal Resistance Genes Across <i>Aspergillus</i> Fungi. <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	2
6832	Genomic and functional evidence reveals convergent evolution in fishes on the Tibetan Plateau. <i>Molecular Ecology</i> , 2021, 30, 5752-5764.	2.0	10
6833	Ancient Mitochondrial Genomes Reveal Extensive Genetic Influence of the Steppe Pastoralists in Western Xinjiang. <i>Frontiers in Genetics</i> , 2021, 12, 740167.	1.1	6
6834	Incipient diploidization of the medicinal plant <i>Perilla</i> within 10,000 years. <i>Nature Communications</i> , 2021, 12, 5508.	5.8	35
6835	A putative de novo evolved gene required for spermatid chromatin condensation in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2021, 17, e1009787.	1.5	20
6837	Comparative transcriptome analysis revealed omnivorous adaptation of the small intestine of <i>Melinae</i> . <i>Scientific Reports</i> , 2021, 11, 19162.	1.6	1
6839	The genomic basis of army ant chemosensory adaptations. <i>Molecular Ecology</i> , 2021, 30, 6627-6641.	2.0	9
6840	Lineage-Specific Variation in IR Boundary Shift Events, Inversions, and Substitution Rates among <i>Caprifoliaceae</i> s.l. (Dipsacales) Plastomes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10485.	1.8	4

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6842	Investigation of Evolutionary History and Origin of the Tre1 Family Suggests a Role in Regulating Hemocytes Cells Infiltration of the Bloodâ€“Brain Barrier. <i>Insects</i> , 2021, 12, 882.	1.0	3
6843	Chloroplast genomes of five <i>Oedogonium</i> species: genome structure, phylogenetic analysis and adaptive evolution. <i>BMC Genomics</i> , 2021, 22, 707.	1.2	11
6844	The evolution of social parasitism in <i>Formica</i> ants revealed by a global phylogeny. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	25
6845	Phylogenomic reconstruction reveals new insights into the evolution and biogeography of <i>Atta</i> leaf-cutting ants (Hymenoptera: Formicidae). <i>Systematic Entomology</i> , 2022, 47, 13-35.	1.7	9
6846	Over-expression of the bottlenose dolphin <i>Hoxd13</i> gene in zebrafish provides new insights into the cetacean flipper formation. <i>Genomics</i> , 2021, 113, 2925-2933.	1.3	2
6847	Diarrheal pathogens trigger rapid evolution of the guanylate cyclase-C signaling axis in bats. <i>Cell Host and Microbe</i> , 2021, 29, 1342-1350.e5.	5.1	5
6848	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
6851	Temperature predicts the rate of molecular evolution in Australian Eugongylinea skinks. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 252-261.	1.1	7
6852	Extensive genomic rearrangements mediated by repetitive sequences in plastomes of <i>Medicago</i> and its relatives. <i>BMC Plant Biology</i> , 2021, 21, 421.	1.6	25
6853	Emerging SARS-CoV-2 variants follow a historical pattern recorded in outgroups infecting non-human hosts. <i>Communications Biology</i> , 2021, 4, 1134.	2.0	3
6855	Molecular evolutionary characteristics of SARSâ€“CoVâ€“2 emerging in the United States. <i>Journal of Medical Virology</i> , 2022, 94, 310-317.	2.5	59
6856	A vast pool of lineage-specific microproteins encoded by long non-coding RNAs in plants. <i>Nucleic Acids Research</i> , 2021, 49, 10328-10346.	6.5	33
6857	Comparative and Phylogenetic Analysis of the Complete Chloroplast Genome of <i>Santalum</i> (Santalaceae). <i>Forests</i> , 2021, 12, 1303.	0.9	9
6858	Patterns of Coevolutionary Adaptations across Time and Space in Mouse Gammaretroviruses and Three Restrictive Host Factors. <i>Viruses</i> , 2021, 13, 1864.	1.5	5
6859	The <i>Euscaphis japonica</i> genome and the evolution of malvids. <i>Plant Journal</i> , 2021, 108, 1382-1399.	2.8	6
6860	A high-quality chromosome-scale assembly of the centipedegrass [<i>Eremochloa ophiuroides</i> (Munro) Hack.] genome provides insights into chromosomal structural evolution and prostrate growth habit. <i>Horticulture Research</i> , 2021, 8, 201.	2.9	8
6862	A tetraploidization event shaped the <i>Aquilaria sinensis</i> genome and contributed to the ability of sesquiterpenes synthesis. <i>BMC Genomics</i> , 2021, 22, 647.	1.2	3
6863	Comparative Mitogenomic Analysis and the Evolution of <i>Rhizoctonia solani</i> Anastomosis Groups. <i>Frontiers in Microbiology</i> , 2021, 12, 707281.	1.5	5

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6865	A high-quality genome assembly of <i>Jasminum sambac</i> provides insight into floral trait formation and Oleaceae genome evolution. <i>Molecular Ecology Resources</i> , 2022, 22, 724-739.	2.2	18
6866	A chromosome-level reference genome of red swamp crayfish <i>Procambarus clarkii</i> provides insights into the gene families regarding growth or development in crustaceans. <i>Genomics</i> , 2021, 113, 3274-3284.	1.3	20
6868	An assembly-free method of phylogeny reconstruction using short-read sequences from pooled samples without barcodes. <i>PLoS Computational Biology</i> , 2021, 17, e1008949.	1.5	0
6869	Segregational Drift Constrains the Evolutionary Rate of Prokaryotic Plasmids. <i>Molecular Biology and Evolution</i> , 2021, 38, 5610-5624.	3.5	14
6870	<i>Zanthoxylum</i> -specific whole genome duplication and recent activity of transposable elements in the highly repetitive paleotetraploid <i>Z. bungeanum</i> genome. <i>Horticulture Research</i> , 2021, 8, 205.	2.9	19
6871	The First Whole Genome Sequencing of <i>Sanghuangporus sanghuang</i> Provides Insights into Its Medicinal Application and Evolution. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 787.	1.5	15
6872	Comparative Chloroplast Genomes of Zosteraceae Species Provide Adaptive Evolution Insights Into Seagrass. <i>Frontiers in Plant Science</i> , 2021, 12, 741152.	1.7	17
6874	Adaptation of Fig Wasps (Agaodinae) to Their Host Revealed by Large-Scale Transcriptomic Data. <i>Insects</i> , 2021, 12, 815.	1.0	5
6876	A high-quality chromosome-level genome of wild <i>Rosa rugosa</i> . <i>DNA Research</i> , 2021, 28, .	1.5	10
6877	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
6878	Phylogenomic approach reveals strong signatures of introgression in the rapid diversification of neotropical true fruit flies (Anastrepha: Tephritidae). <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107200.	1.2	8
6879	Evolutionary rate covariation identifies SLC30A9 (ZnT9) as a mitochondrial zinc transporter. <i>Biochemical Journal</i> , 2021, 478, 3205-3220.	1.7	17
6880	Avian Neo-Sex Chromosomes Reveal Dynamics of Recombination Suppression and W Degeneration. <i>Molecular Biology and Evolution</i> , 2021, 38, 5275-5291.	3.5	25
6881	Comparative molecular evolution of chitinases in ascomycota with emphasis on mycoparasitism lifestyle. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
6882	Plastomes in the holoparasitic family Balanophoraceae: Extremely high AT content, severe gene content reduction, and two independent genetic code changes. <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107208.	1.2	11
6884	Machine learning approaches to identify core and dispensable genes in pangenomes. <i>Plant Genome</i> , 2022, 15, e20135.	1.6	4
6886	A single point mutation causes one-way alteration of pheromone receptor function in two <i>Heliothis</i> species. <i>iScience</i> , 2021, 24, 102981.	1.9	10
6887	Evolutionary origin of a tetraploid <i>Allium</i> species on the Qinghai-Tibet Plateau. <i>Molecular Ecology</i> , 2021, 30, 5780-5795.	2.0	11

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6888	Characterization and expression analysis of wall-associated kinase (WAK) and WAK-like family in cotton. <i>International Journal of Biological Macromolecules</i> , 2021, 187, 867-879.	3.6	20
6889	Multiple independent losses of cell mouth in phylogenetically distant endosymbiotic lineages of oligohymenophorean ciliates: A lesson from <i>Clausilocola</i> . <i>Molecular Phylogenetics and Evolution</i> , 2022, 166, 107310.	1.2	7
6890	Identification and Analysis of GhEXO Gene Family Indicated That GhEXO7_At Promotes Plant Growth and Development Through Brassinosteroid Signaling in Cotton (<i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 719889.	1.7	4
6893	Evolution and dispersal of snakes across the Cretaceous-Paleogene mass extinction. <i>Nature Communications</i> , 2021, 12, 5335.	5.8	13
6895	Whole-Genome Sequencing and Genome-Wide Studies of Spiny Head Croaker (<i>Collichthys lucidus</i>) Reveals Potential Insights for Well-Developed Otoliths in the Family Sciaenidae. <i>Frontiers in Genetics</i> , 2021, 12, 730255.	1.1	0
6897	Frequent intergenotypic recombination between the non-structural and structural genes is a major driver of epidemiological fitness in caliciviruses. <i>Virus Evolution</i> , 2021, 7, veab080.	2.2	24
6898	Insights into angiosperm evolution, floral development and chemical biosynthesis from the <i>Aristolochia fimbriata</i> genome. <i>Nature Plants</i> , 2021, 7, 1239-1253.	4.7	51
6899	The genome sequence provides insights into salt tolerance of <i>Achnatherum splendens</i> (Gramineae), a constructive species of alkaline grassland. <i>Plant Biotechnology Journal</i> , 2022, 20, 116-128.	4.1	18
6900	Genome of the Giant Panda Roundworm Illuminates Its Host Shift and Parasitic Adaptation. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 366-381.	3.0	13
6901	Genomic Resources to Guide Improvement of the Shea Tree. <i>Frontiers in Plant Science</i> , 2021, 12, 720670.	1.7	11
6902	Multi-tissue transcriptome analysis of two <i>Begonia</i> species reveals dynamic patterns of evolution in the chalcone synthase gene family. <i>Scientific Reports</i> , 2021, 11, 17773.	1.6	6
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7289	Genomic and transcriptomic comparisons of closely related malaria parasites differing in virulence and sequestration pattern. <i>Wellcome Open Research</i> , 2018, 3, 142.	0.9	11

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8361	A chromosome-level genome assembly of an alpine plant <i>Crucihimalaya lasiocarpa</i> provides insights into high-altitude adaptation. <i>DNA Research</i> , 2022, 29, .	1.5	13
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8478	Phylogenetic inference of changes in amino acid propensities with single-position resolution. <i>PLoS Computational Biology</i> , 2022, 18, e1009878.	1.5	0
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8480	Insights into the Divergence of Chinese Ips Bark Beetles during Evolutionary Adaptation. <i>Biology</i> , 2022, 11, 384.	1.3	2
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8489	Chromosome-Level Genome Assembly for <i>Acer pseudosieboldianum</i> and Highlights to Mechanisms for Leaf Color and Shape Change. <i>Frontiers in Plant Science</i> , 2022, 13, 850054.	1.7	7
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8491	A chromosome-level genome assembly of <i>Paracymoriza distinctalis</i> (Lepidoptera: Crambidae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	0.6	0
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8505	Landscape of adenosine-to-inosine RNA recoding across human tissues. <i>Nature Communications</i> , 2022, 13, 1184.	5.8	46
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9282	The Visayan Warty Pig (<i>Sus cebifrons</i>) Genome Provides Insight Into Chromosome Evolution and Sensory Adaptation in Pigs. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	3
9283	Genome, genetic evolution, and environmental adaptation mechanisms of <i>Schizophyllum commune</i> in deep seafloor coal-bearing sediments. <i>IScience</i> , 2022, 25, 104417.	1.9	8
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9303	Diet evolution of carnivorous and herbivorous mammals in Laurasiatheria. <i>Bmc Ecology and Evolution</i> , 2022, 22, .	0.7	2
9304	Phylogeny, molecular evolution, and dating of divergences in <i>Lagerstroemia</i> using plastome sequences. <i>Horticultural Plant Journal</i> , 2022, , .	2.3	6
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9310	The First Complete Mitochondrial Genome of <i>Eucrate crenata</i> (Decapoda: Brachyura: Goneplacidae) and Phylogenetic Relationships within Infraorder Brachyura. <i>Genes</i> , 2022, 13, 1127.	1.0	4

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9321	Response to Different Oxygen Partial Pressures and Evolution Analysis of Apoptosis-Related Genes in Plateau Zokor (<i>Myospalax baileyi</i>). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
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9325	The organellar genomes of <i>Silvetia siliquosa</i> (Fucales, Phaeophyceae) and comparative analyses of the brown algae. <i>PLoS ONE</i> , 2022, 17, e0269631.	1.1	0
9326	Centromere drive: model systems and experimental progress. <i>Chromosome Research</i> , 2022, 30, 187-203.	1.0	10
9327	Correlative adaptation between Rubisco and CO ₂ -concentrating mechanisms in seagrasses. <i>Nature Plants</i> , 2022, 8, 706-716.	4.7	15
9329	Genome evolution and diversity of wild and cultivated potatoes. <i>Nature</i> , 2022, 606, 535-541.	13.7	125
9330	Transcriptomic analysis elucidates evolution of the major histocompatibility complex class I in neotropical bats. <i>Journal of Mammalogy</i> , 0, , .	0.6	0
9331	The complete and closed genome of the facultative generalist <i>Candidatus</i> Endoriftia persephone from deep-sea hydrothermal vents. <i>Molecular Ecology Resources</i> , 2022, 22, 3106-3123.	2.2	7

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9333	Molecular Phylogeny and Adaptive Mitochondrial DNA Evolution of Salmonids (Pisces: Salmonidae). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
9335	Cbp1, a fungal virulence factor under positive selection, forms an effector complex that drives macrophage lysis. <i>PLoS Pathogens</i> , 2022, 18, e1010417.	2.1	4
9336	Contextual Constraints: Dynamic Evolution of Snake Venom Phospholipase A2. <i>Toxins</i> , 2022, 14, 420.	1.5	7
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9340	Mitogenomic phylogeny of Typhlocybinae (Hemiptera: Cicadellidae) reveals homoplasy in tribal diagnostic morphological traits. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	11
9341	<i>De novo</i> genes in <i>Arachis hypogaea</i> cv. Tifrunner: systematic identification, molecular evolution, and potential contributions to cultivated peanut. <i>Plant Journal</i> , 0, , .	2.8	0
9342	Evolutionarily conserved odorant-binding proteins participate in establishing tritrophic interactions. <i>IScience</i> , 2022, 25, 104664.	1.9	5
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9347	Plastid and mitochondrial phylogenomics reveal correlated substitution rate variation in <i>Koenigia</i> (Polygonoideae, Polygonaceae) and a reduced plastome for <i>Koenigia delicatula</i> including loss of all <i>ndh</i> genes. <i>Molecular Phylogenetics and Evolution</i> , 2022, 174, 107544.	1.2	5
9348	Clonality and timing of relapsing colorectal cancer metastasis revealed through whole-genome single-cell sequencing. <i>Cancer Letters</i> , 2022, 543, 215767.	3.2	8
9349	Genome assembly provided new insights into the <i>Cinnamomum burmannii</i> evolution and D-borneol biosynthesis differences between chemotypes. <i>Industrial Crops and Products</i> , 2022, 186, 115181.	2.5	6
9350	Chromosome-level genome assembly and annotation of the native Chinese wild blueberry <i>Vaccinium bracteatumFruit Research, 2022, 2, 1-14.	0.9	5

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9352	A chromosome-level genome assembly and intestinal transcriptome of <i>Trypoxylus dichotomus</i> (Coleoptera: Scarabaeidae) to understand its lignocellulose digestion ability. <i>GigaScience</i> , 2022, 11, .	3.3	5
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9354	Integrative genomics analysis of the ever-shrinking pectin methylesterase (PME) gene family in foxtail		

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9387	Genome-wide identification and comparative evolutionary analysis of sorbitol metabolism pathway genes in four Rosaceae species and three model plants. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	5
9388	Genome of <i>Lindera glauca</i> provides insights into the evolution of biosynthesis genes for aromatic compounds. <i>IScience</i> , 2022, 25, 104761.	1.9	2
9389	High-quality ice plant reference genome analysis provides insights into genome evolution and allows exploration of genes involved in the transition from C3 to CAM pathways. <i>Plant Biotechnology Journal</i> , 2022, 20, 2107-2122.	4.1	17
9390	Heat shock protein 70 is a hub gene that underwent adaptive evolution involved in whitefly-wild tomato interaction. <i>Pest Management Science</i> , 2022, 78, 4471-4479.	1.7	1
9391	Secondary reversion to sexual monomorphism associated with tissue-specific loss of <i>doublesex</i> expression. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 2089-2104.	1.1	3
9393	GGDB: A Grameneae genome alignment database of homologous genes hierarchically related to evolutionary events. <i>Plant Physiology</i> , 2022, 190, 340-351.	2.3	1

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9395	Genome-wide local ancestry and evidence for mitonuclear coadaptation in African hybrid cattle populations. <i>IScience</i> , 2022, 25, 104672.	1.9	8
9396	Chromosome-Level Genome Assembly and Transcriptome Comparison Analysis of <i>Cephalopholis sonnerati</i> and Its Related Grouper Species. <i>Biology</i> , 2022, 11, 1053.	1.3	4
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9400	Phylogenomics of the world's otters. <i>Current Biology</i> , 2022, 32, 3650-3658.e4.	1.8	14
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9407	Adaptability and Evolution of Gobiidae: A Genetic Exploration. <i>Animals</i> , 2022, 12, 1741.	1.0	6
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9415	Systematics of the New World bats <i>Eptesicus</i> and <i>Histiotus</i> suggest trans-marine dispersal followed by Neotropical cryptic diversification. <i>Molecular Phylogenetics and Evolution</i> , 2022, 175, 107582.	1.2	4
9416	Pan-genome analysis of three main Chinese chestnut varieties. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
9417	Transcriptomic and gene-family dynamic analyses reveal gene expression pattern and evolution in toxin-producing tissues of Asiatic toad (<i>Bufo gargarizans</i>). <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	1
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9428	A chromosome-level genome assembly of <i>Styphnolobium japonicum</i> combined with comparative genomic analyses offers insights on the evolution of flavonoid and lignin biosynthesis. <i>Industrial Crops and Products</i> , 2022, 187, 115336.	2.5	2
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9438	Evolutionary history of metazoan TMEM16 family. <i>Molecular Phylogenetics and Evolution</i> , 2022, 177, 107595.	1.2	3
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9440	Genetic markers in Andean <i>Puya</i> species (Bromeliaceae) with implications on plastome evolution and phylogeny. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	3
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9451	The genome of the rice planthopper egg parasitoid wasps <i>Anagrus nilaparvatae</i> casts light on the chemo- and mechanosensation in parasitism. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
9452	Comparative Genomics of the Waterfowl Innate Immune System. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	1
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9459	Functional Diversity and Evolution of the <i>Drosophila</i> Sperm Proteome. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100281.	2.5	6
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9462	Chromosome-scale genome assemblies and annotations for Poales species <i>Carex cristatella</i> , <i>Carex scoparia</i> , <i>Juncus effusus</i> , and <i>Juncus inflexus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	9
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9469	Divergent evolution of mitogenomics in Cetartiodactyla niche adaptation. <i>Organisms Diversity and Evolution</i> , 2023, 23, 243-259.	0.7	4
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9471	What snakes and caecilians have in common? Molecular interaction units and the independent origins of similar morphotypes in Tetrapoda. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	1
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9476	Comparative transcriptome and adaptive evolution analysis on the main liver and attaching liver of <i>Pareuchiloglanis macrotrema</i> . <i>Journal of Applied Genetics</i> , 0, .	1.0	0
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9481	Chromosome-level genome assembly and population genomic analyses provide insights into adaptive evolution of the red turpentine beetle, <i>Dendroctonus valens</i> . BMC Biology, 2022, 20, .	1.7	5
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9488	De Novo Whole-Genome Sequencing and Assembly of the Yellow-Throated Bunting (<i>Emberiza elegans</i>) Provides Insights into Its Evolutionary Adaptation. Animals, 2022, 12, 2004.	1.0	0
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9494	Phylotranscriptomic and Evolutionary Analyses of the Green Algal Order Chaetophorales (Chlorophyceae, Chlorophyta). Genes, 2022, 13, 1389.	1.0	1
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9668	Genomic insight into the nocturnal adaptation of the black-crowned night heron (<i>Nycticorax</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742	1.2	2
9669	Novel genome sequence of Chinese cavefish (<i>Triplophysa rosa</i>) reveals pervasive relaxation of natural selection in cavefish genomes. <i>Molecular Ecology</i> , 2022, 31, 5831-5845.	2.0	12
9670	Novel trends of genome evolution in highly complex tropical sponge microbiomes. <i>Microbiome</i> , 2022, 10, .	4.9	9
9671	De novo genome assembly of the medicinal plant <i>Gentiana macrophylla</i> provides insights into the genomic evolution and biosynthesis of iridoids. <i>DNA Research</i> , 2022, 29, .	1.5	10
9673	Lineage-specific protein repeat expansions and contractions reveal malleable regions of immune genes. <i>Genes and Immunity</i> , 2022, 23, 218-234.	2.2	1
9675	The draft genome and multi-omics analyses reveal new insights into geo-herbalism properties of <i>Citrus grandis</i> 'Tomentosa'. <i>Plant Science</i> , 2022, 325, 111489.	1.7	7
9676	Comparative genomics of <i>Sarcoptes scabiei</i> provide new insights into adaptation to permanent parasitism and within-host species divergence. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 3468-3484.	1.3	4
9677	A high-quality <i>Buxus austro-yunnanensis</i> (Buxales) genome provides new insights into karyotype evolution in early eudicots. <i>BMC Biology</i> , 2022, 20, .	1.7	12
9678	A chromosome-level genome assembly for <i>Dracaena cochinchinensis</i> reveals the molecular basis of its longevity and formation of dragon's blood. <i>Plant Communications</i> , 2022, 3, 100456.	3.6	6
9681	Genomes of Two Flying Squid Species Provide Novel Insights into Adaptations of Cephalopods to Pelagic Life. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1053-1065.	3.0	0
9682	The complex genome and adaptive evolution of polyploid Chinese pepper (<i>Zanthoxylum armatum</i>) Tj ETQq0 0 0 rgBT /Overlock 10	4.1	10
9683	Molecular and developmental signatures of genital size macro-evolution in bugs. <i>Molecular Biology and Evolution</i> , 0, , .	3.5	0
9684	An ancient respiratory system in the widespread sedimentary archaea Thermoprofundales. <i>Molecular Biology and Evolution</i> , 0, , .	3.5	2
9685	The Perennial Horse Gram (<i>Macrotyloma axillare</i>) Genome, Phylogeny, and Selection Across the Fabaceae. <i>Compendium of Plant Genomes</i> , 2022, , 255-279.	0.3	2
9686	Genome assembly of the Pendlebury's roundleaf bat, <i>Hipposideros pendleburyi</i> , revealed the expansion of <i>Tc1/Mariner</i> DNA transposons in Rhinolophoidea. <i>DNA Research</i> , 2022, 29, .	1.5	0
9687	Comparative Mitogenomic Analyses and New Insights into the Phylogeny of Thamnocephalidae (Branchiopoda: Anostraca). <i>Genes</i> , 2022, 13, 1765.	1.0	4
9688	Phylogenomics provides insights into the evolution of cactophily and host plant shifts in <i>Drosophila</i> . <i>Molecular Phylogenetics and Evolution</i> , 2023, 178, 107653.	1.2	4
9689	Relationship between genome-wide and MHC class I and II genetic diversity and complementarity in a nonhuman primate. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1

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9691	Genomic Signatures of Mitonuclear Coevolution in Mammals. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	8
9692	Functional Attenuation of <i>UCP1</i> as the Potential Mechanism for Thickened Blubber Layer in Cetaceans. <i>Molecular Biology and Evolution</i> , 0, , .	3.5	0
9693	Cross-species transmission of an ancient endogenous retrovirus and convergent co-option of its envelope gene in two mammalian orders. <i>PLoS Genetics</i> , 2022, 18, e1010458.	1.5	4
9694	The chromosome-level genome of female ginseng (<i>Angelica sinensis</i>) provides insights into molecular mechanisms and evolution of coumarin biosynthesis. <i>Plant Journal</i> , 2022, 112, 1224-1237.	2.8	19
9696	Genomic signatures associated with maintenance of genome stability and venom turnover in two parasitoid wasps. <i>Nature Communications</i> , 2022, 13, .	5.8	16
9697	The pangenome of the wheat pathogen <i>Pyrenophora tritici-repentis</i> reveals novel transposons associated with necrotrophic effectors ToxA and ToxB. <i>BMC Biology</i> , 2022, 20, .	1.7	15
9699	Evolution and antiviral activity of a human protein of retroviral origin. <i>Science</i> , 2022, 378, 422-428.	6.0	37
9701	Population genomics of an icefish reveals mechanisms of glacier-driven adaptive radiation in Antarctic notothenioids. <i>BMC Biology</i> , 2022, 20, .	1.7	5
9702	Characterization and evolutionary diversification of the phospholipase D gene family in mosses. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
9703	Ancient homomorphy of molluscan sex chromosomes sustained by reversible sex-biased genes and sex determiner translocation. <i>Nature Ecology and Evolution</i> , 2022, 6, 1891-1906.	3.4	23
9705	The chromosome-level genome of <i>Akebia trifoliata</i> as an important resource to study plant evolution and environmental adaptation in the Cretaceous. <i>Plant Journal</i> , 2022, 112, 1316-1330.	2.8	14
9706	Phylogenomics reveals the evolution, biogeography, and diversification history of voles in the Hengduan Mountains. <i>Communications Biology</i> , 2022, 5, .	2.0	3
9707	Systematics and evolution of predatory flower flies (Diptera: Syrphidae) based on exon-capture sequencing. <i>Systematic Entomology</i> , 2023, 48, 250-277.	1.7	3
9708	The genome of single-petal jasmine (<i>Jasminum sambac</i>) provides insights into heat stress tolerance and aroma compound biosynthesis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
9710	Multiple origins, one evolutionary trajectory: gradual evolution characterizes distinct lineages of allotetraploid <i>Brachypodium</i> . <i>Genetics</i> , 2023, 223, .	1.2	7
9712	Demographic history and conservation genomics of caribou (<i>Rangifer tarandus</i>) in Québec. <i>Evolutionary Applications</i> , 2022, 15, 2043-2053.	1.5	4
9715	Prediction of a conserved pheromone receptor lineage from antennal transcriptomes of the pine sawyer genus <i>Monochamus</i> (Coleoptera: Cerambycidae). <i>Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology</i> , 0, , .	0.7	0
9718	Biogeography and eye size evolution of the ogre-faced spiders. <i>Scientific Reports</i> , 2022, 12, .	1.6	3

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9720	Evaluation of Genetic Diversity and Parasite-Mediated Selection of MHC Class I Genes in <i>Emberiza godlewskii</i> (Passeriformes: Emberizidae). <i>Diversity</i> , 2022, 14, 925.	0.7	0
9722	Molecular Evolution of Metallothioneins of Antarctic Fish: A Physiological Adaptation to Peculiar Seawater Chemical Characteristics. <i>Journal of Marine Science and Engineering</i> , 2022, 10, 1592.	1.2	2
9723	Characterization and Comparative Analysis of Chloroplast Genomes in Five <i>Uncaria</i> Species Endemic to China. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11617.	1.8	10
9724	Chromosome-scale genome assembly provides insights into the molecular mechanisms of tissue development of <i>Populus wilsonii</i> . <i>Communications Biology</i> , 2022, 5, .	2.0	4
9725	The Chromosome-level genome of <i>Aesculus wilsonii</i> provides new insights into terpenoid biosynthesis and <i>Aesculus</i> evolution. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
9726	Antiviral function and viral antagonism of the rapidly evolving dynein activating adaptor NINL. <i>ELife</i> , 0, 11, .	2.8	6
9727	Natural selection drives the evolution of mitogenomes in <i>Acrossocheilus</i> . <i>PLoS ONE</i> , 2022, 17, e0276056.	1.1	6
9728	Fasulyede Tuz ve Kuraklık Stresi Altında PIF Gen Ailesinin Genom Açığında Analizi ve Karakterizasyonu. <i>Türkiye Tarımsal Araştırmalar Dergisi</i> , 0, , .	0.5	0
9729	Chromosome-level genome assembly of the <i>Verasper variegatus</i> provides insights into left eye migration. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
9730	Integrated phylogenomic analyses unveil reticulate evolution in <i>Parthenocissus</i> (Vitaceae), highlighting speciation dynamics in the Himalayan-Hengduan Mountains. <i>New Phytologist</i> , 2023, 238, 888-903.	3.5	4
9731	Gapless genome assembly of azalea and multi-omics investigation into divergence between two species with distinct flower color. <i>Horticulture Research</i> , 2023, 10, .	2.9	11
9732	A conserved protein disulfide isomerase enhances plant resistance against herbivores. <i>Plant Physiology</i> , 2023, 191, 660-678.	2.3	4
9733	Genome of the endangered Guatemalan Beaded Lizard, <i>Heloderma charlesbogerti</i> , reveals evolutionary relationships of squamates and declines in effective population sizes. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	2
9734	A contiguous <i>de novo</i> genome assembly of sugar beet EL10 (<i>Beta vulgaris</i> L.). <i>DNA Research</i> , 2023, 30, .	1.5	15
9735	The Genetic Diversity and the Divergence Time in Extant Primitive Mayfly, <i>Siphuriscus chinensis</i> Ulmer, 1920 Using the Mitochondrial Genome. <i>Genes</i> , 2022, 13, 1780.	1.0	2
9736	Engineering indel and substitution variants of diverse and ancient enzymes using Graphical Representation of Ancestral Sequence Predictions (GRASP). <i>PLoS Computational Biology</i> , 2022, 18, e1010633.	1.5	16
9737	Probing the origin of prion protein misfolding via reconstruction of ancestral proteins. <i>Protein Science</i> , 0, , .	3.1	2

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9739	Ancestral sequence reconstruction as a tool to study the evolution of wood decaying fungi. <i>Frontiers in Fungal Biology</i> , 0, 3, .	0.9	1
9740	Comprehensive Comparative Analysis and Development of Molecular Markers for <i>Dianthus</i> Species Based on Complete Chloroplast Genome Sequences. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12567.	1.8	4
9741	A Comparative Genomics Approach for Analysis of Complete Mitogenomes of Five Actinidiaceae Plants. <i>Genes</i> , 2022, 13, 1827.	1.0	3
9742	A Chromosome-Scale Genome Assembly of <i>Mitragyna speciosa</i> (Kratom) and the Assessment of Its Genetic Diversity in Thailand. <i>Biology</i> , 2022, 11, 1492.	1.3	2
9744	The characteristics of mRNA m6A methylomes in allopolyploid <i>Brassica napus</i> and its diploid progenitors. <i>Horticulture Research</i> , 2023, 10, .	2.9	2
9745	Two closely related ureotelic fish species of the genus <i>Alcolapia</i> express different levels of ammonium transporters in gills. <i>Biology Open</i> , 2022, 11, .	0.6	1
9746	Thirteen Dipteroidea genomes provide insights into their evolution and borneol biosynthesis. <i>Plant Communications</i> , 2022, 3, 100464.	3.6	6
9747	Meta-analysis of major histocompatibility complex (MHC) class IIA reveals polymorphism and positive selection in many vertebrate species. <i>Molecular Ecology</i> , 2022, 31, 6390-6406.	2.0	6
9749	Comparative genomic and transcriptomic analyses of trans-kingdom pathogen <i>Fusarium solani</i> species complex reveal degrees of compartmentalization. <i>BMC Biology</i> , 2022, 20, .	1.7	3
9751	Genome-Wide Analysis and Characterization of SABATH Gene Family in <i>Phaseolus vulgaris</i> Genotypes Subject to Melatonin under Drought and Salinity Stresses. <i>Plant Molecular Biology Reporter</i> , 2023, 41, 242-259.	1.0	5
9752	Molecular Characterization, Expression, Evolutionary Selection, and Biological Activity Analysis of CD68 Gene from <i>Megalobrama amblycephala</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 13133.	1.8	3
9753	The complete chloroplast genome sequences of three <i>Broussonetia</i> species and comparative analysis within the Moraceae. <i>PeerJ</i> , 0, 10, e14293.	0.9	5
9754	Evolution of increased complexity and specificity at the dawn of form I Rubiscos. <i>Science</i> , 2022, 378, 155-160.	6.0	32
9755	A Comparative Phylogenetic Analysis on the Chloroplast Genome in Different <i>Reynoutria japonica</i> Populations. <i>Genes</i> , 2022, 13, 1979.	1.0	1
9756	The Deadly Toxin Arsenal of the Tree-Dwelling Australian Funnel-Web Spiders. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13077.	1.8	6
9759	Ontogenetic Variation in Macrocytic and Hemicyclic Poplar Rust Fungi. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13062.	1.8	0
9760	Population genetic analyses inferred a limited genetic diversity across the pvama-1 DI domain among <i>Plasmodium vivax</i> isolates from Khyber Pakhtunkhwa regions of Pakistan. <i>BMC Infectious Diseases</i> , 2022, 22, .	1.3	1

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9761	Cistanche Species Mitogenomes Suggest Diversity and Complexity in Lamiales-Order Mitogenomes. <i>Genes</i> , 2022, 13, 1791.	1.0	4
9762	Shared Patterns of Gene Expression and Protein Evolution Associated with Adaptation to Desert Environments in Rodents. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	3
9763	The genome sequence of <i>Hirschfeldia incana</i> , a new Brassicaceae model to improve photosynthetic light-use efficiency. <i>Plant Journal</i> , 0, , .	2.8	2
9764	Unusual Dependence between Gene Expression and Negative Selection in <i>Euplotes</i> . <i>Molecular Biology</i> , 0, , .	0.4	0
9765	Phylogenomics and plastome evolution of a Brazilian mycoheterotrophic orchid, <i>Pogoniopsis schenckii</i> . <i>American Journal of Botany</i> , 2022, 109, 2030-2050.	0.8	8
9766	Evolution of the CBL and CIPK gene families in <i>Medicago</i> : genome-wide characterization, pervasive duplication, and expression pattern under salt and drought stress. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
9767	Chromosome-level genome assembly of the bar-headed goose (<i>Anser indicus</i>). <i>Scientific Data</i> , 2022, 9, .	2.4	2
9768	Inference of Gene Flow between Species under Misspecified Models. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	10
9769	Genome-wide scan for potential CD4+ T-cell vaccine candidates in <i>Candida auris</i> by exploiting reverse vaccinology and evolutionary information. <i>Frontiers in Medicine</i> , 0, , .	1.2	3
9770	Phylogenomics as an effective approach to untangle cross-species hybridization event: A case study in the family Nymphaeaceae. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
9771	Mitochondrial genomic analyses provide new insights into the "missing" <i>atp8</i> and adaptive evolution of Mytilidae. <i>BMC Genomics</i> , 2022, 23, .	1.2	11
9772	The barley DIR gene family: An expanded gene family that is involved in stress responses. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
9773	Whole genome resequencing and comparative genome analysis of three <i>Puccinia striiformis</i> sp. <i>tritici</i> pathotypes prevalent in India. <i>PLoS ONE</i> , 2022, 17, e0261697.	1.1	1
9774	Genomic and phenotypic changes associated with alterations of migratory behaviour in a songbird. <i>Molecular Ecology</i> , 2023, 32, 381-392.	2.0	2
9775	The associated evolution among the extensive RNA editing, GC-biased mutation, and PPR family expansion in the organelle genomes of Selaginellaceae. <i>Journal of Systematics and Evolution</i> , 2023, 61, 890-905.	1.6	2
9776	Evolution of the orthopoxvirus core genome. <i>Virus Research</i> , 2023, 323, 198975.	1.1	3
9777	Olfactory and gustatory receptor genes in fig wasps: Evolutionary insights from comparative studies. <i>Gene</i> , 2023, 850, 146953.	1.0	6
9778	Natural selection pressure exerted on "silent" mutations during the evolution of SARS-CoV-2: Evidence from codon usage and RNA structure. <i>Virus Research</i> , 2023, 323, 198966.	1.1	6

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9780	Dissecting the genome, secretome, and effectome repertoires of <i>Monilinia</i> spp.: The causal agent of brown rot disease: A comparative analysis. <i>Postharvest Biology and Technology</i> , 2023, 195, 112120.	2.9	8
9781	The Soursop Genome (<i>Annona muricata</i> L., Annonaceae). <i>Compendium of Plant Genomes</i> , 2022, , 149-174.	0.3	0
9782	Identification of sex-linked marker and candidate sex determination gene in ornamental fish, African scat (<i>Scatophagus tetracanthus</i>). <i>Aquaculture</i> , 2023, 563, 739023.	1.7	1
9783	Adaptive evolution of <i>scn4aa</i> in Takifugu and Tetraodon. <i>Aquaculture and Fisheries</i> , 2022, , .	1.2	0
9785	Mitochondrial effects on fertility and longevity in <i>Tigriopus californicus</i> contradict predictions of the mother's curse hypothesis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	4
9786	The role of oligomerization in the optimization of cyclohexadienyl dehydratase conformational dynamics and catalytic activity. <i>Protein Science</i> , 2022, 31, .	3.1	4
9787	Identification and Analysis of Stress-Associated Proteins (SAPs) Protein Family and Drought Tolerance of ZmSAP8 in Transgenic Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14109.	1.8	1
9788	Investigating the eukaryotic host-like SLiMs in microbial mimitopes and their potential as novel drug targets for treating autoimmune diseases. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
9789	Whole-genome assembly and annotation for the little yellow croaker (<i>Larimichthys polyactis</i>) provide insights into the evolution of hermaphroditism and gonochorism. <i>Molecular Ecology Resources</i> , 2023, 23, 632-658.	2.2	4
9791	Defensive spines are associated with large geographic range but not diversification in spiny ants (Hymenoptera: Formicidae: <i>Polyrhachis</i>). <i>Systematic Entomology</i> , 0, , .	1.7	1
9792	A high-quality chromosome-level genome assembly of <i>Pelteobagrus vachelli</i> provides insights into its environmental adaptation and population history. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
9793	The highest-elevation frog provides insights into mechanisms and evolution of defenses against high UV radiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	8
9794	The first high-quality chromosome-level genome assembly of Phyllanthaceae (<i>Phyllanthus</i>) Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf 50	1.6	2
9795	The genome of a hadal sea cucumber reveals novel adaptive strategies to deep-sea environments. <i>IScience</i> , 2022, 25, 105545.	1.9	5
9796	A likely autotetraploidization event shaped the Chinese mahogany (<i>Toona sinensis</i>) genome. <i>Horticultural Plant Journal</i> , 2022, , .	2.3	1
9797	Improved assembly and annotation of the sesame genome. <i>DNA Research</i> , 2022, 29, .	1.5	11
9798	Positive selection-driven fixation of a hominin-specific amino acid mutation related to dephosphorylation in IRF9. <i>Bmc Ecology and Evolution</i> , 2022, 22, .	0.7	0

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9800	Whole-genome resequencing reveals complex effects of geographical palaeoclimatic interactions on diversification of moustache toads in East Asia. <i>Molecular Ecology</i> , 2023, 32, 644-659.	2.0	2
9802	Complementary evolution of coding and noncoding sequence underlies mammalian hairlessness. <i>ELife</i> , 0, 11, .	2.8	13
9803	Exploring clade differentiation of the <i>Faecalibacterium prausnitzii</i> complex. <i>IScience</i> , 2022, 25, 105533.	1.9	0
9805	Repeated out-of-Africa expansions of <i>Helicobacter pylori</i> driven by replacement of deleterious mutations. <i>Nature Communications</i> , 2022, 13, .	5.8	5
9806	Gut-specific cardenolide-resistant sodium pump primed an omnivore to feed on toxic oleander. <i>IScience</i> , 2022, 25, 105616.	1.9	1
9807	Plastid phylogenomic insights into relationships, divergence, and evolution of Apiales. <i>Planta</i> , 2022, 256, .	1.6	2
9809	The Mitogenome of <i>Sedum plumbizincicola</i> (Crassulaceae): Insights into RNA Editing, Lateral Gene Transfer, and Phylogenetic Implications. <i>Biology</i> , 2022, 11, 1661.	1.3	1
9810	Chromosome-level genome assembly of the Muscovy duck provides insight into fatty liver susceptibility. <i>Genomics</i> , 2022, 114, 110518.	1.3	2
9811	Plastome sequencing of South American <i>Podocarpus</i> species reveals low rearrangement rates despite ancient gondwanan disjunctions. <i>Molecular Biology Reports</i> , 2023, 50, 309-318.	1.0	2
9813	Genome-wide identification and characterization profile of phosphatidy ethanolamine-binding protein family genes in carrot. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
9815	Draft genome of six Cuban <i>Anolis</i> lizards and insights into genetic changes during their diversification. <i>Bmc Ecology and Evolution</i> , 2022, 22, .	0.7	3
9816	Chromosome-level genome and population genomics reveal evolutionary characteristics and conservation status of Chinese indigenous geese. <i>Communications Biology</i> , 2022, 5, .	2.0	3
9817	Phylogenomics reveals deep relationships and diversification within phylactolaemate bryozoans. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	6
9818	Revisiting ancient polyploidy in leptosporangiate ferns. <i>New Phytologist</i> , 2023, 237, 1405-1417.	3.5	4
9819	De Novo Hybrid Assembly of the <i>Salvia miltiorrhiza</i> Mitochondrial Genome Provides the First Evidence of the Multi-Chromosomal Mitochondrial DNA Structure of <i>Salvia</i> Species. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14267.	1.8	10
9820	Evolutionary analyses of polymeric immunoglobulin receptor (pIgR) in the mammals reveals an outstanding mutation rate in the lagomorphs. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
9822	Sequencing of <i>Camelina neglecta</i> , a diploid progenitor of the hexaploid oilseed <i>Camelina sativa</i> . <i>Plant Biotechnology Journal</i> , 2023, 21, 521-535.	4.1	4

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9824	Characterization of the Chloroplast Genome Structure of <i>Gueldenstaedtia verna</i> (Papilionoideae) and Comparative Analyses among IRLC Species. <i>Forests</i> , 2022, 13, 1942.	0.9	2
9825	Reaction Mechanism of Ancestral α -Lysine Oxidase from <i>Caulobacter</i> Species Studied by Biochemical, Structural, and Computational Analysis. <i>ACS Omega</i> , 2022, 7, 44407-44419.	1.6	2
9827	A Chromosome-level assembly of the Japanese eel genome, insights into gene duplication and chromosomal reorganization. <i>GigaScience</i> , 2022, 11, .	3.3	4
9828	Detection of the peptidyl epitope for vaccine development against MPV. <i>Journal of King Saud University - Science</i> , 2023, 35, 102458.	1.6	3
9829	Ancient origin and conserved gene function in terpene pheromone and defense evolution of stink bugs and hemipteran insects. <i>Insect Biochemistry and Molecular Biology</i> , 2023, 152, 103879.	1.2	9
9830	Chromosomal-level genome and multi-omics dataset provides new insights into leaf pigmentation in <i>Acer palmatum</i> . <i>International Journal of Biological Macromolecules</i> , 2023, 227, 93-104.	3.6	4
9831	Mitogenome-based phylogenomics provides insights into the positions of the enigmatic <i>sinensis</i> group and the <i>sanguinolenta</i> group in Selaginellaceae (Lycophyte). <i>Molecular Phylogenetics and Evolution</i> , 2023, 179, 107673.	1.2	3
9832	Transcriptomic data recover a new superfamily-level phylogeny of Cucujiformia (Coleoptera). <i>Systematic Entomology and Biogeography</i> , 2023, 49, 1-12.	1.2	1
9833	Polymeric structure of the <i>Cannabis sativa</i> L. mitochondrial genome identified with an assembly graph model. <i>Gene</i> , 2023, 853, 147081.	1.0	7
9834	Structural evolution of an amphibian-specific globin: A computational evolutionary biochemistry approach. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2023, 45, 101055.	0.4	0
9835	Chromosome-level genome assembly of the European flat oyster (<i>Ostrea edulis</i>) provides insights into its evolution and adaptation. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2023, 45, 101045.	0.4	6
9836	Genome Wide Analysis and Characterization of NPR-like Gene Family of <i>Phaseolus vulgaris</i> L. , 0, , .		1
9837	Discovering recent selection forces shaping the evolution of dengue viruses based on polymorphism data across geographic scales. <i>Virus Evolution</i> , 2022, 8, .	2.2	0
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9841	Evolutionary Impacts of Pattern Recognition Receptor Genes on Carnivora Complex Habitat Stress Adaptation. <i>Animals</i> , 2022, 12, 3331.	1.0	2
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9882	Genome-Wide Analysis of Wheat GATA Transcription Factor Genes Reveals Their Molecular Evolutionary Characteristics and Involvement in Salt and Drought Tolerance. <i>International Journal of Molecular Sciences</i> , 2023, 24, 27.	1.8	10
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9984	Chromosome fusions repatterned recombination rate and facilitated reproductive isolation during <i>Pristionchus</i> nematode speciation. <i>Nature Ecology and Evolution</i> , 0, , .	3.4	11
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10006	Barbel regeneration and function divergence in red-tail catfish (<i>Hemibagrus wyckioides</i>) based on the chromosome-level genomes and comparative transcriptomes. International Journal of Biological Macromolecules, 2023, 232, 123374.	3.6	1
10007	Plastid phylogenomics and molecular evolution of Thismiaceae (Dioscoreales). American Journal of Botany, 2023, 110, .	0.8	3

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10009	Reduction, evolutionary pattern and positive selection of genes encoding formate dehydrogenase in <i>Woodia-Ljungdahl</i> pathway of gastrointestinal acetogens suggests their adaptation to formate-rich habitats. <i>Environmental Microbiology Reports</i> , 2023, 15, 129-141.	1.0	2
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10108	Life without a sporophyte: the origin and genomic consequences of asexual reproduction in a gametophyte-only fern. <i>International Journal of Plant Sciences</i> , 0, , .	0.6	0
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10110	Chromosome-level reference genome of <i>Tetrastigma hemsleyanum</i> (Vitaceae) provides insights into genomic evolution and the biosynthesis of phenylpropanoids and flavonoids. <i>Plant Journal</i> , 2023, 114, 805-823.	2.8	5

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10137	Genome-Wide Identification of 2-Oxoglutarate and Fe (II)-Dependent Dioxygenase (2ODD-C) Family Genes and Expression Profiles under Different Abiotic Stresses in <i>Camellia sinensis</i> (L.). <i>Plants</i> , 2023, 12, 1302.	1.6	1

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10143	Revealing evolution of tropane alkaloid biosynthesis by analyzing two genomes in the Solanaceae family. <i>Nature Communications</i> , 2023, 14, .	5.8	12
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10148	Comparative genomics reveals the diversification of triterpenoid biosynthesis and origin of ocotillol-type triterpenes in <i>Panax</i> . <i>Plant Communications</i> , 2023, 4, 100591.	3.6	3
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10154	Diversified Mammalian Visual Adaptations to Bright- or Dim-Light Environments. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	3
10155	Chromosome-level de novo genome assembly of two conifer-parasitic wasps, <i>Megastigmus duclouxiana</i> and <i>Megastigmus sabiniae</i> , reveals genomic imprints of adaptation to hosts. <i>Molecular Ecology Resources</i> , 2023, 23, 1142-1154.	2.2	2
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10162	Genome-wide comparative analysis between <i>Cranoglanis boudierius</i> and <i>Pangasianodon hypophthalmus</i> : Reveal the genes related to resistance to low-temperature stress. <i>Journal of the World Aquaculture Society</i> , 2023, 54, 1367-1385.	1.2	1

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10167	Upregulation of ENKD1 disrupts cellular homeostasis to promote lymphoma development. <i>Journal of Cellular Physiology</i> , 0, , .	2.0	0
10168	Genomic convergence underlying high-altitude adaptation in alpine plants. <i>Journal of Integrative Plant Biology</i> , 2023, 65, 1620-1635.	4.1	3
10170	Nuclear phylogeny and insights into whole-genome duplications and reproductive development of Solanaceae plants. <i>Plant Communications</i> , 2023, 4, 100595.	3.6	8
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10193	Extensive MHC class II ^β diversity across multiple loci in the small-spotted catshark (<i>Scyliorhinus</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 5	1.6	1
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