

Bayes Empirical Bayes Inference of Amino Acid Sites Un

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Citation Report

#	ARTICLE	IF	CITATIONS
1	MEDLARS information retrieval in Britain.. Postgraduate Medical Journal, 1966, 42, 69-73.	0.9	6
2	Adaptive Molecular Evolution. , 2004, , .		2
3	Testing for adaptive evolution of the female reproductive protein ZPC in mammals, birds and fishes reveals problems with the M7-M8 likelihood ratio test. BMC Evolutionary Biology, 2005, 5, 65.	3.2	19
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9	Directed Mutagenesis Confirms the Functional Importance of Positively Selected Sites in Polygalacturonase Inhibitor Protein. Molecular Biology and Evolution, 2005, 22, 1531-1534.	3.5	53
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18	Molecular Characterization of Crustacean Visual Pigments and the Evolution of Pancrustacean Opsins. Molecular Biology and Evolution, 2006, 24, 253-268.	3.5	79

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21	Selective Pressures at a Codon-level Predict Deleterious Mutations in Human Disease Genes. <i>Journal of Molecular Biology</i> , 2006, 358, 1390-1404.	2.0	42
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1161	Egernia stokesii (gidgee skink) MHC I positively selected sites lack concordance with HLA peptide binding regions. <i>Immunogenetics</i> , 2017, 69, 49-61.	1.2	5
1162	A Potent Anti-Inflammatory Response in Bat Macrophages May Be Linked to Extended Longevity and Viral Tolerance. <i>Acta Chiropterologica</i> , 2017, 19, 219-228.	0.2	46
1163	Variation in DNA Methylation Is Not Consistently Reflected by Sociality in Hymenoptera. <i>Genome Biology and Evolution</i> , 2017, 9, 1687-1698.	1.1	46
1164	Deciphering the emergence, genetic diversity and evolution of classical swine fever virus. <i>Scientific Reports</i> , 2017, 7, 17887.	1.6	32
1165	Genome-scale detection of positive selection in nine primates predicts human-virus evolutionary conflicts. <i>Nucleic Acids Research</i> , 2017, 45, 10634-10648.	6.5	76
1166	Evolutionary coincidence of adaptive changes in exuperantia and the emergence of bicoid in Cyclorrhapha (Diptera). <i>Development Genes and Evolution</i> , 2017, 227, 355-365.	0.4	11
1167	Host species and pathogenicity effects in the evolution of the mitochondrial genomes of Eimeria species (Apicomplexa; Coccidia; Eimeriidae). <i>Journal of Biological Research</i> , 2017, 24, 13.	2.2	3
1168	Computational Identification of Amino-Acid Mutations that Further Improve the Activity of a Chalcone-Flavonone Isomerase from Glycine max. <i>Frontiers in Plant Science</i> , 2017, 8, 248.	1.7	6
1169	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
1170	Genomic signature of highland adaptation in fish: a case study in Tibetan Schizothoracinae species. <i>BMC Genomics</i> , 2017, 18, 948.	1.2	26
1171	Genome-Wide Comprehensive Analysis the Molecular Phylogenetic Evaluation and Tissue-Specific Expression of SABATH Gene Family in Salvia miltiorrhiza. <i>Genes</i> , 2017, 8, 365.	1.0	14
1172	Recent Positive Selection in Genes of the Mammalian Epidermal Differentiation Complex Locus. <i>Frontiers in Genetics</i> , 2016, 7, 227.	1.1	20

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1173	Adaptive Evolution of Energy Metabolism-Related Genes in Hypoxia-Tolerant Mammals. <i>Frontiers in Genetics</i> , 2017, 8, 205.	1.1	34
1174	Evolution of Anabaenopeptin Peptide Structural Variability in the Cyanobacterium <i>Planktothrix</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 219.	1.5	26
1175	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
1176	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
1177	Genomic Comparisons Reveal Microevolutionary Differences in <i>Mycobacterium abscessus</i> Subspecies. <i>Frontiers in Microbiology</i> , 2017, 8, 2042.	1.5	16
1178	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
1179	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
1180	A novel mitochondrial genome of <i>Arborophila</i> and new insight into <i>Arborophila</i> evolutionary history. <i>PLoS ONE</i> , 2017, 12, e0181649.	1.1	14
1181	Positively selected amino acid replacements within the RuBisCO enzyme of oak trees are associated with ecological adaptations. <i>PLoS ONE</i> , 2017, 12, e0183970.	1.1	11
1182	Positive selection and comparative molecular evolution of reproductive proteins from New Zealand tree weta (Orthoptera, Hemideina). <i>PLoS ONE</i> , 2017, 12, e0188147.	1.1	4
1183	Multilocus Sequence Typing of Pathogens. , 2017, , 383-404.		12
1184	Convergent evolution of SWS2 opsin facilitates adaptive radiation of threespine stickleback into different light environments. <i>PLoS Biology</i> , 2017, 15, e2001627.	2.6	55
1185	Genetic basis of brain size evolution in cetaceans: insights from adaptive evolution of seven primary microcephaly (MCPH) genes. <i>BMC Evolutionary Biology</i> , 2017, 17, 206.	3.2	12
1186	Genome-wide signals of positive selection in stronglylocentrotid sea urchins. <i>BMC Genomics</i> , 2017, 18, 555.	1.2	11
1187	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
1188	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
1189	Polymorphism in the major histocompatibility complex (MHC class II B) genes of the Rufous-backed Bunting (<i>Emberiza jankowskii</i>). <i>PeerJ</i> , 2017, 5, e2917.	0.9	9
1190	Clownfishes evolution below and above the species level. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20171796.	1.2	42

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1191	Distinct domains of the <scp>AVRPM</scp>3^{A2/F2} avirulence protein from wheat powdery mildew are involved in immune receptor recognition and putative effector function. <i>New Phytologist</i> , 2018, 218, 681-695.	3.5	31
1192	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
1193	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
1194	Retained duplications and deletions of CYP2C genes among primates. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 204-212.	1.2	3
1195	A Unique Seminal Plasma Protein, Zona Pellucida 3-Like Protein, has Ca ²⁺ -Dependent Sperm Agglutination Activity. <i>Zoological Science</i> , 2018, 35, 161.	0.3	1
1196	The evolution of immunity in relation to colonization and migration. <i>Nature Ecology and Evolution</i> , 2018, 2, 841-849.	3.4	56
1197	Genetic diversification of chemokine CXCL16 and its receptor CXCR6 in primates. <i>Developmental and Comparative Immunology</i> , 2018, 85, 86-94.	1.0	3
1198	Divergent Selection of Pattern Recognition Receptors in Mammals with Different Ecological Characteristics. <i>Journal of Molecular Evolution</i> , 2018, 86, 138-149.	0.8	22
1199	Footprints of divergent evolution in two Na ⁺ /H ⁺ type antiporter gene families (NHX and SOS1) in the genus <i>Populus</i> . <i>Tree Physiology</i> , 2018, 38, 813-824.	1.4	10
1200	Climate-driven mitochondrial selection: A test in Australian songbirds. <i>Molecular Ecology</i> , 2018, 27, 898-918.	2.0	43
1201	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
1202	Lack of evidence for selection favouring MHC haplotypes that combine high functional diversity. <i>Heredity</i> , 2018, 120, 396-406.	1.2	14
1203	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
1204	Tracing the evolution of the heterotrimeric G protein $\hat{\alpha}$ subunit in Metazoa. <i>BMC Evolutionary Biology</i> , 2018, 18, 51.	3.2	17
1205	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
1206	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
1207	Signature of positive selection in mitochondrial DNA in Cetartiodactyla. <i>Genes and Genetic Systems</i> , 2018, 93, 65-73.	0.2	21
1208	Adaptation to the deep-sea hydrothermal vents and cold seeps: Insights from the transcriptomes of <i>Alvinocaris longirostris</i> in both environments. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2018, 135, 23-33.	0.6	20

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1209	H1N1 seasonal influenza virus evolutionary rate changed over time. <i>Virus Research</i> , 2018, 250, 43-50.	1.1	4
1210	Evolution of Melanoma Antigen-A11 (MAGEA11) During Primate Phylogeny. <i>Journal of Molecular Evolution</i> , 2018, 86, 240-253.	0.8	6
1211	Phenomenological Load on Model Parameters Can Lead to False Biological Conclusions. <i>Molecular Biology and Evolution</i> , 2018, 35, 1473-1488.	3.5	23
1212	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
1213	Genomic Changes Associated with the Evolutionary Transitions of Nostoc to a Plant Symbiont. <i>Molecular Biology and Evolution</i> , 2018, 35, 1160-1175.	3.5	54
1214	Identifying selectively important amino acid positions associated with alternative habitat environments in fish mitochondrial genomes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 511-524.	0.7	4
1215	One-third of the plastid genes evolved under positive selection in PACMAD grasses. <i>Planta</i> , 2018, 247, 255-266.	1.6	99
1216	Lineage-specific evolution of bitter taste receptor genes in the giant and red pandas implies dietary adaptation. <i>Integrative Zoology</i> , 2018, 13, 152-159.	1.3	10
1217	Molecular evolution of myoglobin in the Tibetan Plateau endemic schizothoracine fish (Cyprinidae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i> , 2018, 44, 557-571.	0.9	8
1218	Adaptive evolution of interferon regulatory factors is not correlated with body scale reduction or loss in schizothoracine fish. <i>Fish and Shellfish Immunology</i> , 2018, 73, 145-151.	1.6	8
1219	Convergent selection pressures drive the evolution of rhodopsin kinetics at high altitudes via nonparallel mechanisms. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 170-186.	1.1	16
1220	The complete mitochondrial genome of the alvinocaridid shrimp <i>Shinkaicaris leurokolos</i> (Decapoda). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i> shrimp. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 25, 42-52.	0.4	45
1221	Variations in the breeding behavior of cichlids and the evolution of the multi-functional seminal plasma protein, seminal plasma glycoprotein 120. <i>BMC Evolutionary Biology</i> , 2018, 18, 197.	3.2	3
1222	Genome-wide identification, molecular evolution, and expression analysis of auxin response factor (ARF) gene family in <i>Brachypodium distachyon</i> L. <i>BMC Plant Biology</i> , 2018, 18, 336.	1.6	31
1223	Natural selection in bats with historical exposure to white-nose syndrome. <i>BMC Zoology</i> , 2018, 3, .	0.3	17
1224	Genes Encoding Mammalian Oviductal Proteins Involved in Fertilization are Subjected to Gene Death and Positive Selection. <i>Journal of Molecular Evolution</i> , 2018, 86, 655-667.	0.8	10
1225	Rapidly evolving changes and gene loss associated with host switching in <i>Corynebacterium pseudotuberculosis</i> . <i>PLoS ONE</i> , 2018, 13, e0207304.	1.1	5
1226	Evolutionary conservation of transferrin genomic organization and expression characterization in seven freshwater turtles. <i>Biochemical and Biophysical Research Communications</i> , 2018, 506, 874-882.	1.0	3

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1227	Deciphering the evolutionary signatures of pinnipeds using novel genome sequences: The first genomes of <i>Phoca largha</i> , <i>Callorhinus ursinus</i> , and <i>Eumetopias jubatus</i> . <i>Scientific Reports</i> , 2018, 8, 16877.	1.6	7
1228	Evolutionary Analysis of Plastid Genomes of Seven <i>Lonicera</i> L. Species: Implications for Sequence Divergence and Phylogenetic Relationships. <i>International Journal of Molecular Sciences</i> , 2018, 19, 4039.	1.8	23
1229	Genome sequence of walking catfish (<i>Clarias batrachus</i>) provides insights into terrestrial adaptation. <i>BMC Genomics</i> , 2018, 19, 952.	1.2	36
1230	The first complete mitochondrial genome of the Mariana Trench <i>Freyastera benthophila</i> (Asterozoa: Brisingida: Brisingidae) allows insights into the deep-sea adaptive evolution of Brisingida. <i>Ecology and Evolution</i> , 2018, 8, 10673-10686.	0.8	19
1231	Characterization of a novel N-acylhomoserine lactonase, AidP, from Antarctic <i>Planococcus</i> sp.. <i>Microbial Cell Factories</i> , 2018, 17, 179.	1.9	22
1232	Selective Pressures on Human Cancer Genes along the Evolution of Mammals. <i>Genes</i> , 2018, 9, 582.	1.0	32
1233	Complete mitochondrial genome of <i>Benthodytes marianensis</i> (Holothuroidea: Elasipodida). <i>Journal of Herpetology</i> , 2018, 52, 502-507.	1.1	31
1234	Molecular Evolution of GDP-D-Mannose Epimerase (GME), a Key Gene in Plant Ascorbic Acid Biosynthesis. <i>Frontiers in Plant Science</i> , 2018, 9, 1293.	1.7	23
1235	Positive selection at sites of chemosensory genes is associated with the recent divergence and local ecological adaptation in cactophilic <i>Drosophila</i> . <i>BMC Evolutionary Biology</i> , 2018, 18, 144.	3.2	5
1236	Evidence of positive selection suggests possible role of aquaporins in the water-to-land transition of mudskippers. <i>Organisms Diversity and Evolution</i> , 2018, 18, 499-514.	0.7	8
1237	The evolution of UDP-glycosyl/glucuronosyltransferase 1E (UGT1E) genes in bird lineages is linked to feeding habits but UGT2 genes is not. <i>PLoS ONE</i> , 2018, 13, e0205266.	1.1	4
1238	Comparative Genome-Wide Survey of Single Nucleotide Variation Uncovers the Genetic Diversity and Potential Biomedical Applications among Six <i>Macaca</i> Species. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3123.	1.8	3
1239	Evolutionary Genetics of Hypoxia and Cold Tolerance in Mammals. <i>Journal of Molecular Evolution</i> , 2018, 86, 618-634.	0.8	15
1240	Genome Sequence of Peacock Reveals the Peculiar Case of a Glittering Bird. <i>Frontiers in Genetics</i> , 2018, 9, 392.	1.1	32
1241	Positive Selection in the Evolution of Mammalian CRISPs. <i>Journal of Molecular Evolution</i> , 2018, 86, 635-645.	0.8	6
1242	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
1243	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
1244	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

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1245	Characterization and Expression Patterns of Auxin Response Factors in Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 1395.	1.7	40
1246	Positive selection drives the evolution of endocrine regulatory bone morphogenetic protein system in mammals. <i>Oncotarget</i> , 2018, 9, 18435-18445.	0.8	15
1247	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
1248	Evolutionarily conserved partial gene duplication in the Triticeae tribe of grasses confers pathogen resistance. <i>Genome Biology</i> , 2018, 19, 116.	3.8	9
1249	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
1250	Adaptive genomic evolution of opsins reveals that early mammals flourished in nocturnal environments. <i>BMC Genomics</i> , 2018, 19, 121.	1.2	22
1251	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
1252	Human long intrinsically disordered protein regions are frequent targets of positive selection. <i>Genome Research</i> , 2018, 28, 975-982.	2.4	57
1253	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
1254	Evolution of circadian genes PER and CRY in subterranean rodents. <i>International Journal of Biological Macromolecules</i> , 2018, 118, 1400-1405.	3.6	9
1255	An evolutionary transcriptomics approach links CD36 to membrane remodeling in replicative senescence. <i>Molecular Omics</i> , 2018, 14, 237-246.	1.4	12
1256	Rapid evolutionary dynamics of pepper mild mottle virus. <i>Virus Research</i> , 2018, 256, 96-99.	1.1	7
1257	Positive Selection Driving Cytoplasmic Genome Evolution of the Medicinally Important Ginseng Plant Genus <i>Panax</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 359.	1.7	34
1258	Comparative Chloroplast Genomics of <i>Gossypium</i> Species: Insights Into Repeat Sequence Variations and Phylogeny. <i>Frontiers in Plant Science</i> , 2018, 9, 376.	1.7	86
1259	Comparative Chloroplast Genomics of Dipsacales Species: Insights Into Sequence Variation, Adaptive Evolution, and Phylogenetic Relationships. <i>Frontiers in Plant Science</i> , 2018, 9, 689.	1.7	110
1260	A genome scan of diversifying selection in <i>Ophiocordyceps</i> zombieant fungi suggests a role for enterotoxins in coevolution and host specificity. <i>Molecular Ecology</i> , 2018, 27, 3582-3598.	2.0	22
1261	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
1262	De novo transcriptome assembly and positive selection analysis of an individual deep-sea fish. <i>BMC Genomics</i> , 2018, 19, 394.	1.2	49

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1264	Microbial Community Structure–Function Relationships in Yaquina Bay Estuary Reveal Spatially Distinct Carbon and Nitrogen Cycling Capacities. <i>Frontiers in Microbiology</i> , 2018, 9, 1282.	1.5	48
1265	Molecular evolution of DNMT1 in vertebrates: Duplications in marsupials followed by positive selection. <i>PLoS ONE</i> , 2018, 13, e0195162.	1.1	14
1266	Molecular Evolution and Expression Divergence of HMT Gene Family in Plants. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1248.	1.8	8
1267	Comparative Analysis of the Chloroplast Genomes of the Chinese Endemic Genus <i>Urophysa</i> and Their Contribution to Chloroplast Phylogeny and Adaptive Evolution. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1847.	1.8	92
1268	Genome Sequences of Akhmeta Virus, an Early Divergent Old World Orthopoxvirus. <i>Viruses</i> , 2018, 10, 252.	1.5	32
1269	Genes under positive selection in the core genome of pathogenic <i>Bacillus cereus</i> group members. <i>Infection, Genetics and Evolution</i> , 2018, 65, 55-64.	1.0	11
1270	Genetic variability and lineage phylogeny of human papillomavirus type 45 based on E6 and E7 genes in Southwest China. <i>Virus Research</i> , 2018, 255, 85-89.	1.1	4
1271	Genomic analysis of MHC-based mate choice in the monogamous California mouse. <i>Behavioral Ecology</i> , 2018, 29, 1167-1180.	1.0	9
1272	The polymorphisms of LCR, E6, and E7 of HPV-58 isolates in Yunnan, Southwest China. <i>Virology Journal</i> , 2018, 15, 76.	1.4	9
1273	Discovery of the First Germline-Restricted Gene by Subtractive Transcriptomic Analysis in the Zebra Finch, <i>Taeniopygia guttata</i> . <i>Current Biology</i> , 2018, 28, 1620-1627.e5.	1.8	51
1274	Amino acid compositions contribute to the proteins' evolution under the influence of their abundances and genomic GC content. <i>Scientific Reports</i> , 2018, 8, 7382.	1.6	14
1275	Evolutionary analysis and structural characterization of <i>Aquilaria sinensis</i> sesquiterpene synthase in agarwood formation: A computational study. <i>Journal of Theoretical Biology</i> , 2018, 456, 249-260.	0.8	4
1276	The evolutionary dynamics of H1N1/pdm2009 in India. <i>Infection, Genetics and Evolution</i> , 2018, 65, 276-282.	1.0	13
1277	Floral evolution by simplification in <i>Monanthotaxis</i> (Annonaceae) and hypotheses for pollination system shifts. <i>Scientific Reports</i> , 2018, 8, 12066.	1.6	2
1278	Evolutionary rates of mammalian telomere-stability genes correlate with karyotype features and female germline expression. <i>Nucleic Acids Research</i> , 2018, 46, 7153-7168.	6.5	8
1279	Evolution for extreme living: variation in mitochondrial cytochrome <i>c</i> oxidase genes correlated with elevation in pikas (genus <i>Ochotona</i>). <i>Integrative Zoology</i> , 2018, 13, 517-535.	1.3	8
1280	Genomic organization and adaptive evolution of IGHC genes in marine mammals. <i>Molecular Immunology</i> , 2018, 99, 75-81.	1.0	29

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1281	A transcriptome screen for positive selection in domesticated breadfruit and its wild relatives (<i>T. ETQq0 0 0 rgBT /Overlock 10 Tf 50 74</i>)	0.8	10
1282	Evolution of MHC class I genes in Eurasian badgers, genus <i>Meles</i> (Carnivora, Mustelidae). <i>Heredity</i> , 2019, 122, 205-218.	1.2	9
1283	An evaluation of alternative explanations for widespread cytonuclear discordance in annual sunflowers (<i>Helianthus</i>). <i>New Phytologist</i> , 2019, 221, 515-526.	3.5	118
1284	Contrasting selective patterns across the segmented genome of bluetongue virus in a global reassortment hotspot. <i>Virus Evolution</i> , 2019, 5, vez027.	2.2	17
1285	Diversity, specificity and molecular evolution of the lytic arsenal of <i>Pseudomonas</i> phages: in silico perspective. <i>Environmental Microbiology</i> , 2019, 21, 4136-4150.	1.8	10
1286	Identification of evolutionary and kinetic drivers of NAD-dependent signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15957-15966.	3.3	43
1287	Genome of Alaskapox Virus, A Novel Orthopoxvirus Isolated from Alaska. <i>Viruses</i> , 2019, 11, 708.	1.5	38
1288	Rapid evolution of piRNA pathway and its transposon targets in Japanese flounder (<i>Paralichthys</i>) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 74</i> 100609.	0.4	9
1289	To see or not to see: molecular evolution of the rhodopsin visual pigment in neotropical electric fishes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191182.	1.2	3
1290	AVPR1b variation and the emergence of adaptive phenotypes in Platyrrhini primates. <i>American Journal of Primatology</i> , 2019, 81, e23028.	0.8	13
1291	Genetic structure and variability of tobacco vein banding mosaic virus populations. <i>Archives of Virology</i> , 2019, 164, 2459-2467.	0.9	3
1292	Selection Acting on Genomes. <i>Methods in Molecular Biology</i> , 2019, 1910, 373-397.	0.4	9
1293	Insights into cryptic diversity and adaptive evolution of the clam <i>Coelomactra antiquata</i> (Spengler,) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74</i> 0.3	0.3	2
1294	Genome-Wide Comprehensive Analysis of the SABATH Gene Family in <i>Arabidopsis</i> and Rice. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431986086.	0.6	6
1295	Evolution of <i>Oryza</i> chloroplast genomes promoted adaptation to diverse ecological habitats. <i>Communications Biology</i> , 2019, 2, 278.	2.0	62
1296	Symbiosis, Selection, and Novelty: Freshwater Adaptation in the Unique Sponges of Lake Baikal. <i>Molecular Biology and Evolution</i> , 2019, 36, 2462-2480.	3.5	22
1297	Identification of sex determination genes and their evolution in Phlebotominae sand flies (Diptera,) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74</i> 1.2	1.2	10
1298	The complete mitochondrial genomes of two vent squat lobsters, <i>Munidopsis lauensis</i> and <i>M. Åverrilli</i> : Novel gene arrangements and phylogenetic implications. <i>Ecology and Evolution</i> , 2019, 9, 12390-12407.	0.8	16

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1299	Divergence history and hydrothermal vent adaptation of decapod crustaceans: A mitogenomic perspective. <i>PLoS ONE</i> , 2019, 14, e0224373.	1.1	12
1300	Acute Influenza A virus outbreak in an enzootic infected sow herd: Impact on viral dynamics, genetic and antigenic variability and effect of maternally derived antibodies and vaccination. <i>PLoS ONE</i> , 2019, 14, e0224854.	1.1	24
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1302	Can extreme MHC class I diversity be a feature of a wide geographic range? The example of <i>Seba's</i> short-tailed bat (<i>Carollia perspicillata</i>). <i>Immunogenetics</i> , 2019, 71, 575-587.	1.2	15
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1304	Distinct evolution of toll-like receptor signaling pathway genes in cetaceans. <i>Genes and Genomics</i> , 2019, 41, 1417-1430.	0.5	6
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1366	Comparative Genomic Analysis of the Pheromone Receptor Class 1 Family (V1R) Reveals Extreme Complexity in Mouse Lemurs (Genus, <i>Microcebus</i>) and a Chromosomal Hotspot across Mammals. <i>Genome Biology and Evolution</i> , 2020, 12, 3562-3579.	1.1	12
1367	Comparative plastid genomics of <i>Pinus</i> species: Insights into sequence variations and phylogenetic relationships. <i>Journal of Systematics and Evolution</i> , 2020, 58, 118-132.	1.6	30
1368	A Phenotype-Genotype Codon Model for Detecting Adaptive Evolution. <i>Systematic Biology</i> , 2020, 69, 722-738.	2.7	12
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1391	Comprehensive genomic analysis of the RNase T2 gene family in Rosaceae and expression analysis in <i>Pyrus bretschneideri</i> . <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	7
1392	How Tupanvirus Degrades the Ribosomal RNA of Its Amoebal Host? The Ribonuclease T2 Track. <i>Frontiers in Microbiology</i> , 2020, 11, 1691.	1.5	6
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1398	Senescence and entrenchment in evolution of amino acid sites. <i>Nature Communications</i> , 2020, 11, 4603.	5.8	4
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1400	Comparative ACE2 variation and primate COVID-19 risk. <i>Communications Biology</i> , 2020, 3, 641.	2.0	121
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1417	Genome-wide data reveal discordant mitonuclear introgression in the intermediate horseshoe bat (<i>Rhinolophus affinis</i>). <i>Molecular Phylogenetics and Evolution</i> , 2020, 150, 106886.	1.2	18
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1425	Extensive survey of the <i>ycf4</i> plastid gene throughout the IRLC legumes: Robust evidence of its locus and lineage specific accelerated rate of evolution, pseudogenization and gene loss in the tribe Fabaeae. <i>PLoS ONE</i> , 2020, 15, e0229846.	1.1	10

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1436	A Tale of Two Families: Whole Genome and Segmental Duplications Underlie Glutamine Synthetase and Phosphoenolpyruvate Carboxylase Diversity in Narrow-Leafed Lupin (<i>Lupinus angustifolius</i> L.). <i>International Journal of Molecular Sciences</i> , 2020, 21, 2580.	1.8	7
1437	Antiviral Activity and Adaptive Evolution of Avian Tetherins. <i>Journal of Virology</i> , 2020, 94, .	1.5	4
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1455	Local adaptation in populations of <i>Mycobacterium tuberculosis</i> endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021, 10, 60.	0.8	13
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1467	The complete chloroplast genome of <i>Stauntonia chinensis</i> and compared analysis revealed adaptive evolution of subfamily Lardizabaloideae species in China. <i>BMC Genomics</i> , 2021, 22, 161.	1.2	26

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1475	Molecular Diversity and Evolution of Antimicrobial Peptides in <i>Musca domestica</i> . <i>Diversity</i> , 2021, 13, 107.	0.7	7
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1511	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
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1528	Plastome characterization and comparative analyses of wild crabapples (<i>Malus baccata</i> and <i>M.</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10 and Genomes</i> , 2021, 17, 1.	0.6	11
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1551	A Re-Assessment of Positive Selection on Mitochondrial Genomes of High-Elevation Phrynocephalus Lizards. <i>Journal of Molecular Evolution</i> , 2021, 89, 95-102.	0.8	3
1552	Chloroplast genomic diversity in <i>Bulbophyllum</i> section <i>Macrocaulia</i> (Orchidaceae, Epidendroideae.) <i>Tj ETQq1 1 0.784314 rgBJ/Overlo</i>	1.8	21
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1605	Genome-Wide Identification, Characterization and Phylogenetic Analysis of the Rice LRR-Kinases. <i>PLoS ONE</i> , 2011, 6, e16079.	1.1	69
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1755	The Birth-and-Death Evolution of Cytochrome P450 Genes in Bees. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	11
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1781	Signatures of selection and drivers for novel mutation on transmission-blocking vaccine candidate Pfs25 gene in western Kenya. <i>PLoS ONE</i> , 2022, 17, e0266394.	1.1	2
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1789	Two decades of suspect evidence for adaptive molecular evolutionâ€”negative selection confounding positive-selection signals. <i>National Science Review</i> , 2022, 9, .	4.6	10
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1923	Domain Expansion and Functional Diversification in Vertebrate Reproductive Proteins. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	1
1924	<code>MHCtools</code> â€” an R package for high-throughput sequencing data: Genotyping, haplotype and supertype inference, and downstream genetic analyses in non-model organisms. <i>Molecular Ecology Resources</i> , 2022, 22, 2775-2792.	2.2	4
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1931	The First Complete Mitochondrial Genome of <i>Eucrater crenata</i> (Decapoda: Brachyura: Goneplacidae) and Phylogenetic Relationships within Infraorder Brachyura. <i>Genes</i> , 2022, 13, 1127.	1.0	4
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1940	Comparison of CpG- and UpA-mediated restriction of RNA virus replication in mammalian and avian cells and investigation of potential ZAP-mediated shaping of host transcriptome compositions. <i>Rna</i> , 2022, 28, 1089-1109.	1.6	6
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1942	Comparative Analysis of the Complete Chloroplast Genomes in <i>Allium Section Bromatorrhiza</i> Species (Amaryllidaceae): Phylogenetic Relationship and Adaptive Evolution. <i>Genes</i> , 2022, 13, 1279.	1.0	5
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1952	Variation of natural selection in the Amoebozoa reveals heterogeneity across the phylogeny and adaptive evolution in diverse lineages. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	0
1953	Molecular evolution of vision-related genes may contribute to marsupial photic niche adaptations. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	1
1954	Comparative chloroplast genome analysis of <i>Ficus</i> (Moraceae): Insight into adaptive evolution and mutational hotspot regions. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	16
1955	A Chromosome-Level Genome Assembly of the <i>Rhus</i> Gall Aphid <i>Schlechtendalia chinensis</i> Provides Insight into the Endogenization of Parvovirus-Like DNA Sequences. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1956	Genome-wide identification of wheat ABC1K gene family and functional dissection of TaABC1K3 and TaABC1K6 involved in drought tolerance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
1957	Complete chloroplast genome structure of four <i>Ulmus</i> species and <i>Hemiptelea davidii</i> and comparative analysis within Ulmaceae species. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
1959	Evolutionary rates of body-size-related genes and ecological factors involved in driving body size evolution of squamates. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	0

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1961	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
1962	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
1963	Genomic Signatures of Mitonuclear Coevolution in Mammals. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	8
1964	Detecting signals of adaptive evolution in grape plastomes with a focus on the Cretaceous-Palaeogene (K/Pg) transition. <i>Annals of Botany</i> , 2022, 130, 965-980.	1.4	1
1966	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
1967	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
1968	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
1969	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
1970	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, 9, .	1.2	3
1971	Adaptive evolution of <i>scn4aa</i> in Takifugu and Tetraodon. <i>Aquaculture and Fisheries</i> , 2022, , .	1.2	0
1972	Plastid phylogenomic insights into relationships, divergence, and evolution of <i>Apiales</i> . <i>Planta</i> , 2022, 256, .	1.6	2
1973	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
1974	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
1975	Molecular evolution and diversification of phytoene synthase (PSY) gene family. <i>Genetics and Molecular Biology</i> , 2022, 45, .	0.6	2
1976	Genomic basis of the giga-chromosomes and giga-genome of tree peony <i>Paeonia ostii</i> . <i>Nature Communications</i> , 2022, 13, .	5.8	16
1977	Strategy of micro-environmental adaptation to cold seep among different brittle stars' colonization. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	2
1979	Phylogenetic Analyses of Some Key Genes Provide Information on Pollinator Attraction in Solanaceae. <i>Genes</i> , 2022, 13, 2278.	1.0	1
1980	Comparative analysis of mitochondrial genomes reveals marine adaptation in seagrasses. <i>BMC Genomics</i> , 2022, 23, .	1.2	2

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1981	Stings on wings: Proteotranscriptomic and biochemical profiling of the lesser banded hornet (<i>Vespa</i>) Tj ETQq0 0 0 ggBT /Overlock 10 Tf	1.6	0
1982	Genome-Wide Identification and Phylogenetic Analysis of TRP Gene Family Members in Saurian. <i>Animals</i> , 2022, 12, 3593.	1.0	1
1983	Evaluation of Methods to Detect Shifts in Directional Selection at the Genome Scale. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	4
1984	Molecular and Structural Evolution of Porcine Epidemic Diarrhea Virus. <i>Animals</i> , 2022, 12, 3388.	1.0	2
1985	Rubbing Salt in the Wound: Molecular Evolutionary Analysis of Pain-Related Genes Reveals the Pain Adaptation of Cetaceans in Seawater. <i>Animals</i> , 2022, 12, 3571.	1.0	1
1986	Detection of positive selection acting on protein surfaces at the whole-genome scale in the human malaria parasite <i>Plasmodium falciparum</i> . <i>Infection, Genetics and Evolution</i> , 2023, 107, 105397.	1.0	1
1987	The antigen recognition portion of African buffalo class I MHC is highly polymorphic, consistent with a complex pathogen challenge environment, and the 3â€™™ region suggests distinct haplotype configurations. <i>Immunogenetics</i> , 0, , .	1.2	0
1988	The plastid genome of twenty-two species from <i>Ferula</i> , <i>Talassia</i> , and <i>Soranthus</i> : comparative analysis, phylogenetic implications, and adaptive evolution. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	3
1989	Pollen Coat Proteomes of <i>Arabidopsis thaliana</i> , <i>Arabidopsis lyrata</i> , and <i>Brassica oleracea</i> Reveal Remarkable Diversity of Small Cysteine-Rich Proteins at the Pollen-Stigma Interface. <i>Biomolecules</i> , 2023, 13, 157.	1.8	6
1990	Complete chloroplast genomes and comparative analysis of <i>Ligustrum</i> species. <i>Scientific Reports</i> , 2023, 13, .	1.6	8
1991	Adaptive Evolution of the OAS Gene Family Provides New Insights into the Antiviral Ability of Laurasiatherian Mammals. <i>Animals</i> , 2023, 13, 209.	1.0	2
1992	Near-chromosomal <i>de novo</i> assembly of Bengal tiger genome reveals genetic hallmarks of apex predation. <i>GigaScience</i> , 2022, 12, .	3.3	4
1994	Complete chloroplast genomes provide insights into evolution and phylogeny of Zingiber (<i>Zingiberaceae</i>). <i>BMC Genomics</i> , 2023, 24, .	1.2	11
1995	Nematode gene annotation by machine-learning-assisted proteotranscriptomics enables proteome-wide evolutionary analysis. <i>Genome Research</i> , 2023, 33, 112-128.	2.4	1
1996	Highly Dynamic Gene Family Evolution Suggests Changing Roles for <i>PON</i> Genes Within Metazoa. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	2
1997	Complete chloroplast genome molecular structure, comparative and phylogenetic analyses of <i>Sphaeropteris lepifera</i> of Cyatheaceae family: a tree fern from China. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
1998	Is the Association of the Rare rs35667974 <i>IFIH1</i> Gene Polymorphism With Autoimmune Diseases a Case of RNA Epigenetics?. <i>Journal of Molecular Evolution</i> , 0, , .	0.8	2
1999	Adaptation of Antarctic Icefish Vision to Extreme Environments. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	0

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2000	Reduction, evolutionary pattern and positive selection of genes encoding formate dehydrogenase in <i>Woodia-Jungdahl</i> pathway of gastrointestinal acetogens suggests their adaptation to formate-rich habitats. <i>Environmental Microbiology Reports</i> , 2023, 15, 129-141.	1.0	2
2001	The deep-rooted origin of disulfide-rich spider venom toxins. <i>ELife</i> , 0, 12, .	2.8	3
2002	Organelle genomes of <i>Indigofera amblyantha</i> and <i>Indigofera pseudotinctoria</i> : comparative genome analysis, and intracellular gene transfer. <i>Industrial Crops and Products</i> , 2023, 198, 116674.	2.5	2
2003	Signatures of purifying selection and site-specific positive selection on the mitochondrial DNA of dromedary camels (<i>Camelus dromedarius</i>). <i>Mitochondrion</i> , 2023, 69, 36-42.	1.6	2
2004	Phylogeny and adaptive evolution of subgenus <i>Rhizirideum</i> (Amaryllidaceae, <i>Allium</i>) based on plastid genomes. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	5
2005	Characterization of Megabat-Favored, CA-Dependent Susceptibility to Retrovirus Infection. <i>Journal of Virology</i> , 2023, 97, .	1.5	2
2006	Chloroplast genomic comparison provides insights into the evolution of seagrasses. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	2
2007	Purifying selection decreases the potential for Bangui orthobunyavirus outbreaks in humans. <i>Virus Evolution</i> , 2023, 9, .	2.2	2
2008	Genome-wide identification, expression profile and evolutionary relationships of TPS genes in the neotropical fruit tree species <i>Psidium cattleianum</i> . <i>Scientific Reports</i> , 2023, 13, .	1.6	1
2010	Upregulation of ENKD1 disrupts cellular homeostasis to promote lymphoma development. <i>Journal of Cellular Physiology</i> , 0, , .	2.0	0
2011	Polymorphism analysis of major histocompatibility complex (MHC) DQB gene in the Asiatic black bear (<i>Ursus thibetanus</i>). <i>Mammal Research</i> , 0, , .	0.6	0
2012	Selection in coral mitogenomes, with insights into adaptations in the deep sea. <i>Scientific Reports</i> , 2023, 13, .	1.6	6
2013	The evolution and diurnal expression patterns of photosynthetic pathway genes of the invasive alien weed, <i>Mikania micrantha</i> . <i>Journal of Integrative Agriculture</i> , 2024, 23, 590-604.	1.7	0
2014	Phylogenetic Relationships of the Pseudogobionini Group (Teleostei: Cyprinidae) with Selection Pressure Analyses to Genes of Mitochondrial Genome. <i>Fishes</i> , 2023, 8, 201.	0.7	0
2016	Positive selection on ADAM10 builds species recognition in the synchronous spawning coral <i>Acropora</i> . <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	2
2017	Conservation and variation in the region of the <i>Theileria parva</i> p104 antigen coding gene used for PCR surveillance of the parasite. <i>Parasitology Research</i> , 0, , .	0.6	0