

Masami Hasegawa

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11808887/publications.pdf>

Version: 2024-02-01

185
papers

27,210
citations

13865

67
h-index

5829

161
g-index

186
all docs

186
docs citations

186
times ranked

21822
citing authors

#	ARTICLE	IF	CITATIONS
1	Dating of the human-ape splitting by a molecular clock of mitochondrial DNA. <i>Journal of Molecular Evolution</i> , 1985, 22, 160-174.	1.8	7,690
2	Evaluation of the maximum likelihood estimate of the evolutionary tree topologies from DNA sequence data, and the branching order in hominoidea. <i>Journal of Molecular Evolution</i> , 1989, 29, 170-179.	1.8	3,224
3	CONSEL: for assessing the confidence of phylogenetic tree selection. <i>Bioinformatics</i> , 2001, 17, 1246-1247.	4.1	1,958
4	Evolutionary analysis of Arabidopsis, cyanobacterial, and chloroplast genomes reveals plastid phylogeny and thousands of cyanobacterial genes in the nucleus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12246-12251.	7.1	1,074
5	Maximum likelihood inference of protein phylogeny and the origin of chloroplasts. <i>Journal of Molecular Evolution</i> , 1990, 31, 151-160.	1.8	789
6	Gene transfer to the nucleus and the evolution of chloroplasts. <i>Nature</i> , 1998, 393, 162-165.	27.8	717
7	The yak genome and adaptation to life at high altitude. <i>Nature Genetics</i> , 2012, 44, 946-949.	21.4	708
8	Model of amino acid substitution in proteins encoded by mitochondrial DNA. <i>Journal of Molecular Evolution</i> , 1996, 42, 459-468.	1.8	487
9	Phylogenomic datasets provide both precision and accuracy in estimating the timescale of placental mammal phylogeny. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 3491-3500.	2.6	449
10	Towards Resolving the Interordinal Relationships of Placental Mammals. <i>Systematic Biology</i> , 1999, 48, 1-5.	5.6	306
11	Interordinal Relationships of Birds and Other Reptiles Based on Whole Mitochondrial Genomes. <i>Systematic Biology</i> , 1999, 48, 138-152.	5.6	253
12	Phylogenetic relationships among eutherian orders estimated from inferred sequences of mitochondrial proteins: Instability of a tree based on a single gene. <i>Journal of Molecular Evolution</i> , 1994, 39, 519-27.	1.8	239
13	Ribosomal RNA trees misleading?. <i>Nature</i> , 1993, 361, 23-23.	27.8	230
14	On the maximum likelihood method in molecular phylogenetics. <i>Journal of Molecular Evolution</i> , 1991, 32, 443-445.	1.8	221
15	Conflict Among Individual Mitochondrial Proteins in Resolving the Phylogeny of Eutherian Orders. <i>Journal of Molecular Evolution</i> , 1998, 47, 307-322.	1.8	208
16	Pegasoferae, an unexpected mammalian clade revealed by tracking ancient retroposon insertions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9929-9934.	7.1	207
17	Plastid Genome Phylogeny and a Model of Amino Acid Substitution for Proteins Encoded by Chloroplast DNA. <i>Journal of Molecular Evolution</i> , 2000, 50, 348-358.	1.8	204
18	Toward a more accurate time scale for the human mitochondrial DNA tree. <i>Journal of Molecular Evolution</i> , 1993, 37, 347-354.	1.8	190

#	ARTICLE	IF	CITATIONS
19	Molecular clock of silent substitution: At least six-fold preponderance of silent changes in mitochondrial genes over those in nuclear genes. <i>Journal of Molecular Evolution</i> , 1982, 19, 28-35.	1.8	174
20	Phylogenetic relationships among eukaryotic kingdoms inferred from ribosomal RNA sequences. <i>Journal of Molecular Evolution</i> , 1985, 22, 32-38.	1.8	171
21	Using Novel Phylogenetic Methods to Evaluate Mammalian mtDNA, Including Amino Acid-Invariant Sites-LogDet plus Site Stripping, to Detect Internal Conflicts in the Data, with Special Reference to the Positions of Hedgehog, Armadillo, and Elephant. <i>Systematic Biology</i> , 1999, 48, 31-53.	5.6	153
22	Relative Efficiencies of the Maximum Likelihood, Maximum Parsimony, and Neighbor-Joining Methods for Estimating Protein Phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 1993, 2, 1-5.	2.7	149
23	Early branchings in the evolution of eukaryotes: Ancient divergence of entamoeba that lacks mitochondria revealed by protein sequence data. <i>Journal of Molecular Evolution</i> , 1993, 36, 380-8.	1.8	147
24	Mitochondrial Phylogenetics and Evolution of Mysticete Whales. <i>Systematic Biology</i> , 2005, 54, 77-90.	5.6	143
25	Man's place in Hominoidea as inferred from molecular clocks of DNA. <i>Journal of Molecular Evolution</i> , 1987, 26, 132-147.	1.8	142
26	Combining Multiple Data Sets in a Likelihood Analysis: Which Models are the Best?. <i>Molecular Biology and Evolution</i> , 2002, 19, 2294-2307.	8.9	136
27	Time scale of eutherian evolution estimated without assuming a constant rate of molecular evolution.. <i>Genes and Genetic Systems</i> , 2003, 78, 267-283.	0.7	134
28	Maximum Likelihood Analysis of the Complete Mitochondrial Genomes of Eutherians and a Reevaluation of the Phylogeny of Bats and Insectivores. <i>Journal of Molecular Evolution</i> , 2001, 53, 508-516.	1.8	128
29	[34] Converting distance to time: Application to human evolution. <i>Methods in Enzymology</i> , 1990, 183, 550-570.	1.0	125
30	The Phylogenetic Position of Red Algae Revealed by Multiple Nuclear Genes from Mitochondria-Containing Eukaryotes and an Alternative Hypothesis on the Origin of Plastids. <i>Journal of Molecular Evolution</i> , 2003, 56, 485-497.	1.8	123
31	Phylogenomics and Morphology of Extinct Paleognaths Reveal the Origin and Evolution of the Ratites. <i>Current Biology</i> , 2017, 27, 68-77.	3.9	123
32	Protein phylogeny of translation elongation factor EF-1 α suggests microsporidians are extremely ancient eukaryotes. <i>Journal of Molecular Evolution</i> , 1996, 42, 257-263.	1.8	110
33	Phylogeny, Recombination, and Mechanisms of Stepwise Mitochondrial Genome Reorganization in Mantellid Frogs from Madagascar. <i>Molecular Biology and Evolution</i> , 2008, 25, 874-891.	8.9	108
34	Interordinal relationships and timescale of eutherian evolution as inferred from mitochondrial genome data. <i>Gene</i> , 2000, 259, 149-158.	2.2	107
35	Tempo and mode of mitochondrial DNA evolution in vertebrates at the amino acid sequence level: Rapid evolution in warm-blooded vertebrates. <i>Journal of Molecular Evolution</i> , 1993, 36, 270-281.	1.8	106
36	Relationships between BK virus lineages and human populations. <i>Microbes and Infection</i> , 2007, 9, 204-213.	1.9	106

#	ARTICLE	IF	CITATIONS
37	Molecular phylogeny and evolution of prosimians based on complete sequences of mitochondrial DNAs. <i>Gene</i> , 2009, 441, 53-66.	2.2	105
38	Assessing the Cretaceous Superordinal Divergence Times within Birds and Placental Mammals by Using Whole Mitochondrial Protein Sequences and an Extended Statistical Framework. <i>Systematic Biology</i> , 1999, 48, 119-137.	5.6	104
39	Complete Nucleotide Sequence and Gene Rearrangement of the Mitochondrial Genome of the Japanese Pond Frog <i>Rana nigromaculata</i> .. <i>Genes and Genetic Systems</i> , 2001, 76, 311-325.	0.7	99
40	Intraspecific phylogeny and geographical variation of six species of northeastern Asiatic <i>Sorex</i> shrews based on the mitochondrial cytochrome b sequences. <i>Molecular Ecology</i> , 2001, 10, 2199-2213.	3.9	99
41	A new molecular clock of mitochondrial DNA and the evolution of hominoids.. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 1984, 60, 95-98.	3.8	98
42	Time of the deepest root for polymorphism in human mitochondrial DNA. <i>Journal of Molecular Evolution</i> , 1991, 32, 37-42.	1.8	96
43	Domestication Relaxed Selective Constraints on the Yak Mitochondrial Genome. <i>Molecular Biology and Evolution</i> , 2011, 28, 1553-1556.	8.9	93
44	Phylogenetic Position of <i>Blastocystis hominis</i> and of Stramenopiles Inferred from Multiple Molecular Sequence Data. <i>Journal of Eukaryotic Microbiology</i> , 2002, 49, 42-53.	1.7	92
45	Geometrical models of territory I. Models for synchronous and asynchronous settlement of territories. <i>Journal of Theoretical Biology</i> , 1980, 82, 477-496.	1.7	91
46	Appropriate Likelihood Ratio Tests and Marginal Distributions for Evolutionary Tree Models with Constraints on Parameters. <i>Molecular Biology and Evolution</i> , 2000, 17, 798-803.	8.9	91
47	Extensive mitochondrial gene arrangements in coleoid Cephalopoda and their phylogenetic implications. <i>Molecular Phylogenetics and Evolution</i> , 2006, 38, 648-658.	2.7	91
48	Improved dating of the human/chimpanzee separation in the mitochondrial DNA tree: Heterogeneity among amino acid sites. <i>Journal of Molecular Evolution</i> , 1995, 40, 622-628.	1.8	87
49	Phylogenetic position of turtles among amniotes: evidence from mitochondrial and nuclear genes. <i>Gene</i> , 2000, 259, 139-148.	2.2	87
50	Effects of Character Weighting and Species Sampling on Phylogeny Reconstruction: A Case Study Based on DNA Sequence Data in Cetaceans. <i>Genetics</i> , 1996, 144, 1817-1833.	2.9	85
51	Mammalian Evolution: Timing and Implications from Using the LogDeterminant Transform for Proteins of Differing Amino Acid Composition. <i>Systematic Biology</i> , 1999, 48, 76-93.	5.6	84
52	<i>Balaenoptera omurai</i> is a newly discovered baleen whale that represents an ancient evolutionary lineage. <i>Molecular Phylogenetics and Evolution</i> , 2006, 41, 40-52.	2.7	84
53	Radiation and speciation of pelagic organisms during periods of global warming: the case of the common minke whale, <i>Balaenoptera acutorostrata</i> . <i>Molecular Ecology</i> , 2007, 16, 1481-1495.	3.9	83
54	Rooting the eutherian tree: the power and pitfalls of phylogenomics. <i>Genome Biology</i> , 2007, 8, R199.	9.6	82

#	ARTICLE	IF	CITATIONS
55	The Position of Gnetales among Seed Plants: Overcoming Pitfalls of Chloroplast Phylogenomics. <i>Molecular Biology and Evolution</i> , 2010, 27, 2855-2863.	8.9	82
56	The platypus put in its place. <i>Nature</i> , 1997, 387, 549-550.	27.8	81
57	Ultrastructure of the Dermal Chromatophores in a Lizard (Scincidae: <i>Plestiodon latiscutatus</i>) with Conspicuous Body and Tail Coloration. <i>Zoological Science</i> , 2006, 23, 793-799.	0.7	79
58	The monophyletic origin of sea lions and fur seals (Carnivora; Otariidae) in the Southern Hemisphere. <i>Gene</i> , 2009, 441, 89-99.	2.2	79
59	Root of the Eukaryota Tree as Inferred from Combined Maximum Likelihood Analyses of Multiple Molecular Sequence Data. <i>Molecular Biology and Evolution</i> , 2005, 22, 409-420.	8.9	78
60	Estimation of branching dates among primates by molecular clocks of nuclear DNA which slowed down in Hominoidea. <i>Journal of Human Evolution</i> , 1989, 18, 461-476.	2.6	76
61	Evolution of RNA polymerases and branching patterns of the three major groups of archaeobacteria. <i>Journal of Molecular Evolution</i> , 1991, 32, 70-78.	1.8	76
62	Mitochondrial DNA evolution in primates: Transition rate has been extremely low in the lemur. <i>Journal of Molecular Evolution</i> , 1990, 31, 113-121.	1.8	75
63	Evolution of Human Polyomavirus JC: Implications for the Population History of Humans. <i>Journal of Molecular Evolution</i> , 2002, 54, 285-297.	1.8	75
64	The status of the Japanese and East Asian bats of the genus <i>Myotis</i> (Vespertilionidae) based on mitochondrial sequences. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 297-307.	2.7	74
65	The Origin of Chlorarachniophyte Plastids, as Inferred from Phylogenetic Comparisons of Amino Acid Sequences of EF-Tu. <i>Journal of Molecular Evolution</i> , 1997, 45, 682-687.	1.8	72
66	Confidence Limits of the Maximum-Likelihood Estimate of the Hominoid three from Mitochondrial-DNA Sequences. <i>Evolution; International Journal of Organic Evolution</i> , 1989, 43, 672.	2.3	71
67	CONFIDENCE LIMITS ON THE MAXIMUM-LIKELIHOOD ESTIMATE OF THE HOMINOID TREE FROM MITOCHONDRIAL-DNA SEQUENCES. <i>Evolution; International Journal of Organic Evolution</i> , 1989, 43, 672-677.	2.3	71
68	Secondary structure of MS2 phage RNA and bias in code word usage. <i>Nucleic Acids Research</i> , 1979, 7, 2073-2079.	14.5	69
69	Heterogeneity of tempo and mode of mitochondrial DNA evolution among mammalian orders.. <i>Japanese Journal of Genetics</i> , 1989, 64, 243-258.	1.0	68
70	Close phylogenetic relationship between vestimentifera (tube worms) and annelida revealed by the amino acid sequence of elongation factor-1?. <i>Journal of Molecular Evolution</i> , 1993, 37, 66-70.	1.8	68
71	Molecular phylogenetic study on the origin and evolution of Mustelidae. <i>Gene</i> , 2007, 396, 1-12.	2.2	66
72	Phylogeographical analyses of domestic and wild yaks based on mitochondrial DNA: new data and reappraisal. <i>Journal of Biogeography</i> , 2010, 37, 2332-2344.	3.0	66

#	ARTICLE	IF	CITATIONS
73	Complete Nucleotide Sequences of the Genes Encoding Translation Elongation Factors 1 \hat{A} and 2 from a microsporidian parasite, <i>Glugea plecoglossi</i> : Implications for the Deepest Branching of Eukaryotes. <i>Journal of Biochemistry</i> , 1996, 120, 1095-1103.	1.7	63
74	Monophyletic Origin of the Order Chiroptera and Its Phylogenetic Position Among Mammalia, as Inferred from the Complete Sequence of the Mitochondrial DNA of a Japanese Megabat, the Ryukyu Flying Fox (<i>Pteropus dasymallus</i>). <i>Journal of Molecular Evolution</i> , 2000, 51, 318-328.	1.8	62
75	Differentiation of Oocyte- and Somatic-Type 5S rRNAs in Animals ¹ . <i>Journal of Biochemistry</i> , 1986, 100, 369-374.	1.7	61
76	Mitochondrial phylogeny of hedgehogs and monophyly of Eulipotyphla. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 276-284.	2.7	61
77	Intra- and Interfamily Relationships of Vespertilionidae Inferred by Various Molecular Markers Including SINE Insertion Data. <i>Journal of Molecular Evolution</i> , 2002, 55, 284-301.	1.8	60
78	Estimation of Effective Population Size of HIV-1 Within a Host: A Pseudomaximum-Likelihood Approach. <i>Genetics</i> , 2002, 160, 1283-1293.	2.9	59
79	On the pattern of space division by territories. <i>Annals of the Institute of Statistical Mathematics</i> , 1976, 28, 509-519.	0.8	56
80	Phylogeographic and Demographic Analysis of the Asian Black Bear (<i>Ursus thibetanus</i>) Based on Mitochondrial DNA. <i>PLoS ONE</i> , 2015, 10, e0136398.	2.5	56
81	Phylogeny of Primary Photosynthetic Eukaryotes as Deduced from Slowly Evolving Nuclear Genes. <i>Molecular Biology and Evolution</i> , 2007, 24, 1592-1595.	8.9	55
82	High altitude adaptation of the schizothoracine fishes (Cyprinidae) revealed by the mitochondrial genome analyses. <i>Gene</i> , 2013, 517, 169-178.	2.2	55
83	Episodic Evolution and Adaptation of Chloroplast Genomes in Ancestral Grasses. <i>PLoS ONE</i> , 2009, 4, e5297.	2.5	53
84	Novel phylogeny of whales supported by total molecular evidence. <i>Journal of Molecular Evolution</i> , 1997, 44, S117-S120.	1.8	52
85	Relationship among coelacanths, lungfishes, and tetrapods: A phylogenetic analysis based on mitochondrial cytochrome oxidase I gene sequences. <i>Journal of Molecular Evolution</i> , 1994, 38, 602-9.	1.8	51
86	Complete nucleotide sequence of the mitochondrial genome of a Malagasy poison frog <i>Mantella madagascariensis</i> : Evolutionary implications on mitochondrial genomes of higher anuran groups. <i>Molecular Phylogenetics and Evolution</i> , 2006, 39, 223-236.	2.7	51
87	A viral sampling design for testing the molecular clock and for estimating evolutionary rates and divergence times. <i>Bioinformatics</i> , 2002, 18, 115-123.	4.1	49
88	Afrotherian phylogeny as inferred from complete mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 253-260.	2.7	49
89	Model of Amino Acid Substitution in Proteins Encoded by Mitochondrial DNA. <i>Journal of Molecular Evolution</i> , 1996, 42, 459-468.	1.8	49
90	Phylogenetic relation of lungfish indicated by the amino acid sequence of myelin DM20. <i>Molecular Brain Research</i> , 2000, 80, 256-259.	2.3	48

#	ARTICLE	IF	CITATIONS
91	Topological incongruence between nuclear and chloroplast DNA trees suggesting hybridization in the urophyllum group of the genus <i>Fagopyrum</i> (Polygonaceae). <i>Genes and Genetic Systems</i> , 2003, 78, 139-153.	0.7	48
92	Evolution of BK Virus Based on Complete Genome Data. <i>Journal of Molecular Evolution</i> , 2006, 63, 341-352.	1.8	48
93	Domestication Process of the Goat Revealed by an Analysis of the Nearly Complete Mitochondrial Protein-Encoding Genes. <i>PLoS ONE</i> , 2013, 8, e67775.	2.5	48
94	On the antisymmetry of the amino acid code table. <i>Origins of Life and Evolution of Biospheres</i> , 1980, 10, 265-270.	0.6	47
95	Model dependence of the phylogenetic inference: Relationship among Carnivores, Perissodactyls and Cetartiodactyls as inferred from mitochondrial genome sequences.. <i>Genes and Genetic Systems</i> , 1999, 74, 211-217.	0.7	46
96	Instability of Quartet Analyses of Molecular Sequence Data by the Maximum Likelihood Method: The Cetacea/Artiodactyla Relationships. <i>Molecular Phylogenetics and Evolution</i> , 1996, 6, 72-76.	2.7	43
97	Role of a seasonally specialist bird <i>Zosterops japonica</i> on pollen transfer and reproductive success of <i>Camellia japonica</i> in a temperate area. <i>Plant Species Biology</i> , 2004, 19, 197-201.	1.0	43
98	The Plasmodium Apicoplast Genome: Conserved Structure and Close Relationship of <i>P. ovale</i> to Rodent Malaria Parasites. <i>Molecular Biology and Evolution</i> , 2012, 29, 2095-2099.	8.9	42
99	Rodent polyphyly?. <i>Nature</i> , 1992, 355, 595-595.	27.8	41
100	Phylogenetic Position of the Mitochondrion-Lacking Protozoan <i>Trichomonas tenax</i> , Based on Amino Acid Sequences of Elongation Factors 1± and 2. <i>Journal of Molecular Evolution</i> , 1997, 44, 98-105.	1.8	41
101	Complete nucleotide sequence and gene arrangement of the mitochondrial genome of the crab-eating frog <i>Fejervarya cancrivora</i> and evolutionary implications. <i>Gene</i> , 2009, 441, 148-155.	2.2	41
102	Amino acid substitution of proteins coded for in mitochondrial DNA during mammalian evolution.. <i>Japanese Journal of Genetics</i> , 1992, 67, 187-197.	1.0	38
103	Evolution of Pacific Ocean and the Sea of Japan populations of the gobiid species, <i>Pterogobius elapoides</i> and <i>Pterogobius zonoleucus</i> , based on molecular and morphological analyses. <i>Gene</i> , 2008, 427, 7-18.	2.2	38
104	JC Virus Strains Indigenous to Northeastern Siberians and Canadian Inuits Are Unique But Evolutionally Related to Those Distributed Throughout Europe and Mediterranean Areas. <i>Journal of Molecular Evolution</i> , 2002, 55, 322-335.	1.8	37
105	Phylogeny and molecular evolution in primates.. <i>Japanese Journal of Genetics</i> , 1990, 65, 243-266.	1.0	36
106	Eubacterial origin of nuclear genes for chloroplast and cytosolic glucose-6-phosphate isomerase from spinach: sampling eubacterial gene diversity in eukaryotic chromosomes through symbiosis. <i>Gene</i> , 1998, 214, 205-213.	2.2	35
107	Consistency of SINE Insertion Topology and Flanking Sequence Tree: Quantifying Relationships Among Cetartiodactyls. <i>Molecular Biology and Evolution</i> , 2000, 17, 1417-1424.	8.9	35
108	The Phylogenetic Position of the Pelobiont <i>Mastigamoeba balamuthi</i> Based on Sequences of rDNA and Translation Elongation Factors EF-1alpha and EF-2. <i>Journal of Eukaryotic Microbiology</i> , 2002, 49, 1-10.	1.7	35

#	ARTICLE	IF	CITATIONS
109	Phylogeny mandalas for illustrating the Tree of Life. <i>Molecular Phylogenetics and Evolution</i> , 2017, 117, 168-178.	2.7	34
110	Phylogenetic Relationships Among JC Virus Strains in Japanese/Koreans and Native Americans Speaking Amerind or Na-Dene. <i>Journal of Molecular Evolution</i> , 2003, 56, 18-27.	1.8	33
111	The genome and transcriptome of <i>Trichormus</i> sp. NMC-1: insights into adaptation to extreme environments on the Qinghai-Tibet Plateau. <i>Scientific Reports</i> , 2016, 6, 29404.	3.3	33
112	Phylogenetic place of kinetoplastid protozoa inferred from a protein phylogeny of elongation factor 1 β . <i>Molecular and Biochemical Parasitology</i> , 1995, 70, 181-185.	1.1	30
113	MAXIMUM LIKELIHOOD METHOD OF PHYLOGENETIC INFERENCE FROM DNA SEQUENCE DATA. <i>Japanese Journal of Biometrics</i> , 1984, 5, 1-7.	0.0	30
114	Early evolution of eukaryotes inferred from protein phylogenies of translation elongation factors 1 β and 2. <i>Archiv für Protistenkunde</i> , 1997, 148, 287-295.	0.8	29
115	New candidate species most closely related to penguins. <i>Gene</i> , 2006, 378, 65-73.	2.2	29
116	Phylogeny and classification of hominoidea as inferred from DNA sequence data.. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 1984, 60, 389-392.	3.8	28
117	Eutherian phylogeny as inferred from mitochondrial DNA sequence data.. <i>Japanese Journal of Genetics</i> , 1994, 69, 455-472.	1.0	26
118	Phylogenetic position of <i>Blastocystis hominis</i> that contains cytochrome-free mitochondria, inferred from the protein phylogeny of elongation factor 1 β . <i>Molecular and Biochemical Parasitology</i> , 1996, 77, 241-245.	1.1	25
119	Phylogenetic Analysis of Diprotodontian Marsupials Based on Complete Mitochondrial Genomes. <i>Genes and Genetic Systems</i> , 2006, 81, 181-191.	0.7	25
120	Phylogeny of Asian primate malaria parasites inferred from apicoplast genome-encoded genes with special emphasis on the positions of <i>Plasmodium vivax</i> and <i>P. fragile</i> . <i>Gene</i> , 2010, 450, 32-38.	2.2	25
121	Stability of Mitochondrial Membrane Proteins in Terrestrial Vertebrates Predicts Aerobic Capacity and Longevity. <i>Genome Biology and Evolution</i> , 2011, 3, 1233-1244.	2.5	23
122	Determination of a complete lemur mitochondrial genome from feces. <i>Mammal Study</i> , 2007, 32, 7-16.	0.6	22
123	The genetic code and the entropy of protein. <i>Mathematical Biosciences</i> , 1975, 24, 169-182.	1.9	20
124	Was the universal common ancestry proved?. <i>Nature</i> , 2010, 468, E9-E9.	27.8	20
125	The giant panda is closer to a bear, judged by α - and β -hemoglobin sequences. <i>Journal of Molecular Evolution</i> , 1993, 36, 282-289.	1.8	19
126	Valence Bond Study of the Hydrogen Bond. III. Formation and Migration of Ionic Defects in Water and Ice. <i>Journal of the Physical Society of Japan</i> , 1970, 29, 1329-1334.	1.6	18

#	ARTICLE	IF	CITATIONS
127	Cloning and sequencing of a gene encoding 16S ribosomal RNA from a novel hyperthermophilic archaeobacterium NC12. <i>Gene</i> , 1996, 180, 183-187.	2.2	18
128	Impacts of river alteration for flood control on freshwater turtle populations. <i>Landscape and Ecological Engineering</i> , 2012, 8, 9-16.	1.5	18
129	Snake and Bird Predation Drive the Repeated Convergent Evolution of Correlated Life History Traits and Phenotype in the Izu Island Scincid Lizard (<i>Plestiodon latiscutatus</i>). <i>PLoS ONE</i> , 2014, 9, e92233.	2.5	18
130	Phylogenetic place of a mitochondria-lacking protozoan, <i>Entamoeba histolytica</i> , inferred from amino acid sequences of elongation factor 2.. <i>Japanese Journal of Genetics</i> , 1994, 69, 119-135.	1.0	17
131	Detecting excess radical replacements in phylogenetic trees. <i>Gene</i> , 2003, 319, 127-135.	2.2	17
132	Cyanobacterial Genes Transmitted to the Nucleus Before Divergence of Red Algae in the Chromista. <i>Journal of Molecular Evolution</i> , 2004, 59, 103-13.	1.8	17
133	Adaptive Threonine Increase in Transmembrane Regions of Mitochondrial Proteins in Higher Primates. <i>PLoS ONE</i> , 2008, 3, e3343.	2.5	17
134	Blue, Black, and Stripes: Evolution and Development of Color Production and Pattern Formation in Lizards and Snakes. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	2.2	16
135	Evolutionary implications of error amplification in the self-replicating and protein-synthesizing machinery. <i>Journal of Molecular Evolution</i> , 1984, 20, 77-85.	1.8	15
136	Polyphyletic origins of schizothoracine fish (Cyprinidae, Osteichthyes) and adaptive evolution in their mitochondrial genomes. <i>Genes and Genetic Systems</i> , 2014, 89, 187-191.	0.7	15
137	Polymorphism and evolution of ribosomal DNA in tea (<i>Camellia sinensis</i> , Theaceae). <i>Molecular Phylogenetics and Evolution</i> , 2015, 89, 63-72.	2.7	15
138	Comment on "Nuclear Genomic Sequences Reveal that Polar Bears Are an Old and Distinct Bear Lineage". <i>Science</i> , 2013, 339, 1522-1522.	12.6	14
139	Entropy of the genetic information and evolution. <i>Origins of Life and Evolution of Biospheres</i> , 1975, 6, 219-227.	0.6	13
140	Gene structure and amino acid sequence of <i>Latimeria chalumnae</i> (coelacanth) myelin DM20: phylogenetic relation of the fish. <i>Neurochemical Research</i> , 1999, 24, 867-873.	3.3	13
141	A Close Relationship of Chiroptera with Eulipotyphla (Core Insectivora) Suggested by Four Mitochondrial Genes. <i>Zoological Science</i> , 2000, 17, 1327-1332.	0.7	13
142	Detecting evolutionary rate heterogeneity among mangroves and their close terrestrial relatives. <i>Ecology Letters</i> , 2002, 5, 427-432.	6.4	12
143	The phylogenetic relationships of insectivores with special reference to the lesser hedgehog tenrec as inferred from the complete sequence of their mitochondrial genome.. <i>Genes and Genetic Systems</i> , 2003, 78, 107-112.	0.7	12
144	Molecular Phylogeny and Evolution in Primates. <i>Primate Monographs</i> , 2012, 65, 243-267.	0.8	12

#	ARTICLE	IF	CITATIONS
145	Some Problems in Proving the Existence of the Universal Common Ancestor of Life on Earth. Scientific World Journal, The, 2012, 2012, 1-5.	2.1	12
146	Nucleotide sequences of 5S rRNAs from sponge <i>Halichondria japonica</i> and tunicate <i>Halocynthia roretzi</i> and their phylogenetic positions. Nucleic Acids Research, 1983, 11, 1969-1974.	14.5	11
147	Close evolutionary relatedness of archaeobacteria with eukaryotes.. Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 1990, 66, 63-67.	3.8	11
148	Chronology of the extant African elephant species and case study of the species identification of the small African elephant with the molecular phylogenetic method. Gene, 2009, 441, 176-186.	2.2	11
149	Embryonic developmental process governing the conspicuousness of body stripes and blue tail coloration in the lizard <i>Plestiodon latiscutatus</i> . Evolution & Development, 2017, 19, 29-39.	2.0	11
150	Valence Bond Study of the Hydrogen Bond. I. Journal of the Physical Society of Japan, 1969, 27, 999-1008.	1.6	11
151	Close evolutionary relatedness of archaeobacteria, <i>Methanococcus</i> and <i>Halobacterium</i> , to eukaryotes demonstrated by composite phylogenetic trees of elongation factors EF-Tu and EF-G: Eocyte tree is unlikely.. Japanese Journal of Genetics, 1990, 65, 109-114.	1.0	10
152	Pigment cell mechanism of postembryonic stripe pattern formation in the Japanese four-lined snake. Journal of Morphology, 2016, 277, 196-203.	1.2	9
153	Developmental mechanisms of longitudinal stripes in the Japanese four-lined snake. Journal of Morphology, 2018, 279, 27-36.	1.2	9
154	Evolution of Archaeobacteria: Phylogenetic Relationships Among Archaeobacteria, Eubacteria, and Eukaryotes. , 1991, , 337-351.		9
155	Comparison of pollination characteristics between the insular shrub <i>Clerodendrum izuinisulare</i> and its widespread congener <i>C. trichotomum</i> . Plant Species Biology, 2014, 29, 73-84.	1.0	8
156	Importance of synonymous substitutions under dense taxon sampling and appropriate modeling in reconstructing the mitogenomic tree of Eutheria. Genes and Genetic Systems, 2014, 89, 237-251.	0.7	8
157	Cretaceous origin of giant rhinoceros beetles (Dynastini; Coleoptera) and correlation of their evolution with the Pangean breakup. Genes and Genetic Systems, 2016, 91, 209-215.	0.7	8
158	Speciation of two gobioid species, <i>Pterogobius elapoides</i> and <i>Pterogobius zonoleucus</i> revealed by multi-locus nuclear and mitochondrial DNA analyses. Gene, 2016, 576, 593-602.	2.2	8
159	Molecular phylogeny and man's place in Hominoidea.. Jinruigaku Zasshi = the Journal of the Anthropological Society of Nihon, 1991, 99, 49-61.	0.2	8
160	Distribution of hydrogen bond angles in molecular crystals. Nature, 1975, 254, 212-212.	27.8	6
161	Iridophore- and Xanthophore-Deficient Melanistic Color Variant of the Lizard <i>Plestiodon latiscutatus</i> . Herpetologica, 2016, 72, 189-195.	0.4	6
162	Light reflection from crystal platelets in iridophores determines green or brown skin coloration in <i>Takydromus</i> lizards. Zoology, 2017, 121, 83-90.	1.2	6

#	ARTICLE	IF	CITATIONS
163	Predator presence and recent climatic warming raise body temperatures of island lizards. <i>Ecology Letters</i> , 2021, 24, 533-542.	6.4	6
164	Phylogenetic Analysis of JC Virus DNAs Detected in Ainu: An Attempt to Elucidate the Origin and Diversity of the Ainu. <i>Anthropological Science</i> , 2003, 111, 19-34.	0.1	5
165	Adaptive evolution of chloroplast genomes in ancestral grasses. <i>Plant Signaling and Behavior</i> , 2009, 4, 623-624.	2.4	5
166	Distribution of <i>Eimeria uekii</i> and <i>Eimeria raichoi</i> in cage protection environments for the conservation of Japanese rock ptarmigans (<i>Lagopus muta japonica</i>) in the Japanese Alps. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2021, 15, 225-230.	1.5	5
167	Ancestral Polymorphisms and Sex-Biased Migration Shaped the Demographic History of Brown Bears and Polar Bears. <i>PLoS ONE</i> , 2013, 8, e78813.	2.5	4
168	Mitochondrial determinants of mammalian longevity. <i>Open Biology</i> , 2017, 7, 170083.	3.6	4
169	Parasitic development in intestines and oocyst shedding patterns for infection by <i>Eimeria uekii</i> and <i>Eimeria raichoi</i> in Japanese rock ptarmigans, <i>Lagopus muta japonica</i> , protected by cages in the Southern Japanese Alps. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 12, 19-24.	1.5	4
170	Distribution and Status of Gray-faced Buzzard Eagle <i>Butastur indicus</i> on the Northern Izu Islands, Japan. <i>Japanese Journal of Ornithology</i> , 1996, 45, 83-89.	0.1	4
171	Early evolution of eukaryotes inferred from genome data. <i>International Congress Series</i> , 2002, 1246, 209-215.	0.2	3
172	Assessing the Uncertainty in Phylogenetic Inference. , 2005, , 463-493.		3
173	Extreme nearly neutral evolution in mitochondrial genomes of laboratory mouse strains. <i>Gene</i> , 2014, 534, 444-448.	2.2	3
174	The Origin And The Evolution Of Cellular Organelles. , 1983, , 199-210.		2
175	A Chemical-Distance-Based Test for Positive Darwinian Selection. <i>Lecture Notes in Computer Science</i> , 2001, , 142-155.	1.3	2
176	A Correction to our Paper "Valence Bond Study of the Hydrogen Bond. I." <i>Journal of the Physical Society of Japan</i> , 1970, 28, 275-275.	1.6	2
177	Molecular Orbital Study of the Bent Hydrogen Bond. CNDO/2 Calculation for Dimeric H ₂ O. <i>Journal of the Physical Society of Japan</i> , 1970, 28, 266-266.	1.6	1
178	Red-spotted masu salmon (<i>Oncorhynchus masou ishikawae</i>) with unique jaw morphology collected from central Japan. <i>Ichthyological Research</i> , 2009, 56, 208-209.	0.8	1
179	Phylogeny mandalas of birds using the lithographs of John Gould's folio bird books. <i>Molecular Phylogenetics and Evolution</i> , 2017, 117, 141-149.	2.7	1
180	International symposium on the origin of mammalian orders July 21-25, 1998. <i>Journal of Molecular Evolution</i> , 1998, 46, 498-498.	1.8	0

#	ARTICLE	IF	CITATIONS
181	A Preliminary Study of the Morphological and Ecological Characteristics of <i>Plestiodon japonicus</i> (Scincidae, Squamata) on the Danjo Islands, Western Japan. <i>Current Herpetology</i> , 2021, 40, .	0.5	0
182	Eutherian phylogeny as inferred from mitochondrial DNA sequence data. <i>Genes and Genetic Systems</i> , 1994, 69, 455-472.	0.7	0
183	Inference of Evolutionary Trees from DNA and Protein Sequence Data. , 1994, , 241-248.		0
184	Phylogenetic place of a mitochondria-lacking protozoan, <i>Entamoeba histolytica</i> , inferred from amino acid sequences of elongation factor 2. <i>Genes and Genetic Systems</i> , 1994, 69, 119-135.	0.7	0
185	Effect of Electron Correlation on the Hydrogen Bond. <i>Journal of the Physical Society of Japan</i> , 1971, 31, 1290-1290.	1.6	0