

Masami Hasegawa

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

182
papers

22,626
citations

62
h-index

150
g-index

186
ext. papers

24,878
ext. citations

6
avg, IF

6.6
L-index

#	Paper	IF	Citations
182	Predator presence and recent climatic warming raise body temperatures of island lizards. <i>Ecology Letters</i> , 2021 , 24, 533-542	10	1
181	Distribution of and in cage protection environments for the conservation of Japanese rock ptarmigans () in the Japanese Alps. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2021 , 15, 225-230	2.6	
180	Parasitic development in intestines and oocyst shedding patterns for infection by and in Japanese rock ptarmigans, , protected by cages in the Southern Japanese Alps. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020 , 12, 19-24	2.6	1
179	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,	3.7	3
178	Developmental mechanisms of longitudinal stripes in the Japanese four-lined snake. <i>Journal of Morphology</i> , 2018 , 279, 27-36	1.6	4
177	Embryonic developmental process governing the conspicuousness of body stripes and blue tail coloration in the lizard <i>Plestiodon latiscutatus</i> . <i>Evolution & Development</i> , 2017 , 19, 29-39	2.6	4
176	Phylogeny mandalas of birds using the lithographs of John Gould's folio bird books. <i>Molecular Phylogenetics and Evolution</i> , 2017 , 117, 141-149	4.1	1
175	Phylogenomics and Morphology of Extinct Paleognaths Reveal the Origin and Evolution of the Ratites. <i>Current Biology</i> , 2017 , 27, 68-77	6.3	86
174	Cretaceous origin of giant rhinoceros beetles (Dynastini; Coleoptera) and correlation of their evolution with the Pangean breakup. <i>Genes and Genetic Systems</i> , 2017 , 91, 209-215	1.4	3
173	Mitochondrial determinants of mammalian longevity. <i>Open Biology</i> , 2017 , 7,	7	2
172	Phylogeny mandalas for illustrating the Tree of Life. <i>Molecular Phylogenetics and Evolution</i> , 2017 , 117, 168-178	4.1	26
171	Light reflection from crystal platelets in iridophores determines green or brown skin coloration in <i>Takydromus</i> lizards. <i>Zoology</i> , 2017 , 121, 83-90	1.7	4
170	Iridophore- and Xanthophore-Deficient Melanistic Color Variant of the Lizard <i>Plestiodon latiscutatus</i> . <i>Herpetologica</i> , 2016 , 72, 189-195	1.9	5
169	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	4.9	15
168	Pigment cell mechanism of postembryonic stripe pattern formation in the Japanese four-lined snake. <i>Journal of Morphology</i> , 2016 , 277, 196-203	1.6	8
167	Speciation of two gobioid species, <i>Pterogobius elapoides</i> and <i>Pterogobius zonoleucus</i> revealed by multi-locus nuclear and mitochondrial DNA analyses. <i>Gene</i> , 2016 , 576, 593-602	3.8	8
166	Polymorphism and evolution of ribosomal DNA in tea (<i>Camellia sinensis</i> , Theaceae). <i>Molecular Phylogenetics and Evolution</i> , 2015 , 89, 63-72	4.1	10

165	Phylogeographic and Demographic Analysis of the Asian Black Bear (<i>Ursus thibetanus</i>) Based on Mitochondrial DNA. <i>PLoS ONE</i> , 2015 , 10, e0136398	3.7	45
164	Extreme nearly neutral evolution in mitochondrial genomes of laboratory mouse strains. <i>Gene</i> , 2014 , 534, 444-8	3.8	3
163	Polyphyletic origins of schizothoracine fish (Cyprinidae, Osteichthyes) and adaptive evolution in their mitochondrial genomes. <i>Genes and Genetic Systems</i> , 2014 , 89, 187-91	1.4	9
162	Importance of synonymous substitutions under dense taxon sampling and appropriate modeling in reconstructing the mitogenomic tree of Eutheria. <i>Genes and Genetic Systems</i> , 2014 , 89, 237-51	1.4	6
161	Comparison of pollination characteristics between the insular shrub <i>Clerodendrum izuinsulare</i> and its widespread congener <i>C. trichotomum</i> . <i>Plant Species Biology</i> , 2014 , 29, 73-84	1.3	5
160	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	3.7	14
159	High altitude adaptation of the schizothoracine fishes (Cyprinidae) revealed by the mitochondrial genome analyses. <i>Gene</i> , 2013 , 517, 169-78	3.8	41
158	Comment on "Nuclear genomic sequences reveal that polar bears are an old and distinct bear lineage". <i>Science</i> , 2013 , 339, 1522	33.3	14
157	Domestication process of the goat revealed by an analysis of the nearly complete mitochondrial protein-encoding genes. <i>PLoS ONE</i> , 2013 , 8, e67775	3.7	33
156	Ancestral polymorphisms and sex-biased migration shaped the demographic history of brown bears and polar bears. <i>PLoS ONE</i> , 2013 , 8, e78813	3.7	3
155	Impacts of river alteration for flood control on freshwater turtle populations. <i>Landscape and Ecological Engineering</i> , 2012 , 8, 9-16	2	10
154	Some problems in proving the existence of the universal common ancestor of life on Earth. <i>Scientific World Journal, The</i> , 2012 , 2012, 479824	2.2	9
153	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, 2095-9	8.3	37
152	The yak genome and adaptation to life at high altitude. <i>Nature Genetics</i> , 2012 , 44, 946-9	36.3	472
151	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, 3491-500	4.4	333
150	Stability of mitochondrial membrane proteins in terrestrial vertebrates predicts aerobic capacity and longevity. <i>Genome Biology and Evolution</i> , 2011 , 3, 1233-44	3.9	20
149	Domestication relaxed selective constraints on the yak mitochondrial genome. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1553-6	8.3	62
148	Phylogeographical analyses of domestic and wild yaks based on mitochondrial DNA: new data and reappraisal. <i>Journal of Biogeography</i> , 2010 , 37, 2332-2344	4.1	53

147	Was the universal common ancestry proved?. <i>Nature</i> , 2010 , 468, E9; discussion E10	50.4	19
146	The position of gnetales among seed plants: overcoming pitfalls of chloroplast phylogenomics. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2855-63	8.3	69
145	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, 32-8	3.8	19
144	Adaptive evolution of chloroplast genomes in ancestral grasses. <i>Plant Signaling and Behavior</i> , 2009 , 4, 623-4	2.5	3
143	Molecular phylogeny and evolution of prosimians based on complete sequences of mitochondrial DNAs. <i>Gene</i> , 2009 , 441, 53-66	3.8	95
142	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, 148-55	3.8	34
141	Chronology of the extant African elephant species and case study of the species identification of the small African elephant with the molecular phylogenetic method. <i>Gene</i> , 2009 , 441, 176-86	3.8	7
140	The monophyletic origin of sea lions and fur seals (Carnivora; Otariidae) in the Southern Hemisphere. <i>Gene</i> , 2009 , 441, 89-99	3.8	55
139	Episodic evolution and adaptation of chloroplast genomes in ancestral grasses. <i>PLoS ONE</i> , 2009 , 4, e5293	3.7	41
138	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	3.8	36
137	Phylogeny, recombination, and mechanisms of stepwise mitochondrial genome reorganization in mantellid frogs from Madagascar. <i>Molecular Biology and Evolution</i> , 2008 , 25, 874-91	8.3	96
136	Adaptive threonine increase in transmembrane regions of mitochondrial proteins in higher primates. <i>PLoS ONE</i> , 2008 , 3, e3343	3.7	14
135	Relationships between BK virus lineages and human populations. <i>Microbes and Infection</i> , 2007 , 9, 204-13	9.3	93
134	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, 1481-95	5.7	70
133	Phylogeny of primary photosynthetic eukaryotes as deduced from slowly evolving nuclear genes. <i>Molecular Biology and Evolution</i> , 2007 , 24, 1592-5	8.3	54
132	Determination of a complete lemur mitochondrial genome from feces. <i>Mammal Study</i> , 2007 , 32, 7-16	0.6	18
131	Molecular phylogenetic study on the origin and evolution of Mustelidae. <i>Gene</i> , 2007 , 396, 1-12	3.8	57
130	Rooting the eutherian tree: the power and pitfalls of phylogenomics. <i>Genome Biology</i> , 2007 , 8, R199	18.3	71

129	Evolution of BK virus based on complete genome data. <i>Journal of Molecular Evolution</i> , 2006 , 63, 341-52	3.1	42
128	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, 9929-34	11.5	194
127	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, 793-9	0.8	68
126	New candidate species most closely related to penguins. <i>Gene</i> , 2006 , 378, 65-73	3.8	25
125	Phylogenetic analysis of diprotodontian marsupials based on complete mitochondrial genomes. <i>Genes and Genetic Systems</i> , 2006 , 81, 181-91	1.4	21
124	Extensive mitochondrial gene arrangements in coleoid Cephalopoda and their phylogenetic implications. <i>Molecular Phylogenetics and Evolution</i> , 2006 , 38, 648-58	4.1	76
123	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, 223-36	4.1	44
122	<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	4.1	63
121	Assessing the Uncertainty in Phylogenetic Inference 2005 , 463-493		3
120	Mitochondrial phylogenetics and evolution of mysticete whales. <i>Systematic Biology</i> , 2005 , 54, 77-90	8.4	124
119	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, 409-20	8.3	71
118	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	1.3	38
117	Cyanobacterial genes transmitted to the nucleus before divergence of red algae in the Chromista. <i>Journal of Molecular Evolution</i> , 2004 , 59, 103-13	3.1	14
116	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, 139-53	1.4	42
115	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, 107-12	1.4	11
114	Time scale of eutherian evolution estimated without assuming a constant rate of molecular evolution. <i>Genes and Genetic Systems</i> , 2003 , 78, 267-83	1.4	98
113	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	0.2	4
112	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	3.1	32

111	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, 485-97	3.1	117
110	Afrotherian phylogeny as inferred from complete mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , 2003 , 28, 253-60	4.1	39
109	Mitochondrial phylogeny of hedgehogs and monophyly of Eulipotyphla. <i>Molecular Phylogenetics and Evolution</i> , 2003 , 28, 276-84	4.1	54
108	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	4.1	62
107	Detecting excess radical replacements in phylogenetic trees. <i>Gene</i> , 2003 , 319, 127-35	3.8	17
106	Evolution of human Polyomavirus JC: implications for the population history of humans. <i>Journal of Molecular Evolution</i> , 2002 , 54, 285-97	3.1	71
105	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, 322-35	3.1	33
104	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	3.1	56
103	Detecting evolutionary rate heterogeneity among mangroves and their close terrestrial relatives. <i>Ecology Letters</i> , 2002 , 5, 427-432	10	11
102	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	3.6	33
101	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	3.6	79
100	Combining multiple data sets in a likelihood analysis: which models are the best?. <i>Molecular Biology and Evolution</i> , 2002 , 19, 2294-307	8.3	96
99	A viral sampling design for testing the molecular clock and for estimating evolutionary rates and divergence times. <i>Bioinformatics</i> , 2002 , 18, 115-23	7.2	43
98	Evolutionary analysis of <i>Arabidopsis</i> , 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, 12246-51	11.5	947
97	Early evolution of eukaryotes inferred from genome data. <i>International Congress Series</i> , 2002 , 1246, 209-215		3
96	Estimation of effective population size of HIV-1 within a host: a pseudomaximum-likelihood approach. <i>Genetics</i> , 2002 , 160, 1283-93	4	55
95	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, 508-16	3.1	115
94	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, 2199-213	5.7	89

93	CONSEL: for assessing the confidence of phylogenetic tree selection. <i>Bioinformatics</i> , 2001 , 17, 1246-7	7.2	1772
92	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, 311-25	1.4	85
91	A Chemical-Distance-Based Test for Positive Darwinian Selection. <i>Lecture Notes in Computer Science</i> , 2001 , 142-155	0.9	2
90	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	8.3	82
89	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, 318-28	3.1	51
88	Plastid genome phylogeny and a model of amino acid substitution for proteins encoded by chloroplast DNA. <i>Journal of Molecular Evolution</i> , 2000 , 50, 348-58	3.1	157
87	Consistency of SINE insertion topology and flanking sequence tree: quantifying relationships among cetartiodactyls. <i>Molecular Biology and Evolution</i> , 2000 , 17, 1417-24	8.3	34
86	Phylogenetic position of turtles among amniotes: evidence from mitochondrial and nuclear genes. <i>Gene</i> , 2000 , 259, 139-48	3.8	82
85	Interordinal relationships and timescale of eutherian evolution as inferred from mitochondrial genome data. <i>Gene</i> , 2000 , 259, 149-58	3.8	101
84	Phylogenetic relation of lungfish indicated by the amino acid sequence of myelin DM20. <i>Molecular Brain Research</i> , 2000 , 80, 256-9		43
83	A Close Relationship of Chiroptera with Eulipotyphla (Core Insectivora) Suggested by Four Mitochondrial Genes. <i>Zoological Science</i> , 2000 , 17, 1327-1332	0.8	12
82	Interordinal relationships of birds and other reptiles based on whole mitochondrial genomes. <i>Systematic Biology</i> , 1999 , 48, 138-52	8.4	218
81	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	8.4	78
80	Towards Resolving the Interordinal Relationships of Placental Mammals. <i>Systematic Biology</i> , 1999 , 48, 1-5	8.4	260
79	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, 119-37	8.4	95
78	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	8.4	135
77	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, 867-73	4.6	12
76	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, 211-7	1.4	16

75	Conflict among individual mitochondrial proteins in resolving the phylogeny of eutherian orders. <i>Journal of Molecular Evolution</i> , 1998 , 47, 307-22	3.1	135
74	Gene transfer to the nucleus and the evolution of chloroplasts. <i>Nature</i> , 1998 , 393, 162-5	50.4	638
73	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, 205-13	3.8	33
72	Early evolution of eukaryotes inferred from protein phylogenies of translation elongation factors 1 and 2. <i>Archiv Für Protistenkunde</i> , 1997 , 148, 287-295		26
71	Novel phylogeny of whales supported by total molecular evidence. <i>Journal of Molecular Evolution</i> , 1997 , 44 Suppl 1, S117-20	3.1	24
70	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, 682-7	3.1	61
69	Phylogenetic position of the mitochondrion-lacking protozoan <i>Trichomonas tenax</i> , based on amino acid sequences of elongation factors 1alpha and 2. <i>Journal of Molecular Evolution</i> , 1997 , 44, 98-105	3.1	25
68	Cloning and sequencing of a gene encoding 16S ribosomal RNA from a novel hyperthermophilic archaeobacterium NC12. <i>Gene</i> , 1996 , 180, 183-7	3.8	17
67	Complete nucleotide sequences of the genes encoding translation elongation factors 1 alpha and 2 from a microsporidian parasite, <i>Glugea plecoglossi</i> : implications for the deepest branching of eukaryotes. <i>Journal of Biochemistry</i> , 1996 , 120, 1095-103	3.1	48
66	Phylogenetic position of <i>Blastocystis hominis</i> that contains cytochrome-free mitochondria, inferred from the protein phylogeny of elongation factor 1 alpha. <i>Molecular and Biochemical Parasitology</i> , 1996 , 77, 241-5	1.9	23
65	Model of amino acid substitution in proteins encoded by mitochondrial DNA. <i>Journal of Molecular Evolution</i> , 1996 , 42, 459-68	3.1	407
64	Protein phylogeny of translation elongation factor EF-1 alpha suggests microsporidians are extremely ancient eukaryotes. <i>Journal of Molecular Evolution</i> , 1996 , 42, 257-63	3.1	102
63	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, 72-6	4.1	36
62	Distribution and Status of Gray-faced Buzzard Eagle <i>Buteo indicus</i> on the Northern Izu Islands, Japan. <i>Japanese Journal of Ornithology</i> , 1996 , 45, 83-89	0.1	4
61	Model of amino acid substitution in proteins encoded by mitochondrial DNA 1996 , 42, 459		17
60	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, 1817-33	4	64
59	Dating the Cenacester of Organisms. <i>Science</i> , 1996 , 274, 1750-1750	33.3	4
58	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, 622-8	3.1	81

57	Phylogenetic place of kinetoplastid protozoa inferred from a protein phylogeny of elongation factor 1 alpha. <i>Molecular and Biochemical Parasitology</i> , 1995 , 70, 181-5	1.9	25
56	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	3.1	152
55	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	3.1	41
54	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, 119-35		16
53	Eutherian phylogeny as inferred from mitochondrial DNA sequence data. <i>Japanese Journal of Genetics</i> , 1994 , 69, 455-72		25
52	Eutherian phylogeny as inferred from mitochondrial DNA sequence data. <i>Genes and Genetic Systems</i> , 1994 , 69, 455-472	1.4	
51	Inference of Evolutionary Trees from DNA and Protein Sequence Data 1994 , 241-248		
50	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	1.4	
49	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	4.1	100
48	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, 270-81	3.1	95
47	The giant panda is closer to a bear, judged by β and δ hemoglobin sequences. <i>Journal of Molecular Evolution</i> , 1993 , 36, 282-289	3.1	15
46	Close phylogenetic relationship between Vestimentifera (tube worms) and Annelida revealed by the amino acid sequence of elongation factor-1 alpha. <i>Journal of Molecular Evolution</i> , 1993 , 37, 66-70	3.1	47
45	Toward a more accurate time scale for the human mitochondrial DNA tree. <i>Journal of Molecular Evolution</i> , 1993 , 37, 347-54	3.1	159
44	Early branchings in the evolution of eukaryotes: ancient divergence of <i>entamoeba</i> that lacks mitochondria revealed by protein sequence data. <i>Journal of Molecular Evolution</i> , 1993 , 36, 380-8	3.1	107
43	Ribosomal RNA trees misleading?. <i>Nature</i> , 1993 , 361, 23	50.4	158
42	Amino acid substitution of proteins coded for in mitochondrial DNA during mammalian evolution. <i>Japanese Journal of Genetics</i> , 1992 , 67, 187-97		35
41	Rodent polyphyly?. <i>Nature</i> , 1992 , 355, 595	50.4	39
40	Time of the deepest root for polymorphism in human mitochondrial DNA. <i>Journal of Molecular Evolution</i> , 1991 , 32, 37-42	3.1	79

39	Evolution of RNA polymerases and branching patterns of the three major groups of Archaeobacteria. <i>Journal of Molecular Evolution</i> , 1991 , 32, 70-8	3.1	71
38	On the maximum likelihood method in molecular phylogenetics. <i>Journal of Molecular Evolution</i> , 1991 , 32, 443-5	3.1	167
37	Molecular phylogeny and man's place in Hominoidea.. <i>Jinruigaku Zasshi = the Journal of the Anthropological Society of Nihon</i> , 1991 , 99, 49-61		6
36	Evolution of Archaeobacteria: Phylogenetic Relationships Among Archaeobacteria, Eubacteria, and Eukaryotes 1991 , 337-351		6
35	Phylogeny and molecular evolution in primates. <i>Primate Monographs</i> , 1990 , 65, 243-66	0.3	10
34	Converting distance to time: application to human evolution. <i>Methods in Enzymology</i> , 1990 , 183, 550-70	1.7	72
33	Close evolutionary relatedness of archaeobacteria, Methanococcus and Halobacterium, to eukaryotes demonstrated by composite phylogenetic trees of elongation factors EF-Tu and EF-G: Eocyte tree is unlikely.. <i>Japanese Journal of Genetics</i> , 1990 , 65, 109-114		10
32	Phylogeny and molecular evolution in primates.. <i>Japanese Journal of Genetics</i> , 1990 , 65, 243-266		32
31	Close evolutionary relatedness of archaeobacteria with eukaryotes.. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 1990 , 66, 63-67	4	11
30	Mitochondrial DNA evolution in primates: transition rate has been extremely low in the lemur. <i>Journal of Molecular Evolution</i> , 1990 , 31, 113-21	3.1	68
29	Maximum likelihood inference of protein phylogeny and the origin of chloroplasts. <i>Journal of Molecular Evolution</i> , 1990 , 31, 151-160	3.1	584
28	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	3.1	66
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