

Hirohisa Kishino

List of Publications by Year in descending order

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115
papers

17,706
citations

94433

37
h-index

25787

108
g-index

121
all docs

121
docs citations

121
times ranked

16405
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	Divergence Time and Evolutionary Rate Estimation with Multilocus Data. <i>Systematic Biology</i> , 2002, 51, 689-702.	5.6	895
4	Maximum likelihood inference of protein phylogeny and the origin of chloroplasts. <i>Journal of Molecular Evolution</i> , 1990, 31, 151-160.	1.8	789
5	Performance of a Divergence Time Estimation Method under a Probabilistic Model of Rate Evolution. <i>Molecular Biology and Evolution</i> , 2001, 18, 352-361.	8.9	581
6	An evolutionary model for maximum likelihood alignment of DNA sequences. <i>Journal of Molecular Evolution</i> , 1991, 33, 114-124.	1.8	395
7	Inching toward reality: An improved likelihood model of sequence evolution. <i>Journal of Molecular Evolution</i> , 1992, 34, 3-16.	1.8	323
8	Genomic adaptation to polyphagy and insecticides in a major East Asian noctuid pest. <i>Nature Ecology and Evolution</i> , 2017, 1, 1747-1756.	7.8	269
9	On the maximum likelihood method in molecular phylogenetics. <i>Journal of Molecular Evolution</i> , 1991, 32, 443-445.	1.8	221
10	Protein Evolution with Dependence Among Codons Due to Tertiary Structure. <i>Molecular Biology and Evolution</i> , 2003, 20, 1692-1704.	8.9	180
11	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
12	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
13	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
14	<i>Plasmodium falciparum</i> Accompanied the Human Expansion out of Africa. <i>Current Biology</i> , 2010, 20, 1283-1289.	3.9	121
15	Phylogenetic relationships between tuna species of the genus <i>Thunnus</i> (Scombridae: Teleostei): Inconsistent implications from morphology, nuclear and mitochondrial genomes. <i>Journal of Molecular Evolution</i> , 1995, 41, 741-8.	1.8	114
16	Lessons learned from Japanese marine finfish stock enhancement programmes. <i>Fisheries Research</i> , 2006, 80, 101-112.	1.7	99
17	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
18	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

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19	Estimation of the Size of Genetic Bottlenecks in Cell-to-Cell Movement of <i>Soil-Borne Wheat Mosaic Virus</i> and the Possible Role of the Bottlenecks in Speeding Up Selection of Variations in <i>trans-Acting Genes or Elements</i> . <i>Journal of Virology</i> , 2010, 84, 1828-1837.	3.4	87
20	Estimating Absolute Rates of Synonymous and Nonsynonymous Nucleotide Substitution in Order to Characterize Natural Selection and Date Species Divergences. <i>Molecular Biology and Evolution</i> , 2004, 21, 1201-1213.	8.9	80
21	Effectiveness of a Stock Enhancement Program Evaluated by a Two-Stage Sampling Survey of Commercial Landings. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 1992, 49, 1573-1582.	1.4	77
22	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
23	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
24	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
25	Genetic effects of long-term stock enhancement programs. <i>Aquaculture</i> , 2009, 290, 69-79.	3.5	66
26	Robust Time Estimation Reconciles Views of the Antiquity of Placental Mammals. <i>PLoS ONE</i> , 2007, 2, e384.	2.5	61
27	Expression map of a complete set of gustatory receptor genes in chemosensory organs of <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2017, 82, 74-82.	2.7	61
28	Positive Selection Acting on a Surface Membrane Protein of the Plant-Pathogenic Phytoplasmas. <i>Journal of Bacteriology</i> , 2006, 188, 3424-3428.	2.2	60
29	Viruses Roll the Dice: The Stochastic Behavior of Viral Genome Molecules Accelerates Viral Adaptation at the Cell and Tissue Levels. <i>PLoS Biology</i> , 2015, 13, e1002094.	5.6	59
30	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
31	Quantifying the Impact of Protein Tertiary Structure on Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2007, 24, 1769-1782.	8.9	54
32	Comprehensive Comparison of Self-administered Questionnaires for Measuring Quantitative Autistic Traits in Adults. <i>Journal of Autism and Developmental Disorders</i> , 2014, 44, 993-1007.	2.7	53
33	Rates of Molecular Evolution Suggest Natural History of Life History Traits and a Post-K-Pg Nocturnal Bottleneck of Placentals. <i>Current Biology</i> , 2017, 27, 3025-3033.e5.	3.9	51
34	Incorporating gene-specific variation when inferring and evaluating optimal evolutionary tree topologies from multilocus sequence data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4436-4441.	7.1	45
35	Recent independent evolution of <i>mSP1</i> polymorphism in <i>Plasmodium vivax</i> and related simian malaria parasites. <i>Molecular and Biochemical Parasitology</i> , 2007, 156, 74-79.	1.1	45
36	Synonymous Substitutions Substantially Improve Evolutionary Inference from Highly Diverged Proteins. <i>Systematic Biology</i> , 2008, 57, 367-377.	5.6	44

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37	Bombyx small RNAs: Genomic defense system against transposons in the silkworm, <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 1058-1065.	2.7	41
38	Detection of Closely Linked Multiple Quantitative Trait Loci Using a Genetic Algorithm. <i>Genetics</i> , 2001, 158, 463-475.	2.9	41
39	Population Genetics Without Intraspecific Data. <i>Molecular Biology and Evolution</i> , 2007, 24, 1667-1677.	8.9	40
40	Empirical Bayes Inference of Pairwise F_{ST} and Its Distribution in the Genome. <i>Genetics</i> , 2007, 177, 861-873.	2.9	40
41	Statistical Comparison of Nucleotide, Amino Acid, and Codon Substitution Models for Evolutionary Analysis of Protein-Coding Sequences. <i>Systematic Biology</i> , 2009, 58, 199-210.	5.6	39
42	The empirical Bayes estimators of fine-scale population structure in high gene flow species. <i>Molecular Ecology Resources</i> , 2017, 17, 1210-1222.	4.8	36
43	Time flies, a new molecular time-scale for brachyceran fly evolution without a clock. <i>Systematic Biology</i> , 2003, 52, 745-56.	5.6	28
44	Phylogenetic Detection of Recombination with a Bayesian Prior on the Distance between Trees. <i>PLoS ONE</i> , 2008, 3, e2651.	2.5	27
45	Rigorous monitoring of a large-scale marine stock enhancement program demonstrates the need for comprehensive management of fisheries and nursery habitat. <i>Scientific Reports</i> , 2019, 9, 5290.	3.3	27
46	Estimating mortality rates from tag recoveries: incorporating over-dispersion, correlation, and change points. <i>ICES Journal of Marine Science</i> , 1994, 51, 241-251.	2.5	26
47	Linkage between recycling and consumption: a case of toilet paper in Japan. <i>Resources, Conservation and Recycling</i> , 2000, 30, 177-199.	10.8	26
48	Empirical Bayes Procedure for Estimating Genetic Distance Between Populations and Effective Population Size. <i>Genetics</i> , 2000, 156, 2063-2079.	2.9	26
49	Compartmentalized isozyme genes and the origin of introns. <i>Journal of Molecular Evolution</i> , 1990, 31, 205-210.	1.8	25
50	A population size estimate of the finless porpoise, <i>Neophocaena phocaenoides</i> , from aerial sighting surveys in Ariake Sound and Tachibana Bay, Japan. <i>Researches on Population Ecology</i> , 1997, 39, 239-247.	0.9	24
51	Partial Conservation of LFY Function between Rice and Arabidopsis. <i>Plant and Cell Physiology</i> , 2003, 44, 1311-1319.	3.1	24
52	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
53	Stochastic Variational Inference for Bayesian Phylogenetics: A Case of CAT Model. <i>Molecular Biology and Evolution</i> , 2019, 36, 825-833.	8.9	23
54	Divergence Pattern of Duplicate Genes in Protein-Protein Interactions Follows the Power Law. <i>Molecular Biology and Evolution</i> , 2005, 22, 501-505.	8.9	22

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55	Molecular and morphological evidence of hybridization between native <i>Ruditapes philippinarum</i> and the introduced <i>Ruditapes</i> form in Japan. <i>Conservation Genetics</i> , 2013, 14, 717-733.	1.5	22
56	Renormalized basal metabolic rate describes the human aging process and longevity. <i>Aging Cell</i> , 2019, 18, e12968.	6.7	21
57	Evolutionary History and Mode of the amylase Multigene Family in <i>Drosophila</i> . <i>Journal of Molecular Evolution</i> , 2003, 57, 702-709.	1.8	19
58	Multidimensional Vector Space Representation for Convergent Evolution and Molecular Phylogeny. <i>Molecular Biology and Evolution</i> , 2005, 22, 704-715.	8.9	19
59	Model-Based Tolerance Intervals Derived from Cumulative Historical Composition Data: Application for Substantial Equivalence Assessment of a Genetically Modified Crop. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 9916-9926.	5.2	19
60	Very fast algorithms for evaluating the stability of ML and Bayesian phylogenetic trees from sequence data. <i>Genome Informatics</i> , 2002, 13, 82-92.	0.4	19
61	Rapid Evaluation of the Phylogenetic Congruence of Sequence Data Using Likelihood Ratio Tests. <i>Molecular Biology and Evolution</i> , 2000, 17, 1988-1992.	8.9	18
62	Understanding population structure in an evolutionary context: population-specific <i>F_{ST}</i> and pairwise <i>F_{ST}</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	18
63	Phylogenetic Methodology for Detecting Protein Interactions. <i>Molecular Biology and Evolution</i> , 2006, 24, 650-659.	8.9	17
64	Adaptive Threonine Increase in Transmembrane Regions of Mitochondrial Proteins in Higher Primates. <i>PLoS ONE</i> , 2008, 3, e3343.	2.5	17
65	Recycling and consumption in Germany and Japan: a case of toilet paper. <i>Resources, Conservation and Recycling</i> , 1999, 26, 189-215.	10.8	16
66	Genetic effects of marine stock enhancement: a case study based on the highly piscivorous Japanese Spanish mackerel. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2014, 71, 301-314.	1.4	16
67	An Integrated-Likelihood Method for Estimating Genetic Differentiation Between Populations. <i>Genetics</i> , 2006, 173, 2073-2082.	2.9	15
68	<i>Plasmodium falciparum</i> mitochondrial genetic diversity exhibits isolation-by-distance patterns supporting a sub-Saharan African origin. <i>Mitochondrion</i> , 2013, 13, 630-636.	3.4	15
69	Bias and significance of relative reproductive success estimates based on steelhead trout (<i>Oncorhynchus mykiss</i>) data: a Bayesian meta-analysis. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2011, 68, 1827-1835.	1.4	13
70	Genomic Background Drives the Divergence of Duplicated Amylase Genes at Synonymous Sites in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2003, 21, 222-227.	8.9	12
71	Close evolutionary relatedness of archaeobacteria with eukaryotes.. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 1990, 66, 63-67.	3.8	11
72	Major contribution of dominant inheritance to autism spectrum disorders (ASDs) in population-based families. <i>Journal of Human Genetics</i> , 2009, 54, 721-726.	2.3	11

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73	Detailed Analysis of Japanese Population Substructure with a Focus on the Southwest Islands of Japan. PLoS ONE, 2012, 7, e35000.	2.5	11
74	A cross-species socio-emotional behaviour development revealed by a multivariate analysis. Scientific Reports, 2013, 3, 2630.	3.3	11
75	Detection of heterogeneity and estimation of population characteristics from the field survey data: 1987/88 Japanese feasibility study of the southern hemisphere Minke whales. Annals of the Institute of Statistical Mathematics, 1991, 43, 435-453.	0.8	10
76	A Model of Gene Displacement by Stocking Activities.. Nippon Suisan Gakkaishi, 1995, 61, 326-330.	0.1	10
77	Circulation indices: new tools for analyzing the structure of material cascades. Resources, Conservation and Recycling, 2000, 28, 85-104.	10.8	10
78	Simultaneous Estimation of Mixing Rates and Genetic Drift Under Successive Sampling of Genetic Markers With Application to the Mud Crab (<i>Scylla paramamosain</i>) in Japan. Genetics, 2006, 173, 2063-2072.	2.9	10
79	Fold Recognition of the Human Immunodeficiency Virus Type 1 V3 Loop and Flexibility of Its Crown Structure During the Course of Adaptation to a Host. Genetics, 2006, 172, 1385-1396.	2.9	10
80	Taxon Influence Index: Assessing Taxon-Induced Incongruities in Phylogenetic Inference. Systematic Biology, 2012, 61, 337-345.	5.6	10
81	Bayesian Inference of Baseline Fertility and Treatment Effects via a Crop Yield-Fertility Model. PLoS ONE, 2014, 9, e112785.	2.5	10
82	Global pattern of phylogenetic species composition of shark and its conservation priority. Ecology and Evolution, 2015, 5, 4455-4465.	1.9	10
83	Waves Out of the Korean Peninsula and Inter- and Intra-Species Replacements in Freshwater Fishes in Japan. Genes, 2021, 12, 303.	2.4	10
84	Genomic Background Predicts the Fate of Duplicated Genes: Evidence From the Yeast Genome. Genetics, 2004, 166, 1995-1999.	2.9	10
85	Sampling Scheme for the Estimation of the Stock Composition in the Mixed Population Based on Genetic Data.. Nippon Suisan Gakkaishi, 1994, 60, 359-364.	0.1	9
86	Correspondence analysis of paper recycling society: consumers and paper makers in Japan. Resources, Conservation and Recycling, 1998, 23, 193-208.	10.8	8
87	Simultaneous Detection of Linkage Disequilibrium and Genetic Differentiation of Subdivided Populations. Genetics, 2004, 167, 2003-2013.	2.9	8
88	Phylogenetic skew: an index of community diversity. Molecular Ecology, 2015, 24, 759-770.	3.9	8
89	Potential of a smartphone as a stress-free sensor of daily human behaviour. Behavioural Brain Research, 2015, 276, 181-189.	2.2	7
90	Population structure and persistence of Pacific herring following the Great Tohoku earthquake. Conservation Genetics, 2017, 18, 423-437.	1.5	7

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91	A new approach for comprehensively describing heterogametic sex chromosomes. <i>DNA Research</i> , 2018, 25, 375-382.	3.4	7
92	Evolution of Reproductive Life History in Mammals and the Associated Change of Functional Constraints. <i>Genes</i> , 2021, 12, 740.	2.4	7
93	Population structure of chum salmon and selection on the markers collected for stock identification. <i>Ecology and Evolution</i> , 2021, 11, 13972-13985.	1.9	7
94	A Likelihood-based Index of Protein Protein Binding Affinities with Application to Influenza HA Escape from Antibodies. <i>Molecular Biology and Evolution</i> , 2007, 24, 1627-1638.	8.9	6
95	Structural Considerations in the Fitness Landscape of a Virus. <i>Molecular Biology and Evolution</i> , 2010, 27, 1782-1791.	8.9	6
96	Early-infant diagnostic predictors of the neuro-behavioral development after neonatal care. <i>Behavioural Brain Research</i> , 2015, 276, 143-150.	2.2	6
97	Comparative analysis of farmers engaged in participatory research to cope with climate change versus non-participants in Northeast Thailand. <i>Plant Production Science</i> , 2018, 21, 287-301.	2.0	5
98	Archaeal α -diversity patterns under the seafloor along geochemical gradients. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2014, 119, 1770-1788.	3.0	4
99	A Reference Population-Based Conformance Proportion. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2016, 21, 684-697.	1.4	4
100	Population structure and demographic history of Pacific herring <i>Clupea pallasii</i> around Japan inferred from mitochondrial DNA sequences. <i>Nippon Suisan Gakkaishi</i> , 2017, 83, 163-173.	0.1	4
101	Multiple Isolated Transcription Factors Act as Switches and Contribute to Species Uniqueness. <i>Genes</i> , 2020, 11, 1148.	2.4	4
102	Distribution of distances between topologies and its effect on detection of phylogenetic recombination. <i>Annals of the Institute of Statistical Mathematics</i> , 2010, 62, 145-159.	0.8	3
103	Hypothesis Testing of Inclusion of the Tolerance Interval for the Assessment of Food Safety. <i>PLoS ONE</i> , 2015, 10, e0141117.	2.5	3
104	Estimates of natural selection due to protein tertiary structure inform the ancestry of biallelic loci. <i>Gene</i> , 2009, 441, 45-52.	2.2	2
105	Assessment of the network of protected areas for birds in Taiwan with regard to functional and phylogenetic diversity. <i>Pacific Conservation Biology</i> , 2016, 22, 61.	1.0	2
106	Maximum likelihood procedure adapted to sampling schemes. <i>Journal of Statistical Planning and Inference</i> , 1998, 70, 277-286.	0.6	1
107	Fractional parentage analysis and a scale-free reproductive network of brown trout. <i>Journal of Theoretical Biology</i> , 2013, 336, 18-35.	1.7	1
108	Spatial Distribution of Selection Pressure on a Protein Based on the Hierarchical Bayesian Model. <i>Molecular Biology and Evolution</i> , 2013, 30, 2714-2722.	8.9	1

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109	Exploratory analysis of multi-trait coadaptations in light of population history. <i>Ecology and Evolution</i> , 2022, 12, e8755.	1.9	1
110	The least squares estimation of the transition probabilities of binary processes on the basis of sample paths. <i>Annals of the Institute of Statistical Mathematics</i> , 1983, 35, 425-438.	0.8	0
111	Variance of sightings in the survey of patchily distributed objects. <i>Annals of the Institute of Statistical Mathematics</i> , 1987, 39, 275-287.	0.8	0
112	Population structure and demographic history of Pacific herring <i>Clupea pallasii</i> around Japan inferred from mitochondrial DNA sequences. <i>Nippon Suisan Gakkaishi</i> , 2018, 84, 585-585.	0.1	0
113	Observation Subarea Decision and Population Density Estimation by Space Scale-invariance. <i>Journal of the Japan Statistical Society</i> , 2009, 39, 77-88.	0.1	0
114	An R script for unbiased estimation of stocking effectiveness using a two-stage sampling strategy based on fishery landings. <i>Fisheries Research</i> , 2022, 250, 106266.	1.7	0
115	Molecular Evolutionary Rate Predicts Intraspecific Genetic Polymorphism and Species-Specific Selection. <i>Genes</i> , 2022, 13, 708.	2.4	0