

Hirohisa Kishino

List of Publications by Year in descending order

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Version: 2024-02-01

115
papers

17,706
citations

94433

37
h-index

25787

108
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121
all docs

121
docs citations

121
times ranked

16405
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Exploratory analysis of multi-trait coadaptations in light of population history. <i>Ecology and Evolution</i> , 2022, 12, e8755.	1.9	1
3	Molecular Evolutionary Rate Predicts Intraspecific Genetic Polymorphism and Species-Specific Selection. <i>Genes</i> , 2022, 13, 708.	2.4	0
4	Waves Out of the Korean Peninsula and Inter- and Intra-Species Replacements in Freshwater Fishes in Japan. <i>Genes</i> , 2021, 12, 303.	2.4	10
5	Evolution of Reproductive Life History in Mammals and the Associated Change of Functional Constraints. <i>Genes</i> , 2021, 12, 740.	2.4	7
6	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
7	Understanding population structure in an evolutionary context: population-specific F_{ST} and pairwise F_{ST} . <i>Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	18
8	Multiple Isolated Transcription Factors Act as Switches and Contribute to Species Uniqueness. <i>Genes</i> , 2020, 11, 1148.	2.4	4
9	Renormalized basal metabolic rate describes the human aging process and longevity. <i>Aging Cell</i> , 2019, 18, e12968.	6.7	21
10	Stochastic Variational Inference for Bayesian Phylogenetics: A Case of CAT Model. <i>Molecular Biology and Evolution</i> , 2019, 36, 825-833.	8.9	23
11	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
12	A new approach for comprehensively describing heterogametic sex chromosomes. <i>DNA Research</i> , 2018, 25, 375-382.	3.4	7
13	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
14	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
15	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
16	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
17	Population structure and persistence of Pacific herring following the Great Tohoku earthquake. <i>Conservation Genetics</i> , 2017, 18, 423-437.	1.5	7
18	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

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19	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
20	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
21	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
22	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
23	A Reference Population-Based Conformance Proportion. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2016, 21, 684-697.	1.4	4
24	Global pattern of phylogenetic species composition of shark and its conservation priority. <i>Ecology and Evolution</i> , 2015, 5, 4455-4465.	1.9	10
25	Hypothesis Testing of Inclusion of the Tolerance Interval for the Assessment of Food Safety. <i>PLoS ONE</i> , 2015, 10, e0141117.	2.5	3
26	Phylogenetic skew: an index of community diversity. <i>Molecular Ecology</i> , 2015, 24, 759-770.	3.9	8
27	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
28	Early-infant diagnostic predictors of the neuro-behavioral development after neonatal care. <i>Behavioural Brain Research</i> , 2015, 276, 143-150.	2.2	6
29	Potential of a smartphone as a stress-free sensor of daily human behaviour. <i>Behavioural Brain Research</i> , 2015, 276, 181-189.	2.2	7
30	Bayesian Inference of Baseline Fertility and Treatment Effects via a Crop Yield-Fertility Model. <i>PLoS ONE</i> , 2014, 9, e112785.	2.5	10
31	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
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	Archaeal diversity patterns under the seafloor along geochemical gradients. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2014, 119, 1770-1788.	3.0	4
34	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
35	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
36	<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

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37	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
38	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
39	A cross-species socio-emotional behaviour development revealed by a multivariate analysis. <i>Scientific Reports</i> , 2013, 3, 2630.	3.3	11
40	Taxon Influence Index: Assessing Taxon-Induced Incongruities in Phylogenetic Inference. <i>Systematic Biology</i> , 2012, 61, 337-345.	5.6	10
41	Detailed Analysis of Japanese Population Substructure with a Focus on the Southwest Islands of Japan. <i>PLoS ONE</i> , 2012, 7, e35000.	2.5	11
42	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
43	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
44	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
45	<i>Plasmodium falciparum</i> Accompanied the Human Expansion out of Africa. <i>Current Biology</i> , 2010, 20, 1283-1289.	3.9	121
46	Structural Considerations in the Fitness Landscape of a Virus. <i>Molecular Biology and Evolution</i> , 2010, 27, 1782-1791.	8.9	6
47	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</i> Genes or Elements. <i>Journal of Virology</i> , 2010, 84, 1828-1837.	3.4	87
48	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
49	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
50	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
51	Genetic effects of long-term stock enhancement programs. <i>Aquaculture</i> , 2009, 290, 69-79.	3.5	66
52	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
53	<i>Bombyx</i> 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
54	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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55	Phylogenetic Detection of Recombination with a Bayesian Prior on the Distance between Trees. PLoS ONE, 2008, 3, e2651.	2.5	27
56	Adaptive Threonine Increase in Transmembrane Regions of Mitochondrial Proteins in Higher Primates. PLoS ONE, 2008, 3, e3343.	2.5	17
57	Population Genetics Without Intraspecific Data. Molecular Biology and Evolution, 2007, 24, 1667-1677.	8.9	40
58	Quantifying the Impact of Protein Tertiary Structure on Molecular Evolution. Molecular Biology and Evolution, 2007, 24, 1769-1782.	8.9	54
59	A Likelihood-based Index of Protein Protein Binding Affinities with Application to Influenza HA Escape from Antibodies. Molecular Biology and Evolution, 2007, 24, 1627-1638.	8.9	6
60	Empirical Bayes Inference of Pairwise F_{ST} and Its Distribution in the Genome. Genetics, 2007, 177, 861-873.	2.9	40
61	Robust Time Estimation Reconciles Views of the Antiquity of Placental Mammals. PLoS ONE, 2007, 2, e384.	2.5	61
62	Recent independent evolution of msp1 polymorphism in Plasmodium vivax and related simian malaria parasites. Molecular and Biochemical Parasitology, 2007, 156, 74-79.	1.1	45
63	Lessons learned from Japanese marine finfish stock enhancement programmes. Fisheries Research, 2006, 80, 101-112.	1.7	99
64	Simultaneous Estimation of Mixing Rates and Genetic Drift Under Successive Sampling of Genetic Markers With Application to the Mud Crab (Scylla paramamosain) in Japan. Genetics, 2006, 173, 2063-2072.	2.9	10
65	Phylogenetic Methodology for Detecting Protein Interactions. Molecular Biology and Evolution, 2006, 24, 650-659.	8.9	17
66	Positive Selection Acting on a Surface Membrane Protein of the Plant-Pathogenic Phytoplasmas. Journal of Bacteriology, 2006, 188, 3424-3428.	2.2	60
67	An Integrated-Likelihood Method for Estimating Genetic Differentiation Between Populations. Genetics, 2006, 173, 2073-2082.	2.9	15
68	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
69	Multidimensional Vector Space Representation for Convergent Evolution and Molecular Phylogeny. Molecular Biology and Evolution, 2005, 22, 704-715.	8.9	19
70	Divergence Pattern of Duplicate Genes in Protein-Protein Interactions Follows the Power Law. Molecular Biology and Evolution, 2005, 22, 501-505.	8.9	22
71	Incorporating gene-specific variation when inferring and evaluating optimal evolutionary tree topologies from multilocus sequence data. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4436-4441.	7.1	45
72	Estimating Absolute Rates of Synonymous and Nonsynonymous Nucleotide Substitution in Order to Characterize Natural Selection and Date Species Divergences. Molecular Biology and Evolution, 2004, 21, 1201-1213.	8.9	80

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73	Simultaneous Detection of Linkage Disequilibrium and Genetic Differentiation of Subdivided Populations. <i>Genetics</i> , 2004, 167, 2003-2013.	2.9	8
74	Genomic Background Predicts the Fate of Duplicated Genes: Evidence From the Yeast Genome. <i>Genetics</i> , 2004, 166, 1995-1999.	2.9	10
75	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
76	Partial Conservation of LFY Function between Rice and Arabidopsis. <i>Plant and Cell Physiology</i> , 2003, 44, 1311-1319.	3.1	24
77	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
78	Protein Evolution with Dependence Among Codons Due to Tertiary Structure. <i>Molecular Biology and Evolution</i> , 2003, 20, 1692-1704.	8.9	180
79	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
80	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
81	Divergence Time and Evolutionary Rate Estimation with Multilocus Data. <i>Systematic Biology</i> , 2002, 51, 689-702.	5.6	895
82	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
83	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
84	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
85	Detection of Closely Linked Multiple Quantitative Trait Loci Using a Genetic Algorithm. <i>Genetics</i> , 2001, 158, 463-475.	2.9	41
86	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
87	Circulation indices: new tools for analyzing the structure of material cascades. <i>Resources, Conservation and Recycling</i> , 2000, 28, 85-104.	10.8	10
88	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
89	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
90	Empirical Bayes Procedure for Estimating Genetic Distance Between Populations and Effective Population Size. <i>Genetics</i> , 2000, 156, 2063-2079.	2.9	26

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91	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
92	Correspondence analysis of paper recycling society: consumers and paper makers in Japan. <i>Resources, Conservation and Recycling</i> , 1998, 23, 193-208.	10.8	8
93	Maximum likelihood procedure adapted to sampling schemes. <i>Journal of Statistical Planning and Inference</i> , 1998, 70, 277-286.	0.6	1
94	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
95	A Model of Gene Displacement by Stocking Activities.. <i>Nippon Suisan Gakkaishi</i> , 1995, 61, 326-330.	0.1	10
96	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
97	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
98	Sampling Scheme for the Estimation of the Stock Composition in the Mixed Population Based on Genetic Data.. <i>Nippon Suisan Gakkaishi</i> , 1994, 60, 359-364.	0.1	9
99	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
100	Inching toward reality: An improved likelihood model of sequence evolution. <i>Journal of Molecular Evolution</i> , 1992, 34, 3-16.	1.8	323
101	Evolution of RNA polymerases and branching patterns of the three major groups of archaebacteria. <i>Journal of Molecular Evolution</i> , 1991, 32, 70-78.	1.8	76
102	On the maximum likelihood method in molecular phylogenetics. <i>Journal of Molecular Evolution</i> , 1991, 32, 443-445.	1.8	221
103	An evolutionary model for maximum likelihood alignment of DNA sequences. <i>Journal of Molecular Evolution</i> , 1991, 33, 114-124.	1.8	395
104	Detection of heterogeneity and estimation of population characteristics from the field survey data: 1987/88 Japanese feasibility study of the southern hemisphere Minke whales. <i>Annals of the Institute of Statistical Mathematics</i> , 1991, 43, 435-453.	0.8	10
105	Close evolutionary relatedness of archaebacteria with eukaryotes.. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 1990, 66, 63-67.	3.8	11
106	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
107	Maximum likelihood inference of protein phylogeny and the origin of chloroplasts. <i>Journal of Molecular Evolution</i> , 1990, 31, 151-160.	1.8	789
108	Compartmentalized isozyme genes and the origin of introns. <i>Journal of Molecular Evolution</i> , 1990, 31, 205-210.	1.8	25

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109	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
110	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
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	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
113	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
114	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
115	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