Koichiro Tamura

List of Publications by Year
in descending order

59 papers	206,071 citations	159358 30 h-index	138251 58 g-index
66 all docs	66 docs citations	66 times ranked	145775 citing authors

#	Article	IF	Citations
1	MEGA6: Molecular Evolutionary Genetics Analysis Version 6.0. Molecular Biology and Evolution, 2013, 30, 2725-2729.	3.5	37,728
2	MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. Molecular Biology and Evolution, 2016, 33, 1870-1874.	3.5	36,708
3	MEGA5: Molecular Evolutionary Genetics Analysis Using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. Molecular Biology and Evolution, 2011, 28, 2731-2739.	3.5	36,550
4	MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) Software Version 4.0. Molecular Biology and Evolution, 2007, 24, 1596-1599.	3.5	25,988
5	MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. Molecular Biology and Evolution, 2018, 35, 1547-1549.	3.5	25,630
6	MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. Briefings in Bioinformatics, 2004, 5, 150-163.	3.2	10,598
7	Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees.. Molecular Biology and Evolution, 1993, 10, 512-26.	3.5	8,355
8	MEGA11: Molecular Evolutionary Genetics Analysis Version 11. Molecular Biology and Evolution, 2021, 38, 3022-3027.	3.5	6,189
9	MEGA2: molecular evolutionary genetics analysis software. Bioinformatics, 2001, 17, 1244-1245.	1.8	5,102
10	Prospects for inferring very large phylogenies by using the neighbor-joining method. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11030-11035.	3.3	4,158
11	MEGA: A biologist-centric software for evolutionary analysis of DNA and protein sequences. Briefings in Bioinformatics, 2008, 9, 299-306.	3.2	3,073
12	Molecular Evolutionary Genetics Analysis (MEGA) for macOS. Molecular Biology and Evolution, 2020, 37, 1237-1239.	3.5	1,067
13	MEGA: Molecular Evolutionary Genetics Analysis software for microcomputers. Bioinformatics, 1994, 10, 189-191.	1.8	711
14	POPTREE2: Software for Constructing Population Trees from Allele Frequency Data and Computing Other Population Statistics with Windows Interface. Molecular Biology and Evolution, 2010, 27, 747-752.	3.5	587
15	Estimating divergence times in large molecular phylogenies. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 19333-19338.	3.3	530
16	Temporal Patterns of Fruit Fly (Drosophila) Evolution Revealed by Mutation Clocks. Molecular Biology and Evolution, 2003, 21, 36-44.	3.5	516
17	MEGA-CC: computing core of molecular evolutionary genetics analysis program for automated and iterative data analysis. Bioinformatics, 2012, 28, 2685-2686.	1.8	332
18	Statistics and Truth in Phylogenomics. Molecular Biology and Evolution, 2012, 29, 457-472.	3.5	243

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19	Evolutionary Distance Estimation Under Heterogeneous Substitution Pattern Among Lineages. Molecular Biology and Evolution, 2002, 19, 1727-1736.	3.5	232
20	Replication Origin of Mitochondrial DNA in Insects. Genetics, 2005, 171, 1695-1705.	1.2	216
21	Human origins and analysis of mitochondrial DNA sequences. Science, 1992, 255, 737-739.	6.0	201
22	Theoretical Foundation of the RelTime Method for Estimating Divergence Times from Variable Evolutionary Rates. Molecular Biology and Evolution, 2018, 35, 1770-1782.	3.5	164
23	POPTREEW: Web Version of POPTREE for Constructing Population Trees from Allele Frequency Data and Computing Some Other Quantities. Molecular Biology and Evolution, 2014, 31, 1622-1624.	3.5	156
24	Rapid isolation method of animal mitochondrial DNA by the alkaline lysis procedure. Biochemical Genetics, 1988, 26, 815-819.	0.8	144
25	Deciphering the routes of invasion of <i>Drosophila suzukii</i> by means of ABC random forest. Molecular Biology and Evolution, 2017, 34, msx050.	3.5	132
26	PCR error and molecular population genetics. Biochemical Genetics, 1999, 37, 317-321.	0.8	76
27	Prospects for Building Large Timetrees Using Molecular Data with Incomplete Gene Coverage among Species. Molecular Biology and Evolution, 2014, 31, 2542-2550.	3.5	57
28	Fast and Accurate Estimates of Divergence Times from Big Data. Molecular Biology and Evolution, 2017, 34, 45-50.	3.5	52
29	A Machine Learning Method for Detecting Autocorrelation of Evolutionary Rates in Large Phylogenies. Molecular Biology and Evolution, 2019, 36, 811-824.	3.5	45
30	Phylogenetic relationships between Sophophora and Lordiphosa, with proposition of a hypothesis on the vicariant divergences of tropical lineages between the Old and New Worlds in the family Drosophilidae. Molecular Phylogenetics and Evolution, 2011, 60, 98-107.	1.2	42
31	Reliable Confidence Intervals for RelTime Estimates of Evolutionary Divergence Times. Molecular Biology and Evolution, 2020, 37, 280-290.	3.5	36
32	Phylogenetic Position of the Subgenus Lordiphosa of the Genus Drosophila (Diptera: Drosophilidae) Inferred from Alcohol Dehydrogenase (Adh) Gene Sequences. Journal of Molecular Evolution, 2000, 51, 122-130.	0.8	35
33	MEGA-MD: molecular evolutionary genetics analysis software with mutational diagnosis of amino acid variation. Bioinformatics, 2014, 30, 1305-1307.	1.8	33
34	Molecular Phylogeny of Twelve Asian Species of Epilachnine Ladybird Beetles (Coleoptera,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142 Td	0.3	29
35	Phylogeny of the Drosophila immigrans Species Group (Diptera: Drosophilidae) Based on<i>Adh</i>and<i>Gpdh</i>Sequences. Zoological Science, 2007, 24, 913-921.	0.3	29
36	Model selection in the estimation of the number of nucleotide substitutions.. Molecular Biology and Evolution, 1994, 11, 154-7.	3.5	27

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37	Single column discrepancy and dynamic max-mini optimizations for quickly finding the most parsimonious evolutionary trees. Bioinformatics, 2000, 16, 140-151.	1.8	26
38	RelTime Relaxes the Strict Molecular Clock throughout the Phylogeny. Genome Biology and Evolution, 2018, 10, 1631-1636.	1.1	25
39	Two Cryptic Species of the Phytophagous Ladybird Beetle Epilachna vigintioctopunctata (Coleoptera:) Tj ETQq1 1 0.784314 rgBT /Overl Zoological Science, 2000, 17, 1159-1166.	0.3	22
40	On the estimation of the rate of nucleotide substitution for the control region of human mitochondrial DNA. Gene, 2000, 259, 189-197.	1.0	21
41	A Molecular Evolutionary Reference for the Human Variome. Molecular Biology and Evolution, 2016, 33, 245-254.	3.5	20
42	A new method for inferring timetrees from temporally sampled molecular sequences. PLoS Computational Biology, 2020, 16, e1007046.	1.5	19
43	A Novel Chimeric Gene, siren, With Retroposed Promoter Sequence in the Drosophila bipectinata Complex. Genetics, 2005, 171, 1719-1727.	1.2	18
44	Phylogenetic placement of metagenomic reads using the minimum evolution principle. BMC Genomics, 2015, 16, S13.	1.2	16
45	Efficient Methods for Dating Evolutionary Divergences. , 2020, , 197-219.		14
46	Molecular population genetics of a host-associated sibling species complex of phytophagous ladybird beetles (Coleoptera: Coccinellidae: Epilachninae). Journal of Zoological Systematics and Evolutionary Research, 2011, 49, 16-24.	0.6	12
47	Ancient Male Recombination Shaped Genetic Diversity of Neo-Y Chromosome in *Drosophila albomicans*. Molecular Biology and Evolution, 2016, 33, 367-374.	3.5	12
48	Shared evolutionary trajectories of three independent neo-sex chromosomes in *Drosophila*. Genome Research, 2021, 31, 2069-2079.	2.4	12
49	Cold tolerance and metabolic rate increased by cold acclimation in *Drosophila albomicans* from natural populations. Genes and Genetic Systems, 2013, 88, 289-300.	0.2	11
50	Polymorphism and structure of style–specific arabinogalactan proteins as determinants of pollen tube growth in Nicotiana. BMC Evolutionary Biology, 2017, 17, 186.	3.2	10
51	Adaptive Landscape of Protein Variation in Human Exomes. Molecular Biology and Evolution, 2018, 35, 2015-2025.	3.5	10
52	PathFinder: Bayesian inference of clone migration histories in cancer. Bioinformatics, 2020, 36, i675-i683.	1.8	8
53	Comprehensive identification of odorant-binding protein genes in the seed fly, Delia platura (Diptera:) Tj ETQq1 1 0.784314 rgBT /Overl	0.6	7
54	Inferring the demographic history of Japanese cedar, Cryptomeria japonica, using amplicon sequencing. Heredity, 2019, 123, 371-383.	1.2	7

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55	Semi-automated quantitative Drosophila wings measurements. BMC Bioinformatics, 2017, 18, 319.	1.2	6
56	Identification of odorant-binding protein genes expressed in the antennae and the legs of the onion fly, Delia antiqua (Diptera: Anthomyiidae). Applied Entomology and Zoology, 2014, 49, 89-95.	0.6	5
57	Unusual Evolution of Interspersed Repeat Sequences in the Drosophila ananassae Subgroup. Molecular Biology and Evolution, 2006, 23, 981-987.	3.5	4
58	Extensive Differences in Antifungal Immune Response in Two *Drosophila* Species Revealed by Comparative Transcriptome Analysis. International Journal of Genomics, 2013, 2013, 1-15.	0.8	4
59	Population genetic analysis of two species of Distylium: D. racemosum growing in East Asian evergreen broad-leaved forests and D. lepidotum endemic to the Ogasawara (Bonin) Islands. Tree Genetics and Genomes, 2019, 15, 1.	0.6	3