

# Kazuharu Misawa

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5400040/publications.pdf>

Version: 2024-02-01

44  
papers

13,413  
citations

623188

14  
h-index

276539

41  
g-index

47  
all docs

47  
docs citations

47  
times ranked

22203  
citing authors

#	ARTICLE	IF	CITATIONS
1	MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. <i>Nucleic Acids Research</i> , 2002, 30, 3059-3066.	6.5	12,537
2	Molecular systematics of Volvocales (Chlorophyceae, Chlorophyta) based on exhaustive 18S rRNA phylogenetic analyses. <i>Molecular Phylogenetics and Evolution</i> , 2008, 48, 281-291.	1.2	160
3	Origin and Evolution of the Colonial Volvocales (Chlorophyceae) as Inferred from Multiple, Chloroplast Gene Sequences. <i>Molecular Phylogenetics and Evolution</i> , 2000, 17, 256-268.	1.2	135
4	Phylogenetic positions of Glaucophyta, green plants (Archaeplastida) and Haptophyta (Chromalveolata) as deduced from slowly evolving nuclear genes. <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 872-880.	1.2	62
5	Phylogeny of Primary Photosynthetic Eukaryotes as Deduced from Slowly Evolving Nuclear Genes. <i>Molecular Biology and Evolution</i> , 2007, 24, 1592-1595.	3.5	55
6	A multi-ethnic meta-analysis identifies novel genes, including ACSL5, associated with amyotrophic lateral sclerosis. <i>Communications Biology</i> , 2020, 3, 526.	2.0	49
7	Revisiting the Glires conceptâ€”phylogenetic analysis of nuclear sequences. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 320-327.	1.2	38
8	Cyanobacterial contribution to the genomes of the plastid-lacking protists. <i>BMC Evolutionary Biology</i> , 2009, 9, 197.	3.2	38
9	Reanalysis of Murphy et al.'s Data Gives Various Mammalian Phylogenies and Suggests Overcredibility of Bayesian Trees. <i>Journal of Molecular Evolution</i> , 2003, 57, S290-S296.	0.8	36
10	Genomic structure of nitric oxide synthase in the terrestrial slug is highly conserved. <i>Gene</i> , 2008, 415, 74-81.	1.0	28
11	The Universal Trend of Amino Acid Gainâ€”Loss is Caused by CpG Hypermutable. <i>Journal of Molecular Evolution</i> , 2008, 67, 334-342.	0.8	27
12	Estimation of the Amount of DNA Polymorphism When the Neutral Mutation Rate Varies Among Sites. <i>Genetics</i> , 1997, 147, 1959-1964.	1.2	27
13	Evaluation of the effect of CpG hypermutability on human codon substitution. <i>Gene</i> , 2009, 431, 18-22.	1.0	19
14	Hypouricemia and Urate Transporters. <i>Biomedicines</i> , 2022, 10, 652.	1.4	17
15	Origins of a cyanobacterial 6-phosphogluconate dehydrogenase in plastid-lacking eukaryotes. <i>BMC Evolutionary Biology</i> , 2008, 8, 151.	3.2	16
16	STR-realigner: a realignment method for short tandem repeat regions. <i>BMC Genomics</i> , 2016, 17, 991.	1.2	15
17	Contribution of Rare Variants of the <i>SLC22A12</i> Gene to the Missing Heritability of Serum Urate Levels. <i>Genetics</i> , 2020, 214, 1079-1090.	1.2	15
18	Effect of Group Selection on the Evolution of Altruistic Behavior. <i>Journal of Theoretical Biology</i> , 2003, 220, 55-66.	0.8	13

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19	Construction of full-length Japanese reference panel of class I HLA genes with single-molecule, real-time sequencing. <i>Pharmacogenomics Journal</i> , 2019, 19, 136-146.	0.9	12
20	Relationship between amino acid composition and gene expression in the mouse genome. <i>BMC Research Notes</i> , 2011, 4, 20.	0.6	11
21	A codon substitution model that incorporates the effect of the GC contents, the gene density and the density of CpG islands of human chromosomes. <i>BMC Genomics</i> , 2011, 12, 397.	1.2	10
22	RF: A method for filtering short reads with tandem repeats for genome mapping. <i>Genomics</i> , 2013, 102, 35-37.	1.3	9
23	Construction of JRC (Japanese reference genome) with single-molecule real-time sequencing. <i>Human Genome Variation</i> , 2019, 6, 27.	0.4	9
24	A Simple Method for Classifying Genes and a Bootstrap Test for Classifications. <i>Molecular Biology and Evolution</i> , 2000, 17, 1879-1884.	3.5	8
25	AP-SKAT: highly-efficient genome-wide rare variant association test. <i>BMC Genomics</i> , 2016, 17, 745.	1.2	8
26	Influence of the 3'-UTR-length of mKIAA cDNAs and their Sequence Features to the mRNA Expression Level in the Brain. <i>DNA Research</i> , 2005, 12, 181-189.	1.5	7
27	New correction algorithms for multiple comparisons in case-control multilocus association studies based on haplotypes and diplotype configurations. <i>Journal of Human Genetics</i> , 2008, 53, 789-801.	1.1	7
28	GeneWaltz: A new method for reducing the false positives of gene finding. <i>BioData Mining</i> , 2010, 3, 6.	2.2	7
29	The amount and pattern of DNA polymorphism under the neutral mutation hypothesis. <i>Genetica</i> , 1998, 102/103, 103-107.	0.5	6
30	ParaHaplo: A program package for haplotype-based whole-genome association study using parallel computing. <i>Source Code for Biology and Medicine</i> , 2009, 4, 7.	1.7	5
31	AQUATIC PLANT SPECIATION AFFECTED BY DIVERSIFYING SELECTION OF ORGANELLE DNA REGIONS <sup>1</sup> . <i>Journal of Phycology</i> , 2011, 47, 999-1008.	1.0	5
32	The amount and pattern of DNA polymorphism under the neutral mutation hypothesis. <i>Contemporary Issues in Genetics and Evolution</i> , 1998, , 103-107.	0.9	5
33	ParaHaplo 3.0: A program package for imputation and a haplotype-based whole-genome association study using hybrid parallel computing. <i>Source Code for Biology and Medicine</i> , 2011, 6, 10.	1.7	3
34	Genomic Heritabilities and Correlations of 17 Traits Related to Obesity and Associated Conditions in the Japanese Population. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2221-2228.	0.8	3
35	Antiemetic effects of baclofen in a shrew model of postoperative nausea and vomiting: Whole-transcriptome analysis in the nucleus of the solitary tract. <i>CNS Neuroscience and Therapeutics</i> , 2022, , .	1.9	3
36	New Weighting Methods for Phylogenetic Tree Reconstruction Using Multiple Loci. <i>Journal of Molecular Evolution</i> , 2012, 75, 1-10.	0.8	2

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37	Multiple Sequence Alignments: The Next Generation. <i>Seibutsu Butsuri</i> , 2006, 46, 312-317.	0.0	1
38	ParaHaplo 2.0: a program package for haplotype-estimation and haplotype-based whole-genome association study using parallel computing. <i>Source Code for Biology and Medicine</i> , 2010, 5, 5.	1.7	1
39	PAFFT: A new homology search algorithm for third-generation sequencers. <i>Genomics</i> , 2015, 106, 265-267.	1.3	1
40	Short tandem repeats in the human, cow, mouse, chicken, and lizard genomes are concentrated in the terminal regions of chromosomes. <i>Gene Reports</i> , 2016, 4, 280-285.	0.4	1
41	Population-scale whole genome sequencing identifies 271 highly polymorphic short tandem repeats from Japanese population. <i>Heliyon</i> , 2018, 4, e00625.	1.4	1
42	Is the population of Sado Island genetically close to the population of western Japan?. <i>Human Genome Variation</i> , 2019, 6, 26.	0.4	0
43	Estimating Human Point Mutation Rates from Codon Substitution Rates. , 0, , .		0
44	Genotype Value Decomposition: Simple Methods for the Computation of Kernel Statistics. <i>Genetics &amp; Genomics Next</i> , 0, , 2100066.	0.8	0