

Yumi Yamaguchi-Kabata

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

1,974
citations

430874

18
h-index

361022

35
g-index

35
all docs

35
docs citations

35
times ranked

3842
citing authors

#	ARTICLE	IF	CITATIONS
1	Rare variant discovery by deep whole-genome sequencing of 1,070 Japanese individuals. <i>Nature Communications</i> , 2015, 6, 8018.	12.8	352
2	Japanese Population Structure, Based on SNP Genotypes from 7003 Individuals Compared to Other Ethnic Groups: Effects on Population-Based Association Studies. <i>American Journal of Human Genetics</i> , 2008, 83, 445-456.	6.2	327
3	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	5.6	290
4	3.5KJPNv2: an allele frequency panel of 3552 Japanese individuals including the X chromosome. <i>Human Genome Variation</i> , 2019, 6, 28.	0.7	115
5	Human Immunodeficiency Virus Type 1 Intergroup (M/O) Recombination in Cameroon. <i>Journal of Virology</i> , 1999, 73, 6810-6820.	3.4	109
6	iJGVD: an integrative Japanese genome variation database based on whole-genome sequencing. <i>Human Genome Variation</i> , 2015, 2, 15050.	0.7	100
7	Reevaluation of Amino Acid Variability of the Human Immunodeficiency Virus Type 1 gp120 Envelope Glycoprotein and Prediction of New Discontinuous Epitopes. <i>Journal of Virology</i> , 2000, 74, 4335-4350.	3.4	98
8	Identification of regions in which positive selection may operate in S-RNase of Rosaceae: Implication for S-allele-specific recognition sites in S-RNase. <i>FEBS Letters</i> , 1998, 440, 337-342.	2.8	85
9	Identification of Nine Novel Loci Associated with White Blood Cell Subtypes in a Japanese Population. <i>PLoS Genetics</i> , 2011, 7, e1002067.	3.5	69
10	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2007, 36, D793-D799.	14.5	57
11	Natural Infection of Wild-Born Mandrills (<i>Mandrillus sphinx</i>) with Two Different Types of Simian Immunodeficiency Virus. <i>AIDS Research and Human Retroviruses</i> , 2001, 17, 1143-1154.	1.1	38
12	Distribution and Effects of Nonsense Polymorphisms in Human Genes. <i>PLoS ONE</i> , 2008, 3, e3393.	2.5	35
13	Evaluation of reported pathogenic variants and their frequencies in a Japanese population based on a whole-genome reference panel of 2049 individuals. <i>Journal of Human Genetics</i> , 2018, 63, 213-230.	2.3	35
14	Genome analyses for the Tohoku Medical Megabank Project towards establishment of personalized healthcare. <i>Journal of Biochemistry</i> , 2019, 165, 139-158.	1.7	33
15	Integrated analysis of human genetic association study and mouse transcriptome suggests LBH and SHF genes as novel susceptible genes for amyloid- β accumulation in Alzheimer's disease. <i>Human Genetics</i> , 2018, 137, 521-533.	3.8	22
16	Corticotropin-Releasing Hormone Receptor 2 Gene Variants in Irritable Bowel Syndrome. <i>PLoS ONE</i> , 2016, 11, e0147817.	2.5	21
17	A novel simian immunodeficiency virus from black mangabey (<i>Lophocebus aterrimus</i>) in the Democratic Republic of Congo. <i>Journal of General Virology</i> , 2005, 86, 1967-1971.	2.9	18
18	Investigation of protein functions through data-mining on integrated human transcriptome database, H-Invitational database (H-InvDB). <i>Gene</i> , 2005, 364, 99-107.	2.2	18

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19	The structural origin of metabolic quantitative diversity. <i>Scientific Reports</i> , 2016, 6, 31463.	3.3	18
20	Linkage of Amino Acid Variation and Evolution of Human Immunodeficiency Virus Type 1 gp120 Envelope Glycoprotein (Subtype B) with Usage of the Second Receptor. <i>Journal of Molecular Evolution</i> , 2004, 58, 333-340.	1.8	16
21	Selection pressure on human STR loci and its relevance in repeat expansion disease. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1851-1869.	2.1	15
22	VarySysDB: a human genetic polymorphism database based on all H-InvDB transcripts. <i>Nucleic Acids Research</i> , 2009, 37, D810-D815.	14.5	14
23	Regional genetic differences among Japanese populations and performance of genotype imputation using whole-genome reference panel of the Tohoku Medical Megabank Project. <i>BMC Genomics</i> , 2018, 19, 551.	2.8	14
24	A prioritization analysis of disease association by data-mining of functional annotation of human genes. <i>Genomics</i> , 2012, 99, 1-9.	2.9	11
25	Genetic differences in the two main groups of the Japanese population based on autosomal SNPs and haplotypes. <i>Journal of Human Genetics</i> , 2012, 57, 326-334.	2.3	9
26	The return of individual genomic results to research participants: design and pilot study of Tohoku Medical Megabank Project. <i>Journal of Human Genetics</i> , 2022, 67, 9-17.	2.3	9
27	Establishment of a standardized system to perform population structure analyses with limited sample size or with different sets of SNP genotypes. <i>Journal of Human Genetics</i> , 2010, 55, 525-533.	2.3	8
28	Estimating carrier frequencies of newborn screening disorders using a whole-genome reference panel of 3552 Japanese individuals. <i>Human Genetics</i> , 2019, 138, 389-409.	3.8	7
29	Novel candidates of pathogenic variants of the BRCA1 and BRCA2 genes from a dataset of 3,552 Japanese whole genomes (3.5KJPNv2). <i>PLoS ONE</i> , 2021, 16, e0236907.	2.5	7
30	Prediction of Protein-Destabilizing Polymorphisms by Manual Curation with Protein Structure. <i>PLoS ONE</i> , 2012, 7, e50445.	2.5	4
31	Estimation of the carrier frequencies and proportions of potential patients by detecting causative gene variants associated with autosomal recessive bone dysplasia using a whole-genome reference panel of Japanese individuals. <i>Human Genome Variation</i> , 2021, 8, 2.	0.7	3
32	Making a haplotype catalog with estimated frequencies based on SNP homozygotes. <i>Journal of Human Genetics</i> , 2010, 55, 500-506.	2.3	2
33	Natural infection of chimpanzees with new lentiviruses related to HIV-1/SIVcpz. <i>Journal of Medical Primatology</i> , 1999, 28, 169-173.	0.6	1