Yumi Yamaguchi-Kabata

List of Publications by Year
in descending order

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	The return of individual genomic results to research participants: design and pilot study of Tohoku Medical Megabank Project. Journal of Human Genetics, 2022, 67, 9-17.	2.3	9
2	Novel candidates of pathogenic variants of the BRCA1 and BRCA2 genes from a dataset of 3,552 Japanese whole genomes (3.5KJPNv2). PLoS ONE, 2021, 16, e0236907.	2.5	7
3	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. Human Genome Variation, 2021, 8, 2.	0.7	3
4	3.5KJPNv2: an allele frequency panel of 3552 Japanese individuals including the X chromosome. Human Genome Variation, 2019, 6, 28.	0.7	115
5	Estimating carrier frequencies of newborn screening disorders using a whole-genome reference panel of 3552 Japanese individuals. Human Genetics, 2019, 138, 389-409.	3.8	7
6	Genome analyses for the Tohoku Medical Megabank Project towards establishment of personalized healthcare. Journal of Biochemistry, 2019, 165, 139-158.	1.7	33
7	Evaluation of reported pathogenic variants and their frequencies in a Japanese population based on a whole-genome reference panel of 2049 individuals. Journal of Human Genetics, 2018, 63, 213-230.	2.3	35
8	Regional genetic differences among Japanese populations and performance of genotype imputation using whole-genome reference panel of the Tohoku Medical Megabank Project. BMC Genomics, 2018, 19, 551.	2.8	14
9	Integrated analysis of human genetic association study and mouse transcriptome suggests LBH and SHF genes as novel susceptible genes for amyloid-Î² accumulation in Alzheimerâ€™s disease. Human Genetics, 2018, 137, 521-533.	3.8	22
10	The structural origin of metabolic quantitative diversity. Scientific Reports, 2016, 6, 31463.	3.3	18
11	Selection pressure on human STR loci and its relevance in repeat expansion disease. Molecular Genetics and Genomics, 2016, 291, 1851-1869.	2.1	15
12	Corticotropin-Releasing Hormone Receptor 2 Gene Variants in Irritable Bowel Syndrome. PLoS ONE, 2016, 11, e0147817.	2.5	21
13	iJGVD: an integrative Japanese genome variation database based on whole-genome sequencing. Human Genome Variation, 2015, 2, 15050.	0.7	100
14	Rare variant discovery by deep whole-genome sequencing of 1,070 Japanese individuals. Nature Communications, 2015, 6, 8018.	12.8	352
15	Genetic differences in the two main groups of the Japanese population based on autosomal SNPs and haplotypes. Journal of Human Genetics, 2012, 57, 326-334.	2.3	9
16	A prioritization analysis of disease association by data-mining of functional annotation of human genes. Genomics, 2012, 99, 1-9.	2.9	11
17	Prediction of Protein-Destabilizing Polymorphisms by Manual Curation with Protein Structure. PLoS ONE, 2012, 7, e50445.	2.5	4
18	Identification of Nine Novel Loci Associated with White Blood Cell Subtypes in a Japanese Population. PLoS Genetics, 2011, 7, e1002067.	3.5	69

#	Article	IF	Citations
19	Making a haplotype catalog with estimated frequencies based on SNP homozygotes. Journal of Human Genetics, 2010, 55, 500-506.	2.3	2
20	Establishment of a standardized system to perform population structure analyses with limited sample size or with different sets of SNP genotypes. Journal of Human Genetics, 2010, 55, 525-533.	2.3	8
21	VarySysDB: a human genetic polymorphism database based on all H-InvDB transcripts. Nucleic Acids Research, 2009, 37, D810-D815.	14.5	14
22	Japanese Population Structure, Based on SNP Genotypes from 7003 Individuals Compared to Other Ethnic Groups: Effects on Population-Based Association Studies. American Journal of Human Genetics, 2008, 83, 445-456.	6.2	327
23	Distribution and Effects of Nonsense Polymorphisms in Human Genes. PLoS ONE, 2008, 3, e3393.	2.5	35
24	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. Nucleic Acids Research, 2007, 36, D793-D799.	14.5	57
25	A novel simian immunodeficiency virus from black mangabey (Lophocebus aterrimus) in the Democratic Republic of Congo. Journal of General Virology, 2005, 86, 1967-1971.	2.9	18
26	Investigation of protein functions through data-mining on integrated human transcriptome database, H-Invitational database (H-InvDB). Gene, 2005, 364, 99-107.	2.2	18
27	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	5.6	290
28	Linkage of Amino Acid Variation and Evolution of Human Immunodeficiency Virus Type 1 gp120 Envelope Glycoprotein (Subtype B) with Usage of the Second Receptor. Journal of Molecular Evolution, 2004, 58, 333-340.	1.8	16
29	Natural Infection of Wild-Born Mandrills (Mandrillus sphinx) with Two Different Types of Simian Immunodeficiency Virus. AIDS Research and Human Retroviruses, 2001, 17, 1143-1154.	1.1	38
30	Reevaluation of Amino Acid Variability of the Human Immunodeficiency Virus Type 1 gp120 Envelope Glycoprotein and Prediction of New Discontinuous Epitopes. Journal of Virology, 2000, 74, 4335-4350.	3.4	98
31	Natural infection of chimpanzees with new lentiviruses related to HIVâ€1/SIVcpz. Journal of Medical Primatology, 1999, 28, 169-173.	0.6	1
32	Human Immunodeficiency Virus Type 1 Intergroup (M/O) Recombination in Cameroon. Journal of Virology, 1999, 73, 6810-6820.	3.4	109
33	Identification of regions in which positive selection may operate in S-RNase of Rosaceae: Implication forS-allele-specific recognition sites in S-RNase. FEBS Letters, 1998, 440, 337-342.	2.8	85