Shu Tadaka

List of Publications by Year
in descending order

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29 papers	1,604 citations	516710 16 h-index	454955 30 g-index
37 all docs	37 docs citations	37 times ranked	2895 citing authors

#	Article	IF	Citations
1	ATTED-II in 2018: A Plant Coexpression Database Based on Investigation of the Statistical Property of the Mutual Rank Index. Plant and Cell Physiology, 2018, 59, e3-e3.	3.1	235
2	ATTED-II in 2016: A Plant Coexpression Database Towards Lineage-Specific Coexpression. Plant and Cell Physiology, 2016, 57, e5-e5.	3.1	194
3	COXPRESdb in 2015: coexpression database for animal species by DNA-microarray and RNAseq-based expression data with multiple quality assessment systems. Nucleic Acids Research, 2015, 43, D82-D86.	14.5	137
4	COXPRESdb v7: a gene coexpression database for 11 animal species supported by 23 coexpression platforms for technical evaluation and evolutionary inference. Nucleic Acids Research, 2019, 47, D55-D62.	14.5	125
5	3.5KJPNv2: an allele frequency panel of 3552 Japanese individuals including the X chromosome. Human Genome Variation, 2019, 6, 28.	0.7	115
6	jMorp updates in 2020: large enhancement of multi-omics data resources on the general Japanese population. Nucleic Acids Research, 2021, 49, D536-D544.	14.5	107
7	ATTED-II in 2014: Evaluation of Gene Coexpression in Agriculturally Important Plants. Plant and Cell Physiology, 2014, 55, e6-e6.	3.1	98
8	jMorp: Japanese Multi Omics Reference Panel. Nucleic Acids Research, 2018, 46, D551-D557.	14.5	90
9	COXPRESdb: a database of comparative gene coexpression networks of eleven species for mammals. Nucleic Acids Research, 2012, 41, D1014-D1020.	14.5	71
10	Enhancer remodeling promotes tumor-initiating activity in NRF2-activated non-small cell lung cancers. Nature Communications, 2020, 11, 5911.	12.8	60
11	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. Journal of Biomedical Semantics, 2014, 5, 5.	1.6	47
12	Genome analyses for the Tohoku Medical Megabank Project towards establishment of personalized healthcare. Journal of Biochemistry, 2019, 165, 139-158.	1.7	33
13	Construction and integration of three de novo Japanese human genome assemblies toward a population-specific reference. Nature Communications, 2021, 12, 226.	12.8	31
14	NCMine: Core-peripheral based functional module detection using near-clique mining. Bioinformatics, 2016, 32, 3454-3460.	4.1	22
15	Pathogenic mutations identified by a multimodality approach in 117 Japanese Fanconi anemia patients. Haematologica, 2019, 104, 1962-1973.	3.5	22
16	Functional Characterization of 40 CYP3A4 Variants by Assessing Midazolam 1â€²-Hydroxylation and Testosterone 6Î²-Hydroxylation. Drug Metabolism and Disposition, 2021, 49, 212-220.	3.3	20
17	Japonica Array NEO with increased genome-wide coverage and abundant disease risk SNPs. Journal of Biochemistry, 2021, 170, 399-410.	1.7	17
18	Identification of critical genetic variants associated with metabolic phenotypes of the Japanese population. Communications Biology, 2020, 3, 662.	4.4	16

#	Article	IF	Citations
19	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
20	Genetic loci for lung function in Japanese adults with adjustment for exhaled nitric oxide levels as airway inflammation indicator. Communications Biology, 2021, 4, 1288.	4.4	13
21	A genotype imputation method for de-identified haplotype reference information by using recurrent neural network. PLoS Computational Biology, 2020, 16, e1008207.	3.2	11
22	Comparison of Kit-Based Metabolomics with Other Methodologies in a Large Cohort, towards Establishing Reference Values. Metabolites, 2021, 11, 652.	2.9	10
23	Importance of Rare DPYD Genetic Polymorphisms for 5-Fluorouracil Therapy in the Japanese Population. Frontiers in Pharmacology, 0, 13, .	3.5	9
24	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
25	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
26	Functional Assessment of 12 Rare Allelic CYP2C9 Variants Identified in a Population of 4773 Japanese Individuals. Journal of Personalized Medicine, 2021, 11, 94.	2.5	7
27	dbTMM: an integrated database of large-scale cohort, genome and clinical data for the Tohoku Medical Megabank Project. Human Genome Variation, 2021, 8, 44.	0.7	7
28	Functional Characterization of 21 Rare Allelic CYP1A2 Variants Identified in a Population of 4773 Japanese Individuals by Assessing Phenacetin O-Deethylation. Journal of Personalized Medicine, 2021, 11, 690.	2.5	5
29	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