Yukihide Momozawa

List of Publications by Year
in descending order

46 papers	3,534 citations	279798 23 h-index	233421 45 g-index
49 all docs	49 docs citations	49 times ranked	9138 citing authors

#	Article	IF	Citations
1	Population-based Screening for Hereditary Colorectal Cancer Variants in Japan. Clinical Gastroenterology and Hepatology, 2022, 20, 2132-2141.e9.	4.4	20
2	Genome-wide association study of colorectal polyps identified highly overlapping polygenic architecture with colorectal cancer. Journal of Human Genetics, 2022, 67, 149-156.	2.3	5
3	A genome-wide association study on adherence to low-carbohydrate diets in Japanese. European Journal of Clinical Nutrition, 2022, , .	2.9	1
4	ABO O blood group as a risk factor for platelet reactivity in heparin-induced thrombocytopenia. Blood, 2022, 140, 274-284.	1.4	9
5	Genomic analysis of familial pancreatic cancers and intraductal papillary mucinous neoplasms: A crossâ€sectional study. Cancer Science, 2022, 113, 1821-1829.	3.9	5
6	Federated analysis of BRCA1 and BRCA2 variation in a Japanese cohort. Cell Genomics, 2022, 2, 100109.	6.5	1
7	Expansion of Cancer Risk Profile for BRCA1 and BRCA2 Pathogenic Variants. JAMA Oncology, 2022, 8, 871.	7.1	70
8	Associations of Genome-Wide Polygenic Risk Score and Risk Factors With Hypertension in a Japanese Population. Circulation Genomic and Precision Medicine, 2022, 15, .	3.6	6
9	Unique roles of rare variants in the genetics of complex diseases in humans. Journal of Human Genetics, 2021, 66, 11-23.	2.3	74
10	A genome-wide association study on fish consumption in a Japanese populationâ€”the Japan Multi-Institutional Collaborative Cohort study. European Journal of Clinical Nutrition, 2021, 75, 480-488.	2.9	5
11	Population-Based Impact of Smoking, Drinking, and Genetic Factors on HDL-Cholesterol Levels in J-MICC Study Participants. Journal of Epidemiology, 2021, , .	2.4	0
12	A genome-wide association study on confection consumption in a Japanese population: the Japan Multi-Institutional Collaborative Cohort Study. British Journal of Nutrition, 2021, 126, 1843-1851.	2.3	6
13	Combined inhibition of XIAP and BCL2 drives maximal therapeutic efficacy in genetically diverse aggressive acute myeloid leukemia. Nature Cancer, 2021, 2, 340-356.	13.2	11
14	Update on next generation sequencing of pharmacokinetics-related genes: Development of the PKseq panel, a platform for amplicon sequencing of drug-metabolizing enzyme and drug transporter genes. Drug Metabolism and Pharmacokinetics, 2021, 37, 100370.	2.2	2
15	Germline Pathogenic Variants in 7636 Japanese Patients With Prostate Cancer and 12Â366 Controls. Journal of the National Cancer Institute, 2020, 112, 369-376.	6.3	69
16	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. Genomics, 2020, 112, 1223-1232.	2.9	15
17	Genetic characterization of pancreatic cancer patients and prediction of carrier status of germline pathogenic variants in cancer-predisposing genes. EBioMedicine, 2020, 60, 103033.	6.1	39
18	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. Nature Genetics, 2020, 52, 669-679.	21.4	304

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19	GWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. Nature Human Behaviour, 2020, 4, 308-316.	12.0	80
20	Prevalence and Spectrum of Pathogenic Germline Variants in Japanese Patients With Early-Onset Colorectal, Breast, and Prostate Cancer. JCO Precision Oncology, 2020, 4, 183-191.	3.0	6
21	Genome wide association study of 40 clinical measurements in eight dog breeds. Scientific Reports, 2020, 10, 6520.	3.3	8
22	Polygenic Risk Score of Adolescent Idiopathic Scoliosis for Potential Clinical Use. Journal of Bone and Mineral Research, 2020, 36, 1481-1491.	2.8	5
23	High-throughput functional evaluation of BRCA2 variants of unknown significance. Nature Communications, 2020, 11, 2573.	12.8	38
24	Genome-wide association study identifies 14 previously unreported susceptibility loci for adolescent idiopathic scoliosis in Japanese. Nature Communications, 2019, 10, 3685.	12.8	47
25	Identification of rare coding variants in TYK2 protective for rheumatoid arthritis in the Japanese population and their effects on cytokine signalling. Annals of the Rheumatic Diseases, 2019, 78, 1062-1069.	0.9	16
26	Genome-wide association meta-analysis and Mendelian randomization analysis confirm the influence of ALDH2 on sleep durationin the Japanese population. Sleep, 2019, 42, .	1.1	16
27	A multiethnic meta-analysis defined the association of rs12946942 with severe adolescent idiopathic scoliosis. Journal of Human Genetics, 2019, 64, 493-498.	2.3	11
28	The potential of translational research in dogs in human medicine. Translational and Regulatory Sciences, 2019, 1, 31-36.	0.2	3
29	PPM1D and DNMT3A Mutations in Myelodysplasia and Clonal Hematopoiesis. Blood, 2019, 134, 1709-1709.	1.4	2
30	GWAS identifies two novel colorectal cancer loci at 16q24.1 and 20q13.12. Carcinogenesis, 2018, 39, 652-660.	2.8	52
31	Genetic analysis of quantitative traits in the Japanese population links cell types to complex human diseases. Nature Genetics, 2018, 50, 390-400.	21.4	613
32	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
33	A genome-wide association study in the Japanese population identifies the 12q24 locus for habitual coffee consumption: The J-MICC Study. Scientific Reports, 2018, 8, 1493.	3.3	32
34	Germline pathogenic variants of 11 breast cancer genes in 7,051 Japanese patients and 11,241 controls. Nature Communications, 2018, 9, 4083.	12.8	179
35	A genome-wide association study identifies three novel genetic markers for response to tamoxifen: A prospective multicenter study. PLoS ONE, 2018, 13, e0201606.	2.5	1
36	Blood lipid-related low-frequency variants in LDLR and PCSK9 are associated with onset age and risk of myocardial infarction in Japanese. Scientific Reports, 2018, 8, 8107.	3.3	13

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37	IBD risk loci are enriched in multigenic regulatory modules encompassing putative causative genes. Nature Communications, 2018, 9, 2427.	12.8	159
38	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
39	Polygenic burdens on cell-specific pathways underlie the risk of rheumatoid arthritis. Nature Genetics, 2017, 49, 1120-1125.	21.4	130
40	ZNF384 -related fusion genes define a subgroup of childhood B-cell precursor acute lymphoblastic leukemia with a characteristic immunotype. Haematologica, 2017, 102, 118-129.	3.5	172
41	Fine-mapping inflammatory bowel disease loci to single-variant resolution. Nature, 2017, 547, 173-178.	27.8	473
42	Association between GWAS-identified lung adenocarcinoma susceptibility loci andEGFRmutations in never-smoking Asian women, and comparison with findings from Western populations. Human Molecular Genetics, 2016, 26, ddw414.	2.9	50
43	Low-frequency coding variants inCETPandCFBare associated with susceptibility of exudative age-related macular degeneration in the Japanese population. Human Molecular Genetics, 2016, 25, ddw335.	2.9	42
44	Association of variations in HLA class II and other loci with susceptibility to EGFR-mutated lung adenocarcinoma. Nature Communications, 2016, 7, 12451.	12.8	49
45	CCDC39 is required for assembly of inner dynein arms and the dynein regulatory complex and for normal ciliary motility in humans and dogs. Nature Genetics, 2011, 43, 72-78.	21.4	302
46	Resequencing of positional candidates identifies low frequency IL23R coding variants protecting against inflammatory bowel disease. Nature Genetics, 2011, 43, 43-47.	21.4	175