

Yukihide Momozawa

List of Publications by Year in descending order

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Version: 2024-02-01

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	Genetic analysis of quantitative traits in the Japanese population links cell types to complex human diseases. <i>Nature Genetics</i> , 2018, 50, 390-400.	21.4	613
2	Fine-mapping inflammatory bowel disease loci to single-variant resolution. <i>Nature</i> , 2017, 547, 173-178.	27.8	473
3	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. <i>Nature Genetics</i> , 2020, 52, 669-679.	21.4	304
4	CCDC39 is required for assembly of inner dynein arms and the dynein regulatory complex and for normal ciliary motility in humans and dogs. <i>Nature Genetics</i> , 2011, 43, 72-78.	21.4	302
5	Germline pathogenic variants of 11 breast cancer genes in 7,051 Japanese patients and 11,241 controls. <i>Nature Communications</i> , 2018, 9, 4083.	12.8	179
6	Resequencing of positional candidates identifies low frequency IL23R coding variants protecting against inflammatory bowel disease. <i>Nature Genetics</i> , 2011, 43, 43-47.	21.4	175
7	<i>ZNF384</i> -related fusion genes define a subgroup of childhood B-cell precursor acute lymphoblastic leukemia with a characteristic immunotype. <i>Haematologica</i> , 2017, 102, 118-129.	3.5	172
8	IBD risk loci are enriched in multigenic regulatory modules encompassing putative causative genes. <i>Nature Communications</i> , 2018, 9, 2427.	12.8	159
9	Polygenic burdens on cell-specific pathways underlie the risk of rheumatoid arthritis. <i>Nature Genetics</i> , 2017, 49, 1120-1125.	21.4	130
10	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	6.2	123
11	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	2.5	94
12	GWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. <i>Nature Human Behaviour</i> , 2020, 4, 308-316.	12.0	80
13	Unique roles of rare variants in the genetics of complex diseases in humans. <i>Journal of Human Genetics</i> , 2021, 66, 11-23.	2.3	74
14	Expansion of Cancer Risk Profile for <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>JAMA Oncology</i> , 2022, 8, 871.	7.1	70
15	Germline Pathogenic Variants in 7636 Japanese Patients With Prostate Cancer and 12,366 Controls. <i>Journal of the National Cancer Institute</i> , 2020, 112, 369-376.	6.3	69
16	GWAS identifies two novel colorectal cancer loci at 16q24.1 and 20q13.12. <i>Carcinogenesis</i> , 2018, 39, 652-660.	2.8	52
17	Association between GWAS-identified lung adenocarcinoma susceptibility loci and EGFR mutations in never-smoking Asian women, and comparison with findings from Western populations. <i>Human Molecular Genetics</i> , 2016, 26, ddw414.	2.9	50
18	Association of variations in HLA class II and other loci with susceptibility to EGFR-mutated lung adenocarcinoma. <i>Nature Communications</i> , 2016, 7, 12451.	12.8	49

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19	Genome-wide association study identifies 14 previously unreported susceptibility loci for adolescent idiopathic scoliosis in Japanese. <i>Nature Communications</i> , 2019, 10, 3685.	12.8	47
20	Low-frequency coding variants in <i>CETP</i> and <i>CFB</i> are associated with susceptibility of exudative age-related macular degeneration in the Japanese population. <i>Human Molecular Genetics</i> , 2016, 25, ddw335.	2.9	42
21	Genetic characterization of pancreatic cancer patients and prediction of carrier status of germline pathogenic variants in cancer-predisposing genes. <i>EBioMedicine</i> , 2020, 60, 103033.	6.1	39
22	High-throughput functional evaluation of BRCA2 variants of unknown significance. <i>Nature Communications</i> , 2020, 11, 2573.	12.8	38
23	A genome-wide association study in the Japanese population identifies the 12q24 locus for habitual coffee consumption: The J-MICC Study. <i>Scientific Reports</i> , 2018, 8, 1493.	3.3	32
24	Population-based Screening for Hereditary Colorectal Cancer Variants in Japan. <i>Clinical Gastroenterology and Hepatology</i> , 2022, 20, 2132-2141.e9.	4.4	20
25	Identification of rare coding variants in <i>TYK2</i> protective for rheumatoid arthritis in the Japanese population and their effects on cytokine signalling. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 1062-1069.	0.9	16
26	Genome-wide association meta-analysis and Mendelian randomization analysis confirm the influence of ALDH2 on sleep duration in the Japanese population. <i>Sleep</i> , 2019, 42, .	1.1	16
27	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. <i>Genomics</i> , 2020, 112, 1223-1232.	2.9	15
28	Blood lipid-related low-frequency variants in LDLR and PCSK9 are associated with onset age and risk of myocardial infarction in Japanese. <i>Scientific Reports</i> , 2018, 8, 8107.	3.3	13
29	A multiethnic meta-analysis defined the association of rs12946942 with severe adolescent idiopathic scoliosis. <i>Journal of Human Genetics</i> , 2019, 64, 493-498.	2.3	11
30	Combined inhibition of XIAP and BCL2 drives maximal therapeutic efficacy in genetically diverse aggressive acute myeloid leukemia. <i>Nature Cancer</i> , 2021, 2, 340-356.	13.2	11
31	<i>ABO</i> O blood group as a risk factor for platelet reactivity in heparin-induced thrombocytopenia. <i>Blood</i> , 2022, 140, 274-284.	1.4	9
32	Genome wide association study of 40 clinical measurements in eight dog breeds. <i>Scientific Reports</i> , 2020, 10, 6520.	3.3	8
33	Prevalence and Spectrum of Pathogenic Germline Variants in Japanese Patients With Early-Onset Colorectal, Breast, and Prostate Cancer. <i>JCO Precision Oncology</i> , 2020, 4, 183-191.	3.0	6
34	A genome-wide association study on confection consumption in a Japanese population: the Japan Multi-Institutional Collaborative Cohort Study. <i>British Journal of Nutrition</i> , 2021, 126, 1843-1851.	2.3	6
35	Associations of Genome-Wide Polygenic Risk Score and Risk Factors With Hypertension in a Japanese Population. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, .	3.6	6
36	A genome-wide association study on fish consumption in a Japanese population—the Japan Multi-Institutional Collaborative Cohort study. <i>European Journal of Clinical Nutrition</i> , 2021, 75, 480-488.	2.9	5

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37	Polygenic Risk Score of Adolescent Idiopathic Scoliosis for Potential Clinical Use. <i>Journal of Bone and Mineral Research</i> , 2020, 36, 1481-1491.	2.8	5
38	Genome-wide association study of colorectal polyps identified highly overlapping polygenic architecture with colorectal cancer. <i>Journal of Human Genetics</i> , 2022, 67, 149-156.	2.3	5
39	Genomic analysis of familial pancreatic cancers and intraductal papillary mucinous neoplasms: A cross-sectional study. <i>Cancer Science</i> , 2022, 113, 1821-1829.	3.9	5
40	The potential of translational research in dogs in human medicine. <i>Translational and Regulatory Sciences</i> , 2019, 1, 31-36.	0.2	3
41	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. <i>Drug Metabolism and Pharmacokinetics</i> , 2021, 37, 100370.	2.2	2
42	PPM1D and DNMT3A Mutations in Myelodysplasia and Clonal Hematopoiesis. <i>Blood</i> , 2019, 134, 1709-1709.	1.4	2
43	A genome-wide association study identifies three novel genetic markers for response to tamoxifen: A prospective multicenter study. <i>PLoS ONE</i> , 2018, 13, e0201606.	2.5	1
44	A genome-wide association study on adherence to low-carbohydrate diets in Japanese. <i>European Journal of Clinical Nutrition</i> , 2022, , .	2.9	1
45	Federated analysis of BRCA1 and BRCA2 variation in a Japanese cohort. <i>Cell Genomics</i> , 2022, 2, 100109.	6.5	1
46	Population-Based Impact of Smoking, Drinking, and Genetic Factors on HDL-Cholesterol Levels in J-MICC Study Participants. <i>Journal of Epidemiology</i> , 2021, , .	2.4	0