Koichi K Matsuda

List of Publications by Year
in descending order

196	17,784	18465 62	19169 118
papers	citations	h-index	g-index

229	229	229	25217
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	p53AIP1, a Potential Mediator of p53-Dependent Apoptosis, and Its Regulation by Ser-46-Phosphorylated p53. Cell, 2000, 102, 849-862.	13.5	1,095
2	Genetic analysis of quantitative traits in the Japanese population links cell types to complex human diseases. Nature Genetics, 2018, 50, 390-400.	9.4	613
3	A cross-population atlas of genetic associations for 220 human phenotypes. Nature Genetics, 2021, 53, 1415-1424.	9.4	560
4	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
5	Genome-wide association scan identifies a colorectal cancer susceptibility locus on 11q23 and replicates risk loci at 8q24 and 18q21. Nature Genetics, 2008, 40, 631-637.	9.4	542
6	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	9.4	501
7	A genome-wide association study identifies variants in the HLA-DP locus associated with chronic hepatitis B in Asians. Nature Genetics, 2009, 41, 591-595.	9.4	491
8	Genome-wide association study of hematological and biochemical traits in a Japanese population. Nature Genetics, 2010, 42, 210-215.	9.4	460
9	Overview of the BioBank Japan Project: Study design and profile. Journal of Epidemiology, 2017, 27, S2-S8.	1.1	451
10	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
11	Genome-wide association study identifies 112 new loci for body mass index in the Japanese population. Nature Genetics, 2017, 49, 1458-1467.	9.4	380
12	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	13.5	353
13	Genome-wide association study identifies a susceptibility locus for HCV-induced hepatocellular carcinoma. Nature Genetics, 2011, 43, 455-458.	9.4	332
14	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. Nature Genetics, 2020, 52, 669-679.	9.4	304
15	Functional Variants in ADH1B and ALDH2 Coupled With Alcohol and Smoking Synergistically Enhance Esophageal Cancer Risk. Gastroenterology, 2009, 137, 1768-1775.	0.6	277
16	Large-scale genome-wide association studies in east Asians identify new genetic loci influencing metabolic traits. Nature Genetics, 2011, 43, 990-995.	9.4	270
17	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	9.4	264
18	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251

#	Article	IF	Citations
19	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	5.8	230
20	Large-scale genetic study in East Asians identifies six new loci associated with colorectal cancer risk. Nature Genetics, 2014, 46, 533-542.	9.4	212
21	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. Nature Genetics, 2012, 44, 770-776.	9.4	210
22	Population-specific and trans-ancestry genome-wide analyses identify distinct and shared genetic risk loci for coronary artery disease. Nature Genetics, 2020, 52, 1169-1177.	9.4	206
23	A genome-wide association study of chronic hepatitis B identified novel risk locus in a Japanese population. Human Molecular Genetics, 2011, 20, 3884-3892.	1.4	205
24	A nonsynonymous SNP in PRKCH (protein kinase C Î·) increases the risk of cerebral infarction. Nature Genetics, 2007, 39, 212-217.	9.4	200
25	Germline pathogenic variants of 11 breast cancer genes in 7,051 Japanese patients and 11,241 controls. Nature Communications, 2018, 9, 4083.	5.8	179
26	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
27	Identification of 28 new susceptibility loci for type 2 diabetes in the Japanese population. Nature Genetics, 2019, 51, 379-386.	9.4	164
28	Genome-wide association study of intracranial aneurysms identifies 17 risk loci and genetic overlap with clinical risk factors. Nature Genetics, 2020, 52, 1303-1313.	9.4	163
29	p53RDL1 regulates p53-dependent apoptosis. Nature Cell Biology, 2003, 5, 216-223.	4.6	150
30	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. PLoS Genetics, 2013, 9, e1003796.	1.5	142
31	Genome-wide association analysis in East Asians identifies breast cancer susceptibility loci at 1q32.1, 5q14.3 and 15q26.1. Nature Genetics, 2014, 46, 886-890.	9.4	135
32	Cross-sectional analysis of BioBank Japan clinical data: A large cohort of 200,000 patients with 47 common diseases. Journal of Epidemiology, 2017, 27, S9-S21.	1.1	133
33	Deep whole-genome sequencing reveals recent selection signatures linked to evolution and disease risk of Japanese. Nature Communications, 2018, 9, 1631.	5.8	132
34	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	3.0	129
35	Regulation of histone modification and chromatin structure by the p53â€“PADI4 pathway. Nature Communications, 2012, 3, 676.	5.8	128
36	Improving the trans-ancestry portability of polygenic risk scores by prioritizing variants in predicted cell-type-specific regulatory elements. Nature Genetics, 2020, 52, 1346-1354.	9.4	126

#	Article	IF	Citations
37	Characterizing rare and low-frequency height-associated variants in the Japanese population. Nature Communications, 2019, 10, 4393.	5.8	123
38	Construction of a population-specific HLA imputation reference panel and its application to Graves' disease risk in Japanese. Nature Genetics, 2015, 47, 798-802.	9.4	119
39	A Genome-Wide Association Study Identified AFF1 as a Susceptibility Locus for Systemic Lupus Eyrthematosus in Japanese. PLoS Genetics, 2012, 8, e1002455.	1.5	115
40	A genome-wide association study identifies two susceptibility loci for duodenal ulcer in the Japanese population. Nature Genetics, 2012, 44, 430-434.	9.4	114
41	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. Nature Communications, 2019, 10, 29.	5.8	113
42	Large-Scale Genome-Wide Association Study of East Asians Identifies Loci Associated With Risk for Colorectal Cancer. Gastroenterology, 2019, 156, 1455-1466.	0.6	111
43	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. Nature Medicine, 2021, 27, 1012-1024.	15.2	109
44	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 2022, 54, 450-458.	9.4	109
45	Functional SNPs in CD244 increase the risk of rheumatoid arthritis in a Japanese population. Nature Genetics, 2008, 40, 1224-1229.	9.4	106
46	Regulation of Protein Citrullination through p53/PADI4 Network in DNA Damage Response. Cancer Research, 2009, 69, 8761-8769.	0.4	106
47	A genome-wide association study in 19 633 Japanese subjects identified LHX3-QSOX2 and IGF1 as adult height loci. Human Molecular Genetics, 2010, 19, 2303-2312.	1.4	106
48	Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113.	1.5	106
49	Functional SNP in an Sp1-binding site of AGTRL1 gene is associated with susceptibility to brain infarction. Human Molecular Genetics, 2007, 16, 630-639.	1.4	105
50	Meta-analysis of 208370 East Asians identifies 113 susceptibility loci for systemic lupus erythematosus. Annals of the Rheumatic Diseases, 2021, 80, 632-640.	0.5	103
51	Chromosomal alterations among age-related haematopoietic clones in Japan. Nature, 2020, 584, 130-135.	13.7	102
52	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. Gastroenterology, 2016, 150, 1633-1645.	0.6	97
53	p53AIP1 regulates the mitochondrial apoptotic pathway. Cancer Research, 2002, 62, 2883-9.	0.4	94
54	Orphan receptor tyrosine kinase ROR2 as a potential therapeutic target for osteosarcoma. Cancer Science, 2009, 100, 1227-1233.	1.7	86

#	Article	IF	Citations
55	Citrullination of RGG Motifs in FET Proteins by PAD4 Regulates Protein Aggregation and ALS Susceptibility. Cell Reports, 2018, 22, 1473-1483.	2.9	85
56	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
57	Genome-wide association study for C-reactive protein levels identified pleiotropic associations in the IL6 locus. Human Molecular Genetics, 2011, 20, 1224-1231.	1.4	82
58	Soluble MICA and a MICA Variation as Possible Prognostic Biomarkers for HBV-Induced Hepatocellular Carcinoma. PLoS ONE, 2012, 7, e44743.	1.1	81
59	GWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. Nature Human Behaviour, 2020, 4, 308-316.	6.2	80
60	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. Nature Medicine, 2021, 27, 1239-1249.	15.2	78
61	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. Nature Communications, 2018, 9, 5052.	5.8	75
62	Genetic and phenotypic landscape of the major histocompatibilty complex region in the Japanese population. Nature Genetics, 2019, 51, 470-480.	9.4	75
63	Trans-biobank analysis with 676,000 individuals elucidates the association of polygenic risk scores of complex traits with human lifespan. Nature Medicine, 2020, 26, 542-548.	15.2	74
64	Expansion of Cancer Risk Profile for BRCA1 and BRCA2 Pathogenic Variants. JAMA Oncology, 2022, 8, 871.	3.4	70
65	Identification of Nine Novel Loci Associated with White Blood Cell Subtypes in a Japanese Population. PLoS Genetics, 2011, 7, e1002067.	1.5	69
66	Genetic variants of calcium and vitamin D metabolism in kidney stone disease. Nature Communications, 2019, 10, 5175.	5.8	69
67	Germline Pathogenic Variants in 7636 Japanese Patients With Prostate Cancer and 12Â366 Controls. Journal of the National Cancer Institute, 2020, 112, 369-376.	3.0	69
68	Quantitative T cell repertoire analysis by deep cDNA sequencing of T cell receptor Î± and Î² chains using next-generation sequencing (NGS). OncoImmunology, 2014, 3, e968467.	2.1	68
69	Regulation of iron homeostasis by the p53-ISCU pathway. Scientific Reports, 2015, 5, 16497.	1.6	68
70	Contribution of a Non-classical HLA Gene, HLA-DOA, to the Risk of Rheumatoid Arthritis. American Journal of Human Genetics, 2016, 99, 366-374.	2.6	68
71	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 2016, 99, 636-646.	2.6	67
72	Genome-wide meta-analysis identifies multiple novel loci associated with serum uric acid levels in Japanese individuals. Communications Biology, 2019, 2, 115.	2.0	66

#	Article	IF	Citations
73	Clinical and molecular characteristics of MEF2D fusion-positive B-cell precursor acute lymphoblastic leukemia in childhood, including a novel translocation resulting in MEF2D-HNRNPH1 gene fusion. Haematologica, 2019, 104, 128-137.	1.7	65
74	The histone methyltransferase Wolfâ€“Hirschhorn syndrome candidate 1â€like 1 (WHSC1L1) is involved in human carcinogenesis. Genes Chromosomes and Cancer, 2013, 52, 126-139.	1.5	64
75	A Genome-Wide Association Study of Nephrolithiasis in the Japanese Population Identifies Novel Susceptible Loci at 5q35.3, 7p14.3, and 13q14.1. PLoS Genetics, 2012, 8, e1002541.	1.5	63
76	Claudin-2 deficiency associates with hypercalciuria in mice and human kidney stone disease. Journal of Clinical Investigation, 2020, 130, 1948-1960.	3.9	61
77	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	1.4	60
78	Identification of a Functional Variant in the MICA Promoter Which Regulates MICA Expression and Increases HCV-Related Hepatocellular Carcinoma Risk. PLoS ONE, 2013, 8, e61279.	1.1	59
79	A genome-wide association study of HCV-induced liver cirrhosis in the Japanese population identifies novel susceptibility loci at the MHC region. Journal of Hepatology, 2013, 58, 875-882.	1.8	58
80	Dimensionality reduction reveals fine-scale structure in the Japanese population with consequences for polygenic risk prediction. Nature Communications, 2020, 11, 1569.	5.8	58
81	Identification of a novel p53 target, COL17A1, that inhibits breast cancer cell migration and invasion. Oncotarget, 2017, 8, 55790-55803.	0.8	58
82	GWAS of smoking behaviour in 165,436 Japanese people reveals seven new loci and shared genetic architecture. Nature Human Behaviour, 2019, 3, 471-477.	6.2	54
83	Genomeâ€wide association study identifies a new SMAD7 risk variant associated with colorectal cancer risk in East Asians. International Journal of Cancer, 2014, 135, 948-955.	2.3	52
84	GWAS identifies two novel colorectal cancer loci at 16q24.1 and 20q13.12. Carcinogenesis, 2018, 39, 652-660.	1.3	52
85	Large-scale association analysis in Asians identifies new susceptibility loci for prostate cancer. Nature Communications, 2015, 6, 8469.	5.8	51
86	GWAS of mosaic loss of chromosome Y highlights genetic effects on blood cell differentiation. Nature Communications, 2019, 10, 4719.	5.8	50
87	Common variations in PSMD3â€“CSF3 and PLCB4 are associated with neutrophil count. Human Molecular Genetics, 2010, 19, 2079-2085.	1.4	49
88	Quantitative Structural Characterization of Local N-Glycan Microheterogeneity in Therapeutic Antibodies by Energy-Resolved Oxonium Ion Monitoring. Analytical Chemistry, 2012, 84, 9655-9662.	3.2	49
89	12 new susceptibility loci for prostate cancer identified by genome-wide association study in Japanese population. Nature Communications, 2019, 10, 4422.	5.8	49
90	A genome-wide association study identifies PLCL2 and AP3D1-DOT1L-SF3A2 as new susceptibility loci for myocardial infarction in Japanese. European Journal of Human Genetics, 2015, 23, 374-380.	1.4	48

#	Article	IF	Citations
91	The Transcriptional Landscape of p53 Signalling Pathway. EBioMedicine, 2017, 20, 109-119.	2.7	47
92	Overview of BioBank Japan follow-up data in 32 diseases. Journal of Epidemiology, 2017, 27, S22-S28.	1.1	47
93	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. Nature Communications, 2020, 11, 1217.	5.8	46
94	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. American Journal of Human Genetics, 2017, 100, 51-63.	2.6	45
95	Elucidating the genetic architecture of reproductive ageing in the Japanese population. Nature Communications, 2018, 9, 1977.	5.8	44
96	Transethnic Meta-Analysis of Genome-Wide Association Studies Identifies Three New Loci and Characterizes Population-Specific Differences for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2020, 13, e002670.	1.6	44
97	A deep learning method for HLA imputation and trans-ethnic MHC fine-mapping of type 1 diabetes. Nature Communications, 2021, 12, 1639.	5.8	44
98	Leveraging supervised learning for functionallyÂinformed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. Nature Communications, 2021, 12, 3394.	5.8	44
99	Regulation of myo-inositol biosynthesis by p53-ISYNA1 pathway. International Journal of Oncology, 2016, 48, 2415-2424.	1.4	41
100	Integrated exome and RNA sequencing of dedifferentiated liposarcoma. Nature Communications, 2019, 10, 5683.	5.8	41
101	No association for Chinese HBV-related hepatocellular carcinoma susceptibility SNP in other East Asian populations. BMC Medical Genetics, 2012, 13, 47.	2.1	40
102	Antitumor Activity and Induction of TP53-Dependent Apoptosis toward Ovarian Clear Cell Adenocarcinoma by the Dual PI3K/mTOR Inhibitor DS-7423. PLoS ONE, 2014, 9, e87220.	1.1	40
103	Genome-wide association study in East Asians identifies two novel breast cancer susceptibility loci. Human Molecular Genetics, 2016, 25, 3361-3371.	1.4	40
104	Argininosuccinate synthase 1 is an intrinsic Akt repressor transactivated by p53. Science Advances, 2017, 3, e1603204.	4.7	40
105	Association Study of a Functional Variant on ABCG2 Gene with Sunitinib-Induced Severe Adverse Drug Reaction. PLoS ONE, 2016, 11, e0148177.	1.1	39
106	Genomeâ€wide association study identifies gastric cancer susceptibility loci at 12q24.11â€12 and 20q11.21. Cancer Science, 2018, 109, 4015-4024.	1.7	39
107	Genetic characterization of pancreatic cancer patients and prediction of carrier status of germline pathogenic variants in cancer-predisposing genes. EBioMedicine, 2020, 60, 103033.	2.7	39
108	Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. International Journal of Epidemiology, 2022, 50, 1995-2010.	0.9	39

#	Article	IF	Citations
109	Impact of polymorphisms in drug pathway genes on disease-free survival in adults with acute myeloid leukemia. Journal of Human Genetics, 2013, 58, 353-361.	1.1	38
110	Genome-wide association study identified SNP on 15q24 associated with bladder cancer risk in Japanese population. Human Molecular Genetics, 2015, 24, 1177-1184.	1.4	38
111	Cystatin C as a p53â€inducible apoptotic mediator that regulates cathepsin L activity. Cancer Science, 2016, 107, 298-306.	1.7	38
112	Characteristics and prognosis of Japanese colorectal cancer patients: The BioBank Japan Project. Journal of Epidemiology, 2017, 27, S36-S42.	1.1	38
113	Crosstalk of EDA-A2/XEDAR in the p53 Signaling Pathway. Molecular Cancer Research, 2010, 8, 855-863.	1.5	36
114	Antitumor immunity augments the therapeutic effects of p53 activation on acute myeloid leukemia. Nature Communications, 2019, 10, 4869.	5.8	36
115	Genetic analysis of endometriosis and depression identifies shared loci and implicates causal links with gastric mucosa abnormality. Human Genetics, 2021, 140, 529-552.	1.8	36
116	Association of Common Variants in TNFRSF13B, TNFSF13, and ANXA3 with Serum Levels of Non-Albumin Protein and Immunoglobulin Isotypes in Japanese. PLoS ONE, 2012, 7, e32683.	1.1	34
117	Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. Nature Communications, 2020, 11, 3175.	5.8	34
118	Genome-wide risk prediction of common diseases across ancestries in one million people. Cell Genomics, 2022, 2, 100118.	3.0	34
119	Genetic analysis of right heart structure and function in 40,000 people. Nature Genetics, 2022, 54, 792-803.	9.4	34
120	CLCA2 as a p53-Inducible Senescence Mediator. Neoplasia, 2012, 14, 141-IN9.	2.3	32
121	Demographic and lifestyle factors and survival among patients with esophageal and gastric cancer: The Biobank Japan Project. Journal of Epidemiology, 2017, 27, S29-S35.	1.1	32
122	GWAS of five gynecologic diseases and cross-trait analysis in Japanese. European Journal of Human Genetics, 2020, 28, 95-107.	1.4	32
123	Genetic and phenotypic landscape of the mitochondrial genome in the Japanese population. Communications Biology, 2020, 3, 104.	2.0	32
124	Identification of novel epigenetically inactivated gene PAMR1 in breast carcinoma. Oncology Reports, 2015, 33, 267-273.	1.2	31
125	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	1.4	31
126	Massively parallel sequencing of tenosynovial giant cell tumors reveals novel CSF1 fusion transcripts and novel somatic CBL mutations. International Journal of Cancer, 2019, 145, 3276-3284.	2.3	28

#	Article	IF	Citations
127	Critical Function for Nuclear Envelope Protein TMEM209 in Human Pulmonary Carcinogenesis. Cancer Research, 2012, 72, 4110-4118.	0.4	27
128	Characteristics and prognosis of Japanese female breast cancer patients: The BioBank Japan project. Journal of Epidemiology, 2017, 27, S58-S64.	1.1	27
129	Identification of a significant association of a single nucleotide polymorphism in TNXB with systemic lupus erythematosus in a Japanese population. Journal of Human Genetics, 2008, 53, 64-73.	1.1	26
130	Genome Wide Association Study of Age at Menarche in the Japanese Population. PLoS ONE, 2013, 8, e63821.	1.1	26
131	A functional SNP in the NKX2.5-binding site of ITPR3 promoter is associated with susceptibility to systemic lupus erythematosus in Japanese population. Journal of Human Genetics, 2008, 53, 151-162.	1.1	25
132	Common variants on 14q32 and 13q12 are associated with DLBCL susceptibility. Journal of Human Genetics, 2011, 56, 436-439.	1.1	25
133	Downregulation of the tumor suppressor HSPB7, involved in the p53 pathway, in renal cell carcinoma by hypermethylation. International Journal of Oncology, 2014, 44, 1490-1498.	1.4	25
134	Statin use and all-cause and cancer mortality: BioBank Japan cohort. Journal of Epidemiology, 2017, 27, S84-S91.	1.1	25
135	Novel Risk Loci Identified in a Genome-Wide Association Study of Urolithiasis in a Japanese Population. Journal of the American Society of Nephrology: JASN, 2019, 30, 855-864.	3.0	25
136	Identification of Novel Loci and New Risk Variant in Known Loci for Colorectal Cancer Risk in East Asians. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 477-486.	1.1	25
137	A replication study for three nephrolithiasis loci at 5q35.3, 7p14.3 and 13q14.1 in the Japanese population. Journal of Human Genetics, 2013, 58, 588-593.	1.1	24
138	GALNT6 Stabilizes GRP78 Protein by O-glycosylation and Enhances its Activity to Suppress Apoptosis Under Stress Condition. Neoplasia, 2017, 19, 43-53.	2.3	23
139	The p53 activator overcomes resistance to ALK inhibitors by regulating p53-target selectivity in ALK-driven neuroblastomas. Cell Death Discovery, 2018, 4, 56.	2.0	23
140	Endogenization and excision of human herpesvirus 6 in human genomes. PLoS Genetics, 2020, 16, e1008915.	1.5	22
141	Genome-Wide Natural Selection Signatures Are Linked to Genetic Risk of Modern Phenotypes in the Japanese Population. Molecular Biology and Evolution, 2020, 37, 1306-1316.	3.5	22
142	Adjustment of Cell-Type Composition Minimizes Systematic Bias in Blood DNA Methylation Profiles Derived by DNA Collection Protocols. PLoS ONE, 2016, 11, e0147519.	1.1	21
143	Decrease in PSCA expression caused by Helicobacter pylori infection may promote progression to severe gastritis. Oncotarget, 2018, 9, 3936-3945.	0.8	21
144	Survival of macrovascular disease, chronic kidney disease, chronic respiratory disease, cancer and smoking in patients with type 2 diabetes: BioBank Japan cohort. Journal of Epidemiology, 2017, 27, S98-S106.	1.1	20

#	Article	IF	Citations
145	Population-based Screening for Hereditary Colorectal Cancer Variants in Japan. Clinical Gastroenterology and Hepatology, 2022, 20, 2132-2141.e9.	2.4	20
146	Genetic overlap analysis of endometriosis and asthma identifies shared loci implicating sex hormones and thyroid signalling pathways. Human Reproduction, 2022, 37, 366-383.	0.4	19
147	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	1.8	18
148	Characteristics of patients with liver cancer in the BioBank Japan project. Journal of Epidemiology, 2017, 27, S43-S48.	1.1	17
149	Characteristics and prognosis of Japanese male and female lung cancer patients: The BioBank Japan Project. Journal of Epidemiology, 2017, 27, S49-S57.	1.1	17
150	Association analysis of the NOD2 gene with susceptibility to graft-versus-host disease in a Japanese population. International Journal of Hematology, 2011, 93, 771-778.	0.7	16
151	Late Cornified Envelope Group I, a Novel Target of p53, Regulates PRMT5 Activity. Neoplasia, 2014, 16, 656-664.	2.3	16
152	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.	0.5	16
153	Collagen XVII inhibits breast cancer cell proliferation and growth through deactivation of the AKT/mTOR signaling pathway. PLoS ONE, 2021, 16, e0255179.	1.1	16
154	Impact of PSCA Variation on Gastric Ulcer Susceptibility. PLoS ONE, 2013, 8, e63698.	1.1	15
155	Genetic risk score based on the prevalence of vertebral fracture in Japanese women with osteoporosis. Bone Reports, 2016, 5, 168-172.	0.2	15
156	EPSIN 3, A Novel p53 Target, Regulates the Apoptotic Pathway and Gastric Carcinogenesis. Neoplasia, 2017, 19, 185-195.	2.3	14
157	Functional variants in ADH1B and ALDH2 are non-additively associated with all-cause mortality in Japanese population. European Journal of Human Genetics, 2020, 28, 378-382.	1.4	14
158	Identification of a novel uterine leiomyoma GWAS locus in a Japanese population. Scientific Reports, 2020, 10, 1197.	1.6	14
159	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. EBioMedicine, 2021, 63, 103157.	2.7	14
160	Serum glucose, cholesterol and blood pressure levels in Japanese type 1 and 2 diabetic patients: BioBank Japan. Journal of Epidemiology, 2017, 27, S92-S97.	1.1	12
161	A genome-wide association study identifies a novel candidate locus at the DLGAP1 gene with susceptibility to resistant hypertension in the Japanese population. Scientific Reports, 2021, 11, 19497.	1.6	12
162	Risk prediction models for mortality in patients with cardiovascular disease: The BioBank Japan project. Journal of Epidemiology, 2017, 27, S71-S76.	1.1	11

#	Article	IF	Citations
163	Clinical and histopathological characteristics of patients with prostate cancer in the BioBank Japan project. Journal of Epidemiology, 2017, 27, S65-S70.	1.1	11
164	Endoscopy-based Kyoto classification score of gastritis related to pathological topography of neutrophil activity. World Journal of Gastroenterology, 2020, 26, 5146-5155.	1.4	11
165	The simplified Kyoto classification score is consistent with the ABC method of classification as a grading system for endoscopic gastritis. Journal of Clinical Biochemistry and Nutrition, 2021, 68, 101-104.	0.6	10
166	Comprehensive molecular and clinicopathological profiling of desmoid tumours. European Journal of Cancer, 2021, 145, 109-120.	1.3	10
167	Germline Variants and Advanced Colorectal Adenomas: Adenoma Prevention with Celecoxib Trial Genome-wide Association Study. Clinical Cancer Research, 2013, 19, 6430-6437.	3.2	9
168	Identification of two novel breast cancer loci through large-scale genome-wide association study in the Japanese population. Scientific Reports, 2019, 9, 17332.	1.6	9
169	Single Nucleotide Polymorphisms of HAAO and IRX6 Genes as Risk Factors for Hypospadias. Journal of Urology, 2019, 201, 386-392.	0.2	9
170	Genetic susceptibility to hepatocellular carcinoma in chromosome 22q13.31, findings of a genomeâ€wide association study. JGH Open, 2021, 5, 1363-1372.	0.7	9
171	Biological insights into systemic lupus erythematosus through an immune cell-specific transcriptome-wide association study. Annals of the Rheumatic Diseases, 2022, 81, 1273-1280.	0.5	9
172	Genome-wide association study (GWAS) of ovarian cancer in Japanese predicted regulatory variants in 22q13.1. PLoS ONE, 2018, 13, e0209096.	1.1	8
173	INKA2, a novel p53 target that interacts with the serine/threonine kinase PAK4. International Journal of Oncology, 2019, 54, 1907-1920.	1.4	8
174	Association of circulating 25-Hydroxyvitamin D and its related genetic variations with hepatocellular carcinoma incidence and survival. Annals of Translational Medicine, 2020, 8, 1080-1080.	0.7	8
175	Identification of a nuclear protein, LRRC42, involved in lung carcinogenesis. International Journal of Oncology, 2014, 45, 147-156.	1.4	7
176	Fine Mapping of the Major Histocompatibility Complex Region and Association of the HLA-B*52:01 Allele With Cervical Cancer in Japanese Women. JAMA Network Open, 2020, 3, e2023248.	2.8	7
177	Novel susceptibility loci for hepatocellular carcinoma in chronic HBV carriers. Hepatobiliary Surgery and Nutrition, 2012, 1, 59-60.	0.7	7
178	Influence of Genetic Variants in EGF and Other Genes on Hematological Traits in Korean Populations by a Genome-Wide Approach. BioMed Research International, 2015, 2015, 1-9.	0.9	6
179	Regulation of tubular recycling endosome biogenesis by the p53-MICALL1 pathway. International Journal of Oncology, 2017, 51, 724-736.	1.4	6
180	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.	1.5	6

#	Article	IF	Citations
181	Intracellular Accumulation of IFN-Î»4 Induces ER Stress and Results in Anti-Cirrhotic but Pro-HCV Effects. Frontiers in Immunology, 2021, 12, 692263.	2.2	6
182	Identification of a p53-repressed gene module in breast cancer cells. Oncotarget, 2017, 8, 55821-55836.	0.8	6
183	Decoding the diversity of killer immunoglobulin-like receptors by deep sequencing and a high-resolution imputation method. Cell Genomics, 2022, 2, 100101.	3.0	6
184	A Rare Polymorphic Variant of NBS1 Reduces DNA Repair Activity and Elevates Chromosomal Instability. Cancer Research, 2014, 74, 3707-3715.	0.4	5
185	Genome-wide association study of colorectal polyps identified highly overlapping polygenic architecture with colorectal cancer. Journal of Human Genetics, 2022, 67, 149-156.	1.1	5
186	Genome-Wide Association Study of Intracranial Artery Stenosis Followed by Phenome-Wide Association Study. Translational Stroke Research, 2023, 14, 322-333.	2.3	5
187	A Polymorphic Variant in p19Arf Confers Resistance to Chemically Induced Skin Tumors by Activating the p53 Pathway. Journal of Investigative Dermatology, 2019, 139, 1459-1469.	0.3	4
188	Cholesterol levels of Japanese dyslipidaemic patients with various comorbidities: BioBank Japan. Journal of Epidemiology, 2017, 27, S77-S83.	1.1	3
189	Identification of a p53 target, CD137L, that mediates growth suppression and immune response of osteosarcoma cells. Scientific Reports, 2017, 7, 10739.	1.6	3
190	A single nucleotide polymorphism in <i>Prostate Stem Cell Antigen</i> is associated with endoscopic grading in Kyoto classification of gastritis. Journal of Clinical Biochemistry and Nutrition, 2021, 68, 73-77.	0.6	3
191	Large-scale Integrated Analysis of Genetics and Metabolomic Data Reveals Potential Links Between Lipids and Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1216-1226.	1.1	3
192	Impact of four loci on serum tamsulosin hydrochloride concentration. Journal of Human Genetics, 2013, 58, 21-26.	1.1	2
193	Novel susceptibility loci for steroid-associated osteonecrosis of the femoral head in systemic lupus erythematosus. Human Molecular Genetics, 2022, 31, 1082-1095.	1.4	1
194	Germline Genetic Polymorphisms Are Associated with Disease-Free Survival in Adults with Acute Myeloid Leukemia (AML): A Genomewide Association Study From the Pgrn-Riken Global Alliance.. Blood, 2012, 120, 2548-2548.	0.6	0
195	The Association of Single Nucleotide Polymorphisms with Cancer Risk. , 2019, , 87-144.		0
196	A single-nucleotide-polymorphism in the 5â€²-flanking region of MSX1 gene as a predictive marker candidate for platinum-based therapy of esophageal carcinoma. Therapeutic Advances in Medical Oncology, 2022, 14, 175883592210805.	1.4	0