

Koichi K Matsuda

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201
papers

10,843
citations

51
h-index

99
g-index

229
ext. papers

14,731
ext. citations

12.8
avg, IF

5.45
L-index

#	Paper	IF	Citations
201	p53AIP1, a potential mediator of p53-dependent apoptosis, and its regulation by Ser-46-phosphorylated p53. <i>Cell</i> , 2000 , 102, 849-62	56.2	1005
200	Genome-wide association scan identifies a colorectal cancer susceptibility locus on 11q23 and replicates risk loci at 8q24 and 18q21. <i>Nature Genetics</i> , 2008 , 40, 631-7	36.3	486
199	A genome-wide association study identifies variants in the HLA-DP locus associated with chronic hepatitis B in Asians. <i>Nature Genetics</i> , 2009 , 41, 591-5	36.3	428
198	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011 , 43, 1131-8	36.3	415
197	Genome-wide association study of hematological and biochemical traits in a Japanese population. <i>Nature Genetics</i> , 2010 , 42, 210-5	36.3	388
196	Genetic analysis of quantitative traits in the Japanese population links cell types to complex human diseases. <i>Nature Genetics</i> , 2018 , 50, 390-400	36.3	325
195	Genome-wide association study identifies a susceptibility locus for HCV-induced hepatocellular carcinoma. <i>Nature Genetics</i> , 2011 , 43, 455-8	36.3	296
194	Overview of the BioBank Japan Project: Study design and profile. <i>Journal of Epidemiology</i> , 2017 , 27, S2-S84	38.4	239
193	Functional variants in ADH1B and ALDH2 coupled with alcohol and smoking synergistically enhance esophageal cancer risk. <i>Gastroenterology</i> , 2009 , 137, 1768-75	13.3	232
192	Large-scale genome-wide association studies in East Asians identify new genetic loci influencing metabolic traits. <i>Nature Genetics</i> , 2011 , 43, 990-5	36.3	229
191	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019 , 51, 957-972	36.3	217
190	Genome-wide association study identifies 112 new loci for body mass index in the Japanese population. <i>Nature Genetics</i> , 2017 , 49, 1458-1467	36.3	214
189	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. <i>Nature Genetics</i> , 2012 , 44, 770-6	36.3	184
188	A nonsynonymous SNP in PRKCH (protein kinase C eta) increases the risk of cerebral infarction. <i>Nature Genetics</i> , 2007 , 39, 212-7	36.3	179
187	Large-scale genetic study in East Asians identifies six new loci associated with colorectal cancer risk. <i>Nature Genetics</i> , 2014 , 46, 533-42	36.3	175
186	A genome-wide association study of chronic hepatitis B identified novel risk locus in a Japanese population. <i>Human Molecular Genetics</i> , 2011 , 20, 3884-92	5.6	174
185	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. <i>Nature Communications</i> , 2017 , 8, 15539	17.4	151

184	p53RDL1 regulates p53-dependent apoptosis. <i>Nature Cell Biology</i> , 2003 , 5, 216-23	23.4	144
183	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019 , 51, 1459-1474	36.3	122
182	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015 , 523, 459-462	63.4	119
181	Genome-wide association analysis in East Asians identifies breast cancer susceptibility loci at 1q32.1, 5q14.3 and 15q26.1. <i>Nature Genetics</i> , 2014 , 46, 886-90	36.3	110
180	Meta-analysis of genome-wide association studies identifies six new Loci for serum calcium concentrations. <i>PLoS Genetics</i> , 2013 , 9, e1003796	6	100
179	Germline pathogenic variants of 11 breast cancer genes in 7,051 Japanese patients and 11,241 controls. <i>Nature Communications</i> , 2018 , 9, 4083	17.4	99
178	A genome-wide association study identifies two susceptibility loci for duodenal ulcer in the Japanese population. <i>Nature Genetics</i> , 2012 , 44, 430-4, S1-2	36.3	96
177	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020 , 182, 1214-1231.e11	56.2	96
176	Regulation of histone modification and chromatin structure by the p53-PADI4 pathway. <i>Nature Communications</i> , 2012 , 3, 676	17.4	95
175	Construction of a population-specific HLA imputation reference panel and its application to Graves disease risk in Japanese. <i>Nature Genetics</i> , 2015 , 47, 798-802	36.3	92
174	Multiple loci are associated with white blood cell phenotypes. <i>PLoS Genetics</i> , 2011 , 7, e1002113	6	92
173	Functional SNPs in CD244 increase the risk of rheumatoid arthritis in a Japanese population. <i>Nature Genetics</i> , 2008 , 40, 1224-9	36.3	92
172	A genome-wide association study in 19 633 Japanese subjects identified LHX3-QSOX2 and IGF1 as adult height loci. <i>Human Molecular Genetics</i> , 2010 , 19, 2303-12	5.6	91
171	A genome-wide association study identified AFF1 as a susceptibility locus for systemic lupus erythematosus in Japanese. <i>PLoS Genetics</i> , 2012 , 8, e1002455	6	89
170	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020 , 182, 1198-1213.e14	56.2	88
169	Cross-sectional analysis of BioBank Japan clinical data: A large cohort of 200,000 patients with 47 common diseases. <i>Journal of Epidemiology</i> , 2017 , 27, S9-S21	3.4	85
168	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	36.3	85
167	Deep whole-genome sequencing reveals recent selection signatures linked to evolution and disease risk of Japanese. <i>Nature Communications</i> , 2018 , 9, 1631	17.4	84

166	Identification of 28 new susceptibility loci for type 2 diabetes in the Japanese population. <i>Nature Genetics</i> , 2019 , 51, 379-386	36.3	83
165	p53AIP1 regulates the mitochondrial apoptotic pathway. <i>Cancer Research</i> , 2002 , 62, 2883-9	10.1	83
164	Regulation of protein Citrullination through p53/PADI4 network in DNA damage response. <i>Cancer Research</i> , 2009 , 69, 8761-9	10.1	82
163	Functional SNP in an Sp1-binding site of AGTRL1 gene is associated with susceptibility to brain infarction. <i>Human Molecular Genetics</i> , 2007 , 16, 630-9	5.6	78
162	Genome-wide association study for C-reactive protein levels identified pleiotropic associations in the IL6 locus. <i>Human Molecular Genetics</i> , 2011 , 20, 1224-31	5.6	68
161	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019 , 111, 146-157	9.7	67
160	Orphan receptor tyrosine kinase ROR2 as a potential therapeutic target for osteosarcoma. <i>Cancer Science</i> , 2009 , 100, 1227-33	6.9	67
159	Soluble MICA and a MICA variation as possible prognostic biomarkers for HBV-induced hepatocellular carcinoma. <i>PLoS ONE</i> , 2012 , 7, e44743	3.7	65
158	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. <i>Gastroenterology</i> , 2016 , 150, 1633-1645	13.3	64
157	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. <i>Nature Genetics</i> , 2021 , 53, 65-75	36.3	62
156	Identification of nine novel loci associated with white blood cell subtypes in a Japanese population. <i>PLoS Genetics</i> , 2011 , 7, e1002067	6	61
155	Citrullination of RGG Motifs in FET Proteins by PAD4 Regulates Protein Aggregation and ALS Susceptibility. <i>Cell Reports</i> , 2018 , 22, 1473-1483	10.6	57
154	Quantitative T cell repertoire analysis by deep cDNA sequencing of T cell receptor α and β chains using next-generation sequencing (NGS). <i>Oncotmmunology</i> , 2014 , 3, e968467	7.2	56
153	Large-Scale Genome-Wide Association Study of East Asians Identifies Loci Associated With Risk for Colorectal Cancer. <i>Gastroenterology</i> , 2019 , 156, 1455-1466	13.3	55
152	A genome-wide association study of nephrolithiasis in the Japanese population identifies novel susceptible Loci at 5q35.3, 7p14.3, and 13q14.1. <i>PLoS Genetics</i> , 2012 , 8, e1002541	6	54
151	Characterizing rare and low-frequency height-associated variants in the Japanese population. <i>Nature Communications</i> , 2019 , 10, 4393	17.4	51
150	Population-specific and trans-ancestry genome-wide analyses identify distinct and shared genetic risk loci for coronary artery disease. <i>Nature Genetics</i> , 2020 , 52, 1169-1177	36.3	51
149	Contribution of a Non-classical HLA Gene, HLA-DOA, to the Risk of Rheumatoid Arthritis. <i>American Journal of Human Genetics</i> , 2016 , 99, 366-74	11	51

148	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. <i>Nature Communications</i> , 2019 , 10, 29	17.4	51
147	A genome-wide association study of HCV-induced liver cirrhosis in the Japanese population identifies novel susceptibility loci at the MHC region. <i>Journal of Hepatology</i> , 2013 , 58, 875-82	13.4	50
146	Genome-wide association study identifies a new SMAD7 risk variant associated with colorectal cancer risk in East Asians. <i>International Journal of Cancer</i> , 2014 , 135, 948-55	7.5	49
145	Regulation of iron homeostasis by the p53-ISCU pathway. <i>Scientific Reports</i> , 2015 , 5, 16497	4.9	48
144	Identification of a functional variant in the MICA promoter which regulates MICA expression and increases HCV-related hepatocellular carcinoma risk. <i>PLoS ONE</i> , 2013 , 8, e61279	3.7	47
143	Genetic and phenotypic landscape of the major histocompatibility complex region in the Japanese population. <i>Nature Genetics</i> , 2019 , 51, 470-480	36.3	45
142	Trans-ethnic meta-analysis of white blood cell phenotypes. <i>Human Molecular Genetics</i> , 2014 , 23, 6944-605.6	5.6	45
141	The histone methyltransferase Wolf-Hirschhorn syndrome candidate 1-like 1 (WHSC1L1) is involved in human carcinogenesis. <i>Genes Chromosomes and Cancer</i> , 2013 , 52, 126-39	5	45
140	Common variations in PSMD3-CSF3 and PLCB4 are associated with neutrophil count. <i>Human Molecular Genetics</i> , 2010 , 19, 2079-85	5.6	44
139	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. <i>American Journal of Human Genetics</i> , 2016 , 99, 636-646	11	44
138	Genome-wide association study of intracranial aneurysms identifies 17 risk loci and genetic overlap with clinical risk factors. <i>Nature Genetics</i> , 2020 , 52, 1303-1313	36.3	43
137	Genome-wide meta-analysis identifies multiple novel loci associated with serum uric acid levels in Japanese individuals. <i>Communications Biology</i> , 2019 , 2, 115	6.7	42
136	Overview of BioBank Japan follow-up data in 32 diseases. <i>Journal of Epidemiology</i> , 2017 , 27, S22-S28	3.4	41
135	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
134	Quantitative structural characterization of local N-glycan microheterogeneity in therapeutic antibodies by energy-resolved oxonium ion monitoring. <i>Analytical Chemistry</i> , 2012 , 84, 9655-62	7.8	40
133	A cross-population atlas of genetic associations for 220 human phenotypes. <i>Nature Genetics</i> , 2021 , 53, 1415-1424	36.3	40
132	A genome-wide association study identifies PLCL2 and AP3D1-DOT1L-SF3A2 as new susceptibility loci for myocardial infarction in Japanese. <i>European Journal of Human Genetics</i> , 2015 , 23, 374-80	5.3	39
131	Chromosomal alterations among age-related haematopoietic clones in Japan. <i>Nature</i> , 2020 , 584, 130-135.0.4	5.4	38

130	Large-scale association analysis in Asians identifies new susceptibility loci for prostate cancer. <i>Nature Communications</i> , 2015 , 6, 8469	17.4	37
129	Improving the trans-ancestry portability of polygenic risk scores by prioritizing variants in predicted cell-type-specific regulatory elements. <i>Nature Genetics</i> , 2020 , 52, 1346-1354	36.3	37
128	Trans-biobank analysis with 676,000 individuals elucidates the association of polygenic risk scores of complex traits with human lifespan. <i>Nature Medicine</i> , 2020 , 26, 542-548	50.5	36
127	Antitumor activity and induction of TP53-dependent apoptosis toward ovarian clear cell adenocarcinoma by the dual PI3K/mTOR inhibitor DS-7423. <i>PLoS ONE</i> , 2014 , 9, e87220	3.7	36
126	Clinical and molecular characteristics of fusion-positive B-cell precursor acute lymphoblastic leukemia in childhood, including a novel translocation resulting in gene fusion. <i>Haematologica</i> , 2019 , 104, 128-137	6.6	35
125	No association for Chinese HBV-related hepatocellular carcinoma susceptibility SNP in other East Asian populations. <i>BMC Medical Genetics</i> , 2012 , 13, 47	2.1	34
124	Association Study of a Functional Variant on ABCG2 Gene with Sunitinib-Induced Severe Adverse Drug Reaction. <i>PLoS ONE</i> , 2016 , 11, e0148177	3.7	34
123	Crosstalk of EDA-A2/XEDAR in the p53 signaling pathway. <i>Molecular Cancer Research</i> , 2010 , 8, 855-63	6.6	33
122	Germline Pathogenic Variants in 7636 Japanese Patients With Prostate Cancer and 12366 Controls. <i>Journal of the National Cancer Institute</i> , 2020 , 112, 369-376	9.7	33
121	GWAS identifies two novel colorectal cancer loci at 16q24.1 and 20q13.12. <i>Carcinogenesis</i> , 2018 , 39, 652-660	4.60	32
120	Impact of polymorphisms in drug pathway genes on disease-free survival in adults with acute myeloid leukemia. <i>Journal of Human Genetics</i> , 2013 , 58, 353-61	4.3	32
119	Cystatin C as a p53-inducible apoptotic mediator that regulates cathepsin L activity. <i>Cancer Science</i> , 2016 , 107, 298-306	6.9	31
118	Meta-analysis of 208370 East Asians identifies 113 susceptibility loci for systemic lupus erythematosus. <i>Annals of the Rheumatic Diseases</i> , 2021 , 80, 632-640	2.4	31
117	The Transcriptional Landscape of p53 Signalling Pathway. <i>EBioMedicine</i> , 2017 , 20, 109-119	8.8	30
116	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. <i>American Journal of Human Genetics</i> , 2017 , 100, 51-63	11	30
115	Argininosuccinate synthase 1 is an intrinsic Akt repressor transactivated by p53. <i>Science Advances</i> , 2017 , 3, e1603204	14.3	29
114	Genome-wide association study identified SNP on 15q24 associated with bladder cancer risk in Japanese population. <i>Human Molecular Genetics</i> , 2015 , 24, 1177-84	5.6	29
113	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018 , 9, 5052	17.4	29

112	GWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. <i>Nature Human Behaviour</i> , 2020 , 4, 308-316	12.8	28
111	Regulation of myo-inositol biosynthesis by p53-ISYNA1 pathway. <i>International Journal of Oncology</i> , 2016 , 48, 2415-24	4.4	28
110	CLCA2 as a p53-inducible senescence mediator. <i>Neoplasia</i> , 2012 , 14, 141-9	6.4	28
109	Association of common variants in TNFRSF13B, TNFSF13, and ANXA3 with serum levels of non-albumin protein and immunoglobulin isotypes in Japanese. <i>PLoS ONE</i> , 2012 , 7, e32683	3.7	28
108	Elucidating the genetic architecture of reproductive ageing in the Japanese population. <i>Nature Communications</i> , 2018 , 9, 1977	17.4	28
107	Characteristics and prognosis of Japanese colorectal cancer patients: The BioBank Japan Project. <i>Journal of Epidemiology</i> , 2017 , 27, S36-S42	3.4	27
106	12 new susceptibility loci for prostate cancer identified by genome-wide association study in Japanese population. <i>Nature Communications</i> , 2019 , 10, 4422	17.4	27
105	Genetic variants of calcium and vitamin D metabolism in kidney stone disease. <i>Nature Communications</i> , 2019 , 10, 5175	17.4	27
104	Claudin-2 deficiency associates with hypercalciuria in mice and human kidney stone disease. <i>Journal of Clinical Investigation</i> , 2020 , 130, 1948-1960	15.9	26
103	Integrated exome and RNA sequencing of dedifferentiated liposarcoma. <i>Nature Communications</i> , 2019 , 10, 5683	17.4	26
102	GWAS of smoking behaviour in 165,436 Japanese people reveals seven new loci and shared genetic architecture. <i>Nature Human Behaviour</i> , 2019 , 3, 471-477	12.8	25
101	A replication study for three nephrolithiasis loci at 5q35.3, 7p14.3 and 13q14.1 in the Japanese population. <i>Journal of Human Genetics</i> , 2013 , 58, 588-93	4.3	23
100	Demographic and lifestyle factors and survival among patients with esophageal and gastric cancer: The Biobank Japan Project. <i>Journal of Epidemiology</i> , 2017 , 27, S29-S35	3.4	22
99	Dimensionality reduction reveals fine-scale structure in the Japanese population with consequences for polygenic risk prediction. <i>Nature Communications</i> , 2020 , 11, 1569	17.4	22
98	Genome-wide association study in East Asians identifies two novel breast cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2016 , 25, 3361-3371	5.6	22
97	Common variants on 14q32 and 13q12 are associated with DLBCL susceptibility. <i>Journal of Human Genetics</i> , 2011 , 56, 436-9	4.3	22
96	Critical function for nuclear envelope protein TMEM209 in human pulmonary carcinogenesis. <i>Cancer Research</i> , 2012 , 72, 4110-8	10.1	22
95	Identification of a significant association of a single nucleotide polymorphism in TNXB with systemic lupus erythematosus in a Japanese population. <i>Journal of Human Genetics</i> , 2008 , 53, 64-73	4.3	22

94	Identification of a novel p53 target, COL17A1, that inhibits breast cancer cell migration and invasion. <i>Oncotarget</i> , 2017 , 8, 55790-55803	3.3	22
93	Genome-wide association study identifies gastric cancer susceptibility loci at 12q24.11-12 and 20q11.21. <i>Cancer Science</i> , 2018 , 109, 4015-4024	6.9	22
92	A functional SNP in the NKX2.5-binding site of ITPR3 promoter is associated with susceptibility to systemic lupus erythematosus in Japanese population. <i>Journal of Human Genetics</i> , 2008 , 53, 151-162	4.3	21
91	Genome wide association study of age at menarche in the Japanese population. <i>PLoS ONE</i> , 2013 , 8, e63821	3.7	20
90	GALNT6 Stabilizes GRP78 Protein by O-glycosylation and Enhances its Activity to Suppress Apoptosis Under Stress Condition. <i>Neoplasia</i> , 2017 , 19, 43-53	6.4	19
89	Statin use and all-cause and cancer mortality: BioBank Japan cohort. <i>Journal of Epidemiology</i> , 2017 , 27, S84-S91	3.4	19
88	Characteristics and prognosis of Japanese female breast cancer patients: The BioBank Japan project. <i>Journal of Epidemiology</i> , 2017 , 27, S58-S64	3.4	19
87	GWAS of mosaic loss of chromosome Y highlights genetic effects on blood cell differentiation. <i>Nature Communications</i> , 2019 , 10, 4719	17.4	18
86	Identification of novel epigenetically inactivated gene PAMR1 in breast carcinoma. <i>Oncology Reports</i> , 2015 , 33, 267-73	3.5	18
85	Downregulation of the tumor suppressor HSPB7, involved in the p53 pathway, in renal cell carcinoma by hypermethylation. <i>International Journal of Oncology</i> , 2014 , 44, 1490-8	4.4	18
84	Decrease in expression caused by infection may promote progression to severe gastritis. <i>Oncotarget</i> , 2018 , 9, 3936-3945	3.3	18
83	Adjustment of Cell-Type Composition Minimizes Systematic Bias in Blood DNA Methylation Profiles Derived by DNA Collection Protocols. <i>PLoS ONE</i> , 2016 , 11, e0147519	3.7	17
82	Survival of macrovascular disease, chronic kidney disease, chronic respiratory disease, cancer and smoking in patients with type 2 diabetes: BioBank Japan cohort. <i>Journal of Epidemiology</i> , 2017 , 27, S98-S106	3.4	16
81	Novel Risk Loci Identified in a Genome-Wide Association Study of Urolithiasis in a Japanese Population. <i>Journal of the American Society of Nephrology: JASN</i> , 2019 , 30, 855-864	12.7	16
80	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. <i>Nature Communications</i> , 2020 , 11, 1217	17.4	16
79	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. <i>Nature Medicine</i> , 2021 , 27, 1012-1024	50.5	16
78	Antitumor immunity augments the therapeutic effects of p53 activation on acute myeloid leukemia. <i>Nature Communications</i> , 2019 , 10, 4869	17.4	15
77	GWAS of five gynecologic diseases and cross-trait analysis in Japanese. <i>European Journal of Human Genetics</i> , 2020 , 28, 95-107	5.3	15

76	A deep learning method for HLA imputation and trans-ethnic MHC fine-mapping of type 1 diabetes. <i>Nature Communications</i> , 2021 , 12, 1639	17.4	15
75	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019 , 28, 2615-2633	5.6	14
74	Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. <i>Nature Communications</i> , 2020 , 11, 3175	17.4	14
73	A global atlas of genetic associations of 220 deep phenotypes		14
72	Association analysis of the NOD2 gene with susceptibility to graft-versus-host disease in a Japanese population. <i>International Journal of Hematology</i> , 2011 , 93, 771-778	2.3	13
71	Characteristics of patients with liver cancer in the BioBank Japan project. <i>Journal of Epidemiology</i> , 2017 , 27, S43-S48	3.4	12
70	Characteristics and prognosis of Japanese male and female lung cancer patients: The BioBank Japan Project. <i>Journal of Epidemiology</i> , 2017 , 27, S49-S57	3.4	12
69	Late Cornified Envelope Group I, a novel target of p53, regulates PRMT5 activity. <i>Neoplasia</i> , 2014 , 16, 656-64	6.4	12
68	Risk prediction models for mortality in patients with cardiovascular disease: The BioBank Japan project. <i>Journal of Epidemiology</i> , 2017 , 27, S71-S76	3.4	10
67	The p53 activator overcomes resistance to ALK inhibitors by regulating p53-target selectivity in ALK-driven neuroblastomas. <i>Cell Death Discovery</i> , 2018 , 4, 56	6.9	10
66	Impact of PSCA variation on gastric ulcer susceptibility. <i>PLoS ONE</i> , 2013 , 8, e63698	3.7	10
65	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	8.8	10
64	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. <i>Nature Medicine</i> , 2021 , 27, 1239-1249	50.5	10
63	Massively parallel sequencing of tenosynovial giant cell tumors reveals novel CSF1 fusion transcripts and novel somatic CBL mutations. <i>International Journal of Cancer</i> , 2019 , 145, 3276-3284	7.5	9
62	Transethnic Meta-Analysis of Genome-Wide Association Studies Identifies Three New Loci and Characterizes Population-Specific Differences for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002670	5.2	9
61	Genetic and phenotypic landscape of the mitochondrial genome in the Japanese population. <i>Communications Biology</i> , 2020 , 3, 104	6.7	9
60	Leveraging supervised learning for functionally-informed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. <i>Nature Communications</i> , 2021 , 12, 3394	17.4	9
59	Serum glucose, cholesterol and blood pressure levels in Japanese type 1 and 2 diabetic patients: BioBank Japan. <i>Journal of Epidemiology</i> , 2017 , 27, S92-S97	3.4	8

58	Endogenization and excision of human herpesvirus 6 in human genomes. <i>PLoS Genetics</i> , 2020 , 16, e1008815	8.15	8
57	Genetic risk score based on the prevalence of vertebral fracture in Japanese women with osteoporosis. <i>Bone Reports</i> , 2016 , 5, 168-172	2.6	8
56	Genetic analysis of endometriosis and depression identifies shared loci and implicates causal links with gastric mucosa abnormality. <i>Human Genetics</i> , 2021 , 140, 529-552	6.3	8
55	Clinical and histopathological characteristics of patients with prostate cancer in the BioBank Japan project. <i>Journal of Epidemiology</i> , 2017 , 27, S65-S70	3.4	7
54	Identification of rare coding variants in 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	2.4	7
53	Germline variants and advanced colorectal adenomas: adenoma prevention with celecoxib trial genome-wide association study. <i>Clinical Cancer Research</i> , 2013 , 19, 6430-7	12.9	7
52	Endoscopy-based Kyoto classification score of gastritis related to pathological topography of neutrophil activity. <i>World Journal of Gastroenterology</i> , 2020 , 26, 5146-5155	5.6	7
51	Single Nucleotide Polymorphisms of HAAO and IRX6 Genes as Risk Factors for Hypospadias. <i>Journal of Urology</i> , 2019 , 201, 386-392	2.5	7
50	Functional variants in ADH1B and ALDH2 are non-additively associated with all-cause mortality in Japanese population. <i>European Journal of Human Genetics</i> , 2020 , 28, 378-382	5.3	7
49	The simplified Kyoto classification score is consistent with the ABC method of classification as a grading system for endoscopic gastritis. <i>Journal of Clinical Biochemistry and Nutrition</i> , 2021 , 68, 101-104	3.1	7
48	EPSIN 3, A Novel p53 Target, Regulates the Apoptotic Pathway and Gastric Carcinogenesis. <i>Neoplasia</i> , 2017 , 19, 185-195	6.4	6
47	Identification of a novel uterine leiomyoma GWAS locus in a Japanese population. <i>Scientific Reports</i> , 2020 , 10, 1197	4.9	6
46	Identification of a nuclear protein, LRRC42, involved in lung carcinogenesis. <i>International Journal of Oncology</i> , 2014 , 45, 147-56	4.4	6
45	Global Biobank Meta-analysis Initiative: powering genetic discovery across human diseases		6
44	Novel susceptibility loci for hepatocellular carcinoma in chronic HBV carriers. <i>Hepatobiliary Surgery and Nutrition</i> , 2012 , 1, 59-60	2.1	6
43	Genome-Wide Natural Selection Signatures Are Linked to Genetic Risk of Modern Phenotypes in the Japanese Population. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1306-1316	8.3	6
42	Influence of Genetic Variants in EGF and Other Genes on Hematological Traits in Korean Populations by a Genome-Wide Approach. <i>BioMed Research International</i> , 2015 , 2015, 914965	3	5
41	A rare polymorphic variant of NBS1 reduces DNA repair activity and elevates chromosomal instability. <i>Cancer Research</i> , 2014 , 74, 3707-15	10.1	5

40	Identification of a p53-repressed gene module in breast cancer cells. <i>Oncotarget</i> , 2017 , 8, 55821-55836	3.3	5
39	Identification of two novel breast cancer loci through large-scale genome-wide association study in the Japanese population. <i>Scientific Reports</i> , 2019 , 9, 17332	4.9	5
38	Genome-wide association study (GWAS) of ovarian cancer in Japanese predicted regulatory variants in 22q13.1. <i>PLoS ONE</i> , 2018 , 13, e0209096	3.7	5
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