Yoichiro Kamatani

List of Publications by Year
in descending order

159	24,249	18482 62	11607 135
papers	citations	h-index	g-index

201	201	201	30179
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	27.8	1,974
2	Clinical use of current polygenic risk scores may exacerbate health disparities. Nature Genetics, 2019, 51, 584-591.	21.4	1,664
3	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. Nature Genetics, 2019, 51, 237-244.	21.4	1,307
4	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
5	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	12.6	1,085
6	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
7	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829.	21.4	629
8	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
9	A cross-population atlas of genetic associations for 220 human phenotypes. Nature Genetics, 2021, 53, 1415-1424.	21.4	560
10	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
11	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
12	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.	21.4	491
13	Genome-wide association study of hematological and biochemical traits in a Japanese population. Nature Genetics, 2010, 42, 210-215.	21.4	460
14	Overview of the BioBank Japan Project: Study design and profile. Journal of Epidemiology, 2017, 27, S2-S8.	2.4	451
15	Comparative genetic architectures of schizophrenia in East Asian and European populations. Nature Genetics, 2019, 51, 1670-1678.	21.4	440
16	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
17	Genome-wide association study identifies 112 new loci for body mass index in the Japanese population. Nature Genetics, 2017, 49, 1458-1467.	21.4	380
18	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	28.9	353

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19	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
20	Comprehensive evaluation of structural variation detection algorithms for whole genome sequencing. Genome Biology, 2019, 20, 117.	8.8	311
21	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
22	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	27.8	282
23	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
24	Functional Variants in ADH1B and ALDH2 Coupled With Alcohol and Smoking Synergistically Enhance Esophageal Cancer Risk. Gastroenterology, 2009, 137, 1768-1775.	1.3	277
25	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
26	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
27	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	12.8	230
28	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.	21.4	206
29	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	27.8	198
30	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. Nature Communications, 2021, 12, 1258.	12.8	196
31	Common variation in PHACTR1 is associated with susceptibility to cervical artery dissection. Nature Genetics, 2015, 47, 78-83.	21.4	195
32	Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. Nature Communications, 2019, 10, 2773.	12.8	183
33	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	12.8	181
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	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
36	Identification of 28 new susceptibility loci for type 2 diabetes in the Japanese population. Nature Genetics, 2019, 51, 379-386.	21.4	164

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37	Genome-wide association study of intracranial aneurysms identifies 17 risk loci and genetic overlap with clinical risk factors. Nature Genetics, 2020, 52, 1303-1313.	21.4	163
38	Genetically Determined Levels of Circulating Cytokines and Risk of Stroke. Circulation, 2019, 139, 256-268.	1.6	147
39	Identification of six new genetic loci associated with atrial fibrillation in the Japanese population. Nature Genetics, 2017, 49, 953-958.	21.4	136
40	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.	2.4	133
41	Deep whole-genome sequencing reveals recent selection signatures linked to evolution and disease risk of Japanese. Nature Communications, 2018, 9, 1631.	12.8	132
42	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2016, 15, 695-707.	10.2	130
43	Polygenic burdens on cell-specific pathways underlie the risk of rheumatoid arthritis. Nature Genetics, 2017, 49, 1120-1125.	21.4	130
44	Tractor uses local ancestry to enable the inclusion of admixed individuals in GWAS and to boost power. Nature Genetics, 2021, 53, 195-204.	21.4	125
45	Characterizing rare and low-frequency height-associated variants in the Japanese population. Nature Communications, 2019, 10, 4393.	12.8	123
46	Construction of a population-specific HLA imputation reference panel and its application to Graves' disease risk in Japanese. Nature Genetics, 2015, 47, 798-802.	21.4	119
47	A Functional SNP in BNC2 Is Associated with Adolescent Idiopathic Scoliosis. American Journal of Human Genetics, 2015, 97, 337-342.	6.2	119
48	GWAS of clinically defined gout and subtypes identifies multiple susceptibility loci that include urate transporter genes. Annals of the Rheumatic Diseases, 2017, 76, 869-877.	0.9	114
49	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. Nature Communications, 2019, 10, 29.	12.8	113
50	Genome-wide analysis identifies novel susceptibility loci for myocardial infarction. European Heart Journal, 2021, 42, 919-933.	2.2	113
51	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
52	Genome-wide association study identifies seven novel susceptibility loci for primary open-angle glaucoma. Human Molecular Genetics, 2018, 27, 1486-1496.	2.9	111
53	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. Nature Medicine, 2021, 27, 1012-1024.	30.7	109
54	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 2022, 54, 450-458.	21.4	109

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55	Chromosomal alterations among age-related haematopoietic clones in Japan. Nature, 2020, 584, 130-135.	27.8	102
56	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
57	Polygenic burden in focal and generalized epilepsies. Brain, 2019, 142, 3473-3481.	7.6	90
58	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	12.8	89
59	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
60	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
61	GWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. Nature Human Behaviour, 2020, 4, 308-316.	12.0	80
62	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. Nature Medicine, 2021, 27, 1239-1249.	30.7	78
63	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. Nature Communications, 2018, 9, 5052.	12.8	75
64	Genetic and phenotypic landscape of the major histocompatibilty complex region in the Japanese population. Nature Genetics, 2019, 51, 470-480.	21.4	75
65	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.	30.7	74
66	Genome-wide association study revealed novel loci which aggravate asymptomatic hyperuricaemia into gout. Annals of the Rheumatic Diseases, 2019, 78, 1430-1437.	0.9	73
67	Expansion of Cancer Risk Profile for BRCA1 and BRCA2 Pathogenic Variants. JAMA Oncology, 2022, 8, 871.	7.1	70
68	Identification of Nine Novel Loci Associated with White Blood Cell Subtypes in a Japanese Population. PLoS Genetics, 2011, 7, e1002067.	3.5	69
69	Genetic variants of calcium and vitamin D metabolism in kidney stone disease. Nature Communications, 2019, 10, 5175.	12.8	69
70	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
71	Contribution of a Non-classical HLA Gene, HLA-DOA, to the Risk of Rheumatoid Arthritis. American Journal of Human Genetics, 2016, 99, 366-374.	6.2	68
72	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 2016, 99, 636-646.	6.2	67

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73	Genome-wide meta-analysis identifies multiple novel loci associated with serum uric acid levels in Japanese individuals. Communications Biology, 2019, 2, 115.	4.4	66
74	Genetic Predisposition to Ischemic Stroke. Stroke, 2017, 48, 253-258.	2.0	64
75	Moyamoya Disease Susceptibility Variant RNF213 p.R4810K Increases the Risk of Ischemic Stroke Attributable to Large-Artery Atherosclerosis. Circulation, 2019, 139, 295-298.	1.6	64
76	Claudin-2 deficiency associates with hypercalciuria in mice and human kidney stone disease. Journal of Clinical Investigation, 2020, 130, 1948-1960.	8.2	61
77	Dimensionality reduction reveals fine-scale structure in the Japanese population with consequences for polygenic risk prediction. Nature Communications, 2020, 11, 1569.	12.8	58
78	A polygenic risk score improves risk stratification of coronary artery disease: a large-scale prospective Chinese cohort study. European Heart Journal, 2022, 43, 1702-1711.	2.2	58
79	GWAS of smoking behaviour in 165,436 Japanese people reveals seven new loci and shared genetic architecture. Nature Human Behaviour, 2019, 3, 471-477.	12.0	54
80	GWAS identifies two novel colorectal cancer loci at 16q24.1 and 20q13.12. Carcinogenesis, 2018, 39, 652-660.	2.8	52
81	GWAS of mosaic loss of chromosome Y highlights genetic effects on blood cell differentiation. Nature Communications, 2019, 10, 4719.	12.8	50
82	12 new susceptibility loci for prostate cancer identified by genome-wide association study in Japanese population. Nature Communications, 2019, 10, 4422.	12.8	49
83	A multi-ethnic meta-analysis identifies novel genes, including ACSL5, associated with amyotrophic lateral sclerosis. Communications Biology, 2020, 3, 526.	4.4	49
84	Overview of BioBank Japan follow-up data in 32 diseases. Journal of Epidemiology, 2017, 27, S22-S28.	2.4	47
85	Genome-wide association study identifies 14 previously unreported susceptibility loci for adolescent idiopathic scoliosis in Japanese. Nature Communications, 2019, 10, 3685.	12.8	47
86	Empirical evaluation of variant calling accuracy using ultra-deep whole-genome sequencing data. Scientific Reports, 2019, 9, 1784.	3.3	46
87	Elucidating the genetic architecture of reproductive ageing in the Japanese population. Nature Communications, 2018, 9, 1977.	12.8	44
88	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.	3.6	44
89	A deep learning method for HLA imputation and trans-ethnic MHC fine-mapping of type 1 diabetes. Nature Communications, 2021, 12, 1639.	12.8	44
90	Leveraging supervised learning for functionallyÂinformed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. Nature Communications, 2021, 12, 3394.	12.8	44

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91	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
92	Genomeâ€wide association study identifies gastric cancer susceptibility loci at 12q24.11â€12 and 20q11.21. Cancer Science, 2018, 109, 4015-4024.	3.9	39
93	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
94	Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. International Journal of Epidemiology, 2022, 50, 1995-2010.	1.9	39
95	PLD4 is a genetic determinant to systemic lupus erythematosus and involved in murine autoimmune phenotypes. Annals of the Rheumatic Diseases, 2019, 78, 509-518.	0.9	36
96	Variants encoding a restricted carboxy-terminal domain of SLC12A2 cause hereditary hearing loss in humans. PLoS Genetics, 2020, 16, e1008643.	3.5	36
97	SARS-CoV-2 ORF6 disrupts nucleocytoplasmic trafficking to advance viral replication. Communications Biology, 2022, 5, 483.	4.4	35
98	Integration of Sequence Data from a Consanguineous Family with Genetic Data from an Outbred Population Identifies PLB1 as a Candidate Rheumatoid Arthritis Risk Gene. PLoS ONE, 2014, 9, e87645.	2.5	34
99	Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. Nature Communications, 2020, 11, 3175.	12.8	34
100	Genome-wide association studies identify polygenic effects for completed suicide in the Japanese population. Neuropsychopharmacology, 2019, 44, 2119-2124.	5.4	32
101	GWAS of five gynecologic diseases and cross-trait analysis in Japanese. European Journal of Human Genetics, 2020, 28, 95-107.	2.8	32
102	Genetic and phenotypic landscape of the mitochondrial genome in the Japanese population. Communications Biology, 2020, 3, 104.	4.4	32
103	Eight novel susceptibility loci and putative causal variants in atopic dermatitis. Journal of Allergy and Clinical Immunology, 2021, 148, 1293-1306.	2.9	32
104	Efficient prediction of a spatial transcriptomics profile better characterizes breast cancer tissue sections without costly experimentation. Scientific Reports, 2022, 12, 4133.	3.3	32
105	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.	2.9	31
106	Characteristics and prognosis of Japanese female breast cancer patients: The BioBank Japan project. Journal of Epidemiology, 2017, 27, S58-S64.	2.4	27
107	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.	2.3	26
108	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.	2.3	25

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109	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.	6.1	25
110	Subtype-specific gout susceptibility loci and enrichment of selection pressure on ABCG2 and ALDH2 identified by subtype genome-wide meta-analyses of clinically defined gout patients. Annals of the Rheumatic Diseases, 2020, 79, 657-665.	0.9	24
111	Genome-wide Association Study of Idiopathic Osteonecrosis of the Femoral Head. Scientific Reports, 2017, 7, 15035.	3.3	23
112	Legacy Data Confound Genomics Studies. Molecular Biology and Evolution, 2020, 37, 2-10.	8.9	23
113	Endogenization and excision of human herpesvirus 6 in human genomes. PLoS Genetics, 2020, 16, e1008915.	3.5	22
114	A Mendelian randomization study identified obesity as a causal risk factor of uterine endometrial cancer in Japanese. Cancer Science, 2020, 111, 4646-4651.	3.9	22
115	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.	8.9	22
116	A frequent variant in the Japanese population determines quasi-Mendelian inheritance of rare retinal ciliopathy. Nature Communications, 2019, 10, 2884.	12.8	21
117	Association of the RPA3-UMAD1 locus with interstitial lung diseases complicated with rheumatoid arthritis in Japanese. Annals of the Rheumatic Diseases, 2020, 79, 1305-1309.	0.9	21
118	Multi-trait and cross-population genome-wide association studies across autoimmune and allergic diseases identify shared and distinct genetic component. Annals of the Rheumatic Diseases, 2022, 81, 1301-1312.	0.9	21
119	Population-based Screening for Hereditary Colorectal Cancer Variants in Japan. Clinical Gastroenterology and Hepatology, 2022, 20, 2132-2141.e9.	4.4	20
120	Re-evaluating classical body type theories: genetic correlation between psychiatric disorders and body mass index. Psychological Medicine, 2018, 48, 1745-1748.	4.5	19
121	The schizophrenia genetics knowledgebase: a comprehensive update of findings from candidate gene studies. Translational Psychiatry, 2019, 9, 205.	4.8	19
122	Comparison of effects of UGT1A1*6 and UGT1A1*28 on irinotecan-induced adverse reactions in the Japanese population: analysis of the Biobank Japan Project. Journal of Human Genetics, 2019, 64, 1195-1202.	2.3	19
123	Genome-Wide Association Study of Renal Function Traits: Results from the Japan Multi-Institutional Collaborative Cohort Study. American Journal of Nephrology, 2018, 47, 304-316.	3.1	18
124	Evidence of Polygenic Adaptation in Sardinia at Height-Associated Loci Ascertained from the Biobank Japan. American Journal of Human Genetics, 2020, 107, 60-71.	6.2	18
125	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.	3.8	18
126	Mendelian randomization of genetically independent aging phenotypes identifies LPA and VCAM1 as biological targets for human aging. Nature Aging, 2022, 2, 19-30.	11.6	17

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127	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.	2.8	14
128	Identification of a novel uterine leiomyoma GWAS locus in a Japanese population. Scientific Reports, 2020, 10, 1197.	3.3	14
129	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.	6.1	14
130	HLAâ€B*51:01 and CYP2C9*3 Are Risk Factors for Phenytoinâ€Induced Eruption in the Japanese Population: Analysis of Data From the Biobank Japan Project. Clinical Pharmacology and Therapeutics, 2020, 107, 1170-1178.	4.7	13
131	Whole genome sequencing of 45 Japanese patients with intellectual disability. American Journal of Medical Genetics, Part A, 2021, 185, 1468-1480.	1.2	13
132	A novel PAK3 pathogenic variant identified in two siblings from a Japanese family with X-linked intellectual disability: case report and review of the literature. Journal of Physical Education and Sports Management, 2019, 5, a003988.	1.2	12
133	Polygenic risk scores in schizophrenia with clinically significant copy number variants. Psychiatry and Clinical Neurosciences, 2020, 74, 35-39.	1.8	12
134	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.	3.3	12
135	Clinical and histopathological characteristics of patients with prostate cancer in the BioBank Japan project. Journal of Epidemiology, 2017, 27, S65-S70.	2.4	11
136	Common variants at 2q11.2, 8q21.3, and 11q13.2 are associated with major mood disorders. Translational Psychiatry, 2017, 7, 1273.	4.8	9
137	Identification of two novel breast cancer loci through large-scale genome-wide association study in the Japanese population. Scientific Reports, 2019, 9, 17332.	3.3	9
138	A novel intragenic deletion in OPHN1 in a Japanese patient with Dandy-Walker malformation. Human Genome Variation, 2019, 6, 1.	0.7	9
139	Genomeâ€wide association study of epilepsy in a Japanese population identified an associated region at chromosome 12q24. Epilepsia, 2021, 62, 1391-1400.	5.1	9
140	Genetic susceptibility to hepatocellular carcinoma in chromosome 22q13.31, findings of a genomeâ€wide association study. JGH Open, 2021, 5, 1363-1372.	1.6	9
141	Search for new loci and low-frequency variants influencing glioma risk by exome-array analysis. European Journal of Human Genetics, 2016, 24, 717-724.	2.8	8
142	Genome-wide association study (GWAS) of ovarian cancer in Japanese predicted regulatory variants in 22q13.1. PLoS ONE, 2018, 13, e0209096.	2.5	8
143	Genome-wide SNP data of Izumo and Makurazaki populations support inner-dual structure model for origin of Yamato people. Journal of Human Genetics, 2021, 66, 681-687.	2.3	7
144	Genetics of autosomal mosaic chromosomal alteration (mCA). Journal of Human Genetics, 2021, 66, 879-885.	2.3	7

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145	Using spatio-temporal surveillance data to test the infectious environment of children before type 1 diabetes diagnosis. PLoS ONE, 2017, 12, e0170658.	2.5	6
146	A common variant of LDL receptorÂrelated protein 2 (LRP2) gene is associated with gout susceptibility: a meta-analysis in a Japanese population. Human Cell, 2020, 33, 303-307.	2.7	6
147	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
148	Decoding the diversity of killer immunoglobulin-like receptors by deep sequencing and a high-resolution imputation method. Cell Genomics, 2022, 2, 100101.	6.5	6
149	Polygenic Risk Score of Adolescent Idiopathic Scoliosis for Potential Clinical Use. Journal of Bone and Mineral Research, 2020, 36, 1481-1491.	2.8	5
150	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
151	Genetic variations in medical research in the past, at present and in the future. Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 2021, 97, 324-335.	3.8	4
152	Identification of LEF1 as a Susceptibility Locus for Kawasaki Disease in Patients Younger than 6 Months of Age. Genomics and Informatics, 2018, 16, 36-41.	0.8	4
153	Two decades after Human Genome Project: do large-genetic studies lead to path of the genomic medicine of complex diseases?. Journal of Human Genetics, 2021, 66, 1-1.	2.3	3
154	Whole exome analysis of patients in Japan with hearing loss reveals high heterogeneity among responsible and novel candidate genes. Orphanet Journal of Rare Diseases, 2022, 17, 114.	2.7	3
155	An X chromosome-wide meta-analysis based on Japanese cohorts revealed that non-autosomal variations are associated with serum urate. Rheumatology, 2021, 60, 4430-4432.	1.9	2
156	PPM1D and DNMT3A Mutations in Myelodysplasia and Clonal Hematopoiesis. Blood, 2019, 134, 1709-1709.	1.4	2
157	Trans-Ethnic Mendelian Randomization Study Reveals Causal Relationships Between Cardiometabolic Factors and Chronic Kidney Disease. SSRN Electronic Journal, 0, , .	0.4	1
158	OP0048â€…GENOME-WIDE META-ANALYSIS REVEALED MULTIPLE NOVEL LOCI ASSOCIATED WITH SERUM URIC ACIDLEVELS IN JAPANESE. , 2019, , .		0
159	Editorial: Current Status and Future Challenges of Biobank Data Analysis. Frontiers in Genetics, 2022, 13, 882611.	2.3	0