

Koichi K Matsuda

List of Publications by Year in descending order

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Version: 2024-02-01

196
papers

17,784
citations

18436

62
h-index

19136

118
g-index

229
all docs

229
docs citations

229
times ranked

25217
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Association Study of Intracranial Artery Stenosis Followed by Phenome-Wide Association Study. <i>Translational Stroke Research</i> , 2023, 14, 322-333.	2.3	5
2	Population-based Screening for Hereditary Colorectal Cancer Variants in Japan. <i>Clinical Gastroenterology and Hepatology</i> , 2022, 20, 2132-2141.e9.	2.4	20
3	Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. <i>International Journal of Epidemiology</i> , 2022, 50, 1995-2010.	0.9	39
4	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.	1.1	5
5	Novel susceptibility loci for steroid-associated osteonecrosis of the femoral head in systemic lupus erythematosus. <i>Human Molecular Genetics</i> , 2022, 31, 1082-1095.	1.4	1
6	Genetic overlap analysis of endometriosis and asthma identifies shared loci implicating sex hormones and thyroid signalling pathways. <i>Human Reproduction</i> , 2022, 37, 366-383.	0.4	19
7	A single-nucleotide-polymorphism in the 5' flanking region of <i>MSX1</i> gene as a predictive marker candidate for platinum-based therapy of esophageal carcinoma. <i>Therapeutic Advances in Medical Oncology</i> , 2022, 14, 175883592210805.	1.4	0
8	Decoding the diversity of killer immunoglobulin-like receptors by deep sequencing and a high-resolution imputation method. <i>Cell Genomics</i> , 2022, 2, 100101.	3.0	6
9	Large-scale Integrated Analysis of Genetics and Metabolomic Data Reveals Potential Links Between Lipids and Colorectal Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 1216-1226.	1.1	3
10	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. <i>Nature Genetics</i> , 2022, 54, 450-458.	9.4	109
11	Genome-wide risk prediction of common diseases across ancestries in one million people. <i>Cell Genomics</i> , 2022, 2, 100118.	3.0	34
12	Expansion of Cancer Risk Profile for <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>JAMA Oncology</i> , 2022, 8, 871.	3.4	70
13	Genetic analysis of right heart structure and function in 40,000 people. <i>Nature Genetics</i> , 2022, 54, 792-803.	9.4	34
14	Biological insights into systemic lupus erythematosus through an immune cell-specific transcriptome-wide association study. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, 1273-1280.	0.5	9
15	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.	0.5	103
16	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.	1.8	36
17	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. <i>EBioMedicine</i> , 2021, 63, 103157.	2.7	14
18	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.	9.4	264

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19	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.	0.6	10
20	A deep learning method for HLA imputation and trans-ethnic MHC fine-mapping of type 1 diabetes. <i>Nature Communications</i> , 2021, 12, 1639.	5.8	44
21	Comprehensive molecular and clinicopathological profiling of desmoid tumours. <i>European Journal of Cancer</i> , 2021, 145, 109-120.	1.3	10
22	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.	5.8	44
23	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. <i>Nature Medicine</i> , 2021, 27, 1012-1024.	15.2	109
24	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. <i>Nature Medicine</i> , 2021, 27, 1239-1249.	15.2	78
25	Collagen XVII inhibits breast cancer cell proliferation and growth through deactivation of the AKT/mTOR signaling pathway. <i>PLoS ONE</i> , 2021, 16, e0255179.	1.1	16
26	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. <i>Human Genetics</i> , 2021, 140, 1353-1365.	1.8	18
27	Intracellular Accumulation of IFN- γ Induces ER Stress and Results in Anti-Cirrhotic but Pro-HCV Effects. <i>Frontiers in Immunology</i> , 2021, 12, 692263.	2.2	6
28	A cross-population atlas of genetic associations for 220 human phenotypes. <i>Nature Genetics</i> , 2021, 53, 1415-1424.	9.4	560
29	A genome-wide association study identifies a novel candidate locus at the DLGAP1 gene with susceptibility to resistant hypertension in the Japanese population. <i>Scientific Reports</i> , 2021, 11, 19497.	1.6	12
30	A single nucleotide polymorphism in <i>PSMA</i> is associated with endoscopic grading in Kyoto classification of gastritis. <i>Journal of Clinical Biochemistry and Nutrition</i> , 2021, 68, 73-77.	0.6	3
31	Genetic susceptibility to hepatocellular carcinoma in chromosome 22q13.31, findings of a genome-wide association study. <i>JGH Open</i> , 2021, 5, 1363-1372.	0.7	9
32	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.	3.0	69
33	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.	1.4	14
34	GWAS of five gynecologic diseases and cross-trait analysis in Japanese. <i>European Journal of Human Genetics</i> , 2020, 28, 95-107.	1.4	32
35	Identification of Novel Loci and New Risk Variant in Known Loci for Colorectal Cancer Risk in East Asians. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 477-486.	1.1	25
36	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.	2.7	39

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37	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	13.5	388
38	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.	9.4	206
39	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.	9.4	163
40	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.	9.4	126
41	Endogenization and excision of human herpesvirus 6 in human genomes. <i>PLoS Genetics</i> , 2020, 16, e1008915.	1.5	22
42	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020, 182, 1198-1213.e14.	13.5	353
43	Association of circulating 25-Hydroxyvitamin D and its related genetic variations with hepatocellular carcinoma incidence and survival. <i>Annals of Translational Medicine</i> , 2020, 8, 1080-1080.	0.7	8
44	Fine Mapping of the Major Histocompatibility Complex Region and Association of the HLA-B*52:01 Allele With Cervical Cancer in Japanese Women. <i>JAMA Network Open</i> , 2020, 3, e2023248.	2.8	7
45	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.	1.6	44
46	Chromosomal alterations among age-related haematopoietic clones in Japan. <i>Nature</i> , 2020, 584, 130-135.	13.7	102
47	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.	9.4	304
48	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. <i>Nature Communications</i> , 2020, 11, 1217.	5.8	46
49	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.	15.2	74
50	Genetic and phenotypic landscape of the mitochondrial genome in the Japanese population. <i>Communications Biology</i> , 2020, 3, 104.	2.0	32
51	Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. <i>Nature Communications</i> , 2020, 11, 3175.	5.8	34
52	GWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. <i>Nature Human Behaviour</i> , 2020, 4, 308-316.	6.2	80
53	Identification of a novel uterine leiomyoma GWAS locus in a Japanese population. <i>Scientific Reports</i> , 2020, 10, 1197.	1.6	14
54	Dimensionality reduction reveals fine-scale structure in the Japanese population with consequences for polygenic risk prediction. <i>Nature Communications</i> , 2020, 11, 1569.	5.8	58

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55	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.	1.5	6
56	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.	3.5	22
57	Claudin-2 deficiency associates with hypercalciuria in mice and human kidney stone disease. <i>Journal of Clinical Investigation</i> , 2020, 130, 1948-1960.	3.9	61
58	Endoscopy-based Kyoto classification score of gastritis related to pathological topography of neutrophil activity. <i>World Journal of Gastroenterology</i> , 2020, 26, 5146-5155.	1.4	11
59	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019, 111, 146-157.	3.0	129
60	GWAS of mosaic loss of chromosome Y highlights genetic effects on blood cell differentiation. <i>Nature Communications</i> , 2019, 10, 4719.	5.8	50
61	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	5.8	84
62	Antitumor immunity augments the therapeutic effects of p53 activation on acute myeloid leukemia. <i>Nature Communications</i> , 2019, 10, 4869.	5.8	36
63	12 new susceptibility loci for prostate cancer identified by genome-wide association study in Japanese population. <i>Nature Communications</i> , 2019, 10, 4422.	5.8	49
64	Characterizing rare and low-frequency height-associated variants in the Japanese population. <i>Nature Communications</i> , 2019, 10, 4393.	5.8	123
65	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
66	Genetic and phenotypic landscape of the major histocompatibility complex region in the Japanese population. <i>Nature Genetics</i> , 2019, 51, 470-480.	9.4	75
67	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.	0.5	16
68	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	9.4	549
69	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.	2.3	28
70	INKA2, a novel p53 target that interacts with the serine/threonine kinase PAK4. <i>International Journal of Oncology</i> , 2019, 54, 1907-1920.	1.4	8
71	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.	3.0	25
72	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.	6.2	54

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73	A Polymorphic Variant in p19Arf Confers Resistance to Chemically Induced Skin Tumors by Activating the p53 Pathway. <i>Journal of Investigative Dermatology</i> , 2019, 139, 1459-1469.	0.3	4
74	Genome-wide meta-analysis identifies multiple novel loci associated with serum uric acid levels in Japanese individuals. <i>Communications Biology</i> , 2019, 2, 115.	2.0	66
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.	1.4	31
76	Large-Scale Genome-Wide Association Study of East Asians Identifies Loci Associated With Risk for Colorectal Cancer. <i>Gastroenterology</i> , 2019, 156, 1455-1466.	0.6	111
77	Genetic variants of calcium and vitamin D metabolism in kidney stone disease. <i>Nature Communications</i> , 2019, 10, 5175.	5.8	69
78	Integrated exome and RNA sequencing of dedifferentiated liposarcoma. <i>Nature Communications</i> , 2019, 10, 5683.	5.8	41
79	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.	1.6	9
80	Clinical and molecular characteristics of <i>MEF2D</i> fusion-positive B-cell precursor acute lymphoblastic leukemia in childhood, including a novel translocation resulting in <i>MEF2D-HNRNP1</i> gene fusion. <i>Haematologica</i> , 2019, 104, 128-137.	1.7	65
81	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. <i>Nature Communications</i> , 2019, 10, 29.	5.8	113
82	Single Nucleotide Polymorphisms of <i>HAAO</i> and <i>IRX6</i> Genes as Risk Factors for Hypospadias. <i>Journal of Urology</i> , 2019, 201, 386-392.	0.2	9
83	Identification of 28 new susceptibility loci for type 2 diabetes in the Japanese population. <i>Nature Genetics</i> , 2019, 51, 379-386.	9.4	164
84	The Association of Single Nucleotide Polymorphisms with Cancer Risk. , 2019, , 87-144.		0
85	GWAS identifies two novel colorectal cancer loci at 16q24.1 and 20q13.12. <i>Carcinogenesis</i> , 2018, 39, 652-660.	1.3	52
86	Deep whole-genome sequencing reveals recent selection signatures linked to evolution and disease risk of Japanese. <i>Nature Communications</i> , 2018, 9, 1631.	5.8	132
87	Genetic analysis of quantitative traits in the Japanese population links cell types to complex human diseases. <i>Nature Genetics</i> , 2018, 50, 390-400.	9.4	613
88	Citrullination of RGG Motifs in FET Proteins by PAD4 Regulates Protein Aggregation and ALS Susceptibility. <i>Cell Reports</i> , 2018, 22, 1473-1483.	2.9	85
89	Decrease in <i>PSCA</i> expression caused by <i>Helicobacter pylori</i> infection may promote progression to severe gastritis. <i>Oncotarget</i> , 2018, 9, 3936-3945.	0.8	21
90	Genome-wide association study (GWAS) of ovarian cancer in Japanese predicted regulatory variants in 22q13.1. <i>PLoS ONE</i> , 2018, 13, e0209096.	1.1	8

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91	Genome-wide association study identifies gastric cancer susceptibility loci at 12q24.11 and 20q11.21. <i>Cancer Science</i> , 2018, 109, 4015-4024.	1.7	39
92	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018, 9, 5052.	5.8	75
93	Germline pathogenic variants of 11 breast cancer genes in 7,051 Japanese patients and 11,241 controls. <i>Nature Communications</i> , 2018, 9, 4083.	5.8	179
94	Elucidating the genetic architecture of reproductive ageing in the Japanese population. <i>Nature Communications</i> , 2018, 9, 1977.	5.8	44
95	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.	2.0	23
96	Risk prediction models for mortality in patients with cardiovascular disease: The BioBank Japan project. <i>Journal of Epidemiology</i> , 2017, 27, S71-S76.	1.1	11
97	EPSIN 3, A Novel p53 Target, Regulates the Apoptotic Pathway and Gastric Carcinogenesis. <i>Neoplasia</i> , 2017, 19, 185-195.	2.3	14
98	GALNT6 Stabilizes GRP78 Protein by O-glycosylation and Enhances its Activity to Suppress Apoptosis Under Stress Condition. <i>Neoplasia</i> , 2017, 19, 43-53.	2.3	23
99	Characteristics and prognosis of Japanese colorectal cancer patients: The BioBank Japan Project. <i>Journal of Epidemiology</i> , 2017, 27, S36-S42.	1.1	38
100	Characteristics of patients with liver cancer in the BioBank Japan project. <i>Journal of Epidemiology</i> , 2017, 27, S43-S48.	1.1	17
101	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.	1.1	20
102	Statin use and all-cause and cancer mortality: BioBank Japan cohort. <i>Journal of Epidemiology</i> , 2017, 27, S84-S91.	1.1	25
103	Characteristics and prognosis of Japanese female breast cancer patients: The BioBank Japan project. <i>Journal of Epidemiology</i> , 2017, 27, S58-S64.	1.1	27
104	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.	1.1	32
105	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.	1.1	133
106	Argininosuccinate synthase 1 is an intrinsic Akt repressor transactivated by p53. <i>Science Advances</i> , 2017, 3, e1603204.	4.7	40
107	The Transcriptional Landscape of p53 Signalling Pathway. <i>EBioMedicine</i> , 2017, 20, 109-119.	2.7	47
108	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. <i>Nature Communications</i> , 2017, 8, 15539.	5.8	230

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109	Overview of the BioBank Japan Project: Study design and profile. <i>Journal of Epidemiology</i> , 2017, 27, S2-S8.	1.1	451
110	Overview of BioBank Japan follow-up data in 32 diseases. <i>Journal of Epidemiology</i> , 2017, 27, S22-S28.	1.1	47
111	Cholesterol levels of Japanese dyslipidaemic patients with various comorbidities: BioBank Japan. <i>Journal of Epidemiology</i> , 2017, 27, S77-S83.	1.1	3
112	Clinical and histopathological characteristics of patients with prostate cancer in the BioBank Japan project. <i>Journal of Epidemiology</i> , 2017, 27, S65-S70.	1.1	11
113	Characteristics and prognosis of Japanese male and female lung cancer patients: The BioBank Japan Project. <i>Journal of Epidemiology</i> , 2017, 27, S49-S57.	1.1	17
114	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.	2.6	45
115	Identification of a p53 target, CD137L, that mediates growth suppression and immune response of osteosarcoma cells. <i>Scientific Reports</i> , 2017, 7, 10739.	1.6	3
116	Genome-wide association study identifies 112 new loci for body mass index in the Japanese population. <i>Nature Genetics</i> , 2017, 49, 1458-1467.	9.4	380
117	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.	1.1	12
118	Regulation of tubular recycling endosome biogenesis by the p53-MICALL1 pathway. <i>International Journal of Oncology</i> , 2017, 51, 724-736.	1.4	6
119	Identification of a novel p53 target, COL17A1, that inhibits breast cancer cell migration and invasion. <i>Oncotarget</i> , 2017, 8, 55790-55803.	0.8	58
120	Identification of a p53-repressed gene module in breast cancer cells. <i>Oncotarget</i> , 2017, 8, 55821-55836.	0.8	6
121	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.	1.1	21
122	Association Study of a Functional Variant on ABCG2 Gene with Sunitinib-Induced Severe Adverse Drug Reaction. <i>PLoS ONE</i> , 2016, 11, e0148177.	1.1	39
123	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. <i>American Journal of Human Genetics</i> , 2016, 99, 636-646.	2.6	67
124	Genetic risk score based on the prevalence of vertebral fracture in Japanese women with osteoporosis. <i>Bone Reports</i> , 2016, 5, 168-172.	0.2	15
125	Contribution of a Non-classical HLA Gene, HLA-DOA, to the Risk of Rheumatoid Arthritis. <i>American Journal of Human Genetics</i> , 2016, 99, 366-374.	2.6	68
126	Cystatin C as a p53-inducible apoptotic mediator that regulates cathepsin L activity. <i>Cancer Science</i> , 2016, 107, 298-306.	1.7	38

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127	Regulation of myo-inositol biosynthesis by p53-ISYNA1 pathway. International Journal of Oncology, 2016, 48, 2415-2424.	1.4	41
128	Genome-wide association study in East Asians identifies two novel breast cancer susceptibility loci. Human Molecular Genetics, 2016, 25, 3361-3371.	1.4	40
129	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. Gastroenterology, 2016, 150, 1633-1645.	0.6	97
130	Regulation of iron homeostasis by the p53-ISCU pathway. Scientific Reports, 2015, 5, 16497.	1.6	68
131	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
132	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
133	Identification of novel epigenetically inactivated gene PAMR1 in breast carcinoma. Oncology Reports, 2015, 33, 267-273.	1.2	31
134	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
135	Directional dominance on stature and cognition in diverse human populations. Nature, 2015, 523, 459-462.	13.7	173
136	Large-scale association analysis in Asians identifies new susceptibility loci for prostate cancer. Nature Communications, 2015, 6, 8469.	5.8	51
137	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
138	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
139	Quantitative T cell repertoire analysis by deep cDNA sequencing of T cell receptor α and β chains using next-generation sequencing (NGS). OncoImmunology, 2014, 3, e968467.	2.1	68
140	Late Cornified Envelope Group I, a Novel Target of p53, Regulates PRMT5 Activity. Neoplasia, 2014, 16, 656-664.	2.3	16
141	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
142	A Rare Polymorphic Variant of <i>NBS1</i> Reduces DNA Repair Activity and Elevates Chromosomal Instability. Cancer Research, 2014, 74, 3707-3715.	0.4	5
143	Genome-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
144	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

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145	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, 886-890.	9.4	135
146	Trans-ethnic meta-analysis of white blood cell phenotypes. <i>Human Molecular Genetics</i> , 2014, 23, 6944-6960.	1.4	60
147	Identification of a nuclear protein, LRRC42, involved in lung carcinogenesis. <i>International Journal of Oncology</i> , 2014, 45, 147-156.	1.4	7
148	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, 588-593.	1.1	24
149	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, 875-882.	1.8	58
150	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, 353-361.	1.1	38
151	The histone methyltransferase Wolfâ€“Hirschhorn syndrome candidate 1 (WHSC1L1) is involved in human carcinogenesis. <i>Genes Chromosomes and Cancer</i> , 2013, 52, 126-139.	1.5	64
152	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. <i>PLoS Genetics</i> , 2013, 9, e1003796.	1.5	142
153	Germline Variants and Advanced Colorectal Adenomas: Adenoma Prevention with Celecoxib Trial Genome-wide Association Study. <i>Clinical Cancer Research</i> , 2013, 19, 6430-6437.	3.2	9
154	Impact of four loci on serum tamsulosin hydrochloride concentration. <i>Journal of Human Genetics</i> , 2013, 58, 21-26.	1.1	2
155	Impact of PSCA Variation on Gastric Ulcer Susceptibility. <i>PLoS ONE</i> , 2013, 8, e63698.	1.1	15
156	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.	1.1	59
157	Genome Wide Association Study of Age at Menarche in the Japanese Population. <i>PLoS ONE</i> , 2013, 8, e63821.	1.1	26
158	A Genome-Wide Association Study Identified AFF1 as a Susceptibility Locus for Systemic Lupus Erythematosus in Japanese. <i>PLoS Genetics</i> , 2012, 8, e1002455.	1.5	115
159	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.	1.5	63
160	Critical Function for Nuclear Envelope Protein TMEM209 in Human Pulmonary Carcinogenesis. <i>Cancer Research</i> , 2012, 72, 4110-4118.	0.4	27
161	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. <i>Nature Genetics</i> , 2012, 44, 770-776.	9.4	210
162	A genome-wide association study identifies two susceptibility loci for duodenal ulcer in the Japanese population. <i>Nature Genetics</i> , 2012, 44, 430-434.	9.4	114

#	ARTICLE	IF	CITATIONS
163	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	40
164	Quantitative Structural Characterization of Local N-Glycan Microheterogeneity in Therapeutic Antibodies by Energy-Resolved Oxonium Ion Monitoring. <i>Analytical Chemistry</i> , 2012, 84, 9655-9662.	3.2	49
165	CLCA2 as a p53-Inducible Senescence Mediator. <i>Neoplasia</i> , 2012, 14, 141-IN9.	2.3	32
166	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.	1.1	34
167	Soluble MICA and a MICA Variation as Possible Prognostic Biomarkers for HBV-Induced Hepatocellular Carcinoma. <i>PLoS ONE</i> , 2012, 7, e44743.	1.1	81
168	Regulation of histone modification and chromatin structure by the p53-PADI4 pathway. <i>Nature Communications</i> , 2012, 3, 676.	5.8	128
169	Novel susceptibility loci for hepatocellular carcinoma in chronic HBV carriers. <i>Hepatobiliary Surgery and Nutrition</i> , 2012, 1, 59-60.	0.7	7
170	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.. <i>Blood</i> , 2012, 120, 2548-2548.	0.6	0
171	Genome-wide association study for C-reactive protein levels identified pleiotropic associations in the IL6 locus. <i>Human Molecular Genetics</i> , 2011, 20, 1224-1231.	1.4	82
172	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011, 43, 1131-1138.	9.4	501
173	Large-scale genome-wide association studies in east Asians identify new genetic loci influencing metabolic traits. <i>Nature Genetics</i> , 2011, 43, 990-995.	9.4	270
174	Genome-wide association study identifies a susceptibility locus for HCV-induced hepatocellular carcinoma. <i>Nature Genetics</i> , 2011, 43, 455-458.	9.4	332
175	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.	0.7	16
176	Common variants on 14q32 and 13q12 are associated with DLBCL susceptibility. <i>Journal of Human Genetics</i> , 2011, 56, 436-439.	1.1	25
177	A genome-wide association study of chronic hepatitis B identified novel risk locus in a Japanese population. <i>Human Molecular Genetics</i> , 2011, 20, 3884-3892.	1.4	205
178	Multiple Loci Are Associated with White Blood Cell Phenotypes. <i>PLoS Genetics</i> , 2011, 7, e1002113.	1.5	106
179	Identification of Nine Novel Loci Associated with White Blood Cell Subtypes in a Japanese Population. <i>PLoS Genetics</i> , 2011, 7, e1002067.	1.5	69
180	Genome-wide association study of hematological and biochemical traits in a Japanese population. <i>Nature Genetics</i> , 2010, 42, 210-215.	9.4	460

#	ARTICLE	IF	CITATIONS
181	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, 2303-2312.	1.4	106
182	Crosstalk of EDA-A2/XEDAR in the p53 Signaling Pathway. <i>Molecular Cancer Research</i> , 2010, 8, 855-863.	1.5	36
183	Common variations in PSMD3 and CSF3 and PLCB4 are associated with neutrophil count. <i>Human Molecular Genetics</i> , 2010, 19, 2079-2085.	1.4	49
184	Regulation of Protein Citrullination through p53/PADI4 Network in DNA Damage Response. <i>Cancer Research</i> , 2009, 69, 8761-8769.	0.4	106
185	Orphan receptor tyrosine kinase ROR2 as a potential therapeutic target for osteosarcoma. <i>Cancer Science</i> , 2009, 100, 1227-1233.	1.7	86
186	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, 591-595.	9.4	491
187	Functional Variants in ADH1B and ALDH2 Coupled With Alcohol and Smoking Synergistically Enhance Esophageal Cancer Risk. <i>Gastroenterology</i> , 2009, 137, 1768-1775.	0.6	277
188	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.	1.1	26
189	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.	1.1	25
190	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, 631-637.	9.4	542
191	Functional SNPs in CD244 increase the risk of rheumatoid arthritis in a Japanese population. <i>Nature Genetics</i> , 2008, 40, 1224-1229.	9.4	106
192	Functional SNP in an Sp1-binding site of AGTRL1 gene is associated with susceptibility to brain infarction. <i>Human Molecular Genetics</i> , 2007, 16, 630-639.	1.4	105
193	A nonsynonymous SNP in PRKCH (protein kinase C δ) increases the risk of cerebral infarction. <i>Nature Genetics</i> , 2007, 39, 212-217.	9.4	200
194	p53RDL1 regulates p53-dependent apoptosis. <i>Nature Cell Biology</i> , 2003, 5, 216-223.	4.6	150
195	p53AIP1 regulates the mitochondrial apoptotic pathway. <i>Cancer Research</i> , 2002, 62, 2883-9.	0.4	94
196	p53AIP1, a Potential Mediator of p53-Dependent Apoptosis, and Its Regulation by Ser-46-Phosphorylated p53. <i>Cell</i> , 2000, 102, 849-862.	13.5	1,095