

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 | 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 |
| 2 | 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 |
| 3 | A cross-population atlas of genetic associations for 220 human phenotypes. <i>Nature Genetics</i> , 2021, 53, 1415-1424. | 9.4 | 560 |
| 4 | 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 |
| 5 | 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 |
| 6 | Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 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. <i>Nature Genetics</i> , 2009, 41, 591-595. | 9.4 | 491 |
| 8 | Genome-wide association study of hematological and biochemical traits in a Japanese population. <i>Nature Genetics</i> , 2010, 42, 210-215. | 9.4 | 460 |
| 9 | Overview of the BioBank Japan Project: Study design and profile. <i>Journal of Epidemiology</i> , 2017, 27, S2-S8. | 1.1 | 451 |
| 10 | The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 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. <i>Nature Genetics</i> , 2017, 49, 1458-1467. | 9.4 | 380 |
| 12 | 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 |
| 13 | Genome-wide association study identifies a susceptibility locus for HCV-induced hepatocellular carcinoma. <i>Nature Genetics</i> , 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. <i>Nature Genetics</i> , 2020, 52, 669-679. | 9.4 | 304 |
| 15 | 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 |
| 16 | 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 |
| 17 | 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 |
| 18 | Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 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. <i>Nature Communications</i> , 2017, 8, 15539. | 5.8 | 230 |
| 20 | Large-scale genetic study in East Asians identifies six new loci associated with colorectal cancer risk. <i>Nature Genetics</i> , 2014, 46, 533-542. | 9.4 | 212 |
| 21 | Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. <i>Nature Genetics</i> , 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. <i>Nature Genetics</i> , 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. <i>Human Molecular Genetics</i> , 2011, 20, 3884-3892. | 1.4 | 205 |
| 24 | A nonsynonymous SNP in PRKCH (protein kinase C $\hat{\imath}$) increases the risk of cerebral infarction. <i>Nature Genetics</i> , 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. <i>Nature Communications</i> , 2018, 9, 4083. | 5.8 | 179 |
| 26 | Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462. | 13.7 | 173 |
| 27 | 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 |
| 28 | 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 |
| 29 | p53RDL1 regulates p53-dependent apoptosis. <i>Nature Cell Biology</i> , 2003, 5, 216-223. | 4.6 | 150 |
| 30 | 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 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |
| 34 | Novel Common Genetic Susceptibility Loci for Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019, 111, 146-157. | 3.0 | 129 |
| 35 | Regulation of histone modification and chromatin structure by the p53-PADI4 pathway. <i>Nature Communications</i> , 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. <i>Nature Genetics</i> , 2020, 52, 1346-1354. | 9.4 | 126 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 37 | Characterizing rare and low-frequency height-associated variants in the Japanese population. <i>Nature Communications</i> , 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. <i>Nature Genetics</i> , 2015, 47, 798-802. | 9.4 | 119 |
| 39 | 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 |
| 40 | 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 |
| 41 | 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 |
| 42 | 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 |
| 43 | Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. <i>Nature Medicine</i> , 2021, 27, 1012-1024. | 15.2 | 109 |
| 44 | 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 |
| 45 | 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 |
| 46 | Regulation of Protein Citrullination through p53/PADI4 Network in DNA Damage Response. <i>Cancer Research</i> , 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. <i>Human Molecular Genetics</i> , 2010, 19, 2303-2312. | 1.4 | 106 |
| 48 | Multiple Loci Are Associated with White Blood Cell Phenotypes. <i>PLoS Genetics</i> , 2011, 7, e1002113. | 1.5 | 106 |
| 49 | Functional SNP in an Sp1-binding site of ACTRL1 gene is associated with susceptibility to brain infarction. <i>Human Molecular Genetics</i> , 2007, 16, 630-639. | 1.4 | 105 |
| 50 | 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 |
| 51 | Chromosomal alterations among age-related haematopoietic clones in Japan. <i>Nature</i> , 2020, 584, 130-135. | 13.7 | 102 |
| 52 | Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. <i>Gastroenterology</i> , 2016, 150, 1633-1645. | 0.6 | 97 |
| 53 | p53AIP1 regulates the mitochondrial apoptotic pathway. <i>Cancer Research</i> , 2002, 62, 2883-9. | 0.4 | 94 |
| 54 | Orphan receptor tyrosine kinase ROR2 as a potential therapeutic target for osteosarcoma. <i>Cancer Science</i> , 2009, 100, 1227-1233. | 1.7 | 86 |

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|----|---|------|-----------|
| 55 | 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 |
| 56 | Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957. | 5.8 | 84 |
| 57 | 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 |
| 58 | 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 |
| 59 | CWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. <i>Nature Human Behaviour</i> , 2020, 4, 308-316. | 6.2 | 80 |
| 60 | Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. <i>Nature Medicine</i> , 2021, 27, 1239-1249. | 15.2 | 78 |
| 61 | Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018, 9, 5052. | 5.8 | 75 |
| 62 | 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 |
| 63 | 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 |
| 64 | 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 |
| 65 | 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 |
| 66 | Genetic variants of calcium and vitamin D metabolism in kidney stone disease. <i>Nature Communications</i> , 2019, 10, 5175. | 5.8 | 69 |
| 67 | 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 |
| 68 | Quantitative T cell repertoire analysis by deep cDNA sequencing of T cell receptor α and β chains using next-generation sequencing (NGS). <i>Oncotimmunology</i> , 2014, 3, e968467. | 2.1 | 68 |
| 69 | Regulation of iron homeostasis by the p53-ISCU pathway. <i>Scientific Reports</i> , 2015, 5, 16497. | 1.6 | 68 |
| 70 | 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 |
| 71 | 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 |
| 72 | 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 |

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|----|---|-----|-----------|
| 73 | 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 |
| 74 | The histone methyltransferase Wolf-Hirschhorn syndrome candidate 1-like 1 (WHSC1L1) is involved in human carcinogenesis. <i>Genes Chromosomes and Cancer</i> , 2013, 52, 126-139. | 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. <i>PLoS Genetics</i> , 2012, 8, e1002541. | 1.5 | 63 |
| 76 | 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 |
| 77 | Trans-ethnic meta-analysis of white blood cell phenotypes. <i>Human Molecular Genetics</i> , 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. <i>PLoS ONE</i> , 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. <i>Journal of Hepatology</i> , 2013, 58, 875-882. | 1.8 | 58 |
| 80 | 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 |
| 81 | 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 |
| 82 | 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 |
| 83 | 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, 948-955. | 2.3 | 52 |
| 84 | GWAS identifies two novel colorectal cancer loci at 16q24.1 and 20q13.12. <i>Carcinogenesis</i> , 2018, 39, 652-660. | 1.3 | 52 |
| 85 | Large-scale association analysis in Asians identifies new susceptibility loci for prostate cancer. <i>Nature Communications</i> , 2015, 6, 8469. | 5.8 | 51 |
| 86 | GWAS of mosaic loss of chromosome Y highlights genetic effects on blood cell differentiation. <i>Nature Communications</i> , 2019, 10, 4719. | 5.8 | 50 |
| 87 | Common variations in PSMD3-CSF3 and PLCB4 are associated with neutrophil count. <i>Human Molecular Genetics</i> , 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. <i>Analytical Chemistry</i> , 2012, 84, 9655-9662. | 3.2 | 49 |
| 89 | 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 |
| 90 | 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, 374-380. | 1.4 | 48 |

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|-----|--|-----|-----------|
| 91 | The Transcriptional Landscape of p53 Signalling Pathway. <i>EBioMedicine</i> , 2017, 20, 109-119. | 2.7 | 47 |
| 92 | Overview of BioBank Japan follow-up data in 32 diseases. <i>Journal of Epidemiology</i> , 2017, 27, S22-S28. | 1.1 | 47 |
| 93 | 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 |
| 94 | 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 |
| 95 | Elucidating the genetic architecture of reproductive ageing in the Japanese population. <i>Nature Communications</i> , 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. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002670. | 1.6 | 44 |
| 97 | 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 |
| 98 | 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 |
| 99 | Regulation of myo-inositol biosynthesis by p53-ISYNA1 pathway. <i>International Journal of Oncology</i> , 2016, 48, 2415-2424. | 1.4 | 41 |
| 100 | Integrated exome and RNA sequencing of dedifferentiated liposarcoma. <i>Nature Communications</i> , 2019, 10, 5683. | 5.8 | 41 |
| 101 | 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 |
| 102 | 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. | 1.1 | 40 |
| 103 | Genome-wide association study in East Asians identifies two novel breast cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2016, 25, 3361-3371. | 1.4 | 40 |
| 104 | Argininosuccinate synthase 1 is an intrinsic Akt repressor transactivated by p53. <i>Science Advances</i> , 2017, 3, e1603204. | 4.7 | 40 |
| 105 | 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 |
| 106 | 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 |
| 107 | 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 |
| 108 | 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 |

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|-----|---|-----|-----------|
| 109 | 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 |
| 110 | Genome-wide association study identified SNP on 15q24 associated with bladder cancer risk in Japanese population. <i>Human Molecular Genetics</i> , 2015, 24, 1177-1184. | 1.4 | 38 |
| 111 | Cystatin C as a p53-inducible apoptotic mediator that regulates cathepsin L activity. <i>Cancer Science</i> , 2016, 107, 298-306. | 1.7 | 38 |
| 112 | Characteristics and prognosis of Japanese colorectal cancer patients: The BioBank Japan Project. <i>Journal of Epidemiology</i> , 2017, 27, S36-S42. | 1.1 | 38 |
| 113 | Crosstalk of EDA-A2/XEDAR in the p53 Signaling Pathway. <i>Molecular Cancer Research</i> , 2010, 8, 855-863. | 1.5 | 36 |
| 114 | Antitumor immunity augments the therapeutic effects of p53 activation on acute myeloid leukemia. <i>Nature Communications</i> , 2019, 10, 4869. | 5.8 | 36 |
| 115 | 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 |
| 116 | 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 |
| 117 | Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. <i>Nature Communications</i> , 2020, 11, 3175. | 5.8 | 34 |
| 118 | Genome-wide risk prediction of common diseases across ancestries in one million people. <i>Cell Genomics</i> , 2022, 2, 100118. | 3.0 | 34 |
| 119 | Genetic analysis of right heart structure and function in 40,000 people. <i>Nature Genetics</i> , 2022, 54, 792-803. | 9.4 | 34 |
| 120 | CLCA2 as a p53-Inducible Senescence Mediator. <i>Neoplasia</i> , 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. <i>Journal of Epidemiology</i> , 2017, 27, S29-S35. | 1.1 | 32 |
| 122 | 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 |
| 123 | Genetic and phenotypic landscape of the mitochondrial genome in the Japanese population. <i>Communications Biology</i> , 2020, 3, 104. | 2.0 | 32 |
| 124 | Identification of novel epigenetically inactivated gene PAMR1 in breast carcinoma. <i>Oncology Reports</i> , 2015, 33, 267-273. | 1.2 | 31 |
| 125 | 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 |
| 126 | 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 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 127 | Critical Function for Nuclear Envelope Protein TMEM209 in Human Pulmonary Carcinogenesis. <i>Cancer Research</i> , 2012, 72, 4110-4118. | 0.4 | 27 |
| 128 | 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 |
| 129 | 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 |
| 130 | Genome Wide Association Study of Age at Menarche in the Japanese Population. <i>PLoS ONE</i> , 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. <i>Journal of Human Genetics</i> , 2008, 53, 151-162. | 1.1 | 25 |
| 132 | Common variants on 14q32 and 13q12 are associated with DLBCL susceptibility. <i>Journal of Human Genetics</i> , 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. <i>International Journal of Oncology</i> , 2014, 44, 1490-1498. | 1.4 | 25 |
| 134 | Statin use and all-cause and cancer mortality: BioBank Japan cohort. <i>Journal of Epidemiology</i> , 2017, 27, S84-S91. | 1.1 | 25 |
| 135 | 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 |
| 136 | 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 |
| 137 | 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 |
| 138 | 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 |
| 139 | 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 |
| 140 | Endogenization and excision of human herpesvirus 6 in human genomes. <i>PLoS Genetics</i> , 2020, 16, e1008915. | 1.5 | 22 |
| 141 | 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 |
| 142 | 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 |
| 143 | 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 |
| 144 | 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 |

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|-----|---|-----|-----------|
| 145 | Population-based Screening for Hereditary Colorectal Cancer Variants in Japan. <i>Clinical Gastroenterology and Hepatology</i> , 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. <i>Human Reproduction</i> , 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. <i>Human Genetics</i> , 2021, 140, 1353-1365. | 1.8 | 18 |
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