

Yoichiro Kamatani

List of Publications by Year in descending order

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Version: 2024-02-01

159
papers

24,249
citations

18436

62
h-index

11581

135
g-index

201
all docs

201
docs citations

201
times ranked

30179
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 1 | Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2014, 506, 376-381. | 13.7 | 1,974 |
| 2 | Clinical use of current polygenic risk scores may exacerbate health disparities. <i>Nature Genetics</i> , 2019, 51, 584-591. | 9.4 | 1,664 |
| 3 | Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , 2019, 51, 237-244. | 9.4 | 1,307 |
| 4 | Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018, 50, 524-537. | 9.4 | 1,124 |
| 5 | Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, . | 6.0 | 1,085 |
| 6 | Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508. | 13.7 | 929 |
| 7 | Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. <i>Nature Genetics</i> , 2021, 53, 817-829. | 9.4 | 629 |
| 8 | 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 |
| 9 | A cross-population atlas of genetic associations for 220 human phenotypes. <i>Nature Genetics</i> , 2021, 53, 1415-1424. | 9.4 | 560 |
| 10 | Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233. | 9.4 | 552 |
| 11 | 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 |
| 12 | 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 |
| 13 | Genome-wide association study of hematological and biochemical traits in a Japanese population. <i>Nature Genetics</i> , 2010, 42, 210-215. | 9.4 | 460 |
| 14 | Overview of the BioBank Japan Project: Study design and profile. <i>Journal of Epidemiology</i> , 2017, 27, S2-S8. | 1.1 | 451 |
| 15 | Comparative genetic architectures of schizophrenia in East Asian and European populations. <i>Nature Genetics</i> , 2019, 51, 1670-1678. | 9.4 | 440 |
| 16 | The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11. | 13.5 | 388 |
| 17 | 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 |
| 18 | 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 |

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|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 19 | The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679. | 13.7 | 353 |
| 20 | Comprehensive evaluation of structural variation detection algorithms for whole genome sequencing. <i>Genome Biology</i> , 2019, 20, 117. | 3.8 | 311 |
| 21 | 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 |
| 22 | Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020, 582, 240-245. | 13.7 | 282 |
| 23 | Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017, 49, 946-952. | 9.4 | 279 |
| 24 | 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 |
| 25 | Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474. | 9.4 | 251 |
| 26 | Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572. | 9.4 | 250 |
| 27 | 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 |
| 28 | 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 |
| 29 | Genetic predisposition to mosaic Y chromosome loss in blood. <i>Nature</i> , 2019, 575, 652-657. | 13.7 | 198 |
| 30 | Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. <i>Nature Communications</i> , 2021, 12, 1258. | 5.8 | 196 |
| 31 | Common variation in PHACTR1 is associated with susceptibility to cervical artery dissection. <i>Nature Genetics</i> , 2015, 47, 78-83. | 9.4 | 195 |
| 32 | Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. <i>Nature Communications</i> , 2019, 10, 2773. | 5.8 | 183 |
| 33 | Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. <i>Nature Communications</i> , 2018, 9, 4455. | 5.8 | 181 |
| 34 | 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 |
| 35 | Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462. | 13.7 | 173 |
| 36 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 37 | 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 |
| 38 | Genetically Determined Levels of Circulating Cytokines and Risk of Stroke. <i>Circulation</i> , 2019, 139, 256-268. | 1.6 | 147 |
| 39 | Identification of six new genetic loci associated with atrial fibrillation in the Japanese population. <i>Nature Genetics</i> , 2017, 49, 953-958. | 9.4 | 136 |
| 40 | 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 |
| 41 | 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 |
| 42 | Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , The, 2016, 15, 695-707. | 4.9 | 130 |
| 43 | Polygenic burdens on cell-specific pathways underlie the risk of rheumatoid arthritis. <i>Nature Genetics</i> , 2017, 49, 1120-1125. | 9.4 | 130 |
| 44 | Tractor uses local ancestry to enable the inclusion of admixed individuals in GWAS and to boost power. <i>Nature Genetics</i> , 2021, 53, 195-204. | 9.4 | 125 |
| 45 | Characterizing rare and low-frequency height-associated variants in the Japanese population. <i>Nature Communications</i> , 2019, 10, 4393. | 5.8 | 123 |
| 46 | 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 |
| 47 | A Functional SNP in BNC2 Is Associated with Adolescent Idiopathic Scoliosis. <i>American Journal of Human Genetics</i> , 2015, 97, 337-342. | 2.6 | 119 |
| 48 | GWAS of clinically defined gout and subtypes identifies multiple susceptibility loci that include urate transporter genes. <i>Annals of the Rheumatic Diseases</i> , 2017, 76, 869-877. | 0.5 | 114 |
| 49 | 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 |
| 50 | Genome-wide analysis identifies novel susceptibility loci for myocardial infarction. <i>European Heart Journal</i> , 2021, 42, 919-933. | 1.0 | 113 |
| 51 | Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648. | 9.4 | 112 |
| 52 | Genome-wide association study identifies seven novel susceptibility loci for primary open-angle glaucoma. <i>Human Molecular Genetics</i> , 2018, 27, 1486-1496. | 1.4 | 111 |
| 53 | Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. <i>Nature Medicine</i> , 2021, 27, 1012-1024. | 15.2 | 109 |
| 54 | 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 |

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|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 55 | Chromosomal alterations among age-related haematopoietic clones in Japan. <i>Nature</i> , 2020, 584, 130-135. | 13.7 | 102 |
| 56 | Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166. | 1.1 | 94 |
| 57 | Polygenic burden in focal and generalized epilepsies. <i>Brain</i> , 2019, 142, 3473-3481. | 3.7 | 90 |
| 58 | Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285. | 5.8 | 89 |
| 59 | Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054. | 1.6 | 85 |
| 60 | Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957. | 5.8 | 84 |
| 61 | 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 |
| 62 | Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. <i>Nature Medicine</i> , 2021, 27, 1239-1249. | 15.2 | 78 |
| 63 | Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018, 9, 5052. | 5.8 | 75 |
| 64 | 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 |
| 65 | 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 |
| 66 | Genome-wide association study revealed novel loci which aggravate asymptomatic hyperuricaemia into gout. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 1430-1437. | 0.5 | 73 |
| 67 | 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 |
| 68 | 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 |
| 69 | Genetic variants of calcium and vitamin D metabolism in kidney stone disease. <i>Nature Communications</i> , 2019, 10, 5175. | 5.8 | 69 |
| 70 | 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 |
| 71 | 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 |
| 72 | 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 |

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|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 73 | 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 |
| 74 | Genetic Predisposition to Ischemic Stroke. <i>Stroke</i> , 2017, 48, 253-258. | 1.0 | 64 |
| 75 | Moyamoya Disease Susceptibility Variant <i><i>RNF213</i></i> p.R4810K Increases the Risk of Ischemic Stroke Attributable to Large-Artery Atherosclerosis. <i>Circulation</i> , 2019, 139, 295-298. | 1.6 | 64 |
| 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 | 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 |
| 78 | A polygenic risk score improves risk stratification of coronary artery disease: a large-scale prospective Chinese cohort study. <i>European Heart Journal</i> , 2022, 43, 1702-1711. | 1.0 | 58 |
| 79 | 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 |
| 80 | GWAS identifies two novel colorectal cancer loci at 16q24.1 and 20q13.12. <i>Carcinogenesis</i> , 2018, 39, 652-660. | 1.3 | 52 |
| 81 | GWAS of mosaic loss of chromosome Y highlights genetic effects on blood cell differentiation. <i>Nature Communications</i> , 2019, 10, 4719. | 5.8 | 50 |
| 82 | 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 |
| 83 | A multi-ethnic meta-analysis identifies novel genes, including <i>ACSL5</i> , associated with amyotrophic lateral sclerosis. <i>Communications Biology</i> , 2020, 3, 526. | 2.0 | 49 |
| 84 | Overview of BioBank Japan follow-up data in 32 diseases. <i>Journal of Epidemiology</i> , 2017, 27, S22-S28. | 1.1 | 47 |
| 85 | Genome-wide association study identifies 14 previously unreported susceptibility loci for adolescent idiopathic scoliosis in Japanese. <i>Nature Communications</i> , 2019, 10, 3685. | 5.8 | 47 |
| 86 | Empirical evaluation of variant calling accuracy using ultra-deep whole-genome sequencing data. <i>Scientific Reports</i> , 2019, 9, 1784. | 1.6 | 46 |
| 87 | Elucidating the genetic architecture of reproductive ageing in the Japanese population. <i>Nature Communications</i> , 2018, 9, 1977. | 5.8 | 44 |
| 88 | 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 |
| 89 | 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 |
| 90 | 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 |

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|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 91 | Low-frequency coding variants in <i>CETP</i> and <i>CFB</i> are associated with susceptibility of exudative age-related macular degeneration in the Japanese population. <i>Human Molecular Genetics</i> , 2016, 25, ddw335. | 1.4 | 42 |
| 92 | 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 |
| 93 | 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 |
| 94 | 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 |
| 95 | PLD4 is a genetic determinant to systemic lupus erythematosus and involved in murine autoimmune phenotypes. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 509-518. | 0.5 | 36 |
| 96 | Variants encoding a restricted carboxy-terminal domain of SLC12A2 cause hereditary hearing loss in humans. <i>PLoS Genetics</i> , 2020, 16, e1008643. | 1.5 | 36 |
| 97 | SARS-CoV-2 ORF6 disrupts nucleocytoplasmic trafficking to advance viral replication. <i>Communications Biology</i> , 2022, 5, 483. | 2.0 | 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. <i>PLoS ONE</i> , 2014, 9, e87645. | 1.1 | 34 |
| 99 | Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. <i>Nature Communications</i> , 2020, 11, 3175. | 5.8 | 34 |
| 100 | Genome-wide association studies identify polygenic effects for completed suicide in the Japanese population. <i>Neuropsychopharmacology</i> , 2019, 44, 2119-2124. | 2.8 | 32 |
| 101 | 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 |
| 102 | Genetic and phenotypic landscape of the mitochondrial genome in the Japanese population. <i>Communications Biology</i> , 2020, 3, 104. | 2.0 | 32 |
| 103 | Eight novel susceptibility loci and putative causal variants in atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 148, 1293-1306. | 1.5 | 32 |
| 104 | Efficient prediction of a spatial transcriptomics profile better characterizes breast cancer tissue sections without costly experimentation. <i>Scientific Reports</i> , 2022, 12, 4133. | 1.6 | 32 |
| 105 | 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 |
| 106 | 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 |
| 107 | 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 |
| 108 | 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 |

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|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 109 | 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 |
| 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. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 657-665. | 0.5 | 24 |
| 111 | Genome-wide Association Study of Idiopathic Osteonecrosis of the Femoral Head. <i>Scientific Reports</i> , 2017, 7, 15035. | 1.6 | 23 |
| 112 | Legacy Data Confound Genomics Studies. <i>Molecular Biology and Evolution</i> , 2020, 37, 2-10. | 3.5 | 23 |
| 113 | Endogenization and excision of human herpesvirus 6 in human genomes. <i>PLoS Genetics</i> , 2020, 16, e1008915. | 1.5 | 22 |
| 114 | A Mendelian randomization study identified obesity as a causal risk factor of uterine endometrial cancer in Japanese. <i>Cancer Science</i> , 2020, 111, 4646-4651. | 1.7 | 22 |
| 115 | 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 |
| 116 | A frequent variant in the Japanese population determines quasi-Mendelian inheritance of rare retinal ciliopathy. <i>Nature Communications</i> , 2019, 10, 2884. | 5.8 | 21 |
| 117 | Association of the <i>RPA3-UMAD1</i> locus with interstitial lung diseases complicated with rheumatoid arthritis in Japanese. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 1305-1309. | 0.5 | 21 |
| 118 | Multi-trait and cross-population genome-wide association studies across autoimmune and allergic diseases identify shared and distinct genetic component. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, 1301-1312. | 0.5 | 21 |
| 119 | Population-based Screening for Hereditary Colorectal Cancer Variants in Japan. <i>Clinical Gastroenterology and Hepatology</i> , 2022, 20, 2132-2141.e9. | 2.4 | 20 |
| 120 | Re-evaluating classical body type theories: genetic correlation between psychiatric disorders and body mass index. <i>Psychological Medicine</i> , 2018, 48, 1745-1748. | 2.7 | 19 |
| 121 | The schizophrenia genetics knowledgebase: a comprehensive update of findings from candidate gene studies. <i>Translational Psychiatry</i> , 2019, 9, 205. | 2.4 | 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. <i>Journal of Human Genetics</i> , 2019, 64, 1195-1202. | 1.1 | 19 |
| 123 | Genome-Wide Association Study of Renal Function Traits: Results from the Japan Multi-Institutional Collaborative Cohort Study. <i>American Journal of Nephrology</i> , 2018, 47, 304-316. | 1.4 | 18 |
| 124 | Evidence of Polygenic Adaptation in Sardinia at Height-Associated Loci Ascertained from the Biobank Japan. <i>American Journal of Human Genetics</i> , 2020, 107, 60-71. | 2.6 | 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. <i>Human Genetics</i> , 2021, 140, 1353-1365. | 1.8 | 18 |
| 126 | Mendelian randomization of genetically independent aging phenotypes identifies LPA and VCAM1 as biological targets for human aging. <i>Nature Aging</i> , 2022, 2, 19-30. | 5.3 | 17 |

| # | ARTICLE | IF | CITATIONS |
|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 127 | 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 |
| 128 | Identification of a novel uterine leiomyoma GWAS locus in a Japanese population. <i>Scientific Reports</i> , 2020, 10, 1197. | 1.6 | 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. <i>EBioMedicine</i> , 2021, 63, 103157. | 2.7 | 14 |
| 130 | <i>HLA-B*51:01</i> and <i>CYP2C9*3</i> Are Risk Factors for Phenytoin-Induced Eruption in the Japanese Population: Analysis of Data From the Biobank Japan Project. <i>Clinical Pharmacology and Therapeutics</i> , 2020, 107, 1170-1178. | 2.3 | 13 |
| 131 | Whole genome sequencing of 45 Japanese patients with intellectual disability. <i>American Journal of Medical Genetics, Part A</i> , 2021, 185, 1468-1480. | 0.7 | 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. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a003988. | 0.5 | 12 |
| 133 | Polygenic risk scores in schizophrenia with clinically significant copy number variants. <i>Psychiatry and Clinical Neurosciences</i> , 2020, 74, 35-39. | 1.0 | 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. <i>Scientific Reports</i> , 2021, 11, 19497. | 1.6 | 12 |
| 135 | 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 |
| 136 | Common variants at 2q11.2, 8q21.3, and 11q13.2 are associated with major mood disorders. <i>Translational Psychiatry</i> , 2017, 7, 1273. | 2.4 | 9 |
| 137 | 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 |
| 138 | A novel intragenic deletion in OPHN1 in a Japanese patient with Dandy-Walker malformation. <i>Human Genome Variation</i> , 2019, 6, 1. | 0.4 | 9 |
| 139 | Genome-wide association study of epilepsy in a Japanese population identified an associated region at chromosome 12q24. <i>Epilepsia</i> , 2021, 62, 1391-1400. | 2.6 | 9 |
| 140 | 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 |
| 141 | Search for new loci and low-frequency variants influencing glioma risk by exome-array analysis. <i>European Journal of Human Genetics</i> , 2016, 24, 717-724. | 1.4 | 8 |
| 142 | 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 |
| 143 | Genome-wide SNP data of Izumo and Makurazaki populations support inner-dual structure model for origin of Yamato people. <i>Journal of Human Genetics</i> , 2021, 66, 681-687. | 1.1 | 7 |
| 144 | Genetics of autosomal mosaic chromosomal alteration (mCA). <i>Journal of Human Genetics</i> , 2021, 66, 879-885. | 1.1 | 7 |

| # | ARTICLE | IF | CITATIONS |
|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 145 | Using spatio-temporal surveillance data to test the infectious environment of children before type 1 diabetes diagnosis. PLoS ONE, 2017, 12, e0170658. | 1.1 | 6 |
| 146 | A common variant of LDL receptor-related protein 2 (LRP2) gene is associated with gout susceptibility: a meta-analysis in a Japanese population. Human Cell, 2020, 33, 303-307. | 1.2 | 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. | 1.5 | 6 |
| 148 | Decoding the diversity of killer immunoglobulin-like receptors by deep sequencing and a high-resolution imputation method. Cell Genomics, 2022, 2, 100101. | 3.0 | 6 |
| 149 | Polygenic Risk Score of Adolescent Idiopathic Scoliosis for Potential Clinical Use. Journal of Bone and Mineral Research, 2020, 36, 1481-1491. | 3.1 | 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. | 1.1 | 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. | 1.6 | 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. | 0.4 | 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. | 1.1 | 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. | 1.2 | 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. | 0.9 | 2 |
| 156 | PPM1D and DNMT3A Mutations in Myelodysplasia and Clonal Hematopoiesis. Blood, 2019, 134, 1709-1709. | 0.6 | 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. | 1.1 | 0 |