

Yukinori Okada

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2543821/publications.pdf>

Version: 2024-02-01

196
papers

28,788
citations

16791

66
h-index

9346

148
g-index

238
all docs

238
docs citations

238
times ranked

38692
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206. | 13.7 | 3,823 |
| 2 | Partitioning heritability by functional annotation using genome-wide association summary statistics. <i>Nature Genetics</i> , 2015, 47, 1228-1235. | 9.4 | 2,045 |
| 3 | Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2014, 506, 376-381. | 13.7 | 1,974 |
| 4 | Clinical use of current polygenic risk scores may exacerbate health disparities. <i>Nature Genetics</i> , 2019, 51, 584-591. | 9.4 | 1,664 |
| 5 | 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 |
| 6 | 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 |
| 7 | Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154. | 9.4 | 675 |
| 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 | 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 |
| 11 | Genome-wide association studies. <i>Nature Reviews Methods Primers</i> , 2021, 1, . | 11.8 | 529 |
| 12 | Polarization of the Effects of Autoimmune and Neurodegenerative Risk Alleles in Leukocytes. <i>Science</i> , 2014, 344, 519-523. | 6.0 | 480 |
| 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 | The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11. | 13.5 | 388 |
| 15 | 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 |
| 16 | Meta-analysis identifies common variants associated with body mass index in east Asians. <i>Nature Genetics</i> , 2012, 44, 307-311. | 9.4 | 372 |
| 17 | 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 |
| 18 | The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679. | 13.7 | 353 |

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|----|--|------|-----------|
| 19 | 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 |
| 20 | Meta-analysis identifies nine new loci associated with rheumatoid arthritis in the Japanese population. <i>Nature Genetics</i> , 2012, 44, 511-516. | 9.4 | 285 |
| 21 | Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020, 582, 240-245. | 13.7 | 282 |
| 22 | Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. <i>Nature Genetics</i> , 2012, 44, 904-909. | 9.4 | 254 |
| 23 | Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474. | 9.4 | 251 |
| 24 | 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 |
| 25 | Common variants at CDKAL1 and KLF9 are associated with body mass index in east Asian populations. <i>Nature Genetics</i> , 2012, 44, 302-306. | 9.4 | 240 |
| 26 | A Role for Noncoding Variation in Schizophrenia. <i>Cell Reports</i> , 2014, 9, 1417-1429. | 2.9 | 225 |
| 27 | High-density genotyping of immune-related loci identifies new SLE risk variants in individuals with Asian ancestry. <i>Nature Genetics</i> , 2016, 48, 323-330. | 9.4 | 219 |
| 28 | Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. <i>Nature Medicine</i> , 2021, 27, 1876-1884. | 15.2 | 214 |
| 29 | Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. <i>Human Molecular Genetics</i> , 2014, 23, 5492-5504. | 1.4 | 192 |
| 30 | Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. <i>Nature Communications</i> , 2019, 10, 2773. | 5.8 | 183 |
| 31 | Fine Mapping Major Histocompatibility Complex Associations in Psoriasis and Its Clinical Subtypes. <i>American Journal of Human Genetics</i> , 2014, 95, 162-172. | 2.6 | 182 |
| 32 | Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. <i>Nature Communications</i> , 2018, 9, 4455. | 5.8 | 181 |
| 33 | Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462. | 13.7 | 173 |
| 34 | Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. <i>Nature Genetics</i> , 2015, 47, 1085-1090. | 9.4 | 164 |
| 35 | 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 |
| 36 | Fine Mapping Seronegative and Seropositive Rheumatoid Arthritis to Shared and Distinct HLA Alleles by Adjusting for the Effects of Heterogeneity. <i>American Journal of Human Genetics</i> , 2014, 94, 522-532. | 2.6 | 156 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. <i>Nature Communications</i> , 2016, 7, 10531. | 5.8 | 149 |
| 38 | Metagenome-wide association study of gut microbiome revealed novel aetiology of rheumatoid arthritis in the Japanese population. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 103-111. | 0.5 | 145 |
| 39 | Genetics of rheumatoid arthritis: 2018 status. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 446-453. | 0.5 | 141 |
| 40 | Risk for ACPA-positive rheumatoid arthritis is driven by shared HLA amino acid polymorphisms in Asian and European populations. <i>Human Molecular Genetics</i> , 2014, 23, 6916-6926. | 1.4 | 135 |
| 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 | Suppression of autophagic activity by Rubicon is a signature of aging. <i>Nature Communications</i> , 2019, 10, 847. | 5.8 | 132 |
| 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 | Genetic analyses identify widespread sex-differential participation bias. <i>Nature Genetics</i> , 2021, 53, 663-671. | 9.4 | 124 |
| 46 | Characterizing rare and low-frequency height-associated variants in the Japanese population. <i>Nature Communications</i> , 2019, 10, 4393. | 5.8 | 123 |
| 47 | TYK2 Protein-Coding Variants Protect against Rheumatoid Arthritis and Autoimmunity, with No Evidence of Major Pleiotropic Effects on Non-Autoimmune Complex Traits. <i>PLoS ONE</i> , 2015, 10, e0122271. | 1.1 | 120 |
| 48 | 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 |
| 49 | LC3 lipidation is essential for TFEB activation during the lysosomal damage response to kidney injury. <i>Nature Cell Biology</i> , 2020, 22, 1252-1263. | 4.6 | 117 |
| 50 | 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 |
| 51 | 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 |
| 52 | 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 |
| 53 | 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 |
| 54 | 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 |

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|----|--|------|-----------|
| 55 | Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. <i>Human Molecular Genetics</i> , 2015, 24, 1791-1800. | 1.4 | 105 |
| 56 | Discovery of six new susceptibility loci and analysis of pleiotropic effects in leprosy. <i>Nature Genetics</i> , 2015, 47, 267-271. | 9.4 | 103 |
| 57 | 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 |
| 58 | High-density genotyping of immune loci in Koreans and Europeans identifies eight new rheumatoid arthritis risk loci. <i>Annals of the Rheumatic Diseases</i> , 2015, 74, e13-e13. | 0.5 | 100 |
| 59 | HLA-Cw*1202-B*5201-DRB1*1502 Haplotype Increases Risk for Ulcerative Colitis but Reduces Risk for Crohn's Disease. <i>Gastroenterology</i> , 2011, 141, 864-871.e5. | 0.6 | 90 |
| 60 | Polygenic burden in focal and generalized epilepsies. <i>Brain</i> , 2019, 142, 3473-3481. | 3.7 | 90 |
| 61 | Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285. | 5.8 | 89 |
| 62 | The current landscape of psoriasis genetics in 2020. <i>Journal of Dermatological Science</i> , 2020, 99, 2-8. | 1.0 | 86 |
| 63 | Variation at HLA-DRB1 is associated with resistance to enteric fever. <i>Nature Genetics</i> , 2014, 46, 1333-1336. | 9.4 | 85 |
| 64 | Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study. <i>Lancet Oncology</i> , The, 2016, 17, 1240-1247. | 5.1 | 84 |
| 65 | Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957. | 5.8 | 84 |
| 66 | 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 |
| 67 | The HLA-DRÎ²1 amino acid positions 11â€“13â€“26 explain the majority of SLEâ€“MHC associations. <i>Nature Communications</i> , 2014, 5, 5902. | 5.8 | 80 |
| 68 | Predicting HLA alleles from high-resolution SNP data in three Southeast Asian populations. <i>Human Molecular Genetics</i> , 2014, 23, 4443-4451. | 1.4 | 80 |
| 69 | 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 |
| 70 | Empirical estimation of genome-wide significance thresholds based on the 1000 Genomes Project data set. <i>Journal of Human Genetics</i> , 2016, 61, 861-866. | 1.1 | 75 |
| 71 | 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 |
| 72 | 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 |

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|----|---|-----|-----------|
| 73 | 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 |
| 74 | Regulatory T Cell-Specific Epigenomic Region Variants Are a Key Determinant of Susceptibility to Common Autoimmune Diseases. <i>Immunity</i> , 2020, 52, 1119-1132.e4. | 6.6 | 73 |
| 75 | 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 |
| 76 | A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021, 53, 1504-1516. | 9.4 | 69 |
| 77 | 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 |
| 78 | Population-specific causal disease effect sizes in functionally important regions impacted by selection. <i>Nature Communications</i> , 2021, 12, 1098. | 5.8 | 68 |
| 79 | 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 |
| 80 | 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 |
| 81 | An association analysis of HLA-DRB1 with systemic lupus erythematosus and rheumatoid arthritis in a Japanese population: effects of *09:01 allele on disease phenotypes. <i>Rheumatology</i> , 2013, 52, 1172-1182. | 0.9 | 62 |
| 82 | Multiple Nonglycemic Genomic Loci Are Newly Associated With Blood Level of Glycated Hemoglobin in East Asians. <i>Diabetes</i> , 2014, 63, 2551-2562. | 0.3 | 61 |
| 83 | Trans-ethnic meta-analysis of white blood cell phenotypes. <i>Human Molecular Genetics</i> , 2014, 23, 6944-6960. | 1.4 | 60 |
| 84 | Interactions Between Amino Acid-Defined Major Histocompatibility Complex Class II Variants and Smoking in Seropositive Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2015, 67, 2611-2623. | 2.9 | 58 |
| 85 | 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 |
| 86 | 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 |
| 87 | New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. <i>International Journal of Epidemiology</i> , 2015, 44, 1706-1721. | 0.9 | 53 |
| 88 | Common variations in PSMD3-CSF3 and PLCB4 are associated with neutrophil count. <i>Human Molecular Genetics</i> , 2010, 19, 2079-2085. | 1.4 | 49 |
| 89 | Association of variations in HLA class II and other loci with susceptibility to EGFR-mutated lung adenocarcinoma. <i>Nature Communications</i> , 2016, 7, 12451. | 5.8 | 49 |
| 90 | IMPACT: Genomic Annotation of Cell-State-Specific Regulatory Elements Inferred from the Epigenome of Bound Transcription Factors. <i>American Journal of Human Genetics</i> , 2019, 104, 879-895. | 2.6 | 49 |

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|-----|--|-----|-----------|
| 91 | Empirical evaluation of variant calling accuracy using ultra-deep whole-genome sequencing data. <i>Scientific Reports</i> , 2019, 9, 1784. | 1.6 | 46 |
| 92 | Genetics of rheumatoid arthritis in Asia—present and future. <i>Nature Reviews Rheumatology</i> , 2015, 11, 375-379. | 3.5 | 45 |
| 93 | Haplotypes with Copy Number and Single Nucleotide Polymorphisms in CYP2A6 Locus Are Associated with Smoking Quantity in a Japanese Population. <i>PLoS ONE</i> , 2012, 7, e44507. | 1.1 | 45 |
| 94 | Significant impact of miRNA—target gene networks on genetics of human complex traits. <i>Scientific Reports</i> , 2016, 6, 22223. | 1.6 | 44 |
| 95 | 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 |
| 96 | 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 |
| 97 | Genetic studies of rheumatoid arthritis. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 2015, 91, 410-422. | 1.6 | 43 |
| 98 | Genomic dissection of 43 serum urate-associated loci provides multiple insights into molecular mechanisms of urate control. <i>Human Molecular Genetics</i> , 2020, 29, 923-943. | 1.4 | 40 |
| 99 | Variants at HLA-A, HLA-C, and HLA-DQB1 Confer Risk of Psoriasis Vulgaris in Japanese. <i>Journal of Investigative Dermatology</i> , 2018, 138, 542-548. | 0.3 | 39 |
| 100 | Integration of genetics and miRNA—target gene network identified disease biology implicated in tissue specificity. <i>Nucleic Acids Research</i> , 2018, 46, 11898-11909. | 6.5 | 39 |
| 101 | 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 |
| 102 | Whole gut virome analysis of 476 Japanese revealed a link between phage and autoimmune disease. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, 278-288. | 0.5 | 39 |
| 103 | Metagenome-wide association study revealed disease-specific landscape of the gut microbiome of systemic lupus erythematosus in Japanese. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 1575-1583. | 0.5 | 38 |
| 104 | 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 |
| 105 | GREP: genome for REPositioning drugs. <i>Bioinformatics</i> , 2019, 35, 3821-3823. | 1.8 | 35 |
| 106 | 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 |
| 107 | Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. <i>Nature Communications</i> , 2020, 11, 3175. | 5.8 | 34 |
| 108 | Genome-wide risk prediction of common diseases across ancestries in one million people. <i>Cell Genomics</i> , 2022, 2, 100118. | 3.0 | 34 |

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|-----|--|-----|-----------|
| 109 | Biological characterization of expression quantitative trait loci (eQTLs) showing tissue-specific opposite directional effects. <i>European Journal of Human Genetics</i> , 2019, 27, 1745-1756. | 1.4 | 32 |
| 110 | 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 |
| 111 | Genetic and phenotypic landscape of the mitochondrial genome in the Japanese population. <i>Communications Biology</i> , 2020, 3, 104. | 2.0 | 32 |
| 112 | Common genetic factors for hematological traits in Humans. <i>Journal of Human Genetics</i> , 2012, 57, 161-169. | 1.1 | 31 |
| 113 | High-throughput identification of noncoding functional SNPs via type IIS enzyme restriction. <i>Nature Genetics</i> , 2018, 50, 1180-1188. | 9.4 | 31 |
| 114 | HLA-DRB1*0901 lowers anti-cyclic citrullinated peptide antibody levels in Japanese patients with rheumatoid arthritis. <i>Annals of the Rheumatic Diseases</i> , 2010, 69, 1569-1570. | 0.5 | 29 |
| 115 | Human Leukocyte Antigen Class I Genes Associated With Stevens-Johnson Syndrome and Severe Ocular Complications Following Use of Cold Medicine in a Brazilian Population. <i>JAMA Ophthalmology</i> , 2017, 135, 355. | 1.4 | 29 |
| 116 | A Transethnic Mendelian Randomization Study Identifies Causality of Obesity on Risk of Psoriasis. <i>Journal of Investigative Dermatology</i> , 2019, 139, 1397-1400. | 0.3 | 28 |
| 117 | The Rheumatoid Arthritis Risk Variant CCR6DNP Regulates CCR6 via PARP-1. <i>PLoS Genetics</i> , 2016, 12, e1006292. | 1.5 | 28 |
| 118 | Statistical genetics and polygenic risk score for precision medicine. <i>Inflammation and Regeneration</i> , 2021, 41, 18. | 1.5 | 27 |
| 119 | Dysbiosis of Gut Microbiome Is Associated With Rupture of Cerebral Aneurysms. <i>Stroke</i> , 2022, 53, 895-903. | 1.0 | 27 |
| 120 | Age-associated decline of MondoA drives cellular senescence through impaired autophagy and mitochondrial homeostasis. <i>Cell Reports</i> , 2022, 38, 110444. | 2.9 | 27 |
| 121 | Polygenic risk scores for prediction of breast cancer risk in Asian populations. <i>Genetics in Medicine</i> , 2022, 24, 586-600. | 1.1 | 27 |
| 122 | A Metagenome-Wide Association Study of Gut Microbiome in Patients With Multiple Sclerosis Revealed Novel Disease Pathology. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 585973. | 1.8 | 26 |
| 123 | Genetic determinants of risk in autoimmune pulmonary alveolar proteinosis. <i>Nature Communications</i> , 2021, 12, 1032. | 5.8 | 26 |
| 124 | A Multinational Arab Genome-Wide Association Study Identifies New Genetic Associations for Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2017, 69, 976-985. | 2.9 | 25 |
| 125 | In silico drug screening by using genome-wide association study data repurposed dabrafenib, an anti-melanoma drug, for Parkinson's disease. <i>Human Molecular Genetics</i> , 2018, 27, 3974-3985. | 1.4 | 25 |
| 126 | Identification of secreted phosphoprotein 1 gene as a new rheumatoid arthritis susceptibility gene. <i>Annals of the Rheumatic Diseases</i> , 2015, 74, e19-e19. | 0.5 | 24 |

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|-----|---|-----|-----------|
| 127 | HLA-DQ and RBOFOX1 as susceptibility genes for an outbreak of hydrolyzed wheat allergy. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 1354-1363. | 1.5 | 24 |
| 128 | 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 |
| 129 | Clinical Characteristics of Patients with Coronavirus Disease (COVID-19): Preliminary Baseline Report of Japan COVID-19 Task Force, a Nationwide Consortium to Investigate Host Genetics of COVID-19. <i>International Journal of Infectious Diseases</i> , 2021, 113, 74-81. | 1.5 | 24 |
| 130 | Anti-citrullinated peptide/protein antibody (ACPA)-negative RA shares a large proportion of susceptibility loci with ACPA-positive RA: a meta-analysis of genome-wide association study in a Japanese population. <i>Arthritis Research and Therapy</i> , 2015, 17, 104. | 1.6 | 23 |
| 131 | Advances in genetics toward identifying pathogenic cell states of rheumatoid arthritis. <i>Immunological Reviews</i> , 2020, 294, 188-204. | 2.8 | 23 |
| 132 | Next-generation sequencing identifies contribution of both class I and II HLA genes on susceptibility of multiple sclerosis in Japanese. <i>Journal of Neuroinflammation</i> , 2019, 16, 162. | 3.1 | 22 |
| 133 | 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 |
| 134 | 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 |
| 135 | COX6A2 variants cause a muscle-specific cytochrome c oxidase deficiency. <i>Annals of Neurology</i> , 2019, 86, 193-202. | 2.8 | 21 |
| 136 | Association of the RPA3-UMAD1 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 |
| 137 | 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 |
| 138 | Contribution of a haplotype in the HLA region to anti-cyclic citrullinated peptide antibody positivity in rheumatoid arthritis, independently of HLA-DRB1. <i>Arthritis and Rheumatism</i> , 2009, 60, 3582-3590. | 6.7 | 20 |
| 139 | Loci associated with N-glycosylation of human IgG are not associated with rheumatoid arthritis: a Mendelian randomisation study. <i>Annals of the Rheumatic Diseases</i> , 2016, 75, 317-320. | 0.5 | 19 |
| 140 | Amino acid position 37 of HLA-DRB1 affects susceptibility to Crohn's disease in Asians. <i>Human Molecular Genetics</i> , 2018, 27, 3901-3910. | 1.4 | 19 |
| 141 | Do Genetic Susceptibility Variants Associate with Disease Severity in Early Active Rheumatoid Arthritis?. <i>Journal of Rheumatology</i> , 2015, 42, 1131-1140. | 1.0 | 18 |
| 142 | eLD: entropy-based linkage disequilibrium index between multiallelic sites. <i>Human Genome Variation</i> , 2018, 5, 29. | 0.4 | 18 |
| 143 | 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 |
| 144 | Integration of genetically regulated gene expression and pharmacological library provides therapeutic drug candidates. <i>Human Molecular Genetics</i> , 2021, 30, 294-304. | 1.4 | 17 |

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|-----|--|-----|-----------|
| 145 | 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 |
| 146 | Large-scale plasma-metabolome analysis identifies potential biomarkers of psoriasis and its clinical subtypes. <i>Journal of Dermatological Science</i> , 2021, 102, 78-84. | 1.0 | 15 |
| 147 | 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 |
| 148 | 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 |
| 149 | Trans-ethnic Fine-Mapping of the Major Histocompatibility Complex Region Linked to Parkinson's Disease. <i>Movement Disorders</i> , 2021, 36, 1805-1814. | 2.2 | 14 |
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