

# 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

14655

66  
h-index

8167

148  
g-index

238  
all docs

238  
docs citations

238  
times ranked

35383  
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.	27.8	3,823
2	Partitioning heritability by functional annotation using genome-wide association summary statistics. <i>Nature Genetics</i> , 2015, 47, 1228-1235.	21.4	2,045
3	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2014, 506, 376-381.	27.8	1,974
4	Clinical use of current polygenic risk scores may exacerbate health disparities. <i>Nature Genetics</i> , 2019, 51, 584-591.	21.4	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.	21.4	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.	21.4	1,124
7	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	21.4	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.	21.4	613
9	A cross-population atlas of genetic associations for 220 human phenotypes. <i>Nature Genetics</i> , 2021, 53, 1415-1424.	21.4	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.	21.4	549
11	Genome-wide association studies. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	21.2	529
12	Polarization of the Effects of Autoimmune and Neurodegenerative Risk Alleles in Leukocytes. <i>Science</i> , 2014, 344, 519-523.	12.6	480
13	Genome-wide association study of hematological and biochemical traits in a Japanese population. <i>Nature Genetics</i> , 2010, 42, 210-215.	21.4	460
14	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	28.9	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.	21.4	380
16	Meta-analysis identifies common variants associated with body mass index in east Asians. <i>Nature Genetics</i> , 2012, 44, 307-311.	21.4	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.	28.9	353
18	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	27.8	353

#	ARTICLE	IF	CITATIONS
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.	21.4	304
20	Meta-analysis identifies nine new loci associated with rheumatoid arthritis in the Japanese population. <i>Nature Genetics</i> , 2012, 44, 511-516.	21.4	285
21	Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020, 582, 240-245.	27.8	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.	21.4	254
23	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	21.4	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.	21.4	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.	21.4	240
26	A Role for Noncoding Variation in Schizophrenia. <i>Cell Reports</i> , 2014, 9, 1417-1429.	6.4	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.	21.4	219
28	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. <i>Nature Medicine</i> , 2021, 27, 1876-1884.	30.7	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.	2.9	192
30	Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. <i>Nature Communications</i> , 2019, 10, 2773.	12.8	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.	6.2	182
32	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. <i>Nature Communications</i> , 2018, 9, 4455.	12.8	181
33	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	27.8	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.	21.4	164
35	Identification of 28 new susceptibility loci for type 2 diabetes in the Japanese population. <i>Nature Genetics</i> , 2019, 51, 379-386.	21.4	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.	6.2	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.	12.8	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.	0.9	145
39	Genetics of rheumatoid arthritis: 2018 status. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 446-453.	0.9	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.	2.9	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.	12.8	132
42	Suppression of autophagic activity by Rubicon is a signature of aging. <i>Nature Communications</i> , 2019, 10, 847.	12.8	132
43	Polygenic burdens on cell-specific pathways underlie the risk of rheumatoid arthritis. <i>Nature Genetics</i> , 2017, 49, 1120-1125.	21.4	130
44	Tractor uses local ancestry to enable the inclusion of admixed individuals in GWAS and to boost power. <i>Nature Genetics</i> , 2021, 53, 195-204.	21.4	125
45	Genetic analyses identify widespread sex-differential participation bias. <i>Nature Genetics</i> , 2021, 53, 663-671.	21.4	124
46	Characterizing rare and low-frequency height-associated variants in the Japanese population. <i>Nature Communications</i> , 2019, 10, 4393.	12.8	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.	2.5	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.	21.4	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.	10.3	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.	3.5	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.	0.9	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.	12.8	113
53	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. <i>Nature Genetics</i> , 2022, 54, 450-458.	21.4	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.	2.9	106

#	ARTICLE	IF	CITATIONS
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.	2.9	105
56	Discovery of six new susceptibility loci and analysis of pleiotropic effects in leprosy. <i>Nature Genetics</i> , 2015, 47, 267-271.	21.4	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.	0.9	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.	0.9	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.	1.3	90
60	Polygenic burden in focal and generalized epilepsies. <i>Brain</i> , 2019, 142, 3473-3481.	7.6	90
61	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285.	12.8	89
62	The current landscape of psoriasis genetics in 2020. <i>Journal of Dermatological Science</i> , 2020, 99, 2-8.	1.9	86
63	Variation at HLA-DRB1 is associated with resistance to enteric fever. <i>Nature Genetics</i> , 2014, 46, 1333-1336.	21.4	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.	10.7	84
65	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	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.	2.9	82
67	The HLA-DR $\beta$ 1 amino acid positions 11-13-26 explain the majority of SLE-MHC associations. <i>Nature Communications</i> , 2014, 5, 5902.	12.8	80
68	Predicting HLA alleles from high-resolution SNP data in three Southeast Asian populations. <i>Human Molecular Genetics</i> , 2014, 23, 4443-4451.	2.9	80
69	CWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. <i>Nature Human Behaviour</i> , 2020, 4, 308-316.	12.0	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.	2.3	75
71	Genetic and phenotypic landscape of the major histocompatibility complex region in the Japanese population. <i>Nature Genetics</i> , 2019, 51, 470-480.	21.4	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.	30.7	74

#	ARTICLE	IF	CITATIONS
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.	0.9	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.	14.3	73
75	Identification of Nine Novel Loci Associated with White Blood Cell Subtypes in a Japanese Population. <i>PLoS Genetics</i> , 2011, 7, e1002067.	3.5	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.	21.4	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.	6.2	68
78	Population-specific causal disease effect sizes in functionally important regions impacted by selection. <i>Nature Communications</i> , 2021, 12, 1098.	12.8	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.	6.2	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.	4.4	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.	1.9	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.	0.6	61
83	Trans-ethnic meta-analysis of white blood cell phenotypes. <i>Human Molecular Genetics</i> , 2014, 23, 6944-6960.	2.9	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.	5.6	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.	12.8	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.	12.0	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.	1.9	53
88	Common variations in PSMD3-CSF3 and PLCB4 are associated with neutrophil count. <i>Human Molecular Genetics</i> , 2010, 19, 2079-2085.	2.9	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.	12.8	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.	6.2	49

#	ARTICLE	IF	CITATIONS
91	Empirical evaluation of variant calling accuracy using ultra-deep whole-genome sequencing data. <i>Scientific Reports</i> , 2019, 9, 1784.	3.3	46
92	Genetics of rheumatoid arthritis in Asia—present and future. <i>Nature Reviews Rheumatology</i> , 2015, 11, 375-379.	8.0	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.	2.5	45
94	Significant impact of miRNA—target gene networks on genetics of human complex traits. <i>Scientific Reports</i> , 2016, 6, 22223.	3.3	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.	12.8	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.	12.8	44
97	Genetic studies of rheumatoid arthritis. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 2015, 91, 410-422.	3.8	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.	2.9	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.	0.7	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.	14.5	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.	1.9	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.	0.9	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.	0.9	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.	0.9	36
105	GREP: genome for REPositioning drugs. <i>Bioinformatics</i> , 2019, 35, 3821-3823.	4.1	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.	2.5	34
107	Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. <i>Nature Communications</i> , 2020, 11, 3175.	12.8	34
108	Genome-wide risk prediction of common diseases across ancestries in one million people. <i>Cell Genomics</i> , 2022, 2, 100118.	6.5	34

#	ARTICLE	IF	CITATIONS
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.	2.8	32
110	GWAS of five gynecologic diseases and cross-trait analysis in Japanese. <i>European Journal of Human Genetics</i> , 2020, 28, 95-107.	2.8	32
111	Genetic and phenotypic landscape of the mitochondrial genome in the Japanese population. <i>Communications Biology</i> , 2020, 3, 104.	4.4	32
112	Common genetic factors for hematological traits in Humans. <i>Journal of Human Genetics</i> , 2012, 57, 161-169.	2.3	31
113	High-throughput identification of noncoding functional SNPs via type IIS enzyme restriction. <i>Nature Genetics</i> , 2018, 50, 1180-1188.	21.4	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.	0.9	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.	2.5	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.	0.7	28
117	The Rheumatoid Arthritis Risk Variant CCR6DNP Regulates CCR6 via PARP-1. <i>PLoS Genetics</i> , 2016, 12, e1006292.	3.5	28
118	Statistical genetics and polygenic risk score for precision medicine. <i>Inflammation and Regeneration</i> , 2021, 41, 18.	3.7	27
119	Dysbiosis of Gut Microbiome Is Associated With Rupture of Cerebral Aneurysms. <i>Stroke</i> , 2022, 53, 895-903.	2.0	27
120	Age-associated decline of MondoA drives cellular senescence through impaired autophagy and mitochondrial homeostasis. <i>Cell Reports</i> , 2022, 38, 110444.	6.4	27
121	Polygenic risk scores for prediction of breast cancer risk in Asian populations. <i>Genetics in Medicine</i> , 2022, 24, 586-600.	2.4	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.	3.9	26
123	Genetic determinants of risk in autoimmune pulmonary alveolar proteinosis. <i>Nature Communications</i> , 2021, 12, 1032.	12.8	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.	5.6	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.	2.9	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.	0.9	24



#	ARTICLE	IF	CITATIONS
127	HLA-DQ and RBFOX1 as susceptibility genes for an outbreak of hydrolyzed wheat allergy. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 1354-1363.	2.9	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.	0.9	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.	3.3	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.	3.5	23
131	Advances in genetics toward identifying pathogenic cell states of rheumatoid arthritis. <i>Immunological Reviews</i> , 2020, 294, 188-204.	6.0	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.	7.2	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.	3.9	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.	8.9	22
135	COX6A2 variants cause a muscle-specific cytochrome c oxidase deficiency. <i>Annals of Neurology</i> , 2019, 86, 193-202.	5.3	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.	0.9	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.	0.9	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.	0.9	19
140	Amino acid position 37 of HLA-DR <sup>2</sup> 1 affects susceptibility to Crohn's disease in Asians. <i>Human Molecular Genetics</i> , 2018, 27, 3901-3910.	2.9	19
141	Do Genetic Susceptibility Variants Associate with Disease Severity in Early Active Rheumatoid Arthritis?. <i>Journal of Rheumatology</i> , 2015, 42, 1131-1140.	2.0	18
142	eLD: entropy-based linkage disequilibrium index between multiallelic sites. <i>Human Genome Variation</i> , 2018, 5, 29.	0.7	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.	6.2	18
144	Integration of genetically regulated gene expression and pharmacological library provides therapeutic drug candidates. <i>Human Molecular Genetics</i> , 2021, 30, 294-304.	2.9	17

#	ARTICLE	IF	CITATIONS
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.	11.6	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.	1.9	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.	2.8	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.	6.1	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.	3.9	14
150	HLA imputation and its application to genetic and molecular fine-mapping of the MHC region in autoimmune diseases. <i>Seminars in Immunopathology</i> , 2022, 44, 15-28.	6.1	14
151	Genetic architecture of microRNA expression and its link to complex diseases in the Japanese population. <i>Human Molecular Genetics</i> , 2022, 31, 1806-1820.	2.9	14
152	Mechanistic Characterization of RASGRP1 Variants Identifies an hnRNP-K-Regulated Transcriptional Enhancer Contributing to SLE Susceptibility. <i>Frontiers in Immunology</i> , 2019, 10, 1066.	4.8	13
153	SLC22A4 polymorphism and rheumatoid arthritis susceptibility: a replication study in a Japanese population and a metaanalysis. <i>Journal of Rheumatology</i> , 2008, 35, 1723-8.	2.0	13
154	Transcriptome network analyses in human coronavirus infections suggest a rational use of immunomodulatory drugs for COVID-19 therapy. <i>Genomics</i> , 2021, 113, 564-575.	2.9	12
155	Multi-phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. <i>Journal of Thrombosis and Haemostasis</i> , 2022, 20, 1331-1349.	3.8	12
156	Lysophosphatidylserines derived from microbiota in Crohn's disease elicit pathological Th1 response. <i>Journal of Experimental Medicine</i> , 2022, 219, .	8.5	12
157	Combination of mouse models and genomewide association studies highlights novel genes associated with human kidney function. <i>Kidney International</i> , 2016, 90, 764-773.	5.2	11
158	Grimon: graphical interface to visualize multi-omics networks. <i>Bioinformatics</i> , 2018, 34, 3934-3936.	4.1	11
159	Increased levels of plasma nucleotides in patients with rheumatoid arthritis. <i>International Immunology</i> , 2021, 33, 119-124.	4.0	11
160	Lupus Susceptibility Region Containing <i>CDKN1B</i> rs34330 Mechanistically Influences Expression and Function of Multiple Target Genes, Also Linked to Proliferation and Apoptosis. <i>Arthritis and Rheumatology</i> , 2021, 73, 2303-2313.	5.6	11
161	rs2841277 ( <i>PLD4</i> ) is associated with susceptibility and rs4672495 is associated with disease activity in rheumatoid arthritis. <i>Oncotarget</i> , 2017, 8, 64180-64190.	1.8	11
162	Genomics-driven drug discovery based on disease-susceptibility genes. <i>Inflammation and Regeneration</i> , 2021, 41, 8.	3.7	10

#	ARTICLE	IF	CITATIONS
163	Transcriptome profiling of refractory atopic keratoconjunctivitis by RNA sequencing. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 1610-1614.e6.	2.9	9
164	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.	0.9	9
165	Anti-dsDNA antibodies recognize DNA presented on HLA class II molecules of systemic lupus erythematosus risk alleles. <i>Arthritis and Rheumatology</i> , 2021, , .	5.6	8
166	piRNA/PIWI Protein Complex as a Potential Biomarker in Sporadic Amyotrophic Lateral Sclerosis. <i>Molecular Neurobiology</i> , 2022, 59, 1693-1705.	4.0	8
167	A common variant of MAF/c-MAF, transcriptional factor gene in the kidney, is associated with gout susceptibility. <i>Human Cell</i> , 2018, 31, 10-13.	2.7	7
168	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.	5.9	7
169	Coffee Consumption Reduces Gout Risk Independently of Serum Uric Acid Levels: Mendelian Randomization Analyses Across Ancestry Populations. <i>ACR Open Rheumatology</i> , 2022, 4, 534-539.	2.1	7
170	Editorial: Entering the Age of Whole-Exome Sequencing in Rheumatic Diseases: Novel Insights Into Disease Pathogenicity. <i>Arthritis and Rheumatism</i> , 2013, 65, 1975-1979.	6.7	6
171	Future Directions of Genomics Research in Rheumatic Diseases. <i>Rheumatic Disease Clinics of North America</i> , 2017, 43, 481-487.	1.9	6
172	Response to: "Can sexual dimorphism in rheumatoid arthritis be attributed to the different abundance of <i>Gardnerella</i> ?" by Liu et al. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, e37-e37.	0.9	6
173	Decoding the diversity of killer immunoglobulin-like receptors by deep sequencing and a high-resolution imputation method. <i>Cell Genomics</i> , 2022, 2, 100101.	6.5	6
174	Structural basis of ethnic-specific variants of PAX4 associated with type 2 diabetes. <i>Human Genome Variation</i> , 2021, 8, 25.	0.7	5
175	Genome-Wide Association Study of Intracranial Artery Stenosis Followed by Phenome-Wide Association Study. <i>Translational Stroke Research</i> , 2023, 14, 322-333.	4.2	5
176	Ethnically shared and heterogeneous impacts of molecular pathways suggested by the genome-wide meta-analysis of rheumatoid arthritis: Table 1. <i>Rheumatology</i> , 2016, 55, 186-189.	1.9	4
177	Genetic landscape of interactive effects of <i>HLA-DRB1</i> alleles on susceptibility to ACPA(+) rheumatoid arthritis and ACPA levels in Japanese population. <i>Journal of Medical Genetics</i> , 2017, 54, 853-858.	3.2	3
178	Statistical genetics and its application to neuroimmunology. <i>Clinical and Experimental Neuroimmunology</i> , 2018, 9, 7-12.	1.0	3
179	Response to: "Comment on "Metagenome-wide association study of gut microbiome revealed novel aetiology of rheumatoid arthritis in the Japanese population" by Kishikawa et al." by Kitamura et al. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, e72-e72.	0.9	3
180	Two decades after Human Genome Project: do large-genetic studies lead to path of the genomic medicine of complex diseases?. <i>Journal of Human Genetics</i> , 2021, 66, 1-1.	2.3	3

#	ARTICLE	IF	CITATIONS
181	OMARU: a robust and multifaceted pipeline for metagenome-wide association study. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac019.	3.2	3
182	Human genetics contributes to the understanding of disease pathophysiology and drug discovery. <i>Journal of Orthopaedic Science</i> , 2017, 22, 977-981.	1.1	2
183	Elucidation of disease etiology by trans-layer omics analysis. <i>Inflammation and Regeneration</i> , 2021, 41, 6.	3.7	2
184	An X chromosome-wide meta-analysis based on Japanese cohorts revealed that non-autosomal variations are associated with serum urate. <i>Rheumatology</i> , 2021, 60, 4430-4432.	1.9	2
185	Determining the immune environment of cutaneous T-cell lymphoma lesions through the assessment of lesional blood drops. <i>Scientific Reports</i> , 2021, 11, 19629.	3.3	2
186	Trans-Ethnic Mendelian Randomization Study Reveals Causal Relationships Between Cardiometabolic Factors and Chronic Kidney Disease. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
187	Genotype-Structure-Phenotype Correlations of Disease-Associated IGF1R Variants and Similarities to Those of INSR Variants. <i>Diabetes</i> , 2021, 70, 1874-1884.	0.6	1
188	A massive effort links protein-coding gene variants to health. <i>Nature</i> , 2021, 599, 561-563.	27.8	1
189	Novel susceptibility loci for steroid-associated osteonecrosis of the femoral head in systemic lupus erythematosus. <i>Human Molecular Genetics</i> , 2022, 31, 1082-1095.	2.9	1
190	Obelisc: an identical-by-descent mapping tool based on SNP streak. <i>Bioinformatics</i> , 2021, 36, 5567-5570.	4.1	1
191	A meta-analysis of genome-wide association studies using Japanese and Taiwanese has revealed novel loci associated with gout susceptibility. <i>Human Cell</i> , 2022, 35, 767.	2.7	1
192	OP0048â€¦GENOME-WIDE META-ANALYSIS REVEALED MULTIPLE NOVEL LOCI ASSOCIATED WITH SERUM URIC ACIDLEVELS IN JAPANESE. , 2019, , .		0
193	OP0047â€¦A GENOME-WIDE ASSOCIATION STUDY IDENTIFIED NOVEL LOCI ASSOCIATED WITH THE PROGRESSION FROM ASYMPTOMATIC HYPERURICEMIA TO GOUT. , 2019, , .		0
194	Genetics and functional genetics of autoimmune diseases. <i>Seminars in Immunopathology</i> , 2022, 44, 1-2.	6.1	0
195	of <i>Internal Medicine</i> , 2021, 110, 400-406.	0.0	0
196	An evolving hypothesis in autoimmune disease genetics. <i>Nature Reviews Genetics</i> , 2022, , .	16.3	0