Yukinori Okada

List of Publications by Year
in descending order

196 papers	28,788 citations	14614 66 h-index	8138 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. Nature, 2015, 518, 197-206.	13.7	3,823
2	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	9.4	2,045
3	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	13.7	1,974
4	Clinical use of current polygenic risk scores may exacerbate health disparities. Nature Genetics, 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. Nature Genetics, 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. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
7	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	9.4	675
8	Genetic analysis of quantitative traits in the Japanese population links cell types to complex human diseases. Nature Genetics, 2018, 50, 390-400.	9.4	613
9	A cross-population atlas of genetic associations for 220 human phenotypes. Nature Genetics, 2021, 53, 1415-1424.	9.4	560
10	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
11	Genome-wide association studies. Nature Reviews Methods Primers, 2021, 1, .	11.8	529
12	Polarization of the Effects of Autoimmune and Neurodegenerative Risk Alleles in Leukocytes. Science, 2014, 344, 519-523.	6.0	480
13	Genome-wide association study of hematological and biochemical traits in a Japanese population. Nature Genetics, 2010, 42, 210-215.	9.4	460
14	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 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. Nature Genetics, 2017, 49, 1458-1467.	9.4	380
16	Meta-analysis identifies common variants associated with body mass index in east Asians. Nature Genetics, 2012, 44, 307-311.	9.4	372
17	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	13.5	353
18	The power of genetic diversity in genome-wide association studies of lipids. Nature, 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. Nature Genetics, 2020, 52, 669-679.	9.4	304
20	Meta-analysis identifies nine new loci associated with rheumatoid arthritis in the Japanese population. Nature Genetics, 2012, 44, 511-516.	9.4	285
21	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	13.7	282
22	Meta-analysis identifies multiple loci associated with kidney function–related traits in east Asian populations. Nature Genetics, 2012, 44, 904-909.	9.4	254
23	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 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. Nature Genetics, 2022, 54, 560-572.	9.4	250
25	Common variants at CDKAL1 and KLF9 are associated with body mass index in east Asian populations. Nature Genetics, 2012, 44, 302-306.	9.4	240
26	A Role for Noncoding Variation in Schizophrenia. Cell Reports, 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. Nature Genetics, 2016, 48, 323-330.	9.4	219
28	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. Nature Medicine, 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. Human Molecular Genetics, 2014, 23, 5492-5504.	1.4	192
30	Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. Nature Communications, 2019, 10, 2773.	5.8	183
31	Fine Mapping Major Histocompatibility Complex Associations in Psoriasis and Its Clinical Subtypes. American Journal of Human Genetics, 2014, 95, 162-172.	2.6	182
32	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	5.8	181
33	Directional dominance on stature and cognition in diverse human populations. Nature, 2015, 523, 459-462.	13.7	173
34	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. Nature Genetics, 2015, 47, 1085-1090.	9.4	164
35	Identification of 28 new susceptibility loci for type 2 diabetes in the Japanese population. Nature Genetics, 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. American Journal of Human Genetics, 2014, 94, 522-532.	2.6	156

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37	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. Nature Communications, 2016, 7, 10531.	5.8	149
38	Metagenome-wide association study of gut microbiome revealed novel aetiology of rheumatoid arthritis in the Japanese population. Annals of the Rheumatic Diseases, 2020, 79, 103-111.	0.5	145
39	Genetics of rheumatoid arthritis: 2018 status. Annals of the Rheumatic Diseases, 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. Human Molecular Genetics, 2014, 23, 6916-6926.	1.4	135
41	Deep whole-genome sequencing reveals recent selection signatures linked to evolution and disease risk of Japanese. Nature Communications, 2018, 9, 1631.	5.8	132
42	Suppression of autophagic activity by Rubicon is a signature of aging. Nature Communications, 2019, 10, 847.	5.8	132
43	Polygenic burdens on cell-specific pathways underlie the risk of rheumatoid arthritis. Nature Genetics, 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. Nature Genetics, 2021, 53, 195-204.	9.4	125
45	Genetic analyses identify widespread sex-differential participation bias. Nature Genetics, 2021, 53, 663-671.	9.4	124
46	Characterizing rare and low-frequency height-associated variants in the Japanese population. Nature Communications, 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. PLoS ONE, 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. Nature Genetics, 2015, 47, 798-802.	9.4	119
49	LC3 lipidation is essential for TFEB activation during the lysosomal damage response to kidney injury. Nature Cell Biology, 2020, 22, 1252-1263.	4.6	117
50	A Genome-Wide Association Study Identified AFF1 as a Susceptibility Locus for Systemic Lupus Eyrthematosus in Japanese. PLoS Genetics, 2012, 8, e1002455.	1.5	115
51	GWAS of clinically defined gout and subtypes identifies multiple susceptibility loci that include urate transporter genes. Annals of the Rheumatic Diseases, 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. Nature Communications, 2019, 10, 29.	5.8	113
53	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 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. Human Molecular Genetics, 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. Human Molecular Genetics, 2015, 24, 1791-1800.	1.4	105
56	Discovery of six new susceptibility loci and analysis of pleiotropic effects in leprosy. Nature Genetics, 2015, 47, 267-271.	9.4	103
57	Meta-analysis of 208370 East Asians identifies 113 susceptibility loci for systemic lupus erythematosus. Annals of the Rheumatic Diseases, 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. Annals of the Rheumatic Diseases, 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. Gastroenterology, 2011, 141, 864-871.e5.	0.6	90
60	Polygenic burden in focal and generalized epilepsies. Brain, 2019, 142, 3473-3481.	3.7	90
61	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	5.8	89
62	The current landscape of psoriasis genetics in 2020. Journal of Dermatological Science, 2020, 99, 2-8.	1.0	86
63	Variation at HLA-DRB1 is associated with resistance to enteric fever. Nature Genetics, 2014, 46, 1333-1336.	9.4	85
64	Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study. Lancet Oncology, The, 2016, 17, 1240-1247.	5.1	84
65	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
66	Genome-wide association study for C-reactive protein levels identified pleiotropic associations in the IL6 locus. Human Molecular Genetics, 2011, 20, 1224-1231.	1.4	82
67	The HLA-DRβ1 amino acid positions 11â€"13â€"26 explain the majority of SLEâ€"MHC associations. Nature Communications, 2014, 5, 5902.	5.8	80
68	Predicting HLA alleles from high-resolution SNP data in three Southeast Asian populations. Human Molecular Genetics, 2014, 23, 4443-4451.	1.4	80
69	GWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. Nature Human Behaviour, 2020, 4, 308-316.	6.2	80
70	Empirical estimation of genome-wide significance thresholds based on the 1000 Genomes Project data set. Journal of Human Genetics, 2016, 61, 861-866.	1.1	75
71	Genetic and phenotypic landscape of the major histocompatibilty complex region in the Japanese population. Nature Genetics, 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. Nature Medicine, 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. Annals of the Rheumatic Diseases, 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. Immunity, 2020, 52, 1119-1132.e4.	6.6	73
75	Identification of Nine Novel Loci Associated with White Blood Cell Subtypes in a Japanese Population. PLoS Genetics, 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. Nature Genetics, 2021, 53, 1504-1516.	9.4	69
77	Contribution of a Non-classical HLA Gene, HLA-DOA, to the Risk of Rheumatoid Arthritis. American Journal of Human Genetics, 2016, 99, 366-374.	2.6	68
78	Population-specific causal disease effect sizes in functionally important regions impacted by selection. Nature Communications, 2021, 12, 1098.	5.8	68
79	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 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. Communications Biology, 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. Rheumatology, 2013, 52, 1172-1182.	0.9	62
82	Multiple Nonglycemic Genomic Loci Are Newly Associated With Blood Level of Glycated Hemoglobin in East Asians. Diabetes, 2014, 63, 2551-2562.	0.3	61
83	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 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. Arthritis and Rheumatology, 2015, 67, 2611-2623.	2.9	58
85	Dimensionality reduction reveals fine-scale structure in the Japanese population with consequences for polygenic risk prediction. Nature Communications, 2020, 11, 1569.	5.8	58
86	GWAS of smoking behaviour in 165,436 Japanese people reveals seven new loci and shared genetic architecture. Nature Human Behaviour, 2019, 3, 471-477.	6.2	54
87	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. International Journal of Epidemiology, 2015, 44, 1706-1721.	0.9	53
88	Common variations in PSMD3–CSF3 and PLCB4 are associated with neutrophil count. Human Molecular Genetics, 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. Nature Communications, 2016, 7, 12451.	5.8	49
90	IMPACT: Genomic Annotation of Cell-State-Specific Regulatory Elements Inferred from the Epigenome of Bound Transcription Factors. American Journal of Human Genetics, 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. Scientific Reports, 2019, 9, 1784.	1.6	46
92	Genetics of rheumatoid arthritis in Asia—present and future. Nature Reviews Rheumatology, 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. PLoS ONE, 2012, 7, e44507.	1.1	45
94	Significant impact of miRNA–target gene networks on genetics of human complex traits. Scientific Reports, 2016, 6, 22223.	1.6	44
95	A deep learning method for HLA imputation and trans-ethnic MHC fine-mapping of type 1 diabetes. Nature Communications, 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. Nature Communications, 2021, 12, 3394.	5.8	44
97	Genetic studies of rheumatoid arthritis. Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 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. Human Molecular Genetics, 2020, 29, 923-943.	1.4	40
99	Variants at HLA-A, HLA-C, and HLA-DQB1 Confer Risk of Psoriasis Vulgaris in Japanese. Journal of Investigative Dermatology, 2018, 138, 542-548.	0.3	39
100	Integration of genetics and miRNA–target gene network identified disease biology implicated in tissue specificity. Nucleic Acids Research, 2018, 46, 11898-11909.	6.5	39
101	Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. International Journal of Epidemiology, 2022, 50, 1995-2010.	0.9	39
102	Whole gut virome analysis of 476 Japanese revealed a link between phage and autoimmune disease. Annals of the Rheumatic Diseases, 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. Annals of the Rheumatic Diseases, 2021, 80, 1575-1583.	0.5	38
104	PLD4 is a genetic determinant to systemic lupus erythematosus and involved in murine autoimmune phenotypes. Annals of the Rheumatic Diseases, 2019, 78, 509-518.	0.5	36
105	GREP: genome for REPositioning drugs. Bioinformatics, 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. PLoS ONE, 2014, 9, e87645.	1.1	34
107	Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. Nature Communications, 2020, 11, 3175.	5.8	34
108	Genome-wide risk prediction of common diseases across ancestries in one million people. Cell Genomics, 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. European Journal of Human Genetics, 2019, 27, 1745-1756.	1.4	32
110	GWAS of five gynecologic diseases and cross-trait analysis in Japanese. European Journal of Human Genetics, 2020, 28, 95-107.	1.4	32
111	Genetic and phenotypic landscape of the mitochondrial genome in the Japanese population. Communications Biology, 2020, 3, 104.	2.0	32
112	Common genetic factors for hematological traits in Humans. Journal of Human Genetics, 2012, 57, 161-169.	1.1	31
113	High-throughput identification of noncoding functional SNPs via type IIS enzyme restriction. Nature Genetics, 2018, 50, 1180-1188.	9.4	31
114	HLA-DRB1*0901 lowers anti-cyclic citrullinated peptide antibody levels in Japanese patients with rheumatoid arthritis. Annals of the Rheumatic Diseases, 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. JAMA Ophthalmology, 2017, 135, 355.	1.4	29
116	A Transethnic Mendelian Randomization Study Identifies Causality of Obesity on Risk of Psoriasis. Journal of Investigative Dermatology, 2019, 139, 1397-1400.	0.3	28
117	The Rheumatoid Arthritis Risk Variant CCR6DNP Regulates CCR6 via PARP-1. PLoS Genetics, 2016, 12, e1006292.	1.5	28
118	Statistical genetics and polygenic risk score for precision medicine. Inflammation and Regeneration, 2021, 41, 18.	1.5	27
119	Dysbiosis of Gut Microbiome Is Associated With Rupture of Cerebral Aneurysms. Stroke, 2022, 53, 895-903.	1.0	27
120	Age-associated decline of MondoA drives cellular senescence through impaired autophagy and mitochondrial homeostasis. Cell Reports, 2022, 38, 110444.	2.9	27
121	Polygenic risk scores for prediction of breast cancer risk in Asian populations. Genetics in Medicine, 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. Frontiers in Cellular and Infection Microbiology, 2020, 10, 585973.	1.8	26
123	Genetic determinants of risk in autoimmune pulmonary alveolar proteinosis. Nature Communications, 2021, 12, 1032.	5.8	26
124	A Multinational Arab Genome–Wide Association Study Identifies New Genetic Associations for Rheumatoid Arthritis. Arthritis and Rheumatology, 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. Human Molecular Genetics, 2018, 27, 3974-3985.	1.4	25
126	Identification of secreted phosphoprotein 1 gene as a new rheumatoid arthritis susceptibility gene. Annals of the Rheumatic Diseases, 2015, 74, e19-e19.	0.5	24

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127	HLA-DQ and RBFOX1 as susceptibility genes for an outbreak of hydrolyzed wheat allergy. Journal of Allergy and Clinical Immunology, 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. Annals of the Rheumatic Diseases, 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. International Journal of Infectious Diseases, 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. Arthritis Research and Therapy, 2015, 17, 104.	1.6	23
131	Advances in genetics toward identifying pathogenic cell states of rheumatoid arthritis. Immunological Reviews, 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. Journal of Neuroinflammation, 2019, 16, 162.	3.1	22
133	A Mendelian randomization study identified obesity as a causal risk factor of uterine endometrial cancer in Japanese. Cancer Science, 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. Molecular Biology and Evolution, 2020, 37, 1306-1316.	3.5	22
135	COX6A2 variants cause a muscle–specific cytochrome c oxidase deficiency. Annals of Neurology, 2019, 86, 193-202.	2.8	21
136	Association of the <i>RPA3-UMAD1</i> locus with interstitial lung diseases complicated with rheumatoid arthritis in Japanese. Annals of the Rheumatic Diseases, 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. Annals of the Rheumatic Diseases, 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. Arthritis and Rheumatism, 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. Annals of the Rheumatic Diseases, 2016, 75, 317-320.	0.5	19
140	Amino acid position 37 of HLA-DRβ1 affects susceptibility to Crohn's disease in Asians. Human Molecular Genetics, 2018, 27, 3901-3910.	1.4	19
141	Do Genetic Susceptibility Variants Associate with Disease Severity in Early Active Rheumatoid Arthritis?. Journal of Rheumatology, 2015, 42, 1131-1140.	1.0	18
142	eLD: entropy-based linkage disequilibrium index between multiallelic sites. Human Genome Variation, 2018, 5, 29.	0.4	18
143	Evidence of Polygenic Adaptation in Sardinia at Height-Associated Loci Ascertained from the Biobank Japan. American Journal of Human Genetics, 2020, 107, 60-71.	2.6	18
144	Integration of genetically regulated gene expression and pharmacological library provides therapeutic drug candidates. Human Molecular Genetics, 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. Nature Aging, 2022, 2, 19-30.	5.3	17
146	Large-scale plasma-metabolome analysis identifies potential biomarkers of psoriasis and its clinical subtypes. Journal of Dermatological Science, 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. European Journal of Human Genetics, 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. EBioMedicine, 2021, 63, 103157.	2.7	14
149	Trans‐Ethnic Fine‐Mapping of the Major Histocompatibility Complex Region Linked to Parkinson's Disease. Movement Disorders, 2021, 36, 1805-1814.	2.2	14
150	HLA imputation and its application to genetic and molecular fine-mapping of the MHC region in autoimmune diseases. Seminars in Immunopathology, 2022, 44, 15-28.	2.8	14
151	Genetic architecture of microRNA expression and its link to complex diseases in the Japanese population. Human Molecular Genetics, 2022, 31, 1806-1820.	1.4	14
152	Mechanistic Characterization of RASGRP1 Variants Identifies an hnRNP-K-Regulated Transcriptional Enhancer Contributing to SLE Susceptibility. Frontiers in Immunology, 2019, 10, 1066.	2.2	13
153	SLC22A4 polymorphism and rheumatoid arthritis susceptibility: a replication study in a Japanese population and a metaanalysis. Journal of Rheumatology, 2008, 35, 1723-8.	1.0	13
154	Transcriptome network analyses in human coronavirus infections suggest a rational use of immunomodulatory drugs for COVID-19 therapy. Genomics, 2021, 113, 564-575.	1.3	12
155	Multi‐phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. Journal of Thrombosis and Haemostasis, 2022, 20, 1331-1349.	1.9	12
156	Lysophosphatidylserines derived from microbiota in Crohn's disease elicit pathological Th1 response. Journal of Experimental Medicine, 2022, 219, .	4.2	12
157	Combination of mouse models and genomewide association studies highlights novel genes associated with human kidney function. Kidney International, 2016, 90, 764-773.	2.6	11
158	Grimon: graphical interface to visualize multi-omics networks. Bioinformatics, 2018, 34, 3934-3936.	1.8	11
159	Increased levels of plasma nucleotides in patients with rheumatoid arthritis. International Immunology, 2021, 33, 119-124.	1.8	11
160	Lupus Susceptibility Region Containing *CDKN1B* rs34330 Mechanistically Influences Expression and Function of Multiple Target Genes, Also Linked to Proliferation and Apoptosis. Arthritis and Rheumatology, 2021, 73, 2303-2313.	2.9	11
161	rs2841277 (*PLD4*) is associated with susceptibility and rs4672495 is associated with disease activity in rheumatoid arthritis. Oncotarget, 2017, 8, 64180-64190.	0.8	11
162	Genomics-driven drug discovery based on disease-susceptibility genes. Inflammation and Regeneration, 2021, 41, 8.	1.5	10

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163	Transcriptome profiling of refractory atopic keratoconjunctivitis by RNA sequencing. Journal of Allergy and Clinical Immunology, 2019, 143, 1610-1614.e6.	1.5	9
164	Biological insights into systemic lupus erythematosus through an immune cell-specific transcriptome-wide association study. Annals of the Rheumatic Diseases, 2022, 81, 1273-1280.	0.5	9
165	Antiâ€dsDNA antibodies recognize DNA presented on HLA class II molecules of systemic lupus erythematosus risk alleles. Arthritis and Rheumatology, 2021, , .	2.9	8
166	piRNA/PIWI Protein Complex as a Potential Biomarker in Sporadic Amyotrophic Lateral Sclerosis. Molecular Neurobiology, 2022, 59, 1693-1705.	1.9	8
167	A common variant of MAF/c-MAF, transcriptional factor gene in the kidney, is associated with gout susceptibility. Human Cell, 2018, 31, 10-13.	1.2	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. JAMA Network Open, 2020, 3, e2023248.	2.8	7
169	Coffee Consumption Reduces Gout Risk Independently of Serum Uric Acid Levels: Mendelian Randomization Analyses Across Ancestry Populations. ACR Open Rheumatology, 2022, 4, 534-539.	0.9	7
170	Editorial: Entering the Age of Wholeâ€Exome Sequencing in Rheumatic Diseases: Novel Insights Into Disease Pathogenicity. Arthritis and Rheumatism, 2013, 65, 1975-1979.	6.7	6
171	Future Directions of Genomics Research in Rheumatic Diseases. Rheumatic Disease Clinics of North America, 2017, 43, 481-487.	0.8	6
172	Response to: â€˜Can sexual dimorphism in rheumatoid arthritis be attributed to the different abundance of<i>Gardnerella</i>?â€™ by Liu<i>et al</i>. Annals of the Rheumatic Diseases, 2022, 81, e37-e37.	0.5	6
173	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
174	Structural basis of ethnic-specific variants of PAX4 associated with type 2 diabetes. Human Genome Variation, 2021, 8, 25.	0.4	5
175	Genome-Wide Association Study of Intracranial Artery Stenosis Followed by Phenome-Wide Association Study. Translational Stroke Research, 2023, 14, 322-333.	2.3	5
176	Ethnically shared and heterogeneous impacts of molecular pathways suggested by the genome-wide meta-analysis of rheumatoid arthritis: Table 1. Rheumatology, 2016, 55, 186-189.	0.9	4
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