Yukinori Okada

List of Publications by Year
in descending order

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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	Genome-Wide Association Study of Intracranial Artery Stenosis Followed by Phenome-Wide Association Study. Translational Stroke Research, 2023, 14, 322-333.	2.3	5
2	Response to: â€˜Can sexual dimorphism in rheumatoid arthritis be attributed to the different abundance ofGardnerella?â€™ by Liuet al. Annals of the Rheumatic Diseases, 2022, 81, e37-e37.	0.5	6
3	Response to: â€˜Comment on â€˜Metagenome-wide association study of gut microbiome revealed novel aetiology of rheumatoid arthritis in the Japanese populationâ€™ by Kishikawaet al.â€™ by Kitamuraet al. Annals of the Rheumatic Diseases, 2022, 81, e72-e72.	0.5	3
4	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
5	Novel susceptibility loci for steroid-associated osteonecrosis of the femoral head in systemic lupus erythematosus. Human Molecular Genetics, 2022, 31, 1082-1095.	1.4	1
6	Dysbiosis of Gut Microbiome Is Associated With Rupture of Cerebral Aneurysms. Stroke, 2022, 53, 895-903.	1.0	27
7	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
8	piRNA/PIWI Protein Complex as a Potential Biomarker in Sporadic Amyotrophic Lateral Sclerosis. Molecular Neurobiology, 2022, 59, 1693-1705.	1.9	8
9	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
10	A meta-analysis of genome-wide association studies using Japanese and Taiwanese has revealed novel loci associated with gout susceptibility. Human Cell, 2022, 35, 767.	1.2	1
11	Genetics and functional genetics of autoimmune diseases. Seminars in Immunopathology, 2022, 44, 1-2.	2.8	0
12	OMARU: a robust and multifaceted pipeline for metagenome-wide association study. NAR Genomics and Bioinformatics, 2022, 4, lqac019.	1.5	3
13	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
14	Multiâ€phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. Journal of Thrombosis and Haemostasis, 2022, 20, 1331-1349.	1.9	12
15	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
16	Age-associated decline of MondoA drives cellular senescence through impaired autophagy and mitochondrial homeostasis. Cell Reports, 2022, 38, 110444.	2.9	27
17	An evolving hypothesis in autoimmune disease genetics. Nature Reviews Genetics, 2022, , .	7.7	0
18	Polygenic risk scores for prediction of breast cancer risk in Asian populations. Genetics in Medicine, 2022, 24, 586-600.	1.1	27

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19	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 2022, 54, 450-458.	9.4	109
20	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
21	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
22	Genome-wide risk prediction of common diseases across ancestries in one million people. Cell Genomics, 2022, 2, 100118.	3.0	34
23	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
24	Lysophosphatidylserines derived from microbiota in Crohnâ€™s disease elicit pathological Th1 response. Journal of Experimental Medicine, 2022, 219, .	4.2	12
25	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
26	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
27	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
28	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
29	Increased levels of plasma nucleotides in patients with rheumatoid arthritis. International Immunology, 2021, 33, 119-124.	1.8	11
30	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
31	Population-specific causal disease effect sizes in functionally important regions impacted by selection. Nature Communications, 2021, 12, 1098.	5.8	68
32	Genetic determinants of risk in autoimmune pulmonary alveolar proteinosis. Nature Communications, 2021, 12, 1032.	5.8	26
33	Elucidation of disease etiology by trans-layer omics analysis. Inflammation and Regeneration, 2021, 41, 6.	1.5	2
34	Integration of genetically regulated gene expression and pharmacological library provides therapeutic drug candidates. Human Molecular Genetics, 2021, 30, 294-304.	1.4	17
35	Genomics-driven drug discovery based on disease-susceptibility genes. Inflammation and Regeneration, 2021, 41, 8.	1.5	10
36	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

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37	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
38	Genetic analyses identify widespread sex-differential participation bias. Nature Genetics, 2021, 53, 663-671.	9.4	124
39	Transâ€Ethnic Fineâ€Mapping of the Major Histocompatibility Complex Region Linked to Parkinson's Disease. Movement Disorders, 2021, 36, 1805-1814.	2.2	14
40	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
41	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
42	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
43	Genotype-Structure-Phenotype Correlations of Disease-Associated IGF1R Variants and Similarities to Those of INSR Variants. Diabetes, 2021, 70, 1874-1884.	0.3	1
44	Leveraging supervised learning for functionallyÂinformed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. Nature Communications, 2021, 12, 3394.	5.8	44
45	Statistical genetics and polygenic risk score for precision medicine. Inflammation and Regeneration, 2021, 41, 18.	1.5	27
46	Antiâ€dsDNA antibodies recognize DNA presented on HLA class II molecules of systemic lupus erythematosus risk alleles. Arthritis and Rheumatology, 2021, , .	2.9	8
47	Structural basis of ethnic-specific variants of PAX4 associated with type 2 diabetes. Human Genome Variation, 2021, 8, 25.	0.4	5
48	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
49	Genome-wide association studies. Nature Reviews Methods Primers, 2021, 1, .	11.8	529
50	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
51	A cross-population atlas of genetic associations for 220 human phenotypes. Nature Genetics, 2021, 53, 1415-1424.	9.4	560
52	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
53	Determining the immune environment of cutaneous T-cell lymphoma lesions through the assessment of lesional blood drops. Scientific Reports, 2021, 11, 19629.	1.6	2
54	A massive effort links protein-coding gene variants to health. Nature, 2021, 599, 561-563.	13.7	1

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55	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
56	Obelisc: an identical-by-descent mapping tool based on SNP streak. Bioinformatics, 2021, 36, 5567-5570.	1.8	1
57	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. Nature Medicine, 2021, 27, 1876-1884.	15.2	214
58	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
59	of Internal Medicine, 2021, 110, 400-406.	0.0	0
60	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
61	GWAS of five gynecologic diseases and cross-trait analysis in Japanese. European Journal of Human Genetics, 2020, 28, 95-107.	1.4	32
62	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
63	Advances in genetics toward identifying pathogenic cell states of rheumatoid arthritis. Immunological Reviews, 2020, 294, 188-204.	2.8	23
64	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
65	Association of the RPA3-UMAD1 locus with interstitial lung diseases complicated with rheumatoid arthritis in Japanese. Annals of the Rheumatic Diseases, 2020, 79, 1305-1309.	0.5	21
66	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
67	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
68	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
69	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	5.8	89
70	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
71	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	13.7	282
72	The current landscape of psoriasis genetics in 2020. Journal of Dermatological Science, 2020, 99, 2-8.	1.0	86

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73	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
74	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
75	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
76	Genetic and phenotypic landscape of the mitochondrial genome in the Japanese population. Communications Biology, 2020, 3, 104.	2.0	32
77	Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. Nature Communications, 2020, 11, 3175.	5.8	34
78	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
79	GWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. Nature Human Behaviour, 2020, 4, 308-316.	6.2	80
80	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
81	Dimensionality reduction reveals fine-scale structure in the Japanese population with consequences for polygenic risk prediction. Nature Communications, 2020, 11, 1569.	5.8	58
82	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
83	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
84	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
85	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
86	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
87	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
88	Polygenic burden in focal and generalized epilepsies. Brain, 2019, 142, 3473-3481.	3.7	90
89	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
90	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

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91	Characterizing rare and low-frequency height-associated variants in the Japanese population. Nature Communications, 2019, 10, 4393.	5.8	123
92	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
93	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
94	Genetic and phenotypic landscape of the major histocompatibilty complex region in the Japanese population. Nature Genetics, 2019, 51, 470-480.	9.4	75
95	Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. Nature Communications, 2019, 10, 2773.	5.8	183
96	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
97	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
98	COX6A2 variants cause a muscleâ€specific cytochrome c oxidase deficiency. Annals of Neurology, 2019, 86, 193-202.	2.8	21
99	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
100	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
101	A Transethnic Mendelian Randomization Study Identifies Causality of Obesity on Risk of Psoriasis. Journal of Investigative Dermatology, 2019, 139, 1397-1400.	0.3	28
102	GREP: genome for REPositioning drugs. Bioinformatics, 2019, 35, 3821-3823.	1.8	35
103	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
104	Clinical use of current polygenic risk scores may exacerbate health disparities. Nature Genetics, 2019, 51, 584-591.	9.4	1,664
105	Transcriptome profiling of refractory atopic keratoconjunctivitis by RNA sequencing. Journal of Allergy and Clinical Immunology, 2019, 143, 1610-1614.e6.	1.5	9
106	Suppression of autophagic activity by Rubicon is a signature of aging. Nature Communications, 2019, 10, 847.	5.8	132
107	Empirical evaluation of variant calling accuracy using ultra-deep whole-genome sequencing data. Scientific Reports, 2019, 9, 1784.	1.6	46
108	OP0048â€...GENOME-WIDE META-ANALYSIS REVEALED MULTIPLE NOVEL LOCI ASSOCIATED WITH SERUM URIC ACIDLEVELS IN JAPANESE. , 2019, , .		0

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109	OP0047â€…A GENOME-WIDE ASSOCIATION STUDY IDENTIFIED NOVEL LOCI ASSOCIATED WITH THE PROGRESSION FROM ASYMPTOMATIC HYPERURICEMIA TO GOUT. , 2019, , .		0
110	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
111	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
112	Genetics of rheumatoid arthritis: 2018 status. Annals of the Rheumatic Diseases, 2019, 78, 446-453.	0.5	141
113	Identification of 28 new susceptibility loci for type 2 diabetes in the Japanese population. Nature Genetics, 2019, 51, 379-386.	9.4	164
114	Deep whole-genome sequencing reveals recent selection signatures linked to evolution and disease risk of Japanese. Nature Communications, 2018, 9, 1631.	5.8	132
115	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
116	Statistical genetics and its application to neuroimmunology. Clinical and Experimental Neuroimmunology, 2018, 9, 7-12.	0.5	3
117	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
118	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
119	Integration of genetics and miRNAâ€“target gene network identified disease biology implicated in tissue specificity. Nucleic Acids Research, 2018, 46, 11898-11909.	6.5	39
120	eLD: entropy-based linkage disequilibrium index between multiallelic sites. Human Genome Variation, 2018, 5, 29.	0.4	18
121	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	5.8	181
122	High-throughput identification of noncoding functional SNPs via type IIS enzyme restriction. Nature Genetics, 2018, 50, 1180-1188.	9.4	31
123	In silico drug screening by using genome-wide association study data repurposed dabrafenib, an anti-melanoma drug, for Parkinsonâ€™s disease. Human Molecular Genetics, 2018, 27, 3974-3985.	1.4	25
124	Amino acid position 37 of HLA-DRÎ²1 affects susceptibility to Crohnâ€™s disease in Asians. Human Molecular Genetics, 2018, 27, 3901-3910.	1.4	19
125	Grimon: graphical interface to visualize multi-omics networks. Bioinformatics, 2018, 34, 3934-3936.	1.8	11
126	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

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127	A Multinational Arab Genomeâ€Wide Association Study Identifies New Genetic Associations for Rheumatoid Arthritis. Arthritis and Rheumatology, 2017, 69, 976-985.	2.9	25
128	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
129	Polygenic burdens on cell-specific pathways underlie the risk of rheumatoid arthritis. Nature Genetics, 2017, 49, 1120-1125.	9.4	130
130	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
131	Genetic landscape of interactive effects ofHLA-DRB1alleles on susceptibility to ACPA(+) rheumatoid arthritis and ACPA levels in Japanese population. Journal of Medical Genetics, 2017, 54, 853-858.	1.5	3
132	Human genetics contributes to the understanding of disease pathophysiology and drug discovery. Journal of Orthopaedic Science, 2017, 22, 977-981.	0.5	2
133	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
134	Future Directions of Genomics Research in Rheumatic Diseases. Rheumatic Disease Clinics of North America, 2017, 43, 481-487.	0.8	6
135	rs2841277 (PLD4) is associated with susceptibility and rs4672495 is associated with disease activity in rheumatoid arthritis. Oncotarget, 2017, 8, 64180-64190.	0.8	11
136	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
137	Significant impact of miRNAâ€“target gene networks on genetics of human complex traits. Scientific Reports, 2016, 6, 22223.	1.6	44
138	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 2016, 99, 636-646.	2.6	67
139	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
140	Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study. Lancet Oncology, The, 2016, 17, 1240-1247.	5.1	84
141	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
142	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
143	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
144	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. Nature Communications, 2016, 7, 10531.	5.8	149

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145	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
146	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
147	The Rheumatoid Arthritis Risk Variant CCR6DNP Regulates CCR6 via PARP-1. PLoS Genetics, 2016, 12, e1006292.	1.5	28
148	Genetic studies of rheumatoid arthritis. Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 2015, 91, 410-422.	1.6	43
149	Interactions Between Amino Acidâ€“Defined Major Histocompatibility Complex Class II Variants and Smoking in Seropositive Rheumatoid Arthritis. Arthritis and Rheumatology, 2015, 67, 2611-2623.	2.9	58
150	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
151	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
152	Genetics of rheumatoid arthritis in Asiaâ€”present and future. Nature Reviews Rheumatology, 2015, 11, 375-379.	3.5	45
153	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
154	Discovery of six new susceptibility loci and analysis of pleiotropic effects in leprosy. Nature Genetics, 2015, 47, 267-271.	9.4	103
155	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
156	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
157	Do Genetic Susceptibility Variants Associate with Disease Severity in Early Active Rheumatoid Arthritis?. Journal of Rheumatology, 2015, 42, 1131-1140.	1.0	18
158	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
159	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	9.4	2,045
160	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. Nature Genetics, 2015, 47, 1085-1090.	9.4	164
161	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
162	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

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163	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
164	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
165	The HLA-DRÎ²1 amino acid positions 11â€“13â€“26 explain the majority of SLEâ€“MHC associations. Nature Communications, 2014, 5, 5902.	5.8	80
166	Multiple Nonglycemic Genomic Loci Are Newly Associated With Blood Level of Glycated Hemoglobin in East Asians. Diabetes, 2014, 63, 2551-2562.	0.3	61
167	A Role for Noncoding Variation in Schizophrenia. Cell Reports, 2014, 9, 1417-1429.	2.9	225
168	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
169	Predicting HLA alleles from high-resolution SNP data in three Southeast Asian populations. Human Molecular Genetics, 2014, 23, 4443-4451.	1.4	80
170	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	13.7	1,974
171	Variation at HLA-DRB1 is associated with resistance to enteric fever. Nature Genetics, 2014, 46, 1333-1336.	9.4	85
172	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
173	Fine Mapping Major Histocompatibility Complex Associations in Psoriasis and Its Clinical Subtypes. American Journal of Human Genetics, 2014, 95, 162-172.	2.6	182
174	Polarization of the Effects of Autoimmune and Neurodegenerative Risk Alleles in Leukocytes. Science, 2014, 344, 519-523.	6.0	480
175	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
176	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	1.4	60
177	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
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