

# Kazuyoshi Ishigaki

## List of Publications by Year in descending order

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Version: 2024-02-01

38  
papers

2,934  
citations

257450

24  
h-index

330143

37  
g-index

55  
all docs

55  
docs citations

55  
times ranked

4696  
citing authors

#	ARTICLE	IF	CITATIONS
1	A cross-population atlas of genetic associations for 220 human phenotypes. <i>Nature Genetics</i> , 2021, 53, 1415-1424.	21.4	560
2	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
3	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
4	Dynamic landscape of immune cell-specific gene regulation in immune-mediated diseases. <i>Cell</i> , 2021, 184, 3006-3021.e17.	28.9	147
5	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
6	Polygenic burdens on cell-specific pathways underlie the risk of rheumatoid arthritis. <i>Nature Genetics</i> , 2017, 49, 1120-1125.	21.4	130
7	Improving the trans-ancestry portability of polygenic risk scores by prioritizing variants in predicted cell-type-specific regulatory elements. <i>Nature Genetics</i> , 2020, 52, 1346-1354.	21.4	126
8	Characterizing rare and low-frequency height-associated variants in the Japanese population. <i>Nature Communications</i> , 2019, 10, 4393.	12.8	123
9	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
10	GWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. <i>Nature Human Behaviour</i> , 2020, 4, 308-316.	12.0	80
11	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
12	Single-cell eQTL models reveal dynamic T cell state dependence of disease loci. <i>Nature</i> , 2022, 606, 120-128.	27.8	75
13	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
14	Multimodally profiling memory T cells from a tuberculosis cohort identifies cell state associations with demographics, environment and disease. <i>Nature Immunology</i> , 2021, 22, 781-793.	14.5	52
15	GWAS of mosaic loss of chromosome Y highlights genetic effects on blood cell differentiation. <i>Nature Communications</i> , 2019, 10, 4719.	12.8	50
16	Immunophenotyping of rheumatoid arthritis reveals a linkage between HLA-DRB1 genotype, CXCR4 expression on memory CD4+ T cells and disease activity. <i>Scientific Reports</i> , 2016, 6, 29338.	3.3	49
17	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
18	Early progression to active tuberculosis is a highly heritable trait driven by 3q23 in Peruvians. <i>Nature Communications</i> , 2019, 10, 3765.	12.8	43

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19	Quantitative and qualitative characterization of expanded CD4+ T cell clones in rheumatoid arthritis patients. <i>Scientific Reports</i> , 2015, 5, 12937.	3.3	42
20	HLA autoimmune risk alleles restrict the hypervariable region of T cell receptors. <i>Nature Genetics</i> , 2022, 54, 393-402.	21.4	40
21	Repertoire analyses reveal T cell antigen receptor sequence features that influence T cell fate. <i>Nature Immunology</i> , 2022, 23, 446-457.	14.5	37
22	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
23	Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. <i>Nature Communications</i> , 2020, 11, 3175.	12.8	34
24	TGF- $\beta$ 3 Inhibits Antibody Production by Human B Cells. <i>PLoS ONE</i> , 2017, 12, e0169646.	2.5	34
25	A gene module associated with dysregulated TCR signaling pathways in CD4+ T cell subsets in rheumatoid arthritis. <i>Journal of Autoimmunity</i> , 2018, 89, 21-29.	6.5	32
26	Parsing multiomics landscape of activated synovial fibroblasts highlights drug targets linked to genetic risk of rheumatoid arthritis. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 440-450.	0.9	29
27	Autoantigen BiP-derived HLA-DR4 Epitopes Differentially Recognized by Effector and Regulatory T Cells in Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2015, 67, 1171-1181.	5.6	25
28	Transcriptome analysis of peripheral blood from patients with rheumatoid arthritis: a systematic review. <i>Inflammation and Regeneration</i> , 2018, 38, 21.	3.7	24
29	Skin ulcer is a predictive and prognostic factor of acute or subacute interstitial lung disease in dermatomyositis. <i>Rheumatology International</i> , 2013, 33, 2381-2389.	3.0	23
30	HLA-DRB1 Shared Epitope Alleles and Disease Activity Are Correlated with Reduced T Cell Receptor Repertoire Diversity in CD4+ T Cells in Rheumatoid Arthritis. <i>Journal of Rheumatology</i> , 2018, 45, 905-914.	2.0	23
31	Immune cell multiomics analysis reveals contribution of oxidative phosphorylation to B-cell functions and organ damage of lupus. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, 845-853.	0.9	20
32	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
33	Contribution of a European-prevalent Variant near <i>CD83</i> and an East Asian-prevalent Variant near <i>IL17RB</i> to Herpes Zoster Risk in Tofacitinib Treatment: Results of Genome-wide Association Study Meta-analyses. <i>Arthritis and Rheumatology</i> , 2021, 73, 1155-1166.	5.6	15
34	Beyond GWAS: from simple associations to functional insights. <i>Seminars in Immunopathology</i> , 2022, 44, 3-14.	6.1	13
35	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
36	Genetics of human autoimmunity: From genetic information to functional insights. <i>Clinical Immunology</i> , 2018, 186, 9-13.	3.2	7

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37	Reduction of CD83 Expression on B Cells and the Genetic Basis for Rheumatoid Arthritis: Comment on the Article by Thalayasingam et al. <i>Arthritis and Rheumatology</i> , 2018, 70, 1695-1696.	5.6	2
38	Genetic and Functional Genetics of Autoimmune Diseases. , 2019, , 37-47.		0