

# Masahiro Kanai

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/79135/publications.pdf>

Version: 2024-02-01

51  
papers

10,260  
citations

109264

35  
h-index

175177

52  
g-index

87  
all docs

87  
docs citations

87  
times ranked

14602  
citing authors

#	ARTICLE	IF	CITATIONS
1	Clinical use of current polygenic risk scores may exacerbate health disparities. <i>Nature Genetics</i> , 2019, 51, 584-591.	9.4	1,664
2	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018, 50, 524-537.	9.4	1,124
3	Mapping the human genetic architecture of COVID-19. <i>Nature</i> , 2021, 600, 472-477.	13.7	640
4	Genetic analysis of quantitative traits in the Japanese population links cell types to complex human diseases. <i>Nature Genetics</i> , 2018, 50, 390-400.	9.4	613
5	A cross-population atlas of genetic associations for 220 human phenotypes. <i>Nature Genetics</i> , 2021, 53, 1415-1424.	9.4	560
6	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	9.4	549
7	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	13.5	388
8	Genome-wide association study identifies 112 new loci for body mass index in the Japanese population. <i>Nature Genetics</i> , 2017, 49, 1458-1467.	9.4	380
9	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020, 182, 1198-1213.e14.	13.5	353
10	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
11	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. <i>Nature Genetics</i> , 2020, 52, 669-679.	9.4	304
12	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
13	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. <i>Nature Medicine</i> , 2021, 27, 1876-1884.	15.2	214
14	Identification of 28 new susceptibility loci for type 2 diabetes in the Japanese population. <i>Nature Genetics</i> , 2019, 51, 379-386.	9.4	164
15	Deep whole-genome sequencing reveals recent selection signatures linked to evolution and disease risk of Japanese. <i>Nature Communications</i> , 2018, 9, 1631.	5.8	132
16	Tractor uses local ancestry to enable the inclusion of admixed individuals in GWAS and to boost power. <i>Nature Genetics</i> , 2021, 53, 195-204.	9.4	125
17	Genetic analyses identify widespread sex-differential participation bias. <i>Nature Genetics</i> , 2021, 53, 663-671.	9.4	124
18	Characterizing rare and low-frequency height-associated variants in the Japanese population. <i>Nature Communications</i> , 2019, 10, 4393.	5.8	123

#	ARTICLE	IF	CITATIONS
19	Construction of a population-specific HLA imputation reference panel and its application to Graves' disease risk in Japanese. <i>Nature Genetics</i> , 2015, 47, 798-802.	9.4	119
20	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. <i>Nature Genetics</i> , 2022, 54, 450-458.	9.4	109
21	Polygenic burden in focal and generalized epilepsies. <i>Brain</i> , 2019, 142, 3473-3481.	3.7	90
22	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	5.8	84
23	CWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. <i>Nature Human Behaviour</i> , 2020, 4, 308-316.	6.2	80
24	Empirical estimation of genome-wide significance thresholds based on the 1000 Genomes Project data set. <i>Journal of Human Genetics</i> , 2016, 61, 861-866.	1.1	75
25	Genetic and phenotypic landscape of the major histocompatibility complex region in the Japanese population. <i>Nature Genetics</i> , 2019, 51, 470-480.	9.4	75
26	Trans-biobank analysis with 676,000 individuals elucidates the association of polygenic risk scores of complex traits with human lifespan. <i>Nature Medicine</i> , 2020, 26, 542-548.	15.2	74
27	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021, 53, 1504-1516.	9.4	69
28	Contribution of a Non-classical HLA Gene, HLA-DOA, to the Risk of Rheumatoid Arthritis. <i>American Journal of Human Genetics</i> , 2016, 99, 366-374.	2.6	68
29	Population-specific causal disease effect sizes in functionally important regions impacted by selection. <i>Nature Communications</i> , 2021, 12, 1098.	5.8	68
30	Genome-wide meta-analysis identifies multiple novel loci associated with serum uric acid levels in Japanese individuals. <i>Communications Biology</i> , 2019, 2, 115.	2.0	66
31	Genome-wide functional screen of 3'UTR variants uncovers causal variants for human disease and evolution. <i>Cell</i> , 2021, 184, 5247-5260.e19.	13.5	62
32	Dimensionality reduction reveals fine-scale structure in the Japanese population with consequences for polygenic risk prediction. <i>Nature Communications</i> , 2020, 11, 1569.	5.8	58
33	CWAS of smoking behaviour in 165,436 Japanese people reveals seven new loci and shared genetic architecture. <i>Nature Human Behaviour</i> , 2019, 3, 471-477.	6.2	54
34	Challenges and Opportunities for Developing More Generalizable Polygenic Risk Scores. <i>Annual Review of Biomedical Data Science</i> , 2022, 5, 293-320.	2.8	47
35	Significant impact of miRNA-target gene networks on genetics of human complex traits. <i>Scientific Reports</i> , 2016, 6, 22223.	1.6	44
36	Elucidating the genetic architecture of reproductive ageing in the Japanese population. <i>Nature Communications</i> , 2018, 9, 1977.	5.8	44

#	ARTICLE	IF	CITATIONS
37	Leveraging supervised learning for functionally informed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. <i>Nature Communications</i> , 2021, 12, 3394.	5.8	44
38	Variants at HLA-A, HLA-C, and HLA-DQB1 Confer Risk of Psoriasis Vulgaris in Japanese. <i>Journal of Investigative Dermatology</i> , 2018, 138, 542-548.	0.3	39
39	Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. <i>International Journal of Epidemiology</i> , 2022, 50, 1995-2010.	0.9	39
40	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. <i>Nature Communications</i> , 2020, 11, 1237.	5.8	38
41	Direct characterization of cis-regulatory elements and functional dissection of complex genetic associations using HCR-FlowFISH. <i>Nature Genetics</i> , 2021, 53, 1166-1176.	9.4	36
42	Genome-wide risk prediction of common diseases across ancestries in one million people. <i>Cell Genomics</i> , 2022, 2, 100118.	3.0	34
43	Association of the <i>RPA3-UMAD1</i> locus with interstitial lung diseases complicated with rheumatoid arthritis in Japanese. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 1305-1309.	0.5	21
44	Association of <i>NOD2</i> Mutations with Aggressive Periodontitis. <i>Journal of Dental Research</i> , 2017, 96, 1100-1105.	2.5	17
45	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022, 5, .	2.0	17
46	Multi-phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. <i>Journal of Thrombosis and Haemostasis</i> , 2022, 20, 1331-1349.	1.9	12
47	Grimon: graphical interface to visualize multi-omics networks. <i>Bioinformatics</i> , 2018, 34, 3934-3936.	1.8	11
48	Successfully Treated Lung and Renal Metastases from Primary Chondrosarcoma of the Scapula with Radiofrequency Ablation and Surgical Resection. <i>Case Reports in Oncological Medicine</i> , 2019, 2019, 1-5.	0.2	3
49	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.	0.9	2
50	Trans-Ethnic Mendelian Randomization Study Reveals Causal Relationships Between Cardiometabolic Factors and Chronic Kidney Disease. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
51	OP0048...GENOME-WIDE META-ANALYSIS REVEALED MULTIPLE NOVEL LOCI ASSOCIATED WITH SERUM URIC ACIDLEVELS IN JAPANESE. , 2019, , .		0