Masahiro Kanai

List of Publications by Year
in descending order

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	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
2	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
3	Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. Nature Genetics, 2022, 54, 450-458.	9.4	109
4	Genome-wide risk prediction of common diseases across ancestries in one million people. Cell Genomics, 2022, 2, 100118.	3.0	34
5	Challenges and Opportunities for Developing More Generalizable Polygenic Risk Scores. Annual Review of Biomedical Data Science, 2022, 5, 293-320.	2.8	47
6	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
7	Population-specific causal disease effect sizes in functionally important regions impacted by selection. Nature Communications, 2021, 12, 1098.	5.8	68
8	Genetic analyses identify widespread sex-differential participation bias. Nature Genetics, 2021, 53, 663-671.	9.4	124
9	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
10	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
11	Direct characterization of cis-regulatory elements and functional dissection of complex genetic associations using HCRâ€“FlowFISH. Nature Genetics, 2021, 53, 1166-1176.	9.4	36
12	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	13.7	640
13	Genome-wide functional screen of 3â€²UTR variants uncovers causal variants for human disease and evolution. Cell, 2021, 184, 5247-5260.e19.	13.5	62
14	A cross-population atlas of genetic associations for 220 human phenotypes. Nature Genetics, 2021, 53, 1415-1424.	9.4	560
15	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
16	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
17	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. Nature Medicine, 2021, 27, 1876-1884.	15.2	214
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	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
20	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
21	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
22	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
23	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. Nature Communications, 2020, 11, 1237.	5.8	38
24	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
25	GWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. Nature Human Behaviour, 2020, 4, 308-316.	6.2	80
26	Dimensionality reduction reveals fine-scale structure in the Japanese population with consequences for polygenic risk prediction. Nature Communications, 2020, 11, 1569.	5.8	58
27	Successfully Treated Lung and Renal Metastases from Primary Chondrosarcoma of the Scapula with Radiofrequency Ablation and Surgical Resection. Case Reports in Oncological Medicine, 2019, 2019, 1-5.	0.2	3
28	Polygenic burden in focal and generalized epilepsies. Brain, 2019, 142, 3473-3481.	3.7	90
29	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
30	Characterizing rare and low-frequency height-associated variants in the Japanese population. Nature Communications, 2019, 10, 4393.	5.8	123
31	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
32	Genetic and phenotypic landscape of the major histocompatibilty complex region in the Japanese population. Nature Genetics, 2019, 51, 470-480.	9.4	75
33	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
34	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
35	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
36	Clinical use of current polygenic risk scores may exacerbate health disparities. Nature Genetics, 2019, 51, 584-591.	9.4	1,664

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37	OP0048â€…GENOME-WIDE META-ANALYSIS REVEALED MULTIPLE NOVEL LOCI ASSOCIATED WITH SERUM URIC ACIDLEVELS IN JAPANESE. , 2019, , .		0
38	Identification of 28 new susceptibility loci for type 2 diabetes in the Japanese population. Nature Genetics, 2019, 51, 379-386.	9.4	164
39	Deep whole-genome sequencing reveals recent selection signatures linked to evolution and disease risk of Japanese. Nature Communications, 2018, 9, 1631.	5.8	132
40	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
41	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
42	Elucidating the genetic architecture of reproductive ageing in the Japanese population. Nature Communications, 2018, 9, 1977.	5.8	44
43	Grimon: graphical interface to visualize multi-omics networks. Bioinformatics, 2018, 34, 3934-3936.	1.8	11
44	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
45	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
46	Association of NOD2 Mutations with Aggressive Periodontitis. Journal of Dental Research, 2017, 96, 1100-1105.	2.5	17
47	Significant impact of miRNAâ€“target gene networks on genetics of human complex traits. Scientific Reports, 2016, 6, 22223.	1.6	44
48	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
49	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
50	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
51	Trans-Ethnic Mendelian Randomization Study Reveals Causal Relationships Between Cardiometabolic Factors and Chronic Kidney Disease. SSRN Electronic Journal, 0, , .	0.4	1