Saori Sakaue

List of Publications by Year
in descending order

35 papers	4,007 citations	361296 20 h-index	345118 36 g-index
48 all docs	48 docs citations	48 times ranked	6557 citing authors

#	Article	IF	Citations
1	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
2	A cross-population atlas of genetic associations for 220 human phenotypes. Nature Genetics, 2021, 53, 1415-1424.	9.4	560
3	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
4	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
5	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
6	Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. Nature Communications, 2019, 10, 2773.	5.8	183
7	Deep whole-genome sequencing reveals recent selection signatures linked to evolution and disease risk of Japanese. Nature Communications, 2018, 9, 1631.	5.8	132
8	Characterizing rare and low-frequency height-associated variants in the Japanese population. Nature Communications, 2019, 10, 4393.	5.8	123
9	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	5.8	89
10	Genetic and phenotypic landscape of the major histocompatibilty complex region in the Japanese population. Nature Genetics, 2019, 51, 470-480.	9.4	75
11	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
12	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
13	Dimensionality reduction reveals fine-scale structure in the Japanese population with consequences for polygenic risk prediction. Nature Communications, 2020, 11, 1569.	5.8	58
14	Transethnic Meta-Analysis of Genome-Wide Association Studies Identifies Three New Loci and Characterizes Population-Specific Differences for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2020, 13, e002670.	1.6	44
15	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
16	GREP: genome for REPositioning drugs. Bioinformatics, 2019, 35, 3821-3823.	1.8	35
17	Genetic and phenotypic landscape of the mitochondrial genome in the Japanese population. Communications Biology, 2020, 3, 104.	2.0	32
18	Tocilizumab-induced leucocytoclastic vasculitis in a patient with rheumatoid arthritis. Rheumatology, 2014, 53, 1529-1530.	0.9	31

#	Article	IF	Citations
19	Genetic determinants of risk in autoimmune pulmonary alveolar proteinosis. Nature Communications, 2021, 12, 1032.	5.8	26
20	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
21	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
22	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
23	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
24	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
25	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
26	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
27	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
28	Future Directions of Genomics Research in Rheumatic Diseases. Rheumatic Disease Clinics of North America, 2017, 43, 481-487.	0.8	6
29	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
30	Genome-Wide Association Study of Intracranial Artery Stenosis Followed by Phenome-Wide Association Study. Translational Stroke Research, 2023, 14, 322-333.	2.3	5
31	Takayasuâ€™s Arteritis. New England Journal of Medicine, 2016, 375, 675-675.	13.9	3
32	Human genetics contributes to the understanding of disease pathophysiology and drug discovery. Journal of Orthopaedic Science, 2017, 22, 977-981.	0.5	2
33	Patientsâ€™ demographics of a convenient clinic located in a large railway station in metropolitan Tokyo area. Medicine (United States), 2018, 97, e9646.	0.4	2
34	Unilateral proptosis in a woman with asthma. BMJ Case Reports, 2015, 2015, bcr2014207532-bcr2014207532.	0.2	1
35	Ixekizumab for psoriasis. Lancet, The, 2016, 387, 225-226.	6.3	1