Momoko Horikoshi

List of Publications by Year
in descending order

45 papers	10,631 citations	117625 34 h-index	223800 46 g-index
53 all docs	53 docs citations	53 times ranked	18354 citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
2	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
3	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
4	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
5	SNPs in KCNQ1 are associated with susceptibility to type 2 diabetes in East Asian and European populations. Nature Genetics, 2008, 40, 1098-1102.	21.4	641
6	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. Nature Genetics, 2015, 47, 1449-1456.	21.4	529
7	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
8	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	21.4	402
9	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
10	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. Diabetes, 2011, 60, 2624-2634.	0.6	335
11	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	21.4	310
12	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. Nature Genetics, 2013, 45, 76-82.	21.4	293
13	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	27.8	282
14	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	2.9	275
15	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
16	A genome-wide association study in the Japanese population identifies susceptibility loci for type 2 diabetes at UBE2E2 and C2CD4A-C2CD4B. Nature Genetics, 2010, 42, 864-868.	21.4	245
17	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. JAMA - Journal of the American Medical Association, 2016, 315, 1129.	7.4	220
18	Trans-ethnic meta-regression of genome-wide association studies accounting for ancestry increases power for discovery and improves fine-mapping resolution. Human Molecular Genetics, 2017, 26, 3639-3650.	2.9	170

#	Article	IF	Citations
19	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
20	Identification of 28 new susceptibility loci for type 2 diabetes in the Japanese population. Nature Genetics, 2019, 51, 379-386.	21.4	164
21	Genome-wide association study identifies three novel loci for type 2 diabetes. Human Molecular Genetics, 2014, 23, 239-246.	2.9	158
22	Genome-wide association study of offspring birth weight in 86â€‰577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. Human Molecular Genetics, 2018, 27, 742-756.	2.9	156
23	Expression-based genome-wide association study links the receptor *CD44* in adipose tissue with type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7049-7054.	7.1	144
24	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. Nature Genetics, 2018, 50, 572-580.	21.4	143
25	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
26	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	2.9	109
27	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	12.8	108
28	A single-nucleotide polymorphism in ANK1 is associated with susceptibility to type 2 diabetes in Japanese populations. Human Molecular Genetics, 2012, 21, 3042-3049.	2.9	99
29	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. PLoS Genetics, 2020, 16, e1008718.	3.5	95
30	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
31	Genome-wide association study of primary tooth eruption identifies pleiotropic loci associated with height and craniofacial distances. Human Molecular Genetics, 2013, 22, 3807-3817.	2.9	84
32	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	3.5	77
33	A trans-ancestral meta-analysis of genome-wide association studies reveals loci associated with childhood obesity. Human Molecular Genetics, 2019, 28, 3327-3338.	2.9	76
34	A Polymorphism in the AMPKÂ2 Subunit Gene Is Associated With Insulin Resistance and Type 2 Diabetes in the Japanese Population. Diabetes, 2006, 55, 919-923.	0.6	51
35	Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. Nature Communications, 2020, 11, 3175.	12.8	34
36	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31

#	Article	IF	Citations
37	Variations with modest effects have an important role in the genetic background of type 2 diabetes and diabetes-related traits. Journal of Human Genetics, 2012, 57, 776-779.	2.3	29
38	How Can Genetic Studies Help Us to Understand Links Between Birth Weight and Type 2 Diabetes?. Current Diabetes Reports, 2017, 17, 22.	4.2	28
39	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	2.9	21
40	Associations of variations in the MRF2/ARID5B gene with susceptibility to type 2 diabetes in the Japanese population. Journal of Human Genetics, 2012, 57, 727-733.	2.3	16
41	Genome-wide association studies identify two novel loci conferring susceptibility to diabetic retinopathy in Japanese patients with type 2 diabetes. Human Molecular Genetics, 2021, 30, 716-726.	2.9	13
42	Association Between Genetic Risk and Development of Type 2 Diabetes in a General Japanese Population: The Hisayama Study. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 3213-3222.	3.6	12
43	Genetic Variations of Mrf-2/Arid5b Confer Risk of Coronary Atherosclerosis in the Japanese Population. International Heart Journal, 2008, 49, 313-327.	1.0	8
44	Structural basis of ethnic-specific variants of PAX4 associated with type 2 diabetes. Human Genome Variation, 2021, 8, 25.	0.7	5
45	Genome-Wide Association Study for Type 2 Diabetes. , 2019, , 49-86.		2