

Momoko Horikoshi

List of Publications by Year in descending order

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Version: 2024-02-01

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	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	21.4	250
2	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	12.8	87
3	Genome-wide association studies identify two novel loci conferring susceptibility to diabetic retinopathy in Japanese patients with type 2 diabetes. <i>Human Molecular Genetics</i> , 2021, 30, 716-726.	2.9	13
4	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
5	Structural basis of ethnic-specific variants of PAX4 associated with type 2 diabetes. <i>Human Genome Variation</i> , 2021, 8, 25.	0.7	5
6	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. <i>PLoS Genetics</i> , 2020, 16, e1008718.	3.5	95
7	Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020, 582, 240-245.	27.8	282
8	Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. <i>Nature Communications</i> , 2020, 11, 3175.	12.8	34
9	A trans-ancestral meta-analysis of genome-wide association studies reveals loci associated with childhood obesity. <i>Human Molecular Genetics</i> , 2019, 28, 3327-3338.	2.9	76
10	Association Between Genetic Risk and Development of Type 2 Diabetes in a General Japanese Population: The Hisayama Study. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 3213-3222.	3.6	12
11	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019, 51, 804-814.	21.4	402
12	Genome-Wide Association Study for Type 2 Diabetes. , 2019, , 49-86.		2
13	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
14	Genome-wide association study of offspring birth weight in 86,577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. <i>Human Molecular Genetics</i> , 2018, 27, 742-756.	2.9	156
15	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. <i>Nature Genetics</i> , 2018, 50, 572-580.	21.4	143
16	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	12.8	169
17	How Can Genetic Studies Help Us to Understand Links Between Birth Weight and Type 2 Diabetes?. <i>Current Diabetes Reports</i> , 2017, 17, 22.	4.2	28
18	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	5.3	31

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19	Trans-ethnic meta-regression of genome-wide association studies accounting for ancestry increases power for discovery and improves fine-mapping resolution. <i>Human Molecular Genetics</i> , 2017, 26, 3639-3650.	2.9	170
20	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	27.8	952
21	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	27.8	1,204
22	Genome-wide associations for birth weight and correlations with adult disease. <i>Nature</i> , 2016, 538, 248-252.	27.8	406
23	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	7.1	110
24	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. <i>Human Molecular Genetics</i> , 2016, 25, 2070-2081.	2.9	21
25	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. <i>JAMA - Journal of the American Medical Association</i> , 2016, 315, 1129.	7.4	220
26	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. <i>Human Molecular Genetics</i> , 2016, 25, 389-403.	2.9	275
27	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. <i>PLoS Genetics</i> , 2015, 11, e1005230.	3.5	77
28	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. <i>Nature Communications</i> , 2015, 6, 8658.	12.8	108
29	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015, 47, 589-597.	21.4	310
30	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. <i>Nature Genetics</i> , 2015, 47, 1449-1456.	21.4	529
31	A novel common variant in DCST2 is associated with length in early life and height in adulthood. <i>Human Molecular Genetics</i> , 2015, 24, 1155-1168.	2.9	109
32	Genome-wide association study identifies three novel loci for type 2 diabetes. <i>Human Molecular Genetics</i> , 2014, 23, 239-246.	2.9	158
33	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	21.4	959
34	Genome-wide association study of primary tooth eruption identifies pleiotropic loci associated with height and craniofacial distances. <i>Human Molecular Genetics</i> , 2013, 22, 3807-3817.	2.9	84
35	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. <i>Nature Genetics</i> , 2013, 45, 76-82.	21.4	293
36	A single-nucleotide polymorphism in ANK1 is associated with susceptibility to type 2 diabetes in Japanese populations. <i>Human Molecular Genetics</i> , 2012, 21, 3042-3049.	2.9	99

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37	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012, 44, 991-1005.	21.4	746
38	Expression-based genome-wide association study links the receptor <i>CD44</i> in adipose tissue with type 2 diabetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7049-7054.	7.1	144
39	Associations of variations in the <i>MRF2/ARID5B</i> gene with susceptibility to type 2 diabetes in the Japanese population. <i>Journal of Human Genetics</i> , 2012, 57, 727-733.	2.3	16
40	Variations with modest effects have an important role in the genetic background of type 2 diabetes and diabetes-related traits. <i>Journal of Human Genetics</i> , 2012, 57, 776-779.	2.3	29
41	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. <i>Diabetes</i> , 2011, 60, 2624-2634.	0.6	335
42	A genome-wide association study in the Japanese population identifies susceptibility loci for type 2 diabetes at <i>UBE2E2</i> and <i>C2CD4A-C2CD4B</i> . <i>Nature Genetics</i> , 2010, 42, 864-868.	21.4	245
43	SNPs in <i>KCNQ1</i> are associated with susceptibility to type 2 diabetes in East Asian and European populations. <i>Nature Genetics</i> , 2008, 40, 1098-1102.	21.4	641
44	Genetic Variations of <i>Mrf-2/Arid5b</i> Confer Risk of Coronary Atherosclerosis in the Japanese Population. <i>International Heart Journal</i> , 2008, 49, 313-327.	1.0	8
45	A Polymorphism in the <i>AMPKα2</i> Subunit Gene Is Associated With Insulin Resistance and Type 2 Diabetes in the Japanese Population. <i>Diabetes</i> , 2006, 55, 919-923.	0.6	51