

# Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Evaluation of Common Type 2 Diabetes Risk Variants in a South Asian Population of Sri Lankan Descent. PLoS ONE, 2014, 9, e98608.	1.1	8
2	The ras responsive transcription factor RREB1 is a novel candidate gene for type 2 diabetes associated end-stage kidney disease. Human Molecular Genetics, 2014, 23, 6441-6447.	1.4	34
3	Variants associated with type 2 diabetes identified by the transethnic meta-analysis study: assessment in American Indians and evidence for a new signal in LPP. Diabetologia, 2014, 57, 2334-2338.	2.9	9
4	Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies. PLoS Genetics, 2014, 10, e1004722.	1.5	475
5	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	1.5	191
6	Identification of a Novel Gene for Diabetic Traits in Rats, Mice, and Humans. Genetics, 2014, 198, 17-29.	1.2	44
7	Science and Medicine. Yearbook of Paediatric Endocrinology, 2014, , 199-212.	0.0	0
9	Trans-ethnic genome-wide association studies: advantages and challenges of mapping in diverse populations. Genome Medicine, 2014, 6, 91.	3.6	167
10	Fine Mapping of Type 2 Diabetes Susceptibility Loci. Current Diabetes Reports, 2014, 14, 549.	1.7	22
11	Association of a Low-Frequency Variant in <i>HNF1A</i> With Type 2 Diabetes in a Latino Population. JAMA - Journal of the American Medical Association, 2014, 311, 2305.	3.8	230
12	ABCC8 genetic variants and risk of diabetes mellitus. Gene, 2014, 545, 198-204.	1.0	34
13	Insights into the Genetic Susceptibility to Type 2 Diabetes from Genome-Wide Association Studies of Glycaemic Traits. Current Diabetes Reports, 2014, 14, 551.	1.7	38
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18	The pancreatic $\beta^2$ cell: recent insights from human genetics. Trends in Endocrinology and Metabolism, 2014, 25, 425-434.	3.1	29
19	Genetic architecture of type 2 diabetes. Biochemical and Biophysical Research Communications, 2014, 452, 213-220.	1.0	48

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20	<i>Dorothy Hodgkin Lecture 2014</i> Understanding genes identified by genome-wide association studies for Type 2 diabetes. <i>Diabetic Medicine</i> , 2014, 31, 1480-1487.	1.2	29
21	Dissecting complex traits using the <i>Drosophila</i> Synthetic Population Resource. <i>Trends in Genetics</i> , 2014, 30, 488-495.	2.9	82
22	Sex differences in disease genetics: evidence, evolution, and detection. <i>Trends in Genetics</i> , 2014, 30, 453-463.	2.9	98
23	Genetic susceptibility to type 2 diabetes and obesity: from genome-wide association studies to rare variants and beyond. <i>Diabetologia</i> , 2014, 57, 1528-1541.	2.9	162
24	Insulin resistance, selfish brain, and selfish immune system: an evolutionarily positively selected program used in chronic inflammatory diseases. <i>Arthritis Research and Therapy</i> , 2014, 16, S4.	1.6	62
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67	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. <i>Nature Genetics</i> , 2015, 47, 979-986.	9.4	1,965
68	An ImmunoChip study of multiple sclerosis risk in African Americans. <i>Brain</i> , 2015, 138, 1518-1530.	3.7	60
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132	Common germline variants within the CDKN2A/2B region affect risk of pancreatic neuroendocrine tumors. <i>Scientific Reports</i> , 2016, 6, 39565.	1.6	15
134	Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. <i>Cell Systems</i> , 2016, 3, 572-584.e3.	2.9	261
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147	Genetics of Type 2 Diabetes. <i>Endocrine Development</i> , 2016, 31, 203-220.	1.3	59
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171	Can genetic evidence help us to understand the fetal origins of type 2 diabetes?. Diabetologia, 2016, 59, 1850-1854.	2.9	10
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