Karen L Mohlke

List of Publications by Year
in descending order

218	65,186	3668 92	1875 215
papers	citations	h-index	g-index

242	242	242	57713
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
3	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
4	A Genome-Wide Association Study of Type 2 Diabetes in Finns Detects Multiple Susceptibility Variants. Science, 2007, 316, 1341-1345.	6.0	2,534
5	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
6	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	6.3	1,937
7	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
8	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
9	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
10	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	9.4	1,683
11	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
12	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	9.4	1,572
13	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. Nature Genetics, 2008, 40, 161-169.	9.4	1,488
14	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	9.4	1,331
15	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
16	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. Nature Genetics, 2019, 51, 237-244.	9.4	1,307
17	Common variants at 30 loci contribute to polygenic dyslipidemia. Nature Genetics, 2009, 41, 56-65.	9.4	1,234
18	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179

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19	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104
20	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
21	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
22	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	9.4	836
23	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	9.4	762
24	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
25	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
26	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662
27	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
28	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	9.4	591
29	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
30	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
31	Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. Nature Genetics, 2012, 44, 67-72.	9.4	545
32	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
33	Identification of ten loci associated with height highlights new biological pathways in human growth. Nature Genetics, 2008, 40, 584-591.	9.4	537
34	A map of open chromatin in human pancreatic islets. Nature Genetics, 2010, 42, 255-259.	9.4	515
35	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
36	Physical Activity Attenuates the Influence of FTO Variants on Obesity Risk: A Meta-Analysis of 218,166 Adults and 19,268 Children. PLoS Medicine, 2011, 8, e1001116.	3.9	446

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37	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	9.4	428
38	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
39	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406
40	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402
41	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
42	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.3	387
43	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
44	Common variants in the GDF5-UQCC region are associated with variation in human height. Nature Genetics, 2008, 40, 198-203.	9.4	369
45	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
46	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
47	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
48	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
49	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
50	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
51	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	1.5	331
52	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
53	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. Diabetes, 2014, 63, 2158-2171.	0.3	297
54	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	9.4	294

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55	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. Nature Genetics, 2013, 45, 76-82.	9.4	293
56	Quantifying prion disease penetrance using large population control cohorts. Science Translational Medicine, 2016, 8, 322ra9.	5.8	289
57	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
58	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	13.7	282
59	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
60	Genetic Variation Near the Hepatocyte Nuclear Factor-4Â Gene Predicts Susceptibility to Type 2 Diabetes. Diabetes, 2004, 53, 1141-1149.	0.3	255
61	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
62	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
63	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
64	Exome array analysis identifies new loci and low-frequency variants influencing insulin processing and secretion. Nature Genetics, 2013, 45, 197-201.	9.4	247
65	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
66	Detailed Physiologic Characterization Reveals Diverse Mechanisms for Novel Genetic Loci Regulating Glucose and Insulin Metabolism in Humans. Diabetes, 2010, 59, 1266-1275.	0.3	237
67	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. Nature Genetics, 2010, 42, 430-435.	9.4	223
68	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
69	Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. Human Molecular Genetics, 2014, 23, 5492-5504.	1.4	192
70	Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in LAMA1 and Enrichment for Risk Variants in Lean Compared to Obese Cases. PLoS Genetics, 2012, 8, e1002741.	1.5	190
71	Genetic regulatory signatures underlying islet gene expression and type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2301-2306.	3.3	189
72	The Finlandâ€“United States Investigation of Nonâ€“Insulinâ€Dependent Diabetes Mellitus Genetics (FUSION) Study. I. An Autosomal Genome Scan for Genes That Predispose to Type 2 Diabetes. American Journal of Human Genetics, 2000, 67, 1174-1185.	2.6	186

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73	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	5.8	173
74	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
75	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	5.8	169
76	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
77	The Finland-United States investigation of non-insulin-dependent diabetes mellitus genetics (FUSION) study. I. An autosomal genome scan for genes that predispose to type 2 diabetes. American Journal of Human Genetics, 2000, 67, 1174-85.	2.6	154
78	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13127-13132.	3.3	152
79	The Metabolic Syndrome in Men study: a resource for studies of metabolic and cardiovascular diseases. Journal of Lipid Research, 2017, 58, 481-493.	2.0	147
80	GREGOR: evaluating global enrichment of trait-associated variants in epigenomic features using a systematic, data-driven approach. Bioinformatics, 2015, 31, 2601-2606.	1.8	146
81	Variations in the G6PC2/ABCB11 genomic region are associated with fasting glucose levels. Journal of Clinical Investigation, 2008, 118, 2620-8.	3.9	146
82	FTO genetic variants, dietary intake and body mass index: insights from 177 330 individuals. Human Molecular Genetics, 2014, 23, 6961-6972.	1.4	143
83	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. American Journal of Human Genetics, 2017, 100, 428-443.	2.6	141
84	Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. Human Molecular Genetics, 2017, 26, 1770-1784.	1.4	135
85	Exome chip meta-analysis identifies novel loci and East Asianâ€“specific coding variants that contribute to lipid levels and coronary artery disease. Nature Genetics, 2017, 49, 1722-1730.	9.4	129
86	High-throughput screening for evidence of association by using mass spectrometry genotyping on DNA pools. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16928-16933.	3.3	117
87	Mendelian Randomization Studies Do Not Support a Causal Role for Reduced Circulating Adiponectin Levels in Insulin Resistance and Type 2 Diabetes. Diabetes, 2013, 62, 3589-3598.	0.3	116
88	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. Nature Communications, 2016, 7, 11764.	5.8	114
89	Trans-Ethnic Fine-Mapping of Lipid Loci Identifies Population-Specific Signals and Allelic Heterogeneity That Increases the Trait Variance Explained. PLoS Genetics, 2013, 9, e1003379.	1.5	112
90	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	9.4	112

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91	Recent advances in understanding the genetic architecture of type 2 diabetes. Human Molecular Genetics, 2015, 24, R85-R92.	1.4	107
92	Metabolic reprogramming through fatty acid transport protein 1 (FATP1) regulates macrophage inflammatory potential and adipose inflammation. Molecular Metabolism, 2016, 5, 506-526.	3.0	107
93	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Human Molecular Genetics, 2015, 24, 1791-1800.	1.4	105
94	A Genome-Wide Association Study of IVGTT-Based Measures of First-Phase Insulin Secretion Refines the Underlying Physiology of Type 2 Diabetes Variants. Diabetes, 2017, 66, 2296-2309.	0.3	102
95	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	5.8	100
96	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	1.5	95
97	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
98	Deciphering the Emerging Complexities of Molecular Mechanisms at GWAS Loci. American Journal of Human Genetics, 2018, 103, 637-653.	2.6	93
99	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
100	Phenotype-Specific Enrichment of Mendelian Disorder Genes near GWAS Regions across 62 Complex Traits. American Journal of Human Genetics, 2018, 103, 535-552.	2.6	90
101	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
102	Genetic variant effects on gene expression in human pancreatic islets and their implications for T2D. Nature Communications, 2020, 11, 4912.	5.8	89
103	Variation in the resistin gene is associated with obesity and insulin-related phenotypes in Finnish subjects. Diabetologia, 2004, 47, 1782-1788.	2.9	85
104	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
105	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
106	Identification of a Regulatory Variant That Binds FOXA1 and FOXA2 at the CDC123/CAMK1D Type 2 Diabetes GWAS Locus. PLoS Genetics, 2014, 10, e1004633.	1.5	80
107	Metabolic and cardiovascular traits: an abundance of recently identified common genetic variants. Human Molecular Genetics, 2008, 17, R102-R108.	1.4	75
108	Integration of human adipocyte chromosomal interactions with adipose gene expression prioritizes obesity-related genes from GWAS. Nature Communications, 2018, 9, 1512.	5.8	75

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109	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. Nature Communications, 2018, 9, 5052.	5.8	75
110	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	6.2	75
111	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74
112	A Large Set of Finnish Affected Sibling Pair Families With Type 2 Diabetes Suggests Susceptibility Loci on Chromosomes 6, 11, and 14. Diabetes, 2004, 53, 821-829.	0.3	73
113	Mitochondrial polymorphisms and susceptibility to type 2 diabetes-related traits in Finns. Human Genetics, 2005, 118, 245-254.	1.8	73
114	Genomeâ€Wide Association Study of Anthropometric Traits and Evidence of Interactions With Age and Study Year in Filipino Women. Obesity, 2011, 19, 1019-1027.	1.5	72
115	Evaluation of the Metabochip Genotyping Array in African Americans and Implications for Fine Mapping of GWAS-Identified Loci: The PAGE Study. PLoS ONE, 2012, 7, e35651.	1.1	71
116	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. American Journal of Human Genetics, 2016, 98, 229-242.	2.6	71
117	Common Variants in Maturity-Onset Diabetes of the Young Genes Contribute to Risk of Type 2 Diabetes in Finns. Diabetes, 2006, 55, 2534-2540.	0.3	69
118	HUGIn: Hi-C Unifying Genomic Interrogator. Bioinformatics, 2017, 33, 3793-3795.	1.8	69
119	A meta-analysis of genome-wide association studies for adiponectin levels in East Asians identifies a novel locus near WDR11-FGFR2. Human Molecular Genetics, 2014, 23, 1108-1119.	1.4	68
120	A Common Functional Regulatory Variant at a Type 2 Diabetes Locus Upregulates ARAP1 Expression in the Pancreatic Beta Cell. American Journal of Human Genetics, 2014, 94, 186-197.	2.6	67
121	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci. Diabetes, 2016, 65, 3200-3211.	0.3	67
122	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	5.8	64
123	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. Nature Communications, 2022, 13, 1644.	5.8	63
124	Genome-wide association study of homocysteine levels in Filipinos provides evidence for CPS1 in women and a stronger MTHFR effect in young adults. Human Molecular Genetics, 2010, 19, 2050-2058.	1.4	62
125	Association of FTO With Obesity-Related Traits in the Cebu Longitudinal Health and Nutrition Survey (CLHNS) Cohort. Diabetes, 2008, 57, 1987-1991.	0.3	61
126	Linkage Disequilibrium Between Microsatellite Markers Extends Beyond 1 cM on Chromosome 20 in Finns. Genome Research, 2001, 11, 1221-1226.	2.4	60

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127	Genome-Wide Association Meta-analysis Identifies Novel Variants Associated With Fasting Plasma Glucose in East Asians. Diabetes, 2015, 64, 291-298.	0.3	59
128	Genome-wide association studies in East Asians identify new loci for waist-hip ratio and waist circumference. Scientific Reports, 2016, 6, 17958.	1.6	58
129	Content and Performance of the MiniMUGA Genotyping Array: A New Tool To Improve Rigor and Reproducibility in Mouse Research. Genetics, 2020, 216, 905-930.	1.2	58
130	Tag SNP selection for Finnish individuals based on the CEPH Utah HapMap database. Genetic Epidemiology, 2006, 30, 180-190.	0.6	54
131	A Type 2 Diabetesâ€“Associated Functional Regulatory Variant in a Pancreatic Islet Enhancer at the ADCY5 Locus. Diabetes, 2017, 66, 2521-2530.	0.3	54
132	Multiple Hepatic Regulatory Variants at the GALNT2 GWAS Locus Associated with High-Density Lipoprotein Cholesterol. American Journal of Human Genetics, 2015, 97, 801-815.	2.6	49
133	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	5.8	49
134	Common, low-frequency, and rare genetic variants associated with lipoprotein subclasses and triglyceride measures in Finnish men from the METSIM study. PLoS Genetics, 2017, 13, e1007079.	1.5	49
135	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
136	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
137	A Common Type 2 Diabetes Risk Variant Potentiates Activity of an Evolutionarily Conserved Islet Stretch Enhancer and Increases C2CD4A and C2CD4B Expression. American Journal of Human Genetics, 2018, 102, 620-635.	2.6	47
138	Finding genes and variants for lipid levels after genome-wide association analysis. Current Opinion in Lipidology, 2012, 23, 98-103.	1.2	46
139	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. American Journal of Human Genetics, 2019, 105, 773-787.	2.6	45
140	Multi-ethnic fine-mapping of 14 central adiposity loci. Human Molecular Genetics, 2014, 23, 4738-4744.	1.4	41
141	Colocalization of GWAS and eQTL signals at loci with multiple signals identifies additional candidate genes for body fat distribution. Human Molecular Genetics, 2019, 28, 4161-4172.	1.4	41
142	Association of Birth Weight With Type 2 Diabetes and Glycemic Traits. JAMA Network Open, 2019, 2, e1910915.	2.8	41
143	FUT2 Variants Confer Susceptibility to Familial Otitis Media. American Journal of Human Genetics, 2018, 103, 679-690.	2.6	40
144	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	3.0	39

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145	Epigenome-wide association in adipose tissue from the METSIM cohort. Human Molecular Genetics, 2018, 27, 1830-1846.	1.4	38
146	Population-specific coding variant underlies genome-wide association with adiponectin level. Human Molecular Genetics, 2012, 21, 463-471.	1.4	37
147	A Partial Loss-of-Function Variant in AKT2 Is Associated With Reduced Insulin-Mediated Glucose Uptake in Multiple Insulin-Sensitive Tissues: A Genotype-Based Callback Positron Emission Tomography Study. Diabetes, 2018, 67, 334-342.	0.3	37
148	Allelic expression imbalance at high-density lipoprotein cholesterol locus MMAB-MVK. Human Molecular Genetics, 2010, 19, 1921-1929.	1.4	35
149	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
150	Human and rat skeletal muscle single-nuclei multi-omic integrative analyses nominate causal cell types, regulatory elements, and SNPs for complex traits. Genome Research, 2021, 31, 2258-2275.	2.4	31
151	Alterations to chromatin in intestinal macrophages link ILâ€10 deficiency to inappropriate inflammatory responses. European Journal of Immunology, 2016, 46, 1912-1925.	1.6	30
152	Identification of seven novel loci associated with amino acid levels using single-variant and gene-based tests in 8545 Finnish men from the METSIM study. Human Molecular Genetics, 2018, 27, 1664-1674.	1.4	30
153	Identification and functional analysis of glycemic trait loci in the China Health and Nutrition Survey. PLoS Genetics, 2018, 14, e1007275.	1.5	30
154	The causal effect of obesity on prediabetes and insulin resistance reveals the important role of adipose tissue in insulin resistance. PLoS Genetics, 2020, 16, e1009018.	1.5	29
155	The role of HNF4A variants in the risk of type 2 diabetes. Current Diabetes Reports, 2005, 5, 149-156.	1.7	28
156	Genetic association with lipids in Filipinos: waist circumference modifies an APOA5 effect on triglyceride levels. Journal of Lipid Research, 2013, 54, 3198-3205.	2.0	28
157	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	3.3	28
158	Genetic risk scores in the prediction of plasma glucose, impaired insulin secretion, insulin resistance and incident type 2 diabetes in the METSIM study. Diabetologia, 2017, 60, 1722-1730.	2.9	26
159	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.3	26
160	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. American Journal of Human Genetics, 2014, 94, 710-720.	2.6	24
161	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	2.6	24
162	BMI loci and longitudinal BMI from adolescence to young adulthood in an ethnically diverse cohort. International Journal of Obesity, 2017, 41, 759-768.	1.6	23

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163	Multi-SNP mediation intersection-union test. Bioinformatics, 2019, 35, 4724-4729.	1.8	23
164	Identification of TBX15 as an adipose master trans regulator of abdominal obesity genes. Genome Medicine, 2021, 13, 123.	3.6	23
165	Genetic effects on liver chromatin accessibility identify disease regulatory variants. American Journal of Human Genetics, 2021, 108, 1169-1189.	2.6	22
166	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	1.4	21
167	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	2.6	21
168	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. Communications Biology, 2022, 5, 329.	2.0	21
169	Genetic Determinants of Circulating Glycine Levels and Risk of Coronary Artery Disease. Journal of the American Heart Association, 2019, 8, e011922.	1.6	20
170	A New Liver Expression Quantitative Trait Locus Map From 1,183 Individuals Provides Evidence for Novel Expression Quantitative Trait Loci of Drug Response, Metabolic, and Sexâ€Biased Phenotypes. Clinical Pharmacology and Therapeutics, 2020, 107, 1383-1393.	2.3	20
171	Trans-ancestry Fine Mapping and Molecular Assays Identify Regulatory Variants at the ANGPTL8 HDL-C GWAS Locus. G3: Genes, Genomes, Genetics, 2017, 7, 3217-3227.	0.8	19
172	Open Chromatin Profiling in Adipose Tissue Marks Genomic Regions with Functional Roles in Cardiometabolic Traits. G3: Genes, Genomes, Genetics, 2019, 9, 2521-2533.	0.8	19
173	Evaluation of SLC2A10 (GLUT10) as a candidate gene for type 2 diabetes and related traits in Finns. Molecular Genetics and Metabolism, 2005, 85, 323-327.	0.5	18
174	A comprehensive SNP and indel imputability database. Bioinformatics, 2013, 29, 528-531.	1.8	18
175	ACE2 expression in adipose tissue is associated with cardio-metabolic risk factors and cell type compositionâ€"implications for COVID-19. International Journal of Obesity, 2022, 46, 1478-1486.	1.6	18
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