List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Relationship between glucose homeostasis and obesity in early life—a study of Italian children and adolescents. Human Molecular Genetics, 2022, 31, 816-826.	1.4	10
2	The use of polygenic risk scores in pre-implantation genetic testing: an unproven, unethical practice. European Journal of Human Genetics, 2022, 30, 493-495.	1.4	38
3	Bifidobacterium Is Enriched in Gut Microbiome of Kashmiri Women with Polycystic Ovary Syndrome. Genes, 2022, 13, 379.	1.0	13
4	LongITools: Dynamic longitudinal exposome trajectories in cardiovascular and metabolic noncommunicable diseases. Environmental Epidemiology, 2022, 6, e184.	1.4	6
5	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
6	Risk of Recurrent Pregnancy Loss in the Ukrainian Population Using a Combined Effect of Genetic Variants: A Case-Control Study. Genes, 2021, 12, 64.	1.0	6
7	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87
8	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
9	Functional Effects In Silico Prediction for Androgen Receptor Ligand-Binding Domain Novel 1836S Mutation. Life, 2021, 11, 659.	1.1	6
10	The Role of the European Society of Human Genetics in Delivering Genomic Education. Frontiers in Genetics, 2021, 12, 693952.	1.1	6
11	Measurement invariance testing of the patient health questionnaire-9 (PHQ-9) across people with and without diabetes mellitus from the NHANES, EMHS and UK Biobank datasets. Journal of Affective Disorders, 2021, 292, 311-318.	2.0	5
12	Exploring the role of genetic confounding in the association between maternal and offspring body mass index: evidence from three birth cohorts. International Journal of Epidemiology, 2020, 49, 233-243.	0.9	18
13	Characterization of <i>GDF2</i> Mutations and Levels of BMP9 and BMP10 in Pulmonary Arterial Hypertension. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 575-585.	2.5	80
14	Understanding the cumulative risk of maternal prenatal biopsychosocial factors on birth weight: a DynaHEALTH study on two birth cohorts. Journal of Epidemiology and Community Health, 2020, 74, jech-2019-213154.	2.0	5
15	Heterogeneous Effects of Calorie Content and Nutritional Components Underlie Dietary Influence on Pancreatic Cancer Susceptibility. Cell Reports, 2020, 32, 107880.	2.9	6
16	Expression Quantitative Trait Locus Mapping in Pulmonary Arterial Hypertension. Genes, 2020, 11, 1247.	1.0	3
17	Whole-Blood RNA Profiles Associated with Pulmonary Arterial Hypertension and Clinical Outcome. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 586-594.	2.5	45
18	Mendelian randomisation analysis of red cell distribution width in pulmonary arterial hypertension. European Respiratory Journal, 2020, 55, 1901486.	3.1	26

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19	Understanding the complexity of glycaemic health: systematic bio-psychosocial modelling of fasting glucose in middle-age adults; a DynaHEALTH study. International Journal of Obesity, 2019, 43, 1181-1192.	1.6	11
20	Cohort Profile: The DynaHEALTH consortium – a European consortium for a life-course bio-psychosocial model of healthy ageing of glucose homeostasis. International Journal of Epidemiology, 2019, 48, 1051-1051k.	0.9	10
21	Human pancreatic islet three-dimensional chromatin architecture provides insights into the genetics of type 2 diabetes. Nature Genetics, 2019, 51, 1137-1148.	9.4	208
22	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. Scientific Reports, 2019, 9, 9439.	1.6	5
23	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. Science Advances, 2019, 5, eaaw3095.	4.7	86
24	miRNAs Identify Shared Pathways in Alzheimer's and Parkinson's Diseases. Trends in Molecular Medicine, 2019, 25, 662-672.	3.5	44
25	Multilocus associations of inflammatory genes with the risk of type 1 diabetes. Gene, 2019, 707, 1-8.	1.0	4
26	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
27	Genetic correlations of psychiatric traits with body composition and glycemic traits are sex- and age-dependent. Nature Communications, 2019, 10, 5765.	5.8	59
28	Alzheimer's disease pathology explains association between dementia with Lewy bodies and APOEâ€îµ4/TOMM40 long polyâ€ī repeat allele variants. Alzheimer's and Dementia: Translational Research and Clinical Interventions, 2019, 5, 814-824.	1.8	14
29	A meta-analysis of Italian and Estonian individuals shows an effect of common variants in HMGCR on blood apoB levels. Biomarkers in Medicine, 2019, 13, 931-940.	0.6	0
30	Genetic determinants of risk in pulmonary arterial hypertension: international genome-wide association studies and meta-analysis. Lancet Respiratory Medicine,the, 2019, 7, 227-238.	5.2	122
31	Genomics of body fat percentage may contribute to sex bias in anorexia nervosa. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 428-438.	1.1	87
32	Identification of rare sequence variation underlying heritable pulmonary arterial hypertension. Nature Communications, 2018, 9, 1416.	5.8	279
33	Genome-wide meta-analysis identifies novel determinants of circulating serum progranulin. Human Molecular Genetics, 2018, 27, 546-558.	1.4	15
34	Genetic Determinants of Circulating Estrogen Levels and Evidence of a Causal Effect of Estradiol on Bone Density in Men. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 991-1004.	1.8	60
35	Evidence for three genetic loci involved in both anorexia nervosa risk and variation of body mass index. Molecular Psychiatry, 2017, 22, 192-201.	4.1	63
36	SCOPA and META-SCOPA: software for the analysis and aggregation of genome-wide association studies of multiple correlated phenotypes. BMC Bioinformatics, 2017, 18, 25.	1.2	25

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37	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
38	A Low-Frequency Inactivating <i>AKT2</i> 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
39	The TAD-pathway for GWAS signals. European Journal of Human Genetics, 2017, 25, 1179-1180.	1.4	2
40	A rare-variant test for high-dimensional data. European Journal of Human Genetics, 2017, 25, 988-994.	1.4	15
41	MARV: a tool for genome-wide multi-phenotype analysis of rare variants. BMC Bioinformatics, 2017, 18, 110.	1.2	17
42	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
43	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. PLoS Medicine, 2017, 14, e1002383.	3.9	341
44	Genome-wide physical activity interactions in adiposity ― A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
45	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
46	Associations between TOMM40 Poly-T Repeat Variants and Dementia in Cases with Parkinsonism. Journal of Parkinson's Disease, 2016, 6, 99-108.	1.5	6
47	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. American Journal of Human Genetics, 2016, 98, 857-868.	2.6	21
48	Genome-Wide Association Studies of Type 2 Diabetes. , 2016, , 13-61.		8
49	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406
50	Genomewide metaâ€analysis identifies loci associated with <scp>IGF</scp> â€I and <scp>IGFBP</scp> â€3 levels with impact on ageâ€related traits. Aging Cell, 2016, 15, 811-824.	3.0	83
51	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74
52	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies <i>BCL2</i> and <i>FAM19A2</i> as Novel Insulin Sensitivity Loci. Diabetes, 2016, 65, 3200-3211.	0.3	67
53	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284
54	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245

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55	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
56	Harmonising and linking biomedical and clinical data across disparate data archives to enable integrative cross-biobank research. European Journal of Human Genetics, 2016, 24, 521-528.	1.4	27
57	A new strategy for enhancing imputation quality of rare variants from next-generation sequencing data via combining SNP and exome chip data. BMC Genomics, 2015, 16, 1109.	1.2	13
58	Prevalence and Regional Distribution of Autoantibodies Against GAD65Ab in a European Population Without Diabetes: The EPIC-InterAct Study. Diabetes Care, 2015, 38, e114-e115.	4.3	8
59	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
60	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	1.5	77
61	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	0.9	123
62	1A.11. Journal of Hypertension, 2015, 33, e3-e4.	0.3	1
63	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
64	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
65	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	5.8	706
66	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.3	63
67	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
68	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
69	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
70	Genome-wide enrichment analysis between endometriosis and obesity-related traits reveals novel susceptibility loci. Human Molecular Genetics, 2015, 24, 1185-1199.	1.4	71
71	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
72	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	4.1	235

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73	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. Diabetes, 2014, 63, 2158-2171.	0.3	297
74	A Central Role for GRB10 in Regulation of Islet Function in Man. PLoS Genetics, 2014, 10, e1004235.	1.5	164
75	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	1.5	80
76	Genome Wide Meta-analysis Highlights the Role of Genetic Variation in RARRES2 in the Regulation of Circulating Serum Chemerin. PLoS Genetics, 2014, 10, e1004854.	1.5	31
77	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	0.5	107
78	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	13.5	113
79	Revisiting the Thrifty Gene Hypothesis via 65 Loci Associated with Susceptibility to Type 2 Diabetes. American Journal of Human Genetics, 2014, 94, 176-185.	2.6	72
80	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
81	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
82	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
83	Expression of Phosphofructokinase in Skeletal Muscle Is Influenced by Genetic Variation and Associated With Insulin Sensitivity. Diabetes, 2014, 63, 1154-1165.	0.3	41
84	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
85	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	2.6	60
86	Genome-wide association and longitudinal analyses reveal genetic loci linking pubertal height growth, pubertal timing and childhood adiposity. Human Molecular Genetics, 2013, 22, 2735-2747.	1.4	188
87	Meta-Analysis Investigating Associations Between Healthy Diet and Fasting Glucose and Insulin Levels and Modification by Loci Associated With Glucose Homeostasis in Data From 15 Cohorts. American Journal of Epidemiology, 2013, 177, 103-115.	1.6	74
88	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	9.4	675
89	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. Journal of the American Society of Nephrology: JASN, 2013, 24, 2105-2117.	3.0	33
90	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	9.4	808

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91	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
92	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
93	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	3.9	178
94	Higher Magnesium Intake Is Associated with Lower Fasting Glucose and Insulin, with No Evidence of Interaction with Select Genetic Loci, in a Meta-Analysis of 15 CHARGE Consortium Studies. Journal of Nutrition, 2013, 143, 345-353.	1.3	47
95	Genome-wide association study of primary tooth eruption identifies pleiotropic loci associated with height and craniofacial distances. Human Molecular Genetics, 2013, 22, 3807-3817.	1.4	84
96	A common biological basis of obesity and nicotine addiction. Translational Psychiatry, 2013, 3, e308-e308.	2.4	51
97	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
98	A Genome-Wide Association Meta-Analysis of Circulating Sex Hormone–Binding Globulin Reveals Multiple Loci Implicated in Sex Steroid Hormone Regulation. PLoS Genetics, 2012, 8, e1002805.	1.5	151
99	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	1.5	79
100	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	1.5	166
101	The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. PLoS Genetics, 2012, 8, e1002793.	1.5	448
102	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
103	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
104	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	1.4	64
105	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
106	Common variants at 12q15 and 12q24 are associated with infant head circumference. Nature Genetics, 2012, 44, 532-538.	9.4	130
107	No Interactions Between Previously Associated 2-Hour Glucose Gene Variants and Physical Activity or BMI on 2-Hour Glucose Levels. Diabetes, 2012, 61, 1291-1296.	0.3	23
108	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320

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109	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
110	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
111	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
112	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
113	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. Nature Genetics, 2011, 43, 984-989.	9.4	481
114	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
115	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	9.4	501
116	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	13.7	401
117	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.	0.3	335
118	Abdominal Aortic Aneurysm Is Associated with a Variant in Low-Density Lipoprotein Receptor-Related Protein 1. American Journal of Human Genetics, 2011, 89, 619-627.	2.6	185
119	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	3.0	208
120	SAILâ $\in$ "a software system for sample and phenotype availability across biobanks and cohorts. Bioinformatics, 2011, 27, 589-591.	1.8	14
121	Sequence variants at CYP1A1–CYP1A2 and AHR associate with coffee consumption. Human Molecular Genetics, 2011, 20, 2071-2077.	1.4	114
122	Obesity-susceptibility loci have a limited influence on birth weight: a meta-analysis of up to 28,219 individuals. American Journal of Clinical Nutrition, 2011, 93, 851-860.	2.2	58
123	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	1.4	168
124	Association of Genetic Loci With Glucose Levels in Childhood and Adolescence. Diabetes, 2011, 60, 1805-1812.	0.3	103
125	Genome-wide association and genetic functional studies identify <i>autism susceptibility candidate 2</i> gene ( <i>AUTS2</i> ) in the regulation of alcohol consumption. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7119-7124.	3.3	258
126	Total Zinc Intake May Modify the Glucose-Raising Effect of a Zinc Transporter (SLC30A8) Variant: A 14-Cohort Meta-analysis. Diabetes, 2011, 60, 2407-2416.	0.3	91

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127	Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113.	1.5	106
128	A Genome-Wide Screen for Interactions Reveals a New Locus on 4p15 Modifying the Effect of Waist-to-Hip Ratio on Total Cholesterol. PLoS Genetics, 2011, 7, e1002333.	1.5	29
129	Association of FTO variants with BMI and fat mass in the self-contained population of Sorbs in Germany. European Journal of Human Genetics, 2010, 18, 104-110.	1.4	81
130	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	13.7	737
131	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
132	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	9.4	591
133	Genetic loci influencing kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 373-375.	9.4	246
134	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. Nature Genetics, 2010, 42, 430-435.	9.4	223
135	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	9.4	710
136	Sequence variants at CHRNB3–CHRNA6 and CYP2A6 affect smoking behavior. Nature Genetics, 2010, 42, 448-453.	9.4	649
137	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
138	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
139	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
140	Integrated Genetic and Epigenetic Analysis Identifies Haplotype-Specific Methylation in the FTO Type 2 Diabetes and Obesity Susceptibility Locus. PLoS ONE, 2010, 5, e14040.	1.1	215
141	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
142	Interactions of Dietary Whole-Grain Intake With Fasting Glucose- and Insulin-Related Genetic Loci in Individuals of European Descent: A meta-analysis of 14 cohort studies. Diabetes Care, 2010, 33, 2684-2691.	4.3	127
143	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.3	387
144	Genome-Wide Association Study Identifies Two Novel Regions at 11p15.5-p13 and 1p31 with Major Impact on Acute-Phase Serum Amyloid A. PLoS Genetics, 2010, 6, e1001213.	1.5	24

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145	Two New Loci for Body-Weight Regulation Identified in a Joint Analysis of Genome-Wide Association Studies for Early-Onset Extreme Obesity in French and German Study Groups. PLoS Genetics, 2010, 6, e1000916.	1.5	287
146	Plasma Protein Biomarkers for Depression and Schizophrenia by Multi Analyte Profiling of Case-Control Collections. PLoS ONE, 2010, 5, e9166.	1.1	294
147	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
148	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
149	Linkage Disequilibrium Mapping of the Replicated Type 2 Diabetes Linkage Signal on Chromosome 1q. Diabetes, 2009, 58, 1704-1709.	0.3	30
150	A Genome-Wide Association Study Reveals Variants in ARL15 that Influence Adiponectin Levels. PLoS Genetics, 2009, 5, e1000768.	1.5	148
151	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
152	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662
153	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	9.4	742
154	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
155	Type 2 diabetes: new genes, new understanding. Trends in Genetics, 2008, 24, 613-621.	2.9	229
156	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
157	Family history of depression is associated with younger age of onset in patients with recurrent depression. Psychological Medicine, 2008, 38, 641-649.	2.7	53
158	Association between the ACCN1 Gene and Multiple Sclerosis in Central East Sardinia. PLoS ONE, 2007, 2, e480.	1.1	36
159	Risk for Relatives of Patients with Multiple Sclerosis in Central Sardinia, Italy. Neuroepidemiology, 2003, 22, 290-296.	1.1	13
160	Multiple sclerosis recurrence risk for siblings in an isolated population of Central Sardinia, Italy. Genetic Epidemiology, 2002, 22, 265-271.	0.6	19