

CITATION REPORT

List of articles citing

A genome-wide association study of type 2 diabetes in Finns detects multiple susceptibility variants

DOI: 10.1126/science.1142382
Science, 2007, 316, 1341-5.

Source: <https://exaly.com/paper-pdf/42378817/citation-report.pdf>

Version: 2024-04-25

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
2309	Genome-wide association studies of cancer. 2007 , 3, 419-27		10
2308	A search for variants associated with young-onset type 2 diabetes in American Indians in a 100K genotyping array. 2007 , 56, 3045-52		79
2307	Common variants of the novel type 2 diabetes genes CDKAL1 and HHEX/IDE are associated with decreased pancreatic beta-cell function. 2007 , 56, 3101-4		203
2306	Identification of type 2 diabetes genes in Mexican Americans through genome-wide association studies. 2007 , 56, 3033-44		105
2305	Genomic copy number and expression variation within the C57BL/6J inbred mouse strain. 2008 , 18, 60-6		91
2304	Tyrosine hydroxylase: another piece of the genetics of hypertension puzzle. 2007 , 116, 970-2		2
2303	Genetics of the cardiometabolic syndrome: new insights and therapeutic implications. 2007 , 1, 37-47		12
2302	Metabolic and electrical oscillations: partners in controlling pulsatile insulin secretion. 2007 , 293, E890-900		127
2301	Association study of the genetic polymorphisms of the transcription factor 7-like 2 (TCF7L2) gene and type 2 diabetes in the Chinese population. 2007 , 56, 2631-7		149
2300	Functional effects of nonsynonymous polymorphisms in the human TRPV1 gene. 2007 , 293, F1865-76		46
2299	Linkage disequilibrium in wild mice. 2007 , 3, e144		89
2298	Power to detect risk alleles using genome-wide tag SNP panels. 2007 , 3, 1827-37		77
2297	Copy number variants and common disorders: filling the gaps and exploring complexity in genome-wide association studies. 2007 , 3, 1787-99		157
2296	Orchestration of glucose homeostasis: from a small acorn to the California oak. 2007 , 56, 1489-501		91
2295	Genomewide association analysis of coronary artery disease. 2007 , 357, 443-53		1608
2294	Gone with the Wnts: beta-catenin, T-cell factor, forkhead box O, and oxidative stress in age-dependent diseases of bone, lipid, and glucose metabolism. 2007 , 21, 2605-14		262
2293	Impact of family history of diabetes and ethnicity on β -cell function in obese, glucose-tolerant individuals. 2007 , 92, 4656-63		28

2292	Obesity. 2007 ,	11
2291	The genomics gold rush. 2007 , 298, 218-21	59
2290	Genetics of cardiovascular diseases: from single mutations to the whole genome. 2007 , 116, 1714-24	78
2289	Genetic susceptibility to peripheral arterial disease: a dark corner in vascular biology. 2007 , 27, 2068-78	49
2288	Problems with genome-wide association studies. <i>Science</i> , 2007 , 316, 1840-2	33-3 71
2287	Successful design and conduct of genome-wide association studies. 2007 , 16 Spec No. 2, R220-5	61
2286	A 100K genome-wide association scan for diabetes and related traits in the Framingham Heart Study: replication and integration with other genome-wide datasets. 2007 , 56, 3063-74	74
2285	Genetic factors in diabetic nephropathy. 2007 , 2, 1306-16	145
2284	Genome-wide association: which do you want first: the good news, the bad news, or the good news?. 2007 , 56, 2844-8	6
2283	Validity of Reported Genetic Risk Factors for Acute Coronary SyndromeReply. 2007 , 298, 1757	
2282	Interpreting P values in pharmacogenetic studies: a call for process and perspective. 2007 , 25, 4513-5	33
2281	A genotype calling algorithm for the Illumina BeadArray platform. 2007 , 23, 2741-6	194
2280	Validity of reported genetic risk factors for acute coronary syndrome. 2007 , 298, 1757; author reply 1759	
2279	Validity of reported genetic risk factors for acute coronary syndrome. 2007 , 298, 1758; author reply 1759	
2278	Point: genetic risk feedback for common disease time to test the waters. 2007 , 16, 1724-6	10
2277	Relevance of cost-effectiveness analysis to clinicians and policy makers. 2007 , 298, 221-4	79
2276	Validity of reported genetic risk factors for acute coronary syndrome. 2007 , 298, 1757-8; author reply 1759	
2275	Studies of association of variants near the HHEX, CDKN2A/B, and IGF2BP2 genes with type 2 diabetes and impaired insulin release in 10,705 Danish subjects: validation and extension of genome-wide association studies. 2007 , 56, 3105-11	207

2274	Evaluation of genome-wide power of genetic association studies based on empirical data from the HapMap project. 2007 , 16, 2494-505		25
2273	Generating new candidate genes for neonatal diabetes: functional and genetic studies of insulin secretion in type 2 diabetes. 2007 , 12, 75-85		1
2272	Monogenic disorders of the pancreatic β -cell: personalizing treatment for rare forms of diabetes and hypoglycemia. 2007 , 4, 247-259		3
2271	Validity of reported genetic risk factors for acute coronary syndrome. 2007 , 298, 1758-9; author reply 1759		
2270	Genome-wide association scans for Type 2 diabetes: new insights into biology and therapy. 2007 , 28, 598-601		20
2269	Cellular senescence in cancer and aging. 2007 , 130, 223-33		1245
2268	Implementation of genetics to personalize medicine. 2007 , 4, 248-65		20
2267	Genome-wide association analysis identifies loci for type 2 diabetes and triglyceride levels. <i>Science</i> , 2007 , 316, 1331-6	33.3	2364
2266	The obesity-associated FTO gene encodes a 2-oxoglutarate-dependent nucleic acid demethylase. <i>Science</i> , 2007 , 318, 1469-72	33.3	1119
2265	Risk alleles for multiple sclerosis identified by a genomewide study. 2007 , 357, 851-62		1327
2264	Les aspects g�n�tiques de l'ob�sit�. 2007 , 1, 22-27		
2263	Replication of genome-wide association signals in UK samples reveals risk loci for type 2 diabetes. <i>Science</i> , 2007 , 316, 1336-41	33.3	1823
2262	Noncoding miRNAs as key controllers of pancreatic β -cell functions. 2007 , 2, 461-468		
2261	Multidrug resistance in epilepsy: a pharmacogenomic update. 2007 , 8, 1441-9		38
2260	The biotechnology era: has the promise been fulfilled?. 2007 , 2, 1549-53		2
2259	Genetics and genomics in human lung transplantation. 2007 , 1, 271-8		1
2258	Prediction of individual genetic risk to disease from genome-wide association studies. 2007 , 17, 1520-8		436
2257	Future use of genomics in coronary artery disease. 2007 , 50, 1933-40		49

2256	The replication of beta cells in normal physiology, in disease and for therapy. 2007 , 3, 758-68	210
2255	Genome wide association (GWA) study for early onset extreme obesity supports the role of fat mass and obesity associated gene (FTO) variants. 2007 , 2, e1361	388
2254	Heterogeneity in meta-analyses of genome-wide association investigations. 2007 , 2, e841	246
2253	Admixture mapping provides evidence of association of the VNN1 gene with hypertension. 2007 , 2, e1244	43
2252	[Anatomical and functional plasticity of pancreatic beta-cells and type 2 diabetes]. 2007 , 23, 885-94	5
2251	Genome-Wide Association Studies: Progress in Identifying Genetic Biomarkers in Common, Complex Diseases. 2007 , 2, 117727190700200	18
2250	A beginning of the end of the holism versus reductionism debate?: Molecular biology goes cellular and organismic. 2007 , 13, 10-13	7
2249	The Framingham Heart Study 100K SNP genome-wide association study resource: overview of 17 phenotype working group reports. 2007 , 8 Suppl 1, S1	152
2248	Genome-wide association study for subclinical atherosclerosis in major arterial territories in the NHLBI's Framingham Heart Study. 2007 , 8 Suppl 1, S4	110
2247	Genome miners rush to stake claims. 2007 , 447, 623	3
2246	Replicating genotype-phenotype associations. 2007 , 447, 655-60	1363
2245	Genomics: Encyclopaedia of humble DNA. 2007 , 447, 782-3	22
2244	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. 2007 , 39, 1329-37	1130
2243	From fused toes in mice to human obesity. 2007 , 39, 706-7	19
2242	Guilt beyond a reasonable doubt. 2007 , 39, 813-5	130
2241	Conjuring SNPs to detect associations. 2007 , 39, 815-6	24
2240	New models of collaboration in genome-wide association studies: the Genetic Association Information Network. 2007 , 39, 1045-51	258
2239	Copy number variants and genetic traits: closer to the resolution of phenotypic to genotypic variability. 2007 , 8, 639-46	335

2238	Genome-wide association studies provide new insights into type 2 diabetes aetiology. 2007 , 8, 657-62	468
2237	How stem cells age and why this makes us grow old. 2007 , 8, 703-13	688
2236	A common variant of the interleukin 6 receptor (IL-6r) gene increases IL-6r and IL-6 levels, without other inflammatory effects. 2007 , 8, 552-9	98
2235	Introduction to genetic association studies. 2007 , 127, 2283-7	7
2234	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. 2007 , 447, 661-78	7801
2233	A second generation human haplotype map of over 3.1 million SNPs. 2007 , 449, 851-61	3647
2232	Genetics and type 2 diabetes in youth. 2007 , 8 Suppl 9, 42-7	17
2231	The importance of TCF7L2. 2007 , 24, 1062-6	70
2230	A new era for Type 2 diabetes genetics. 2007 , 24, 1181-6	28
2229	What will whole genome searches for susceptibility genes for common complex disease offer to clinical practice?. 2008 , 263, 16-27	43
2228	Susceptibility genes and B-chronic lymphocytic leukaemia. 2007 , 139, 762-71	23
2227	Identification of novel candidate genes for type 2 diabetes from a genome-wide association scan in the Old Order Amish: evidence for replication from diabetes-related quantitative traits and from independent populations. 2007 , 56, 3053-62	136
2226	Mechanisms of disease: The genetic basis of coronary heart disease. 2007 , 4, 558-69	52
2225	Variation in the HHEX-IDE gene region predisposes to type 2 diabetes in the prospective, population-based EPIC-Potsdam cohort. 2007 , 50, 2405-7	21
2224	Mutations in the SLC30A8 gene are not a major cause of MODY or other forms of early-onset, autosomal dominant type 2 diabetes. 2007 , 50, 2224-6	7
2223	Genetic studies of diabetes following the advent of the genome-wide association study: where do we go from here?. 2007 , 50, 2229-33	25
2222	Variations in the HHEX gene are associated with increased risk of type 2 diabetes in the Japanese population. 2007 , 50, 2461-6	178
2221	Variation in the FTO gene locus is associated with cerebrocortical insulin resistance in humans. 2007 , 50, 2602-3	89

2220	Polymorphisms in the gene encoding the voltage-dependent Ca(2+) channel Ca (V)2.3 (CACNA1E) are associated with type 2 diabetes and impaired insulin secretion. 2007 , 50, 2467-75	34
2219	TCF7L2 is associated with high serum triacylglycerol and differentially expressed in adipose tissue in families with familial combined hyperlipidaemia. 2008 , 51, 62-9	41
2218	The GCKR rs780094 polymorphism is associated with elevated fasting serum triacylglycerol, reduced fasting and OGTT-related insulinaemia, and reduced risk of type 2 diabetes. 2008 , 51, 70-5	137
2217	Molecular genetics of human growth hormone, insulin-like growth factors and their pathways in common disease. 2007 , 122, 1-21	57
2216	Sideways Glance: Genome wide association studies for type 2 diabetes mellitus. 2007 , 2, 245-8	5
2215	Genome-wide association studies: A new era in human genetics. 2007 , 1, 271-272	
2214	Association of the TCF7L2 polymorphism with colorectal cancer and adenoma risk. 2008 , 19, 975-80	33
2213	Genetische Disposition für die Entwicklung von Adipositas und Typ-2-Diabetes im Mausmodell und beim Menschen. 2008 , 3, 86-88	
2212	Genetic factors for human obesity. 2008 , 65, 1086-98	47
2211	Realistic expectations of prepulse inhibition in translational models for schizophrenia research. 2008 , 199, 331-88	412
2210	The FTO gene, implicated in human obesity, is found only in vertebrates and marine algae. 2008 , 66, 80-4	50
2209	Drug resistance and genetic mapping in Plasmodium falciparum. 2008 , 54, 223-39	51
2208	Diabetic modifier QTLs in F(2) intercrosses carrying homozygous transgene of TGF-beta. 2008 , 19, 15-25	4
2207	[Congestive heart failure is a common disease with complex inheritance--new perspectives through genome wide association studies]. 2008 , 49, 405-10, 412	1
2206	Analysis of novel risk loci for type 2 diabetes in a general French population: the D.E.S.I.R. study. 2008 , 86, 341-8	60
2205	Replication of the association between variants in WFS1 and risk of type 2 diabetes in European populations. 2008 , 51, 458-63	89
2204	Candidate gene studies reveal that the WFS1 gene joins the expanding list of novel type 2 diabetes genes. 2008 , 51, 391-3	20
2203	Polymorphisms in AHI1 are not associated with type 2 diabetes or related phenotypes in Danes: non-replication of a genome-wide association result. 2008 , 51, 609-14	1

2202	Polymorphisms in the TCF7L2, CDKAL1 and SLC30A8 genes are associated with impaired proinsulin conversion. 2008 , 51, 597-601	215
2201	The common SLC30A8 Arg325Trp variant is associated with reduced first-phase insulin release in 846 non-diabetic offspring of type 2 diabetes patients--the EUGENE2 study. 2008 , 51, 816-20	101
2200	Strong association of common variants in the CDKN2A/CDKN2B region with type 2 diabetes in French Europids. 2008 , 51, 821-6	30
2199	Genetic analysis of recently identified type 2 diabetes loci in 1,638 unselected patients with type 2 diabetes and 1,858 control participants from a Norwegian population-based cohort (the HUNT study). 2008 , 51, 971-7	76
2198	Newly identified loci highlight beta cell dysfunction as a key cause of type 2 diabetes: where are the insulin resistance genes?. 2008 , 51, 1100-10	237
2197	Beta cell glucose sensitivity is decreased by 39% in non-diabetic individuals carrying multiple diabetes-risk alleles compared with those with no risk alleles. 2008 , 51, 1989-92	41
2196	Positive association between variations in CDKAL1 and type 2 diabetes in Han Chinese individuals. 2008 , 51, 2134-7	40
2195	The search for putative unifying genetic factors for components of the metabolic syndrome. 2008 , 51, 2242-51	56
2194	Assessing gene-treatment interactions at the FTO and INSIG2 loci on obesity-related traits in the Diabetes Prevention Program. 2008 , 51, 2214-23	80
2193	Gene variants influencing measures of inflammation or predisposing to autoimmune and inflammatory diseases are not associated with the risk of type 2 diabetes. 2008 , 51, 2205-13	38
2192	Common variants in the TCF7L2 gene help to differentiate autoimmune from non-autoimmune diabetes in young (15-34 years) but not in middle-aged (40-59 years) diabetic patients. 2008 , 51, 2224-32	28
2191	Association of chromosome 9p21 SNPs with cardiovascular phenotypes in morbid obesity using electronic health record data. 2008 , 2, 33-43	17
2190	Molecular genetics of myocardial infarction. 2008 , 2, 7-22	28
2189	Genome-wide association study of susceptibility alleles for coronary artery disease. 2008 , 10, 183-5	
2188	Common and rare alleles as causes of complex phenotypes. 2008 , 10, 194-200	13
2187	TCF7L2 genetic defect and type 2 diabetes. 2008 , 8, 149-55	63
2186	Genes and type 2 diabetes mellitus. 2008 , 8, 192-7	46
2185	Genetic susceptibility of diabetic retinopathy. 2008 , 8, 257-62	23

2184	Therapeutic options for premature coronary artery disease. 2008 , 10, 294-303	1
2183	Search for type 2 diabetes susceptibility genes on chromosomes 1q, 3q and 12q. 2008 , 53, 314-324	33
2182	Structural genomic variation in ischemic stroke. 2008 , 9, 101-8	26
2181	Methods for meta-analysis in genetic association studies: a review of their potential and pitfalls. 2008 , 123, 1-14	159
2180	Haplotypic analysis of Wellcome Trust Case Control Consortium data. 2008 , 123, 273-80	60
2179	Genome-wide screen for asthma in Puerto Ricans: evidence for association with 5q23 region. 2008 , 123, 455-68	63
2178	Type 2 diabetes susceptibility loci in the Ashkenazi Jewish population. 2008 , 124, 101-4	23
2177	Evaluation of a SNP map of 6q24-27 confirms diabetic nephropathy loci and identifies novel associations in type 2 diabetes patients with nephropathy from an African-American population. 2008 , 124, 63-71	14
2176	Missing data imputation and haplotype phase inference for genome-wide association studies. 2008 , 124, 439-50	124
2175	Lack of association between PKLR rs3020781 and NOS1AP rs7538490 and type 2 diabetes, overweight, obesity and related metabolic phenotypes in a Danish large-scale study: case-control studies and analyses of quantitative traits. 2008 , 9, 118	11
2174	Evaluating the association of common PBX1 variants with type 2 diabetes. 2008 , 9, 14	2
2173	Aryl hydrocarbon receptor nuclear translocator (ARNT) gene as a positional and functional candidate for type 2 diabetes and prediabetic intermediate traits: Mutation detection, case-control studies, and gene expression analysis. 2008 , 9, 16	14
2172	Lack of association of genetic variation in chromosome region 15q14-22.1 with type 2 diabetes in a Japanese population. 2008 , 9, 22	1
2171	Genome-wide association study for renal traits in the Framingham Heart and Atherosclerosis Risk in Communities Studies. 2008 , 9, 49	26
2170	Impact of nine common type 2 diabetes risk polymorphisms in Asian Indian Sikhs: PPARG2 (Pro12Ala), IGF2BP2, TCF7L2 and FTO variants confer a significant risk. 2008 , 9, 59	199
2169	'Fat mass and obesity associated' gene (FTO): no significant association of variant rs9939609 with weight loss in a lifestyle intervention and lipid metabolism markers in German obese children and adolescents. 2008 , 9, 85	76
2168	Association between the FTO rs9939609 polymorphism and the metabolic syndrome in a non-Caucasian multi-ethnic sample. 2008 , 7, 5	73
2167	Worldwide population differentiation at disease-associated SNPs. 2008 , 1, 22	98

2166	In search of causal variants: refining disease association signals using cross-population contrasts. 2008 , 9, 58	27
2165	Cardiovascular GO annotation initiative year 1 report: why cardiovascular GO?. 2008 , 8, 1950-3	12
2164	Type 2 diabetes genetics: starting to solve the puzzle. 2008 , 25, 214-215	
2163	Susceptibility genes in movement disorders. 2008 , 23, 927-934	2
2162	Mechanisms of β cell failure in the pathogenesis of Type 2 diabetes. 2008 , 69, 111-115	4
2161	Microarray-based DNA profiling to study genomic aberrations. 2008 , 60, 437-40	10
2160	CHOP T/C and C/T haplotypes contribute to early-onset type 2 diabetes in Italians. 2008 , 217, 291-5	9
2159	A support vector machine approach for detecting gene-gene interaction. 2008 , 32, 152-67	81
2158	Increasing the power of identifying gene x gene interactions in genome-wide association studies. 2008 , 32, 255-63	146
2157	Estimation of the multiple testing burden for genomewide association studies of nearly all common variants. 2008 , 32, 381-5	584
2156	Evaluating cost efficiency of SNP chips in genome-wide association studies. 2008 , 32, 387-95	21
2155	The thrifty epigenotype: an acquired and heritable predisposition for obesity and diabetes?. 2008 , 30, 156-66	186
2154	Calibration of credibility of agnostic genome-wide associations. 2008 , 147B, 964-72	18
2153	The positives, protocols, and perils of genome-wide association. 2008 , 147B, 1288-94	34
2152	Perspective on the genetics of attention deficit/hyperactivity disorder. 2008 , 147B, 1334-6	3
2151	(ii) Family-based linkage and case control association studies. 2008 , 22, 245-250	2
2150	(iv) Genetics of disc degeneration. 2008 , 22, 259-266	4
2149	Nutrigenomics research for personalized nutrition and medicine. 2008 , 19, 110-20	87

2148	Array-based DNA diagnostics: let the revolution begin. 2008 , 59, 113-29	118
2147	Defining pancreatic endocrine precursors and their descendants. 2008 , 57, 654-68	61
2146	Autism genetics: strategies, challenges, and opportunities. 2008 , 1, 4-17	95
2145	The use of SNP markers for estimation of individual genetic predisposition to diabetes mellitus type 1 and 2. 2008 , 2, 126-132	
2144	Genetic effects, gene-lifestyle interactions, and type 2 diabetes. 2008 , 3, 1-7	
2143	Using the optimal receiver operating characteristic curve to design a predictive genetic test, exemplified with type 2 diabetes. 2008 , 82, 641-51	49
2142	Detection, imputation, and association analysis of small deletions and null alleles on oligonucleotide arrays. 2008 , 82, 1316-33	32
2141	A test for genetic association that incorporates information about deviation from Hardy-Weinberg proportions in cases. 2008 , 83, 53-63	32
2140	WW-domain-containing oxidoreductase is associated with low plasma HDL-C levels. 2008 , 83, 180-92	41
2139	The Population Reference Sample, POPRES: a resource for population, disease, and pharmacological genetics research. 2008 , 83, 347-58	238
2138	Common coding variant in the TCF7L2 gene and study of the association with type 2 diabetes in Japanese subjects. 2008 , 53, 972-982	7
2137	Association between polymorphisms in SLC30A8, HHEX, CDKN2A/B, IGF2BP2, FTO, WFS1, CDKAL1, KCNQ1 and type 2 diabetes in the Korean population. 2008 , 53, 991-998	126
2136	Novel UBE2B-associated polymorphisms in an azoospermic/oligozoospermic population. 2008 , 10, 461-6	16
2135	The success of the genome-wide association approach: a brief story of a long struggle. 2008 , 16, 554-64	85
2134	Hzf regulates adipogenesis through translational control of C/EBPalpha. 2008 , 27, 1481-90	21
2133	Genomewide association for schizophrenia in the CATIE study: results of stage 1. 2008 , 13, 570-84	308
2132	Progress and challenges in genome-wide association studies in humans. 2008 , 456, 728-31	286
2131	Inactivation of the Rb pathway and overexpression of both isoforms of E2F3 are obligate events in bladder tumours with 6p22 amplification. 2008 , 27, 2716-27	65

2130	What for genetics?. 2008 , 16, 507-8	1
2129	FTO polymorphisms are associated with obesity but not diabetes risk in postmenopausal women. 2008 , 16, 2472-80	61
2128	Rare independent mutations in renal salt handling genes contribute to blood pressure variation. 2008 , 40, 592-599	639
2127	Identification of ten loci associated with height highlights new biological pathways in human growth. 2008 , 40, 584-91	482
2126	Common variants near MC4R are associated with fat mass, weight and risk of obesity. 2008 , 40, 768-75	1048
2125	Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. 2008 , 40, 955-62	2092
2124	Estimating coverage and power for genetic association studies using near-complete variation data. 2008 , 40, 841-3	74
2123	Variants in KCNQ1 are associated with susceptibility to type 2 diabetes mellitus. 2008 , 40, 1092-7	598
2122	SNPs in KCNQ1 are associated with susceptibility to type 2 diabetes in East Asian and European populations. 2008 , 40, 1098-102	555
2121	Susceptibility loci for intracranial aneurysm in European and Japanese populations. 2008 , 40, 1472-7	222
2120	The same sequence variant on 9p21 associates with myocardial infarction, abdominal aortic aneurysm and intracranial aneurysm. 2008 , 40, 217-24	596
2119	Common variants in the GDF5-UQCC region are associated with variation in human height. 2008 , 40, 198-203	315
2118	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. 2008 , 40, 161-9	1304
2117	Genome-wide association studies: progress and potential for drug discovery and development. 2008 , 7, 221-30	91
2116	Pharmacogenetics in drug discovery and development: a translational perspective. 2008 , 7, 807-17	99
2115	The molecular epidemiology of pain: a new discipline for drug discovery. 2008 , 7, 647-58	62
2114	Genetic programming of liver and pancreas progenitors: lessons for stem-cell differentiation. 2008 , 9, 329-40	231
2113	Genome-wide association studies for complex traits: consensus, uncertainty and challenges. 2008 , 9, 356-69	2126

2112	Linkage disequilibrium--understanding the evolutionary past and mapping the medical future. 2008 , 9, 477-85	695
2111	Psychiatric genetics: progress amid controversy. 2008 , 9, 527-40	377
2110	Metabolic syndrome: from epidemiology to systems biology. 2008 , 9, 819-30	233
2109	Popper revisited: GWAS here, last year. 2008 , 16, 1-2	18
2108	Genome-wide association studies of quantitative traits with related individuals: little (power) lost but much to be gained. 2008 , 16, 387-90	40
2107	HHEX gene polymorphisms are associated with type 2 diabetes in the Dutch Breda cohort. 2008 , 16, 652-6	18
2106	Whole-genome association study of bipolar disorder. 2008 , 13, 558-69	571
2105	TCF7L2 polymorphisms are associated with type 2 diabetes in Khatri Sikhs from North India: genetic variation affects lipid levels. 2008 , 72, 499-509	49
2104	Effect of RBP4 gene variants on circulating RBP4 concentration and type 2 diabetes in a Chinese population. 2008 , 25, 11-8	26
2103	Genetics: how the UKPDS contributed to determining the genetic landscape of Type 2 diabetes. 2008 , 25 Suppl 2, 35-40	7
2102	The genetics of birth timing: insights into a fundamental component of human development. 2008 , 74, 493-501	36
2101	The G/G genotype of a single nucleotide polymorphism at -1066 of c-Jun N-terminal kinase 1 gene (MAPK8) does not affect type 2 diabetes susceptibility despite the specific binding of AP2alpha. 2008 , 69, 36-44	0
2100	Genetic association analysis: a primer on how it works, its strengths and its weaknesses. 2008 , 31, 546-56	22
2099	Identifying the susceptibility genes for coronary artery disease: from hyperbole through doubt to cautious optimism. 2008 , 263, 538-52	37
2098	Using the longest significance run to estimate region-specific p-values in genetic association mapping studies. 2008 , 9, 246	3
2097	Assessing batch effects of genotype calling algorithm BRLMM for the Affymetrix GeneChip Human Mapping 500 K array set using 270 HapMap samples. 2008 , 9 Suppl 9, S17	51
2096	Detection of genome-wide polymorphisms in the AT-rich Plasmodium falciparum genome using a high-density microarray. 2008 , 9, 398	51
2095	An optimized procedure for the design and evaluation of Ecotilling assays. 2008 , 9, 510	6

2094	The CoLaus study: a population-based study to investigate the epidemiology and genetic determinants of cardiovascular risk factors and metabolic syndrome. 2008 , 8, 6	433
2093	Oxidative demethylation of 3-methylthymine and 3-methyluracil in single-stranded DNA and RNA by mouse and human FTO. 2008 , 582, 3313-9	302
2092	Genome-wide association studies in aging-related processes such as diabetes mellitus, atherosclerosis and cancer. 2008 , 43, 39-43	32
2091	Genome-wide association studies in neurological disorders. 2008 , 7, 1067-72	43
2090	The human lexinome: genes of language and reading. 2008 , 41, 409-20	25
2089	Type 2 diabetes: new genes, new understanding. 2008 , 24, 613-21	204
2088	Study designs for genome-wide association studies. 2008 , 60, 465-504	40
2087	Concept, design and implementation of a cardiovascular gene-centric 50 k SNP array for large-scale genomic association studies. 2008 , 3, e3583	321
2086	Study Design and Statistical Issues in Pharmacogenetics Research. 2008 , 185-206	
2085	Introduction: Why Molecular Epidemiology?. 1-5	
2084	Impact of genetic and epigenetic factors from early life to later disease. 2008 , 57 Suppl 2, S27-31	33
2083	Preventing type 2 diabetes: genes or lifestyle?. 2008 , 2, 65-6	6
2082	Learning from molecular genetics: novel insights arising from the definition of genes for monogenic and type 2 diabetes. 2008 , 57, 2889-98	96
2081	Metabolomics: a global biochemical approach to drug response and disease. 2008 , 48, 653-83	517
2080	The dice are rolling for schizophrenia genetics. 2008 , 38, 1693-6; discussion 1818-20	13
2079	Genetic susceptibility to type 2 diabetes and implications for antidiabetic therapy. 2008 , 59, 95-111	40
2078	Bayesian meta-analysis of genetic association studies with different sets of markers. 2008 , 82, 859-72	49
2077	The year in atherothrombosis. 2008 , 51, 944-55	11

2076	Gene-environment interactions and susceptibility to metabolic syndrome and other chronic diseases. 2008 , 79, 1508-13	56
2075	Telomeres and Telomerase in Ageing, Disease, and Cancer. 2008 ,	1
2074	FitSNPs: highly differentially expressed genes are more likely to have variants associated with disease. 2008 , 9, R170	57
2073	Isolated populations and complex disease gene identification. 2008 , 9, 109	104
2072	Genetic determinants of phenotypic diversity in humans. 2008 , 9, 215	24
2071	Validation and extension of an empirical Bayes method for SNP calling on Affymetrix microarrays. 2008 , 9, R63	28
2070	Classification of genetic profiles of Crohn's disease: a focus on the ATG16L1 gene. 2008 , 8, 199-207	10
2069	Genotype score in addition to common risk factors for prediction of type 2 diabetes. 2008 , 359, 2208-19	608
2068	Clinical risk factors, DNA variants, and the development of type 2 diabetes. 2008 , 359, 2220-32	698
2067	Admixture mapping and the role of population structure for localizing disease genes. 2008 , 60, 547-69	49
2066	Assessing the combined impact of 18 common genetic variants of modest effect sizes on type 2 diabetes risk. 2008 , 57, 3129-35	245
2065	Pharmacogenetics: potential role in the treatment of diabetes and obesity. 2008 , 9, 1109-19	11
2064	Performance of whole-genome amplified DNA isolated from serum and plasma on high-density single nucleotide polymorphism arrays. 2008 , 10, 249-57	16
2063	Common variants in maturity-onset diabetes of the young genes and future risk of type 2 diabetes. 2008 , 57, 1738-44	63
2062	Genetics of diabetic nephropathy. 2008 , 2, 363-71	20
2061	Glucolipotoxicity: fuel excess and beta-cell dysfunction. 2008 , 29, 351-66	801
2060	Assessment of cumulative evidence on genetic associations: interim guidelines. 2008 , 37, 120-32	451
2059	Gaining insights in coronary disease genomics. 2008 , 52, 385-6	3

2058	Monogenic diabetes in the young, pharmacogenetics and relevance to multifactorial forms of type 2 diabetes. 2008 , 29, 254-64		118
2057	Pharmacogenomics and Personalized Medicine. 2008 ,		2
2056	Interaction Between Physical Activity and Genetic Factors in Complex Metabolic Disease. 2007 , 155-173		
2055	The future of mouse QTL mapping to diagnose disease in mice in the age of whole-genome association studies. 2008 , 42, 131-41		63
2054	A polymorphism within the G6PC2 gene is associated with fasting plasma glucose levels. <i>Science</i> , 2008 , 320, 1085-8	33-3	199
2053	Innovative Endocrinology of Cancer. 2008 ,		5
2052	Zinc signalling and subcellular distribution: emerging targets in type 2 diabetes. 2008 , 14, 419-28		66
2051	Candidate gene polymorphisms and the 9p21 locus in acute coronary syndromes. 2008 , 14, 441-9		19
2050	Estimating odds ratios in genome scans: an approximate conditional likelihood approach. 2008 , 82, 1064-74		53
2049	Consistently replicating locus linked to migraine on 10q22-q23. 2008 , 82, 1051-63		36
2048	Detecting AIDS restriction genes: from candidate genes to genome-wide association discovery. 2008 , 26, 2951-65		13
2047	A role for metallothionein in the pathogenesis of diabetes and its cardiovascular complications. 2008 , 94, 1-3		11
2046	A non-synonymous variant in SLC30A8 is not associated with type 1 diabetes in the Danish population. 2008 , 94, 386-8		18
2045	Atypical protein kinase C dysfunction and the metabolic syndrome. 2008 , 19, 39-41		2
2044	The role for endoplasmic reticulum stress in diabetes mellitus. 2008 , 29, 42-61		868
2043	Epigenetics and obesity. 2008 , 9, 1851-60		60
2042	The emerging genetic architecture of type 2 diabetes. 2008 , 8, 186-200		239
2041	Can geneticists help clinicians to understand and treat non-autoimmune diabetes?. 2008 , 82 Suppl 2, S83-93		5

2040	Future impact of integrated high-throughput methylome analyses on human health and disease. 2008 , 35, 391-401	36
2039	Meta-analysis approach identifies candidate genes and associated molecular networks for type-2 diabetes mellitus. 2008 , 9, 310	45
2038	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. 2008 , 40, 638-45	1496
2037	Prevalence in the United States of selected candidate gene variants: Third National Health and Nutrition Examination Survey, 1991-1994. 2009 , 169, 54-66	72
2036	Applying novel genome-wide linkage strategies to search for loci influencing type 2 diabetes and adult height in American Samoa. 2008 , 80, 99-123	3
2035	How to interpret a genome-wide association study. 2008 , 299, 1335-44	626
2034	Genetic mapping in human disease. <i>Science</i> , 2008 , 322, 881-8	33.3 1086
2033	Considerations regarding the genetics of obesity. 2008 , 16 Suppl 3, S33-9	33
2032	Obesity genes and gene-environment-behavior interactions: recommendations for a way forward. 2008 , 16 Suppl 3, S79-81	16
2031	Gene-environment interactions in the etiology of obesity: defining the fundamentals. 2008 , 16 Suppl 3, S5-S10	120
2030	Genetics of type 2 diabetes mellitus and obesity--a review. 2008 , 40, 2-10	24
2029	Molecular signatures of cardiovascular disease risk: potential for test development and clinical application. 2008 , 12, 281-7	4
2028	Zinc transporter-8 gene (SLC30A8) is associated with type 2 diabetes in Chinese. 2008 , 93, 4107-12	62
2027	The search for genes contributing to endometriosis risk. 2008 , 14, 447-57	156
2026	Primer: strategies for identifying genes involved in renal disease. 2008 , 4, 265-76	18
2025	Population differences in breast cancer severity. 2008 , 9, 323-33	24
2024	Common variation in the fat mass and obesity-associated (FTO) gene confers risk of obesity and modulates BMI in the Chinese population. 2008 , 57, 2245-52	179
2023	Identifying Disease Susceptible DNA Regions Using Underlying Odds Ratio Contour Analysis. 2008 ,	0

2022 Developmental Toxicology. **2008**,

2021	Mechanisms of disease: genetic insights into the etiology of type 2 diabetes and obesity. 2008 , 4, 156-63	36
2020	Implication of genetic variants near TCF7L2, SLC30A8, HHEX, CDKAL1, CDKN2A/B, IGF2BP2, and FTO in type 2 diabetes and obesity in 6,719 Asians. 2008 , 57, 2226-33	291
2019	Genome-wide association studies: potential next steps on a genetic journey. 2008 , 17, R156-65	263
2018	Predicting type 2 diabetes based on polymorphisms from genome-wide association studies: a population-based study. 2008 , 57, 3122-8	231
2017	Sequence Analysis in Vicinity of Type 2 Diabetes Related SNP rs7903146. 2008 ,	
2016	Common variants in CDKAL1, CDKN2A/B, IGF2BP2, SLC30A8, and HHEX/IDE genes are associated with type 2 diabetes and impaired fasting glucose in a Chinese Han population. 2008 , 57, 2834-42	199
2015	Introduction to the Special Issue on Society and Genetics. 2008 , 37, 159-163	12
2014	Required sample size and nonreplicability thresholds for heterogeneous genetic associations. 2008 , 105, 617-22	91
2013	Generating Linkage Disequilibrium Patterns in Data Simulations Using genomeSIMLA. 2008 , 24-35	29
2012	Mitochondria as chi. 2008 , 179, 727-35	116
2011	Physical activity and the association of common FTO gene variants with body mass index and obesity. 2008 , 168, 1791-7	207
2010	A polymorphism in the zinc transporter gene SLC30A8 confers resistance against posttransplantation diabetes mellitus in renal allograft recipients. 2008 , 57, 1043-7	66
2009	Looking for polycystic ovary syndrome genes: rational and best strategy. 2008 , 26, 5-13	61
2008	Commentary: Genetic association studies see light at the end of the tunnel. 2008 , 37, 133-5	7
2007	Into the post-HapMap era. 2008 , 60, 727-42	16
2006	Anthropometry, carbohydrate and lipid metabolism in the East Flanders Prospective Twin Survey: linkage of candidate genes using two sib-pair based variance components analyses. 2008 , 11, 505-16	6
2005	Genomewide association analysis followed by a replication study implicates a novel candidate gene for neuroticism. 2008 , 65, 1062-71	109

2004	PCLO variants are nominally associated with early-onset type 2 diabetes and insulin resistance in Pima Indians. 2008 , 57, 3156-60	10
2003	Haplotype structure of the ENPP1 Gene and Nominal Association of the K121Q missense single nucleotide polymorphism with glycemic traits in the Framingham Heart Study. 2008 , 57, 1971-7	39
2002	Association analysis of type 2 diabetes Loci in type 1 diabetes. 2008 , 57, 1983-6	39
2001	Extension of type 2 diabetes genome-wide association scan results in the diabetes prevention program. 2008 , 57, 2503-10	86
2000	Cardiovascular genomics, personalized medicine, and the National Heart, Lung, and Blood Institute: part I: the beginning of an era. 2008 , 1, 51-7	29
1999	Mechanisms of mammalian zinc-regulated gene expression. 2008 , 36, 1262-6	46
1998	[Genome-wide association study on complex diseases: study design and genetic markers]. 2008 , 30, 400-6	2
1997	Pharmacogenomics: candidate gene identification, functional validation and mechanisms. 2008 , 17, R174-9	49
1996	Clinical review: the genetics of type 2 diabetes: a realistic appraisal in 2008. 2008 , 93, 4633-42	90
1995	Lifetime body mass index and later atherosclerosis risk in young adults: examining causal links using Mendelian randomization in the Cardiovascular Risk in Young Finns study. 2008 , 29, 2552-60	52
1994	Whole genome analyses suggest ischemic stroke and heart disease share an association with polymorphisms on chromosome 9p21. 2008 , 39, 1586-9	138
1993	Meta-analysis of 23 type 2 diabetes linkage studies from the International Type 2 Diabetes Linkage Analysis Consortium. 2008 , 66, 35-49	34
1992	Pathogenesis, risk assessment and prevention of type 2 diabetes mellitus. 2008 , 1, 128-37	19
1991	A common nonsynonymous single nucleotide polymorphism in the SLC30A8 gene determines ZnT8 autoantibody specificity in type 1 diabetes. 2008 , 57, 2693-7	165
1990	Association of CDKAL1, IGF2BP2, CDKN2A/B, HHEX, SLC30A8, and KCNJ11 with susceptibility to type 2 diabetes in a Japanese population. 2008 , 57, 791-5	233
1989	Genetic variants of FTO influence adiposity, insulin sensitivity, leptin levels, and resting metabolic rate in the Quebec Family Study. 2008 , 57, 1147-50	184
1988	Dissecting the nutrigenomics, diabetes, and gastrointestinal disease interface: from risk assessment to health intervention. 2008 , 12, 237-44	10
1987	Common variation in the FTO gene alters diabetes-related metabolic traits to the extent expected given its effect on BMI. 2008 , 57, 1419-26	260

1986	Association of variants in the sterol regulatory element-binding factor 1 (SREBF1) gene with type 2 diabetes, glycemia, and insulin resistance: a study of 15,734 Danish subjects. 2008 , 57, 1136-42	36
1985	Transcription factor 7-like 2 regulates beta-cell survival and function in human pancreatic islets. 2008 , 57, 645-53	221
1984	Long-range enhancers are required to maintain expression of the autoantigen islet-specific glucose-6-phosphatase catalytic subunit-related protein in adult mouse islets in vivo. 2008 , 57, 133-41	15
1983	Fat mass-and obesity-associated (FTO) gene variant is associated with obesity: longitudinal analyses in two cohort studies and functional test. 2008 , 57, 3145-51	123
1982	Exclusion of Polymorphisms in Carnosinase Genes (CNDP1 and CNDP2) as a Cause of Diabetic Nephropathy in Type 1 Diabetes: Results of Large Case-Control and Follow-Up Studies. 2008 , 57, 2547-2551	40
1981	Evaluation of the association of IGF2BP2 variants with type 2 diabetes in French Caucasians. 2008 , 57, 1992-6	23
1980	Investigation of transport mechanisms and regulation of intracellular Zn ²⁺ in pancreatic alpha-cells. 2008 , 283, 10184-97	87
1979	Transcription factor 7-like 2 polymorphism and colon cancer. 2008 , 17, 978-82	36
1978	The Importance of GeneEnvironment Interaction: Implications for Social Scientists. 2008 , 37, 164-200	12
1977	Four SNPs on chromosome 9p21 in a South Korean population implicate a genetic locus that confers high cross-race risk for development of coronary artery disease. 2008 , 28, 360-5	157
1976	The sulfonylurea receptor, an atypical ATP-binding cassette protein, and its regulation of the KATP channel. 2008 , 102, 164-76	97
1975	Rationale, design, and methodology of the Women's Genome Health Study: a genome-wide association study of more than 25,000 initially healthy american women. 2008 , 54, 249-55	145
1974	A candidate type 2 diabetes polymorphism near the HHEX locus affects acute glucose-stimulated insulin release in European populations: results from the EUGENE2 study. 2008 , 57, 514-7	47
1973	A novel susceptibility locus for type 1 diabetes on Chr12q13 identified by a genome-wide association study. 2008 , 57, 1143-6	118
1972	American College of Endocrinology Pre-Diabetes Consensus Conference: part three. 2008 , 31, 2404-9	9
1971	Regulation of Fto/Ftm gene expression in mice and humans. 2008 , 294, R1185-96	238
1970	Genetic variation in an individual human exome. 2008 , 4, e1000160	205
1969	Polymorphisms in the IDE-KIF11-HHEX gene locus are reproducibly associated with type 2 diabetes in a Japanese population. 2008 , 93, 310-4	51

1968	Diabetes. 2008 ,	1
1967	Predicting unobserved phenotypes for complex traits from whole-genome SNP data. 2008 , 4, e1000231	147
1966	Positional cloning of "Lisch-Like", a candidate modifier of susceptibility to type 2 diabetes in mice. 2008 , 4, e1000137	53
1965	Associations among multiple markers and complex disease: models, algorithms, and applications. 2008 , 60, 437-64	1
1964	Novel association of HK1 with glycated hemoglobin in a non-diabetic population: a genome-wide evaluation of 14,618 participants in the Women's Genome Health Study. 2008 , 4, e1000312	77
1963	Gene set enrichment in eQTL data identifies novel annotations and pathway regulators. 2008 , 4, e1000070	79
1962	Replication of genome-wide association studies of type 2 diabetes susceptibility in Japan. 2008 , 93, 3136-41	117
1961	Common missense variant in the glucokinase regulatory protein gene is associated with increased plasma triglyceride and C-reactive protein but lower fasting glucose concentrations. 2008 , 57, 3112-21	223
1960	Polygenic obesity in humans. 2008 , 1, 35-42	45
1959	Epithelial sodium channel: mendelian versus essential hypertension. 2008 , 52, 595-600	58
1958	What can genome-wide association studies tell us about the genetics of common disease?. 2008 , 4, e33	102
1957	Practical issues in imputation-based association mapping. 2008 , 4, e1000279	144
1956	Genes influencing susceptibility to infection. 2008 , 197, 4-6	9
1955	Microarray technology and applications in the arena of genome-wide association. 2008 , 54, 1116-24	61
1954	Adaptations to climate in candidate genes for common metabolic disorders. 2008 , 4, e32	204
1953	Data and theory point to mainly additive genetic variance for complex traits. 2008 , 4, e1000008	643
1952	Tracing sub-structure in the European American population with PCA-informative markers. 2008 , 4, e1000114	53
1951	Association testing of novel type 2 diabetes risk alleles in the JAZF1, CDC123/CAMK1D, TSPAN8, THADA, ADAMTS9, and NOTCH2 loci with insulin release, insulin sensitivity, and obesity in a population-based sample of 4,516 glucose-tolerant middle-aged Danes. 2008 , 57, 2534-40	116

1950	Association analysis in african americans of European-derived type 2 diabetes single nucleotide polymorphisms from whole-genome association studies. 2008 , 57, 2220-5	118
1949	Common variation in the WNK1 gene and blood pressure in childhood: the Avon Longitudinal Study of Parents and Children. 2008 , 52, 974-9	31
1948	Practical aspects of imputation-driven meta-analysis of genome-wide association studies. 2008 , 17, R122-8	423
1947	Associations between single nucleotide polymorphisms on chromosome 9p21 and risk of coronary heart disease in Chinese Han population. 2008 , 28, 2085-9	65
1946	Comprehensive association study of type 2 diabetes and related quantitative traits with 222 candidate genes. 2008 , 57, 3136-44	82
1945	Impact of common type 2 diabetes risk polymorphisms in the DESIR prospective study. 2008 , 57, 244-54	137
1944	Evidence that the gene encoding insulin degrading enzyme influences human lifespan. 2008 , 17, 2370-8	8
1943	Quantitative trait analysis of type 2 diabetes susceptibility loci identified from whole genome association studies in the Insulin Resistance Atherosclerosis Family Study. 2008 , 57, 1093-100	93
1942	Susceptibility to coronary artery disease and diabetes is encoded by distinct, tightly linked SNPs in the ANRIL locus on chromosome 9p. 2008 , 17, 806-14	420
1941	Genome-wide association scans identified CTNBL1 as a novel gene for obesity. 2008 , 17, 1803-13	152
1940	HapMap and mapping genes for cardiovascular disease. 2008 , 1, 66-71	12
1939	A weighted-Holm procedure accounting for allele frequencies in genomewide association studies. 2008 , 180, 697-702	5
1938	Metabolic and cardiovascular traits: an abundance of recently identified common genetic variants. 2008 , 17, R102-8	64
1937	Gene-environment interaction in genome-wide association studies. 2009 , 169, 219-26	208
1936	Proinflammatory gene polymorphisms and ischemic stroke. 2008 , 14, 3590-600	22
1935	Genetic analysis of Kruppel-like zinc finger 11 variants in 5864 Danish individuals: potential effect on insulin resistance and modified signal transducer and activator of transcription-3 binding by promoter variant -1659G>C. 2008 , 93, 3128-35	12
1934	Single-nucleotide polymorphism rs7754840 of CDKAL1 is associated with impaired insulin secretion in nondiabetic offspring of type 2 diabetic subjects and in a large sample of men with normal glucose tolerance. 2008 , 93, 1924-30	71
1933	[Diabetology 2008]. 2008 , 133, 1377-80	

1932	Impact of TCF7L2 rs7903146 on insulin secretion and action in young and elderly Danish twins. 2008 , 93, 4013-9	51
1931	Variants of the PPARG, IGF2BP2, CDKAL1, HHEX, and TCF7L2 genes confer risk of type 2 diabetes independently of BMI in the German KORA studies. 2008 , 40, 722-6	65
1930	The complex genetics of multiple sclerosis: pitfalls and prospects. 2008 , 131, 3118-31	83
1929	Genes associated with risk of type 2 diabetes identified by a candidate-wide association scan: as a trickle becomes a flood. 2008 , 57, 2915-7	10
1928	A meta-analysis of QTL for diabetes-related traits in rodents. 2008 , 34, 42-53	37
1927	Delineating slowly and rapidly evolving fractions of the Drosophila genome. 2008 , 15, 407-30	16
1926	The clinical utility of genetic risk variants in type 2 diabetes. 2008 , 2, 991-1002	
1925	Exchangeable models of complex inherited diseases. 2008 , 179, 2253-61	30
1924	A gene expression network model of type 2 diabetes links cell cycle regulation in islets with diabetes susceptibility. 2008 , 18, 706-16	269
1923	Control of pancreatic beta-cell fate by insulin signaling: The sweet spot hypothesis. 2008 , 7, 1343-7	28
1922	Defining targets for investigating the pharmacogenomics of adverse drug reactions to antifungal agents. 2008 , 9, 561-84	18
1921	Advances in endophenotyping schizophrenia. 2008 , 7, 11-8	75
1920	On Sequence Variants that Influence the Risk of Common Diseases. 2008 ,	
1919	A genome-wide association study identifies novel risk loci for type 2 diabetes. 2008 , 2008, 36-37	
1918	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. 2008 , 2008, 38-39	19
1917	Interaction between poor glycemic control and 9p21 locus on risk of coronary artery disease in type 2 diabetes. 2008 , 300, 2389-97	92
1916	Gene by social context interactions for number of sexual partners among white male youths: genetics-informed sociology. 2008 , 114 Suppl, S36-66	39
1915	The pancreatic beta-cell: birth, life and death. 2008 , 36, 267-71	5

1914	Genes, environment, and interactions in prevention of type 2 diabetes: a focus on physical activity and lifestyle changes. 2008 , 8, 519-32	105
1913	Common statistical issues in genome-wide association studies: a review on power, data quality control, genotype calling and population structure. 2008 , 19, 133-43	73
1912	Single gene contributions: genetic variants of peroxisome proliferator-activated receptor (isoforms alpha, beta/delta and gamma) and mechanisms of dyslipidemias. 2008 , 19, 106-12	24
1911	Family study designs in the age of genome-wide association studies: experience from the Framingham Heart Study. 2008 , 19, 144-50	11
1910	Maintenance of Glucose Control in Patients With Type 1 Diabetes During Acute Mental Stress by Riding High-Speed Rollercoasters. 2008 , 2008, 39-41	
1909	New gene variants alter type 2 diabetes risk predominantly through reduced beta-cell function. 2008 , 11, 371-7	86
1908	Emergence of TCF7L2 as a Most Promising Gene in Predisposition of Diabetes Type II. 2008 , 8, 199-215	8
1907	Polygenic contribution to obesity: genome-wide strategies reveal new targets. 2008 , 36, 12-36	26
1906	The transcription factor 7-like 2 gene and increased risk of type 2 diabetes: an update. 2008 , 11, 385-92	32
1905	Defining the spectrum of alleles that contribute to blood lipid concentrations in humans. 2008 , 19, 122-7	40
1904	Hypertension and genome-wide association studies: combining high fidelity phenotyping and hypercontrols. 2008 , 26, 1275-81	29
1903	. 2008 ,	8
1902	Diabetes Mellitus. 2008 , 374-421	2
1901	The HapMap: charting a course for genetic discovery in neurological diseases. 2008 , 65, 319-21	7
1900	Association of common polymorphisms in GLUT9 gene with gout but not with coronary artery disease in a large case-control study. 2008 , 3, e1948	64
1899	Post genome-wide association studies of novel genes associated with type 2 diabetes show gene-gene interaction and high predictive value. 2008 , 3, e2031	124
1898	Variations in the ghrelin receptor gene associate with obesity and glucose metabolism in individuals with impaired glucose tolerance. 2008 , 3, e2941	26
1897	Novel meta-analysis-derived type 2 diabetes risk loci do not determine prediabetic phenotypes. 2008 , 3, e3019	35

1896	Analyses and comparison of accuracy of different genotype imputation methods. 2008 , 3, e3551	100
1895	Bitter taste receptors influence glucose homeostasis. 2008 , 3, e3974	187
1894	Chromosome 9p21.3 is associated with early-onset coronary heart disease in the Irish population. 2008 , 25, 81-5	17
1893	Polymorphisms of the ENPP1 gene are not associated with type 2 diabetes or obesity in the Chinese Han population. 2008 ,	
1892	Gene and Pathway-Based Analysis: Second Wave of Genome-wide Association Studies. 2008 ,	
1891	A HapMap harvest of insights into the genetics of common disease. 2008 , 118, 1590-605	683
1890	Genetic Testing: Moving to the Bedside When and How?. 47-64	
1889	Genomic Approaches to Complex Disease. 2009 , 33-46	
1888	. 2009 ,	59
1887	Type 1 Diabetes: Clinical and Experimental. 2009 , 111-131	
1886	References. 231-243	
1885	Mining Potential Functionally Significant Polymorphisms at the ATP-Binding- Cassette Transporter Genes. 2009 , 7, 40-58	6
1884	Candidate Gene and Genome-Wide Association Studies. 1-19	
1883	Human genetics of diabetes mellitus in Taiwan. 2009 , 14, 4535-45	2
1882	Comparative characterization of a temperature responsive gene (lactate dehydrogenase-B, ldh-b) in two congeneric tropical fish, Lates calcarifer and Lates niloticus. 2009 , 5, 558-69	6
1881	Molecular Signatures of Obstructive Sleep Apnea in Adults: A Review and Perspective. 2009 ,	
1880	A Bayesian Method for Detecting and Characterizing Allelic Heterogeneity and Boosting Signals in Genome-Wide Association Studies. 2009 , 24,	17
1879	Mitochondria, bioenergetics, and the epigenome in eukaryotic and human evolution. 2009 , 74, 383-93	39

1878	Disruptive insights in psychiatry: transforming a clinical discipline. 2009 , 119, 700-5	106
1877	Translational Genomics: From Discovery to Clinical Practice. 2009 , 262-274	2
1876	Use of Obesity Biomarkers in Cardiovascular Epidemiology. 2009 , 26, 247-263	20
1875	Genome-wide Association: A Revolutionary Approach 2009 , 9, 97-103	
1874	Molecular signatures of obstructive sleep apnea in adults: a review and perspective. 2009 , 32, 447-70	243
1873	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. 2009 , 5, e1000508	393
1872	Positional cloning of zinc finger domain transcription factor Zfp69, a candidate gene for obesity-associated diabetes contributed by mouse locus Nidd/SJL. 2009 , 5, e1000541	59
1871	STrengthening the REporting of Genetic Association Studies (STREGA): an extension of the STROBE statement. 2009 , 6, e22	264
1870	INK4/ARF transcript expression is associated with chromosome 9p21 variants linked to atherosclerosis. 2009 , 4, e5027	196
1869	Down-regulation of ZnT8 expression in INS-1 rat pancreatic beta cells reduces insulin content and glucose-inducible insulin secretion. 2009 , 4, e5679	63
1868	The type 2 diabetes associated minor allele of rs2237895 KCNQ1 associates with reduced insulin release following an oral glucose load. 2009 , 4, e5872	40
1867	Replication study of candidate genes associated with type 2 diabetes based on genome-wide screening. 2009 , 58, 493-8	115
1866	Age-dependent decline in beta-cell proliferation restricts the capacity of beta-cell regeneration in mice. 2009 , 58, 1312-20	252
1865	Finding common susceptibility variants for complex disease: past, present and future. 2009 , 8, 345-52	17
1864	Nonmetric multidimensional scaling corrects for population structure in association mapping with different sample types. 2009 , 182, 875-88	89
1863	Confirmation of multiple risk Loci and genetic impacts by a genome-wide association study of type 2 diabetes in the Japanese population. 2009 , 58, 1690-9	196
1862	Interrogating type 2 diabetes genome-wide association data using a biological pathway-based approach. 2009 , 58, 1463-7	87
1861	Breast-feeding modifies the association of PPARgamma2 polymorphism Pro12Ala with growth in early life: the Generation R Study. 2009 , 58, 992-8	16

1860	Genomewide association studies of stroke. 2009 , 360, 1718-28	376
1859	Genome-wide association and meta-analysis of bipolar disorder in individuals of European ancestry. 2009 , 106, 7501-6	239
1858	The T-381C SNP in BNP gene may be modestly associated with type 2 diabetes: an updated meta-analysis in 49 279 subjects. 2009 , 18, 2495-501	26
1857	Previously associated type 2 diabetes variants may interact with physical activity to modify the risk of impaired glucose regulation and type 2 diabetes: a study of 16,003 Swedish adults. 2009 , 58, 1411-8	55
1856	Genetic architecture of quantitative traits in mice, flies, and humans. 2009 , 19, 723-33	321
1855	Methods for analysis in pharmacogenomics: lessons from the Pharmacogenetics Research Network Analysis Group. 2009 , 10, 243-51	10
1854	Genome-wide association scan for diabetic nephropathy susceptibility genes in type 1 diabetes. 2009 , 58, 1403-10	227
1853	Examination of type 2 diabetes loci implicates CDKAL1 as a birth weight gene. 2009 , 58, 2414-8	52
1852	Association of type 2 diabetes candidate polymorphisms in KCNQ1 with incretin and insulin secretion. 2009 , 58, 1715-20	89
1851	Underlying genetic models of inheritance in established type 2 diabetes associations. 2009 , 170, 537-45	60
1850	Progress in genome-wide association studies of human height. 2009 , 71 Suppl 2, 5-13	36
1849	The role of the PGC1 α Gly482Ser polymorphism in weight gain due to intensive diabetes therapy. 2009 , 2009, 649286	7
1848	Data integration in genetics and genomics: methods and challenges. 2009 , 2009,	80
1847	A neurologist's guide to genome-wide association studies. 2009 , 72, 558-65	26
1846	Size matters: just how big is BIG?: Quantifying realistic sample size requirements for human genome epidemiology. 2009 , 38, 263-73	192
1845	From the Cover: Whole-genome association study identifies STK39 as a hypertension susceptibility gene. 2009 , 106, 226-31	240
1844	GWAS GUI: graphical browser for the results of whole-genome association studies with high-dimensional phenotypes. 2009 , 25, 284-5	8
1843	Risk loci for type 2 diabetes - quo vadis?. 2009 , 47, 383-6	3

1842	ATOM: a powerful gene-based association test by combining optimally weighted markers. 2009 , 25, 497-503	42
1841	A common variant in the FTO gene is associated with body mass index in males and postmenopausal females but not in premenopausal females. Czech post-MONICA and 3PMFs studies. 2009 , 47, 387-90	34
1840	Recent progress in the genetics of diabetes. 2009 , 71 Suppl 1, 17-23	5
1839	A genomics study of type 2 diabetes mellitus in U.S. Air Force personnel. 2009 , 3, 770-5	2
1838	Statistical screening method for genetic factors influencing susceptibility to common diseases in a two-stage genome-wide association study. 2009 , 8, Article 46	
1837	Adiposity-related heterogeneity in patterns of type 2 diabetes susceptibility observed in genome-wide association data. 2009 , 58, 505-10	98
1836	Linkage disequilibrium mapping of the replicated type 2 diabetes linkage signal on chromosome 1q. 2009 , 58, 1704-9	23
1835	Linking the genetics of type 2 diabetes with low birth weight: a role for prenatal islet maldevelopment?. 2009 , 58, 1255-6	26
1834	Novel insights into the etiology of diabetes from genome-wide association studies. 2009 , 58, 2444-7	2
1833	Genetic predisposition, Western dietary pattern, and the risk of type 2 diabetes in men. 2009 , 89, 1453-8	113
1832	A genetic variant on chromosome 9p21 and incident heart failure in the ARIC study. 2009 , 30, 1222-8	44
1831	Clinical translation of genetic predictors for type 2 diabetes. 2009 , 16, 100-6	14
1830	Proteomic identification of carboxypeptidase E connects lipid-induced beta-cell apoptosis and dysfunction in type 2 diabetes. 2009 , 8, 38-42	12
1829	Current World Literature. 2009 , 20, 135-42	
1828	Genetic variants of TCF7L2 are associated with insulin resistance and related metabolic phenotypes in Taiwanese adolescents and Caucasian young adults. 2009 , 94, 3575-82	39
1827	Genetic variant in the IGF2BP2 gene may interact with fetal malnutrition to affect glucose metabolism. 2009 , 58, 1440-4	41
1826	Collaborative genome-wide association studies of diverse diseases: programs of the NHGRI's office of population genomics. 2009 , 10, 235-41	36
1825	The medical and economic roles of pipeline pharmacogenetics: Alzheimer's disease as a model of efficacy and HLA-B(*)5701 as a model of safety. 2009 , 34, 6-17	35

1824	Loci of TCF7L2, HHEX and IDE on chromosome 10q and the susceptibility of their genetic polymorphisms to type 2 diabetes. 2009 , 117, 186-90	15
1823	Single nucleotide transcription factor 7-like 2 (TCF7L2) gene polymorphisms in antiislet autoantibody-negative patients at onset of diabetes. 2009 , 94, 504-10	10
1822	Racial differences in the interaction between family history and risk factors associated with diabetes in the National Health and Nutritional Examination Survey, 1999-2004. 2009 , 11, 542-7	19
1821	Downregulation of ZnT8 expression in pancreatic β -cells of diabetic mice. 2009 , 1, 124-8	37
1820	Evaluation of risk prediction updates from commercial genome-wide scans. 2009 , 11, 588-94	63
1819	Singapore Genome Variation Project: a haplotype map of three Southeast Asian populations. 2009 , 19, 2154-62	129
1818	Genome-wide association studies for atherosclerotic vascular disease and its risk factors. 2009 , 2, 63-72	36
1817	The E23K variation in the KCNJ11 gene is associated with type 2 diabetes in Chinese and East Asian population. 2009 , 54, 433-5	48
1816	Evidence for interaction between PPARG Pro12Ala and PPARGC1A Gly482Ser polymorphisms in determining type 2 diabetes intermediate phenotypes in overweight subjects. 2009 , 117, 455-9	13
1815	Minireview: Meeting the demand for insulin: molecular mechanisms of adaptive postnatal beta-cell mass expansion. 2009 , 23, 747-58	122
1814	The inhibitory effect of recent type 2 diabetes risk loci on insulin secretion is modulated by insulin sensitivity. 2009 , 94, 1775-80	18
1813	Interpretation of genetic association studies: markers with replicated highly significant odds ratios may be poor classifiers. 2009 , 5, e1000337	191
1812	Identification of a shared genetic susceptibility locus for coronary heart disease and periodontitis. 2009 , 5, e1000378	162
1811	A genome-wide association study of pulmonary function measures in the Framingham Heart Study. 2009 , 5, e1000429	242
1810	The genetic signatures of noncoding RNAs. 2009 , 5, e1000459	553
1809	Common type 2 diabetes risk gene variants associate with gestational diabetes. 2009 , 94, 145-50	169
1808	Genome-wide analysis of haplotype interaction for the data from the North American Rheumatoid Arthritis Consortium. 2009 , 3 Suppl 7, S34	7
1807	A genome-wide investigation of SNPs and CNVs in schizophrenia. 2009 , 5, e1000373	357

1806	PPARG, KCNJ11, CDKAL1, CDKN2A-CDKN2B, IDE-KIF11-HHEX, IGF2BP2 and SLC30A8 are associated with type 2 diabetes in a Chinese population. 2009 , 4, e7643	137
1805	Genome-wide uH2A localization analysis highlights Bmi1-dependent deposition of the mark at repressed genes. 2009 , 5, e1000506	48
1804	Genetics and the general physician: insights, applications and future challenges. 2009 , 102, 757-72	10
1803	Personalized medicine: are we there yet?. 2009 , 9, 85	5
1802	Testing the association of novel meta-analysis-derived diabetes risk genes with type II diabetes and related metabolic traits in Asian Indian Sikhs. 2009 , 54, 162-8	33
1801	PPAR gamma variant influences angiographic outcome and 10-year cardiovascular risk in male symptomatic coronary artery disease patients. 2009 , 32, 839-44	25
1800	Joint effects of common genetic variants on the risk for type 2 diabetes in U.S. men and women of European ancestry. 2009 , 150, 541-50	191
1799	The 9p21 myocardial infarction risk allele increases risk of peripheral artery disease in older people. 2009 , 2, 347-53	76
1798	A genome-wide association study of schizophrenia using brain activation as a quantitative phenotype. 2009 , 35, 96-108	179
1797	Polycomb protein Ezh2 regulates pancreatic beta-cell Ink4a/Arf expression and regeneration in diabetes mellitus. 2009 , 23, 975-85	296
1796	IGF2 mRNA-binding protein 2: biological function and putative role in type 2 diabetes. 2009 , 43, 187-95	123
1795	GRM7 variants confer susceptibility to age-related hearing impairment. 2009 , 18, 785-96	145
1794	Genetic variant in HK1 is associated with a proanemic state and A1C but not other glycemic control-related traits. 2009 , 58, 2687-97	29
1793	TCF7L2 polymorphism associates with new-onset diabetes after transplantation. 2009 , 20, 2459-67	55
1792	Gene X environment interaction of vigorous exercise and body mass index among male Vietnam-era twins. 2009 , 89, 1011-8	61
1791	Reduced expression of the Kinesin-Associated Protein 3 (KIFAP3) gene increases survival in sporadic amyotrophic lateral sclerosis. 2009 , 106, 9004-9	149
1790	Common polymorphic transcript variation in human disease. 2009 , 19, 567-75	64
1789	Integrating siRNA and protein-protein interaction data to identify an expanded insulin signaling network. 2009 , 19, 1057-67	45

1788	Gene prioritization based on biological plausibility over genome wide association studies renders new loci associated with type 2 diabetes. 2009 , 11, 338-43	15
1787	Type 2 diabetes risk alleles are associated with reduced size at birth. 2009 , 58, 1428-33	117
1786	Regulation of pancreatic juxtaductal endocrine cell formation by FoxO1. 2009 , 29, 4417-30	46
1785	Genome-wide linkage scan in Gullah-speaking African American families with type 2 diabetes: the Sea Islands Genetic African American Registry (Project SuGAR). 2009 , 58, 260-7	24
1784	RARRES2, encoding the novel adipokine chemerin, is a genetic determinant of disproportionate regional body fat distribution: a comparative magnetic resonance imaging study. 2009 , 58, 519-24	46
1783	Effect of an FTO polymorphism on fat mass, obesity, and type 2 diabetes mellitus in the French MONICA Study. 2009 , 58, 971-5	56
1782	Preliminary report: genetic variation within the GPBAR1 gene is not associated with metabolic traits in white subjects at an increased risk for type 2 diabetes mellitus. 2009 , 58, 1809-11	13
1781	Understanding cardiovascular disease through the lens of genome-wide association studies. 2009 , 25, 387-94	55
1780	Human genetic variations: Beacons on the pathways to successful ageing. 2009 , 130, 553-63	21
1779	Identifying hypothetical genetic influences on complex disease phenotypes. 2009 , 10 Suppl 2, S13	5
1778	The 9p21 susceptibility locus for coronary artery disease and the severity of coronary atherosclerosis. 2009 , 9, 3	31
1777	PPAR gamma protects cardiomyocytes against oxidative stress and apoptosis via Bcl-2 upregulation. 2009 , 51, 169-74	68
1776	Cell intrinsic and extrinsic mechanisms of stem cell aging depend on telomere status. 2009 , 44, 75-82	25
1775	Genetic-epidemiological evidence on genes associated with HDL cholesterol levels: a systematic in-depth review. 2009 , 44, 136-60	96
1774	Estudio del componente genético de la cardiopatía isquémica: de los estudios de ligamiento al genotipado integral del genoma. 2009 , 9, 24-38	2
1773	Genome-wide autozygosity mapping in human populations. 2009 , 33, 172-80	50
1772	An optimal dose-effect mode trend test for SNP genotype tables. 2009 , 33, 114-27	16
1771	Using genome-wide pathway analysis to unravel the etiology of complex diseases. 2009 , 33, 419-31	159

1770	Genotype-based matching to correct for population stratification in large-scale case-control genetic association studies. 2009 , 33, 508-17	37
1769	A modified forward multiple regression in high-density genome-wide association studies for complex traits. 2009 , 33, 518-25	5
1768	STrengthening the REporting of Genetic Association Studies (STREGA)--an extension of the STROBE statement. 2009 , 33, 581-98	134
1767	VALID: visualization of association study results and linkage disequilibrium. 2009 , 33, 599-603	1
1766	Meta-analysis of genome-wide association studies: no efficiency gain in using individual participant data. 2010 , 34, 60-6	95
1765	Correcting "winner's curse" in odds ratios from genomewide association findings for major complex human diseases. 2010 , 34, 78-91	58
1764	Searching genetic risk factors for schizophrenia and bipolar disorder: learn from the past and back to the future. 2009 , 30, 1139-52	44
1763	Strengthening the reporting of genetic association studies (STREGA): an extension of the STROBE Statement. 2009 , 125, 131-51	136
1762	Analysis of FTO gene variants with measures of obesity and glucose homeostasis in the IRAS Family Study. 2009 , 125, 615-26	77
1761	Glucokinase regulatory protein gene polymorphism affects postprandial lipemic response in a dietary intervention study. 2009 , 126, 567-74	22
1760	Association between insulin secretion, insulin sensitivity and type 2 diabetes susceptibility variants identified in genome-wide association studies. 2009 , 46, 217-26	81
1759	The genetics of autoimmune diseases: a networked perspective. 2009 , 21, 596-605	110
1758	In vitro modulation of TCF7L2 gene expression in human pancreatic cells. 2009 , 36, 2329-32	7
1757	Strengthening the reporting of genetic association studies (STREGA): an extension of the STROBE statement. 2009 , 24, 37-55	35
1756	Human QTL linkage mapping. 2009 , 136, 333-40	29
1755	Advanced technologies for genomic analysis in farm animals and its application for QTL mapping. 2009 , 136, 371-86	22
1754	The molecular genetic basis of age-related macular degeneration: an overview. 2009 , 88, 425-49	82
1753	Genetic basis of myocardial infarction: Novel insights from genome-wide association studies. 2009 , 3, 426-433	2

1752	Genome-wide association studies in type 2 diabetes. 2009 , 9, 164-71	174
1751	Update Typ-2-Diabetes anhand ausgewählter aktueller Publikationen. 2009 , 5, 177-189	
1750	The null distributions of test statistics in genomewide association studies. 2009 , 1, 214-227	
1749	Polymorphisms within insulin-degrading enzyme (IDE) gene determine insulin metabolism and risk of type 2 diabetes. 2009 , 87, 1145-51	51
1748	Type 2 diabetes-associated genetic variants discovered in the recent genome-wide association studies are related to gestational diabetes mellitus in the Korean population. 2009 , 52, 253-61	177
1747	The risk allele load accelerates the age-dependent decline in beta cell function. 2009 , 52, 457-62	23
1746	Risk prediction of prevalent diabetes in a Swiss population using a weighted genetic score--the CoLaus Study. 2009 , 52, 600-8	95
1745	A common genetic variant in WFS1 determines impaired glucagon-like peptide-1-induced insulin secretion. 2009 , 52, 1075-82	67
1744	Combined analysis of 19 common validated type 2 diabetes susceptibility gene variants shows moderate discriminative value and no evidence of gene-gene interaction. 2009 , 52, 1308-14	51
1743	A genome-wide association scan for acute insulin response to glucose in Hispanic-Americans: the Insulin Resistance Atherosclerosis Family Study (IRAS FS). 2009 , 52, 1326-33	29
1742	Variants in KCNQ1 are associated with susceptibility to type 2 diabetes in the population of mainland China. 2009 , 52, 1315-21	54
1741	No association of multiple type 2 diabetes loci with type 1 diabetes. 2009 , 52, 2109-16	63
1740	Replication study for the association of new meta-analysis-derived risk loci with susceptibility to type 2 diabetes in 6,244 Japanese individuals. 2009 , 52, 1554-60	26
1739	Autoantibodies to zinc transporter 8 and SLC30A8 genotype stratify type 1 diabetes risk. 2009 , 52, 1881-8	137
1738	Association analysis of v-AKT murine thymoma viral oncogene homolog 1 (AKT1) polymorphisms and type 2 diabetes mellitus in the Korean population. 2009 , 31, 73-83	1
1737	Variation in genetic admixture and population structure among Latinos: the Los Angeles Latino eye study (LALES). 2009 , 10, 71	22
1736	Evaluating the association of common APOA2 variants with type 2 diabetes. 2009 , 10, 13	9
1735	Association between TCF7L2 gene polymorphisms and susceptibility to type 2 diabetes mellitus: a large Human Genome Epidemiology (HuGE) review and meta-analysis. 2009 , 10, 15	173

1734	Studies of CTNNB1 and FDFT1 variants and measures of obesity: analyses of quantitative traits and case-control studies in 18,014 Danes. 2009 , 10, 17	13
1733	FTO gene variation and measures of body mass in an African population. 2009 , 10, 21	77
1732	Functional and genetic analysis in type 2 diabetes of liver X receptor alleles--a cohort study. 2009 , 10, 27	20
1731	Contribution of type 2 diabetes associated loci in the Arabic population from Tunisia: a case-control study. 2009 , 10, 33	54
1730	Type 2 diabetes gene TCF7L2 polymorphism is not associated with fetal and postnatal growth in two birth cohort studies. 2009 , 10, 67	12
1729	Common polymorphisms within the NR4A3 locus, encoding the orphan nuclear receptor Nor-1, are associated with enhanced beta-cell function in non-diabetic subjects. 2009 , 10, 77	20
1728	SLC6A3 and body mass index in the Prostate, Lung, Colorectal and Ovarian Cancer Screening Trial. 2009 , 10, 9	4
1727	Zinc transporter gene expression is regulated by pro-inflammatory cytokines: a potential role for zinc transporters in beta-cell apoptosis?. 2009 , 9, 7	42
1726	Strengthening the REporting of Genetic Association studies (STREGA)--an extension of the STROBE statement. 2009 , 39, 247-66	190
1725	Association of genetic variation on chromosome 9p21.3 and arterial stiffness. 2009 , 265, 373-81	43
1724	Sequence variant on 9p21 is associated with the presence of abdominal aortic aneurysm disease but does not have an impact on aneurysmal expansion. 2009 , 17, 391-4	46
1723	GENESTAT: an information portal for design and analysis of genetic association studies. 2009 , 17, 533-6	5
1722	Genetic association analysis of 13 nuclear-encoded mitochondrial candidate genes with type II diabetes mellitus: the DAMAGE study. 2009 , 17, 1056-62	12
1721	Joint analysis of tightly linked SNPs in screening step of genome-wide association studies leads to increased power. 2009 , 17, 1043-9	15
1720	Recovering unused information in genome-wide association studies: the benefit of analyzing SNPs out of Hardy-Weinberg equilibrium. 2009 , 17, 1676-82	28
1719	Shared susceptibility variations in autoimmune diseases: a brief perspective on common issues. 2009 , 10, 1-4	21
1718	Differential contribution of CDKAL1 variants to psoriasis, Crohn's disease and type II diabetes. 2009 , 10, 654-8	43
1717	Effect of BSN-MST1 locus on inflammatory bowel disease and multiple sclerosis susceptibility. 2009 , 10, 631-5	16

1716	Genome-wide association for major depressive disorder: a possible role for the presynaptic protein piccolo. 2009 , 14, 359-75	322
1715	Inactivation of the Fto gene protects from obesity. 2009 , 458, 894-8	709
1714	Human genetics illuminates the paths to metabolic disease. 2009 , 462, 307-14	260
1713	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. 2009 , 41, 47-55	708
1712	Common variant in MTNR1B associated with increased risk of type 2 diabetes and impaired early insulin secretion. 2009 , 41, 82-8	550
1711	Variants in MTNR1B influence fasting glucose levels. 2009 , 41, 77-81	584
1710	Common variants at 30 loci contribute to polygenic dyslipidemia. 2009 , 41, 56-65	1095
1709	Genome-wide scan reveals association of psoriasis with IL-23 and NF-kappaB pathways. 2009 , 41, 199-204	1038
1708	Genome-wide association study identifies five susceptibility loci for glioma. 2009 , 41, 899-904	640
1707	New common variants affecting susceptibility to basal cell carcinoma. 2009 , 41, 909-14	275
1706	Genetic variant near IRS1 is associated with type 2 diabetes, insulin resistance and hyperinsulinemia. 2009 , 41, 1110-5	356
1705	New insights into the genetics of addiction. 2009 , 10, 225-31	171
1704	Human genetic variation and its contribution to complex traits. 2009 , 10, 241-51	778
1703	Bayesian statistical methods for genetic association studies. 2009 , 10, 681-90	339
1702	Structural basis for autoregulation of the zinc transporter YiiP. 2009 , 16, 1063-7	192
1701	Association of the FTO rs9939609 single nucleotide polymorphism with C-reactive protein levels. 2009 , 17, 330-4	31
1700	Association analyses between type 2 diabetes genes and obesity traits in pigs. 2009 , 17, 323-9	22
1699	Variation in IGF2BP2 interacts with adiposity to alter insulin sensitivity in Mexican Americans. 2009 , 17, 729-36	30

1698	The common variant in the FTO gene did not modify the effect of lifestyle changes on body weight: the Finnish Diabetes Prevention Study. 2009 , 17, 832-6	83
1697	A rare variant in the visfatin gene (NAMPT/PBEF1) is associated with protection from obesity. 2009 , 17, 1549-53	52
1696	Sudden cardiac death: The larger problem... The larger genome. 2009 , 20, 585-96	18
1695	CADISP-genetics: an International project searching for genetic risk factors of cervical artery dissections. 2009 , 4, 224-30	60
1694	Genetic gains on the obesity and metabolic disease fronts. 2009 , 76, 236-41	1
1693	1. DNA Collection in a Randomized Social Science Study of College Peer Effects. 2009 , 39, 1-29	9
1692	Genetic and biochemical pathways of beta-cell failure in type 2 diabetes. 2009 , 11 Suppl 4, 38-45	49
1691	Genetic basis of beta-cell dysfunction in man. 2009 , 11 Suppl 4, 149-58	15
1690	RD Lawrence Lecture 2009. Old genes, new tricks: learning about blood glucose regulation from naturally occurring genetic variation in humans. 2009 , 26, 1083-9	2
1689	Expression of p16(INK4a) in peripheral blood T-cells is a biomarker of human aging. 2009 , 8, 439-48	285
1688	Zinc and diabetes--clinical links and molecular mechanisms. 2009 , 20, 399-417	290
1687	Emerging therapies for metabolic diseases--the focus is on diabetes and obesity. 2009 , 13, 332-7	24
1686	A Fast Implementation of a Scan Statistic for Identifying Chromosomal Patterns of Genome Wide Association Studies. 2009 , 53, 1794-1801	8
1685	Zn(2+)-transporter-8: a dual role in diabetes. 2009 , 35, 356-63	15
1684	Meta-analysis of genetic association studies: methodologies, between-study heterogeneity and winner's curse. 2009 , 54, 615-23	80
1683	Design of tag SNP whole genome genotyping arrays. 2009 , 529, 51-61	10
1682	Construction of a prediction model for type 2 diabetes mellitus in the Japanese population based on 11 genes with strong evidence of the association. 2009 , 54, 236-41	62
1681	The polarizing effect of news media messages about the social determinants of health. 2009 , 99, 2160-7	130

1680	Genotype-imputation accuracy across worldwide human populations. 2009 , 84, 235-50	191
1679	The relationship between imputation error and statistical power in genetic association studies in diverse populations. 2009 , 85, 692-8	58
1678	ATRIUM: testing untyped SNPs in case-control association studies with related individuals. 2009 , 85, 667-78	6
1677	Meta-analysis of genome-wide association studies with overlapping subjects. 2009 , 85, 862-72	101
1676	Genetic architecture of type 2 diabetes: recent progress and clinical implications. 2009 , 32, 1107-14	51
1675	Human serum metabonomic analysis reveals progression axes for glucose intolerance and insulin resistance statuses. 2009 , 8, 5188-95	112
1674	Adaptive beta-cell proliferation is severely restricted with advanced age. 2009 , 58, 1365-72	257
1673	Insulin crystallization depends on zinc transporter ZnT8 expression, but is not required for normal glucose homeostasis in mice. 2009 , 106, 14872-7	257
1672	Association of 18 confirmed susceptibility loci for type 2 diabetes with indices of insulin release, proinsulin conversion, and insulin sensitivity in 5,327 nondiabetic Finnish men. 2009 , 58, 2129-36	149
1671	Relationship between human periodontitis and type 2 diabetes at a genomic level: a data-mining study. 2009 , 80, 1265-73	20
1670	Association analysis of variation in/near FTO, CDKAL1, SLC30A8, HHEX, EXT2, IGF2BP2, LOC387761, and CDKN2B with type 2 diabetes and related quantitative traits in Pima Indians. 2009 , 58, 478-88	120
1669	Genetic variants on chromosome 9p21 and ischemic stroke in Chinese. 2009 , 79, 431-5	29
1668	Genetic variations of solute carrier family 30 (zinc transporter) member 8 (SLC30A8) are not associated with polycystic ovary syndrome. 2009 , 91, 1598-601	4
1667	The Pro12Ala PPARgamma2 variant determines metabolism at the gene-environment interface. 2009 , 9, 88-98	57
1666	Beta-cell deterioration during diabetes: what's in the gun?. 2009 , 20, 388-93	77
1665	Genome-wide association studies in type 1 diabetes, inflammatory bowel disease and other immune-mediated disorders. 2009 , 21, 355-62	15
1664	Genetic dissection of type 2 diabetes. 2009 , 297, 10-7	111
1663	Strengthening the reporting of genetic association studies (STREGA): an extension of the strengthening the reporting of observational studies in epidemiology (STROBE) statement. 2009 , 62, 597-608.e4	77

1662	Healing and hurting: molecular mechanisms, functions, and pathologies of cellular senescence. 2009 , 36, 2-14	249
1661	TCF7L2 rs12255372 and SLC30A8 rs13266634 confer susceptibility to type 2 diabetes in a Russian population. 2009 , 3, 219-223	3
1660	A systematic method for estimating individual responses to treatment with antipsychotics in CATIE. 2009 , 107, 13-21	34
1659	Genetic risk factors for type 2 diabetes with pharmacologic intervention in African-American patients with schizophrenia or schizoaffective disorder. 2009 , 114, 50-6	12
1658	Comparison of genetic risk in three candidate genes (TCF7L2, PPARG, KCNJ11) with traditional risk factors for type 2 diabetes in a population-based study--the HUNT study. 2009 , 69, 282-7	22
1657	Latent autoimmune diabetes in adults. 2009 , 94, 4635-44	149
1656	The Molecular Genetics of Type 2 Diabetes: Past, Present and Future. 2009 ,	1
1655	Epigenetics: a molecular link between environmental factors and type 2 diabetes. 2009 , 58, 2718-25	439
1654	Mammalian zinc transporters: nutritional and physiologic regulation. 2009 , 29, 153-76	539
1653	Genes and GeneEnvironment Interactions in the Pathogenesis of Obesity and the Metabolic Syndrome. 2009 , 11-39	
1652	The genetics of cervical artery dissection: a systematic review. 2009 , 40, e459-66	73
1651	The HapMap and genome-wide association studies in diagnosis and therapy. 2009 , 60, 443-56	155
1650	Pathomechanisms of type 2 diabetes genes. 2009 , 30, 557-85	102
1649	Meta-analysis in genome-wide association studies. 2009 , 10, 191-201	199
1648	Significance of genome-wide association studies in molecular anthropology. 2009 , 13, 711-5	
1647	Nature versus nurture in determining athletic ability. 2009 , 54, 11-27	6
1646	DNA Microarrays for Biomedical Research. 2009 ,	10
1645	Genome-wide association study in humans. 2009 , 573, 231-58	15

1644	Cardiovascular Genomics. 2009 ,	1
1643	Enrichment of sequencing targets from the human genome by solution hybridization. 2009 , 10, R116	92
1642	Using prior knowledge and genome-wide association to identify pathways involved in multiple sclerosis. 2009 , 1, 65	21
1641	Worldwide patterns of haplotype diversity at 9p21.3, a locus associated with type 2 diabetes and coronary heart disease. 2009 , 1, 51	31
1640	Gene-gene and gene-environment interactions: new insights into the prevention, detection and management of coronary artery disease. 2009 , 1, 28	42
1639	DNA variations in human and medical genetics: 25 years of my experience. 2009 , 54, 1-8	52
1638	Molecular Endocrinology. 2009 ,	4
1637	Genetics of diabetic nephropathy: are there clues to the understanding of common kidney diseases?. 2009 , 112, c213-21	24
1636	Tissue-specific alternative splicing of TCF7L2. 2009 , 18, 3795-804	89
1635	Genetic determinants and molecular pathways in the pathogenesis of Type 2 diabetes. 2009 , 116, 99-111	52
1634	Signals of recent positive selection in a worldwide sample of human populations. 2009 , 19, 826-37	557
1633	Genomic regulatory blocks in vertebrates and implications in human disease. 2009 , 8, 333-42	27
1632	Haplotypic background of a private allele at high frequency in the Americas. 2009 , 26, 995-1016	48
1631	Pancreatic islet inflammation in type 2 diabetes: from alpha and beta cell compensation to dysfunction. 2009 , 115, 240-7	73
1630	Genomics of type 2 diabetes mellitus: implications for the clinician. 2009 , 5, 429-36	68
1629	Disclosing the disclosure: factors associated with communicating the results of genetic susceptibility testing for Alzheimer's disease. 2009 , 14, 768-84	24
1628	Genetic variants associated with Lp(a) lipoprotein level and coronary disease. 2009 , 361, 2518-28	935
1627	Three SNPs on chromosome 9p21 confer increased risk of myocardial infarction in Chinese subjects. 2009 , 207, 26-8	22

1626	Population-Based Association Studies. 2009 , 171-190	1
1625	The role of genetics in susceptibility to diabetic retinopathy. 2009 , 49, 35-52	72
1624	Association of the CPT1B gene with skeletal muscle fat infiltration in Afro-Caribbean men. 2009 , 17, 1396-401	15
1623	A genome-wide association study primer for clinicians. 2009 , 48, 89-95	15
1622	Evidence of interaction between type 2 diabetes susceptibility genes and dietary fat intake for adiposity and glucose homeostasis-related phenotypes. 2009 , 2, 225-34	23
1621	Genotype imputation. 2009 , 10, 387-406	812
1620	Genetic epidemiology in aging research. 2009 , 64, 47-60	17
1619	Environmental and genetic risk factors in obesity. 2009 , 18, 83-94	92
1618	Association of common type 2 diabetes risk gene variants and posttransplantation diabetes mellitus in renal allograft recipients in Korea. 2009 , 88, 693-8	32
1617	Genome-wide association study for type 2 diabetes: clinical applications. 2009 , 20, 87-91	34
1616	Fostering translation of genetics research: an NIDDK perspective. 2009 , 6, 579-588	1
1615	Replication in genome-wide association studies. 2009 , 24, 561-573	177
1614	Conference on "Multidisciplinary approaches to nutritional problems". Symposium on "Diabetes and health". Nutrition and its contribution to obesity and diabetes: a life-course approach to disease prevention?. 2009 , 68, 71-7	14
1613	Deletion of the mouse Slc30a8 gene encoding zinc transporter-8 results in impaired insulin secretion. 2009 , 421, 371-6	141
1612	Genome-wide association study to identify novel loci associated with therapy-related myeloid leukemia susceptibility. 2009 , 113, 5575-82	80
1611	STrengthening the REporting of Genetic Association studies (STREGA): an extension of the STROBE Statement. 2009 , 150, 206-15	87
1610	Cardiovascular disease risk prediction with and without knowledge of genetic variation at chromosome 9p21.3. 2009 , 150, 65-72	181
1609	Erratum. 2009 , 11, 594-594	

1608	Prioritizing genes for follow-up from genome wide association studies using information on gene expression in tissues relevant for type 2 diabetes mellitus. 2009 , 2, 72	32
1607	Type 2 Diabetes Mellitus: New Genetic Insights will Lead to New Therapeutics. 2009 , 10, 110-8	25
1606	Mining the genome for susceptibility to complex neurological disorders. 2009 , 9, 801-13	3
1605	Pharmacogenetics and functional genomics in asthma. 2009 , 6, 409-416	0
1604	Novel biological insights emerging from genetic studies of type 2 diabetes and related metabolic traits. 2010 , 21, 44-50	32
1603	Recent advances in the genetics and genomics of asthma and related traits. 2010 , 22, 307-12	9
1602	Interactions between genetic factors that predict diabetes and dietary factors that ultimately impact on risk of diabetes. 2010 , 21, 31-7	25
1601	Genes and Response to Training. 2010 , 177-184	1
1600	A genome-wide association study of amygdala activation in youths with and without bipolar disorder. 2010 , 49, 33-41	9
1599	TCF7L2 rs12255372 and SLC30A8 rs13266634 confer susceptibility to type 2 diabetes in a Russian population. 2010 , 46, 1001-1008	1
1598	Genome-wide association study for femoral neck bone geometry. 2010 , 25, 320-9	34
1597	Identification of KCNJ15 as a susceptibility gene in Asian patients with type 2 diabetes mellitus. 2010 , 86, 54-64	45
1596	Integrating pathway analysis and genetics of gene expression for genome-wide association studies. 2010 , 86, 581-91	202
1595	Powerful SNP-set analysis for case-control genome-wide association studies. 2010 , 86, 929-42	425
1594	To identify associations with rare variants, just WHaIT: Weighted haplotype and imputation-based tests. 2010 , 87, 728-35	78
1593	Gene expression in skin and lymphoblastoid cells: Refined statistical method reveals extensive overlap in cis-eQTL signals. 2010 , 87, 779-89	144
1592	Coronary artery calcification and its relationship to validated genetic variants for diabetes mellitus assessed in the Heinz Nixdorf recall cohort. 2010 , 30, 1867-72	23
1591	Genetics of coronary artery disease. 2010 , 11, 91-108	67

1590	[Genetic determinants of obesity. Current issues]. 2010 , 53, 674-80	6
1589	Diet-induced gene expression of isolated pancreatic islets from a polygenic mouse model of the metabolic syndrome. 2010 , 53, 309-20	39
1588	Candidate loci for insulin sensitivity and disposition index from a genome-wide association analysis of Hispanic participants in the Insulin Resistance Atherosclerosis (IRAS) Family Study. 2010 , 53, 281-9	22
1587	Improvements in glucose homeostasis in response to regular exercise are influenced by the PPARG Pro12Ala variant: results from the HERITAGE Family Study. 2010 , 53, 679-89	52
1586	Evidence for neuroendocrine function of a unique splicing form of TCF7L2 in human brain, islets and gut. 2010 , 53, 712-6	17
1585	Beta cell-specific Znt8 deletion in mice causes marked defects in insulin processing, crystallisation and secretion. 2010 , 53, 1656-68	228
1584	Type 2 diabetes risk alleles near ADCY5, CDKAL1 and HHEX-IDE are associated with reduced birthweight. 2010 , 53, 1908-16	56
1583	Disease-associated loci are significantly over-represented among genes bound by transcription factor 7-like 2 (TCF7L2) in vivo. 2010 , 53, 2340-6	37
1582	Genetic variants affecting incretin sensitivity and incretin secretion. 2010 , 53, 2289-97	32
1581	Association analysis of SLC30A8 rs13266634 and rs16889462 polymorphisms with type 2 diabetes mellitus and repaglinide response in Chinese patients. 2010 , 66, 1207-15	51
1580	From monogenic to polygenic obesity: recent advances. 2010 , 19, 297-310	149
1579	Evaluating variations of genotype calling: a potential source of spurious associations in genome-wide association studies. 2010 , 89, 55-64	11
1578	Type 2 Diabetes and Genetics, 2010: Translating Knowledge into Understanding. 2010 , 4, 437-445	3
1577	The genetics of insulin resistance: Where's Waldo?. 2010 , 10, 476-84	27
1576	From genetic association to molecular mechanism. 2010 , 10, 452-66	27
1575	Toll-like receptor 4 and inducible nitric oxide synthase gene polymorphisms are associated with Type 2 diabetes. 2010 , 24, 192-8	35
1574	Association of Gly972Arg polymorphism of IRS1 gene with type 2 diabetes mellitus in lean participants of a national health survey in Mexico: a candidate gene study. 2010 , 59, 38-45	31
1573	PPARG and ADIPOQ gene polymorphisms increase type 2 diabetes mellitus risk in Asian Indian Sikhs: Pro12Ala still remains as the strongest predictor. 2010 , 59, 492-501	54

1572	Replication of recently described type 2 diabetes gene variants in a South Indian population. 2010 , 59, 1760-6	39
1571	The genetics of obesity: FTO leads the way. 2010 , 26, 266-74	233
1570	Evaluating diabetes and hypertension disease causality using mouse phenotypes. 2010 , 4, 97	3
1569	Three-dimensional structure of beta-cell-specific zinc transporter, ZnT-8, predicted from the type 2 diabetes-associated gene variant SLC30A8 R325W. 2010 , 2, 33	24
1568	Identification of genetic factors associated with Type 2 Diabetes in Saudis: The lessons from European studies. 2010 , 2, 133-136	1
1567	Over-expression of ZnT7 increases insulin synthesis and secretion in pancreatic beta-cells by promoting insulin gene transcription. 2010 , 316, 2630-43	47
1566	Were genome-wide linkage studies a waste of time? Exploiting candidate regions within genome-wide association studies. 2010 , 34, 107-18	18
1565	Bayesian mixture models for the incorporation of prior knowledge to inform genetic association studies. 2010 , 34, 418-26	14
1564	Design of association studies with pooled or un-pooled next-generation sequencing data. 2010 , 34, 479-91	69
1563	Resequencing of pooled DNA for detecting disease associations with rare variants. 2010 , 34, 492-501	21
1562	Identifying genetic interactions in genome-wide data using Bayesian networks. 2010 , 34, 575-81	48
1561	Identifying candidate causal variants via trans-population fine-mapping. 2010 , 34, 653-64	27
1560	MaCH: using sequence and genotype data to estimate haplotypes and unobserved genotypes. 2010 , 34, 816-34	1535
1559	SNP selection in genome-wide and candidate gene studies via penalized logistic regression. 2010 , 34, 879-91	133
1558	Genome-wide pleiotropy of osteoporosis-related phenotypes: the Framingham Study. 2010 , 25, 1555-63	44
1557	Candidate gene association study conditioning on individual ancestry in patients with type 2 diabetes and metabolic syndrome from Mexico City. 2010 , 26, 261-70	82
1556	Genetic Mapping of Complex Traits. 2010 , 67-90	1
1555	Association study of 182 candidate genes in anorexia nervosa. 2010 , 153B, 1070-80	45

1554	The AlkB Domain of Mammalian ABH8 Catalyzes Hydroxylation of 5-Methoxycarbonylmethyluridine at the Wobble Position of tRNA. 2010 , 122, 9069-9072	6
1553	The AlkB domain of mammalian ABH8 catalyzes hydroxylation of 5-methoxycarbonylmethyluridine at the wobble position of tRNA. 2010 , 49, 8885-8	113
1552	Identification of type 2 diabetes-associated combination of SNPs using support vector machine. 2010 , 11, 26	60
1551	Obesity and diabetes genes are associated with being born small for gestational age: results from the Auckland Birthweight Collaborative study. 2010 , 11, 125	47
1550	The longitudinal association of common susceptibility variants for type 2 diabetes and obesity with fasting glucose level and BMI. 2010 , 11, 140	14
1549	Common genetic variants on chromosome 9p21 are associated with myocardial infarction and type 2 diabetes in an Italian population. 2010 , 11, 60	16
1548	Large-scale association analysis of TNF/LTA gene region polymorphisms in type 2 diabetes. 2010 , 11, 69	34
1547	Implication of genetic variants near SLC30A8, HHEX, CDKAL1, CDKN2A/B, IGF2BP2, FTO, TCF2, KCNQ1, and WFS1 in type 2 diabetes in a Chinese population. 2010 , 11, 81	95
1546	Association study of genetic variants in eight genes/loci with type 2 diabetes in a Han Chinese population. 2010 , 11, 97	66
1545	Translating type 2 diabetes genetics: what does it add to clinical practice?. 2010 , 27, 264-266	
1544	Interactions between TCF7L2 genotype and growth hormone-induced changes in glucose homeostasis in small for gestational age children. 2010 , 72, 47-52	5
1543	Transferrin receptor-1 gene polymorphisms are associated with type 2 diabetes. 2010 , 40, 600-7	19
1542	Forearm vasodilator reactivity in homozygous carriers of the 9p21.3 rs1333049 G>C polymorphism. 2010 , 40, 700-5	4
1541	FTO genotype is associated with exercise training-induced changes in body composition. 2010 , 18, 322-6	38
1540	Meta-analysis added power to identify variants in FTO associated with type 2 diabetes and obesity in the Asian population. 2010 , 18, 1619-24	87
1539	Gene and pathway-based second-wave analysis of genome-wide association studies. 2010 , 18, 111-7	189
1538	Assessing sources of inconsistencies in genotypes and their effects on genome-wide association studies with HapMap samples. 2010 , 10, 364-74	18
1537	IGF2BP2 variations influence repaglinide response and risk of type 2 diabetes in Chinese population. 2010 , 31, 709-17	38

1536	Grand challenge commentary: RNA epigenetics?. 2010 , 6, 863-5	292
1535	Variation in CDKN2A at 9p21.3 influences childhood acute lymphoblastic leukemia risk. 2010 , 42, 492-4	214
1534	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. 2010 , 42, 579-89	1449
1533	A genome-wide association study identifies genetic variants in the CDKN2BAS locus associated with endometriosis in Japanese. 2010 , 42, 707-10	195
1532	A genome-wide association study in the Japanese population identifies susceptibility loci for type 2 diabetes at UBE2E2 and C2CD4A-C2CD4B. 2010 , 42, 864-8	214
1531	Genome-wide association analysis identifies three psoriasis susceptibility loci. 2010 , 42, 1000-4	251
1530	The role of peroxisome proliferator-activated receptor α in pancreatic β cell function and survival: therapeutic implications for the treatment of type 2 diabetes mellitus. 2010 , 12, 1036-47	50
1529	References. 235-268	
1528	Zinc, alpha cells and glucagon secretion. 2010 , 6, 52-7	29
1527	Analysis of Osteocalcin as a Candidate Gene for Type 2 Diabetes (T2D) and Intermediate Traits in Caucasians and African Americans. 2010 , 28, 281-286	24
1526	Longitudinal genome-wide association of cardiovascular disease risk factors in the Bogalusa heart study. 2010 , 6, e1001094	105
1525	Association between type 2 diabetes loci and measures of fatness. 2010 , 5, e8541	15
1524	Common SNPs in FTO gene are associated with obesity related anthropometric traits in an island population from the eastern Adriatic coast of Croatia. 2010 , 5, e10375	26
1523	Risk of type 2 diabetes and obesity is differentially associated with variation in FTO in whites and African-Americans in the ARIC study. 2010 , 5, e10521	61
1522	Analyses and comparison of imputation-based association methods. 2010 , 5, e10827	26
1521	Multiethnic genetic association studies improve power for locus discovery. 2010 , 5, e12600	44
1520	Genome wide association studies for milk production traits in Chinese Holstein population. 2010 , 5, e13661	164
1519	Unifying candidate gene and GWAS Approaches in Asthma. 2010 , 5, e13894	74

1518	Integrated genetic and epigenetic analysis identifies haplotype-specific methylation in the FTO type 2 diabetes and obesity susceptibility locus. 2010 , 5, e14040	193
1517	Analyses of copy number variation of GK rat reveal new putative type 2 diabetes susceptibility loci. 2010 , 5, e14077	10
1516	Presymptomatic risk assessment for chronic non-communicable diseases. 2010 , 5, e14338	11
1515	CDKAL1 and type 2 diabetes: a global meta-analysis. 2010 , 9, 1109-20	60
1514	Phenotypic and Genotypic Variation. 155-156	
1513	Human Adaptation to High Altitude. 170-191	1
1512	High Fat Diet Regulation of β -Cell Proliferation and β -Cell Mass. 2010 , 4,	40
1511	Fine-mapping a locus for glucose tolerance using heterogeneous stock rats. 2010 , 41, 102-8	40
1510	The epidemiology of diabetes in Korea: from the economics to genetics. 2010 , 34, 10-5	16
1509	The Common FTO Genetic Polymorphism rs9939609 is Associated with Increased BMI in Type 1 Diabetes but not with Diabetic Nephropathy. 2010 , 5, 29-32	10
1508	METAL: fast and efficient meta-analysis of genomewide association scans. 2010 , 26, 2190-1	2697
1507	Dyslipidemia in HIV-infected individuals: from pharmacogenetics to pharmacogenomics. 2010 , 11, 587-94	19
1506	Impact of single nucleotide polymorphisms and of clinical risk factors on new-onset diabetes mellitus in HIV-infected individuals. 2010 , 51, 1090-8	21
1505	Genetic variants in ABO blood group region, plasma soluble E-selectin levels and risk of type 2 diabetes. 2010 , 19, 1856-62	131
1504	Investigation of type 2 diabetes risk alleles support CDKN2A/B, CDKAL1, and TCF7L2 as susceptibility genes in a Han Chinese cohort. 2010 , 5, e9153	94
1503	Association of the CTLA4 gene with Graves' disease in the Chinese Han population. 2010 , 5, e9821	37
1502	Epigenetic regulation of p16Ink4a and Arf by JDP2 in cellular senescence. 2010 , 1, 49-58	
1501	No association between FTO or HHEX and endometrial cancer risk. 2010 , 19, 2106-9	22

1500	The PPARgamma Pro12Ala variant is associated with insulin sensitivity in Russian normoglycaemic and type 2 diabetic subjects. 2010 , 7, 56-62	19
1499	Association of single nucleotide polymorphisms on chromosome 9p21.3 with platelet reactivity: a potential mechanism for increased vascular disease. 2010 , 3, 445-53	48
1498	Prepulse inhibition of the startle reflex: a window on the brain in schizophrenia. 2010 , 4, 349-71	79
1497	Cyclin D2 is essential for the compensatory beta-cell hyperplastic response to insulin resistance in rodents. 2010 , 59, 987-96	54
1496	Considerations for designing a prototype genetic test for use in translational research. 2010 , 13, 155-65	22
1495	Genetic variants influencing circulating lipid levels and risk of coronary artery disease. 2010 , 30, 2264-76	318
1494	Acute cytokine-mediated downregulation of the zinc transporter ZnT8 alters pancreatic beta-cell function. 2010 , 206, 159-69	43
1493	Genetic variants identified in a European genome-wide association study that were found to predict incident coronary heart disease in the atherosclerosis risk in communities study. 2010 , 171, 14-23	41
1492	The possible role of epigenetics in gestational diabetes: cause, consequence, or both. 2010 , 2010, 605163	30
1491	The genetics of obesity and the metabolic syndrome. 2010 , 10, 86-108	47
1490	DataSHIELD: resolving a conflict in contemporary bioscience--performing a pooled analysis of individual-level data without sharing the data. 2010 , 39, 1372-82	102
1489	Association between a literature-based genetic risk score and cardiovascular events in women. 2010 , 303, 631-7	256
1488	Diabetes in Women. 2010 ,	1
1487	Can the genetics of type 1 and type 2 diabetes shed light on the genetics of latent autoimmune diabetes in adults?. 2010 , 31, 183-93	46
1486	The genetics of type 2 diabetes: what have we learned from GWAS?. 2010 , 1212, 59-77	264
1485	Empirical Data Indicates a Primarily Additive Genetic Model for Expressional QTLs. 2010 ,	
1484	Combining genetic markers and clinical risk factors improves the risk assessment of impaired glucose metabolism. 2010 , 42, 196-206	10
1483	Genetic variants at 2q24 are associated with susceptibility to type 2 diabetes. 2010 , 19, 2706-15	164

1482	EMINIM: an adaptive and memory-efficient algorithm for genotype imputation. 2010 , 17, 547-60	12
1481	Gene variants in the novel type 2 diabetes loci CDC123/CAMK1D, THADA, ADAMTS9, BCL11A, and MTNR1B affect different aspects of pancreatic beta-cell function. 2010 , 59, 293-301	106
1480	Long-range gene regulation links genomic type 2 diabetes and obesity risk regions to HHEX, SOX4, and IRX3. 2010 , 107, 775-80	159
1479	Progress in the genetics of common obesity and type 2 diabetes. 2010 , 12, e7	67
1478	Genetic influences on the association between fetal growth and susceptibility to type 2 diabetes. 2010 , 1, 96-105	6
1477	Polygenic risk variants for type 2 diabetes susceptibility modify age at diagnosis in monogenic HNF1A diabetes. 2010 , 59, 266-71	25
1476	Combined risk allele score of eight type 2 diabetes genes is associated with reduced first-phase glucose-stimulated insulin secretion during hyperglycemic clamps. 2010 , 59, 287-92	48
1475	Anonymization of electronic medical records for validating genome-wide association studies. 2010 , 107, 7898-903	98
1474	Genetic heterogeneity in latent autoimmune diabetes is linked to various degrees of autoimmune activity: results from the Nord-Trøndelag Health Study. 2010 , 59, 302-10	59
1473	Colloquium paper: bioenergetics, the origins of complexity, and the ascent of man. 2010 , 107 Suppl 2, 8947-53	93
1472	Examination of all type 2 diabetes GWAS loci reveals HHEX-IDE as a locus influencing pediatric BMI. 2010 , 59, 751-5	49
1471	Functional analysis of two single nucleotide polymorphisms in SLC30A2 (ZnT2): implications for mammary gland function and breast disease in women. 2010 , 42A, 219-27	37
1470	Identification of new genetic risk variants for type 2 diabetes. 2010 , 6, e1001127	168
1469	Genome-wide significant associations for variants with minor allele frequency of 5% or less--an overview: A HuGE review. 2010 , 172, 869-89	38
1468	The use of animal models to study stem cell therapies for diabetes mellitus. 2009 , 51, 74-81	6
1467	Genetic variants of cyclin-dependent kinase 5 regulatory subunit associated protein 1-like 1 and transcription factor 7-like 2 are not associated with polycystic ovary syndrome in Chinese women. 2010 , 26, 129-34	9
1466	A genome-wide association study identifies susceptibility variants for type 2 diabetes in Han Chinese. 2010 , 6, e1000847	251
1465	Common inherited variation in mitochondrial genes is not enriched for associations with type 2 diabetes or related glyceic traits. 2010 , 6, e1001058	366

1464	Expression of linear and novel circular forms of an INK4/ARF-associated non-coding RNA correlates with atherosclerosis risk. 2010 , 6, e1001233	653
1463	Chromosome 9p21 SNPs Associated with Multiple Disease Phenotypes Correlate with ANRIL Expression. 2010 , 6, e1000899	291
1462	Quantification of population structure using correlated SNPs by shrinkage principal components. 2010 , 70, 9-22	40
1461	Genome-wide association study of coronary artery disease. 2010 , 2010, 790539	12
1460	Consistent association of type 2 diabetes risk variants found in europeans in diverse racial and ethnic groups. 2010 , 6, e1001078	142
1459	Family-based association analysis of 42 hereditary prostate cancer families identifies the Apolipoprotein L3 region on chromosome 22q12 as a risk locus. 2010 , 19, 3852-62	15
1458	Utility of genetic and non-genetic risk factors in prediction of type 2 diabetes: Whitehall II prospective cohort study. 2010 , 340, b4838	211
1457	Liver and adipose expression associated SNPs are enriched for association to type 2 diabetes. 2010 , 6, e1000932	139
1456	An interactive effect of batch size and composition contributes to discordant results in GWAS with the CHIAMO genotyping algorithm. 2010 , 10, 355-63	10
1455	Combined effects of 19 common variations on type 2 diabetes in Chinese: results from two community-based studies. 2010 , 5, e14022	68
1454	Epigenetic regulation of the INK4b-ARF-INK4a locus: in sickness and in health. 2010 , 5, 685-90	168
1453	Explaining inter-individual variability in phenotype: is epigenetics up to the challenge?. 2010 , 5, 16-9	39
1452	Lack of significant effects of the type 2 diabetes susceptibility loci JAZF1, CDC123/CAMK1D, NOTCH2, ADAMTS9, THADA, and TSPAN8/LGR5 on diabetes and quantitative metabolic traits. 2010 , 42, 14-22	18
1451	Cutting the Fat: The Genetic Dissection of Body Weight. 2010 , 94, 197-212	5
1450	Polymorphisms in NRXN3, TFAP2B, MSRA, LYPLAL1, FTO and MC4R and their effect on visceral fat area in the Japanese population. 2010 , 55, 738-42	32
1449	Multigenic condition risk assessment in direct-to-consumer genomic services. 2010 , 12, 279-88	32
1448	Variations in/nearby genes coding for JAZF1, TSPAN8/LGR5 and HHEX-IDE and risk of type 2 diabetes in Han Chinese. 2010 , 55, 810-5	18
1447	Polymorphisms identified through genome-wide association studies and their associations with type 2 diabetes in Chinese, Malays, and Asian-Indians in Singapore. 2010 , 95, 390-7	68

1446	The genetics of autism: key issues, recent findings, and clinical implications. 2010 , 33, 83-105	98
1445	Genetic research into bipolar disorder: the need for a research framework that integrates sophisticated molecular biology and clinically informed phenotype characterization. 2010 , 33, 67-82	52
1444	Translating associations between common kidney diseases and genetic variation into the clinic. 2010 , 30, 195-202	2
1443	Genomics of heart failure. 2010 , 6, 115-24	9
1442	Genetic variants in MTNR1B affecting insulin secretion. 2010 , 42, 387-93	32
1441	Genomewide association studies and assessment of the risk of disease. 2010 , 363, 166-76	1098
1440	Wnt signaling in pancreatic islets. 2010 , 654, 391-419	68
1439	Two-stage testing strategies for genome-wide association studies in family-based designs. 2010 , 620, 485-96	5
1438	[Association of FTO gene polymorphisms and morbid obesity in the population of Extremadura (Spain)]. 2010 , 57, 203-9	12
1437	Rethinking the genetic basis for comorbidity of schizophrenia and type 2 diabetes. 2010 , 123, 234-43	88
1436	Clinical differences between patients with MODY-3, MODY-2 and type 2 diabetes mellitus with I27L polymorphism in the HNF1alpha gene. 2010 , 57, 4-8	6
1435	Genetics of psychiatric disorders methods: molecular approaches. 2010 , 30, 815-27	2
1434	Genetics of psychiatric disorders methods: molecular approaches. 2010 , 33, 1-13	13
1433	A Genome-Wide Association Study of Amygdala Activation in Youths With and Without Bipolar Disorder. 2010 , 49, 33-41	25
1432	FoxM1 is up-regulated by obesity and stimulates beta-cell proliferation. 2010 , 24, 1822-34	69
1431	Impact of common variants of PPARG, KCNJ11, TCF7L2, SLC30A8, HHEX, CDKN2A, IGF2BP2, and CDKAL1 on the risk of type 2 diabetes in 5,164 Indians. 2010 , 59, 2068-74	146
1430	No association between polymorphisms in the INSIG1 gene and the risk of type 2 diabetes and related traits. 2010 , 92, 252-7	8
1429	Role of Nutrition in the Pathophysiology, Prevention, and Treatment of Type 2 Diabetes and the Spectrum of Cardiometabolic Disease. 2010 , 371-387	

1428	Genetic susceptibility to type 2 diabetes is associated with reduced prostate cancer risk. 2010 , 69, 193-201	30
1427	IGF2BP1, IGF2BP2 and IGF2BP3 genotype, haplotype and genetic model studies in metabolic syndrome traits and diabetes. 2010 , 20, 310-8	27
1426	Gestational diabetes mellitus screening based on the gene chip technique. 2010 , 89, 167-73	15
1425	Antidiabetic effects of IGFBP2, a leptin-regulated gene. 2010 , 11, 11-22	203
1424	TCF7L2 is associated with type 2 diabetes in nonobese individuals from Tunisia. 2010 , 58, 426-9	13
1423	Expansion of beta-cell mass in response to pregnancy. 2010 , 21, 151-8	229
1422	Analysis of candidate genes on chromosome 20q12-13.1 reveals evidence for BMI mediated association of PREX1 with type 2 diabetes in European Americans. 2010 , 96, 211-9	30
1421	Meta-analysis and functional effects of the SLC30A8 rs13266634 polymorphism on isolated human pancreatic islets. 2010 , 100, 77-82	83
1420	Apolipoprotein E polymorphisms and type 2 diabetes: a meta-analysis of 30 studies including 5423 cases and 8197 controls. 2010 , 100, 283-91	57
1419	The pursuit of genome-wide association studies: where are we now?. 2010 , 55, 195-206	172
1418	Uncovering the roles of rare variants in common disease through whole-genome sequencing. 2010 , 11, 415-25	1082
1417	Histone chaperone Jun dimerization protein 2 (JDP2): role in cellular senescence and aging. 2010 , 26, 515-31	10
1416	Replication of association between schizophrenia and ZNF804A in the Irish Case-Control Study of Schizophrenia sample. 2010 , 15, 29-37	182
1415	Probability theory-based SNP association study method for identifying susceptibility loci and genetic disease models in human case-control data. 2010 , 9, 232-41	1
1414	Genome-wide association studies: a primer. 2010 , 40, 1063-77	73
1413	Handbook on Analyzing Human Genetic Data. 2010 ,	5
1412	A hidden Markov random field model for genome-wide association studies. 2010 , 11, 139-50	33
1411	Genomics, type 2 diabetes, and obesity. 2010 , 363, 2339-50	696

1410	Practical issues in building risk-predicting models for complex diseases. 2010 , 20, 415-40	16
1409	Statistical Methods in Molecular Biology. 2010 ,	10
1408	Evolutionary adaptations to dietary changes. 2010 , 30, 291-314	119
1407	Genome-Wide Association Studies and Genotyping Technologies. 2010 , 38-45	
1406	Genomics of Myocardial Infarction. 2010 , 289-302	
1405	Diabetes. 2010 , 676-684	
1404	Pharmacogenetics of Anti-Diabetes Drugs. 2010 , 3, 2610-2646	70
1403	Obesity and the brain: a possible genetic link. 2010 , 2, 27	6
1402	Behavioral Neurobiology of Schizophrenia and Its Treatment. 2010 ,	6
1401	Lipoprotein Disorders. 2010 , 269-288	1
1400	Association of gene polymorphism of the fat-mass and obesity-associated gene with insulin resistance in Japanese. 2010 , 33, 214-8	23
1399	From estrogen-centric to aging and oxidative stress: a revised perspective of the pathogenesis of osteoporosis. 2010 , 31, 266-300	742
1398	Erythrocyte fatty acid composition and insulin sensitivity in daughters of Type 2 diabetic patients and women with no family history of diabetes. 2010 , 33, 306-12	1
1397	Human genetic variation recognizes functional elements in noncoding sequence. 2010 , 20, 311-9	46
1396	Inherited destiny? Genetics and gestational diabetes mellitus. 2011 , 3, 18	17
1395	LOC387761 polymorphism is associated with type 2 diabetes in the Mexican population. 2011 , 15, 79-83	10
1394	ANRIL, a long, noncoding RNA, is an unexpected major hotspot in GWAS. 2011 , 25, 444-8	361
1393	Variants in the Toll-interacting protein gene are associated with susceptibility to sepsis in the Chinese Han population. 2011 , 15, R12	38

1392	The same chromosome 9p21.3 locus is associated with type 2 diabetes and coronary artery disease in a Chinese Han population. 2011 , 60, 680-4	41
1391	Type 2 diabetes (T2D) associated polymorphisms regulate expression of adjacent transcripts in transformed lymphocytes, adipose, and muscle from Caucasian and African-American subjects. 2011 , 96, E394-403	17
1390	Type 2 diabetes risk variants and colorectal cancer risk: the Multiethnic Cohort and PAGE studies. 2011 , 60, 1703-11	35
1389	1. Diabetes in the Elderly Population: Pathophysiology, Prevention, and Management. 2011 , 9-37	1
1388	Common variants of FTO and the risk of obesity and type 2 diabetes in Indians. 2011 , 56, 720-6	50
1387	Cyclin-dependent kinase 5 promotes pancreatic β -cell survival via Fak-Akt signaling pathways. 2011 , 60, 1186-97	34
1386	At-risk variant in TCF7L2 for type II diabetes increases risk of schizophrenia. 2011 , 70, 59-63	101
1385	Statistical issues in gene association studies. 2011 , 700, 17-36	10
1384	An overview of the genetic susceptibility to alcoholism. 2011 , 51 Suppl 1, S2-6	22
1383	Association of genetic variations in TCF7L2, SLC30A8, HHEX, LOC387761, and EXT2 with Type 2 diabetes mellitus in Tunisia. 2011 , 15, 399-405	28
1382	Development of a predictive model for type 2 diabetes mellitus using genetic and clinical data. 2011 , 2, 75-82	13
1381	Two non-synonymous markers in PTPN21, identified by genome-wide association study data-mining and replication, are associated with schizophrenia. 2011 , 131, 43-51	19
1380	CDKN2BAS is associated with periodontitis in different European populations and is activated by bacterial infection. 2011 , 48, 38-47	57
1379	Role of WNT signalling in the determination of human mesenchymal stem cells into preadipocytes. 2011 , 46, R65-72	94
1378	Epigenetic Aspects of Chronic Diseases. 2011 ,	2
1377	Comprehensive Cardiovascular Medicine in the Primary Care Setting. 2011 ,	
1376	N6-methyladenosine in nuclear RNA is a major substrate of the obesity-associated FTO. 2011 , 7, 885-7	1937
1375	Comparing strategies to fine-map the association of common SNPs at chromosome 9p21 with type 2 diabetes and myocardial infarction. 2011 , 43, 801-5	75

1374	Resequencing and analysis of variation in the TCF7L2 gene in African Americans suggests that SNP rs7903146 is the causal diabetes susceptibility variant. 2011 , 60, 662-8	65
1373	Clinical Cardiogenetics. 2011 ,	3
1372	Planning a genome-wide association study: points to consider. 2011 , 43, 451-60	14
1371	Genetic Epidemiology. 2011 ,	2
1370	New-onset diabetes after transplantation: risk factors and clinical impact. 2011 , 37, 1-14	33
1369	Behavioral strategies in diabetes prevention programs: a systematic review of randomized controlled trials. 2011 , 91, 1-12	102
1368	Association between rs13266634 C/T polymorphisms of solute carrier family 30 member 8 (SLC30A8) and type 2 diabetes, impaired glucose tolerance, type 1 diabetes--a meta-analysis. 2011 , 91, 195-202	33
1367	Association between polymorphisms in RAPGEF1, TP53, NRF1 and type 2 diabetes in Chinese Han population. 2011 , 91, 171-6	22
1366	Transcription factor 7-like 2 (TCF7L2) gene polymorphism and complication/comorbidity profile in type 2 diabetes patients. 2011 , 93, 390-5	24
1365	Type 2 diabetes susceptibility single-nucleotide polymorphisms are not associated with polycystic ovary syndrome. 2011 , 95, 2538-41.e1-6	25
1364	What is a functional locus? Understanding the genetic basis of complex phenotypic traits. 2011 , 76, 638-42	7
1363	Quantitative assessment of the influence of hematopoietically expressed homeobox variant (rs1111875) on type 2 diabetes risk. 2011 , 102, 194-9	9
1362	Association of ACACB polymorphisms with obesity and diabetes. 2011 , 104, 670-6	29
1361	Where to go with FTO?. 2011 , 22, 53-9	55
1360	Endoplasmic reticulum stress and pancreatic β -cell death. 2011 , 22, 266-74	245
1359	Acceleration Genotype Imputation for Large Dataset on GPU. 2011 , 8, 457-463	1
1358	SLC30A8 polymorphism and type 2 diabetes risk: evidence from 27 study groups. 2011 , 21, 398-405	22
1357	Association of the FTO gene variant (rs9939609) with cardiovascular disease in men with abnormal glucose metabolism--the Finnish Diabetes Prevention Study. 2011 , 21, 691-8	37

1356	[Genetic variants, cardiovascular risk and genome-wide association studies]. 2011 , 64, 509-14	16
1355	The chromosome 9p21 region and myocardial infarction in a European population. 2011 , 217, 220-6	20
1354	Genome-wide association studies: results from the first few years and potential implications for clinical medicine. 2011 , 62, 11-24	73
1353	Genome-wide association studies and type 2 diabetes. 2011 , 10, 52-60	82
1352	The ENPP1 K121Q polymorphism is not associated with type 2 diabetes or obesity in the Chinese Han population. 2011 , 56, 12-6	20
1351	Genetic Variants, Cardiovascular Risk and Genome-Wide Association Studies. 2011 , 64, 509-514	
1350	Genetics of non-alcoholic fatty liver disease and associated metabolic disorders. 2011 , 27, 186-197	1
1349	New type 2 diabetes risk genes provide new insights in insulin secretion mechanisms. 2011 , 93 Suppl 1, S9-24	55
1348	Delineating Signals from Association Studies. 2011 , 277-293	
1347	The search for genetic risk factors of type 2 diabetes mellitus. 2011 , 35, 12-22	26
1346	Pharmacogenetics for T2DM and Anti-Diabetic Drugs. 2011 ,	
1345	Data Quality Control. 2011 , 95-108	3
1344	Aging and Insulin Secretion. 2011 , 373-384	3
1343	Genetics of childhood obesity. 2011 , 2011, 845148	38
1342	Association of genetic variation on chromosome 9p21 with polypoidal choroidal vasculopathy and neovascular age-related macular degeneration. 2011 , 52, 8063-7	19
1341	Genetic variants of diabetes risk and incident cardiovascular events in chronic coronary artery disease. 2011 , 6, e16341	6
1340	A genome-wide association study confirms previously reported loci for type 2 diabetes in Han Chinese. 2011 , 6, e22353	49
1339	Association of new loci identified in European genome-wide association studies with susceptibility to type 2 diabetes in the Japanese. 2011 , 6, e26911	48

1338	Association of six single nucleotide polymorphisms with gestational diabetes mellitus in a Chinese population. 2011 , 6, e26953	63
1337	Large scale association analysis identifies three susceptibility loci for coronary artery disease. 2011 , 6, e29427	63
1336	Genetic and clinical risk factors of new-onset diabetes after transplantation in Hispanic kidney transplant recipients. 2011 , 91, 1114-9	34
1335	Association between two key SNPs on chromosome 12p13 and ischemic stroke in Chinese Han population. 2011 , 21, 572-8	13
1334	Two common genetic variants near nuclear-encoded OXPHOS genes are associated with insulin secretion in vivo. 2011 , 164, 765-71	24
1333	Genetic risk factors for type 2 diabetes mellitus and response to sulfonylurea treatment. 2011 , 21, 461-8	7
1332	The interplay of lifestyle and genetic susceptibility in Type 2 diabetes risk. 2011 , 1, 299-307	4
1331	The pancreatic islet β -cell-enriched transcription factor Pdx-1 regulates Slc30a8 gene transcription through an intronic enhancer. 2011 , 433, 95-105	23
1330	Genetics of Type 2 diabetes in Asian Indians. 2011 , 1, 309-324	5
1329	THE INTERPRETATION OF THE GENETIC CODE. 2011 , 113-131	
1328	Genetics of type 2 diabetes: the GWAS era and future perspectives [Review]. 2011 , 58, 723-39	116
1327	Genome-wide association studies of Type 2 diabetes: are these ready to make an impact in the clinic?. 2011 , 1, 379-387	
1326	Bone metabolism and fracture risk in type 2 diabetes mellitus [Review]. 2011 , 58, 613-24	56
1325	Genetic interaction between hyperglycemic QTLs is manifested under a high calorie diet in OLETF-derived congenic rats. 2011 , 60, 125-32	4
1324	Classical Genetic Studies of Schizophrenia. 2011 , 245-268	1
1323	KCNQ1 gene variants and risk of new-onset diabetes in tacrolimus-treated renal-transplanted patients. 2011 , 25, E284-91	27
1322	Association between the FTO gene and overweight in Japanese children and adolescents. 2011 , 12, 494-500	13
1321	Dorothy Hodgkin Lecture 2010. From hype to hope? A journey through the genetics of Type 2 diabetes. 2011 , 28, 132-40	14

1320	Genetics of type 2 diabetes: pathophysiologic and clinical relevance. 2011 , 41, 679-92	91
1319	Genome-wide association scan allowing for epistasis in type 2 diabetes. 2011 , 75, 10-9	29
1318	Genetic mapping of vascular calcified plaque loci on chromosome 16p in European Americans from the diabetes heart study. 2011 , 75, 222-35	7
1317	rs9939609 in the FTO gene is associated with obesity but not with several biochemical parameters in Sardinian obese children. 2011 , 75, 648-54	19
1316	Periodontal genetics: a decade of genetic association studies mandates better study designs. 2011 , 38, 103-7	49
1315	Obesity-induced overexpression of miRNA-143 inhibits insulin-stimulated AKT activation and impairs glucose metabolism. 2011 , 13, 434-46	390
1314	Genome-wide association study identifies a susceptibility locus for HCV-induced hepatocellular carcinoma. 2011 , 43, 455-8	296
1313	Genome-wide association study identifies susceptibility loci for open angle glaucoma at TMCO1 and CDKN2B-AS1. 2011 , 43, 574-8	329
1312	Long non-coding RNA ANRIL is required for the PRC2 recruitment to and silencing of p15(INK4B) tumor suppressor gene. 2011 , 30, 1956-62	799
1311	Replication of genetic variants from genome-wide association studies with metabolic traits in an island population of the Adriatic coast of Croatia. 2011 , 19, 341-6	13
1310	Genetic testing and common disorders in a public health framework: how to assess relevance and possibilities. Background Document to the ESHG recommendations on genetic testing and common disorders. 2011 , 19 Suppl 1, S6-44	60
1309	Heterogeneity of genetic associations of CDKAL1 and HHEX with susceptibility of type 2 diabetes mellitus by gender. 2011 , 19, 672-5	22
1308	The growth hormone-IGF-I axis as a mediator for the association between FTO variants and body mass index: results of the Study of Health in Pomerania. 2011 , 35, 364-72	14
1307	Reduced body weight in male Tspan8-deficient mice. 2011 , 35, 605-17	19
1306	Analysis of FTO gene variants with obesity and glucose homeostasis measures in the multiethnic Insulin Resistance Atherosclerosis Study cohort. 2011 , 35, 1173-82	41
1305	Genome-wide association study of recurrent early-onset major depressive disorder. 2011 , 16, 193-201	206
1304	Novel loci for major depression identified by genome-wide association study of Sequenced Treatment Alternatives to Relieve Depression and meta-analysis of three studies. 2011 , 16, 202-15	209
1303	Genome-wide pharmacogenomic analysis of response to treatment with antipsychotics. 2011 , 16, 76-85	124

1302	GWA study data mining and independent replication identify cardiomyopathy-associated 5 (CMYA5) as a risk gene for schizophrenia. 2011 , 16, 1117-29	58
1301	9p21 DNA variants associated with coronary artery disease impair interferon- β signalling response. 2011 , 470, 264-8	490
1300	Long noncoding RNAs and human disease. 2011 , 21, 354-61	1544
1299	Genetic variation within the TRPM5 locus associates with prediabetic phenotypes in subjects at increased risk for type 2 diabetes. 2011 , 60, 1325-33	33
1298	A powerful hybrid approach to select top single-nucleotide polymorphisms for genome-wide association study. 2011 , 12, 3	2
1297	Early peroxisome proliferator-activated receptor gamma regulated genes involved in expansion of pancreatic beta cell mass. 2011 , 4, 86	14
1296	An analysis of single nucleotide polymorphisms of 125 DNA repair genes in the Texas genome-wide association study of lung cancer with a replication for the XRCC4 SNPs. 2011 , 10, 398-407	23
1295	Association between IGF2BP2 rs4402960 polymorphism and risk of type 2 diabetes mellitus: a meta-analysis. 2011 , 42, 361-7	16
1294	Impact of genetic polymorphisms of cytochrome P450 2 C (CYP2C) enzymes on the drug metabolism and design of antidiabetics. 2011 , 194, 159-67	12
1293	mTOR phosphorylates IMP2 to promote IGF2 mRNA translation by internal ribosomal entry. 2011 , 25, 1159-72	120
1292	New IBD genetics: common pathways with other diseases. 2011 , 60, 1739-53	418
1291	A Synopsis of Exercise Genomics Research and a Vision for its Future Translation into Practice. 2011 , 231-254	
1290	Emerging applications of metabolomic and genomic profiling in diabetic clinical medicine. 2011 , 34, 2624-30	36
1289	Epigenomics of human embryonic stem cells and induced pluripotent stem cells: insights into pluripotency and implications for disease. 2011 , 3, 36	39
1288	Random-effects model aimed at discovering associations in meta-analysis of genome-wide association studies. 2011 , 88, 586-98	351
1287	Association study of type 2 diabetes genetic susceptibility variants and risk of pancreatic cancer: an analysis of PanScan-I data. 2011 , 22, 877-83	48
1286	AKT1 polymorphisms are associated with risk for metabolic syndrome. 2011 , 129, 129-39	22
1285	Type 2 diabetes and obesity: genomics and the clinic. 2011 , 130, 41-58	62

1284	Realizing the promise of population biobanks: a new model for translation. 2011 , 130, 333-45	25
1283	The carriage of risk variants of CDKAL1 impairs beta-cell function in both diabetic and non-diabetic patients and reduces response to non-sulfonylurea and sulfonylurea agonists of the pancreatic KATP channel. 2011 , 48, 227-35	34
1282	Mouse models and type 2 diabetes: translational opportunities. 2011 , 22, 390-400	12
1281	Genetic variation within the NR1H2 gene encoding liver X receptor α associates with insulin secretion in subjects at increased risk for type 2 diabetes. 2011 , 89, 75-81	20
1280	A role for coding functional variants in HNF4A in type 2 diabetes susceptibility. 2011 , 54, 111-9	24
1279	Insulin promoter DNA methylation correlates negatively with insulin gene expression and positively with HbA(1c) levels in human pancreatic islets. 2011 , 54, 360-7	179
1278	Glucose tolerance, insulin sensitivity and insulin release in European non-diabetic carriers of a polymorphism upstream of CDKN2A and CDKN2B. 2011 , 54, 795-802	26
1277	Replication of 13 genome-wide association (GWA)-validated risk variants for type 2 diabetes in Pakistani populations. 2011 , 54, 1368-74	77
1276	Genome-wide association study of type 2 diabetes in a sample from Mexico City and a meta-analysis of a Mexican-American sample from Starr County, Texas. 2011 , 54, 2038-46	99
1275	Design and cohort description of the InterAct Project: an examination of the interaction of genetic and lifestyle factors on the incidence of type 2 diabetes in the EPIC Study. 2011 , 54, 2272-82	155
1274	UCP2 -866G/A and Ala55Val, and UCP3 -55C/T polymorphisms in association with type 2 diabetes susceptibility: a meta-analysis study. 2011 , 54, 2315-24	30
1273	Heritability and familiarity of type 2 diabetes and related quantitative traits in the Botnia Study. 2011 , 54, 2811-9	150
1272	Ant colony optimisation to identify genetic variant association with type 2 diabetes. 2011 , 181, 1609-1622	27
1271	Combined effects of FTO rs9939609 and MC4R rs17782313 on obesity and BMI in Chinese Han populations. 2011 , 39, 69-74	48
1270	Roles of autophagy in pancreatic β -cell function and type 2 diabetes. 2011 , 2, 1-9	7
1269	How pleiotropic genetics of the musculoskeletal system can inform genomics and phenomics of aging. 2011 , 33, 49-62	20
1268	Effects of SNPs at newly identified lipids loci on blood lipid levels and risk of coronary heart disease in Chinese Han population: a case control study. 2011 , 31, 452	3
1267	Testing the thrifty gene hypothesis: the Gly482Ser variant in PPARGC1A is associated with BMI in Tongans. 2011 , 12, 10	28

1266	Variants in KCNQ1 increase type II diabetes susceptibility in South Asians: a study of 3,310 subjects from India and the US. 2011 , 12, 18	46
1265	Capability of common SNPs to tag rare variants. 2011 , 5 Suppl 9, S88	11
1264	Estimation of allele frequency and association mapping using next-generation sequencing data. 2011 , 12, 231	126
1263	Predicting functionally important SNP classes based on negative selection. 2011 , 12, 26	9
1262	Analysis of genome-wide association study data using the protein knowledge base. 2011 , 12, 98	9
1261	Comparative analysis of methods for detecting interacting loci. 2011 , 12, 344	30
1260	PPAR α Pro12Ala interacts with fat intake for obesity and weight loss in a behavioural treatment based on the Mediterranean diet. 2011 , 55, 1771-9	50
1259	A comparison of approaches to account for uncertainty in analysis of imputed genotypes. 2011 , 35, 102-10	78
1258	Sample size requirements to detect gene-environment interactions in genome-wide association studies. 2011 , 35, 201-10	73
1257	Optimal methods for meta-analysis of genome-wide association studies. 2011 , 35, 581-91	20
1256	Genome-wide association studies (GWAS): impact on elucidating the aetiology of diabetes. 2011 , 27, 685-96	26
1255	Meta-analysis of published studies identified eight additional common susceptibility loci for Crohn's disease and ulcerative colitis. 2011 , 17, 2407-15	84
1254	A polymorphism in the chromosome 9p21 ANRIL locus is associated to Philadelphia positive acute lymphoblastic leukemia. 2011 , 35, 1052-9	64
1253	MicroRNA links obesity and impaired glucose metabolism. 2011 , 21, 864-6	25
1252	FTO polymorphisms are associated with adult body mass index (BMI) and colorectal adenomas in African-Americans. 2011 , 32, 748-56	36
1251	PWD/PhJ and WSB/EiJ mice are resistant to diet-induced obesity but have abnormal insulin secretion. 2011 , 152, 3005-17	20
1250	Guidelines and recommendations for laboratory analysis in the diagnosis and management of diabetes mellitus. 2011 , 57, e1-e47	293
1249	Correlations between islet autoantibody specificity and the SLC30A8 genotype with HLA-DQB1 and metabolic control in new onset type 1 diabetes. 2011 , 44, 107-14	26

1248	An overview of a wide range of functions of ZnT and Zip zinc transporters in the secretory pathway. 2011 , 75, 1036-43	85
1247	Susceptibility genes for coronary heart disease and myocardial infarction. 2011 , 13, 136-42	19
1246	Genomics and genetics in the biology of adaptation to exercise. 2011 , 1, 1603-48	102
1245	FTO, type 2 diabetes, and weight gain throughout adult life: a meta-analysis of 41,504 subjects from the Scandinavian HUNT, MDC, and MPP studies. 2011 , 60, 1637-44	102
1244	Discovery and assessment of conserved Pax6 target genes and enhancers. 2011 , 21, 1349-59	35
1243	Epigenetics meets endocrinology. 2011 , 46, R11-32	189
1242	Characterization of the human SLC30A8 promoter and intronic enhancer. 2011 , 47, 251-9	13
1241	The role of KRAS rs61764370 in invasive epithelial ovarian cancer: implications for clinical testing. 2011 , 17, 3742-50	45
1240	DNA methylation profiling identifies epigenetic differences between diabetes patients with ESRD and diabetes patients without nephropathy. 2011 , 6, 20-8	152
1239	cn.FARMS: a latent variable model to detect copy number variations in microarray data with a low false discovery rate. 2011 , 39, e79	18
1238	Epigenetics and Type 2 Diabetes. 2011 , 135-145	1
1237	Insulin resistance and epigenetic regulation: insights from human studies and prospects for future research. 2011 , 2, 445-57	2
1236	Genetics of type 2 diabetes. 2011 , 57, 241-54	113
1235	Frequent loss of genome gap region in 4p16.3 subtelomere in early-onset type 2 diabetes mellitus. 2011 , 2011, 498460	8
1234	Genomics, Proteomics, and the Nervous System. 2011 ,	1
1233	Latent Autoimmune Diabetes in Adults. 2011 , 315-329	
1232	Mouse models and the interpretation of human GWAS in type 2 diabetes and obesity. 2011 , 4, 155-64	32
1231	Glucose regulates free cytosolic Zn ²⁺ concentration, Slc39 (ZIP), and metallothionein gene expression in primary pancreatic islet β -cells. 2011 , 286, 25778-89	91

1230	Is diabetes mellitus a continuous spectrum?. 2011 , 57, 158-61	31
1229	Generation of N-ethyl-N-nitrosourea (ENU) diabetes models in mice demonstrates genotype-specific action of glucokinase activators. 2011 , 286, 39560-72	12
1228	Diabetes and biomarkers. 2011 , 5, 192-7	20
1227	Meta-analysis of the effect of HHEX gene polymorphism on the risk of type 2 diabetes. 2011 , 26, 309-14	21
1226	Notice of Retraction: ABCC8 and Type 2 Diabetes: A Global Meta-Analysis. 2011 ,	
1225	Total zinc intake may modify the glucose-raising effect of a zinc transporter (SLC30A8) variant: a 14-cohort meta-analysis. 2011 , 60, 2407-16	81
1224	Diabesity: an overview of a rising epidemic. 2011 , 26, 28-35	187
1223	Genome-wide association analysis of ischemic stroke in young adults. 2011 , 1, 505-14	26
1222	Guidelines and recommendations for laboratory analysis in the diagnosis and management of diabetes mellitus. 2011 , 34, e61-99	316
1221	Transferability of type 2 diabetes implicated loci in multi-ethnic cohorts from Southeast Asia. 2011 , 7, e1001363	119
1220	Body mass index and obesity- and diabetes-associated genotypes and risk for pancreatic cancer. 2011 , 20, 779-92	64
1219	Jun dimerization protein 2 controls senescence and differentiation via regulating histone modification. 2011 , 2011, 569034	12
1218	Eight common genetic variants associated with serum DHEAS levels suggest a key role in ageing mechanisms. 2011 , 7, e1002025	69
1217	Conditional expression of the FTO gene product in rat INS-1 cells reveals its rapid turnover and a role in the profile of glucose-induced insulin secretion. 2011 , 120, 403-13	16
1216	Fine mapping of five loci associated with low-density lipoprotein cholesterol detects variants that double the explained heritability. 2011 , 7, e1002198	118
1215	Using gene-network landscape to dissect genotype effects of TCF7L2 genetic variant on diabetes and cardiovascular risk. 2012 , 44, 903-14	17
1214	The fat-mass and obesity-associated gene (FTO) predicts mortality in chronic kidney disease of various severity. 2012 , 27 Suppl 4, iv58-62	12
1213	Effects of high-fat diet feeding on Znt8-null mice: differences between β -cell and global knockout of Znt8. 2012 , 302, E1084-96	54

1212	Chapter 13: Mining electronic health records in the genomics era. 2012 , 8, e1002823	122
1211	Interpreting meta-analyses of genome-wide association studies. 2012 , 8, e1002555	109
1210	Intracranial aneurysm risk locus 5q23.2 is associated with elevated systolic blood pressure. 2012 , 8, e1002563	18
1209	The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. 2012 , 8, e1002793	395
1208	Analysis of case-control association studies with known risk variants. 2012 , 28, 1729-37	25
1207	Genetic risk score constructed using 14 susceptibility alleles for type 2 diabetes is associated with the early onset of diabetes and may predict the future requirement of insulin injections among Japanese individuals. 2012 , 35, 1763-70	71
1206	Gestational diabetes mellitus: a positive predictor of type 2 diabetes?. 2012 , 2012, 721653	8
1205	A genome-wide association study of nephrolithiasis in the Japanese population identifies novel susceptible Loci at 5q35.3, 7p14.3, and 13q14.1. 2012 , 8, e1002541	54
1204	A single-nucleotide polymorphism in ANK1 is associated with susceptibility to type 2 diabetes in Japanese populations. 2012 , 21, 3042-9	86
1203	Assumption weighting for incorporating heterogeneity into meta-analysis of genomic data. 2012 , 28, 807-14	6
1202	Genotype prediction of adult type 2 diabetes from adolescence in a multiracial population. 2012 , 130, e1235-42	37
1201	The evolution and refinement of traditional risk factors for cardiovascular disease. 2012 , 20, 118-29	39
1200	Factors Affecting the Accuracy of Genotype Imputation in Populations from Several Maize Breeding Programs. 2012 , 52, 654-663	98
1199	Imp2 controls oxidative phosphorylation and is crucial for preserving glioblastoma cancer stem cells. 2012 , 26, 1926-44	275
1198	Novel Target Identification Technologies for the Personalised Therapy of Type II Diabetes and Obesity. 2012 , 12, 183-207	2
1197	Development of type 2 diabetes caused by a deficiency of a tRNA(lys) modification. 2012 , 4, 71-3	7
1196	Response to comment on: Marquez et al. Low-frequency variants in HMGA1 are not associated with type 2 diabetes risk. Diabetes 2012;61:524-530. 2012 , 61, e15	7
1195	Efficiency of trans-ethnic genome-wide meta-analysis and fine-mapping. 2012 , 20, 1300-7	20

1194	From genotype to human cell phenotype and beyond. 2012 , 4, 323-32	11
1193	Bone metabolism and fracture risk in type 2 diabetes mellitus. 2012 , 1, 36	11
1192	Genetic variants on chromosome 6p21.1 and 6p22.3 are associated with type 2 diabetes risk: a case-control study in Han Chinese. 2012 , 57, 320-5	22
1191	Association of TCF7L2 and ADIPOQ with body mass index, waist-hip ratio, and systolic blood pressure in an endogamous ethnic group of India. 2012 , 16, 948-51	17
1190	Beyond the fourth wave of genome-wide obesity association studies. 2012 , 2, e37	45
1189	A statistical method for region-based meta-analysis of genome-wide association studies in genetically diverse populations. 2012 , 20, 469-75	12
1188	Single nucleotide polymorphisms in JAZF1 and BCL11A gene are nominally associated with type 2 diabetes in African-American families from the GENNID study. 2012 , 57, 57-61	22
1187	Znt7-null mice are more susceptible to diet-induced glucose intolerance and insulin resistance. 2012 , 287, 33883-96	54
1186	Comparative analysis of genome-wide association studies signals for lipids, diabetes, and coronary heart disease: Cardiovascular Biomarker Genetics Collaboration. 2012 , 33, 393-407	75
1185	Consistent directions of effect for established type 2 diabetes risk variants across populations: the population architecture using Genomics and Epidemiology (PAGE) Consortium. 2012 , 61, 1642-7	42
1184	Chemical and genetic evidence for the involvement of Wnt antagonist Dickkopf2 in regulation of glucose metabolism. 2012 , 109, 11402-7	42
1183	Expression-based genome-wide association study links the receptor CD44 in adipose tissue with type 2 diabetes. 2012 , 109, 7049-54	109
1182	Evaluation of genome-wide association study-identified type 2 diabetes loci in African Americans. 2012 , 176, 995-1001	32
1181	Using multiple genetic variants as instrumental variables for modifiable risk factors. 2012 , 21, 223-42	288
1180	Harnessing the potential clinical use of medicinal plants as anti-diabetic agents. 2012 , 7	11
1179	Single diabetic QTL derived from OLETF rat is a sufficient agent for severe diabetic phenotype in combination with leptin-signaling deficiency. 2012 , 2012, 858121	3
1178	Nuclear receptor variants in liver disease. 2012 , 2012, 934707	4
1177	Rising intracellular zinc by membrane depolarization and glucose in insulin-secreting clonal HIT-T15 beta cells. 2012 , 2012, 190309	12

1176	A genome-wide association study in the Japanese population confirms 9p21 and 14q23 as susceptibility loci for primary open angle glaucoma. 2012 , 21, 2836-42	100
1175	Alternative methods to a TaqMan assay to detect a tri-allelic single nucleotide polymorphism rs757210 in the HNF1 β gene. 2011 , 50, 279-84	7
1174	Epigenetic differences in normal colon mucosa of cancer patients suggest altered dietary metabolic pathways. 2012 , 5, 374-84	40
1173	Performance of genotype imputations using data from the 1000 Genomes Project. 2012 , 73, 18-25	31
1172	Stochastic model search with binary outcomes for genome-wide association studies. 2012 , 19, e13-20	7
1171	Ancestral susceptibility to colorectal cancer. 2012 , 27, 197-204	2
1170	Complex-disease networks of trait-associated single-nucleotide polymorphisms (SNPs) unveiled by information theory. 2012 , 19, 295-305	36
1169	Genes related to diabetes may be associated with pancreatic cancer in a population-based case-control study in Minnesota. 2012 , 41, 50-3	20
1168	Increased β -cell replication and β -cell mass regeneration in syngeneically transplanted rat islets overexpressing insulin-like growth factor II. 2012 , 21, 2119-29	12
1167	Reduction in Tcf7l2 expression decreases diabetic susceptibility in mice. 2012 , 8, 791-801	20
1166	Genetic risk factors for type 2 diabetes: insights from the emerging genomic evidence. 2012 , 10, 147-55	19
1165	Low density lipoprotein (LDL) receptor-related protein 6 (LRP6) regulates body fat and glucose homeostasis by modulating nutrient sensing pathways and mitochondrial energy expenditure. 2012 , 287, 7213-23	58
1164	A genome-wide association study of gestational diabetes mellitus in Korean women. 2012 , 61, 531-41	169
1163	Gene-exercise interactions. 2012 , 108, 447-60	13
1162	Diabetes and obesity-related genes and the risk of neural tube defects in the national birth defects prevention study. 2012 , 176, 1101-9	37
1161	Polycystic ovary syndrome is not associated with polymorphisms of the TCF7L2, CDKAL1, HHEX, KCNJ11, FTO and SLC30A8 genes. 2012 , 77, 439-45	31
1160	Chromatin structure, epigenetic mechanisms and long-range interactions in the human insulin locus. 2012 , 14 Suppl 3, 1-11	15
1159	Interactions between genetic background, insulin resistance and β -cell function. 2012 , 14 Suppl 3, 46-56	15

1158	Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. 2011 , 44, 67-72	475
1157	The epigenetic lorax: gene-environment interactions in human health. 2012 , 4, 383-402	44
1156	Association between IGF2BP2 rs4402960 polymorphism and risk of type 2 diabetes mellitus: need for clarification of data in a recent meta-analysis. 2012 , 43, 411; author reply 412-3	
1155	Reply: Clarification of Data in the Recent Meta-analysis About Association Between IGF2BP2 rs4402960 Polymorphism and Risk of Type 2 Diabetes Mellitus. 2012 , 43, 412-413	
1154	Genetic determinants of the ankle-brachial index: a meta-analysis of a cardiovascular candidate gene 50K SNP panel in the candidate gene association resource (CARE) consortium. 2012 , 222, 138-47	18
1153	Premature myocardial infarction is associated with low serum levels of Wnt-1. 2012 , 222, 251-6	35
1152	. 2012 ,	
1151	The FTO rs9939609, ADIPOQ rs1501299, rs822391, and ADIPOR2 rs16928662 Polymorphisms Relationship to Obesity and Metabolic Syndrome in Bulgarian Sample. 2012 , 26, 65-71	2
1150	What should the genome-wide significance threshold be? Empirical replication of borderline genetic associations. 2012 , 41, 273-86	189
1149	Genome-wide meta-regression of gene-environment interaction. 2012 ,	1
1148	Agaricus bisporus lectins mediates islet β -cell proliferation through regulation of cell cycle proteins. 2012 , 237, 287-96	25
1147	Effect of type 2 diabetes predisposing genetic variants on colorectal cancer risk. 2012 , 97, E845-51	43
1146	Association of the C677T polymorphism in the human methylenetetrahydrofolate reductase (MTHFR) gene with the genetic predisposition for type 2 diabetes mellitus in a Moroccan population. 2012 , 16, 383-7	21
1145	A genome-wide scan for common variants affecting the rate of age-related cognitive decline. 2012 , 33, 1017.e1-15	115
1144	Glaucoma risk alleles at CDKN2B-AS1 are associated with lower intraocular pressure, normal-tension glaucoma, and advanced glaucoma. 2012 , 119, 1539-45	64
1143	Validation of candidate genes associated with cardiovascular risk factors in psychiatric patients. 2012 , 36, 213-9	2
1142	Association between a common KCNJ11 polymorphism (rs5219) and new-onset posttransplant diabetes in patients treated with Tacrolimus. 2012 , 105, 525-7	24
1141	Strategies beyond genome-wide association studies for atherosclerosis. 2012 , 32, 170-81	32

1140	A metagenome-wide association study of gut microbiota in type 2 diabetes. 2012 , 490, 55-60	3779
1139	A genome-wide association study identifies two susceptibility loci for duodenal ulcer in the Japanese population. 2012 , 44, 430-4, S1-2	96
1138	Use of diverse electronic medical record systems to identify genetic risk for type 2 diabetes within a genome-wide association study. 2012 , 19, 212-8	216
1137	Presence of multiple independent effects in risk loci of common complex human diseases. 2012 , 91, 185-92	25
1136	Malaria evolution in South Asia: knowledge for control and elimination. 2012 , 121, 256-66	14
1135	Association between polymorphisms in cytokine genes IL-17A and IL-17F and development of allergic rhinitis and comorbid asthma in Chinese subjects. 2012 , 73, 647-53	29
1134	Twin studies in autoimmune disease: genetics, gender and environment. 2012 , 38, J156-69	189
1133	Is genetic testing useful to predict type 2 diabetes?. 2012 , 26, 189-201	43
1132	Genetic determinants of glucose homeostasis. 2012 , 26, 159-70	9
1131	Association of the PPAR γ Pro12Ala polymorphism with type 2 diabetes and incident coronary heart disease in a Hong Kong Chinese population. 2012 , 97, 483-91	23
1130	Genetic prediction of postpartum diabetes in women with gestational diabetes mellitus. 2012 , 97, 394-8	37
1129	Zinc transporter expression in zebrafish (<i>Danio rerio</i>) during development. 2012 , 155, 26-32	22
1128	Association between FTO 1st intron tagging variant and telomere length in middle aged females. 3PMFs study. 2012 , 413, 1222-5	22
1127	A systems genetics approach identifies genes and pathways for type 2 diabetes in human islets. 2012 , 16, 122-34	266
1126	Cloning and characterization of chicken fat mass and obesity associated (Fto) gene: fasting affects Fto expression. 2012 , 42, 1-10	19
1125	The obesity gene and colorectal cancer risk: a population study in Northern Italy. 2012 , 23, 65-9	18
1124	A novel locus for body mass index on 5p15.2: a meta-analysis of two genome-wide association studies. 2012 , 500, 80-4	10
1123	Higher incidence of death in multi-vessel coronary artery disease patients associated with polymorphisms in chromosome 9p21. 2012 , 12, 61	15

1122	Association between 9p21 genetic variants and mortality risk in a prospective cohort of patients with type 2 diabetes (ZODIAC-15). 2012 , 11, 138	10
1121	Identification of shared genetic susceptibility locus for coronary artery disease, type 2 diabetes and obesity: a meta-analysis of genome-wide studies. 2012 , 11, 68	17
1120	Evaluation of the imputation performance of the program IMPUTE in an admixed sample from Mexico City using several model designs. 2012 , 5, 12	7
1119	Regulation and functional effects of ZNT8 in human pancreatic islets. 2012 , 214, 225-32	26
1118	Variations with modest effects have an important role in the genetic background of type 2 diabetes and diabetes-related traits. 2012 , 57, 776-9	23
1117	Transferability and fine-mapping of glucose and insulin quantitative trait loci across populations: CARE, the Candidate Gene Association Resource. 2012 , 55, 2970-84	23
1116	Epigenetics of Diabetes in Humans. 2012 , 321-329	
1115	The effect of KCNJ11 polymorphism on the risk of type 2 diabetes: a global meta-analysis based on 49 case-control studies. 2012 , 31, 801-10	15
1114	Fast and accurate genotype imputation in genome-wide association studies through pre-phasing. 2012 , 44, 955-9	1292
1113	Contribution of common genetic variation to the risk of type 2 diabetes in the Mexican Mestizo population. 2012 , 61, 3314-21	71
1112	Rare variants in complex traits: novel identification strategies and the role of de novo mutations. 2012 , 74, 215-25	4
1111	Individualized therapy for type 2 diabetes: clinical implications of pharmacogenetic data. 2012 , 16, 285-302	27
1110	Association of type 2 diabetes susceptibility loci with one-year weight loss in the look AHEAD clinical trial. 2012 , 20, 1675-82	23
1109	IGF2BP2 and IGF2 genetic effects in diabetes and diabetic nephropathy. 2012 , 26, 393-8	20
1108	Genetic investigation into the endophenotypic status of central corneal thickness and optic disc parameters in relation to open-angle glaucoma. 2012 , 154, 833-842.e2	25
1107	Identification and function of auxiliary iron-sulfur clusters in radical SAM enzymes. 2012 , 1824, 1196-212	56
1106	The potential of 2-oxoglutarate oxygenases acting on nucleic acids as therapeutic targets. 2012 , 9, e91-e100	9
1105	European genetic variants associated with type 2 diabetes in North African Arabs. 2012 , 38, 316-23	55

1104	Influence of PTPN1 polymorphism among people with type 2 diabetes: A Thanjavur-based study. 2012 , 4, 94-97	
1103	Type 2 diabetes and polymorphisms on chromosome 9p21: a meta-analysis. 2012 , 22, 619-25	31
1102	Epigenetic regulation of pancreas development and function. 2012 , 23, 693-700	25
1101	Disturbed zinc homeostasis in diabetic patients by in vitro and in vivo analysis of insulinomimetic activity of zinc. 2012 , 23, 1458-66	89
1100	Impact of FTO genotypes on BMI and weight in polycystic ovary syndrome: a systematic review and meta-analysis. 2012 , 55, 2636-2645	64
1099	A noncoding RNA antisense to moesin at 5p14.1 in autism. 2012 , 4, 128ra40	104
1098	Development of cell-active N6-methyladenosine RNA demethylase FTO inhibitor. 2012 , 134, 17963-71	188
1097	From mice to humans. 2012 , 12, 651-8	10
1096	Genetics of type 2 diabetes in East Asian populations. 2012 , 12, 686-96	46
1095	Transcription factor 7-like 2 (TCF7L2) variations associated with earlier age-onset of type 2 diabetes in Thai patients. 2012 , 91, 251-5	10
1094	A genetic risk score is associated with incident cardiovascular disease and coronary artery calcium: the Framingham Heart Study. 2012 , 5, 113-21	162
1093	Quantitative assessment of the variation in IGF2BP2 gene and type 2 diabetes risk. 2012 , 49 Suppl 1, S87-97	9
1092	Widespread expression of zinc transporter ZnT (SLC30) family members in mouse endocrine cells. 2012 , 138, 605-16	13
1091	Effect of a common variant of the PCSK2 gene on reduced insulin secretion. 2012 , 55, 3245-51	13
1090	Abnormal glucose tolerance and insulin secretion in pancreas-specific Tcf7l2-null mice. 2012 , 55, 2667-2676	88
1089	SNP in the genome-wide association study hotspot on chromosome 9p21 confers susceptibility to diabetic nephropathy in type 1 diabetes. 2012 , 55, 2386-93	18
1088	Impact of common type 2 diabetes risk gene variants on future type 2 diabetes in the non-diabetic population in Korea. 2012 , 57, 265-8	8
1087	Genetic risk assessment of type 2 diabetes-associated polymorphisms in African Americans. 2012 , 35, 287-92	42

1086	DNA methylation profiling identifies epigenetic dysregulation in pancreatic islets from type 2 diabetic patients. 2012 , 31, 1405-26	301
1085	Genetics of type 2 diabetes in European populations. 2012 , 4, 203-12	27
1084	Lack of association between genetic polymorphisms within KCNQ1 locus and type 2 diabetes in Tunisian Arabs. 2012 , 98, 452-8	15
1083	Investigation on cardiovascular risk prediction using genetic information. 2012 , 16, 795-808	18
1082	Prediabetes Genes in Pima and Amish. 2012 , 61-80	
1081	Analysis of common type 2 diabetes mellitus genetic risk factors in new-onset diabetes after transplantation in kidney transplant patients medicated with tacrolimus. 2012 , 68, 1587-94	32
1080	Expression analyses of the genes harbored by the type 2 diabetes and pediatric BMI associated locus on 10q23. 2012 , 13, 89	10
1079	Genome-wide meta-analysis of genetic susceptible genes for Type 2 Diabetes. 2012 , 6 Suppl 3, S16	28
1078	The Rise and Fall of Thrift. 2012 , 73-94	
1077	Fat: Beyond Energy Storage. 2012 , 219-244	1
1076	Applying semantic web technologies for phenome-wide scan using an electronic health record linked Biobank. 2012 , 3, 10	27
1075	African ancestry and its correlation to type 2 diabetes in African Americans: a genetic admixture analysis in three U.S. population cohorts. 2012 , 7, e32840	56
1074	A genome-wide association search for type 2 diabetes genes in African Americans. 2012 , 7, e29202	138
1073	Association of the type 2 diabetes mellitus susceptibility gene, TCF7L2, with schizophrenia in an Arab-Israeli family sample. 2012 , 7, e29228	46
1072	Cryptic distant relatives are common in both isolated and cosmopolitan genetic samples. 2012 , 7, e34267	126
1071	Genetic variants of IDE-KIF11-HHEX at 10q23.33 associated with type 2 diabetes risk: a fine-mapping study in Chinese population. 2012 , 7, e35060	29
1070	CDKN2B polymorphism is associated with primary open-angle glaucoma (POAG) in the Afro-Caribbean population of Barbados, West Indies. 2012 , 7, e39278	69
1069	The chromosome 9p21.3 coronary heart disease risk allele is associated with altered gene expression in normal heart and vascular tissues. 2012 , 7, e39574	32

1068	IGF2BP2 alternative variants associated with glutamic acid decarboxylase antibodies negative diabetes in Malaysian subjects. 2012 , 7, e45573	4
1067	Meta-analysis of the relationship between common type 2 diabetes risk gene variants with gestational diabetes mellitus. 2012 , 7, e45882	90
1066	Joint effect of genetic and lifestyle risk factors on type 2 diabetes risk among Chinese men and women. 2012 , 7, e49464	12
1065	The rs11705701 G>A polymorphism of IGF2BP2 is associated with IGF2BP2 mRNA and protein levels in the visceral adipose tissue - a link to type 2 diabetes susceptibility. 2012 , 9, 112-22	18
1064	Epigenetics in the Pathophysiology of Type 2 Diabetes. 2012 , 225-232	
1063	Genotype Imputation for Latinos Using the HapMap and 1000 Genomes Project Reference Panels. 2012 , 3, 117	15
1062	Type 2 Diabetes Genetics: Beyond GWAS. 2012 , 3,	84
1061	Alzheimer's disease. 371-381	1
1060	Replication analysis for severe diabetic retinopathy. 2012 , 53, 2377-81	39
1059	A more rapid approach to systematically assessing published associations of genetic polymorphisms and disease risk: type 2 diabetes as a test case. 2012 , 1	
1058	Ausência de associação entre o genótipo CC do polimorfismo rs7903146 no gene TCF7L2 e artrite reumatoide. 2012 , 52, 523-528	3
1057	Finding genetic risk factors of gestational diabetes. 2012 , 10, 239-43	17
1056	The rs10830963 variant of melatonin receptor MTNR1B is associated with increased risk for gestational diabetes mellitus in a Greek population. 2012 , 11, 70-6	29
1055	Tyrosine hydroxylase gene: another piece of the genetic puzzle of Parkinson's disease. 2012 , 11, 469-81	13
1054	SLC30A8 (ZnT8) variations and type 2 diabetes in the Chinese Han population. 2012 , 11, 1592-8	21
1053	Stratification-score matching improves correction for confounding by population stratification in case-control association studies. 2012 , 36, 195-205	16
1052	Accurate imputation of rare and common variants in a founder population from a small number of sequenced individuals. 2012 , 36, 312-9	18
1051	Genotype imputation for African Americans using data from HapMap phase II versus 1000 genomes projects. 2012 , 36, 508-16	10

1050	A likelihood ratio-based Mann-Whitney approach finds novel replicable joint gene action for type 2 diabetes. 2012 , 36, 583-93	15
1049	Direct genetic effects and their estimation from matched case-control data. 2012 , 36, 652-62	7
1048	Investigation of allelic heterogeneity of the CCK-A receptor gene in paranoid schizophrenia. 2012 , 159B, 741-7	9
1047	IGF2BP2 genetic variation and type 2 diabetes: a global meta-analysis. 2012 , 31, 713-20	9
1046	Randomized trial of personal genomics for preventive cardiology: design and challenges. 2012 , 5, 368-76	23
1045	Generating cells of the gastrointestinal system: current approaches and applications for the differentiation of human pluripotent stem cells. 2012 , 90, 763-71	15
1044	The prevalence of Type 2 Diabetes Mellitus in the United Arab Emirates: justification for the establishment of the Emirates Family Registry. 2012 , 32, 25-32	26
1043	Genetic variation in the carbonyl reductase 3 gene confers risk of type 2 diabetes and insulin resistance: a potential regulator of adipogenesis. 2012 , 90, 847-58	8
1042	Superior beta cell proliferation, function and gene expression in a subpopulation of rat islets identified by high blood perfusion. 2012 , 55, 1390-9	28
1041	Genetic association of zinc transporter 8 (ZnT8) autoantibodies in type 1 diabetes cases. 2012 , 55, 1978-84	35
1040	Large-scale gene-centric meta-analysis across 39 studies identifies type 2 diabetes loci. 2012 , 90, 410-25	214
1039	Replication of genome-wide association signals of type 2 diabetes in Han Chinese in a prospective cohort. 2012 , 76, 365-72	27
1038	Integration of GWAS SNPs and tissue specific expression profiling reveal discrete eQTLs for human traits in blood and brain. 2012 , 47, 20-8	100
1037	FTO gene is related to obesity in Chilean Amerindian children and impairs HOMA-IR in prepubertal girls. 2012 , 13, 384-91	11
1036	Association between autoantibodies to the Arginine variant of the Zinc transporter 8 (ZnT8) and stimulated C-peptide levels in Danish children and adolescents with newly diagnosed type 1 diabetes. 2012 , 13, 454-62	21
1035	The combined effect of the T2DM susceptibility genes is an important risk factor for T2DM in non-obese Japanese: a population based case-control study. 2012 , 13, 11	19
1034	Determining genetic risk factors for pediatric type 2 diabetes. 2012 , 12, 88-92	4
1033	Association analysis of 31 common polymorphisms with type 2 diabetes and its related traits in Indian sib pairs. 2012 , 55, 349-57	41

1032	Association between KCNJ11 gene polymorphisms and risk of type 2 diabetes mellitus in East Asian populations: a meta-analysis in 42,573 individuals. 2012 , 39, 645-59	23
1031	Association between type 2 diabetes and CDKN2A/B: a meta-analysis study. 2012 , 39, 1609-16	22
1030	Replication study of novel risk variants in six genes with type 2 diabetes and related quantitative traits in the Han Chinese lean individuals. 2012 , 39, 2447-54	20
1029	Artifact due to differential error when cases and controls are imputed from different platforms. 2012 , 131, 111-9	24
1028	Association of glucokinase regulatory protein polymorphism with type 2 diabetes and fasting plasma glucose: a meta-analysis. 2013 , 40, 3935-42	23
1027	Association between 9p21.3 genomic markers and coronary artery disease in East Asians: a meta-analysis involving 9,813 cases and 10,710 controls. 2013 , 40, 337-43	15
1026	Diagnostics in Plant Breeding. 2013 ,	1
1025	Genome-wide association study of multiple congenital heart disease phenotypes identifies a susceptibility locus for atrial septal defect at chromosome 4p16. 2013 , 45, 822-4	91
1024	Meta-analysis of the effect of KCNQ1 gene polymorphism on the risk of type 2 diabetes. 2013 , 40, 3557-67	12
1023	Inflammatory mechanisms linking periodontal diseases to cardiovascular diseases. 2013 , 84, S51-69	105
1022	Emerging Intelligent Computing Technology and Applications. 2013 ,	1
1021	Metabolic regulation of the cell cycle. 2013 , 25, 724-9	37
1020	Genotype imputation in genome-wide association studies. 2013 , Chapter 1, Unit 1.25	29
1019	Diabetes genes identified by genome-wide association studies are regulated in mice by nutritional factors in metabolically relevant tissues and by glucose concentrations in islets. 2013 , 14, 10	16
1018	A Drosophila functional evaluation of candidates from human genome-wide association studies of type 2 diabetes and related metabolic traits identifies tissue-specific roles for dHHEX. 2013 , 14, 136	27
1017	Association between variations in the fat mass and obesity-associated gene and pancreatic cancer risk: a case-control study in Japan. 2013 , 13, 337	37
1016	Variants at the 9p21 locus and melanoma risk. 2013 , 13, 325	23
1015	Obesity-related genetic variants, human pigmentation, and risk of melanoma. 2013 , 132, 793-801	21

1014	ACE I/D and MTHFR C677T polymorphisms are significantly associated with type 2 diabetes in Arab ethnicity: a meta-analysis. 2013 , 520, 166-77	34
1013	Association between type 2 diabetes and rs10811661 polymorphism upstream of CDKN2A/B: a meta-analysis. 2013 , 50, 657-62	12
1012	Polycystic ovary syndrome is not associated with genetic variants that mark risk of type 2 diabetes. 2013 , 50, 451-7	22
1011	LRP6 enhances glucose metabolism by promoting TCF7L2-dependent insulin receptor expression and IGF receptor stabilization in humans. 2013 , 17, 197-209	62
1010	Privacy-Preserving Data Exploration in Genome-Wide Association Studies. 2013 , 2013, 1079-1087	83
1009	No detectable association of IGF2BP2 and SLC30A8 genes with type 2 diabetes in the population of Hyderabad, India. 2013 , 1, 15-23	21
1008	Hippocampal calcium dysregulation at the nexus of diabetes and brain aging. 2013 , 719, 34-43	22
1007	A genome-wide association study of HCV-induced liver cirrhosis in the Japanese population identifies novel susceptibility loci at the MHC region. 2013 , 58, 875-82	50
1006	Functional characterization of Cdkal1, a risk factor of type 2 diabetes, and the translational opportunities. 2013 , 10, e65-e69	2
1005	Subset-based ant colony optimisation for the discovery of gene-gene interactions in genome wide association studies. 2013 ,	4
1004	Association of the ADRA2A polymorphisms with the risk of type 2 diabetes: a meta-analysis. 2013 , 46, 722-6	11
1003	The relationship between five widely-evaluated variants in CDKN2A/B and CDKAL1 genes and the risk of type 2 diabetes: a meta-analysis. 2013 , 531, 435-43	25
1002	Identification of an intermediate methyl carrier in the radical S-adenosylmethionine methyltransferases RimO and MiaB. 2013 , 135, 15404-15416	47
1001	TCF7L2 gene polymorphisms and type 2 diabetes risk: a comprehensive and updated meta-analysis involving 121,174 subjects. 2013 , 28, 25-37	60
1000	Assessing the clinical utility of a genetic risk score constructed using 49 susceptibility alleles for type 2 diabetes in a Japanese population. 2013 , 98, E1667-73	29
999	The role of FTO genotype on eating behavior in obese Sardinian children and adolescents. 2013 , 26, 539-44	11
998	Association between donor and recipient TCF7L2 gene polymorphisms and the risk of new-onset diabetes mellitus after liver transplantation in a Han Chinese population. 2013 , 58, 271-7	57
997	Human genetics of diabetic vascular complications. 2013 , 92, 677-94	16

996	The large non-coding RNA ANRIL, which is associated with atherosclerosis, periodontitis and several forms of cancer, regulates ADIPOR1, VAMP3 and C11ORF10. 2013 , 22, 4516-27	163
995	A genome-wide search for type 2 diabetes susceptibility genes in an extended Arab family. 2013 , 77, 488-503	24
994	Trans-ethnic fine mapping identifies a novel independent locus at the 3' end of CDKAL1 and novel variants of several susceptibility loci for type 2 diabetes in a Han Chinese population. 2013 , 56, 2619-28	25
993	Studies of association of AGPAT6 variants with type 2 diabetes and related metabolic phenotypes in 12,068 Danes. 2013 , 14, 113	2
992	Genetic variant in fat mass and obesity-associated gene associated with type 2 diabetes risk in Han Chinese. 2013 , 14, 86	13
991	Association between polymorphisms in long non-coding RNA PRNCR1 in 8q24 and risk of colorectal cancer. 2013 , 32, 104	69
990	Senescent cells and their secretory phenotype as targets for cancer therapy. 2013 , 38, 17-27	83
989	Chromosome 9p21 rs10757278 polymorphism is associated with the risk of metabolic syndrome. 2013 , 379, 77-85	10
988	Meta-regression of gene-environment interaction in genome-wide association studies. 2013 , 12, 354-62	9
987	Towards Mining Frequent Patterns in Genome Wide Association. 2013 ,	0
986	Biomarkers for early diagnosis of type 2 diabetic nephropathy: a study based on an integrated biomarker system. 2013 , 9, 2134-41	27
985	Genetics and genomics for the prevention and treatment of cardiovascular disease: update: a scientific statement from the American Heart Association. 2013 , 128, 2813-51	76
984	Intra- and inter-sparse multiple output regression with application on environmental microbial community study. 2013 ,	0
983	ALKBH5 is a mammalian RNA demethylase that impacts RNA metabolism and mouse fertility. 2013 , 49, 18-29	1627
982	Prevalence of ZnT8 antibody in relation to phenotype and SLC30A8 polymorphism in adult autoimmune diabetes: results from the HUNT study, Norway. 2013 , 46, 74-9	13
981	MaCH-admix: genotype imputation for admixed populations. 2013 , 37, 25-37	100
980	Single nucleotide polymorphism in genome-wide association of human population: A tool for broad spectrum service. 2013 , 14, 123-134	42
979	A population-based association study of 2q32.3 and 8q21.3 loci with schizophrenia in Han Chinese. 2013 , 47, 712-7	43

978	Genetic ablation of phospholipase C delta 1 increases survival in SOD1(G93A) mice. 2013 , 60, 11-7	15
977	Cellular and animal models of type 2 diabetes GWAS gene polymorphisms: what can we learn?. 2013 , 10, e59-e64	
976	MicroRNA-106b induces mitochondrial dysfunction and insulin resistance in C2C12 myotubes by targeting mitofusin-2. 2013 , 381, 230-40	72
975	A distant, cis-acting enhancer drives induction of Arf by Tgf β in the developing eye. 2013 , 380, 49-57	10
974	Recent Developments in the Genetic and Genomic Basis of Type 2 Diabetes. 2013 , 7, 66-72	
973	Genome wide association studies for diabetes: perspective on results and challenges. 2013 , 14, 90-6	25
972	The genetics of type 2 diabetes and its clinical relevance. 2013 , 83, 297-306	37
971	Increased dosage of Ink4/Arf protects against glucose intolerance and insulin resistance associated with aging. 2013 , 12, 102-11	26
970	Assessment of the 9p21.3 locus in severity of coronary artery disease in the presence and absence of type 2 diabetes. 2013 , 14, 11	21
969	Systematic evaluation of validated type 2 diabetes and glycaemic trait loci for association with insulin clearance. 2013 , 56, 1282-90	33
968	Hereditary Transmission of Diabetes Mellitus. 2013 , 283-322	
967	A variant in FTO shows association with melanoma risk not due to BMI. 2013 , 45, 428-32, 432e1	95
966	The SLC30 family of zinc transporters - a review of current understanding of their biological and pathophysiological roles. 2013 , 34, 548-60	229
965	Genetics of type 2 diabetes and potential clinical implications. 2013 , 36, 167-77	21
964	A genome-wide association study identifies GRK5 and RASGRP1 as type 2 diabetes loci in Chinese Hans. 2013 , 62, 291-8	142
963	Diabetes Mellitus. 2013 , 1-58	3
962	Recent progress in the use of genetics to understand links between type 2 diabetes and related metabolic traits. 2013 , 14, 203	7
961	Genome-wide association analysis for multiple continuous secondary phenotypes. 2013 , 92, 744-59	57

960	Prospects and Limitations for Development and Application of Functional Markers in Plants. 2013 , 329-346	4
959	Mapping and significance of the mRNA methylome. 2013 , 4, 397-422	73
958	Inflammatory mechanisms linking periodontal diseases to cardiovascular diseases. 2013 , 40 Suppl 14, S51-69	126
957	Genome-wide association study for type 2 diabetes in Indians identifies a new susceptibility locus at 2q21. 2013 , 62, 977-86	132
956	Apolipoprotein E2 accentuates postprandial inflammation and diet-induced obesity to promote hyperinsulinemia in mice. 2013 , 62, 382-91	30
955	A simple but effective modeling strategy for structural properties of non-heme Fe(II) sites in proteins: test of force field models and application to proteins in the AlkB family. 2013 , 34, 1620-35	9
954	Association between obesity-related gene FTO and ADHD. 2013 , 21, E738-44	51
953	Genetics of canine diabetes mellitus: are the diabetes susceptibility genes identified in humans involved in breed susceptibility to diabetes mellitus in dogs?. 2013 , 195, 139-47	42
952	Identification of CpG-SNPs associated with type 2 diabetes and differential DNA methylation in human pancreatic islets. 2013 , 56, 1036-46	143
951	The type 2 diabetes-associated gene <i>ide</i> is required for insulin secretion and suppression of β -synuclein levels in β -cells. 2013 , 62, 2004-14	73
950	Network models of genome-wide association studies uncover the topological centrality of protein interactions in complex diseases. 2013 , 20, 619-29	35
949	Identification of a genetic locus on chromosome 4q34-35 for type 2 diabetes with overweight. 2013 , 45, e7	10
948	Minireview: intraislet regulation of insulin secretion in humans. 2013 , 27, 1984-95	51
947	Fat mass and obesity gene and cognitive decline: the Atherosclerosis Risk in Communities Study. 2013 , 80, 92-9	22
946	A cross-platform analysis of 14,177 expression quantitative trait loci derived from lymphoblastoid cell lines. 2013 , 23, 716-26	117
945	Diabetes. 2013 , 990-1005	
944	ALKBH4-dependent demethylation of actin regulates actomyosin dynamics. 2013 , 4, 1832	51
943	Blood-Based Indicators of Insulin Resistance and Metabolic Syndrome in Bottlenose Dolphins (<i>Tursiops truncatus</i>). 2013 , 4, 136	37

942	Contribution of Genes to the Changes on Body Composition Components: a Two-Year Longitudinal Study in a Small Cohort of Twins. 2013 , 9, 489-498	1
941	Adult onset global loss of the fto gene alters body composition and metabolism in the mouse. 2013 , 9, e1003166	103
940	Long-term sustained autoimmune response to beta cell specific zinc transporter (ZnT8, W, R, Q) in young adult patients with preserved beta cell function at diagnosis of diabetes. 2013 , 46, 50-61	6
939	Trans-ethnic fine-mapping of lipid loci identifies population-specific signals and allelic heterogeneity that increases the trait variance explained. 2013 , 9, e1003379	94
938	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. 2013 , 9, e1003500	277
937	Long non-coding RNAs in haematological malignancies. 2013 , 14, 15386-422	34
936	Bioenergetics in human evolution and disease: implications for the origins of biological complexity and the missing genetic variation of common diseases. 2013 , 368, 20120267	90
935	Re-thinking cell cycle regulators: the cross-talk with metabolism. 2013 , 3, 4	48
934	Comparing methods for performing trans-ethnic meta-analysis of genome-wide association studies. 2013 , 22, 2303-11	48
933	Lack of tRNA modification isopentenyl-A37 alters mRNA decoding and causes metabolic deficiencies in fission yeast. 2013 , 33, 2918-29	54
932	Association of risk variants for type 2 diabetes and hyperglycemia with gestational diabetes. 2013 , 169, 291-7	82
931	HuR maintains a replicative life span by repressing the ARF tumor suppressor. 2013 , 33, 1886-900	9
930	Transferability and fine mapping of type 2 diabetes loci in African Americans: the Candidate Gene Association Resource Plus Study. 2013 , 62, 965-76	51
929	Crystallization and preliminary X-ray diffraction of the RNA demethylase ALKBH5. 2013 , 69, 1231-4	6
928	Animal models of GWAS-identified type 2 diabetes genes. 2013 , 2013, 906590	27
927	Genetic factors in the etiology of type 2 diabetes: linkage analyses, candidate gene association, and genome-wide association and #8211; still a long way to go!. 2013 , 3, 57	3
926	Linkage of type 2 diabetes on chromosome 9p24 in Mexican Americans: additional evidence from the Veterans Administration Genetic Epidemiology Study (VAGES). 2013 , 76, 36-46	4
925	Rare nonconservative LRP6 mutations are associated with metabolic syndrome. 2013 , 34, 1221-5	51

924	Gene Smoking interactions on human brain gene expression: finding common mechanisms in adolescents and adults. 2013 , 54, 1109-19	11
923	Multiple neurofibromas as the presenting feature of familial atypical multiple malignant melanoma (FAMMM) syndrome. 2013 , 161A, 1425-31	9
922	Association between the rs1333040 polymorphism on the chromosomal 9p21 locus and sporadic brain arteriovenous malformations. 2013 , 84, 1059-62	11
921	The human disease network. 2013 , 1, 20-28	22
920	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. 2013 , 45, 76-82	232
919	FTO predicts weight regain in the Look AHEAD clinical trial. 2013 , 37, 1545-52	37
918	QTL replication and targeted association highlight the nerve growth factor gene for nonverbal communication deficits in autism spectrum disorders. 2013 , 18, 226-35	16
917	Replication study for the association of a single-nucleotide polymorphism, rs3746876, within KCNJ15, with susceptibility to type 2 diabetes in a Japanese population. 2013 , 58, 490-3	5
916	A note on statistical method for genotype calling of high-throughput SNP arrays. 2013 , 40, 1372-1381	1
915	MicroRNAs in farm animals. 2013 , 7, 1567-75	24
914	Novel common and rare genetic determinants of paraoxonase activity: FTO, SERPINA12, and ITGAL. 2013 , 54, 552-60	15
913	Type 2 diabetes and risk of rupture of saccular intracranial aneurysm in eastern Finland. 2013 , 36, 2020-6	34
912	CDKAL1 gene rs7756992 A/G polymorphism and type 2 diabetes mellitus: a meta-analysis of 62,567 subjects. 2013 , 3, 3131	12
911	Association of rs734312 and rs10010131 polymorphisms in WFS1 gene with type 2 diabetes mellitus: a meta-analysis. 2013 , 60, 441-447	13
910	Variations in Solute Transporter Genes Affecting Micronutrient Solute Transport and Human Health. 2013 , 25-82	
909	FTO first intron rs1558902 variant and platelets count in white middle-aged women: prague pre- and post-menopausal females (3PMFs) study. 2013 , 61, 291-3	
908	First Phase Insulin Secretion and Type 2 Diabetes. 2013 , 13, 126-139	18
907	The new perspectives on genetic studies of type 2 diabetes and thyroid diseases. 2013 , 14, 33-48	3

906	Regulation of Insulin Synthesis and Secretion and Pancreatic Beta-Cell Dysfunction in Diabetes. 2013 , 9, 25-53	377
905	Generation of high quality chromatin immunoprecipitation DNA template for high-throughput sequencing (ChIP-seq). 2013 ,	10
904	The role of gut microbiota on insulin resistance. 2013 , 5, 829-51	123
903	Common dysfunctional variants in ABCG2 are a major cause of early-onset gout. 2013 , 3, 2014	88
902	Association of FTO and PPARG polymorphisms with obesity in Portuguese women. 2013 , 6, 241-5	10
901	Association of variants in PPAR α , IGF2BP2, and KCNQ1 with a susceptibility to gestational diabetes mellitus in a Korean population. 2013 , 54, 352-7	30
900	Obesity-associated endometrial and cervical cancers. 2013 , 5, 109-18	16
899	The diabetes-susceptible gene SLC30A8/ZnT8 regulates hepatic insulin clearance. 2013 , 123, 4513-24	166
898	Cost-effective GPU-grid for genome-wide epistasis calculations. 2013 , 52, 91-5	6
897	Association study of 25 type 2 diabetes related Loci with measures of obesity in Indian sib pairs. 2013 , 8, e53944	17
896	On combining reference data to improve imputation accuracy. 2013 , 8, e55600	8
895	Common variant rs9939609 in gene FTO confers risk to polycystic ovary syndrome. 2013 , 8, e66250	29
894	Association of genetic variants with isolated fasting hyperglycaemia and isolated postprandial hyperglycaemia in a Han Chinese population. 2013 , 8, e71399	8
893	A study assessing the association of glycated hemoglobin A1C (HbA1C) associated variants with HbA1C, chronic kidney disease and diabetic retinopathy in populations of Asian ancestry. 2013 , 8, e79767	20
892	Replication study for the association of 9 East Asian GWAS-derived loci with susceptibility to type 2 diabetes in a Japanese population. 2013 , 8, e76317	36
891	An f2 pig resource population as a model for genetic studies of obesity and obesity-related diseases in humans: design and genetic parameters. 2013 , 4, 29	30
890	Autoimmune Disorders. 2013 , 822-838	3
889	Admixture mapping and subsequent fine-mapping suggests a biologically relevant and novel association on chromosome 11 for type 2 diabetes in African Americans. 2014 , 9, e86931	11

888	Simultaneous copy number losses within multiple subtelomeric regions in early-onset type 2 diabetes mellitus. 2014 , 9, e88602	
887	Association between 9p21 genomic markers and ischemic stroke risk: evidence based on 21 studies. 2014 , 9, e90255	16
886	Cross-sectional and longitudinal replication analyses of genome-wide association loci of type 2 diabetes in Han Chinese. 2014 , 9, e91790	16
885	Quantitative assessment of the effect of KCNJ11 gene polymorphism on the risk of type 2 diabetes. 2014 , 9, e93961	32
884	Validation of type 2 diabetes risk variants identified by genome-wide association studies in Han Chinese population: a replication study and meta-analysis. 2014 , 9, e95045	26
883	Drosophila 3' UTRs are more complex than protein-coding sequences. 2014 , 9, e97336	5
882	Evaluation of common type 2 diabetes risk variants in a South Asian population of Sri Lankan descent. 2014 , 9, e98608	6
881	Genetic association study with metabolic syndrome and metabolic-related traits in a cross-sectional sample and a 10-year longitudinal sample of chinese elderly population. 2014 , 9, e100548	11
880	Obesity-related genomic loci are associated with type 2 diabetes in a Han Chinese population. 2014 , 9, e104486	21
879	Polymorphism of 9p21.3 locus is associated with 5-year survival in high-risk patients with myocardial infarction. 2014 , 9, e104635	11
878	Can evidence from genome-wide association studies and positive natural selection surveys be used to evaluate the thrifty gene hypothesis in East Asians?. 2014 , 9, e110974	5
877	Genome-wide linkage scan identifies two novel genetic loci for coronary artery disease: in GeneQuest families. 2014 , 9, e113935	6
876	Genetic and Epigenetics of Type 2 Diabetes. 2014 , 467-476	
875	Association of CDKN2BAS polymorphism rs4977574 with coronary heart disease: a case-control study and a meta-analysis. 2014 , 15, 17478-92	33
874	Risk factors contributing to type 2 diabetes and recent advances in the treatment and prevention. 2014 , 11, 1185-200	426
873	Lessons from Genome-Wide Search for Disease-Related Genes with Special Reference to HLA-Disease Associations. 2014 , 5, 84-96	3
872	Genome-wide association study identifies two novel Loci with sex-specific effects for type 2 diabetes mellitus and glycemic traits in a korean population. 2014 , 38, 375-87	27
871	Genetic and epigenetic catalysts in early-life programming of adult cardiometabolic disorders. 2014 , 7, 575-86	8

870	Association between FTO, MC4R, SLC30A8, and KCNQ1 gene variants and type 2 diabetes in Saudi population. 2014 , 13, 10194-203	30
869	Modify or die?—RNA modification defects in metazoans. 2014 , 11, 1555-67	51
868	The ras responsive transcription factor RREB1 is a novel candidate gene for type 2 diabetes associated end-stage kidney disease. 2014 , 23, 6441-7	26
867	Multiple nonglycemic genomic loci are newly associated with blood level of glycated hemoglobin in East Asians. 2014 , 63, 2551-62	46
866	Lack of genetic susceptibility of KCNJ11 E23K polymorphism with risk of type 2 diabetes in an Iranian population. 2014 , 39, 120-5	13
865	Effect of polymorphisms in the CSN3 (β casein) gene on milk production traits in Chinese Holstein Cattle. 2014 , 41, 7585-93	10
864	Next-Generation Sequencing Studies: Optimal Design and Analysis, Missing Heritability and Rare Variants. 2014 , 1, 213-219	2
863	Circulating dickkopf-1 in diabetes mellitus: association with platelet activation and effects of improved metabolic control and low-dose aspirin. 2014 , 3,	40
862	The diabetes gene Hhex maintains β cell differentiation and islet function. 2014 , 28, 829-34	78
861	Zinc-ing about diabetes. 2014 , 7, 276-276	
860	Introduction to the Molecular Biology of the Cell. 2014 , 3-14	
859	Moving into a new era of periodontal genetic studies: relevance of large case-control samples using severe phenotypes for genome-wide association studies. 2014 , 49, 683-95	37
858	Association analyses of insulin signaling pathway gene polymorphisms with healthy aging and longevity in Americans of Japanese ancestry. 2014 , 69, 270-3	10
857	The architecture of risk for type 2 diabetes: understanding Asia in the context of global findings. 2014 , 2014, 593982	27
856	Genetic Variations in the Kir6.2 Subunit (KCNJ11) of Pancreatic ATP-Sensitive Potassium Channel Gene Are Associated with Insulin Response to Glucose Loading and Early Onset of Type 2 Diabetes in Childhood and Adolescence in Taiwan. 2014 , 2014, 983016	8
855	Genome-wide associations between genetic and epigenetic variation influence mRNA expression and insulin secretion in human pancreatic islets. 2014 , 10, e1004735	118
854	A central role for GRB10 in regulation of islet function in man. 2014 , 10, e1004235	124
853	Genetic susceptibility to type 2 diabetes and obesity: follow-up of findings from genome-wide association studies. 2014 , 2014, 769671	50

852	Diabetes Mellitus. 2014,	3
851	Mangiferin facilitates islet regeneration and β -cell proliferation through upregulation of cell cycle and β -cell regeneration regulators. 2014, 15, 9016-35	28
850	Genetics of type 2 diabetes: insights into the pathogenesis and its clinical application. 2014, 2014, 926713	49
849	Principal component analysis characterizes shared pathogenetics from genome-wide association studies. 2014, 10, e1003820	13
848	TCF7L2 is a master regulator of insulin production and processing. 2014, 23, 6419-31	118
847	Fat mass and obesity-associated gene rs11642015 polymorphism is significantly associated with prediabetes and type 2 diabetes subsequent to adjustment for body mass index. 2014, 2, 681-686	3
846	Detecting local haplotype sharing and haplotype association. 2014, 197, 823-38	18
845	Investigating the potential effect of consanguinity on type 2 diabetes susceptibility in a Saudi population. 2014, 77, 197-206	17
844	High cardiorespiratory fitness can reduce glycosylated hemoglobin levels regardless of polygenic risk for Type 2 diabetes mellitus in nondiabetic Japanese men. 2014, 46, 497-504	3
843	Two novel type 2 diabetes loci revealed through integration of TCF7L2 DNA occupancy and SNP association data. 2014, 2, e000052	12
842	Association of IRS1, CAPN10, and PPARG gene polymorphisms with type 2 diabetes mellitus in the high-risk population of Hyderabad, India. 2014, 6, 564-73	26
841	Genetics of alcohol dependence: a review of clinical studies. 2014, 70, 77-94	21
840	The effect of FTO variation on increased osteoarthritis risk is mediated through body mass index: a Mendelian randomisation study. 2014, 73, 2082-6	32
839	Imputation without doing imputation: a new method for the detection of non-genotyped causal variants. 2014, 38, 173-90	8
838	Protein truncating variants of SLC30A8 reduce type 2 diabetes mellitus risk in humans. 2014, 86, 121-2	1
837	Global metabolomic and isobaric tagging capillary liquid chromatography-tandem mass spectrometry approaches for uncovering pathway dysfunction in diabetic mouse aorta. 2014, 13, 6121-34	22
836	Hydrochlorothiazide-induced hyperuricaemia in the pharmacogenomic evaluation of antihypertensive responses study. 2014, 276, 486-97	22
835	Frequency of fat mass and obesity-associated gene rs9939609 and peroxisome proliferator-activated receptor gamma 2 gene rs1801282 polymorphisms among Trinidadian neonates of different ethnicities and their relationship to anthropometry at birth. 2014, 7, 39-47	

834	Association between polymorphisms rs1333040 and rs7865618 of chromosome 9p21 and sporadic brain arteriovenous malformations. 2014 , 37, 290-5	11
833	Current knowledge and trends in age-related macular degeneration: genetics, epidemiology, and prevention. 2014 , 34, 423-41	84
832	Type 2 Diabetes. 2014 ,	1
831	Statistical properties of single-marker tests for rare variants. 2014 , 17, 143-50	10
830	Antiretroviral therapy modifies the genetic effect of known type 2 diabetes-associated risk variants in HIV-infected women. 2014 , 28, 1815-23	3
829	Cellular senescence mediated by p16INK4A-coupled miRNA pathways. 2014 , 42, 1606-18	50
828	FTO genotype, physical activity, and coronary heart disease risk in Swedish men and women. 2014 , 7, 171-7	26
827	Mining Frequent Patterns for Genetic Variants Associated to Diabetes. 2014 ,	1
826	Age-related impairment of pancreatic Beta-cell function: pathophysiological and cellular mechanisms. 2014 , 5, 138	65
825	Re-sequencing expands our understanding of the phenotypic impact of variants at GWAS loci. 2014 , 10, e1004147	42
824	Association of common genetic variants with diabetes and metabolic syndrome related traits in the Arizona Insulin Resistance registry: a focus on Mexican American families in the Southwest. 2014 , 78, 47-58	31
823	Genetic Testing and Type 2 Diabetes Risk Awareness. 2014 , 40, 427-433	1
822	Identification of Hipk2 as an essential regulator of white fat development. 2014 , 111, 7373-8	27
821	The Adiponectin variants contribute to the genetic background of type 2 diabetes in Turkish population. 2014 , 534, 10-16	22
820	Weight loss independent association of TCF7 L2 gene polymorphism with fasting blood glucose after Roux-en-Y gastric bypass in type 2 diabetic patients. 2014 , 10, 679-83	2
819	Mitochondrial DNA haplogroups and risk of new-onset diabetes among tacrolimus-treated renal transplanted patients. 2014 , 538, 195-8	18
818	Contribution of SLC30A8 variants to the risk of type 2 diabetes in a multi-ethnic population: a case control study. 2014 , 14, 2	6
817	FTO and obesity: mechanisms of association. 2014 , 14, 486	72

816	Targeting the pancreatic β -cell to treat diabetes. 2014 , 13, 278-89	192
815	Genome-wide association study identifies three novel loci for type 2 diabetes. 2014 , 23, 239-46	138
814	Co-occurrence of risk alleles in or near genes modulating insulin secretion predisposes obese youth to prediabetes. 2014 , 37, 475-82	28
813	Beneficial modulation of the gut microbiota. 2014 , 588, 4120-30	166
812	Transcription factor 7-like 2 (TCF7L2) gene polymorphism and clinical phenotype in end-stage renal disease patients. 2014 , 41, 4063-8	15
811	Nutrigenetics: bridging two worlds to understand type 2 diabetes. 2014 , 14, 477	9
810	Personal history of diabetes, genetic susceptibility to diabetes, and risk of brain glioma: a pooled analysis of observational studies. 2014 , 23, 47-54	28
809	Elite athletes' genetic predisposition for altered risk of complex metabolic traits. 2015 , 16, 25	14
808	Association of FTO, KCNJ11, SLC30A8, and CDKN2B polymorphisms with type 2 diabetes mellitus. 2015 , 49, 103-111	6
807	Imp2 regulates GBM progression by activating IGF2/PI3K/Akt pathway. 2015 , 16, 623-33	45
806	Assessing gene-environment interactions for common and rare variants with binary traits using gene-trait similarity regression. 2015 , 199, 695-710	15
805	Correlation between and gene polymorphisms and type 2 and post-transplant diabetes mellitus in the Asian Indian population. 2015 , 2, 276-282	21
804	Ink4/Arf locus restores glucose tolerance and insulin sensitivity by reducing hepatic steatosis and inflammation in mice with impaired IRS2-dependent signalling. 2015 , 1852, 1729-42	7
803	Long Non-coding RNA ANRIL and Polycomb in Human Cancers and Cardiovascular Disease. 2016 , 394, 29-39	55
802	A cautionary note on using secondary phenotypes in neuroimaging genetic studies. 2015 , 121, 136-45	5
801	Gene polymorphisms and increased DNA damage in morbidly obese women. 2015 , 776, 111-7	10
800	Krüppel-like factor 14 increases insulin sensitivity through activation of PI3K/Akt signal pathway. 2015 , 27, 2201-8	33
799	Characterization of the transcriptional machinery bound across the widely presumed type 2 diabetes causal variant, rs7903146, within TCF7L2. 2015 , 23, 103-9	17

798	Long Noncoding RNAs. 2015,	2
797	Molecular genetics of coronary artery disease and ischemic stroke. 2015, 4, 4-12	1
796	The Physiological, Biochemical, and Molecular Roles of Zinc Transporters in Zinc Homeostasis and Metabolism. 2015, 95, 749-84	493
795	SNP imputation bias reduces effect size determination. 2015, 6, 30	4
794	Structural forms of the human amylase locus and their relationships to SNPs, haplotypes and obesity. 2015, 47, 921-5	92
793	SLC transporters as therapeutic targets: emerging opportunities. 2015, 14, 543-60	363
792	Genetics of type 2 diabetes-pitfalls and possibilities. 2015, 6, 87-123	257
791	The expression of dominant negative TCF7L2 in pancreatic beta cells during the embryonic stage causes impaired glucose homeostasis. 2015, 4, 344-52	20
790	Genetic modifiers of response to glucose-insulin-potassium (GIK) infusion in acute coronary syndromes and associations with clinical outcomes in the IMMEDIATE trial. 2015, 15, 488-95	7
789	Joint effect of CENTD2 and KCNQ1 polymorphisms on the risk of type 2 diabetes mellitus among Chinese Han population. 2015, 407, 46-51	9
788	Is the adiposity-associated FTO gene variant related to all-cause mortality independent of adiposity? Meta-analysis of data from 169,551 Caucasian adults. 2015, 16, 327-340	7
787	Habitual coffee intake, genetic polymorphisms, and type 2 diabetes. 2015, 172, 595-601	21
786	Replication study of the association of rs7578597 in THADA, rs10886471 in GRK5, and rs7403531 in RASGRP1 with susceptibility to type 2 diabetes among a Japanese population. 2015, 6, 306-312	1
785	Increased DNA methylation of the SLC30A8 gene promoter is associated with type 2 diabetes in a Malay population. 2015, 7, 30	28
784	The CELSR1 polymorphisms rs6007897 and rs4044210 are associated with ischaemic stroke in Chinese Han population. 2015, 42, 26-30	4
783	Functional mechanisms for type 2 diabetes-associated genetic variants. 2015, 29, 497-501	1
782	Longevity Genes. 2015,	2
781	Understanding Interindividual Epigenetic Variations in Obesity and Its Management. 2015, 429-460	3

780	Models to explore genetics of human aging. 2015 , 847, 141-61	3
779	minimac2: faster genotype imputation. 2015 , 31, 782-4	264
778	The Uyghur population and genetic susceptibility to type 2 diabetes: potential role for variants in CDKAL1, JAZF1, and IGF1 genes. 2015 , 19, 230-7	20
777	The genetics of type 2 diabetes. 2015 , 401-412	
776	The genetics of diabetic complications. 2015 , 11, 277-87	99
775	Genome Mapping and Genomics in Human and Non-Human Primates. 2015 ,	
774	Bisphenol-A treatment during pregnancy in mice: a new window of susceptibility for the development of diabetes in mothers later in life. 2015 , 156, 1659-70	93
773	Pleiotropy analysis of quantitative traits at gene level by multivariate functional linear models. 2015 , 39, 259-75	43
772	IGF2BP2/IMP2-Deficient mice resist obesity through enhanced translation of Ucp1 mRNA and Other mRNAs encoding mitochondrial proteins. 2015 , 21, 609-21	87
771	Diabetes susceptibility in Mayas: Evidence for the involvement of polymorphisms in HHEX, HNF4B, KCNJ11, PPARA, CDKN2A/2B, SLC30A8, CDC123/CAMK1D, TCF7L2, ABCA1 and SLC16A11 genes. 2015 , 565, 68-75	45
770	Anatomy of success: 100 most cited articles in diabetes research. 2015 , 6, 163-73	27
769	Genomics, Personalized Medicine and Oral Disease. 2015 ,	1
768	The uniform-score gene set analysis for identifying common pathways associated with different diabetes traits. 2015 , 16, 336	4
767	Changes in Zinc Transporter 8 Autoantibodies Following Type 1 Diabetes Onset: The Type 1 Diabetes Genetics Consortium Autoantibody Workshop. 2015 , 38 Suppl 2, S14-20	16
766	Community members' engagement with and involvement in genomic research: lessons to learn from the field. 2015 , 15, 1-7	12
765	ABCC8 R1420H Loss-of-Function Variant in a Southwest American Indian Community: Association With Increased Birth Weight and Doubled Risk of Type 2 Diabetes. 2015 , 64, 4322-32	37
764	The HHEX rs1111875A/G gene polymorphism is associated with susceptibility to type 2 diabetes in the Iranian population. 2015 , 49, 535-542	6
763	Genetics of Type 2 Diabetes. 2015 , 1-21	

762	Genome of The Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. 2015 , 6, 6065	32
761	Three missense variants of metabolic syndrome-related genes are associated with alpha-1 antitrypsin levels. 2015 , 6, 7754	24
760	Paternal BPA exposure in early life alters Igf2 epigenetic status in sperm and induces pancreatic impairment in rat offspring. 2015 , 238, 30-8	49
759	Circadian rhythm of RNA N6-methyladenosine and the role of cryptochrome. 2015 , 465, 88-94	27
758	Genetics of Type 2 Diabetes in African Americans. 2015 , 15, 74	14
757	Consumption of meat is associated with higher fasting glucose and insulin concentrations regardless of glucose and insulin genetic risk scores: a meta-analysis of 50,345 Caucasians. 2015 , 102, 1266-78	51
756	Common Variants Associated with Type 2 Diabetes in a Black South African Population of Setswana Descent: African Populations Diverge. 2015 , 19, 617-26	8
755	Type 2 diabetes-related variants influence the risk of developing multiple myeloma: results from the IMMEnSE consortium. 2015 , 22, 545-59	10
754	Insulin-degrading enzyme is activated by the C-terminus of β -synuclein. 2015 , 466, 192-5	18
753	Evidence of non-pancreatic beta cell-dependent roles of Tcf7l2 in the regulation of glucose metabolism in mice. 2015 , 24, 1646-54	23
752	Identification of novel genes for glucose metabolism based upon expression pattern in human islets and effect on insulin secretion and glycemia. 2015 , 24, 1945-55	60
751	T2DM GWAS in the Lebanese population confirms the role of TCF7L2 and CDKAL1 in disease susceptibility. 2014 , 4, 7351	22
750	Genome-wide association study identified SNP on 15q24 associated with bladder cancer risk in Japanese population. 2015 , 24, 1177-84	29
749	Quality control metrics improve repeatability and reproducibility of single-nucleotide variants derived from whole-genome sequencing. 2015 , 15, 298-309	8
748	Effect of zinc supplementation on insulin secretion: interaction between zinc and SLC30A8 genotype in Old Order Amish. 2015 , 58, 295-303	30
747	Selective disruption of Tcf7l2 in the pancreatic β cell impairs secretory function and lowers β cell mass. 2015 , 24, 1390-9	68
746	SLC30A8 mutations in type 2 diabetes. 2015 , 58, 31-6	73
745	Regenerative Medicine. 2015 ,	

744	Role of lncRNAs in health and disease-size and shape matter. 2015 , 14, 115-29	23
743	The genetics of diabetic pregnancy. 2015 , 29, 102-9	1
742	Contribution of CDKAL1 rs7756992 and IGF2BP2 rs4402960 polymorphisms in type 2 diabetes, diabetic complications, obesity risk and hypertension in the Tunisian population. 2015 , 7, 102-13	24
741	Genes Associated with Increased Fasting Glucose in Patients with Schizophrenia Spectrum Disorders. 2016 , 6,	
740	snpGeneSets: An R Package for Genome-Wide Study Annotation. 2016 , 6, 4087-4095	8
739	Genetic Susceptibility to Cardiovascular Diseases: From Mendelian Disorders to Common Variants. 2016 , 137-157	
738	Association between IGF2BP2 Polymorphisms and Type 2 Diabetes Mellitus: A Case-Control Study and Meta-Analysis. 2016 , 13,	25
737	Obesity – Are we continuing to play the genetic “blame game”?. 2016 , Volume 6, 11-23	1
736	Identification of matrix metalloproteinase-12 as a candidate molecule for prevention and treatment of cardiometabolic disease. 2016 , 22, 487-496	9
735	Lack of Association between Variants and Type 2 Diabetes in Mexican American Families. 2016 , 2016, 6463214	6
734	Identification of trends in scientific publications related to genetic polymorphisms in gestational diabetes mellitus. 2016 , 15,	7
733	Multiple Genetic Associations with Irish Wolfhound Dilated Cardiomyopathy. 2016 , 2016, 6374082	20
732	The Decay of Disease Association with Declining Linkage Disequilibrium: A Fine Mapping Theorem. 2016 , 7, 217	1
731	The Functions of Metallothionein and ZIP and ZnT Transporters: An Overview and Perspective. 2016 , 17, 336	221
730	Allelic Imbalance in Regulation of ANRIL through Chromatin Interaction at 9p21 Endometriosis Risk Locus. 2016 , 12, e1005893	34
729	The Transcription Factor Nfatc2 Regulates β -Cell Proliferation and Genes Associated with Type 2 Diabetes in Mouse and Human Islets. 2016 , 12, e1006466	22
728	. 2016 ,	1
727	Type 2 diabetes: genetic data sharing to advance complex disease research. 2016 , 17, 535-49	92

726	Discovery and Development of Small Molecules Targeting Epigenetic Enzymes with Computational Methods. 2016 , 75-112	2
725	Binomial Mixture Model Based Association Testing to Account for Genetic Heterogeneity for GWAS. 2016 , 40, 202-9	1
724	IMP2 axonal localization, RNA interactome, and function in the development of axon trajectories. 2016 , 143, 2753-9	12
723	Reverse geroscience: how does exposure to early diseases accelerate the age-related decline in health?. 2016 , 1386, 30-44	18
722	Evaluation of common variants in and the risk of type 2 diabetes and insulin resistance in Han Chinese. 2016 , 5, 612	3
721	Diabetes mellitus and the risk of aneurysmal subarachnoid haemorrhage: A systematic review and meta-analysis of current evidence. 2016 , 44, 1141-1155	8
720	IMPs: an RNA-binding protein family that provides a link between stem cell maintenance in normal development and cancer. 2016 , 30, 2459-2474	132
719	Common germline variants within the CDKN2A/2B region affect risk of pancreatic neuroendocrine tumors. 2016 , 6, 39565	9
718	Genetic Architecture of Type 2 Diabetes. 2016 , 187-204	
717	Novel variation at chr11p13 associated with cystic fibrosis lung disease severity. 2016 , 3, 16020	8
716	Common variants in TCF7L2 and CDKAL1 genes and risk of type 2 diabetes mellitus in Egyptians. 2016 , 14, 247-251	10
715	The analysis of association between type 2 diabetes and polymorphic markers in the CDKAL1 gene and in the HHEX/IDE locus. 2016 , 52, 1192-1199	1
714	Hypomethylation of FAM63B in bipolar disorder patients. 2016 , 8, 52	14
713	Genetics of Type 2 Diabetes: the Power of Isolated Populations. 2016 , 16, 65	17
712	Assignment of Functional Relevance to Genes at Type 2 Diabetes-Associated Loci Through Investigation of β -Cell Mass Deficits. 2016 , 30, 429-45	13
711	Genetics of Type 2 Diabetes. 2016 , 31, 203-20	42
710	Nrf2 as molecular target for polyphenols: A novel therapeutic strategy in diabetic retinopathy. 2016 , 53, 293-312	45
709	Long Non-coding RNAs in Human Disease. 2016 ,	3

708	The Genetics of Type 2 Diabetes and Related Traits. 2016,	3
707	Genome-Wide Association Studies of Type 2 Diabetes. 2016, 13-61	4
706	Evaluation of type 2 diabetes genetic risk variants in Chinese adults: findings from 93,000 individuals from the China Kadoorie Biobank. 2016, 59, 1446-1457	37
705	GCKR: How Genetic Variation Across the Allelic Spectrum Influences Protein Function and Metabolic Traits in Humans. 2016, 317-336	0
704	Physiology Insights. 2016, 207-221	
703	Computational Intelligence Techniques in Health Care. 2016,	0
702	Established BMI-associated genetic variants and their prospective associations with BMI and other cardiometabolic traits: the GLACIER Study. 2016, 40, 1346-52	16
701	Radical S-Adenosylmethionine Enzymes in Human Health and Disease. 2016, 85, 485-514	147
700	Improved Performance of Dynamic Measures of Insulin Response Over Surrogate Indices to Identify Genetic Contributors of Type 2 Diabetes: The GUARDIAN Consortium. 2016, 65, 2072-80	3
699	Long non-coding RNAs: An emerging powerhouse in the battle between life and death of tumor cells. 2016, 26, 28-42	64
698	The prevalence and predictive value of the SLC30A8 R325W polymorphism and zinc transporter 8 autoantibodies in the development of GDM and postpartum type 1 diabetes. 2016, 53, 740-6	11
697	Islet biology, the CDKN2A/B locus and type 2 diabetes risk. 2016, 59, 1579-93	50
696	Interaction between the obesity-risk gene FTO and the dopamine D2 receptor gene ANKK1/TaqIA on insulin sensitivity. 2016, 59, 2622-2631	31
695	Zinc-Associated Variant in SLC30A8 Gene Interacts With Gestational Weight Gain on Postpartum Glycemic Changes: A Longitudinal Study in Women With Prior Gestational Diabetes Mellitus. 2016, 65, 3786-3793	3
694	Lack of association between genetic polymorphism of FTO, AKT1 and AKTIP in childhood overweight and obesity. 2016, 92, 521-527	2
693	Diabetes mellitus. Criterios diagn3sticos y clasificaci3n. Epidemiolog3a. Etiopatogenia. Evaluaci3n inicial del paciente con diabetes. 2016, 12, 935-946	1
692	Predictive utility of a genetic risk score of common variants associated with type 2 diabetes in a black South African population. 2016, 122, 1-8	11
691	Genetic susceptibility for insulin resistance among Egyptian women. 2016, 14, 189-193	1

690	Post-Transcriptional Modifications of RNA: Impact on RNA Function and Human Health. 2016 , 91-130	3
689	An Isogenic Human ESC Platform for Functional Evaluation of Genome-wide-Association-Study-Identified Diabetes Genes and Drug Discovery. 2016 , 19, 326-40	63
688	Lack of association between genetic polymorphism of FTO, AKT1 and AKTIP in childhood overweight and obesity. 2016 , 92, 521-7	11
687	Genetic markers of type 2 diabetes: Progress in genome-wide association studies and clinical application for risk prediction. 2016 , 8, 24-35	49
686	Genetics of cardiovascular and renal complications in diabetes. 2016 , 7, 139-54	26
685	Replication of genome-wide association signals in Asian Indians with early-onset type 2 diabetes. 2016 , 53, 915-923	11
684	What to expect from an evolutionary hypothesis for a human disease: The case of type 2 diabetes. 2016 , 67, 349-368	5
683	Examining how p16(INK4a) expression levels are linked to handgrip strength in the elderly. 2016 , 6, 31905	5
682	Epigenetic Regulation of Islet Development and Regeneration. 2016 , 83-109	
681	Post-transcriptional modifications in development and stem cells. 2016 , 143, 3871-3881	48
680	Cross-talk between amyloidogenic proteins in type-2 diabetes and Parkinson's disease. 2016 , 113, 12473-12478	0
679	Meta-Analysis of the Association of IGF2BP2 Gene rs1470579 Polymorphisms with T2DM. 2016 ,	
678	eMERGE Phenome-Wide Association Study (PheWAS) identifies clinical associations and pleiotropy for stop-gain variants. 2016 , 9 Suppl 1, 32	23
677	Genetic variants associated with lean and obese type 2 diabetes in a Han Chinese population: A case-control study. 2016 , 95, e3841	19
676	Whole-genome re-sequencing for the identification of high contribution susceptibility gene variants in patients with type 2 diabetes. 2016 , 13, 3735-46	5
675	Transcription Factor 7-Like 2 (TCF7L2). 2016 , 297-316	0
674	SLC30A8: A Complex Road from Association to Function. 2016 , 379-401	1
673	Genome-Wide Association Studies of Quantitative Glycaemic Traits. 2016 , 63-89	

672	Fine-Mapping of Type 2 Diabetes Loci. 2016 , 127-151	
671	Caenorhabditis elegans susceptibility to gut Enterococcus faecalis infection is associated with fat metabolism and epithelial junction integrity. 2016 , 16, 6	24
670	FTO rs 9939609 SNP Is Associated With Adiponectin and Leptin Levels and the Risk of Obesity in a Cohort of Romanian Children Population. 2016 , 95, e3709	24
669	Role of PPARG (Pro12Ala) in Malaysian type 2 diabetes mellitus patients. 2016 , 36, 449-456	3
668	Genetics of Type 2 Diabetes. 2016 , 141-157	
667	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. 2016 , 7, 10531	99
666	KATP Channels in the Cardiovascular System. 2016 , 96, 177-252	130
665	Assessing statistical significance in multivariable genome wide association analysis. 2016 , 32, 1990-2000	22
664	Increased Expression of the Diabetes Gene SOX4 Reduces Insulin Secretion by Impaired Fusion Pore Expansion. 2016 , 65, 1952-61	39
663	Genetic and clinical variables identify predictors for chronic kidney disease in type 2 diabetes. 2016 , 89, 411-20	12
662	PAX4 preserves endoplasmic reticulum integrity preventing beta cell degeneration in a mouse model of type 1 diabetes mellitus. 2016 , 59, 755-65	29
661	Association of SLC30A8 gene polymorphism with type 2 diabetes, evidence from 46 studies: a meta-analysis. 2016 , 53, 381-94	23
660	Polymorphisms in the long non-coding RNA CDKN2B-AS1 may contribute to higher systolic blood pressure levels in hypertensive patients. 2016 , 49, 821-7	25
659	Recent progress in genetic and epigenetic research on type 2 diabetes. 2016 , 48, e220	92
658	Overexpression of a glucokinase point mutant in the treatment of diabetes mellitus. 2016 , 23, 323-9	5
657	A Radioactivity-Based Assay for Screening Human m6A-RNA Methyltransferase, METTL3-METTL14 Complex, and Demethylase ALKBH5. 2016 , 21, 290-7	47
656	A genome-wide analysis of the response to inhaled β_2 -agonists in chronic obstructive pulmonary disease. 2016 , 16, 326-35	21
655	Review: High-performance computing to detect epistasis in genome scale data sets. 2016 , 17, 368-79	29

654	Animal models for diabetes: Understanding the pathogenesis and finding new treatments. 2016 , 99, 1-10	92
653	Association of FTO and IRX3 genetic variants to obesity risk in north India. 2016 , 43, 451-6	21
652	Genes associated with diabetes: potential for novel therapeutic targets?. 2016 , 20, 255-67	12
651	Molecular genetics of coronary artery disease. 2016 , 61, 71-7	47
650	Type 2 Diabetes Mellitus. 2016 , 691-714.e6	4
649	Is the association between insulin resistance and diabetogenic haematopoietically expressed homeobox (HHEX) polymorphism (rs1111875) affected by polycystic ovary syndrome status?. 2017 , 29, 670-678	4
648	Computational analyses of type 2 diabetes-associated loci identified by genome-wide association studies. 2017 , 9, 362-377	14
647	The Correlation Between 9p21 Chromosome rs4977574 Polymorphism Genotypes and the Development of Coronary Artery Heart Disease. 2017 , 17, 185-189	5
646	Long noncoding RNA variations in cardiometabolic diseases. 2017 , 62, 97-104	33
645	Disturbance of zinc and glucose homeostasis by methyl tert-butyl ether (MTBE); evidence for type 2 diabetes. 2017 , 47, 547-552	3
644	Association of a type 2 diabetes genetic risk score with insulin secretion modulated by insulin sensitivity among Chinese Hans. 2017 , 91, 832-842	8
643	CDC123/CAMK1D gene rs12779790 polymorphism and rs10811661 polymorphism upstream of the CDKN2A/2B gene in women with gestational diabetes. 2017 , 37, 345-348	8
642	Transdisciplinary approaches enhance the production of translational knowledge. 2017 , 182, 123-134	31
641	Additional Evidence Supports Association of Common Variants in COL11A1 with Increased Risk of Hip Osteoarthritis Susceptibility. 2017 , 21, 86-91	4
640	Characterization of globulin storage proteins of a low prolamin cereal species in relation to celiac disease. 2017 , 7, 39876	9
639	New insights into the genetics of primary open-angle glaucoma based on meta-analyses of intraocular pressure and optic disc characteristics. 2017 , 26, 438-453	80
638	Fat mass and obesity-associated gene variations are related to fatty liver disease in HIV-infected patients. 2017 , 18, 546-554	4
637	Bioinformatics in the Identification of Novel Targets and Pathways in Neurodegenerative Diseases. 2017 , 5, 15-21	

636	Sequence robust association test for familial data. 2017 , 73, 876-884	1
635	Genomics of Islet (Dys)function and Type 2 Diabetes. 2017 , 33, 244-255	44
634	Pancreatic impairment and Igf2 hypermethylation induced by developmental exposure to bisphenol A can be counteracted by maternal folate supplementation. 2017 , 37, 825-835	12
633	Association of CDKAL1 gene rs7756992 A/G polymorphism with type 2 diabetes mellitus and diabetic nephropathy in the Egyptian population. 2017 , 7, 142-146	2
632	Perinatal DNA Methylation at CDKN2A Is Associated With Offspring Bone Mass: Findings From the Southampton Women's Survey. 2017 , 32, 2030-2040	24
631	SOX4 Allows Facultative β -Cell Proliferation Through Repression of. 2017 , 66, 2213-2219	13
630	Using genetics to inform new therapeutics for diabetes. 2017 , 12, 159-169	
629	ANRIL Promoter DNA Methylation: A Perinatal Marker for Later Adiposity. 2017 , 19, 60-72	49
628	Engaging Hmong adults in genomic and pharmacogenomic research: Toward reducing health disparities in genomic knowledge using a community-based participatory research approach. 2017 , 8, 117-125	19
627	Exploring the Association Between Demographics, SLC30A8 Genotype, and Human Islet Content of Zinc, Cadmium, Copper, Iron, Manganese and Nickel. 2017 , 7, 473	25
626	The dynamic plasticity of insulin production in β -cells. 2017 , 6, 958-973	66
625	MicroRNA profiling in clear cell renal cell carcinoma tissues potentially links tumorigenesis and recurrence with obesity. 2017 , 116, 77-84	30
624	Multiancestry Study of Gene-Lifestyle Interactions for Cardiovascular Traits in 610 475 Individuals From 124 Cohorts: Design and Rationale. 2017 , 10,	30
623	Using hESCs to Probe the Interaction of the Diabetes-Associated Genes CDKAL1 and MT1E. 2017 , 19, 1512-1521	20
622	FTO gene polymorphisms (rs9939609 and rs17817449) as predictors of Type 2 Diabetes Mellitus in obese Iraqi population. 2017 , 627, 79-84	13
621	Gene variants in the FTO gene are associated with adiponectin and TNF-alpha levels in gestational diabetes mellitus. 2017 , 9, 32	17
620	Identification of genetic variants affecting vitamin D receptor binding and associations with autoimmune disease. 2017 , 26, 2164-2176	21
619	FTO is required for myogenesis by positively regulating mTOR-PGC-1 β pathway-mediated mitochondria biogenesis. 2017 , 8, e2702	64

618	Obstacles to Translating Genotype-Phenotype Correlates in Metabolic Disease. 2017 , 32, 42-50	2
617	Introduction. 2017 , 1-34	
616	Pancreatic alpha cell-selective deletion of Tcf7l2 impairs glucagon secretion and counter-regulatory responses to hypoglycaemia in mice. 2017 , 60, 1043-1050	13
615	A fly view on the roles and mechanisms of the mA mRNA modification and its players. 2017 , 14, 1232-1240	27
614	The druggable genome and support for target identification and validation in drug development. 2017 , 9,	212
613	Genome-Wide Association Study Meta-Analysis of Long-Term Average Blood Pressure in East Asians. 2017 , 10, e001527	20
612	hZnT8 (Slc30a8) Transgenic Mice That Overexpress the R325W Polymorph Have Reduced Islet Zn ²⁺ and Proinsulin Levels, Increased Glucose Tolerance After a High-Fat Diet, and Altered Levels of Pancreatic Zinc Binding Proteins. 2017 , 66, 551-559	18
611	Prevalence and Clinical Significance of Diabetes in Asian Versus White Patients With Heart Failure. 2017 , 5, 14-24	42
610	Dwarfism and Altered Craniofacial Development in Rabbits Is Caused by a 12.1 kb Deletion at the HMGA2 Locus. 2017 , 205, 955-965	21
609	Gene expression signature: a powerful approach for drug discovery in diabetes. 2017 , 232, R131-R139	6
608	Further analysis reveals new gut microbiome markers of type 2 diabetes mellitus. 2017 , 110, 445-453	21
607	easyGWAS: A Cloud-Based Platform for Comparing the Results of Genome-Wide Association Studies. 2017 , 29, 5-19	56
606	RNA Binding Protein Ybx2 Regulates RNA Stability During Cold-Induced Brown Fat Activation. 2017 , 66, 2987-3000	15
605	A Loss-of-Function Splice Acceptor Variant in Is Protective for Type 2 Diabetes. 2017 , 66, 2903-2914	32
604	Zinc, Insulin and IGF-I Interplay in Aging. 2017 , 57-90	0
603	Genetic Basis for Increased Risk for Vascular Diseases in Diabetes. 2017 , 27-71	
602	Cdkal1, a type 2 diabetes susceptibility gene, regulates mitochondrial function in adipose tissue. 2017 , 6, 1212-1225	25
601	Effects of Lactobacillus casei CCFM419 on insulin resistance and gut microbiota in type 2 diabetic mice. 2017 , 8, 421-432	65

600	Human beta cell mass and function in diabetes: Recent advances in knowledge and technologies to understand disease pathogenesis. 2017 , 6, 943-957	215
599	Meta-analysis of gene-environment interaction exploiting gene-environment independence across multiple case-control studies. 2017 , 36, 3895-3909	1
598	ANRIL polymorphism rs1333049, a novel genetic predictor for diabetic retinopathy complication. 2017 , 14, 33-37	2
597	Diversity and inclusion in genomic research: why the uneven progress?. 2017 , 8, 255-266	146
596	CDK5 Regulatory Subunit-Associated Protein 1-like 1 Negatively Regulates Adipocyte Differentiation through Activation of Wnt Signaling Pathway. 2017 , 7, 7326	6
595	Association between Sugar Intake, Oral Health, and the Impact on Overall Health: Raising Public Awareness. 2017 , 4, 176-183	6
594	Genetic variants of increased waist circumference in psychosis. 2017 , 27, 210-218	3
593	A genetic stochastic process model for genome-wide joint analysis of biomarker dynamics and disease susceptibility with longitudinal data. 2017 , 41, 620-635	3
592	Concise Review: Challenges in Regenerating the Diabetic Heart: A Comprehensive Review. 2017 , 35, 2009-2026	9
591	Differential cytolocation and functional assays of the two major human SLC30A8 (ZnT8) isoforms. 2017 , 44, 116-124	15
590	Introduction of the DiaGene study: clinical characteristics, pathophysiology and determinants of vascular complications of type 2 diabetes. 2017 , 9, 47	11
589	Acute Lung Injury and Repair. 2017 ,	
588	Impact of Genetic Testing and Family Health History Based Risk Counseling on Behavior Change and Cognitive Precursors for Type 2 Diabetes. 2017 , 26, 133-140	16
587	Cellular senescence: Implications for metabolic disease. 2017 , 455, 93-102	35
586	Polymorphisms in PDLIM5 gene are associated with alcohol dependence, type 2 diabetes, and hypertension. 2017 , 84, 27-34	10
585	Metabolomics in Sepsis and Its Impact on Public Health. 2017 , 20, 274-285	16
584	A POWERFUL METHOD FOR INCLUDING GENOTYPE UNCERTAINTY IN TESTS OF HARDY-WEINBERG EQUILIBRIUM. 2017 , 22, 368-379	1
583	Primary Open-Angle Glaucoma Genetics in African Americans. 2017 , 5, 167-174	7

582	The function-on-scalar LASSO with applications to longitudinal GWAS. 2017 , 11,	20
581	Genetic aetiology of glycaemic traits: approaches and insights. 2017 , 26, R172-R184	8
580	Identification of candidate protective variants for common diseases and evaluation of their protective potential. 2017 , 18, 575	11
579	FTO Genotype and Type 2 Diabetes Mellitus: Spatial Analysis and Meta-Analysis of 62 Case-Control Studies from Different Regions. 2017 , 8,	22
578	Diabetes. 2017 , 245-282	1
577	Genetic Variations as Modifying Factors to Dietary Zinc Requirements-A Systematic Review. 2017 , 9,	11
576	Long Noncoding RNAs as Diagnostic and Therapeutic Targets in Type 2 Diabetes and Related Complications. 2017 , 8,	53
575	Meta-Analysis of the association of IGF2BP2 gene rs4402960 polymorphisms with T2DM in Asia. 2017 , 8, 02003	1
574	Type 2 Diabetes Susceptibility in the Greek-Cypriot Population: Replication of Associations with TCF7L2, FTO, HHEX, SLC30A8 and IGF2BP2 Polymorphisms. 2017 , 8,	15
573	An Efficient Test for Gene-Environment Interaction in Generalized Linear Mixed Models with Family Data. 2017 , 14,	3
572	Gene-Diet Interaction and Precision Nutrition in Obesity. 2017 , 18,	79
571	A Nutrigenomic Approach to Non-Alcoholic Fatty Liver Disease. 2017 , 18,	39
570	Long Noncoding RNAs and RNA-Binding Proteins in Oxidative Stress, Cellular Senescence, and Age-Related Diseases. 2017 , 2017, 2062384	63
569	Transcription factor 7-like 2 (TCF7L2) gene polymorphisms are strong predictors of type 2 diabetes among nonobese diabetics in the Turkish population. 2017 , 47, 22-28	10
568	Association between 28 single nucleotide polymorphisms and type 2 diabetes mellitus in the Kazakh population: a case-control study. 2017 , 18, 76	13
567	Spectrum of mutations in monogenic diabetes genes identified from high-throughput DNA sequencing of 6888 individuals. 2017 , 15, 213	45
566	Association between serum osteocalcin and glucose/lipid metabolism in Chinese Han and Uygur populations with type 2 diabetes mellitus in Xinjiang: two cross-sectional studies. 2017 , 16, 139	11
565	Polygene Varianten und Epigenetik bei Adipositas. 2017 , 29, 365-373	

564	Genetics and Diabetes. 2017 , 659-675	
563	Association of polymorphic markers of genes , and with type 2 diabetes mellitus in the Russian population. 2017 , 5, e3414	17
562	LncRNAs: key players and novel insights into diabetes mellitus. 2017 , 8, 71325-71341	54
561	The pathogenetic role of β -cell mitochondria in type 2 diabetes. 2018 , 236, R145-R159	46
560	Association of genetic variants with macronutrient intake in Circassian and Chechan populations in relation to diabetes. 2018 , 16, 199-207	
559	GWAS identifies two novel colorectal cancer loci at 16q24.1 and 20q13.12. 2018 , 39, 652-660	32
558	Progress in defining the genetic contribution to type 2 diabetes susceptibility. 2018 , 50, 41-51	15
557	Precision medicine in diabetes prevention, classification and management. 2018 , 9, 998-1015	32
556	Novel association between CDKAL1 and cholesterol efflux capacity: Replication after GWAS-based discovery. 2018 , 273, 21-27	2
555	A multifactor dimensionality reduction model of gene polymorphisms and an environmental interaction analysis in type 2 diabetes mellitus study among Punjabi, a North India population. 2018 , 16, 39-49	1
554	SLC30A family expression in the pancreatic islets of humans and mice: cellular localization in the β -cells. 2018 , 49, 133-145	6
553	Functional polymorphisms of the neuropilin 1 gene are associated with the risk of tetralogy of Fallot in a Chinese Han population. 2018 , 653, 72-79	3
552	T2D Genome-Wide Association Study Risk SNPs Impact Locus Gene Expression and Proliferation in Human Islets. 2018 , 67, 872-884	28
551	Disease Gene Identification. 2018 ,	1
550	Physiologic Interpretation of GWAS Signals for Type 2 Diabetes. 2018 , 1706, 323-351	1
549	Association of CDKAL1 nucleotide variants with the risk of non-syndromic cleft lip with or without cleft palate. 2018 , 63, 397-406	4
548	Genetics and Genomics of Coronary Artery Disease. 2018 , 661-678	1
547	DNA methylation at the 9p21 glaucoma susceptibility locus is associated with normal-tension glaucoma. 2018 , 39, 221-227	10

546	Emerging roles of RNA-binding proteins in diabetes and their therapeutic potential in diabetic complications. 2018 , 9, e1459	27
545	A candidate functional SNP rs7074440 in TCF7L2 alters gene expression through C-FOS in hepatocytes. 2018 , 592, 422-433	8
544	Polygenic Obesity. 2018 , 183-202	1
543	Histochemical evidence of IGF2 mRNA-binding protein 2-mediated regulation of osteoclast function and adhesive ability. 2018 , 149, 343-351	3
542	The FTO variant is associated with chronic complications of diabetes mellitus in Czech population. 2018 , 642, 220-224	12
541	Metabolomics study on the association between nicotinamide N-methyltransferase gene polymorphisms and type 2 diabetes. 2018 , 38, 409-416	3
540	The AraGWAS Catalog: a curated and standardized Arabidopsis thaliana GWAS catalog. 2018 , 46, D1150-D115639	
539	LncRNAs in genetic basis of glaucoma. 2018 , 3, e000131	13
538	FTO variant is not associated with osteoarthritis in the Chinese Han population: replication study for a genome-wide association study identified risk loci. 2018 , 13, 65	8
537	Improved score statistics for meta-analysis in single-variant and gene-level association studies. 2018 , 42, 333-343	3
536	Variants of CDKAL1 rs7754840 (G/C) and CDKN2A/2B rs10811661 (C/T) with gestational diabetes: insignificant association. 2018 , 11, 181	8
535	Replicability and Prediction: Lessons and Challenges from GWAS. 2018 , 34, 504-517	77
534	Paraneoplastic Syndromes in Pancreatic Cancer. 2018 , 633-657	2
533	Prevalence of type 2 diabetes and prediabetes in the Faroe Islands. 2018 , 140, 162-173	8
532	Genome-Wide Association Studies and Heritability Estimation in the Functional Genomics Era. 2018 , 361-425	4
531	The emerging role of mRNA methylation in normal and pathological behavior. 2018 , 17, e12428	48
530	Inhibition of Cdk5 Promotes β -Cell Differentiation From Ductal Progenitors. 2018 , 67, 58-70	24
529	Metabolic pathways at the crossroads of diabetes and inborn errors. 2018 , 41, 5-17	4

528	Genetic risk scores and family history as predictors of schizophrenia in Nordic registers. 2018 , 48, 1201-1208	18
527	Interrelationship of the rs7903146 TCF7L2 gene variant with measures of glucose metabolism and adiposity: The NEO study. 2018 , 28, 150-157	8
526	The role of cellular senescence in aging through the prism of Koch-like criteria. 2018 , 41, 18-33	27
525	Investigation of CAV1/CAV2 rs4236601 and CDKN2B-AS1 rs2157719 in primary open-angle glaucoma patients from Brazil. 2018 , 39, 194-199	12
524	Detection of SNPs of T2DM susceptibility genes by a ligase detection reaction-fluorescent nanosphere technique. 2018 , 540-541, 38-44	2
523	Genetic Approaches to the Study of Gene Variants and Their Impact on the Pathophysiology of Type 2 Diabetes. 2018 , 56, 22-55	17
522	The GAIT translational control system. 2018 , 9, e1441	28
521	The clinical potential of adipogenesis and obesity-related microRNAs. 2018 , 28, 91-111	53
520	Fetuin-A levels and risk of type 2 diabetes mellitus: a systematic review and meta-analysis. 2018 , 55, 87-98	30
519	Impact of variants on type-2 diabetes risk genes identified through genomewide association studies in polycystic ovary syndrome: a case-control study. 2018 , 97, 1213-1223	1
518	Subset-Based Analysis Using Gene-Environment Interactions for Discovery of Genetic Associations across Multiple Studies or Phenotypes. 2018 , 83, 283-314	3
517	Nutrient Sensing, Signaling and Ageing: The Role of IGF-1 and mTOR in Ageing and Age-Related Disease. 2018 , 90, 49-97	21
516	Periodontal, metabolic, and cardiovascular disease: Exploring the role of inflammation and mental health. 2018 , 29, 124-163	16
515	Genes associated with Type 2 Diabetes and vascular complications. 2018 , 10, 178-196	27
514	Methods and Tools in Genome-wide Association Studies. 2018 , 1819, 93-136	7
513	Evaluation of the roles of the cytosolic N-terminus and His-rich loop of ZNT proteins using ZNT2 and ZNT3 chimeric mutants. 2018 , 8, 14084	12
512	Into the Wild: GWAS Exploration of Non-coding RNAs. 2018 , 5, 181	49
511	Genome-wide association study (GWAS) of ovarian cancer in Japanese predicted regulatory variants in 22q13.1. 2018 , 13, e0209096	5

510	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. 2018 , 14, e1007813	166
509	Genome-wide association study identifies gastric cancer susceptibility loci at 12q24.11-12 and 20q11.21. 2018 , 109, 4015-4024	22
508	A novel SNP-set analytical method without distinguishing common variants or rare variants in genome-wide association study. 2018 , 11, 1850094	2
507	A novel role for zinc transporter 8 in the facilitation of zinc accumulation and regulation of testosterone synthesis in Leydig cells of human and mouse testicles. 2018 , 88, 40-50	11
506	Central Circadian Clock Regulates Energy Metabolism. 2018 , 1090, 79-103	11
505	RBPs Play Important Roles in Vascular Endothelial Dysfunction Under Diabetic Conditions. 2018 , 9, 1310	12
504	Association Between SLC30A8 rs13266634 Polymorphism and Risk of T2DM and IGR in Chinese Population: A Systematic Review and Meta-Analysis. 2018 , 9, 564	4
503	Long Noncoding RNA : Lnc-ing Genetic Variation at the Chromosome 9p21 Locus to Molecular Mechanisms of Atherosclerosis. 2018 , 5, 145	49
502	Analysis of the 9p21.3 sequence associated with coronary artery disease reveals a tendency for duplication in a CAD patient. 2018 , 9, 15275-15291	4
501	Highly specific monoclonal antibodies for allosteric inhibition and immunodetection of the human pancreatic zinc transporter ZnT8. 2018 , 293, 16206-16216	8
500	tRNA modifications and islet function. 2018 , 20 Suppl 2, 20-27	10
499	Pathophysiology of Type 2 Diabetes in Koreans. 2018 , 33, 9-16	8
498	Hematopoietically expressed homeobox gene is associated with type 2 diabetes in KK Cg-A/J mice and a Taiwanese Han Chinese population. 2018 , 16, 185-191	6
497	Genotype Imputation from Large Reference Panels. 2018 , 19, 73-96	68
496	The ADRA2A rs553668 variant is associated with type 2 diabetes and five variants were associated at nominal significance levels in a population-based case-control study from Mexico City. 2018 , 669, 28-34	8
495	Glycogen synthase kinase-3 (GSK-3) activity regulates mRNA methylation in mouse embryonic stem cells. 2018 , 293, 10731-10743	14
494	Molecular functions and specific roles of circRNAs in the cardiovascular system. 2018 , 3, 75-98	38
493	Genetic variation of the transcription factor GATA3, not STAT4, is associated with the risk of type 2 diabetes in the Bangladeshi population. 2018 , 13, e0198507	15

492	Impact of KCNQ1, CDKN2A/2B, CDKAL1, HHEX, MTNR1B, SLC30A8, TCF7L2, and UBE2E2 on risk of developing type 2 diabetes in Thai population. 2018 , 19, 93	19
491	The ciliary protein Rpgrip1l in development and disease. 2018 , 442, 60-68	14
490	Type 2 Diabetes Mellitus and Cardiovascular Disease: Genetic and Epigenetic Links. 2018 , 9, 2	138
489	The rs4712527 Polymorphism in the CDKAL1 Gene: A Protective Factor for Proliferative Diabetic Retinopathy Progress in Type 2 Diabetes. 2018 , 2, 200-207	
488	Diabetes Mellitus. 2018 , 341-352	
487	Genetics of Diabetes and Diabetic Complications. 2018 , 1-60	
486	Pilot genome-wide association study identifying novel risk loci for type 2 diabetes in a Maya population. 2018 , 677, 324-331	9
485	From SNPs to pathways: Biological interpretation of type 2 diabetes (T2DM) genome wide association study (GWAS) results. 2018 , 13, e0193515	24
484	The journey of gut microbiome [An introduction and its influence on metabolic disorders. 2018 , 13, 327-341	4
483	Association of type 2 diabetes susceptible genes GCKR, SLC30A8, and FTO polymorphisms with gestational diabetes mellitus risk: a meta-analysis. 2018 , 62, 34-45	12
482	Silencing of the FTO gene inhibits insulin secretion: An in vitro study using GRINCH cells. 2018 , 472, 10-17	12
481	Interrogation of nonconserved human adipose lincRNAs identifies a regulatory role of in adipocyte metabolism. 2018 , 10,	28
480	MicroRNA-99a mimics inhibit M1 macrophage phenotype and adipose tissue inflammation by targeting TNF α . 2019 , 16, 495-507	40
479	Assessment of FTO Gene Polymorphism and its Association with Type 2 Diabetes Mellitus in North Indian Populations. 2019 , 34, 479-484	2
478	Genetic Variation in Long-Range Enhancers. 2019 , 42, 35-50	1
477	RNAs and RNA-Binding Proteins in Immuno-Metabolic Homeostasis and Diseases. 2019 , 6, 106	13
476	The Niemann-Pick C1-like 1 rs2073547 polymorphism is associated with type 2 diabetes mellitus in a Chinese population. 2019 , 47, 4260-4271	0
475	Recent advances and perspectives in next generation sequencing application to the genetic research of type 2 diabetes. 2019 , 10, 376-395	8

474	Meclofenamic acid represses spermatogonial proliferation through modulating mA RNA modification. 2019 , 10, 63	16
473	Regulation of growth hormone biosynthesis by Cdk5 regulatory subunit associated protein 1-like 1 (CDKAL1) in pituitary adenomas. 2019 , 66, 807-816	4
472	Investigating the association of rs7903146 of TCF7L2 gene, rs5219 of KCNJ11 gene, rs10946398 of CDKAL1 gene, and rs9939609 of FTO gene with type 2 diabetes mellitus in Emirati population. 2019 , 21, 100600	5
471	Contemplating the role of genetic variants of HHEX, CDKAL1, WFS1 and SLC30A8 genes of TYPE-2 diabetes in Asians ethnic groups. 2019 , 17, 100465	4
470	Genetic Determinants of Type 2 Diabetes. 2019 , 117-125	
469	Genetics, adaptation to environmental changes and archaic admixture in the pathogenesis of diabetes mellitus in Indigenous Australians. 2019 , 20, 321-332	2
468	A Novel Polymorphism (rs35612982) in CDKAL1 Is a Risk Factor of Type 2 Diabetes: A Case-Control Study. 2019 , 44, 1313-1326	10
467	Nutrigenomics and personalized nutrition for the prevention of hyperglycemia and type 2 diabetes mellitus. 2019 , 339-352	1
466	"Omics" and "epi-omics" underlying the β -cell adaptation to insulin resistance. 2019 , 27S, S42-S48	9
465	Lack of association between TCF7L2 gene variants and type 2 diabetes mellitus in a Brazilian sample of patients with the risk for cardiovascular disease. 2019 , 53, 1-7	3
464	Increased Expression of Lipid Metabolism Genes in Early Stages of Wooden Breast Links Myopathy of Broilers to Metabolic Syndrome in Humans. 2019 , 10,	24
463	12 new susceptibility loci for prostate cancer identified by genome-wide association study in Japanese population. 2019 , 10, 4422	27
462	Endothelial Function Assessed by Digital Volume Plethysmography Predicts the Development and Progression of Type 2 Diabetes Mellitus. 2019 , 8, e012509	15
461	Genotype Imputation in Genome-Wide Association Studies. 2019 , 102, e84	10
460	Liver-specific deletion of IGF2 mRNA binding protein-2/IMP2 reduces hepatic fatty acid oxidation and increases hepatic triglyceride accumulation. 2019 , 294, 11944-11951	17
459	Cross-population analysis for functional characterization of type II diabetes variants. 2019 , 20, 320	0
458	HHEX gene polymorphisms and type 2 diabetes mellitus: A case-control report from Iran. 2019 , 120, 16445-16461	
457	Genetic Insights for Drug Development in NAFLD. 2019 , 40, 506-516	34

456	Genetics of Type 2 Diabetes: A Review. 2019 , 6, 59-63	1
455	The hypertension advantage and natural selection: Since type 2 diabetes associates with co-morbidities and premature death, why have the genetic variants remained in the human genome?. 2019 , 129, 109237	2
454	Function and Mechanism of Long Noncoding RNAs in Adipocyte Biology. 2019 , 68, 887-896	29
453	Identification of entacapone as a chemical inhibitor of FTO mediating metabolic regulation through FOXO1. 2019 , 11,	97
452	The association between the FTO gene variant and alcohol consumption and binge and problem drinking in different gene-environment background: The HAPIEE study. 2019 , 707, 30-35	3
451	The RNA N-methyladenosine modification landscape of human fetal tissues. 2019 , 21, 651-661	67
450	Long Non-Coding RNA in Vascular Disease and Aging. 2019 , 5,	12
449	Locus-specific DNA methylation prediction in cord blood and placenta. 2019 , 14, 405-420	8
448	Genetic, Functional, and Immunological Study of ZnT8 in Diabetes. 2019 , 2019, 1524905	5
447	Multi-Ancestry Genome-Wide Association Study of Spontaneous Clearance of Hepatitis C Virus. 2019 , 156, 1496-1507.e7	20
446	FTO haplotyping underlines high obesity risk for European populations. 2019 , 12, 46	9
445	Ancestry-specific association mapping in admixed populations. 2019 , 43, 506-521	19
444	Robust Reference Powered Association Test of Genome-Wide Association Studies. 2019 , 10, 319	1
443	Deficiency of ZnT8 Promotes Adiposity and Metabolic Dysfunction by Increasing Peripheral Serotonin Production. 2019 , 68, 1197-1209	11
442	Epigenetics of Diabetic Nephropathy. 2019 , 865-884	
441	Influence of obesity, parental history of diabetes, and genes in type 2 diabetes: A case-control study. 2019 , 9, 2748	8
440	Completing the genetic spectrum influencing coronary artery disease: from germline to somatic variation. 2019 , 115, 830-843	7
439	Zinc and its regulators in pancreas. 2019 , 27, 453-464	14

438	A resource-efficient tool for mixed model association analysis of large-scale data. 2019 , 51, 1749-1755	102
437	The Impact of Working Hours on Cardiovascular Diseases and Moderating Effects of Sex and Type of Work: Results From a Longitudinal Analysis of the Korean Working Population. 2019 , 61, e247-e252	9
436	Type 2 Diabetes-Associated Genetic Polymorphisms as Potential Disease Predictors. 2019 , 12, 2689-2706	14
435	Retracted Article: Long noncoding RNA ANRIL protects cardiomyocytes against hypoxia/reoxygenation injury by sponging miR-195-5p and upregulating Bcl-2. 2019 , 9, 35624-35635	1
434	The Role of De Novo Noncoding Regulatory Mutations in Neurodevelopmental Disorders. 2019 , 42, 115-127	33
433	Irx3, a new leader on obesity genetics. 2019 , 39, 19-20	6
432	Precision medicine in type 2 diabetes. 2019 , 285, 40-48	41
431	Interaction of amylin species with transition metals and membranes. 2019 , 191, 69-76	24
430	The variant at TGFBRAP1 is significantly associated with type 2 diabetes mellitus and affects diabetes-related miRNA expression. 2019 , 23, 83-92	4
429	CYC27 Synthetic Derivative of Bromophenol from Red Alga : Anti-Diabetic Effects of Sensitizing Insulin Signaling Pathways and Modulating RNA Splicing-Associated RBPs. 2019 , 17,	7
428	Genetic Polymorphisms and Zinc Status: Implications for Supplementation in Metabolic Diseases. 2018 , 24, 4131-4143	2
427	Association of vascular endothelial growth factor expression and polymorphisms with the risk of gestational diabetes mellitus. 2019 , 33, e22686	10
426	Deciphering Cardiovascular Genomics and How They Apply to Cardiovascular Disease Prevention. 2019 , 99-111	
425	Discovery of common and rare genetic risk variants for colorectal cancer. 2019 , 51, 76-87	177
424	Interdisciplinary Care Model: Diabetes and Oral Health. 2019 , 47-61	2
423	Computational models for lncRNA function prediction and functional similarity calculation. 2019 , 18, 58-82	88
422	Linking diabetic vascular complications with lncRNAs. 2019 , 114, 139-144	22
421	Peripheral Artery Disease and Aortic Disease. 2016 , 11, 313-326	6

420	Insights into the structure-function relationship of both wild and mutant zinc transporter ZnT8 in human: a computational structural biology approach. 2020 , 38, 137-151	14
419	Interaction analysis of gene variants of TCF7L2 and body mass index and waist circumference on type 2 diabetes. 2020 , 39, 192-197	10
418	Diabetes and cancer risk: A Mendelian randomization study. 2020 , 146, 712-719	14
417	Cattle genomics: genome projects, current status, and future applications. 2020 , 3-28	0
416	Improving Imputation Quality in BEAGLE for Crop and Livestock Data. 2020 , 10, 177-188	16
415	New sights in cancer: Component and function of N6-methyladenosine modification. 2020 , 122, 109694	13
414	Solute Carrier Transporters as Potential Targets for the Treatment of Metabolic Disease. 2020 , 72, 343-379	44
413	Role of inflammasomes in the pathogenesis of periodontal disease and therapeutics. 2020 , 82, 93-114	38
412	PRMT1 Is Required for the Maintenance of Mature β -Cell Identity. 2020 , 69, 355-368	9
411	Hyaluronic Acid Nanoparticles as Nanomedicine for Treatment of Inflammatory Diseases. 2020 , 12,	21
410	Hepatic FTO is dispensable for the regulation of metabolism but counteracts HCC development in vivo. 2020 , 42, 101085	18
409	PPAR γ Chromatin Repression during Activation of Lung Monocyte-Macrophages in Severe COVID-19. 2020 , 23, 101611	17
408	Association between genetic variants at chromosome 9p21 and risk of coronary artery disease in Emirati Type 2 Diabetes patients. 2020 , 21, 100892	
407	The Diverse Functions of IMP2/IGF2BP2 in Metabolism. 2020 , 31, 670-679	24
406	Gut microbiome: Current development, challenges, and perspectives. 2020 , 227-241	1
405	Genome plasticity and endocrine diseases. 2020 , 211-235	
404	Analysis of the interaction effect of 48 SNPs and obesity on type 2 diabetes in Chinese Hans. 2020 , 8,	1
403	Disease-Causing Mutations and Rearrangements in Long Non-coding RNA Gene Loci. 2020 , 11, 527484	11

402	Genetic Studies of Gestational Diabetes and Glucose Metabolism in Pregnancy. 2020 , 20, 69	13
401	PPARG (Pro12Ala) genetic variant and risk of T2DM: a systematic review and meta-analysis. 2020 , 10, 12764	20
400	S-adenosylmethionine tRNA modification: unexpected/unsuspected implications of former/new players. 2020 , 16, 3018-3027	2
399	A Multiancestry Sex-Stratified Genome-Wide Association Study of Spontaneous Clearance of Hepatitis C Virus. 2021 , 223, 2090-2098	1
398	Nutrient consumption-dependent association of a glucagon-like peptide-1 receptor gene polymorphism with insulin secretion. 2020 , 10, 16382	1
397	Early childhood education and life-cycle health. 2020 ,	0
396	A shared genetic contribution to breast cancer and schizophrenia. 2020 , 11, 4637	11
395	Functional Genomics in Pancreatic β Cells: Recent Advances in Gene Deletion and Genome Editing Technologies for Diabetes Research. 2020 , 11, 576632	7
394	Genetic predisposition in type 2 diabetes: A promising approach toward a personalized management of diabetes. 2020 , 98, 525-547	16
393	Drivers for the comorbidity of type 2 diabetes mellitus and epilepsy: A scoping review. 2020 , 106, 107043	5
392	High-Resolution mRNA and Secretome Atlas of Human Enteroendocrine Cells. 2020 , 181, 1291-1306.e19	41
391	Ranbow: A fast and accurate method for polyploid haplotype reconstruction. 2020 , 16, e1007843	11
390	Computational determination of human PPARG gene: SNPs and prediction of their effect on protein functions of diabetic patients. 2020 , 9, 7	7
389	Integrative analysis of Mendelian randomization and Bayesian colocalization highlights four genes with putative BMI-mediated causal pathways to diabetes. 2020 , 10, 7476	1
388	Validating the doubly weighted genetic risk score for the prediction of type 2 diabetes in the Lifelines and Estonian Biobank cohorts. 2020 , 44, 589-600	3
387	Replication of FTO Gene associated with lean mass in a Meta-Analysis of Genome-Wide Association Studies. 2020 , 10, 5057	5
386	Human and Arabidopsis alpha-ketoglutarate-dependent dioxygenase homolog proteins-New players in important regulatory processes. 2020 , 72, 1126-1144	5
385	Systematic Review of Polygenic Risk Scores for Type 1 and Type 2 Diabetes. 2020 , 21,	15

384	Sequencing and imputation in GWAS: Cost-effective strategies to increase power and genomic coverage across diverse populations. 2020 , 44, 537-549	10
383	A comparative study of microbial community and functions of type 2 diabetes mellitus patients with obesity and healthy people. 2020 , 104, 7143-7153	13
382	Structure/Function Analysis of human ZnT8 (SLC30A8): A Diabetes Risk Factor and Zinc Transporter. 2020 , 2, 144-155	4
381	Genetic factors for short life span associated with evolution of the loss of flight ability. 2020 , 10, 6020-6029	1
380	Insights into pancreatic islet cell dysfunction from type 2 diabetes mellitus genetics. 2020 , 16, 202-212	50
379	Lifestyle intervention in individuals with impaired glucose regulation affects Caveolin-1 expression and DNA methylation. 2020 , 9, 96-107	3
378	Analysis on the polymorphisms of site RS4977574, and RS1333045 in region 9p21 and the susceptibility of coronary heart disease in Chinese population. 2020 , 21, 36	3
377	Genome-wide meta-analysis associates GPSM1 with type 2 diabetes, a plausible gene involved in skeletal muscle function. 2020 , 65, 411-420	3
376	Irp2 regulates insulin production through iron-mediated Cdkal1-catalyzed tRNA modification. 2020 , 11, 296	28
375	The Effect Sizes of rs1801282 rs9939609, and rs2229616 Variants on Type 2 Diabetes Mellitus Risk among the Western Saudi Population: A Cross-Sectional Prospective Study. 2020 , 11,	7
374	Using Crystal Structures of Drug-Metabolizing Enzymes in Mechanism-Based Modeling for Drug Design. 2020 , 567-585	
373	Hierarchical inference for genome-wide association studies: a view on methodology with software. 2020 , 35, 1-40	5
372	E2f8 and Dlg2 genes have independent effects on impaired insulin secretion associated with hyperglycaemia. 2020 , 63, 1333-1348	5
371	FTO Demethylates Cyclin D1 mRNA and Controls Cell-Cycle Progression. 2020 , 31, 107464	16
370	Diabetes and Genetics: A Relationship Between Genetic Risk Alleles, Clinical Phenotypes and Therapeutic Approaches. 2021 , 1307, 457-498	6
369	and are Associated with Type 2 Diabetes Mellitus in Iranian Patients. 2020 , 13, 897-906	14
368	Obesity-induced overexpression of miR-802 impairs insulin transcription and secretion. 2020 , 11, 1822	18
367	Multi-substrate selectivity based on key loops and non-homologous domains: new insight into ALKBH family. 2021 , 78, 129-141	21

366	Adeno-Associated Virus-Mediated Knockdown of SLC16A11 Improves Glucose Tolerance and Hepatic Insulin Signaling in High Fat Diet-Fed Mice. 2021 , 129, 104-111	2
365	Genetic risk score constructed from common genetic variants is associated with cardiovascular disease risk in type 2 diabetes mellitus. 2021 , 23, e3305	2
364	SIRT1 functional polymorphisms (rs12778366, rs3758391) as genetic biomarkers of susceptibility to type 2 diabetes mellitus in Iranians: a case-control study and computational analysis. 2021 , 41, 447-455	0
363	Common Variants Associated to Type 2 Diabetes in the Italian Population. 2021 , 11, 24-42	1
362	Combining twin-family designs with measured genetic variants to study the causes of epigenetic variation. 2021 , 239-259	
361	Critical roles of FTO-mediated mRNA m6A demethylation in regulating adipogenesis and lipid metabolism: Implications in lipid metabolic disorders.. 2022 , 9, 51-61	6
360	Long non-coding RNA-regulated pathways in pancreatic β cells: Their role in diabetes. 2021 , 359, 325-355	1
359	Diabetes Mellitus. 2021 , 814-883	1
358	RNA Modification by mA Methylation in Cardiovascular Disease. 2021 , 2021, 8813909	3
357	An Improved Genome-Wide Polygenic Score Model for Predicting the Risk of Type 2 Diabetes. 2021 , 12, 632385	5
356	Loss of 9p21 Regulatory Hub Promotes Kidney Cancer Progression by Upregulating HOXB13. 2021 , 19, 979-990	2
355	Is type 2 diabetes an adiposity-based metabolic disease? From the origin of insulin resistance to the concept of dysfunctional adipose tissue. 2021 , 26, 2429-2441	7
354	Analysis of coding variants in the human FTO gene from the ExAC (gnomAD) Database.	
353	HICANCER: accurate and complete cancer genome phasing with Hi-C reads. 2021 , 11, 6609	
352	The type 2 diabetes mellitus susceptibility gene CDKAL1 polymorphism is associated with depressive symptom in first-episode drug-naive schizophrenic patients. 2021 , 36, e2790	0
351	Genetics of Cardiovascular Disease: How Far Are We from Personalized CVD Risk Prediction and Management?. 2021 , 22,	2
350	Genetic architecture of type 2 diabetes and its shared genetic component with low birth weight in African Americans. 2021 , 24, 326-332	1
349	Diabetes and Renin-Angiotensin-Aldosterone System: Pathophysiology and Genetics.	

348	Role of the gut microbiota in type 2 diabetes and related diseases. 2021 , 117, 154712	32
347	FTO regulates myoblast proliferation by controlling CCND1 expression in an m ⁶ A-YTHDF2-dependent manner. 2021 , 401, 112524	5
346	RNA-Binding Proteins Hold Key Roles in Function, Dysfunction, and Disease. 2021 , 10,	4
345	Progress in Defining the Genetic Contribution to Type 2 Diabetes in Individuals of East Asian Ancestry. 2021 , 21, 17	2
344	Kidney Disease in Diabetic Patients: From Pathophysiology to Pharmacological Aspects with a Focus on Therapeutic Inertia. 2021 , 22,	7
343	Pancreatic β -cell-selective zinc transporter 8 insufficiency accelerates diabetes associated with islet amyloidosis. 2021 , 6,	3
342	Investigative genetic genealogy: Current methods, knowledge and practice. 2021 , 52, 102474	16
341	Correlations between FTO Gene Polymorphisms and TSH Level in Uyghur Chinese Patients with Type 2 Diabetes. 2021 , 2021, 6646750	
340	Insulin-like Growth Factor 2 mRNA-Binding Protein 2-a Potential Link Between Type 2 Diabetes Mellitus and Cancer. 2021 , 106, 2807-2818	5
339	Prognostic SLC family genes promote cell proliferation, migration, and invasion in hepatocellular carcinoma. 2021 , 53, 1065-1075	6
338	Impact of family history of diabetes on blood glucose, lipid levels and perinatal outcomes in pregnant women with gestational diabetes mellitus. 2021 , 50, 329-334	1
337	RNA m ⁶ A reader IMP2/IGF2BP2 promotes pancreatic β -cell proliferation and insulin secretion by enhancing PDX1 expression. 2021 , 48, 101209	9
336	Novel Reclassification of Adult Diabetes Is Useful to Distinguish Stages of β -Cell Function Linked to the Risk of Vascular Complications: The DOLCE Study From Northern Ukraine. 2021 , 12, 637945	2
335	Epigenetic regulation of energy metabolism in obesity. 2021 , 13, 480-499	6
334	An imputed whole-genome sequence-based GWAS approach pinpoints causal mutations for complex traits in a specific swine population. 2021 , 1	0
333	Multi-omics profiling: the way towards precision medicine in metabolic diseases. 2021 ,	4
332	The detection and functions of RNA modification m ⁶ A based on m ⁶ A writers and erasers. 2021 , 297, 100973	9
331	Genome-wide association studies. 2021 , 1,	50

330	Genetics of Type 2 Diabetes: Opportunities for Precision Medicine: JACC Focus Seminar. 2021 , 78, 496-512	2
329	The haplotype of the gene is associated with primary open-angle glaucoma and pseudoexfoliation glaucoma in the Caucasian population of Central Russia. 2021 , 42, 698-705	2
328	What the Jackson Heart Study Has Taught Us About Diabetes and Cardiovascular Disease in the African American Community: a 20-year Appreciation. 2021 , 21, 39	0
327	Anticipation of Precision Diabetes and Promise of Integrative Multi-Omics. 2021 , 50, 559-574	
326	Role of FOXP3 gene polymorphisms (SNPs rs3761547, rs3761549, and rs2232365) in the development of Type 2 diabetes mellitus. 2021 , 24, 101253	1
325	Non-Coding RNA as Biomarkers for Type 2 Diabetes Development and Clinical Management. 2021 , 12, 630032	5
324	Adaptive function-on-scalar regression with a smoothing elastic net. 2021 , 185, 104765	1
323	The role of long non-coding RNAs in the regulation of pancreatic beta cell identity. 2021 , 49, 2153-2161	1
322	Association of polymorphic loci of susceptibility to diabetes mellitus type 2 in various ethnic groups of the Russian Federation. 2021 , 24, 262-272	0
321	IGF-2 mRNA binding protein 2 regulates primordial germ cell development in zebrafish. 2021 , 313, 113875	0
320	Zinc transporters and their functional integration in mammalian cells. 2021 , 296, 100320	33
319	Senotherapeutics: Experimental therapy of cellular senescence. 2021 , 251-284	
318	Association of type 2 diabetes mellitus and periodontal disease susceptibility with genome-wide association-identified risk variants in a Southeastern Brazilian population. 2021 , 25, 3873-3892	4
317	Assessment of immune-alternations and their correlations with therapeutic outcomes of transplantation of autologous Mesenchymal and Allogenic fetal stem cells in patients with type 1 diabetes: a study protocol. 2021 , 20, 1067-1073	
316	Redefining Disease and Pharmaceutical Targets Through Molecular Definitions and Personalized Medicine. 1	0
315	The Main Events in the History of Diabetes Mellitus. 2010 , 3-16	16
314	Paraneoplastic Syndromes in Pancreatic Cancer. 2010 , 651-673	1
313	Pharmacogenomics of endocrine therapy in breast cancer. 2008 , 630, 220-31	14

312	Genomic Risk Information for Common Health Conditions: Maximizing Kinship-Based Health Promotion. 2010 , 407-433	5
311	Family Influences on Children's Well-Being: Potential Roles of Molecular Genetics and Epigenetics. 2011 , 181-204	1
310	Basic molecular techniques for the detection of single nucleotide polymorphisms: genome-wide applications in search for endocrine tumor related genes. 2009 , 590, 143-63	2
309	Genome-wide association studies. 2011 , 713, 89-103	3
308	The Main Events in the History of Diabetes Mellitus. 2017 , 3-19	1
307	The Genetics of Anxiety Disorders. 2009 , 165-185	2
306	What Do We Learn from Network-Based Analysis of Genome-Wide Association Data?. 2014 , 865-876	2
305	The genetic basis of bipolar disorder. 2009 , 59-76	2
304	Regulation of pRB and p53 Pathways by the Long Noncoding RNAs ANRIL, lincRNA-p21, lincRNA-RoR, and PANDA. 2015 , 175-189	1
303	Cytotoxic Mechanisms of Islet Amyloid Polypeptide in the Pathogenesis of Type-2 Diabetes Mellitus (T2DM). 2012 , 217-255	1
302	Wnt Signaling in Pancreatic Islets. 2014 , 1-31	1
301	Bioinformatics, Genomics and Diabetes. 2016 , 1-18	0
300	Genome-Wide Association Study for Type 2 Diabetes. 2019 , 49-86	1
299	Epigenetic Basis of Oxidative Stress in Diabetic Coronary Atherosclerosis: A Shift in Focus from Genetic Prerogative. 2019 , 419-455	1
298	Epigenetic processes and DNA repair in embryonic stem cells. 2020 , 1-23	0
297	Type 2 Diabetes Mellitus. 2010 , 765-787	2
296	Sleep-related breathing disorders. 279-301	1
295	The association of TNF- β 308G/A and -238G/A polymorphisms with type 2 diabetes mellitus: a meta-analysis. 2019 , 39,	3

294	Genetic Predictors of Obesity. 2008 , 437-460	4
293	The disruption of trace element homeostasis due to aneuploidy as a unifying theme in the etiology of cancer.	2
292	Ancestry-specific association mapping in admixed populations.	5
291	Identifying tissues implicated in Anorexia Nervosa using Transcriptomic Imputation.	1
290	Sequencing and Imputation in GWAS: Cost-Effective Strategies to Increase Power and Genomic Coverage Across Diverse Populations.	2
289	Improving imputation quality in BEAGLE for crop and livestock data.	2
288	A resource-efficient tool for mixed model association analysis of large-scale data.	10
287	Efficient approaches for large scale GWAS studies with genotype uncertainty.	1
286	Parental lifespan and the likelihood of reaching the age of 90 years in the Netherlands Cohort Study. 2021 , 21, 215-221	1
285	Genetics Insights in the Relationship Between Type 2 Diabetes and Coronary Heart Disease. 2020 , 126, 1526-1548	22
284	Claudin-2 deficiency associates with hypercalciuria in mice and human kidney stone disease. 2020 , 130, 1948-1960	26
283	Mechanisms by which common variants in the TCF7L2 gene increase risk of type 2 diabetes. 2007 , 117, 2155-63	574
282	Genetic and epigenetic factors are associated with expression of respiratory chain component NDUFB6 in human skeletal muscle. 2007 , 117, 3427-35	146
281	Prime suspect: the TCF7L2 gene and type 2 diabetes risk. 2007 , 117, 2077-9	37
280	Cholesterol in islet dysfunction and type 2 diabetes. 2008 , 118, 403-8	105
279	Variations in the G6PC2/ABCB11 genomic region are associated with fasting glucose levels. 2008 , 118, 2620-8	127
278	Correlation of rare coding variants in the gene encoding human glucokinase regulatory protein with phenotypic, cellular, and kinetic outcomes. 2012 , 122, 205-17	31
277	Deficit of tRNA(Lys) modification by Cdkal1 causes the development of type 2 diabetes in mice. 2011 , 121, 3598-608	173

276	The role of aging upon β cell turnover. 2013 , 123, 990-5	114
275	iPSC-derived β cells model diabetes due to glucokinase deficiency. 2013 , 123, 3146-53	77
274	Distinct but complementary contributions of PPAR isotypes to energy homeostasis. 2017 , 127, 1202-1214	174
273	The Regulatory and Signaling Functions of Zinc Ions in Human Cellular Physiology. 2010 , 181-212	3
272	Heritable Variation in Fat Preference. 2009 , 395-415	1
271	Gene Polymorphism Association with Type 2 Diabetes and Related Gene-Gene and Gene-Environment Interactions in a Uyghur Population. 2016 , 22, 474-87	13
270	On quality control measures in genome-wide association studies: a test to assess the genotyping quality of individual probands in family-based association studies and an application to the HapMap data. 2009 , 5, e1000572	6
269	Expression Quantitative Trait Locus Mapping Studies in Mid-secretory Phase Endometrial Cells Identifies HLA-F and TAP2 as Fecundability-Associated Genes. 2016 , 12, e1005858	23
268	HHEX_23 AA Genotype Exacerbates Effect of Diabetes on Dementia and Alzheimer Disease: A Population-Based Longitudinal Study. 2015 , 12, e1001853	6
267	Polymorphisms within novel risk loci for type 2 diabetes determine beta-cell function. 2007 , 2, e832	127
266	Polymorphisms within the novel type 2 diabetes risk locus MTNR1B determine beta-cell function. 2008 , 3, e3962	93
265	Is replication the gold standard for validating genome-wide association findings?. 2008 , 3, e4037	38
264	Low frequency variants in the exons only encoding isoform A of HNF1A do not contribute to susceptibility to type 2 diabetes. 2009 , 4, e6615	4
263	Variant near ADAMTS9 known to associate with type 2 diabetes is related to insulin resistance in offspring of type 2 diabetes patients--EUGENE2 study. 2009 , 4, e7236	43
262	The dopamine transporter gene, a spectrum of most common risky behaviors, and the legal status of the behaviors. 2010 , 5, e9352	40
261	Type 2 diabetes susceptibility gene expression in normal or diabetic sorted human alpha and beta cells: correlations with age or BMI of islet donors. 2010 , 5, e11053	39
260	Case-control analysis of SNPs in GLUT4, RBP4 and STRA6: association of SNPs in STRA6 with type 2 diabetes in a South Indian population. 2010 , 5, e11444	41
259	A genome-wide association study of the metabolic syndrome in Indian Asian men. 2010 , 5, e11961	94

258	Deletion of CDKAL1 affects mitochondrial ATP generation and first-phase insulin exocytosis. 2010 , 5, e15553	57
257	Short telomeres compromise β -cell signaling and survival. 2011 , 6, e17858	64
256	Novel susceptibility locus at 22q11 for diabetic nephropathy in type 1 diabetes. 2011 , 6, e24053	8
255	Genomewide analysis of inherited variation associated with phosphorylation of PI3K/AKT/mTOR signaling proteins. 2011 , 6, e24873	7
254	The role of inflammatory pathway genetic variation on maternal metabolic phenotypes during pregnancy. 2012 , 7, e32958	19
253	Two isoforms of the mRNA binding protein IGF2BP2 are generated by alternative translational initiation. 2012 , 7, e33140	14
252	Common variants in CDKN2B-AS1 associated with optic-nerve vulnerability of glaucoma identified by genome-wide association studies in Japanese. 2012 , 7, e33389	69
251	Amerind ancestry, socioeconomic status and the genetics of type 2 diabetes in a Colombian population. 2012 , 7, e33570	40
250	European American stratification in ovarian cancer case control data: the utility of genome-wide data for inferring ancestry. 2012 , 7, e35235	3
249	A replication study of GWAS-derived lipid genes in Asian Indians: the chromosomal region 11q23.3 harbors loci contributing to triglycerides. 2012 , 7, e37056	56
248	The physiological effects of deleting the mouse SLC30A8 gene encoding zinc transporter-8 are influenced by gender and genetic background. 2012 , 7, e40972	55
247	Improved minimum cost and maximum power two stage genome-wide association study designs. 2012 , 7, e42367	5
246	Technical reproducibility of genotyping SNP arrays used in genome-wide association studies. 2012 , 7, e44483	46
245	A single nucleotide polymorphism within DUSP9 is associated with susceptibility to type 2 diabetes in a Japanese population. 2012 , 7, e46263	27
244	Deletion of CDKAL1 affects high-fat diet-induced fat accumulation and glucose-stimulated insulin secretion in mice, indicating relevance to diabetes. 2012 , 7, e49055	22
243	Hematopoietically-expressed homeobox gene three widely-evaluated polymorphisms and risk for diabetes: a meta-analysis. 2012 , 7, e49917	13
242	Rs4074134 near BDNF gene is associated with type 2 diabetes mellitus in Chinese Han population independently of body mass index. 2013 , 8, e56898	16
241	Replication of type 2 diabetes candidate genes variations in three geographically unrelated Indian population groups. 2013 , 8, e58881	23

240	Identification of a functional variant in the MICA promoter which regulates MICA expression and increases HCV-related hepatocellular carcinoma risk. 2013 , 8, e61279	47
239	Mutations in Mll2, an H3K4 methyltransferase, result in insulin resistance and impaired glucose tolerance in mice. 2013 , 8, e61870	31
238	RNAi screening in primary human hepatocytes of genes implicated in genome-wide association studies for roles in type 2 diabetes identifies roles for CAMK1D and CDKAL1, among others, in hepatic glucose regulation. 2013 , 8, e64946	15
237	Polymorphism of 9p21.3 locus is associated with 5-year survival in high-risk patients with myocardial infarction. 2013 , 8, e72333	6
236	Ocular expression and distribution of products of the POAG-associated chromosome 9p21 gene region. 2013 , 8, e75067	10
235	Use of net reclassification improvement (NRI) method confirms the utility of combined genetic risk score to predict type 2 diabetes. 2013 , 8, e83093	29
234	Genomic data and disease forecasting: application to type 2 diabetes (T2D). 2014 , 9, e85684	2
233	Joint effects of known type 2 diabetes susceptibility loci in genome-wide association study of Singapore Chinese: the Singapore Chinese health study. 2014 , 9, e87762	14
232	Genome-wide identification of expression quantitative trait loci (eQTLs) in human heart. 2014 , 9, e97380	35
231	Population specific impact of genetic variants in KCNJ11 gene to type 2 diabetes: a case-control and meta-analysis study. 2014 , 9, e107021	25
230	Genome-wide association study for wool production traits in a Chinese Merino sheep population. 2014 , 9, e107101	47
229	Do variants associated with susceptibility to pancreatic cancer and type 2 diabetes reciprocally affect risk?. 2015 , 10, e0117230	13
228	Zip4 mediated zinc influx stimulates insulin secretion in pancreatic beta cells. 2015 , 10, e0119136	23
227	Can data science inform environmental justice and community risk screening for type 2 diabetes?. 2015 , 10, e0121855	3
226	Replication Study in a Japanese Population to Evaluate the Association between 10 SNP Loci, Identified in European Genome-Wide Association Studies, and Type 2 Diabetes. 2015 , 10, e0126363	9
225	Comparative Genome of GK and Wistar Rats Reveals Genetic Basis of Type 2 Diabetes. 2015 , 10, e0141859	11
224	The Association of Type 2 Diabetes Loci Identified in Genome-Wide Association Studies with Metabolic Syndrome and Its Components in a Chinese Population with Type 2 Diabetes. 2015 , 10, e0143607	33
223	Association between the rs7903146 Polymorphism in the TCF7L2 Gene and Parameters Derived with Continuous Glucose Monitoring in Individuals without Diabetes. 2016 , 11, e0149992	8

222	Replication Study in a Japanese Population of Six Susceptibility Loci for Type 2 Diabetes Originally Identified by a Transethnic Meta-Analysis of Genome-Wide Association Studies. 2016 , 11, e0154093	8
221	Replication and Relevance of Multiple Susceptibility Loci Discovered from Genome Wide Association Studies for Type 2 Diabetes in an Indian Population. 2016 , 11, e0157364	18
220	Extending the use of GWAS data by combining data from different genetic platforms. 2017 , 12, e0172082	4
219	Common and rare exonic MUC5B variants associated with type 2 diabetes in Han Chinese. 2017 , 12, e0173784	5
218	Evaluating the glucose raising effect of established loci via a genetic risk score. 2017 , 12, e0186669	5
217	Genetic framework of type 2 diabetes mellitus. 2013 , 16, 11-16	4
216	The role of melatonin in development of gestational diabetes mellitus. 2018 , 67, 85-91	8
215	Polymorphisms associated with type 2 diabetes in familial longevity: The Leiden Longevity Study. 2011 , 3, 55-62	17
214	Screening of a kinase library reveals novel pro-senescence kinases and their common NF- κ B-dependent transcriptional program. 2015 , 7, 986-1003	26
213	A common variant within the HNF1B gene is associated with overall survival of multiple myeloma patients: results from the IMMEnSE consortium and meta-analysis. 2016 , 7, 59029-59048	14
212	Functional single nucleotide polymorphisms within the cyclin-dependent kinase inhibitor 2A/2B region affect pancreatic cancer risk. 2016 , 7, 57011-57020	27
211	Impact of diabetes-related gene polymorphisms on the clinical characteristics of type 2 diabetes Chinese Han population. 2016 , 7, 85464-85471	10
210	PPARGC1A rs3736265 G>A polymorphism is associated with decreased risk of type 2 diabetes mellitus and fasting plasma glucose level. 2017 , 8, 37308-37320	13
209	Mitochondrial DNA variants in the pathogenesis of type 2 diabetes - relevance of asian population studies. 2009 , 6, 237-46	18
208	Zinc and zinc transporter regulation in pancreatic islets and the potential role of zinc in islet transplantation. 2010 , 7, 263-74	25
207	Association between genetics of diabetes, coronary artery disease, and macrovascular complications: exploring a common ground hypothesis. 2011 , 8, 230-44	21
206	Beyond the Protein-Coding Sequence: Noncoding RNAs in the Pathogenesis of Type 2 Diabetes. 2015 , 12, 260-76	7
205	Complex Genetics of Type 2 Diabetes and Effect Size: What have We Learned from Isolated Populations?. 2015 , 12, 299-319	11

204	Understanding Genetic Heterogeneity in Type 2 Diabetes by Delineating Physiological Phenotypes: SIRT1 and its Gene Network in Impaired Insulin Secretion. 2016 , 13, 17-34	8
203	The Link between Parental and Offspring Longevity.	0
202	Association of PPARG Gene Polymorphisms Pro12Ala with Type 2 Diabetes Mellitus: A Meta-analysis. 2019 , 15, 277-283	5
201	The Pathway Less Traveled: Moving from Candidate Genes to Candidate Pathways in the Analysis of Genome-Wide Data from Large Scale Pharmacogenetic Association Studies. 2008 , 6, 150-159	36
200	Exclusion of polymorphisms in carnosinase genes (CNDP1 and CNDP2) as a cause of diabetic nephropathy in type 1 diabetes: results of large case-control and follow-up studies. 2008 , 57, 2547-51	29
199	Association of FTO Gene Variant (rs8050136) with Type 2 Diabetes and Markers of Obesity, Glycaemic Control and Inflammation. 2019 , 38, 153-163	18
198	Genomewide Association Studies. 2008 , 225-238	3
197	Nature and nurture in neuropsychiatric genetics: where do we stand?. 2010 , 12, 7-23	35
196	Variation in CDKAL1 gene is associated with therapeutic response to sulphonylureas. 2012 , 61, 177-83	14
195	Fat mass and obesity associated gene variants are associated with increased growth hormone levels and affect glucose and lipid metabolism in lean women. 2015 , 64, S177-85	2
194	Strong gender-specific additive effects of the NYD-SP18 and FTO variants on BMI values. 2015 , 64, S419-26	7
193	Common genetic variants shared among five major psychiatric disorders: a large-scale genome-wide combined analysis. 2019 , 21-30	6
192	[Current status of genome-wide association study]. 2011 , 33, 25-35	2
191	Association of single-nucleotide polymorphisms on chromosome 1p13 and 9p21 with acute myocardial infarction in a Chinese population: the AMI study in China. 2011 , 31, 822-829	4
190	Association of CDKAL1, CDKN2A/B & HHEX gene polymorphisms with type 2 diabetes mellitus in the population of Hyderabad, India. 2016 , 143, 455-63	18
189	Significance of a common variant in the CDKAL1 gene with susceptibility to type 2 diabetes mellitus in Iranian population. 2015 , 4, 45	14
188	Pharmacogenomics of Sulphonylureas Response in Relation to rs7754840 Polymorphisms in Cyclin-Dependent Kinase 5 Regulatory Subunit-associated Protein 1-like (CDKAL1) Gene in Iranian Type 2 Diabetes Patients. 2018 , 7, 96	4
187	Association of gene variants with susceptibility to type 2 diabetes among Omanis. 2015 , 6, 358-66	31

186	False-Negative-Rate Based Approach for Selecting Top Single-Nucleotide Polymorphisms in the First Stage of a Two-Stage Genome-Wide Association Study. 2011 , 4, 359-371	1
185	Bone fragility in type 2 diabetes mellitus. 2010 , 1, 3-9	18
184	Pathway Analysis of Metabolic Syndrome Using a Genome-Wide Association Study of Korea Associated Resource (KARE) Cohorts. 2014 , 12, 195-202	8
183	Risk Prediction Using Genome-Wide Association Studies on Type 2 Diabetes. 2016 , 14, 138-148	9
182	Cryo-EM structures of human ZnT8 in both outward- and inward-facing conformations. 2020 , 9,	17
181	Epigenetics and the International Classification of Functioning, Disability and Health Model: Bridging Nature, Nurture, and Patient-Centered Population Health. 2021 ,	1
180	Genetics and Clinical Characteristics of PPAR γ Variant-Induced Diabetes in a Chinese Han Population. 2021 , 12, 677130	1
179	Meta-Analysis of Joint Test of SNP and SNP-Environment Interaction with Heterogeneity. 2021 , 1-9	0
178	Neuron-Specific IMP2 Overexpression by Synapsin Promoter-Driven AAV9: A Tool to Study Its Role in Axon Regeneration. 2021 , 10,	
177	Ocular expression of cyclin-dependent kinase 5 in patients with proliferative diabetic retinopathy. 2021 ,	0
176	The Genetics of Diabetes: What We Can Learn from. 2021 , 22,	1
175	Pharmacogenomic Applications in Children. 2008 , 447-477	
174	p16INK4a and Stem Cell Ageing: A Telomere-Independent Process?. 2008 , 181-202	
173	Cyclin-Dependent Kinase 5 and Insulin Secretion. 2008 , 145-158	
172	Reporting and Interpreting Results. 2008 , 275-292	
171	Diabetes. 2009 , 1187-1193	
170	Genome-Wide Association Studies and Genotyping Technologies. 2009 , 101-107	
169	No Association of Obesity and Type 2 Diabetes Mellitus Related Genetic Variants With Colon Cancer. 2009 , 2, 311-316	

168 High-Density Lipoprotein Mutations. **2009**, 85-92

1

167 Encyclopedia of Complexity and Systems Science. **2009**, 3964-3985

166 Genetic Dyslipidemia. **2009**, 71-84

165 The Genetic Basis of Diabetes. **2009**, 377-413

164 Inter-Species Comparative Sequence Analysis: A Tool for Genomic Medicine. **2009**, 120-130

163 Genomics of Myocardial Infarction. **2009**, 665-679

162 Lipoprotein Disorders. **2009**, 634-651

161 Molecular Genetics of Susceptibility to Coronary Heart Disease.

160 Genetics of Type 2 Diabetes: From Candidate Genes to Genome-Wide Association Analysis. **2010**, 147-163

159 Genetics of Obesity and Diabetes. **2010**, 499-521

0

158 Role of Jun dimerization protein 2 (JDP2) in cellular senescence. **2010**, 30, 507-519

157 Functional Genomics and Proteomics in Allergy Research. **2010**, 1-18

156 Genetic Loci Influencing Plasma High Density Lipoprotein Cholesterol Concentrations in Humans. **2010**, 111-120

155 Genetics of Gestational Diabetes Mellitus and Type 2 Diabetes. **2010**, 181-193

154 12 Lichaamsmetabolisme. **2010**, 415-458

153 Polygenic Obesity. **2010**, 65-73

1

152 Molecular Genetics of Myocardial Infarction.

151 Deciphering Cardiovascular Genomics and How They Apply to Cardiovascular Disease Prevention. **2011**, 125-136

- 150 Genetics of (Premature) Coronary Artery Disease. **2011**, 369-383
- 149 Public Health Genomics of Type 1 Diabetes, Type 2 Diabetes, and Diabetic Complications. **2010**, 665-686
- 148 The Winner's Curse.
- 147 Genetic Studies of Schizophrenia. **2011**, 333-380
- 146 Genome-wide association studies: Where we are heading?. **2011**, 1, 23 0
- 145 Pharmacogenomics. **2011**, 81-93
- 144 Interaction Between Exercise and Genetics in Type 2 Diabetes Mellitus: An Epidemiological Perspective. **2011**, 73-100
- 143 Molecular genetics of atherosclerosis and acute coronary syndromes. **2011**, 35-43
- 142 DNA Variations, Impaired Insulin Secretion and Type 2 Diabetes. **2011**, 275-297
- 141 Association of KCNJ11 with impaired glucose regulation in essential hypertension. **2011**, 10, 1111-9 2
- 140 Biomarkers and obstructive sleep apnea. **2011**, 216-235
- 139 Pharmacogenomics and Organ Transplantation. 133-145
- 138 [Advances of genetics in diabetic nephropathy]. **2012**, 34, 1537-44 1
- 137 Biweight Midcorrelation-Based Gene Differential Coexpression Analysis and Its Application to Type II Diabetes. **2013**, 81-87
- 136 Genetics of Childhood Obesity. **2013**, 1-21
- 135 Acne and Genetics. **2014**, 109-130 1
- 134 Zinc and Its Role in the Pathogenesis of Type 2 Diabetes. **2014**, 269-283
- 133 Vascular Complications of Diabetes Mellitus. **2014**, 1-65

- 132 Genetic variants at 10q23.33 are associated with plasma lipid levels in a Chinese population. **2014**, 28, 53-8 3
- 131 Genetic Epidemiology of Atherosclerotic Vascular Disease. **2014**, 1-24
- 130 Obesity research: Status quo and future outlooks. **2014**, 3, 119
- 129 Wnt Signaling in Pancreatic Islets. **2015**, 707-741 1
- 128 Adjusting sampling bias in case-control genetic association studies. **2014**, 25, 1127-1135
- 127 Concern for Pharmacogenomics and Autologous Cell Therapy: Can This Be a Direction Toward Medicine for the Future?. **2015**, 267-272
- 126 Linkage Mapping: Localizing the Genes That Shape Human Variation. **2015**, 33-52
- 125 Mapping of Susceptibility Genes for Obesity, Type 2 Diabetes, and the Metabolic Syndrome in Human Populations. **2015**, 181-245
- 124 Lichaamsmetabolisme. **2015**, 403-445
- 123 Periodontal Disease. **2015**, 145-166
- 122 Genetic Epidemiology of Atherosclerotic Vascular Disease. **2015**, 1517-1539
- 121 The Main Events in the History of Diabetes Mellitus. **2015**, 1-17
- 120 Genetic Determinants of Type 2 Diabetes in Asians. **2015**, 2015, 6
- 119 Skim-Based Genotyping by Sequencing Using a Double Haploid Population to Call SNPs, Infer Gene Conversions, and Improve Genome Assemblies. **2016**, 1374, 285-92 1
- 118 Genetics of Type 2 Diabetes: From Candidate Genes to Genome-Wide Association Analysis. **2016**, 1-24
- 117 Identification of genetic variants affecting vitamin D receptor binding and associations with autoimmune disease.
- 116 Genetic and Genomic Approaches to Acute Lung Injury. **2017**, 133-159
- 115 Genetics of Type 2 Diabetes: From Candidate Genes to Genome-Wide Association Analysis. **2017**, 1-24

- 114 Epigenetics of Diabetic Nephropathy. **2017**, 1-20
- 113 Genetics of Type 2 Diabetes: From Candidate Genes to Genome-Wide Association Analysis. **2017**, 191-214
- 112 Improved Score Statistics for Meta-analysis in Single-variant and Gene-level Association Studies.
- 111 Myeloid-Derived Suppressor Cells in Aged Humans. **2018**, 1-12
- 110 Paraneoplastic Syndromes in Pancreatic Cancer. **2018**, 1-25
- 109 The effects of an acute exercise bout on GH and IGF-1 in prediabetic and healthy African Americans: A pilot study investigating gene expression. **2018**, 13, e0191331 0
- 108 Genetics of Diabetes and Diabetic Complications. **2018**, 81-139 1
- 107 The association between the chromosome 9p21 CDKN2B-AS1 gene variants and the lipid metabolism: A pre-diagnostic biomarker for coronary artery disease. **2019**, 21, 31-38 7
- 106 Foraging theory and the propensity to be obese: an alternative to thrift. 0
- 105 Large-Scale Genome-Wide Meta Analysis of Polycystic Ovary Syndrome Suggests Shared Genetic Architecture for Different Diagnosis Criteria.
- 104 Subset-Based Analysis using Gene-Environment Interactions for Discovery of Genetic Associations across Multiple Studies or Phenotypes. 0
- 103 Robust Reference Powered Association Test of genome-wide association studies.
- 102 Role of Zinc Transporters in Type 2 Diabetes and Obesity. **2019**, 229-242
- 101 Lichaamsmetabolisme. **2019**, 417-458
- 100 Myeloid-Derived Suppressor Cells in Aged Humans. **2019**, 733-744
- 99 Long Noncoding RNAs in Cardiovascular Disease. **2019**, 199-288 0
- 98 An Understanding of Diabetes Mellitus Associated Complications, Treatment Modalities and Management Strategies. **2019**, 16, 195-209 0
- 97 Impact of type 2 diabetes variants identified through genome-wide association studies in early-onset type 2 diabetes from South Indian population. **2020**, 18, e27 2

96	CTNNA3 genetic polymorphism may be a new genetic signal of type 2 diabetes in the Chinese Han population: a case control study. 2021 , 14, 257	0
95	Whole-exome analysis in Tunisian Imazighen and Arabs shows the impact of demography in functional variation. 2021 , 11, 21125	1
94	Recovering high-quality host genomes from gut metagenomic data through genotype imputation.	
93	Sex, Age and Gene Interactions in Cardiometabolic Diseases. 2020 , 179-190	
92	Bivariate traits association analysis using generalized estimating equations in family data. 2020 , 19,	1
91	An adipocyte-specific lncRAP2 Δ gf2bp2 complex enhances adipogenesis and energy expenditure by stabilizing target mRNAs.	
90	Adult nontwin sib concordance rates for type 2 diabetes, hypertension and metabolic syndrome among Asian Indians: the Indian Atherosclerosis Research Study. 2007 , 3, 1063-8	4
89	Genome-wide association studies: progress in identifying genetic biomarkers in common, complex diseases. 2007 , 2, 283-92	12
88	Genomic approaches to coronary artery disease. 2010 , 132, 567-78	16
87	Biomolecular Systems of Disease Buried Across Multiple GWAS Unveiled by Information Theory and Ontology. 2010 , 2010, 31-5	5
86	Whole genome association analysis shows that ACE is a risk factor for Alzheimer's disease and fails to replicate most candidates from Meta-analysis. 2010 , 1, 19-30	4
85	Mining the human phenome using semantic web technologies: a case study for Type 2 Diabetes. 2012 , 2012, 699-708	8
84	The association of Pro12Ala polymorphism in the peroxisome proliferator-activated receptor-gamma2 gene with the metabolic characteristics in Chinese women with polycystic ovary syndrome. 2013 , 6, 1894-902	9
83	Regulation of insulin synthesis and secretion and pancreatic Beta-cell dysfunction in diabetes. 2013 , 9, 25-53	174
82	Cumulative Effect of Common Genetic Variants Predicts Incident Type 2 Diabetes: A Study of 21,183 Subjects from Three Large Prospective Cohorts. 2011 , 1, 108	1
81	Association of Type 2 Diabetes Mellitus related SNP genotypes with altered serum adipokine levels and metabolic syndrome phenotypes. 2015 , 8, 4464-71	3
80	Gene-by-Environment Interactions in Pancreatic Cancer: Implications for Prevention. 2015 , 88, 115-26	9
79	Correlation between polymorphism of FTO gene and type 2 diabetes mellitus in Uygur people from northwest China. 2015 , 8, 9744-50	9

78	Part 1: The Human Gut Microbiome in Health and Disease. 2014 , 13, 17-22	93
77	Association of rs7754840 G/C polymorphisms in CDKAL1 with type 2 diabetes: a meta-analysis of 70141 subjects. 2015 , 8, 17392-405	9
76	Common Variations in Perilipin rs1052700 and FTO rs3751812 Gene Variants, and Risk for Obesity and Type-2 Diabetes. 2017 , 6, 80-87	3
75	Transcription factor 7-like 2 (TCF7L2): a culprit gene in Type 2 Diabetes Mellitus. 2021 , 24, 371-376	
74	Stem Cell-Derived β Cells: A Versatile Research Platform to Interrogate the Genetic Basis of β Cell Dysfunction.. 2022 , 23,	0
73	MRSF: A Meta-analysis Method Based on Random Sign Flip. 2021 ,	
72	Significance of the lncRNAs MALAT1 and ANRIL in occurrence and development of glaucoma.. 2022 , e24215	1
71	Skim-Based Genotyping by Sequencing Using a Double Haploid Population to Call SNPs, Infer Gene Conversions, and Improve Genome Assemblies.. 2022 , 2443, 405-413	
70	Analysis of coding variants in the human FTO gene from the gnomAD database.. 2022 , 17, e0248610	
69	CDKAL1 gene rs7756992 A/G and rs7754840 G/C polymorphisms are associated with gestational diabetes mellitus in a sample of Bangladeshi population: implication for future T2DM prophylaxis.. 2022 , 14, 18	0
68	Cis-regulation of antisense noncoding RNA at the JAZF1 locus in type 2 diabetes.. 2022 , e3407	0
67	Artificial intelligence perspective in the future of endocrine diseases. 1	2
66	Different Associations Between Variants and Type 2 Diabetes Mellitus Susceptibility: A Meta-analysis.. 2021 , 12, 783078	
65	An adipose lncRAP2-Igf2bp2 complex enhances adipogenesis and energy expenditure by stabilizing target mRNAs.. 2022 , 25, 103680	0
64	Novel diabetes gene discovery through comprehensive characterization and integrative analysis of longitudinal gene expression changes.. 2022 ,	0
63	Common variants in genes involved in islet amyloid polypeptide (IAPP) processing and the degradation pathway are associated with T2DM risk: A Chinese population study.. 2022 , 109235	0
62	Challenges and future directions for studying effects of host genetics on the gut microbiome.. 2022 , 54, 100-106	6
61	Impact of variants on type-2 diabetes risk genes identified through genomewide association studies in polycystic ovary syndrome: a case-control study. 2018 , 97, 1213-1223	1

- 60 Ramadan Diurnal Intermittent Fasting Is Associated With Attenuated FTO Gene Expression in Subjects With Overweight and Obesity: A Prospective Cohort Study.. **2021**, 8, 741811 ○
- 59 Prenatal exposure to phthalates and peripheral blood and buccal epithelial DNA methylation in infants: An epigenome-wide association study.. **2022**, 163, 107183 ○
- 58 Genetic risk factors associated with gestational diabetes in a multi-ethnic population.. **2021**, 16, e0261137 ○
- 57 PPARG genindeki Pro12Ala polimorfizmi, Türk populasyonunda insülin direnci ve tip 2 diyabet ile ilişkili değildir: Bir vaka-kontrol çalışması.. **2021**, 31, 339-343
- 56 Efficient approaches for large-scale GWAS with genotype uncertainty. **2021**, ○
- 55 Image_1.TIFF. **2019**,
- 54 Image_2.TIFF. **2019**,
- 53 Image_3.TIFF. **2019**,
- 52 Image_4.TIFF. **2019**,
- 51 Table_1.XLS. **2019**,
- 50 Table_2.XLS. **2019**,
- 49 Table_3.XLS. **2019**,
- 48 Table_4.xls. **2019**,
- 47 Table_5.xls. **2019**,
- 46 Table_6.xls. **2019**,
- 45 Table_1.DOCX. **2018**,
- 44 Table_2.DOCX. **2018**,
- 43 Table_3.DOCX. **2018**,

42	Glucose-Related Traits and Risk of Migraine: A Potential Mechanism and Treatment Consideration. 2022 , 13, 730	0
41	Studies on the fat mass and obesity-associated (FTO) gene and its impact on obesity-associated diseases. 2022 ,	0
40	Type 2 Diabetes-Related Variants Influence the Risk of Developing Prostate Cancer: A Population-Based Case-Control Study and Meta-Analysis. 2022 , 14, 2376	1
39	Identification of Candidate Genes Regulating Carcass Depth and Hind Leg Circumference in Simmental Beef Cattle Using Illumina Bovine Beadchip and Next-Generation Sequencing Analyses.. 2022 , 12,	1
38	A Brief Review on Deep Learning Applications in Genomic Studies. 2022 , 2,	0
37	The IGF2BP family of RNA binding proteins links epitranscriptomics to cancer. 2022 ,	0
36	Role of EPO and TCF7L2 Gene Polymorphism Contribution to the Occurrence of Diabetic Retinopathy. 2022 , 2022, 1-7	
35	Human Multi-omics Data Pre-processing for Predictive Purposes Using Machine Learning: A Case Study in Childhood Obesity. 2022 , 359-374	0
34	Inherited basis of visceral, abdominal subcutaneous and gluteofemoral fat depots. 2022 , 13,	0
33	The role of proton in a eukaryotic zinc transporter.	
32	Association of polymorphisms of genes SLC30A8 and MC4R with the prognosis of the development of type 2 diabetes mellitus. 2022 , 25, 215-225	
31	Genetics of Type 2 Diabetes: Past, Present, and Future. 2022 , 14, 3201	2
30	Association of SLC30A8 (rs13266634) and GLIS3 (rs7034200) gene variant in development of type 2 diabetes mellitus in Indian population: A case-control study. 2022 , 28, 101655	
29	Genetics of type 2 diabetes mellitus in Indian and Global Population: A Review. 2022 , 23,	0
28	Association between glycemic traits and primary open-angle glaucoma: A Mendelian randomization study in the Japanese population. 2022 ,	1
27	The comprehensive detection of miRNA and circRNA in the regulation of intramuscular and subcutaneous adipose tissue of Laiwu pig. 2022 , 12,	0
26	Insulin, Glucose, and the Metabolic Syndrome in Cardiovascular Behavioral Medicine. 2022 , 809-831	0
25	The Mechanism and Role of N6-methyladenosine (m6A) Modification in Atherosclerosis and Atherosclerotic Diseases. 2022 , 9, 367	0

24	FTO and Anthropometrics: The Role of Modifiable Factors. 2022 , 7, 90	1
23	Age-dependent topic modelling of comorbidities in UK Biobank identifies disease subtypes with differential genetic risk.	0
22	Smooth muscle cell FTO regulates contractile function.	0
21	Human T2D Associated Gene IMP2/IGF2BP2 Promotes the Commitment of Mesenchymal Stem Cells into Adipogenic Lineage.	1
20	An autoencoder-based deep learning method for genotype imputation. 5,	0
19	Advances in multi-omics study of biomarkers of glycolipid metabolism disorder. 2022 , 20, 5935-5951	0
18	Genetic Risk Factors and GeneLifestyle Interactions in Gestational Diabetes. 2022 , 14, 4799	2
17	Protective effects of black onion polysaccharide on liver and kidney injury in T2DM rats through the synergistic impact of hypolipidemic and antioxidant abilities. 2022 , 223, 378-390	0
16	Association of an intronic SNP rs9939609 in FTO gene with type 2 diabetes mellitus among Bangladeshi population: A casecontrol study combined with updated meta-analysis. 2023 , 35, 201133	0
15	Cryo-EM structure of a eukaryotic zinc transporter at a low pH suggests its Zn ²⁺ -releasing mechanism. 2023 , 215, 107926	0
14	Insight into genetic, biological, and environmental determinants of sexual-dimorphism in type 2 diabetes and glucose-related traits. 9,	0
13	Integrative analysis of blood cells DNA methylation, transcriptomics and genomics identifies novel epigenetic regulatory mechanisms of insulin resistance during puberty in children with obesity.	1
12	Risk Factors of Severe COVID-19: A Review of Host, Viral and Environmental Factors. 2023 , 15, 175	5
11	Integrating Common Risk Factors with Polygenic Scores Improves the Prediction of Type 2 Diabetes. 2023 , 24, 984	0
10	Progress in genetics of type 2 diabetes and diabetic complications.	0
9	Decoding type 2 diabetes mellitus genetic risk variants in Pakistani Pashtun ethnic population using the nascent whole exome sequencing and MassARRAY genotyping: A case-control association study. 2023 , 18, e0281070	1
8	Modeling SILAC Data to Assess Protein Turnover in a Cellular Model of Diabetic Nephropathy. 2023 , 24, 2811	0
7	GeneEnvironment interactions in the associations of PFAS exposure with insulin sensitivity and beta-cell function in a Faroese cohort followed from birth to adulthood. 2023 , 226, 115600	0

- 6 CDKAL1 Drives the Maintenance of Cancer Stem-Like Cells by Assembling the eIF4F Translation Initiation Complex. 2206542 ○
- 5 Genetic Variants of HNF4A, WFS1, DUSP9, FTO, and ZFAND6 Genes Are Associated with Prediabetes Susceptibility and Inflammatory Markers in the Saudi Arabian Population. **2023**, 14, 536 ○
- 4 Functionally Significant Variants in Genes Associated with Abdominal Obesity: A Review. **2023**, 13, 460 ○
- 3 Split-Transformer Impute (STI): Genotype Imputation Using a Transformer-Based Model. ○
- 2 Methyltransferase Inhibition Enables Tgf β Driven Induction of CDKN2A and B in Cancer Cells. **2023**, 43, 115-129 ○
- 1 Association of the CDKAL1 gene polymorphism with gestational diabetes mellitus in Chinese women. **2023**, 11, e003164 ○