Replication of genome-wide association signals in UK samples reveals risk loci for type 2 diabetes

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#	Paper	IF	Citations
1949	.		
1948	The status of genetic investigations of schizophrenia. 288-308		
1947	A search for variants associated with young-onset type 2 diabetes in American Indians in a 100K genotyping array. **2007**, 56, 3045-52		79
1946	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
1945	Identification of type 2 diabetes genes in Mexican Americans through genome-wide association studies. **2007**, 56, 3033-44		105
1944	Tyrosine hydroxylase: another piece of the genetics of hypertension puzzle. **2007**, 116, 970-2		2
1943	Genetics of the cardiometabolic syndrome: new insights and therapeutic implications. **2007**, 1, 37-47		12
1942	Genome-wide association study for Crohn's disease in the Quebec Founder Population identifies multiple validated disease loci. **2007**, 104, 14747-52		175
1941	Aryl hydrocarbon receptor nuclear translocator-like (BMAL1) is associated with susceptibility to hypertension and type 2 diabetes. **2007**, 104, 14412-7		284
1940	The Walter B. Cannon Physiology in Perspective Lecture, 2007. ATP-sensitive K+ channels and disease: from molecule to malady. **2007**, 293, E880-9		91
1939	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
1938	Functional effects of nonsynonymous polymorphisms in the human TRPV1 gene. **2007**, 293, F1865-76		46
1937	Power to detect risk alleles using genome-wide tag SNP panels. **2007**, 3, 1827-37		77
1936	Orchestration of glucose homeostasis: from a small acorn to the California oak. **2007**, 56, 1489-501		91
1935	Genomewide association analysis of coronary artery disease. **2007**, 357, 443-53		1608
1934	Genetics of late-onset Alzheimer's disease: progress and prospect. **2007**, 8, 1747-55		12
1933	Obesity. **2007**,		11

1932	The genomics gold rush. **2007**, 298, 218-21		59
1931	Genetics of cardiovascular diseases: from single mutations to the whole genome. **2007**, 116, 1714-24		78
1930	Psoriasis is associated with pleiotropic susceptibility loci identified in type II diabetes and Crohn disease. **2008**, 45, 114-6		104
1929	Genetic susceptibility to age-related macular degeneration: a paradigm for dissecting complex disease traits. *Human Molecular Genetics*, **2007**, 16 Spec No. 2, R174-82	5.6	146
1928	Genetic susceptibility to peripheral arterial disease: a dark corner in vascular biology. **2007**, 27, 2068-78		49
1927	Response to Comment on: Chang et al. (2007) Association Study of the Genetic Polymorphisms of the Transcription Factor 7-like 2 (TCF7L2) Gene and Type 2 Diabetes in the Chinese Population: Diabetes 56:2631 2637. **2007**, 56, e23-e23		5
1926	Problems with genome-wide association studies. *Science*, **2007**, 316, 1840-2	33.3	71
1925	Successful design and conduct of genome-wide association studies. *Human Molecular Genetics*, **2007**, 16 Spec No. 2, R220-5	5.6	61
1924	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
1923	Genome-wide association: which do you want first: the good news, the bad news, or the good news?. **2007**, 56, 2844-8		6
1922	Interpreting P values in pharmacogenetic studies: a call for process and perspective. **2007**, 25, 4513-5		33
1921	Point: genetic risk feedback for common disease time to test the waters. **2007**, 16, 1724-6		10
1920	Relevance of cost-effectiveness analysis to clinicians and policy makers. **2007**, 298, 221-4		79
1919	Turning the pump handle: evolving methods for integrating the evidence on gene-disease association. **2007**, 166, 863-6		22
1918	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
1917	Evaluation of genome-wide power of genetic association studies based on empirical data from the HapMap project. *Human Molecular Genetics*, **2007**, 16, 2494-505	5.6	25
1916	Generating new candidate genes for neonatal diabetes: functional and genetic studies of insulin secretion in type 2 diabetes. **2007**, 12, 75-85		1
1915	Genetic determinants of diabetes are similarly associated with other immune-mediated diseases. **2007**, 7, 468-74		19

1914	Monogenic disorders of the pancreatic β-cell: personalizing treatment for rare forms of diabetes and hypoglycemia. **2007**, 4, 247-259		3
1913	Genome-wide association scans for Type 2 diabetes: new insights into biology and therapy. **2007**, 28, 598-601		20
1912	Cellular senescence in cancer and aging. **2007**, 130, 223-33		1245
1911	Implementation of genetics to personalize medicine. **2007**, 4, 248-65		20
1910	Genome-wide association analysis identifies loci for type 2 diabetes and triglyceride levels. *Science*, **2007**, 316, 1331-6	33.3	2364
1909	Risk alleles for multiple sclerosis identified by a genomewide study. **2007**, 357, 851-62		1327
1908	Genetics and genomics in human lung transplantation. **2007**, 1, 271-8		1
1907	Prediction of individual genetic risk to disease from genome-wide association studies. **2007**, 17, 1520-8		436
1906	A genome-wide association study of type 2 diabetes in Finns detects multiple susceptibility variants. *Science*, **2007**, 316, 1341-5	33.3	2269
1905	Future use of genomics in coronary artery disease. **2007**, 50, 1933-40		49
1904	The replication of beta cells in normal physiology, in disease and for therapy. **2007**, 3, 758-68		210
1903	Heterogeneity in meta-analyses of genome-wide association investigations. *PLoS ONE*, **2007**, 2, e841	3.7	246
1902	[Anatomical and functional plasticity of pancreatic beta-cells and type 2 diabetes]. **2007**, 23, 885-94		5
1901	Genome-Wide Association Studies: Progress in Identifying Genetic Biomarkers in Common, Complex Diseases. **2007**, 2, 117727190700200		18
1900	The candidate genes TAF5L, TCF7, PDCD1, IL6 and ICAM1 cannot be excluded from having effects in type 1 diabetes. **2007**, 8, 71		37
1899	The Framingham Heart Study 100K SNP genome-wide association study resource: overview of 17 phenotype working group reports. **2007**, 8 Suppl 1, S1		152
1898	Genome-wide association study for subclinical atherosclerosis in major arterial territories in the NHLBI's Framingham Heart Study. **2007**, 8 Suppl 1, S4		110
1897	Genome miners rush to stake claims. **2007**, 447, 623		3

1896	Genomics: guilt by association. **2007**, 447, 645-6	34
1895	Replicating genotype-phenotype associations. **2007**, 447, 655-60	1363
1894	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. **2007**, 39, 1329-37	1130
1893	Guilt beyond a reasonable doubt. **2007**, 39, 813-5	130
1892	A common variant of HMGA2 is associated with adult and childhood height in the general population. **2007**, 39, 1245-50	330
1891	Population genomics of human gene expression. **2007**, 39, 1217-24	936
1890	Copy number variants and genetic traits: closer to the resolution of phenotypic to genotypic variability. **2007**, 8, 639-46	335
1889	Genome-wide association studies provide new insights into type 2 diabetes aetiology. **2007**, 8, 657-62	468
1888	Recent and ongoing selection in the human genome. **2007**, 8, 857-68	365
1887	How stem cells age and why this makes us grow old. **2007**, 8, 703-13	688
1886	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
1885	Introduction to genetic association studies. **2007**, 127, 2283-7	7
1884	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. **2007**, 447, 661-78	7801
1883	Genetics and type 2 diabetes in youth. **2007**, 8 Suppl 9, 42-7	17
1882	The importance of TCF7L2. **2007**, 24, 1062-6	70
1881	A new era for Type 2 diabetes genetics. **2007**, 24, 1181-6	28
1880	What will whole genome searches for susceptibility genes for common complex disease offer to clinical practice?. **2008**, 263, 16-27	43
1879	Common pathological processes in Alzheimer disease and type 2 diabetes: a review. **2007**, 56, 384-402	277

1878	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
1877	Mechanisms of disease: The genetic basis of coronary heart disease. **2007**, 4, 558-69	52
1876	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
1875	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
1874	Genetic studies of diabetes following the advent of the genome-wide association study: where do we go from here?. **2007**, 50, 2229-33	25
1873	Variations in the HHEX gene are associated with increased risk of type 2 diabetes in the Japanese population. **2007**, 50, 2461-6	178
1872	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
1871	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
1870	The Generation R Study Biobank: a resource for epidemiological studies in children and their parents. **2007**, 22, 917-23	179
1869	Molecular genetics of human growth hormone, insulin-like growth factors and their pathways in common disease. **2007**, 122, 1-21	57
1868	Sideways Glance: Genome wide association studies for type 2 diabetes mellitus. **2007**, 2, 245-8	5
1867	Genome-wide association studies: A new era in human genetics. **2007**, 1, 271-272	
1866	Maternal nutrition, intrauterine programming and consequential risks in the offspring. **2008**, 9, 203-11	123
1865	Pharmacogenetics: data, concepts and tools to improve drug discovery and drug treatment. **2008**, 64, 133-57	42
1864	Diabetic modifier QTLs in F(2) intercrosses carrying homozygous transgene of TGF-beta. **2008**, 19, 15-25	4
1863	[Congestive heart failure is a common disease with complex inheritance--new perspectives through genome wide association studies]. **2008**, 49, 405-10, 412	1
1862	beta-cell Regeneration: neogenesis, replication or both?. **2008**, 86, 247-58	32
1861	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

1860	Testing of diabetes-associated WFS1 polymorphisms in the Diabetes Prevention Program. **2008**, 51, 451-7	54
1859	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
1858	Polymorphisms in the TCF7L2, CDKAL1 and SLC30A8 genes are associated with impaired proinsulin conversion. **2008**, 51, 597-601	215
1857	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
1856	Strong association of common variants in the CDKN2A/CDKN2B region with type 2 diabetes in French Europids. **2008**, 51, 821-6	30
1855	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
1854	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
1853	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
1852	Positive association between variations in CDKAL1 and type 2 diabetes in Han Chinese individuals. **2008**, 51, 2134-7	40
1851	The search for putative unifying genetic factors for components of the metabolic syndrome. **2008**, 51, 2242-51	56
1850	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
1849	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
1848	Association of chromosome 9p21 SNPs with cardiovascular phenotypes in morbid obesity using electronic health record data. **2008**, 2, 33-43	17
1847	Molecular genetics of myocardial infarction. **2008**, 2, 7-22	28
1846	Common and rare alleles as causes of complex phenotypes. **2008**, 10, 194-200	13
1845	TCF7L2 genetic defect and type 2 diabetes. **2008**, 8, 149-55	63
1844	Genes and type 2 diabetes mellitus. **2008**, 8, 192-7	46
1843	Genetic susceptibility of diabetic retinopathy. **2008**, 8, 257-62	23

1842	The challenges for molecular nutrition research 1: linking genotype to healthy nutrition. **2008**, 3, 41-9	39
1841	Therapeutic options for premature coronary artery disease. **2008**, 10, 294-303	1
1840	Search for type 2 diabetes susceptibility genes on chromosomes 1q, 3q and 12q. **2008**, 53, 314-324	33
1839	Structural genomic variation in ischemic stroke. **2008**, 9, 101-8	26
1838	Expression of insulin-like growth factor-1 receptors, Wilm's tumor-1 protein, c-kit and p16 in primary fallopian tube carcinoma in diabetic patients. **2008**, 277, 449-55	0
1837	Methods for meta-analysis in genetic association studies: a review of their potential and pitfalls. **2008**, 123, 1-14	159
1836	Mendelian randomization: can genetic epidemiology help redress the failures of observational epidemiology?. **2008**, 123, 15-33	200
1835	Haplotypic analysis of Wellcome Trust Case Control Consortium data. **2008**, 123, 273-80	60
1834	Genome-wide screen for asthma in Puerto Ricans: evidence for association with 5q23 region. **2008**, 123, 455-68	63
1833	Type 2 diabetes susceptibility loci in the Ashkenazi Jewish population. **2008**, 124, 101-4	23
1832	Missing data imputation and haplotype phase inference for genome-wide association studies. **2008**, 124, 439-50	124
1831	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
1830	Evaluating the association of common PBX1 variants with type 2 diabetes. **2008**, 9, 14	2
1829	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
1828	Lack of association of genetic variation in chromosome region 15q14-22.1 with type 2 diabetes in a Japanese population. **2008**, 9, 22	1
1827	Genome-wide association study for renal traits in the Framingham Heart and Atherosclerosis Risk in Communities Studies. **2008**, 9, 49	26
1826	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
1825	Worldwide population differentiation at disease-associated SNPs. **2008**, 1, 22	98

1824	In search of causal variants: refining disease association signals using cross-population contrasts. **2008**, 9, 58	27
1823	Cardiovascular GO annotation initiative year 1 report: why cardiovascular GO?. **2008**, 8, 1950-3	12
1822	Type 2 diabetes genetics: starting to solve the puzzle. **2008**, 25, 214-215	
1821	Susceptibility genes in movement disorders. **2008**, 23, 927-934	2
1820	Mechanisms of □cell failure in the pathogenesis of Type 2 diabetes. **2008**, 69, 111-115	4
1819	Microarray-based DNA profiling to study genomic aberrations. **2008**, 60, 437-40	10
1818	CHOP T/C and C/T haplotypes contribute to early-onset type 2 diabetes in Italians. **2008**, 217, 291-5	9
1817	Examining the statistical properties of fine-scale mapping in large-scale association studies. **2008**, 32, 204-14	5
1816	Estimation of the multiple testing burden for genomewide association studies of nearly all common variants. **2008**, 32, 381-5	584
1815	Evaluating cost efficiency of SNP chips in genome-wide association studies. **2008**, 32, 387-95	21
1814	On the utility of gene set methods in genomewide association studies of quantitative traits. **2008**, 32, 658-68	49
1813	CANDID: a flexible method for prioritizing candidate genes for complex human traits. **2008**, 32, 779-90	67
1812	Calibration of credibility of agnostic genome-wide associations. **2008**, 147B, 964-72	18
1811	The positives, protocols, and perils of genome-wide association. **2008**, 147B, 1288-94	34
1810	Combined effects of exonic polymorphisms in CRHR1 and AVPR1B genes in a case/control study for panic disorder. **2008**, 147B, 1196-204	88
1809	Perspective on the genetics of attention deficit/hyperactivity disorder. **2008**, 147B, 1334-6	3
1808	Exploring case-control genetic association tests using phase diagrams. **2008**, 32, 391-9	4
1807	Nutrigenomics research for personalized nutrition and medicine. **2008**, 19, 110-20	87

1806	Array-based DNA diagnostics: let the revolution begin. **2008**, 59, 113-29	118
1805	Defining pancreatic endocrine precursors and their descendants. **2008**, 57, 654-68	61
1804	Autism genetics: strategies, challenges, and opportunities. **2008**, 1, 4-17	95
1803	Stem cells use distinct self-renewal programs at different ages. **2008**, 73, 539-53	41
1802	The use of SNP markers for estimation of individual genetic predisposition to diabetes mellitus type 1 and 2. **2008**, 2, 126-132	
1801	Genetic effects, gene-lifestyle interactions, and type 2 diabetes. **2008**, 3, 1-7	
1800	WW-domain-containing oxidoreductase is associated with low plasma HDL-C levels. **2008**, 83, 180-92	41
1799	Common coding variant in the TCF7L2 gene and study of the association with type 2 diabetes in Japanese subjects. **2008**, 53, 972-982	7
1798	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
1797	Development of a large-scale de-identified DNA biobank to enable personalized medicine. **2008**, 84, 362-9	627
1796	The success of the genome-wide association approach: a brief story of a long struggle. **2008**, 16, 554-64	85
1795	Hzf regulates adipogenesis through translational control of C/EBPalpha. **2008**, 27, 1481-90	21
1794	Polycystic ovary syndrome in adolescents. **2008**, 32, 1035-41	129
1793	Genomewide association for schizophrenia in the CATIE study: results of stage 1. **2008**, 13, 570-84	308
1792	Genome-wide association studies in psychiatry: lessons from early studies of non-psychiatric and psychiatric phenotypes. **2008**, 13, 649-53	55
1791	Progress and challenges in genome-wide association studies in humans. **2008**, 456, 728-31	286
1790	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
1789	Polymorphic markers associated with genes responsible for lipid and carbohydrate metabolism disorders and insulin resistance in cancer patients. **2008**, 42, 843-851	7

1788	FTO polymorphisms are associated with obesity but not diabetes risk in postmenopausal women. **2008**, 16, 2472-80	61
1787	Most gene test sales are misleading. **2008**, 26, 1221	6
1786	Newly identified genetic risk variants for celiac disease related to the immune response. **2008**, 40, 395-402	524
1785	Rare independent mutations in renal salt handling genes contribute to blood pressure variation. **2008**, 40, 592-599	639
1784	Genome-wide association analysis identifies 20 loci that influence adult height. **2008**, 40, 575-83	654
1783	Common variants near MC4R are associated with fat mass, weight and risk of obesity. **2008**, 40, 768-75	1048
1782	Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. **2008**, 40, 955-62	2092
1781	Estimating coverage and power for genetic association studies using near-complete variation data. **2008**, 40, 841-3	74
1780	Genome-wide scan identifies variation in MLXIPL associated with plasma triglycerides. **2008**, 40, 149-51	262
1779	Identification of loci associated with schizophrenia by genome-wide association and follow-up. **2008**, 40, 1053-5	877
1778	Variants in KCNQ1 are associated with susceptibility to type 2 diabetes mellitus. **2008**, 40, 1092-7	598
1777	SNPs in KCNQ1 are associated with susceptibility to type 2 diabetes in East Asian and European populations. **2008**, 40, 1098-102	555
1776	Susceptibility loci for intracranial aneurysm in European and Japanese populations. **2008**, 40, 1472-7	222
1775	Tbc1d1 mutation in lean mouse strain confers leanness and protects from diet-induced obesity. **2008**, 40, 1354-9	156
1774	The same sequence variant on 9p21 associates with myocardial infarction, abdominal aortic aneurysm and intracranial aneurysm. **2008**, 40, 217-24	596
1773	Genome-wide association studies: progress and potential for drug discovery and development. **2008**, 7, 221-30	91
1772	Pharmacogenetics in drug discovery and development: a translational perspective. **2008**, 7, 807-17	99
1771	Genetic programming of liver and pancreas progenitors: lessons for stem-cell differentiation. **2008**, 9, 329-40	231

1770	Genome-wide association studies for complex traits: consensus, uncertainty and challenges. **2008**, 9, 356-69	2126
1769	Linkage disequilibrium--understanding the evolutionary past and mapping the medical future. **2008**, 9, 477-85	695
1768	Popper revisited: GWAS here, last year. **2008**, 16, 1-2	18
1767	Singleton SNPs in the human genome and implications for genome-wide association studies. **2008**, 16, 506-15	31
1766	HHEX gene polymorphisms are associated with type 2 diabetes in the Dutch Breda cohort. **2008**, 16, 652-6	18
1765	To what extent do scans of non-synonymous SNPs complement denser genome-wide association studies?. **2008**, 16, 718-23	23
1764	Whole-genome association study of bipolar disorder. **2008**, 13, 558-69	571
1763	Developmental Neuroscience Perspectives on Emotion Regulation. **2008**, 2, 132-140	87
1762	TCF7L2 polymorphisms are associated with type 2 diabetes in Khatri Sikhs from North India: genetic variation affects lipid levels. **2008**, 72, 499-509	49
1761	Relationship between beta-cell mass and diabetes onset. **2008**, 10 Suppl 4, 23-31	179
1760	Effect of RBP4 gene variants on circulating RBP4 concentration and type 2 diabetes in a Chinese population. **2008**, 25, 11-8	26
1759	Genetics: how the UKPDS contributed to determining the genetic landscape of Type 2 diabetes. **2008**, 25 Suppl 2, 35-40	7
1758	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
1757	Identifying the susceptibility genes for coronary artery disease: from hyperbole through doubt to cautious optimism. **2008**, 263, 538-52	37
1756	Using the longest significance run to estimate region-specific p-values in genetic association mapping studies. **2008**, 9, 246	3
1755	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
1754	Impact of mitochondrial calcium on the coupling of metabolism to insulin secretion in the pancreatic beta-cell. **2008**, 44, 64-76	79
1753	Genome-wide association studies in aging-related processes such as diabetes mellitus, atherosclerosis and cancer. **2008**, 43, 39-43	32

1752	Genome-wide association studies in neurological disorders. **2008**, 7, 1067-72		43
1751	A Genetics Primer for Social Health Research. **2008**, 2, 785-816		9
1750	Genetic markers for prediction of normal tissue toxicity after radiotherapy. **2008**, 18, 126-35		90
1749	Type 2 diabetes: new genes, new understanding. **2008**, 24, 613-21		204
1748	Study designs for genome-wide association studies. **2008**, 60, 465-504		40
1747	Concept, design and implementation of a cardiovascular gene-centric 50 k SNP array for large-scale genomic association studies. *PLoS ONE*, **2008**, 3, e3583	3.7	321
1746	Study Design and Statistical Issues in Pharmacogenetics Research. **2008**, 185-206		
1745	Introduction: Why Molecular Epidemiology?. 1-5		
1744	Integrating genomic and clinical medicine: searching for susceptibility genes in complex lung diseases. **2008**, 151, 181-93		11
1743	Preventing type 2 diabetes: genes or lifestyle?. **2008**, 2, 65-6		6
1742	Learning from molecular genetics: novel insights arising from the definition of genes for monogenic and type 2 diabetes. **2008**, 57, 2889-98		96
1741	Metabolomics: a global biochemical approach to drug response and disease. **2008**, 48, 653-83		517
1740	Genetic susceptibility to type 2 diabetes and implications for antidiabetic therapy. **2008**, 59, 95-111		40
1739	Support for neuregulin 1 as a susceptibility gene for bipolar disorder and schizophrenia. **2008**, 64, 419-27		95
1738	Developments in psoriasis and psoriatic arthritis. **2008**, 5, e47-e54		1
1737	Gene-environment interactions and susceptibility to metabolic syndrome and other chronic diseases. **2008**, 79, 1508-13		56
1736	Telomeres and Telomerase in Ageing, Disease, and Cancer. **2008**,		1
1735	Validation and extension of an empirical Bayes method for SNP calling on Affymetrix microarrays. **2008**, 9, R63		28

1734	Classification of genetic profiles of Crohn's disease: a focus on the ATG16L1 gene. **2008**, 8, 199-207		10
1733	Genotype score in addition to common risk factors for prediction of type 2 diabetes. **2008**, 359, 2208-19		608
1732	Clinical risk factors, DNA variants, and the development of type 2 diabetes. **2008**, 359, 2220-32		698
1731	Admixture mapping and the role of population structure for localizing disease genes. **2008**, 60, 547-69		49
1730	Assessing the combined impact of 18 common genetic variants of modest effect sizes on type 2 diabetes risk. **2008**, 57, 3129-35		245
1729	Pharmacogenetics: potential role in the treatment of diabetes and obesity. **2008**, 9, 1109-19		11
1728	Common variants in maturity-onset diabetes of the young genes and future risk of type 2 diabetes. **2008**, 57, 1738-44		63
1727	Genetics of diabetic nephropathy. **2008**, 2, 363-71		20
1726	Glucolipotoxicity: fuel excess and beta-cell dysfunction. **2008**, 29, 351-66		801
1725	Assessment of cumulative evidence on genetic associations: interim guidelines. **2008**, 37, 120-32		451
1724	Gaining insights in coronary disease genomics. **2008**, 52, 385-6		3
1723	Monogenic diabetes in the young, pharmacogenetics and relevance to multifactorial forms of type 2 diabetes. **2008**, 29, 254-64		118
1722	Pharmacogenomics and Personalized Medicine. **2008**,		2
1721	Interaction Between Physical Activity and Genetic Factors in Complex Metabolic Disease. **2007**, 155-173		
1720	A polymorphism within the G6PC2 gene is associated with fasting plasma glucose levels. *Science*, **2008**, 320, 1085-8	33.3	199
1719	Innovative Endocrinology of Cancer. **2008**,		5
1718	Zinc signalling and subcellular distribution: emerging targets in type 2 diabetes. **2008**, 14, 419-28		66
1717	Candidate gene polymorphisms and the 9p21 locus in acute coronary syndromes. **2008**, 14, 441-9		19

1716	Genome-wide association study identifies genes for biomarkers of cardiovascular disease: serum urate and dyslipidemia. **2008**, 82, 139-49	361
1715	Heterogeneity in gene loci associated with type 2 diabetes on human chromosome 20q13.1. **2008**, 92, 226-34	32
1714	A role for metallothionein in the pathogenesis of diabetes and its cardiovascular complications. **2008**, 94, 1-3	11
1713	A non-synonymous variant in SLC30A8 is not associated with type 1 diabetes in the Danish population. **2008**, 94, 386-8	18
1712	Atypical protein kinase C dysfunction and the metabolic syndrome. **2008**, 19, 39-41	2
1711	The role for endoplasmic reticulum stress in diabetes mellitus. **2008**, 29, 42-61	868
1710	Epigenetics and obesity. **2008**, 9, 1851-60	60
1709	An ancient evolutionary origin of genes associated with human genetic diseases. **2008**, 25, 2699-707	133
1708	The emerging genetic architecture of type 2 diabetes. **2008**, 8, 186-200	239
1707	Can geneticists help clinicians to understand and treat non-autoimmune diabetes?. **2008**, 82 Suppl 2, S83-93	5
1706	Future impact of integrated high-throughput methylome analyses on human health and disease. **2008**, 35, 391-401	36
1705	Meta-analysis approach identifies candidate genes and associated molecular networks for type-2 diabetes mellitus. **2008**, 9, 310	45
1704	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. **2008**, 40, 638-45	1496
1703	Variation in inflammation-related genes and risk of incident nonfatal myocardial infarction or ischemic stroke. **2008**, 198, 166-73	65
1702	A roadmap to disentangle the molecular etiology of schizophrenia. **2008**, 23, 224-32	7
1701	Genes for multiple sclerosis. **2008**, 371, 283-5	38
1700	Type 2 diabetes: pathogenesis and treatment. **2008**, 371, 2153-6	92
1699	Prevalence in the United States of selected candidate gene variants: Third National Health and Nutrition Examination Survey, 1991-1994. **2009**, 169, 54-66	72

1698	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
1697	Genetic mapping in human disease. *Science*, **2008**, 322, 881-8	33.3	1086
1696	Considerations regarding the genetics of obesity. **2008**, 16 Suppl 3, S33-9		33
1695	Obesity genes and gene-environment-behavior interactions: recommendations for a way forward. **2008**, 16 Suppl 3, S79-81		16
1694	Gene-environment interactions in the etiology of obesity: defining the fundamentals. **2008**, 16 Suppl 3, S5-S10		120
1693	Genetics of type 2 diabetes mellitus and obesity--a review. **2008**, 40, 2-10		24
1692	Molecular signatures of cardiovascular disease risk: potential for test development and clinical application. **2008**, 12, 281-7		4
1691	Pharmacogenetics of major depression: insights from level 1 of the Sequenced Treatment Alternatives to Relieve Depression (STAR*D) trial. **2008**, 12, 321-30		17
1690	Zinc transporter-8 gene (SLC30A8) is associated with type 2 diabetes in Chinese. **2008**, 93, 4107-12		62
1689	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
1688	Developmental Toxicology. **2008**,		
1687	Mechanisms of disease: genetic insights into the etiology of type 2 diabetes and obesity. **2008**, 4, 156-63		36
1686	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
1685	Genome-wide association studies: potential next steps on a genetic journey. *Human Molecular Genetics*, **2008**, 17, R156-65	5.6	263
1684	Predicting type 2 diabetes based on polymorphisms from genome-wide association studies: a population-based study. **2008**, 57, 3122-8		231
1683	Proteomic characterization of mouse cytosolic and membrane prostate fractions: high levels of free SUMO peptides are androgen-regulated. **2008**, 7, 4492-9		8
1682	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
1681	Introduction to the Special Issue on Society and Genetics. **2008**, 37, 159-163		12

1680	Required sample size and nonreplicability thresholds for heterogeneous genetic associations. **2008**, 105, 617-22		91
1679	Generating Linkage Disequilibrium Patterns in Data Simulations Using genomeSIMLA. **2008**, 24-35		29
1678	Mitochondria as chi. **2008**, 179, 727-35		116
1677	Physical activity and the association of common FTO gene variants with body mass index and obesity. **2008**, 168, 1791-7		207
1676	A polymorphism in the zinc transporter gene SLC30A8 confers resistance against posttransplantation diabetes mellitus in renal allograft recipients. **2008**, 57, 1043-7		66
1675	Looking for polycystic ovary syndrome genes: rational and best strategy. **2008**, 26, 5-13		61
1674	Commentary: Genetic association studies see light at the end of the tunnel. **2008**, 37, 133-5		7
1673	Into the post-HapMap era. **2008**, 60, 727-42		16
1672	A study of diabetes mellitus within a large sample of Australian twins. **2008**, 11, 28-40		25
1671	Beta-cell replication is the primary mechanism subserving the postnatal expansion of beta-cell mass in humans. **2008**, 57, 1584-94		529
1670	PCLO variants are nominally associated with early-onset type 2 diabetes and insulin resistance in Pima Indians. **2008**, 57, 3156-60		10
1669	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
1668	Association analysis of type 2 diabetes Loci in type 1 diabetes. **2008**, 57, 1983-6		39
1667	Extension of type 2 diabetes genome-wide association scan results in the diabetes prevention program. **2008**, 57, 2503-10		86
1666	Cardiovascular genomics, personalized medicine, and the National Heart, Lung, and Blood Institute: part I: the beginning of an era. **2008**, 1, 51-7		29
1665	Mechanisms of mammalian zinc-regulated gene expression. **2008**, 36, 1262-6		46
1664	Pharmacogenomics: candidate gene identification, functional validation and mechanisms. *Human Molecular Genetics*, **2008**, 17, R174-9	5.6	49
1663	The emerging role of structural variations in common disorders: initial findings and discovery challenges. **2008**, 123, 108-17		5

1662	Aliskiren. **2008**, 118, 773-84	106
1661	The heritability of HbA1c and fasting blood glucose in different measurement settings. **2008**, 11, 597-602	46
1660	Why most discovered true associations are inflated. **2008**, 19, 640-8	1078
1659	Clinical review: the genetics of type 2 diabetes: a realistic appraisal in 2008. **2008**, 93, 4633-42	90
1658	Whole genome analyses suggest ischemic stroke and heart disease share an association with polymorphisms on chromosome 9p21. **2008**, 39, 1586-9	138
1657	Meta-analysis of 23 type 2 diabetes linkage studies from the International Type 2 Diabetes Linkage Analysis Consortium. **2008**, 66, 35-49	34
1656	A common nonsynonymous single nucleotide polymorphism in the SLC30A8 gene determines ZnT8 autoantibody specificity in type 1 diabetes. **2008**, 57, 2693-7	165
1655	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
1654	Bioinformatics and Systems Biology. **2008**,	7
1653	Molecular genetics of Alzheimer's disease: an update. **2008**, 40, 562-83	175
1652	Dissecting the nutrigenomics, diabetes, and gastrointestinal disease interface: from risk assessment to health intervention. **2008**, 12, 237-44	10
1651	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
1650	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
1649	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
1648	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
1647	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
1646	Evaluation of the association of IGF2BP2 variants with type 2 diabetes in French Caucasians. **2008**, 57, 1992-6	23
1645	Investigation of transport mechanisms and regulation of intracellular Zn2+ in pancreatic alpha-cells. **2008**, 283, 10184-97	87

1644	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
1643	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
1642	A novel susceptibility locus for type 1 diabetes on Chr12q13 identified by a genome-wide association study. **2008**, 57, 1143-6		118
1641	Polymorphisms in the IDE-KIF11-HHEX gene locus are reproducibly associated with type 2 diabetes in a Japanese population. **2008**, 93, 310-4		51
1640	Diabetes. **2008**,		1
1639	Positional cloning of "Lisch-Like", a candidate modifier of susceptibility to type 2 diabetes in mice. **2008**, 4, e1000137		53
1638	Associations among multiple markers and complex disease: models, algorithms, and applications. **2008**, 60, 437-64		1
1637	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
1636	Gene set enrichment in eQTL data identifies novel annotations and pathway regulators. **2008**, 4, e1000070		79
1635	What can genome-wide association studies tell us about the genetics of common disease?. **2008**, 4, e33		102
1634	Genes influencing susceptibility to infection. **2008**, 197, 4-6		9
1633	Microarray technology and applications in the arena of genome-wide association. **2008**, 54, 1116-24		61
1632	Adaptations to climate in candidate genes for common metabolic disorders. **2008**, 4, e32		204
1631	Tracing sub-structure in the European American population with PCA-informative markers. **2008**, 4, e1000114		53
1630	Inflammation, insulin resistance, and diabetes--Mendelian randomization using CRP haplotypes points upstream. **2008**, 5, e155		114
1629	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
1628	Association analysis in african americans of European-derived type 2 diabetes single nucleotide polymorphisms from whole-genome association studies. **2008**, 57, 2220-5		118
1627	Practical aspects of imputation-driven meta-analysis of genome-wide association studies. *Human Molecular Genetics*, **2008**, 17, R122-8	5.6	423

1626	Evaluation of the potential excess of statistically significant findings in published genetic association studies: application to Alzheimer's disease. **2008**, 168, 855-65		34
1625	Associations between single nucleotide polymorphisms on chromosome 9p21 and risk of coronary heart disease in Chinese Han population. **2008**, 28, 2085-9		65
1624	Comprehensive association study of type 2 diabetes and related quantitative traits with 222 candidate genes. **2008**, 57, 3136-44		82
1623	Molecular basis for the thiol sensitivity of insulin-degrading enzyme. **2008**, 105, 9582-7		50
1622	An appreciation of Robert Turner. **2008**, 57, 2918-21		2
1621	Evidence that the gene encoding insulin degrading enzyme influences human lifespan. *Human Molecular Genetics*, **2008**, 17, 2370-8	5.6	8
1620	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
1619	Susceptibility to coronary artery disease and diabetes is encoded by distinct, tightly linked SNPs in the ANRIL locus on chromosome 9p. *Human Molecular Genetics*, **2008**, 17, 806-14	5.6	420
1618	HapMap and mapping genes for cardiovascular disease. **2008**, 1, 66-71		12
1617	A weighted-Holm procedure accounting for allele frequencies in genomewide association studies. **2008**, 180, 697-702		5
1616	Metabolic and cardiovascular traits: an abundance of recently identified common genetic variants. *Human Molecular Genetics*, **2008**, 17, R102-8	5.6	64
1615	Gene-environment interaction in genome-wide association studies. **2009**, 169, 219-26		208
1614	Update on the genetics of stroke and cerebrovascular disease 2007. **2008**, 39, 252-4		5
1613	Proinflammatory gene polymorphisms and ischemic stroke. **2008**, 14, 3590-600		22
1612	Islet amyloid in type 2 diabetes, and the toxic oligomer hypothesis. **2008**, 29, 303-16		467
1611	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
1610	[Diabetology 2008]. **2008**, 133, 1377-80		
1609	Association analysis of Krüppel-like factor 11 variants with type 2 diabetes in Pima Indians. **2008**, 93, 3644-9		9

1608	Impact of TCF7L2 rs7903146 on insulin secretion and action in young and elderly Danish twins. **2008**, 93, 4013-9	51
1607	Severe intrauterine growth retardation and atypical diabetes associated with a translocation breakpoint disrupting regulation of the insulin-like growth factor 2 gene. **2008**, 93, 4373-80	30
1606	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
1605	Regulatory variation and evolution: implications for disease. **2008**, 61, 295-306	2
1604	A meta-analysis of QTL for diabetes-related traits in rodents. **2008**, 34, 42-53	37
1603	Delineating slowly and rapidly evolving fractions of the Drosophila genome. **2008**, 15, 407-30	16
1602	Primer: immunity and autoimmunity. **2008**, 57, 2872-82	28
1601	The clinical utility of genetic risk variants in type 2 diabetes. **2008**, 2, 991-1002	
1600	Exchangeable models of complex inherited diseases. **2008**, 179, 2253-61	30
1599	A gene expression network model of type 2 diabetes links cell cycle regulation in islets with diabetes susceptibility. **2008**, 18, 706-16	269
1598	Defining targets for investigating the pharmacogenomics of adverse drug reactions to antifungal agents. **2008**, 9, 561-84	18
1597	On Sequence Variants that Influence the Risk of Common Diseases. **2008**,	
1596	Transmission of raised blood pressure and endothelial dysfunction to the F2 generation induced by maternal protein restriction in the F0, in the absence of dietary challenge in the F1 generation. **2008**, 100, 760-6	93
1595	A genome-wide association study identifies novel risk loci for type 2 diabetes. **2008**, 2008, 36-37	
1594	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. **2008**, 2008, 38-39	19
1593	Interaction between poor glycemic control and 9p21 locus on risk of coronary artery disease in type 2 diabetes. **2008**, 300, 2389-97	92
1592	Gene by social context interactions for number of sexual partners among white male youths: genetics-informed sociology. **2008**, 114 Suppl, S36-66	39
1591	The pancreatic beta-cell: birth, life and death. **2008**, 36, 267-71	5

1590	Identification of human minor histocompatibility antigens based on genetic association with highly parallel genotyping of pooled DNA. **2008**, 111, 3286-94		43
1589	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
1588	Family study designs in the age of genome-wide association studies: experience from the Framingham Heart Study. **2008**, 19, 144-50		11
1587	Maintenance of Glucose Control in Patients With Type 1 Diabetes During Acute Mental Stress by Riding High-Speed Rollercoasters. **2008**, 2008, 39-41		
1586	New gene variants alter type 2 diabetes risk predominantly through reduced beta-cell function. **2008**, 11, 371-7		86
1585	Polygenic contribution to obesity: genome-wide strategies reveal new targets. **2008**, 36, 12-36		26
1584	The transcription factor 7-like 2 gene and increased risk of type 2 diabetes: an update. **2008**, 11, 385-92		32
1583	Defining the spectrum of alleles that contribute to blood lipid concentrations in humans. **2008**, 19, 122-7		40
1582	Forum: Interactions between gene and environment. **2008**, 21, 315-7		31
1581	Hypertension and genome-wide association studies: combining high fidelity phenotyping and hypercontrols. **2008**, 26, 1275-81		29
1580	. **2008**,		8
1579	Diabetes Mellitus. **2008**, 374-421		2
1578	[What is new in the genetics of type 2 diabetes]. **2008**, 24, 241-2		1
1577	The HapMap: charting a course for genetic discovery in neurological diseases. **2008**, 65, 319-21		7
1576	Association analysis of the FTO gene with obesity in children of Caucasian and African ancestry reveals a common tagging SNP. *PLoS ONE*, **2008**, 3, e1746	3.7	161
1575	Association of common polymorphisms in GLUT9 gene with gout but not with coronary artery disease in a large case-control study. *PLoS ONE*, **2008**, 3, e1948	3.7	64
1574	Post genome-wide association studies of novel genes associated with type 2 diabetes show gene-gene interaction and high predictive value. *PLoS ONE*, **2008**, 3, e2031	3.7	124
1573	Density of common complex ocular traits in the aging eye: analysis of secondary traits in genome-wide association studies. *PLoS ONE*, **2008**, 3, e2510	3.7	2

1572	Novel meta-analysis-derived type 2 diabetes risk loci do not determine prediabetic phenotypes. *PLoS ONE*, **2008**, 3, e3019	3.7	35
1571	Regeneration of pancreatic beta cells. **2008**, 13, 6170-82		12
1570	Gene and Pathway-Based Analysis: Second Wave of Genome-wide Association Studies. **2008**,		
1569	A HapMap harvest of insights into the genetics of common disease. **2008**, 118, 1590-605		683
1568	Genomic Approaches to Complex Disease. **2009**, 33-46		
1567	. **2009**,		59
1566	References. 231-243		
1565	Candidate Gene and Genome-Wide Association Studies. 1-19		
1564	Genetics of Gestational Diabetes Mellitus. **2009**, 52, 688		3
1563	Therapeutic approaches based on beta-cell mass preservation and/or regeneration. **2009**, 14, 1835-50		14
1562	The genetic and neurobiologic compass points toward common signaling dysfunctions in autism spectrum disorders. **2009**, 119, 747-54		165
1561	Host genetic and epigenetic factors in toxoplasmosis. **2009**, 104, 162-9		18
1560	Molecular Signatures of Obstructive Sleep Apnea in Adults: A Review and Perspective. **2009**,		
1559	A Bayesian Method for Detecting and Characterizing Allelic Heterogeneity and Boosting Signals in Genome-Wide Association Studies. **2009**, 24,		17
1558	Mitochondria, bioenergetics, and the epigenome in eukaryotic and human evolution. **2009**, 74, 383-93		39
1557	Disruptive insights in psychiatry: transforming a clinical discipline. **2009**, 119, 700-5		106
1556	Translational Genomics: From Discovery to Clinical Practice. **2009**, 262-274		2
1555	Genome-wide Association: A Revolutionary Approach**2009**, 9, 97-103		

1554	Molecular signatures of obstructive sleep apnea in adults: a review and perspective. **2009**, 32, 447-70		243
1553	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
1552	STrengthening the REporting of Genetic Association Studies (STREGA): an extension of the STROBE statement. **2009**, 6, e22		264
1551	INK4/ARF transcript expression is associated with chromosome 9p21 variants linked to atherosclerosis. *PLoS ONE*, **2009**, 4, e5027	3.7	196
1550	Down-regulation of ZnT8 expression in INS-1 rat pancreatic beta cells reduces insulin content and glucose-inducible insulin secretion. *PLoS ONE*, **2009**, 4, e5679	3.7	63
1549	The type 2 diabetes associated minor allele of rs2237895 KCNQ1 associates with reduced insulin release following an oral glucose load. *PLoS ONE*, **2009**, 4, e5872	3.7	40
1548	Replication study of candidate genes associated with type 2 diabetes based on genome-wide screening. **2009**, 58, 493-8		115
1547	Age-dependent decline in beta-cell proliferation restricts the capacity of beta-cell regeneration in mice. **2009**, 58, 1312-20		252
1546	Finding common susceptibility variants for complex disease: past, present and future. **2009**, 8, 345-52		17
1545	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
1544	High-throughput, high-accuracy array-based resequencing. **2009**, 106, 6712-7		20
1543	Interrogating type 2 diabetes genome-wide association data using a biological pathway-based approach. **2009**, 58, 1463-7		87
1542	Insulin storage and glucose homeostasis in mice null for the granule zinc transporter ZnT8 and studies of the type 2 diabetes-associated variants. **2009**, 58, 2070-83		302
1541	Breast-feeding modifies the association of PPARgamma2 polymorphism Pro12Ala with growth in early life: the Generation R Study. **2009**, 58, 992-8		16
1540	Ethical issues of predictive genetic testing for diabetes. **2009**, 3, 781-8		13
1539	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
1538	Genetic architecture of quantitative traits in mice, flies, and humans. **2009**, 19, 723-33		321
1537	Methods for analysis in pharmacogenomics: lessons from the Pharmacogenetics Research Network Analysis Group. **2009**, 10, 243-51		10

1536	Kir6.2 variant E23K increases ATP-sensitive K+ channel activity and is associated with impaired insulin release and enhanced insulin sensitivity in adults with normal glucose tolerance. **2009**, 58, 1869-78	68
1535	Examination of type 2 diabetes loci implicates CDKAL1 as a birth weight gene. **2009**, 58, 2414-8	52
1534	Association of type 2 diabetes candidate polymorphisms in KCNQ1 with incretin and insulin secretion. **2009**, 58, 1715-20	89
1533	Genome-wide association studies, field synopses, and the development of the knowledge base on genetic variation and human diseases. **2009**, 170, 269-79	117
1532	Underlying genetic models of inheritance in established type 2 diabetes associations. **2009**, 170, 537-45	60
1531	Progress in genome-wide association studies of human height. **2009**, 71 Suppl 2, 5-13	36
1530	Whole genome association study in a homogenous population in Shandong peninsula of China reveals JARID2 as a susceptibility gene for schizophrenia. **2009**, 2009, 536918	26
1529	Data integration in genetics and genomics: methods and challenges. **2009**, 2009,	80
1528	Size matters: just how big is BIG?: Quantifying realistic sample size requirements for human genome epidemiology. **2009**, 38, 263-73	192
1527	Risk loci for type 2 diabetes - quo vadis?. **2009**, 47, 383-6	3
1526	ATOM: a powerful gene-based association test by combining optimally weighted markers. **2009**, 25, 497-503	42
1525	Integration of heterogeneous expression data sets extends the role of the retinol pathway in diabetes and insulin resistance. **2009**, 25, 3121-7	17
1524	Recent progress in the genetics of diabetes. **2009**, 71 Suppl 1, 17-23	5
1523	Statistical screening method for genetic factors influencing susceptibility to common diseases in a two-stage genome-wide association study. **2009**, 8, Article 46	
1522	Adiposity-related heterogeneity in patterns of type 2 diabetes susceptibility observed in genome-wide association data. **2009**, 58, 505-10	98
1521	Successful versus failed adaptation to high-fat diet-induced insulin resistance: the role of IAPP-induced beta-cell endoplasmic reticulum stress. **2009**, 58, 906-16	75
1520	Linkage disequilibrium mapping of the replicated type 2 diabetes linkage signal on chromosome 1q. **2009**, 58, 1704-9	23
1519	Linking the genetics of type 2 diabetes with low birth weight: a role for prenatal islet maldevelopment?. **2009**, 58, 1255-6	26

1518	Novel insights into the etiology of diabetes from genome-wide association studies. **2009**, 58, 2444-7	2
1517	Genetic predisposition, Western dietary pattern, and the risk of type 2 diabetes in men. **2009**, 89, 1453-8	113
1516	A genetic variant on chromosome 9p21 and incident heart failure in the ARIC study. **2009**, 30, 1222-8	44
1515	Clinical translation of genetic predictors for type 2 diabetes. **2009**, 16, 100-6	14
1514	Current World Literature. **2009**, 20, 135-42	
1513	Update to Terwilliger and G□ing's "Gene mapping in the 20th and 21st centuries" (2000): gene mapping when rare variants are common and common variants are rare. **2009**, 81, 729-33	11
1512	Genetic variant in the IGF2BP2 gene may interact with fetal malnutrition to affect glucose metabolism. **2009**, 58, 1440-4	41
1511	Collaborative genome-wide association studies of diverse diseases: programs of the NHGRI's office of population genomics. **2009**, 10, 235-41	36
1510	Learning your identity and disease from research papers. **2009**,	113
1509	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
1508	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
1507	Involvement of 4E-BP1 in the protection induced by HDLs on pancreatic beta-cells. **2009**, 23, 1572-86	18
1506	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
1505	Downregulation of ZnT8 expression in pancreatic □-cells of diabetic mice. **2009**, 1, 124-8	37
1504	Evaluation of risk prediction updates from commercial genome-wide scans. **2009**, 11, 588-94	63
1503	Singapore Genome Variation Project: a haplotype map of three Southeast Asian populations. **2009**, 19, 2154-62	129
1502	Genome-wide association studies for atherosclerotic vascular disease and its risk factors. **2009**, 2, 63-72	36
1501	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

1500	Minireview: Meeting the demand for insulin: molecular mechanisms of adaptive postnatal beta-cell mass expansion. **2009**, 23, 747-58		122
1499	Evidence for association between polycystic ovary syndrome (PCOS) and TCF7L2 and glucose intolerance in women with PCOS and TCF7L2. **2009**, 94, 2617-25		49
1498	Genetic architecture of coronary artery disease in the genome-wide era: implications for the emerging "golden dozen" loci. **2009**, 35, 671-82		29
1497	Identification of a shared genetic susceptibility locus for coronary heart disease and periodontitis. **2009**, 5, e1000378		162
1496	The genetic signatures of noncoding RNAs. **2009**, 5, e1000459		553
1495	Common type 2 diabetes risk gene variants associate with gestational diabetes. **2009**, 94, 145-50		169
1494	The effect of multiple genetic variants in predicting the risk of type 2 diabetes. **2009**, 3 Suppl 7, S49		12
1493	Ensuring the safe use of genomic medicine in children. **2009**, 48, 703-8		7
1492	PPARG, KCNJ11, CDKAL1, CDKN2A-CDKN2B, IDE-KIF11-HHEX, IGF2BP2 and SLC30A8 are associated with type 2 diabetes in a Chinese population. *PLoS ONE*, **2009**, 4, e7643	3.7	137
1491	Genetics and the general physician: insights, applications and future challenges. **2009**, 102, 757-72		10
1490	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
1489	Genetic variations in sex steroid-related genes as predictors of serum estrogen levels in men. **2009**, 94, 1033-41		55
1488	Additive effects of genetic variation in GCK and G6PC2 on insulin secretion and fasting glucose. **2009**, 58, 2946-53		28
1487	The 9p21 myocardial infarction risk allele increases risk of peripheral artery disease in older people. **2009**, 2, 347-53		76
1486	Polycomb protein Ezh2 regulates pancreatic beta-cell Ink4a/Arf expression and regeneration in diabetes mellitus. **2009**, 23, 975-85		296
1485	IGF2 mRNA-binding protein 2: biological function and putative role in type 2 diabetes. **2009**, 43, 187-95		123
1484	Genetic variant in HK1 is associated with a proanemic state and A1C but not other glycemic control-related traits. **2009**, 58, 2687-97		29
1483	TCF7L2 polymorphism associates with new-onset diabetes after transplantation. **2009**, 20, 2459-67		55

1482	Ranking of genome-wide association scan signals by different measures. **2009**, 38, 1364-73	9
1481	Reduced expression of the Kinesin-Associated Protein 3 (KIFAP3) gene increases survival in sporadic amyotrophic lateral sclerosis. **2009**, 106, 9004-9	149
1480	Common polymorphic transcript variation in human disease. **2009**, 19, 567-75	64
1479	Glucagon-like peptide-1 protects beta-cells against apoptosis by increasing the activity of an IGF-2/IGF-1 receptor autocrine loop. **2009**, 58, 1816-25	105
1478	Association and interaction analyses of genetic variants in ADIPOQ, ENPP1, GHSR, PPARgamma and TCF7L2 genes for diabetic nephropathy in a Taiwanese population with type 2 diabetes. **2009**, 24, 3360-6	66
1477	Gene prioritization based on biological plausibility over genome wide association studies renders new loci associated with type 2 diabetes. **2009**, 11, 338-43	15
1476	Type 2 diabetes risk alleles are associated with reduced size at birth. **2009**, 58, 1428-33	117
1475	Association of regions on chromosomes 6 and 7 with blood pressure in Nigerian families. **2009**, 2, 38-45	14
1474	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
1473	An update on preventive and regenerative therapies in diabetes mellitus. **2009**, 121, 317-31	36
1472	Understanding cardiovascular disease through the lens of genome-wide association studies. **2009**, 25, 387-94	55
1471	Human genetic variations: Beacons on the pathways to successful ageing. **2009**, 130, 553-63	21
1470	Cell intrinsic and extrinsic mechanisms of stem cell aging depend on telomere status. **2009**, 44, 75-82	25
1469	Estudio del componente genético de la cardiopatía isquémica: de los estudios de ligamiento al genotipado integral del genoma. **2009**, 9, 24-38	2
1468	Convergent functional genomics of genome-wide association data for bipolar disorder: comprehensive identification of candidate genes, pathways and mechanisms. **2009**, 150B, 155-81	152
1467	Sequence variants on chromosome 9p21.3 confer risk for atherosclerotic stroke. **2009**, 65, 531-9	185
1466	An optimal dose-effect mode trend test for SNP genotype tables. **2009**, 33, 114-27	16
1465	Using genome-wide pathway analysis to unravel the etiology of complex diseases. **2009**, 33, 419-31	159

1464	Genotype-based matching to correct for population stratification in large-scale case-control genetic association studies. **2009**, 33, 508-17	37
1463	STrengthening the REporting of Genetic Association Studies (STREGA)--an extension of the STROBE statement. **2009**, 33, 581-98	134
1462	Meta-analysis of genome-wide association studies: no efficiency gain in using individual participant data. **2010**, 34, 60-6	95
1461	The influence of genetic variations in HHEX gene on insulin metabolism in the German MESYBEPO cohort. **2009**, 25, 156-62	20
1460	Strengthening the reporting of genetic association studies (STREGA): an extension of the STROBE Statement. **2009**, 125, 131-51	136
1459	Analysis of FTO gene variants with measures of obesity and glucose homeostasis in the IRAS Family Study. **2009**, 125, 615-26	77
1458	Genome-wide association studies in ADHD. **2009**, 126, 13-50	316
1457	Strategies and issues in the detection of pathway enrichment in genome-wide association studies. **2009**, 126, 289-301	106
1456	Association between insulin secretion, insulin sensitivity and type 2 diabetes susceptibility variants identified in genome-wide association studies. **2009**, 46, 217-26	81
1455	The genetics of autoimmune diseases: a networked perspective. **2009**, 21, 596-605	110
1454	Strengthening the reporting of genetic association studies (STREGA): an extension of the STROBE statement. **2009**, 24, 37-55	35
1453	Empirical Bayes and semi-Bayes adjustments for a vast number of estimations. **2009**, 24, 737-41	10
1452	Association of the common rs9939609 variant of FTO gene with polycystic ovary syndrome in Chinese women. **2009**, 36, 377-82	29
1451	Novel antigens in type 1 diabetes: the importance of ZnT8. **2009**, 9, 105-12	49
1450	Genome-wide association studies in type 2 diabetes. **2009**, 9, 164-71	174
1449	Update Typ-2-Diabetes anhand ausgewÄlter aktueller Publikationen. **2009**, 5, 177-189	
1448	The null distributions of test statistics in genomewide association studies. **2009**, 1, 214-227	
1447	Polymorphisms within insulin-degrading enzyme (IDE) gene determine insulin metabolism and risk of type 2 diabetes. **2009**, 87, 1145-51	51

1446	The association of common genetic variants in the APOA5, LPL and GCK genes with longitudinal changes in metabolic and cardiovascular traits. **2009**, 52, 106-14	22
1445	FTO gene variants are strongly associated with type 2 diabetes in South Asian Indians. **2009**, 52, 247-52	145
1444	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
1443	The risk allele load accelerates the age-dependent decline in beta cell function. **2009**, 52, 457-62	23
1442	Risk prediction of prevalent diabetes in a Swiss population using a weighted genetic score--the CoLaus Study. **2009**, 52, 600-8	95
1441	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
1440	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
1439	Variants in KCNQ1 are associated with susceptibility to type 2 diabetes in the population of mainland China. **2009**, 52, 1315-21	54
1438	No association of multiple type 2 diabetes loci with type 1 diabetes. **2009**, 52, 2109-16	63
1437	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
1436	Autoantibodies to zinc transporter 8 and SLC30A8 genotype stratify type 1 diabetes risk. **2009**, 52, 1881-8	137
1435	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
1434	Genetic factors for resistance to diet-induced obesity and associated metabolic traits on mouse chromosome 17. **2009**, 20, 71-82	33
1433	Variation in genetic admixture and population structure among Latinos: the Los Angeles Latino eye study (LALES). **2009**, 10, 71	22
1432	Single nucleotide polymorphisms in obesity-related genes and all-cause and cause-specific mortality: a prospective cohort study. **2009**, 10, 103	20
1431	Evaluating the association of common APOA2 variants with type 2 diabetes. **2009**, 10, 13	9
1430	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
1429	Functional and genetic analysis in type 2 diabetes of liver X receptor alleles--a cohort study. **2009**, 10, 27	20

1428	Contribution of type 2 diabetes associated loci in the Arabic population from Tunisia: a case-control study. **2009**, 10, 33	54
1427	Type 2 diabetes gene TCF7L2 polymorphism is not associated with fetal and postnatal growth in two birth cohort studies. **2009**, 10, 67	12
1426	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
1425	SLC6A3 and body mass index in the Prostate, Lung, Colorectal and Ovarian Cancer Screening Trial. **2009**, 10, 9	4
1424	Zinc transporter gene expression is regulated by pro-inflammatory cytokines: a potential role for zinc transporters in beta-cell apoptosis?. **2009**, 9, 7	42
1423	MODY-like diabetes associated with an apparently balanced translocation: possible involvement of MPP7 gene and cell polarity in the pathogenesis of diabetes. **2009**, 2, 5	7
1422	Genetics and visceral leishmaniasis: of mice and man. **2009**, 31, 254-66	80
1421	STrengthening the REporting of Genetic Association studies (STREGA)--an extension of the STROBE statement. **2009**, 39, 247-66	190
1420	Association of genetic variation on chromosome 9p21.3 and arterial stiffness. **2009**, 265, 373-81	43
1419	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
1418	Global similarity with local differences in linkage disequilibrium between the Dutch and HapMap-CEU populations. **2009**, 17, 802-10	12
1417	Genetic association analysis of 13 nuclear-encoded mitochondrial candidate genes with type II diabetes mellitus: the DAMAGE study. **2009**, 17, 1056-62	12
1416	Joint analysis of tightly linked SNPs in screening step of genome-wide association studies leads to increased power. **2009**, 17, 1043-9	15
1415	Differential contribution of CDKAL1 variants to psoriasis, Crohn's disease and type II diabetes. **2009** , 10, 654-8	43
1414	Effect of BSN-MST1 locus on inflammatory bowel disease and multiple sclerosis susceptibility. **2009** , 10, 631-5	16
1413	Human genetics illuminates the paths to metabolic disease. **2009**, 462, 307-14	260
1412	Common variant in MTNR1B associated with increased risk of type 2 diabetes and impaired early insulin secretion. **2009**, 41, 82-8	550
1411	Variants in MTNR1B influence fasting glucose levels. **2009**, 41, 77-81	584

1410	New common variants affecting susceptibility to basal cell carcinoma. **2009**, 41, 909-14	275
1409	Genetic variant near IRS1 is associated with type 2 diabetes, insulin resistance and hyperinsulinemia. **2009**, 41, 1110-5	356
1408	Genetic prognostic and predictive markers in colorectal cancer. **2009**, 9, 489-99	517
1407	Beyond odds ratios--communicating disease risk based on genetic profiles. **2009**, 10, 264-9	113
1406	Validating, augmenting and refining genome-wide association signals. **2009**, 10, 318-29	306
1405	Human genetic variation and its contribution to complex traits. **2009**, 10, 241-51	778
1404	Detecting gene-gene interactions that underlie human diseases. **2009**, 10, 392-404	990
1403	Structural basis for autoregulation of the zinc transporter YiiP. **2009**, 16, 1063-7	192
1402	Association analyses between type 2 diabetes genes and obesity traits in pigs. **2009**, 17, 323-9	22
1401	Variation in IGF2BP2 interacts with adiposity to alter insulin sensitivity in Mexican Americans. **2009**, 17, 729-36	30
1400	A rare variant in the visfatin gene (NAMPT/PBEF1) is associated with protection from obesity. **2009**, 17, 1549-53	52
1399	Genetic gains on the obesity and metabolic disease fronts. **2009**, 76, 236-41	1
1398	1. DNA Collection in a Randomized Social Science Study of College Peer Effects. **2009**, 39, 1-29	9
1397	Genetic and biochemical pathways of beta-cell failure in type 2 diabetes. **2009**, 11 Suppl 4, 38-45	49
1396	Genetic basis of beta-cell dysfunction in man. **2009**, 11 Suppl 4, 149-58	15
1395	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
1394	Expression of p16(INK4a) in peripheral blood T-cells is a biomarker of human aging. **2009**, 8, 439-48	285
1393	Zinc and diabetes--clinical links and molecular mechanisms. **2009**, 20, 399-417	290

1392	Zn(2+)-transporter-8: a dual role in diabetes. **2009**, 35, 356-63	15
1391	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
1390	Gene ontology analysis of GWA study data sets provides insights into the biology of bipolar disorder. **2009**, 85, 13-24	333
1389	ATRIUM: testing untyped SNPs in case-control association studies with related individuals. **2009**, 85, 667-78	6
1388	Meta-analysis of genome-wide association studies with overlapping subjects. **2009**, 85, 862-72	101
1387	Simultaneous genotype calling and haplotype phasing improves genotype accuracy and reduces false-positive associations for genome-wide association studies. **2009**, 85, 847-61	165
1386	Genetic architecture of type 2 diabetes: recent progress and clinical implications. **2009**, 32, 1107-14	51
1385	Adaptive beta-cell proliferation is severely restricted with advanced age. **2009**, 58, 1365-72	257
1384	Insulin crystallization depends on zinc transporter ZnT8 expression, but is not required for normal glucose homeostasis in mice. **2009**, 106, 14872-7	257
1383	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
1382	Prediction of cardiovascular disease outcomes and established cardiovascular risk factors by genome-wide association markers. **2009**, 2, 7-15	60
1381	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
1380	Bench-to-bedside review: Association of genetic variation with sepsis. **2009**, 13, 210	63
1379	TCF7L2 regulates late events in insulin secretion from pancreatic islet beta-cells. **2009**, 58, 894-905	157
1378	The FTO gene modifies weight, fat mass and insulin sensitivity in women with polycystic ovary syndrome, where its role may be larger than in other phenotypes. **2009**, 35, 328-31	31
1377	Genetic variations of solute carrier family 30 (zinc transporter) member 8 (SLC30A8) are not associated with polycystic ovary syndrome. **2009**, 91, 1598-601	4
1376	The Pro12Ala PPARgamma2 variant determines metabolism at the gene-environment interface. **2009**, 9, 88-98	57
1375	Hyperinsulinism and diabetes: genetic dissection of beta cell metabolism-excitation coupling in mice. **2009**, 10, 442-53	30

1374	Beta-cell deterioration during diabetes: what's in the gun?. **2009**, 20, 388-93	77
1373	Pilot study: association of traditional and genetic risk factors and new-onset diabetes mellitus following kidney transplantation. **2009**, 41, 4172-7	27
1372	Genome-wide association studies in type 1 diabetes, inflammatory bowel disease and other immune-mediated disorders. **2009**, 21, 355-62	15
1371	Mitochondrial dysfunction in pancreatic beta-cells in Type 2 diabetes. **2009**, 297, 34-40	92
1370	The AMP-regulated kinase family: enigmatic targets for diabetes therapy. **2009**, 297, 41-9	64
1369	Genetic dissection of type 2 diabetes. **2009**, 297, 10-7	111
1368	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
1367	Genome-wide association studies reach hepatology. **2009**, 50, 1278-80	1
1366	Healing and hurting: molecular mechanisms, functions, and pathologies of cellular senescence. **2009**, 36, 2-14	249
1365	Use of multiple metabolic and genetic markers to improve the prediction of type 2 diabetes: the EPIC-Potsdam Study. **2009**, 32, 2116-9	107
1364	TCF7L2 rs12255372 and SLC30A8 rs13266634 confer susceptibility to type 2 diabetes in a Russian population. **2009**, 3, 219-223	3
1363	Genetic risk factors for type 2 diabetes with pharmacologic intervention in African-American patients with schizophrenia or schizoaffective disorder. **2009**, 114, 50-6	12
1362	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
1361	Latent autoimmune diabetes in adults. **2009**, 94, 4635-44	149
1360	The Molecular Genetics of Type 2 Diabetes: Past, Present and Future. **2009**,	1
1359	Investigation of Crohn's disease risk loci in ulcerative colitis further defines their molecular relationship. **2009**, 136, 523-9.e3	152
1358	Epigenetics: a molecular link between environmental factors and type 2 diabetes. **2009**, 58, 2718-25	439
1357	Mammalian zinc transporters: nutritional and physiologic regulation. **2009**, 29, 153-76	539

1356 Genes and Gene Environment Interactions in the Pathogenesis of Obesity and the Metabolic Syndrome. **2009**, 11-39

1355 Single Nucleotide Polymorphisms. **2009**, 23

1354 The HapMap and genome-wide association studies in diagnosis and therapy. **2009**, 60, 443-56 155

1353 How to use an article about genetic association: B: Are the results of the study valid?. **2009**, 301, 191-7 98

1352 How to use an article about genetic association: A: Background concepts. **2009**, 301, 74-81 68

1351 Meta-analysis in genome-wide association studies. **2009**, 10, 191-201 199

1350 Significance of genome-wide association studies in molecular anthropology. **2009**, 13, 711-5

1349 Genome-wide association study in humans. **2009**, 573, 231-58 15

1348 Cardiovascular Genomics. **2009**, 1

1347 Role of MAPK in apolipoprotein CIII-induced apoptosis in INS-1E cells. **2009**, 8, 3 22

1346 Enrichment of sequencing targets from the human genome by solution hybridization. **2009**, 10, R116 92

1345 Worldwide patterns of haplotype diversity at 9p21.3, a locus associated with type 2 diabetes and coronary heart disease. **2009**, 1, 51 31

1344 DNA variations in human and medical genetics: 25 years of my experience. **2009**, 54, 1-8 52

1343 Molecular Endocrinology. **2009**, 4

1342 A fingerprint marker from early gestation associated with diabetes in middle age: the Dutch Hunger Winter Families Study. **2009**, 38, 101-9 33

1341 Genetics of diabetic nephropathy: are there clues to the understanding of common kidney diseases?. **2009**, 112, c213-21 24

1340 Tissue-specific alternative splicing of TCF7L2. *Human Molecular Genetics*, **2009**, 18, 3795-804 5.6 89

1339 Genetic determinants and molecular pathways in the pathogenesis of Type 2 diabetes. **2009**, 116, 99-111 52

1338	Molecular time: an often overlooked dimension to cardiovascular disease. **2009**, 105, 1047-61	86
1337	Genomic regulatory blocks in vertebrates and implications in human disease. **2009**, 8, 333-42	27
1336	An overview of recent developments in genomics and associated statistical methods. **2009**, 367, 4313-37	24
1335	Haplotypic background of a private allele at high frequency in the Americas. **2009**, 26, 995-1016	48
1334	Discovery properties of genome-wide association signals from cumulatively combined data sets. **2009**, 170, 1197-206	50
1333	Pancreatic islet inflammation in type 2 diabetes: from alpha and beta cell compensation to dysfunction. **2009**, 115, 240-7	73
1332	Shared genomics: A platform for emerging interpretation of genetic epidemiology. **2009**,	
1331	Genomics of type 2 diabetes mellitus: implications for the clinician. **2009**, 5, 429-36	68
1330	Genetic variants associated with Lp(a) lipoprotein level and coronary disease. **2009**, 361, 2518-28	935
1329	FTO polymorphisms are associated with obesity but not with diabetes in East Asian populations: a meta-analysis. **2009**, 22, 449-57	31
1328	Association of the CPT1B gene with skeletal muscle fat infiltration in Afro-Caribbean men. **2009**, 17, 1396-401	15
1327	A genome-wide association study primer for clinicians. **2009**, 48, 89-95	15
1326	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
1325	Genotype imputation. **2009**, 10, 387-406	812
1324	Genetic epidemiology in aging research. **2009**, 64, 47-60	17
1323	Genotyping technologies for genetic research. **2009**, 10, 117-33	164
1322	Genetic regulation of adult stature. **2009**, 21, 515-22	50
1321	Selected summaries from the XVI World Congress of Psychiatric Genetics, Osaka, Japan, 11-15 October 2008. **2009**, 19, 219-36	2

1320	Association of common type 2 diabetes risk gene variants and posttransplantation diabetes mellitus in renal allograft recipients in Korea. **2009**, 88, 693-8	32
1319	Genome-wide association study for type 2 diabetes: clinical applications. **2009**, 20, 87-91	34
1318	Fostering translation of genetics research: an NIDDK perspective. **2009**, 6, 579-588	1
1317	Selective inference in complex research. **2009**, 367, 4255-71	55
1316	Does direct-to-consumer prescription drug advertising do more harm than good?. **2009**, 151, 823-4; author reply 824	1
1315	Replication in genome-wide association studies. **2009**, 24, 561-573	177
1314	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
1313	Deletion of the mouse Slc30a8 gene encoding zinc transporter-8 results in impaired insulin secretion. **2009**, 421, 371-6	141
1312	Cardiovascular disease risk prediction with and without knowledge of genetic variation at chromosome 9p21.3. **2009**, 150, 65-72	181
1311	Is lifelong anticoagulation worth the risk in patients with unprovoked DVT?. **2009**, 151, 827; author reply 827	
1310	Racial differences in myocardial infarction outcomes. **2009**, 151, 823; author reply 823	
1309	Ultrasonography to guide duration of anticoagulation in DVT. **2009**, 151, 826; author reply 826-7	
1308	Ultrasonography to guide duration of anticoagulation in DVT. **2009**, 151, 825-6; author reply 826-7	
1307	Racial differences in myocardial infarction outcomes. **2009**, 151, 823; author reply 823	
1306	Erratum. **2009**, 11, 594-594	
1305	Understanding the combined effects of conventional risk factors and genetic loci on diabetes incidence. **2009**, 151, 824-5; author reply 825	
1304	Correction: In the Clinic: Community-Acquired Pneumonia. **2009**, 151, 827	
1303	Dissecting the phenotype in genome-wide association studies of psychiatric illness. **2009**, 195, 97-9	54

1302	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
1301	Type 2 Diabetes Mellitus: New Genetic Insights will Lead to New Therapeutics. **2009**, 10, 110-8	25
1300	Pharmacogenetics and functional genomics in asthma. **2009**, 6, 409-416	0
1299	Novel biological insights emerging from genetic studies of type 2 diabetes and related metabolic traits. **2010**, 21, 44-50	32
1298	Genetics of type 2 diabetes. **2010**, 13, 471-7	26
1297	Recent advances in the genetics and genomics of asthma and related traits. **2010**, 22, 307-12	9
1296	Interactions between genetic factors that predict diabetes and dietary factors that ultimately impact on risk of diabetes. **2010**, 21, 31-7	25
1295	Genes and Response to Training. **2010**, 177-184	1
1294	TCF7L2 rs12255372 and SLC30A8 rs13266634 confer susceptibility to type 2 diabetes in a Russian population. **2010**, 46, 1001-1008	1
1293	Identification of KCNJ15 as a susceptibility gene in Asian patients with type 2 diabetes mellitus. **2010**, 86, 54-64	45
1292	Robust replication of genotype-phenotype associations across multiple diseases in an electronic medical record. **2010**, 86, 560-72	264
1291	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
1290	Genetics of coronary artery disease. **2010**, 11, 91-108	67
1289	Effects of ascertainment bias and marker number on estimations of barley diversity from high-throughput SNP genotype data. **2010**, 120, 1525-34	91
1288	Genetic association analysis of LARS2 with type 2 diabetes. **2010**, 53, 103-10	8
1287	Diet-induced gene expression of isolated pancreatic islets from a polygenic mouse model of the metabolic syndrome. **2010**, 53, 309-20	39
1286	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
1285	The ENPP1 K121Q polymorphism determines individual susceptibility to the insulin-sensitising effect of lifestyle intervention. **2010**, 53, 504-9	12

1284	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
1283	Beta cell-specific Znt8 deletion in mice causes marked defects in insulin processing, crystallisation and secretion. **2010**, 53, 1656-68	228
1282	Evidence that BMI and type 2 diabetes share only a minor fraction of genetic variance: a follow-up study of 23,585 monozygotic and dizygotic twins from the Finnish Twin Cohort Study. **2010**, 53, 1314-21	46
1281	The suppressor of cytokine signalling 2 (SOCS2) is a key repressor of insulin secretion. **2010**, 53, 1935-46	21
1280	Type 2 diabetes risk alleles near ADCY5, CDKAL1 and HHEX-IDE are associated with reduced birthweight. **2010**, 53, 1908-16	56
1279	Disease-associated loci are significantly over-represented among genes bound by transcription factor 7-like 2 (TCF7L2) in vivo. **2010**, 53, 2340-6	37
1278	Genetic variants affecting incretin sensitivity and incretin secretion. **2010**, 53, 2289-97	32
1277	Association analysis of SLC30A8 rs13266634 and rs16889462 polymorphisms with type 2 diabetes mellitus and repaglinide response in Chinese patients. **2010**, 66, 1207-15	51
1276	K(ATP) channelopathies in the pancreas. **2010**, 460, 307-20	27
1275	Evaluating variations of genotype calling: a potential source of spurious associations in genome-wide association studies. **2010**, 89, 55-64	11
1274	Type 2 Diabetes and Genetics, 2010: Translating Knowledge into Understanding. **2010**, 4, 437-445	3
1273	The genetics of insulin resistance: Where's Waldo?. **2010**, 10, 476-84	27
1272	From genetic association to molecular mechanism. **2010**, 10, 452-66	27
1271	Polymorphisms of TCF7L2 and HHEX genes in Chinese women with polycystic ovary syndrome. **2010**, 27, 23-8	26
1270	Association study of four variants in KCNQ1 with type 2 diabetes mellitus and premature coronary artery disease in a Chinese population. **2010**, 37, 207-12	26
1269	Toll-like receptor 4 and inducible nitric oxide synthase gene polymorphisms are associated with Type 2 diabetes. **2010**, 24, 192-8	35
1268	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
1267	Replication of recently described type 2 diabetes gene variants in a South Indian population. **2010**, 59, 1760-6	39

1266	Evaluating diabetes and hypertension disease causality using mouse phenotypes. **2010**, 4, 97	3
1265	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
1264	Experimental approaches to the study of epigenomic dysregulation in ageing. **2010**, 45, 255-68	14
1263	Identification of genetic factors associated with Type 2 Diabetes in Saudis: The lessons from European studies. **2010**, 2, 133-136	1
1262	Over-expression of ZnT7 increases insulin synthesis and secretion in pancreatic beta-cells by promoting insulin gene transcription. **2010**, 316, 2630-43	47
1261	Detecting rare variants for complex traits using family and unrelated data. **2010**, 34, 171-87	103
1260	Optimizing the power of genome-wide association studies by using publicly available reference samples to expand the control group. **2010**, 34, 319-26	13
1259	A powerful approach to sub-phenotype analysis in population-based genetic association studies. **2010**, 34, 335-43	39
1258	Resequencing of pooled DNA for detecting disease associations with rare variants. **2010**, 34, 492-501	21
1257	Identifying candidate causal variants via trans-population fine-mapping. **2010**, 34, 653-64	27
1256	SNP selection in genome-wide and candidate gene studies via penalized logistic regression. **2010**, 34, 879-91	133
1255	A genetic variation in the fat mass- and obesity-associated gene is associated with obesity and newly diagnosed type 2 diabetes in a Chinese population. **2010**, 26, 128-32	27
1254	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
1253	Genetic Mapping of Complex Traits. **2010**, 67-90	1
1252	Simultaneous and selective inference: Current successes and future challenges. **2010**, 52, 708-21	91
1251	Obesity and diabetes genes are associated with being born small for gestational age: results from the Auckland Birthweight Collaborative study. **2010**, 11, 125	47
1250	The longitudinal association of common susceptibility variants for type 2 diabetes and obesity with fasting glucose level and BMI. **2010**, 11, 140	14
1249	Chromosome 7p linkage and association study for diabetes related traits and type 2 diabetes in an African-American population enriched for nephropathy. **2010**, 11, 22	11

1248	Common genetic variants on chromosome 9p21 are associated with myocardial infarction and type 2 diabetes in an Italian population. **2010**, 11, 60		16
1247	Large-scale association analysis of TNF/LTA gene region polymorphisms in type 2 diabetes. **2010**, 11, 69		34
1246	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
1245	Association study of genetic variants in eight genes/loci with type 2 diabetes in a Han Chinese population. **2010**, 11, 97		66
1244	KCNQ1 gene polymorphisms are associated with lipid parameters in a Chinese Han population. *Cardiovascular Diabetology*, **2010**, 9, 35	8.7	22
1243	Translating type 2 diabetes genetics: what does it add to clinical practice?. **2010**, 27, 264-266		
1242	Bayesian methods for examining Hardy-Weinberg equilibrium. **2010**, 66, 257-65		24
1241	FTO genotype is associated with exercise training-induced changes in body composition. **2010**, 18, 322-6		38
1240	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
1239	Association of FTO variants with BMI and fat mass in the self-contained population of Sorbs in Germany. **2010**, 18, 104-10		71
1238	Gene and pathway-based second-wave analysis of genome-wide association studies. **2010**, 18, 111-7		189
1237	Replication of past candidate loci for common diseases and phenotypes in 100 genome-wide association studies. **2010**, 18, 832-7		94
1236	Assessing sources of inconsistencies in genotypes and their effects on genome-wide association studies with HapMap samples. **2010**, 10, 364-74		18
1235	IGF2BP2 variations influence repaglinide response and risk of type 2 diabetes in Chinese population. **2010**, 31, 709-17		38
1234	Genome-wide association study identifies five new breast cancer susceptibility loci. **2010**, 42, 504-7		582
1233	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. **2010**, 42, 579-89		1449
1232	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
1231	Kinase mutations in human disease: interpreting genotype-phenotype relationships. **2010**, 11, 60-74		250

1230	Genotype imputation for genome-wide association studies. **2010**, 11, 499-511		1134
1229	Nutrigenomics: where are we with genetic and epigenetic markers for disposition and susceptibility?. **2010**, 68 Suppl 1, S38-47		34
1228	The role of peroxisome proliferator-activated receptor □n pancreatic □cell function and survival: therapeutic implications for the treatment of type 2 diabetes mellitus. **2010**, 12, 1036-47		50
1227	Fertile soil or no man□ land:. 165-173		11
1226	The search for susceptibility genes. 174-182		
1225	Genetics and pathogenesis of polycystic ovary syndrome. 13-24		
1224	Association between type 2 diabetes loci and measures of fatness. *PLoS ONE*, **2010**, 5, e8541	3.7	15
1223	A new statistic to evaluate imputation reliability. *PLoS ONE*, **2010**, 5, e9697	3.7	47
1222	Common SNPs in FTO gene are associated with obesity related anthropometric traits in an island population from the eastern Adriatic coast of Croatia. *PLoS ONE*, **2010**, 5, e10375	3.7	26
1221	Risk of type 2 diabetes and obesity is differentially associated with variation in FTO in whites and African-Americans in the ARIC study. *PLoS ONE*, **2010**, 5, e10521	3.7	61
1220	Multiethnic genetic association studies improve power for locus discovery. *PLoS ONE*, **2010**, 5, e12600	3.7	44
1219	Integrated genetic and epigenetic analysis identifies haplotype-specific methylation in the FTO type 2 diabetes and obesity susceptibility locus. *PLoS ONE*, **2010**, 5, e14040	3.7	193
1218	Analyses of copy number variation of GK rat reveal new putative type 2 diabetes susceptibility loci. *PLoS ONE*, **2010**, 5, e14077	3.7	10
1217	Identification of genes and networks driving cardiovascular and metabolic phenotypes in a mouse F2 intercross. *PLoS ONE*, **2010**, 5, e14319	3.7	36
1216	Presymptomatic risk assessment for chronic non-communicable diseases. *PLoS ONE*, **2010**, 5, e14338	3.7	11
1215	CDKAL1 and type 2 diabetes: a global meta-analysis. **2010**, 9, 1109-20		60
1214	High Fat Diet Regulation of □-Cell Proliferation and □-Cell Mass. **2010**, 4,		40
1213	Fine-mapping a locus for glucose tolerance using heterogeneous stock rats. **2010**, 41, 102-8		40

1212	The epidemiology of diabetes in Korea: from the economics to genetics. **2010**, 34, 10-5		16
1211	[The amazing story of ANRIL, a long non-coding RNA]. **2010**, 26, 564-6		4
1210	Impact of single nucleotide polymorphisms and of clinical risk factors on new-onset diabetes mellitus in HIV-infected individuals. **2010**, 51, 1090-8		21
1209	Genetic variants in ABO blood group region, plasma soluble E-selectin levels and risk of type 2 diabetes. *Human Molecular Genetics*, **2010**, 19, 1856-62	5.6	131
1208	Investigation of type 2 diabetes risk alleles support CDKN2A/B, CDKAL1, and TCF7L2 as susceptibility genes in a Han Chinese cohort. *PLoS ONE*, **2010**, 5, e9153	3.7	94
1207	Epigenetic regulation of p16Ink4a and Arf by JDP2 in cellular senescence. **2010**, 1, 49-58		
1206	Use of mouse models in studying type 2 diabetes mellitus. **2011**, 13, e1		20
1205	Genetic variation at the FTO locus influences RBL2 gene expression. **2010**, 59, 726-32		42
1204	Association of single nucleotide polymorphisms on chromosome 9p21.3 with platelet reactivity: a potential mechanism for increased vascular disease. **2010**, 3, 445-53		48
1203	Cyclin D2 is essential for the compensatory beta-cell hyperplastic response to insulin resistance in rodents. **2010**, 59, 987-96		54
1202	Functional variants in MBL2 are associated with type 2 diabetes and pre-diabetes traits in Pima Indians and the old order Amish. **2010**, 59, 2080-5		14
1201	Acute cytokine-mediated downregulation of the zinc transporter ZnT8 alters pancreatic beta-cell function. **2010**, 206, 159-69		43
1200	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
1199	The genetics of obesity and the metabolic syndrome. **2010**, 10, 86-108		47
1198	DataSHIELD: resolving a conflict in contemporary bioscience--performing a pooled analysis of individual-level data without sharing the data. **2010**, 39, 1372-82		102
1197	Association between a literature-based genetic risk score and cardiovascular events in women. **2010**, 303, 631-7		256
1196	Diabetes in Women. **2010**,		1
1195	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

1194	The genetics of type 2 diabetes: what have we learned from GWAS?. **2010**, 1212, 59-77	264
1193	Combining genetic markers and clinical risk factors improves the risk assessment of impaired glucose metabolism. **2010**, 42, 196-206	10
1192	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
1191	Long-range gene regulation links genomic type 2 diabetes and obesity risk regions to HHEX, SOX4, and IRX3. **2010**, 107, 775-80	159
1190	Progress in the genetics of common obesity and type 2 diabetes. **2010**, 12, e7	67
1189	Genetic influences on the association between fetal growth and susceptibility to type 2 diabetes. **2010**, 1, 96-105	6
1188	Polygenic risk variants for type 2 diabetes susceptibility modify age at diagnosis in monogenic HNF1A diabetes. **2010**, 59, 266-71	25
1187	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
1186	Genetic heterogeneity in latent autoimmune diabetes is linked to various degrees of autoimmune activity: results from the Nord-Tr□delag Health Study. **2010**, 59, 302-10	59
1185	Colloquium paper: bioenergetics, the origins of complexity, and the ascent of man. **2010**, 107 Suppl 2, 8947-53	93
1184	Screening the mammalian extracellular proteome for regulators of embryonic human stem cell pluripotency. **2010**, 107, 3552-7	82
1183	Examination of all type 2 diabetes GWAS loci reveals HHEX-IDE as a locus influencing pediatric BMI. **2010**, 59, 751-5	49
1182	Aging induces a distinct gene expression program in mouse islets. **2010**, 2, 345-52	33
1181	A European evidence-based guideline for the prevention of type 2 diabetes. **2010**, 42 Suppl 1, S3-36	317
1180	Identification of new genetic risk variants for type 2 diabetes. **2010**, 6, e1001127	168
1179	Genome-wide significant associations for variants with minor allele frequency of 5% or less--an overview: A HuGE review. **2010**, 172, 869-89	38
1178	Association of a cyclin-dependent kinase 5 regulatory subunit-associated protein 1-like 1 (CDKAL1) polymorphism with elevated hemoglobin A□c) levels and the prevalence of metabolic syndrome in Japanese men: interaction with dietary energy intake. **2010**, 172, 985-91	16
1177	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

1176	A genome-wide association study identifies susceptibility variants for type 2 diabetes in Han Chinese. **2010**, 6, e1000847		251
1175	Common inherited variation in mitochondrial genes is not enriched for associations with type 2 diabetes or related glycemic traits. **2010**, 6, e1001058		366
1174	Expression of linear and novel circular forms of an INK4/ARF-associated non-coding RNA correlates with atherosclerosis risk. **2010**, 6, e1001233		653
1173	Chromosome 9p21 SNPs Associated with Multiple Disease Phenotypes Correlate with ANRIL Expression. **2010**, 6, e1000899		291
1172	A genome-wide association study of optic disc parameters. **2010**, 6, e1000978		157
1171	Whole-genome linkage and association scan in primary, nonsyndromic vesicoureteric reflux. **2010**, 21, 113-23		51
1170	Ethical considerations in the collection of genetic data from critically ill patients: what do published studies reveal about potential directions for empirical ethics research?. **2010**, 10, 77-85		8
1169	Quantification of population structure using correlated SNPs by shrinkage principal components. **2010**, 70, 9-22		40
1168	Genome-wide association study of coronary artery disease. **2010**, 2010, 790539		12
1167	Consistent association of type 2 diabetes risk variants found in europeans in diverse racial and ethnic groups. **2010**, 6, e1001078		142
1166	Experimental approaches for identifying schizophrenia risk genes. **2010**, 4, 587-610		4
1165	Utility of genetic and non-genetic risk factors in prediction of type 2 diabetes: Whitehall II prospective cohort study. **2010**, 340, b4838		211
1164	An interactive effect of batch size and composition contributes to discordant results in GWAS with the CHIAMO genotyping algorithm. **2010**, 10, 355-63		10
1163	Combined effects of 19 common variations on type 2 diabetes in Chinese: results from two community-based studies. *PLoS ONE*, **2010**, 5, e14022	3.7	68
1162	Association of variants at 1q32 and STAT3 with ankylosing spondylitis suggests genetic overlap with Crohn's disease. **2010**, 6, e1001195		162
1161	Epigenetic regulation of the INK4b-ARF-INK4a locus: in sickness and in health. **2010**, 5, 685-90		168
1160	The relationship between smoking and replicated sequence variants on chromosomes 8 and 9 with familial intracranial aneurysm. **2010**, 41, 1132-7		44
1159	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

1158	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
1157	The genetics of autism: key issues, recent findings, and clinical implications. **2010**, 33, 83-105	98
1156	Factores genéticos frente a factores ambientales en el desarrollo de la diabetes tipo 2. **2010**, 26, 268-269	1
1155	Genetic variants in MTNR1B affecting insulin secretion. **2010**, 42, 387-93	32
1154	Wnt signaling in pancreatic islets. **2010**, 654, 391-419	68
1153	Two-stage testing strategies for genome-wide association studies in family-based designs. **2010**, 620, 485-96	5
1152	[Association of FTO gene polymorphisms and morbid obesity in the population of Extremadura (Spain)]. **2010**, 57, 203-9	12
1151	Genomewide association study of movement-related adverse antipsychotic effects. **2010**, 67, 279-82	107
1150	Gene-wide association study between the methylenetetrahydrofolate reductase gene (MTHFR) and schizophrenia in the Japanese population, with an updated meta-analysis on currently available data. **2010**, 124, 216-22	26
1149	FoxM1 is up-regulated by obesity and stimulates beta-cell proliferation. **2010**, 24, 1822-34	69
1148	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
1147	No association between polymorphisms in the INSIG1 gene and the risk of type 2 diabetes and related traits. **2010**, 92, 252-7	8
1146	Role of zinc in human islet amyloid polypeptide aggregation. **2010**, 132, 8973-83	181
1145	Role of Nutrition in the Pathophysiology, Prevention, and Treatment of Type 2 Diabetes and the Spectrum of Cardiometabolic Disease. **2010**, 371-387	
1144	Association of the ADIPOQ rs17360539 and rs266729 polymorphisms with type 2 diabetes: a meta-analysis. **2010**, 325, 78-83	37
1143	IGF2BP1, IGF2BP2 and IGF2BP3 genotype, haplotype and genetic model studies in metabolic syndrome traits and diabetes. **2010**, 20, 310-8	27
1142	Gestational diabetes mellitus screening based on the gene chip technique. **2010**, 89, 167-73	15
1141	Antidiabetic effects of IGFBP2, a leptin-regulated gene. **2010**, 11, 11-22	203

1140	TCF7L2 is associated with type 2 diabetes in nonobese individuals from Tunisia. **2010**, 58, 426-9	13
1139	Expansion of beta-cell mass in response to pregnancy. **2010**, 21, 151-8	229
1138	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
1137	Meta-analysis and functional effects of the SLC30A8 rs13266634 polymorphism on isolated human pancreatic islets. **2010**, 100, 77-82	83
1136	Apolipoprotein E polymorphisms and type 2 diabetes: a meta-analysis of 30 studies including 5423 cases and 8197 controls. **2010**, 100, 283-91	57
1135	The pursuit of genome-wide association studies: where are we now?. **2010**, 55, 195-206	172
1134	Histone chaperone Jun dimerization protein 2 (JDP2): role in cellular senescence and aging. **2010**, 26, 515-31	10
1133	Replication of association between schizophrenia and ZNF804A in the Irish Case-Control Study of Schizophrenia sample. **2010**, 15, 29-37	182
1132	Statins and risk of incident diabetes: a collaborative meta-analysis of randomised statin trials. **2010**, 375, 735-42	1644
1131	Genomics, type 2 diabetes, and obesity. **2010**, 363, 2339-50	696
1130	Statistical Methods in Molecular Biology. **2010**,	10
1129	Evolutionary adaptations to dietary changes. **2010**, 30, 291-314	119
1128	Genomics of Myocardial Infarction. **2010**, 289-302	
1127	Diabetes. **2010**, 676-684	
1126	Pharmacogenetics of Anti-Diabetes Drugs. **2010**, 3, 2610-2646	70
1125	Zinc-dependent effects of small molecules on the insulin-sensitive transcription factor FOXO1a and gluconeogenic genes. **2010**, 2, 195-203	17
1124	Inherited destiny? Genetics and gestational diabetes mellitus. **2011**, 3, 18	17
1123	LOC387761 polymorphism is associated with type 2 diabetes in the Mexican population. **2011**, 15, 79-83	10

1122	ANRIL, a long, noncoding RNA, is an unexpected major hotspot in GWAS. **2011**, 25, 444-8	361
1121	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
1120	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
1119	Type 2 diabetes risk variants and colorectal cancer risk: the Multiethnic Cohort and PAGE studies. **2011**, 60, 1703-11	35
1118	1. Diabetes in the Elderly Population: Pathophysiology, Prevention, and Management. **2011**, 9-37	1
1117	Association of obesity-related genetic variants with endometrial cancer risk: a report from the Shanghai Endometrial Cancer Genetics Study. **2011**, 174, 1115-26	49
1116	Cyclin-dependent kinase 5 promotes pancreatic □-cell survival via Fak-Akt signaling pathways. **2011**, 60, 1186-97	34
1115	At-risk variant in TCF7L2 for type II diabetes increases risk of schizophrenia. **2011**, 70, 59-63	101
1114	Statistical issues in gene association studies. **2011**, 700, 17-36	10
1113	Association of genetic variations in TCF7L2, SLC30A8, HHEX, LOC387761, and EXT2 with Type 2 diabetes mellitus in Tunisia. **2011**, 15, 399-405	28
1112	Development of a predictive model for type 2 diabetes mellitus using genetic and clinical data. **2011**, 2, 75-82	13
1111	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
1110	Does a short breastfeeding period protect from FTO-induced adiposity in children?. **2011**, 6, e326-35	16
1109	CDKN2BAS is associated with periodontitis in different European populations and is activated by bacterial infection. **2011**, 48, 38-47	57
1108	Epigenetic Aspects of Chronic Diseases. **2011**,	2
1107	Genetic variations in the FTO gene are associated with type 2 diabetes and obesity in south Indians (CURES-79). **2011**, 13, 33-42	52
1106	Comprehensive Cardiovascular Medicine in the Primary Care Setting. **2011**,	
1105	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

1104	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
1103	Planning a genome-wide association study: points to consider. **2011**, 43, 451-60	14
1102	Genetic Epidemiology. **2011**,	2
1101	Cardiovascular diseases and genome-wide association studies. **2011**, 412, 1697-701	19
1100	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
1099	Association between polymorphisms in RAPGEF1, TP53, NRF1 and type 2 diabetes in Chinese Han population. **2011**, 91, 171-6	22
1098	Transcription factor 7-like 2 (TCF7L2) gene polymorphism and complication/comorbidity profile in type 2 diabetes patients. **2011**, 93, 390-5	24
1097	Molecular genetics in glaucoma. **2011**, 93, 331-9	95
1096	Genetics and epigenetics of obesity. **2011**, 69, 41-9	190
1095	Quantitative assessment of the influence of hematopoietically expressed homeobox variant (rs1111875) on type 2 diabetes risk. **2011**, 102, 194-9	9
1094	Association of ACACB polymorphisms with obesity and diabetes. **2011**, 104, 670-6	29
1093	Endoplasmic reticulum stress and pancreatic □-cell death. **2011**, 22, 266-74	245
1092	SLC30A8 polymorphism and type 2 diabetes risk: evidence from 27 study groups. **2011**, 21, 398-405	22
1091	Variants at the endocannabinoid receptor CB1 gene (CNR1) and insulin sensitivity, type 2 diabetes, and coronary heart disease. **2011**, 19, 2031-7	13
1090	The chromosome 9p21 region and myocardial infarction in a European population. **2011**, 217, 220-6	20
1089	Efficacy and safety of statin treatment for cardiovascular disease: a network meta-analysis of 170,255 patients from 76 randomized trials. **2011**, 104, 109-24	222
1088	Cell cycle control of □-cell replication in the prenatal and postnatal human pancreas. **2011**, 300, E221-30	54
1087	Genome-wide association studies: results from the first few years and potential implications for clinical medicine. **2011**, 62, 11-24	73

1086	Genome-wide association studies and type 2 diabetes. **2011**, 10, 52-60		82
1085	New type 2 diabetes risk genes provide new insights in insulin secretion mechanisms. **2011**, 93 Suppl 1, S9-24		55
1084	Genetic Polymorphisms in the Fat Mass and Obesity-Associated Gene Confers Risk of Obesity in Iraqi Population. **2011**, 7, 40-44		
1083	Bioinformatics Approaches. **2011**, 251-260		
1082	Delineating Signals from Association Studies. **2011**, 277-293		
1081	The search for genetic risk factors of type 2 diabetes mellitus. **2011**, 35, 12-22		26
1080	Pharmacogenetics for T2DM and Anti-Diabetic Drugs. **2011**,		
1079	A Genome-wide Association Case Study on Obesity. **2011**, 295-306		
1078	Data Quality Control. **2011**, 95-108		3
1077	Genetic Association Study Design. **2011**, 25-48		1
1076	Aging and Insulin Secretion. **2011**, 373-384		3
1075	Genetics of childhood obesity. **2011**, 2011, 845148		38
1074	Association of genetic variation on chromosome 9p21 with polypoidal choroidal vasculopathy and neovascular age-related macular degeneration. **2011**, 52, 8063-7		19
1073	Genetic variants of diabetes risk and incident cardiovascular events in chronic coronary artery disease. *PLoS ONE*, **2011**, 6, e16341	3.7	6
1072	A genome-wide association study confirms previously reported loci for type 2 diabetes in Han Chinese. *PLoS ONE*, **2011**, 6, e22353	3.7	49
1071	Association of new loci identified in European genome-wide association studies with susceptibility to type 2 diabetes in the Japanese. *PLoS ONE*, **2011**, 6, e26911	3.7	48
1070	Association of six single nucleotide polymorphisms with gestational diabetes mellitus in a Chinese population. *PLoS ONE*, **2011**, 6, e26953	3.7	63
1069	Large scale association analysis identifies three susceptibility loci for coronary artery disease. *PLoS ONE*, **2011**, 6, e29427	3.7	63

1068	The false-positive to false-negative ratio in epidemiologic studies. **2011**, 22, 450-6	209
1067	Two common genetic variants near nuclear-encoded OXPHOS genes are associated with insulin secretion in vivo. **2011**, 164, 765-71	24
1066	Genetic risk factors for type 2 diabetes mellitus and response to sulfonylurea treatment. **2011**, 21, 461-8	7
1065	The interplay of lifestyle and genetic susceptibility in Type 2 diabetes risk. **2011**, 1, 299-307	4
1064	Pharmacogenomic Research in South Africa: Lessons Learned and Future Opportunities in the Rainbow Nation. **2011**, 9, 191-207	49
1063	The pancreatic islet □-cell-enriched transcription factor Pdx-1 regulates Slc30a8 gene transcription through an intronic enhancer. **2011**, 433, 95-105	23
1062	Genetics of Type 2 diabetes in Asian Indians. **2011**, 1, 309-324	5
1061	Genetics of type 2 diabetes: the GWAS era and future perspectives [Review]. **2011**, 58, 723-39	116
1060	Functional loss of Cdkal1, a novel tRNA modification enzyme, causes the development of type 2 diabetes. **2011**, 58, 819-25	60
1059	Genome-wide association studies of Type 2 diabetes: are these ready to make an impact in the clinic?. **2011**, 1, 379-387	
1058	Genetic interaction between hyperglycemic QTLs is manifested under a high calorie diet in OLETF-derived congenic rats. **2011**, 60, 125-32	4
1057	Classical Genetic Studies of Schizophrenia. **2011**, 245-268	1
1056	Ancestry-informative markers on chromosomes 2, 8 and 15 are associated with insulin-related traits in a racially diverse sample of children. **2011**, 5, 79-89	19
1055	KCNQ1 gene variants and risk of new-onset diabetes in tacrolimus-treated renal-transplanted patients. **2011**, 25, E284-91	27
1054	Dorothy Hodgkin Lecture 2010. From hype to hope? A journey through the genetics of Type 2 diabetes. **2011**, 28, 132-40	14
1053	Messenger RNA processing and its role in diabetes. **2011**, 28, 1010-7	
1052	Assessment of the functionality of genome-wide canine SNP arrays and implications for canine disease association studies. **2011**, 42, 181-90	11
1051	Genetics of type 2 diabetes: pathophysiologic and clinical relevance. **2011**, 41, 679-92	91

1050	Genome-wide association scan allowing for epistasis in type 2 diabetes. **2011**, 75, 10-9	29
1049	Genetic mapping of vascular calcified plaque loci on chromosome 16p in European Americans from the diabetes heart study. **2011**, 75, 222-35	7
1048	Periodontal genetics: a decade of genetic association studies mandates better study designs. **2011**, 38, 103-7	49
1047	Common variants near ATM are associated with glycemic response to metformin in type 2 diabetes. **2011**, 43, 117-20	319
1046	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
1045	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
1044	Heterogeneity of genetic associations of CDKAL1 and HHEX with susceptibility of type 2 diabetes mellitus by gender. **2011**, 19, 672-5	22
1043	Reduced body weight in male Tspan8-deficient mice. **2011**, 35, 605-17	19
1042	Analysis of FTO gene variants with obesity and glucose homeostasis measures in the multiethnic Insulin Resistance Atherosclerosis Study cohort. **2011**, 35, 1173-82	41
1041	Genome-wide pharmacogenomic analysis of response to treatment with antipsychotics. **2011**, 16, 76-85	124
1040	GWA study data mining and independent replication identify cardiomyopathy-associated 5 (CMYA5) as a risk gene for schizophrenia. **2011**, 16, 1117-29	58
1039	Genetic variation within the TRPM5 locus associates with prediabetic phenotypes in subjects at increased risk for type 2 diabetes. **2011**, 60, 1325-33	33
1038	A powerful hybrid approach to select top single-nucleotide polymorphisms for genome-wide association study. **2011**, 12, 3	2
1037	Early peroxisome proliferator-activated receptor gamma regulated genes involved in expansion of pancreatic beta cell mass. **2011**, 4, 86	14
1036	Association between IGF2BP2 rs4402960 polymorphism and risk of type 2 diabetes mellitus: a meta-analysis. **2011**, 42, 361-7	16
1035	mTOR phosphorylates IMP2 to promote IGF2 mRNA translation by internal ribosomal entry. **2011**, 25, 1159-72	120
1034	New IBD genetics: common pathways with other diseases. **2011**, 60, 1739-53	418
1033	A Synopsis of Exercise Genomics Research and a Vision for its Future Translation into Practice. **2011**, 231-254	

1032	Emerging applications of metabolomic and genomic profiling in diabetic clinical medicine. **2011**, 34, 2624-30	36
1031	Random-effects model aimed at discovering associations in meta-analysis of genome-wide association studies. **2011**, 88, 586-98	351
1030	The porcine TBC1D1 gene: mapping, SNP identification, and association study with meat, carcass and production traits in Italian heavy pigs. **2011**, 38, 1425-31	24
1029	Type 2 diabetes and obesity: genomics and the clinic. **2011**, 130, 41-58	62
1028	Realizing the promise of population biobanks: a new model for translation. **2011**, 130, 333-45	25
1027	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
1026	Genetic variation within the NR1H2 gene encoding liver X receptor associates with insulin secretion in subjects at increased risk for type 2 diabetes. **2011**, 89, 75-81	20
1025	A role for coding functional variants in HNF4A in type 2 diabetes susceptibility. **2011**, 54, 111-9	24
1024	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
1023	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
1022	Genetic predisposition to obesity leads to increased risk of type 2 diabetes. **2011**, 54, 776-82	49
1021	Replication of 13 genome-wide association (GWA)-validated risk variants for type 2 diabetes in Pakistani populations. **2011**, 54, 1368-74	77
1020	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
1019	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
1018	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
1017	Heritability and familiality of type 2 diabetes and related quantitative traits in the Botnia Study. **2011**, 54, 2811-9	150
1016	Ant colony optimisation to identify genetic variant association with type 2 diabetes. **2011**, 181, 1609-1622	27
1015	Combined effects of FTO rs9939609 and MC4R rs17782313 on obesity and BMI in Chinese Han populations. **2011**, 39, 69-74	48

1014	Meet me halfway: when genomics meets structural bioinformatics. **2011**, 4, 281-303	10
1013	Testing the thrifty gene hypothesis: the Gly482Ser variant in PPARGC1A is associated with BMI in Tongans. **2011**, 12, 10	28
1012	Predicting functionally important SNP classes based on negative selection. **2011**, 12, 26	9
1011	SNP-based pathway enrichment analysis for genome-wide association studies. **2011**, 12, 99	86
1010	Gene- or region-based association study via kernel principal component analysis. **2011**, 12, 75	12
1009	Analysis of genome-wide association study data using the protein knowledge base. **2011**, 12, 98	9
1008	PPARPro12Ala interacts with fat intake for obesity and weight loss in a behavioural treatment based on the Mediterranean diet. **2011**, 55, 1771-9	50
1007	Bayesian semiparametric meta-analysis for genetic association studies. **2011**, 35, 333-40	5
1006	Optimal methods for meta-analysis of genome-wide association studies. **2011**, 35, 581-91	20
1005	Stability selection for genome-wide association. **2011**, 35, 722-8	40
1004	Genome-wide association studies (GWAS): impact on elucidating the aetiology of diabetes. **2011**, 27, 685-96	26
1003	Examining the overlap between genome-wide rare variant association signals and linkage peaks in rheumatoid arthritis. **2011**, 63, 1522-6	7
1002	A polymorphism in the chromosome 9p21 ANRIL locus is associated to Philadelphia positive acute lymphoblastic leukemia. **2011**, 35, 1052-9	64
1001	Four out of eight genes in a mouse chromosome 7 congenic donor region are candidate obesity genes. **2011**, 43, 1049-55	7
1000	FTO polymorphisms are associated with adult body mass index (BMI) and colorectal adenomas in African-Americans. **2011**, 32, 748-56	36
999	At the end of the beginning. Foreword. **2011**, 31, 111-3	
998	World Congress on Insulin Resistance, Diabetes, and Cardiovascular Disease: part 2. **2011**, 34, e126-31	4
997	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

996	An overview of a wide range of functions of ZnT and Zip zinc transporters in the secretory pathway. **2011**, 75, 1036-43	85
995	Genomics and genetics in the biology of adaptation to exercise. **2011**, 1, 1603-48	102
994	Genetic analysis of adult-onset autoimmune diabetes. **2011**, 60, 2645-53	92
993	Characterization of the human SLC30A8 promoter and intronic enhancer. **2011**, 47, 251-9	13
992	cn.FARMS: a latent variable model to detect copy number variations in microarray data with a low false discovery rate. **2011**, 39, e79	18
991	Epigenetics and Type 2 Diabetes. **2011**, 135-145	1
990	Insulin resistance and epigenetic regulation: insights from human studies and prospects for future research. **2011**, 2, 445-57	2
989	Genetics of type 2 diabetes. **2011**, 57, 241-54	113
988	Frequent loss of genome gap region in 4p16.3 subtelomere in early-onset type 2 diabetes mellitus. **2011**, 2011, 498460	8
987	Exploration of empirical Bayes hierarchical modeling for the analysis of genome-wide association study data. **2011**, 12, 445-61	13
986	Genomics, Proteomics, and the Nervous System. **2011**,	1
985	Latent Autoimmune Diabetes in Adults. **2011**, 315-329	
984	Genome-wide association studies: is there a genotype for cognitive decline in older persons with type 2 diabetes?. **2011**, 17, 347-56	10
983	Comparison of effect sizes associated with biomarkers reported in highly cited individual articles and in subsequent meta-analyses. **2011**, 305, 2200-10	185
982	Mouse models and the interpretation of human GWAS in type 2 diabetes and obesity. **2011**, 4, 155-64	32
981	Glucose regulates free cytosolic Zn2+ concentration, Slc39 (ZiP), and metallothionein gene expression in primary pancreatic islet β-cells. **2011**, 286, 25778-89	91
980	Generation of N-ethyl-N-nitrosourea (ENU) diabetes models in mice demonstrates genotype-specific action of glucokinase activators. **2011**, 286, 39560-72	12
979	Diabetes and biomarkers. **2011**, 5, 192-7	20

978	Meta-analysis of the effect of HHEX gene polymorphism on the risk of type 2 diabetes. **2011**, 26, 309-14		21
977	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
976	Diabesity: an overview of a rising epidemic. **2011**, 26, 28-35		187
975	Genome-wide association analysis of ischemic stroke in young adults. **2011**, 1, 505-14		26
974	Transferability of type 2 diabetes implicated loci in multi-ethnic cohorts from Southeast Asia. **2011**, 7, e1001363		119
973	Jun dimerization protein 2 controls senescence and differentiation via regulating histone modification. **2011**, 2011, 569034		12
972	Eight common genetic variants associated with serum DHEAS levels suggest a key role in ageing mechanisms. **2011**, 7, e1002025		69
971	Using gene-network landscape to dissect genotype effects of TCF7L2 genetic variant on diabetes and cardiovascular risk. **2012**, 44, 903-14		17
970	Identification of novel type 2 diabetes candidate genes involved in the crosstalk between the mitochondrial and the insulin signaling systems. **2012**, 8, e1003046		17
969	The fat-mass and obesity-associated gene (FTO) predicts mortality in chronic kidney disease of various severity. **2012**, 27 Suppl 4, iv58-62		12
968	Effects of high-fat diet feeding on Znt8-null mice: differences between □-cell and global knockout of Znt8. **2012**, 302, E1084-96		54
967	Interpreting meta-analyses of genome-wide association studies. **2012**, 8, e1002555		109
966	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
965	Gestational diabetes mellitus: a positive predictor of type 2 diabetes?. **2012**, 2012, 721653		8
964	A single-nucleotide polymorphism in ANK1 is associated with susceptibility to type 2 diabetes in Japanese populations. *Human Molecular Genetics*, **2012**, 21, 3042-9	5.6	86
963	Genotype prediction of adult type 2 diabetes from adolescence in a multiracial population. **2012**, 130, e1235-42		37
962	The evolution and refinement of traditional risk factors for cardiovascular disease. **2012**, 20, 118-29		39
961	Do genome-wide association scans have potential for translation?. **2011**, 50, 255-60		4

960	Data-driven integration of epidemiological and toxicological data to select candidate interacting genes and environmental factors in association with disease. **2012**, 28, i121-6	23
959	Novel Target Identification Technologies for the Personalised Therapy of Type II Diabetes and Obesity. **2012**, 12, 183-207	2
958	Development of type 2 diabetes caused by a deficiency of a tRNA(lys) modification. **2012**, 4, 71-3	7
957	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
956	Psoriasis and other complex trait dermatoses: from Loci to functional pathways. **2012**, 132, 915-22	68
955	The association of genetic variants of type 2 diabetes with kidney function. **2012**, 82, 220-5	36
954	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
953	Genome-wide pharmacogenomic study of citalopram-induced side effects in STAR*D. **2012**, 2, e129	34
952	Bias in high-tier medical journals concerning physician-academic relationships with industry. **2012**, 30, 320-2	11
951	A statistical method for region-based meta-analysis of genome-wide association studies in genetically diverse populations. **2012**, 20, 469-75	12
950	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
949	Znt7-null mice are more susceptible to diet-induced glucose intolerance and insulin resistance. **2012**, 287, 33883-96	54
948	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
947	Genetic variation in peroxisome proliferator-activated receptor gamma, soy, and mammographic density in Singapore Chinese women. **2012**, 21, 635-44	14
946	Evaluation of genome-wide association study-identified type 2 diabetes loci in African Americans. **2012**, 176, 995-1001	32
945	Rosuvastatin and atorvastatin: comparative effects on glucose metabolism in non-diabetic patients with dyslipidaemia. **2012**, 5, 13-30	11
944	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
943	Nuclear receptor variants in liver disease. **2012**, 2012, 934707	4

942	Rising intracellular zinc by membrane depolarization and glucose in insulin-secreting clonal HIT-T15 beta cells. **2012**, 2012, 190309		12
941	A genome-wide association study in the Japanese population confirms 9p21 and 14q23 as susceptibility loci for primary open angle glaucoma. *Human Molecular Genetics*, **2012**, 21, 2836-42	5.6	100
940	Alternative methods to a TaqMan assay to detect a tri-allelic single nucleotide polymorphism rs757210 in the HNF1gene. **2011**, 50, 279-84		7
939	Editorial: current topics on the epidemiology, pathogenesis, and treatment of diabetes mellitus and its complications. **2012**, 10, 138-9		
938	Genes related to diabetes may be associated with pancreatic cancer in a population-based case-control study in Minnesota. **2012**, 41, 50-3		20
937	Genetic basis, nutritional challenges and adaptive responses in the prenatal origin of obesity and type-2 diabetes. **2012**, 8, 144-54		21
936	Increased -cell replication and -cell mass regeneration in syngeneically transplanted rat islets overexpressing insulin-like growth factor II. **2012**, 21, 2119-29		12
935	Genetic risk factors for type 2 diabetes: insights from the emerging genomic evidence. **2012**, 10, 147-55		19
934	Extraneuronal activities and regulatory mechanisms of the atypical cyclin-dependent kinase Cdk5. **2012**, 84, 985-93		61
933	A genome-wide association study of gestational diabetes mellitus in Korean women. **2012**, 61, 531-41		169
932	Gene-exercise interactions. **2012**, 108, 447-60		13
931	Polycystic ovary syndrome is not associated with polymorphisms of the TCF7L2, CDKAL1, HHEX, KCNJ11, FTO and SLC30A8 genes. **2012**, 77, 439-45		31
930	Interactions between genetic background, insulin resistance and -cell function. **2012**, 14 Suppl 3, 46-56		15
929	Genetic variants at 6p21.1 and 7p15.3 are associated with risk of multiple cancers in Han Chinese. **2012**, 91, 928-34		59
928	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
927	RCM: a novel association approach to search for coronary artery disease genetic related metabolites based on SNPs and metabolic network. **2012**, 100, 282-8		1
926	Recent Findings on the Genetics of Obesity: Is there Public Health Relevance?. **2012**, 1, 239-248		3
925	. **2012**,		

924	What should the genome-wide significance threshold be? Empirical replication of borderline genetic associations. **2012**, 41, 273-86		189
923	Peptidomics approach to elucidate the proteolytic regulation of bioactive peptides. **2012**, 109, 8523-7		29
922	Effect of type 2 diabetes predisposing genetic variants on colorectal cancer risk. **2012**, 97, E845-51		43
921	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. **2012**, 44, 981-90		1482
920	Disease liability prediction from large scale genotyping data using classifiers with a reject option. **2012**, 9, 88-97		7
919	Validation of candidate genes associated with cardiovascular risk factors in psychiatric patients. **2012**, 36, 213-9		2
918	Metabolic and cardiovascular genes in polycystic ovary syndrome: a candidate-wide association study (CWAS). **2012**, 77, 317-22		23
917	Strategies beyond genome-wide association studies for atherosclerosis. **2012**, 32, 170-81		32
916	A review of familial, genetic, and congenital aspects of primary varicose vein disease. **2012**, 5, 460-6		35
915	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
914	Twin studies in autoimmune disease: genetics, gender and environment. **2012**, 38, J156-69		189
913	Is genetic testing useful to predict type 2 diabetes?. **2012**, 26, 189-201		43
912	Genetic determinants of glucose homeostasis. **2012**, 26, 159-70		9
911	Higher incidence of death in multi-vessel coronary artery disease patients associated with polymorphisms in chromosome 9p21. **2012**, 12, 61		15
910	Effect of communicating genetic and phenotypic risk for type 2 diabetes in combination with lifestyle advice on objectively measured physical activity: protocol of a randomised controlled trial. **2012**, 12, 444		20
909	Association between 9p21 genetic variants and mortality risk in a prospective cohort of patients with type 2 diabetes (ZODIAC-15). *Cardiovascular Diabetology*, **2012**, 11, 138	8.7	10
908	Identification of shared genetic susceptibility locus for coronary artery disease, type 2 diabetes and obesity: a meta-analysis of genome-wide studies. *Cardiovascular Diabetology*, **2012**, 11, 68	8.7	17
907	Regulation and functional effects of ZNT8 in human pancreatic islets. **2012**, 214, 225-32		26

906	Transferability and fine-mapping of glucose and insulin quantitative trait loci across populations: CARe, the Candidate Gene Association Resource. **2012**, 55, 2970-84	23
905	Epigenetics of Diabetes in Humans. **2012**, 321-329	
904	Contribution of common genetic variation to the risk of type 2 diabetes in the Mexican Mestizo population. **2012**, 61, 3314-21	71
903	Individualized therapy for type 2 diabetes: clinical implications of pharmacogenetic data. **2012**, 16, 285-302	27
902	Association of type 2 diabetes susceptibility loci with one-year weight loss in the look AHEAD clinical trial. **2012**, 20, 1675-82	23
901	IGF2BP2 and IGF2 genetic effects in diabetes and diabetic nephropathy. **2012**, 26, 393-8	20
900	Identification and function of auxiliary iron-sulfur clusters in radical SAM enzymes. **2012**, 1824, 1196-212	56
899	Human □cell transcriptome analysis uncovers lncRNAs that are tissue-specific, dynamically regulated, and abnormally expressed in type 2 diabetes. **2012**, 16, 435-48	345
898	European genetic variants associated with type 2 diabetes in North African Arabs. **2012**, 38, 316-23	55
897	Influence of PTPN1 polymorphism among people with type 2 diabetes: A Thanjavur-based study. **2012**, 4, 94-97	
896	Type 2 diabetes and polymorphisms on chromosome 9p21: a meta-analysis. **2012**, 22, 619-25	31
895	IRS1 gene variants, dysglycaemic metabolic changes and type-2 diabetes risk. **2012**, 22, 1024-30	15
894	Epigenetic regulation of pancreas development and function. **2012**, 23, 693-700	25
893	Disturbed zinc homeostasis in diabetic patients by in vitro and in vivo analysis of insulinomimetic activity of zinc. **2012**, 23, 1458-66	89
892	Impact of FTO genotypes on BMI and weight in polycystic ovary syndrome: a systematic review and meta-analysis. **2012**, 55, 2636-2645	64
891	Meta-analysis identifies common variants associated with body mass index in east Asians. **2012**, 44, 307-11	301
890	A noncoding RNA antisense to moesin at 5p14.1 in autism. **2012**, 4, 128ra40	104
889	From mice to humans. **2012**, 12, 651-8	10

888	Genetics of type 2 diabetes in East Asian populations. **2012**, 12, 686-96	46
887	Genetic predisposition to type 2 diabetes is associated with impaired insulin secretion but does not modify insulin resistance or secretion in response to an intervention to lower dietary saturated fat. **2012**, 7, 529-36	3
886	Quantitative assessment of the variation in IGF2BP2 gene and type 2 diabetes risk. **2012**, 49 Suppl 1, S87-97	9
885	Widespread expression of zinc transporter ZnT (SLC30) family members in mouse endocrine cells. **2012**, 138, 605-16	13
884	Effect of a common variant of the PCSK2 gene on reduced insulin secretion. **2012**, 55, 3245-51	13
883	Impact of transcription factor 7-like 2 (TCF7L2) on pancreatic islet function and morphology in mice and men. **2012**, 55, 2559-2561	7
882	Abnormal glucose tolerance and insulin secretion in pancreas-specific Tcf7l2-null mice. **2012**, 55, 2667-2676	88
881	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
880	Genetic risk assessment of type 2 diabetes-associated polymorphisms in African Americans. **2012**, 35, 287-92	42
879	DNA methylation profiling identifies epigenetic dysregulation in pancreatic islets from type 2 diabetic patients. **2012**, 31, 1405-26	301
878	Genetics of type 2 diabetes in European populations. **2012**, 4, 203-12	27
877	Lack of association between genetic polymorphisms within KCNQ1 locus and type 2 diabetes in Tunisian Arabs. **2012**, 98, 452-8	15
876	Investigation on cardiovascular risk prediction using genetic information. **2012**, 16, 795-808	18
875	Prediabetes Genes in Pima and Amish. **2012**, 61-80	
874	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
873	Maternal and offspring fasting glucose and type 2 diabetes-associated genetic variants and cognitive function at age 8: a Mendelian randomization study in the Avon Longitudinal Study of Parents and Children. **2012**, 13, 90	19
872	Expression analyses of the genes harbored by the type 2 diabetes and pediatric BMI associated locus on 10q23. **2012**, 13, 89	10
871	Applying semantic web technologies for phenome-wide scan using an electronic health record linked Biobank. **2012**, 3, 10	27

870	African ancestry and its correlation to type 2 diabetes in African Americans: a genetic admixture analysis in three U.S. population cohorts. *PLoS ONE*, **2012**, 7, e32840	3.7	56
869	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
868	Genetic variants of IDE-KIF11-HHEX at 10q23.33 associated with type 2 diabetes risk: a fine-mapping study in Chinese population. *PLoS ONE*, **2012**, 7, e35060	3.7	29
867	The chromosome 9p21.3 coronary heart disease risk allele is associated with altered gene expression in normal heart and vascular tissues. *PLoS ONE*, **2012**, 7, e39574	3.7	32
866	IGF2BP2 alternative variants associated with glutamic acid decarboxylase antibodies negative diabetes in Malaysian subjects. *PLoS ONE*, **2012**, 7, e45573	3.7	4
865	Joint effect of genetic and lifestyle risk factors on type 2 diabetes risk among Chinese men and women. *PLoS ONE*, **2012**, 7, e49464	3.7	12
864	cDNA cloning and mRNA expression of cat and dog. **2012**, 3, 65-69		
863	Epigenetics in the Pathophysiology of Type 2 Diabetes. **2012**, 225-232		
862	Type 2 Diabetes Genetics: Beyond GWAS. **2012**, 3,		84
861	Alzheimer's disease. 371-381		1
860	Replication analysis for severe diabetic retinopathy. **2012**, 53, 2377-81		39
859	A more rapid approach to systematically assessing published associations of genetic polymorphisms and disease risk: type 2 diabetes as a test case. **2012**, 1		
858	Tyrosine hydroxylase gene: another piece of the genetic puzzle of Parkinson's disease. **2012**, 11, 469-81		13
857	SLC30A8 (ZnT8) variations and type 2 diabetes in the Chinese Han population. **2012**, 11, 1592-8		21
856	Use of genome-wide association studies for drug repositioning. **2012**, 30, 317-20		275
855	Genomewide association studies in cardiovascular disease--an update 2011. **2012**, 58, 92-103		53
854	Recent studies of the human chromosome 9p21 locus, which is associated with atherosclerosis in human populations. **2012**, 32, 196-206		145
853	Two adaptive weighting methods to test for rare variant associations in family-based designs. **2012**, 36, 499-507		21

852	Detecting association of rare and common variants by testing an optimally weighted combination of variants. **2012**, 36, 561-71	55
851	A likelihood ratio-based Mann-Whitney approach finds novel replicable joint gene action for type 2 diabetes. **2012**, 36, 583-93	15
850	Direct genetic effects and their estimation from matched case-control data. **2012**, 36, 652-62	7
849	11q13 is a susceptibility locus for hormone receptor positive breast cancer. **2012**, 33, 1123-32	33
848	IGF2BP2 genetic variation and type 2 diabetes: a global meta-analysis. **2012**, 31, 713-20	9
847	Genetic association of zinc transporter 8 (ZnT8) autoantibodies in type 1 diabetes cases. **2012**, 55, 1978-84	35
846	Genetic variants in FTO associated with metabolic syndrome: a meta- and gene-based analysis. **2012**, 39, 5691-8	43
845	Genetic variants at chromosome 9p21, 10p15 and 10q22 and breast cancer susceptibility in a Chinese population. **2012**, 132, 741-6	8
844	Large-scale gene-centric meta-analysis across 39 studies identifies type 2 diabetes loci. **2012**, 90, 410-25	214
843	Replication of genome-wide association signals of type 2 diabetes in Han Chinese in a prospective cohort. **2012**, 76, 365-72	27
842	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
841	Association of glycosylated hemoglobin with the gene encoding CDKAL1 in the Korean Association Resource (KARE) study. **2012**, 33, 655-9	25
840	Common genetic variants differentially influence the transition from clinically defined states of fasting glucose metabolism. **2012**, 55, 331-9	32
839	Association analysis of 31 common polymorphisms with type 2 diabetes and its related traits in Indian sib pairs. **2012**, 55, 349-57	41
838	Association of type 2 diabetes susceptibility genes (TCF7L2, SLC30A8, PCSK1 and PCSK2) and proinsulin conversion in a Chinese population. **2012**, 39, 17-23	37
837	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
836	Association between type 2 diabetes and CDKN2A/B: a meta-analysis study. **2012**, 39, 1609-16	22
835	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

834	Discovery by the Epistasis Project of an epistatic interaction between the GSTM3 gene and the HHEX/IDE/KIF11 locus in the risk of Alzheimer's disease. **2013**, 34, 1309.e1-7	24
833	Evaluation of serum metallothionein-1, selenium, zinc, and copper in Ghanaian type 2 diabetes mellitus patients. **2013**, 33, 86-95	6
832	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
831	Meta-analysis of the effect of KCNQ1 gene polymorphism on the risk of type 2 diabetes. **2013**, 40, 3557-67	12
830	Inflammatory mechanisms linking periodontal diseases to cardiovascular diseases. **2013**, 84, S51-69	105
829	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
828	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
827	The link between family history and risk of type 2 diabetes is not explained by anthropometric, lifestyle or genetic risk factors: the EPIC-InterAct study. **2013**, 56, 60-9	158
826	Systematic identification of interaction effects between genome- and environment-wide associations in type 2 diabetes mellitus. **2013**, 132, 495-508	86
825	HMGA2 expression in white adipose tissue linking cellular senescence with diabetes. **2013**, 8, 449-56	38
824	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
823	Association between type 2 diabetes and rs10811661 polymorphism upstream of CDKN2A/B: a meta-analysis. **2013**, 50, 657-62	12
822	Polycystic ovary syndrome is not associated with genetic variants that mark risk of type 2 diabetes. **2013**, 50, 451-7	22
821	No detectable association of IGF2BP2 and SLC30A8 genes with type 2 diabetes in the population of Hyderabad, India. **2013**, 1, 15-23	21
820	Functional characterization of Cdkal1, a risk factor of type 2 diabetes, and the translational opportunities. **2013**, 10, e65-e69	2
819	Subset-based ant colony optimisation for the discovery of gene-gene interactions in genome wide association studies. **2013**,	4
818	Bridging the gap between genetic associations and molecular mechanisms for type 2 diabetes. **2013**, 13, 778-85	8
817	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

816	Identification of an intermediate methyl carrier in the radical S-adenosylmethionine methylthiotransferases RimO and MiaB. **2013**, 135, 15404-15416		47
815	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
814	The large non-coding RNA ANRIL, which is associated with atherosclerosis, periodontitis and several forms of cancer, regulates ADIPOR1, VAMP3 and C11ORF10. *Human Molecular Genetics*, **2013**, 22, 4516-27	5.6	163
813	A genome-wide search for type 2 diabetes susceptibility genes in an extended Arab family. **2013**, 77, 488-503		24
812	The genetic influence on body fat distribution. **2013**, 10, e5-e13		7
811	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
810	Genetic variant in fat mass and obesity-associated gene associated with type 2 diabetes risk in Han Chinese. **2013**, 14, 86		13
809	A multiclass likelihood ratio approach for genetic risk prediction allowing for phenotypic heterogeneity. **2013**, 37, 715-25		5
808	Senescent cells and their secretory phenotype as targets for cancer therapy. **2013**, 38, 17-27		83
807	Chromosome 9p21 rs10757278 polymorphism is associated with the risk of metabolic syndrome. **2013**, 379, 77-85		10
806	Discovering Findings That Replicate From a Primary Study of High Dimension to a Follow-Up Study. **2013**, 108, 1480-1492		16
805	Towards Mining Frequent Patterns in Genome Wide Association. **2013**,		0
804	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
803	Zinc, pancreatic islet cell function and diabetes: new insights into an old story. **2013**, 26, 1-11		67
802	Single nucleotide polymorphism in genome-wide association of human population: A tool for broad spectrum service. *Egyptian Journal of Medical Human Genetics*, **2013**, 14, 123-134	2	42
801	A population-based association study of 2q32.3 and 8q21.3 loci with schizophrenia in Han Chinese. **2013**, 47, 712-7		43
800	Cellular and animal models of type 2 diabetes GWAS gene polymorphisms: what can we learn?. **2013**, 10, e59-e64		
799	A distant, cis-acting enhancer drives induction of Arf by Tgf□in the developing eye. **2013**, 380, 49-57		10

798	Recent Developments in the Genetic and Genomic Basis of Type 2 Diabetes. **2013**, 7, 66-72		
797	Genome wide association studies for diabetes: perspective on results and challenges. **2013**, 14, 90-6		25
796	The genetics of type 2 diabetes and its clinical relevance. **2013**, 83, 297-306		37
795	Increased dosage of Ink4/Arf protects against glucose intolerance and insulin resistance associated with aging. **2013**, 12, 102-11		26
794	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
793	Systematic evaluation of validated type 2 diabetes and glycaemic trait loci for association with insulin clearance. **2013**, 56, 1282-90		33
792	A variant in FTO shows association with melanoma risk not due to BMI. **2013**, 45, 428-32, 432e1		95
791	Association study of genetic variants of 17 diabetes-related genes/loci and cardiovascular risk and diabetic nephropathy in the Chinese She population. **2013**, 5, 136-45		40
790	Genetics of type 2 diabetes and potential clinical implications. **2013**, 36, 167-77		21
789	A genome-wide association study identifies GRK5 and RASGRP1 as type 2 diabetes loci in Chinese Hans. **2013**, 62, 291-8		142
788	Diabetes Mellitus. **2013**, 1-58		3
787	Recent progress in the use of genetics to understand links between type 2 diabetes and related metabolic traits. **2013**, 14, 203		7
786	AdipoQ polymorphisms are associated with type 2 diabetes mellitus: a meta-analysis study. **2013**, 29, 532-45		18
785	Inflammatory mechanisms linking periodontal diseases to cardiovascular diseases. **2013**, 40 Suppl 14, S51-69		126
784	Apolipoprotein E2 accentuates postprandial inflammation and diet-induced obesity to promote hyperinsulinemia in mice. **2013**, 62, 382-91		30
783	Association of ANRIL polymorphism (rs1333049:C>G) with myocardial infarction and its pharmacogenomic role in hypercholesterolemia. **2013**, 515, 416-20		22
782	Identification of CpG-SNPs associated with type 2 diabetes and differential DNA methylation in human pancreatic islets. **2013**, 56, 1036-46		143
781	Association of TCF7L2 gene polymorphisms with T2DM in the population of Hyderabad, India. *PLoS ONE*, **2013**, 8, e60212	3.7	36

780	Genome-wide association study meta-analysis of European and Asian-ancestry samples identifies three novel loci associated with bipolar disorder. **2013**, 18, 195-205	155
779	The type 2 diabetes-associated gene ide is required for insulin secretion and suppression of -synuclein levels in -cells. **2013**, 62, 2004-14	73
778	Ethical and practical challenges to studying patients who opt out of large-scale biorepository research. **2013**, 20, e221-5	3
777	Identification of a genetic locus on chromosome 4q34-35 for type 2 diabetes with overweight. **2013**, 45, e7	10
776	Diabetes. **2013**, 990-1005	
775	Adaptive clustering and adaptive weighting methods to detect disease associated rare variants. **2013**, 21, 332-7	10
774	Genome-wide association studies of human growth traits. **2013**, 71, 29-38	
773	Correlations between psoriasis and inflammatory bowel diseases. **2013**, 2013, 983902	61
772	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
771	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. **2013**, 9, e1003500	277
770	Phenome-wide association study (PheWAS) for detection of pleiotropy within the Population Architecture using Genomics and Epidemiology (PAGE) Network. **2013**, 9, e1003087	126
769	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
768	Impact of TCF7L2 single nucleotide polymorphisms on hydrochlorothiazide-induced diabetes. **2013**, 23, 697-705	12
767	Familial atrial fibrillation predicts increased risk of mortality: a study in Danish twins. **2013**, 6, 10-5	11
766	Dysregulation of Long Non-coding RNAs in Human Disease. **2013**, 115-136	
765	HuR maintains a replicative life span by repressing the ARF tumor suppressor. **2013**, 33, 1886-900	9
764	Transferability and fine mapping of type 2 diabetes loci in African Americans: the Candidate Gene Association Resource Plus Study. **2013**, 62, 965-76	51
763	Animal models of GWAS-identified type 2 diabetes genes. **2013**, 2013, 906590	27

762	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
761	The genetics of human obesity. **2013**, 1281, 178-90	120
760	Insights into the genetic basis of type 2 diabetes. **2013**, 4, 233-44	44
759	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
758	Multiple neurofibromas as the presenting feature of familial atypical multiple malignant melanoma (FAMMM) syndrome. **2013**, 161A, 1425-31	9
757	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. **2013**, 45, 76-82	232
756	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
755	The current state of play on the molecular genetics of depression. **2013**, 43, 673-87	66
754	Novel common and rare genetic determinants of paraoxonase activity: FTO, SERPINA12, and ITGAL. **2013**, 54, 552-60	15
753	Genome-wide association study identifies possible genetic risk factors for colorectal adenomas. **2013**, 22, 1219-26	11
752	Association of rs734312 and rs10010131 polymorphisms in WFS1 gene with type 2 diabetes mellitus: a meta-analysis. **2013**, 60, 441-447	13
751	Variations in Solute Transporter Genes Affecting Micronutrient Solute Transport and Human Health. **2013**, 25-82	
750	Molecular Genetics of Primary Varicose Vein Disease. **2013**,	
749	The new perspectives on genetic studies of type 2 diabetes and thyroid diseases. **2013**, 14, 33-48	3
748	Lack of interaction of beta-cell-function-associated variants with hypertension on change in fasting glucose and diabetes risk: the Framingham Offspring Study. **2013**, 31, 1001-9	
747	Generation of high quality chromatin immunoprecipitation DNA template for high-throughput sequencing (ChIP-seq). **2013**,	10
746	Association of variants in PPAR□, IGF2BP2, and KCNQ1 with a susceptibility to gestational diabetes mellitus in a Korean population. **2013**, 54, 352-7	30
745	The diabetes-susceptible gene SLC30A8/ZnT8 regulates hepatic insulin clearance. **2013**, 123, 4513-24	166

744	Association of genetic variants with isolated fasting hyperglycaemia and isolated postprandial hyperglycaemia in a Han Chinese population. *PLoS ONE*, **2013**, 8, e71399	3.7	8
743	Replication study for the association of 9 East Asian GWAS-derived loci with susceptibility to type 2 diabetes in a Japanese population. *PLoS ONE*, **2013**, 8, e76317	3.7	36
742	Autoimmune Disorders. **2013**, 822-838		3
741	Predictive value of genomics in the screening of type 2 diabetes: limitations and current status. **2014**, 45		
740	Admixture mapping and subsequent fine-mapping suggests a biologically relevant and novel association on chromosome 11 for type 2 diabetes in African Americans. *PLoS ONE*, **2014**, 9, e86931	3.7	11
739	Cross-sectional and longitudinal replication analyses of genome-wide association loci of type 2 diabetes in Han Chinese. *PLoS ONE*, **2014**, 9, e91790	3.7	16
738	Validation of type 2 diabetes risk variants identified by genome-wide association studies in Han Chinese population: a replication study and meta-analysis. *PLoS ONE*, **2014**, 9, e95045	3.7	26
737	Drosophila 3' UTRs are more complex than protein-coding sequences. *PLoS ONE*, **2014**, 9, e97336	3.7	5
736	Evaluation of common type 2 diabetes risk variants in a South Asian population of Sri Lankan descent. *PLoS ONE*, **2014**, 9, e98608	3.7	6
735	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. *PLoS ONE*, **2014**, 9, e100548	3.7	11
734	Obesity-related genomic loci are associated with type 2 diabetes in a Han Chinese population. *PLoS ONE*, **2014**, 9, e104486	3.7	21
733	Polymorphism of 9p21.3 locus is associated with 5-year survival in high-risk patients with myocardial infarction. *PLoS ONE*, **2014**, 9, e104635	3.7	11
732	Genetic and Epigenetics of Type 2 Diabetes. **2014**, 467-476		
731	Association of CDKN2BAS polymorphism rs4977574 with coronary heart disease: a case-control study and a meta-analysis. *International Journal of Molecular Sciences*, **2014**, 15, 17478-92	6.3	33
730	Risk factors contributing to type 2 diabetes and recent advances in the treatment and prevention. **2014**, 11, 1185-200		426
729	Computer aided screening of secreted frizzled-related protein 4 (SFRP4): a potential control for diabetes mellitus. **2014**, 19, 10129-36		11
728	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
727	Association between FTO, MC4R, SLC30A8, and KCNQ1 gene variants and type 2 diabetes in Saudi population. **2014**, 13, 10194-203		30

726	Legal Aspects of Biobanking as Key Issues for Personalized Medicine & Translational Exploitation. **2014**,	
725	Polymorphisms of cell cycle control genes influence the development of sporadic medullary thyroid carcinoma. **2014**, 171, 761-7	15
724	Modify or die?--RNA modification defects in metazoans. **2014**, 11, 1555-67	51
723	Lack of genetic susceptibility of KCNJ11 E23K polymorphism with risk of type 2 diabetes in an Iranian population. **2014**, 39, 120-5	13
722	Next-Generation Sequencing Studies: Optimal Design and Analysis, Missing Heritability and Rare Variants. **2014**, 1, 213-219	2
721	Disease risk factors identified through shared genetic architecture and electronic medical records. **2014**, 6, 234ra57	33
720	Zinc-ing about diabetes. **2014**, 7, 276-276	
719	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
718	Association analyses of insulin signaling pathway gene polymorphisms with healthy aging and longevity in Americans of Japanese ancestry. **2014**, 69, 270-3	10
717	The architecture of risk for type 2 diabetes: understanding Asia in the context of global findings. **2014**, 2014, 593982	27
716	Maternal genotype and gestational diabetes. **2014**, 31, 69-76	30
715	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
714	Genome-wide associations between genetic and epigenetic variation influence mRNA expression and insulin secretion in human pancreatic islets. **2014**, 10, e1004735	118
713	A central role for GRB10 in regulation of islet function in man. **2014**, 10, e1004235	124
712	Genetic susceptibility to type 2 diabetes and obesity: follow-up of findings from genome-wide association studies. **2014**, 2014, 769671	50
711	Diabetes Mellitus. **2014**,	3
710	Genetics of type 2 diabetes: insights into the pathogenesis and its clinical application. **2014**, 2014, 926713	49
709	Spontaneous preterm birth in African-American and Caucasian women receiving 17□hydroxyprogesterone caproate. **2014**, 31, 55-60	12

708	TCF7L2 is a master regulator of insulin production and processing. *Human Molecular Genetics*, **2014**, 23, 6419-31	5.6	118
707	Investigating the potential effect of consanguinity on type 2 diabetes susceptibility in a Saudi population. **2014**, 77, 197-206		17
706	Two novel type 2 diabetes loci revealed through integration of TCF7L2 DNA occupancy and SNP association data. **2014**, 2, e000052		12
705	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
704	CDKAL1 and HHEX are associated with type 2 diabetes-related traits among Yup'ik people. **2014**, 6, 251-9		11
703	A polymorphism in the melanocortin 4 receptor gene (MC4R:c.92C>T) is associated with diabetes mellitus in overweight domestic shorthaired cats. **2014**, 28, 458-64		19
702	Genome-wide association study of height-adjusted BMI in childhood identifies functional variant in ADCY3. **2014**, 22, 2252-9		53
701	Candidate disease gene prediction using Gentrepid: application to a genome-wide association study on coronary artery disease. **2014**, 2, 44-57		10
700	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		
699	Modulation of the pancreatic islet-stress axis as a novel potential therapeutic target in diabetes mellitus. **2014**, 95, 195-222		6
698	Type 2 Diabetes. **2014**,		1
697	Antiretroviral therapy modifies the genetic effect of known type 2 diabetes-associated risk variants in HIV-infected women. **2014**, 28, 1815-23		3
696	Cellular senescence mediated by p16INK4A-coupled miRNA pathways. **2014**, 42, 1606-18		50
695	Mining Frequent Patterns for Genetic Variants Associated to Diabetes. **2014**,		1
694	Age-related impairment of pancreatic Beta-cell function: pathophysiological and cellular mechanisms. *Frontiers in Endocrinology*, **2014**, 5, 138	5.7	65
693	DataSHIELD: taking the analysis to the data, not the data to the analysis. **2014**, 43, 1929-44		116
692	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
691	Genetic Testing and Type 2 Diabetes Risk Awareness. **2014**, 40, 427-433		1

690	Using volcano plots and regularized-chi statistics in genetic association studies. **2014**, 48, 77-83		19
689	Pleiotropic genes for metabolic syndrome and inflammation. **2014**, 112, 317-38		81
688	Contribution of SLC30A8 variants to the risk of type 2 diabetes in a multi-ethnic population: a case control study. **2014**, 14, 2		6
687	FTO and obesity: mechanisms of association. **2014**, 14, 486		72
686	Targeting the pancreatic □-cell to treat diabetes. **2014**, 13, 278-89		192
685	Co-occurrence of risk alleles in or near genes modulating insulin secretion predisposes obese youth to prediabetes. **2014**, 37, 475-82		28
684	Transcription factor 7-like 2 (TCF7L2) gene polymorphism and clinical phenotype in end-stage renal disease patients. **2014**, 41, 4063-8		15
683	Current Insights into the Joint Genetic Basis of Type 2 Diabetes and Coronary Heart Disease. **2014**, 8, 368		17
682	Nutrigenetics: bridging two worlds to understand type 2 diabetes. **2014**, 14, 477		9
681	Nutrigenomics: the role of nutrients in gene expression. **2014**, 64, 154-60		15
680	System-based approaches to decode the molecular links in Parkinson's disease and diabetes. **2014**, 72 Pt A, 84-91		66
679	Identification of a splicing variant that regulates type 2 diabetes risk factor CDKAL1 level by a coding-independent mechanism in human. *Human Molecular Genetics*, **2014**, 23, 4639-50	5.6	36
678	Cdkn2a/p16Ink4a regulates fasting-induced hepatic gluconeogenesis through the PKA-CREB-PGC1□pathway. **2014**, 63, 3199-209		27
677	Anti-diabetic activity of insulin-degrading enzyme inhibitors mediated by multiple hormones. **2014**, 511, 94-8		164
676	Cyclin D1-Cdk4 controls glucose metabolism independently of cell cycle progression. **2014**, 510, 547-51		158
675	Current understanding of ZIP and ZnT zinc transporters in human health and diseases. **2014**, 71, 3281-95		154
674	Genetic comorbidities in Parkinson's disease. *Human Molecular Genetics*, **2014**, 23, 831-41	5.6	49
673	SLC30A8 nonsynonymous variant is associated with recovery following exercise and skeletal muscle size and strength. **2014**, 63, 363-8		19

672	A robust method for genome-wide association meta-analysis with the application to circulating insulin-like growth factor I concentrations. **2014**, 38, 162-71	4
671	Association between type 2 diabetes mellitus-related SNP variants and obesity traits in a Saudi population. **2014**, 41, 1731-40	18
670	The Genetics of Obesity. **2014**,	
669	Identifying causal variants at loci with multiple signals of association. **2014**, 198, 497-508	266
668	Interactions between zinc transporter-8 gene (SLC30A8) and plasma zinc concentrations for impaired glucose regulation and type 2 diabetes. **2014**, 63, 1796-803	66
667	Inhibition of secreted frizzled-related protein 5 improves glucose metabolism. **2014**, 307, E1144-52	14
666	Cross-tissue and tissue-specific eQTLs: partitioning the heritability of a complex trait. **2014**, 95, 521-34	61
665	Exploring the genetic basis of stroke. Spanish stroke genetics consortium. **2014**, 29, 560-566	0
664	Insights into the genetic susceptibility to type 2 diabetes from genome-wide association studies of glycaemic traits. **2014**, 14, 551	34
663	A comparison of type 2 diabetes risk allele load between African Americans and European Americans. **2014**, 133, 1487-95	40
662	Diabetes mellitus. **2014**, 846-900.e1	6
661	CREB-regulated transcription coactivator 3 (CRTC3) polymorphism associated with type 2 diabetes and hyperlipidemia in the Taiwanese population. **2014**, 26, 114-118	1
660	Associations of genetic variants in/near body mass index-associated genes with type 2 diabetes: a systematic meta-analysis. **2014**, 81, 702-10	27
659	Gene-Diet Interactions in Type 2 Diabetes. **2014**, 3, 302-323	4
658	Etiology of diabetes mellitus. **2014**, 1-26	
657	Gene dose effect between a fat mass and obesity-associated polymorphism and body mass index was observed in Korean women with polycystic ovary syndrome but not in control women. **2014**, 102, 1143-1148.e2	13
656	Overlap of genetic susceptibility to type 1 diabetes, type 2 diabetes, and latent autoimmune diabetes in adults. **2014**, 14, 550	29
655	The role of metallothionein-3 in streptozotocin-induced beta-islet cell death and diabetes in mice. **2014**, 6, 1748-57	9

654	Utility of large consanguineous family-based model for investigating the genetics of type 2 diabetes mellitus. **2014**, 548, 22-8	4
653	A gene variant in the transcription factor 7-like 2 (TCF7L2) is associated with an increased risk of gestational diabetes mellitus. **2014**, 180, 77-82	24
652	Analysis of metabolic syndrome components in >15 000 african americans identifies pleiotropic variants: results from the population architecture using genomics and epidemiology study. **2014**, 7, 505-13	32
651	Genetic architecture of type 2 diabetes. **2014**, 452, 213-20	42
650	TBC1D1 reduces palmitate oxidation by inhibiting □-HAD activity in skeletal muscle. **2014**, 307, R1115-23	13
649	Diverse convergent evidence in the genetic analysis of complex disease: coordinating omic, informatic, and experimental evidence to better identify and validate risk factors. **2014**, 7, 10	22
648	Zinc-finger BED domain-containing 3 (Zbed3) is a novel secreted protein associated with insulin resistance in humans. **2014**, 275, 522-33	26
647	Meta-analysis of sequencing studies with heterogeneous genetic associations. **2014**, 38, 389-401	22
646	Genetic and epigenetic risk factors for diabetic kidney disease. **2014**, 21, 287-96	26
645	Exploring the genetic basis of stroke. Spanish stroke genetics consortium. **2014**, 29, 560-6	3
644	The regulation of pre- and post-maturational plasticity of mammalian islet cell mass. **2014**, 57, 1291-303	27
643	Association analysis of IGF2BP2, KCNJ11, and CDKAL1 polymorphisms with type 2 diabetes mellitus in a Moroccan population: a case-control study and meta-analysis. **2014**, 52, 430-42	19
642	Zinc transporter 8 (ZnT8) and □cell function. **2014**, 25, 415-24	96
641	Assessing the contribution of 38 genetic loci to the risk of type 2 diabetes in the Saudi Arabian Population. **2014**, 80, 532-7	29
640	Genetics of diabetes--are we missing the genes or the disease?. **2014**, 382, 726-739	107
639	Recent advances in the molecular genetics of type 2 diabetes mellitus. **2014**, 5, 128-40	83
638	Replicability analysis for genome-wide association studies. **2014**, 8,	23
637	The effect of IGF2BP2 gene polymorphisms on pioglitazone response in Chinese type 2 diabetes patients. **2014**, 94, 115-22	8

636	Fine Mapping Type 2 Diabetes Susceptibility Loci. **2014**, 14-28		1
635	Genome-Wide Association Studies of Glycaemic Traits: A MAGICal Journey. **2014**, 42-57		
634	Diabetes and Health Care. **2014**, 1-129		1
633	Legal aspects of biobanking as key issues for personalized medicine and translational exploitation. **2014**, 11, 497-508		4
632	Milk: an epigenetic amplifier of FTO-mediated transcription? Implications for Western diseases. **2015**, 13, 385		49
631	Candidate gene analysis supports a role for polymorphisms at TCF7L2 as risk factors for type 2 diabetes in Sudan. **2015**, 15, 4		8
630	CDKN2A-rs10811661 polymorphism, waist-hip ratio, systolic blood pressure, and dyslipidemia are the independent risk factors for prediabetes in a Vietnamese population. **2015**, 16, 107		6
629	Genome-wide association studies in biliary atresia. **2015**, 7, 267-73		15
628	Association study of polymorphisms in miRNAs with T2DM in Chinese population. **2015**, 12, 875-80		21
627	Diabetes mellitus: The epidemic of the century. **2015**, 6, 850-67		398
626	DNA Methylation and MicroRNA-Based Biomarkers for Risk of Type 2 Diabetes. **2016**, 12, 20-9		13
625	Cumulative effect and predictive value of genetic variants associated with type 2 diabetes in Han Chinese: a case-control study. *PLoS ONE*, **2015**, 10, e0116537	3.7	14
624	Structural Properties of Gene Promoters Highlight More than Two Phenotypes of Diabetes. *PLoS ONE*, **2015**, 10, e0137950	3.7	3
623	Polymorphism on Chromosome 9p21.3 Is Associated with Severity and Early-Onset CAD in Type 2 Diabetic Tunisian Population. **2015**, 2015, 792679		3
622	The Chromosome 9p21 CVD- and T2D-Associated Regions in a Norwegian Population (The HUNT2 Survey). **2015**, 2015, 164652		3
621	Association between SLC30A8 rs13266634 Polymorphism and Type 2 Diabetes Risk: A Meta-Analysis. **2015**, 21, 2178-89		20
620	Deterministic identification of specific individuals from GWAS results. **2015**, 31, 1701-7		22
619	Type 2 diabetes as a protein misfolding disease. **2015**, 21, 439-49		190

618	Insulin-like Growth Factor 2 Overexpression Induces -Cell Dysfunction and Increases Beta-cell Susceptibility to Damage. **2015**, 290, 16772-85		35
617	Association study of the miRNA-binding site polymorphisms of CDKN2A/B genes with gestational diabetes mellitus susceptibility. **2015**, 52, 951-8		21
616	The Zinc Transporter Slc30a8/ZnT8 Is Required in a Subpopulation of Pancreatic -Cells for Hypoglycemia-induced Glucagon Secretion. **2015**, 290, 21432-42		32
615	Genetic variants associated with motion sickness point to roles for inner ear development, neurological processes and glucose homeostasis. *Human Molecular Genetics*, **2015**, 24, 2700-8	5.6	53
614	Genetics and epigenetics of obesity. **2015**, 5, 538-547		1
613	CDKAL1 gene variants affect the anti-TNF response among Psoriasis patients. **2015**, 29, 947-949		13
612	High density methylation QTL analysis in human blood via next-generation sequencing of the methylated genomic DNA fraction. **2015**, 16, 291		86
611	An Ant Colony Optimization and Tabu List Approach to the Detection of Gene-Gene Interactions in Genome-Wide Association Studies [Research Frontier]. **2015**, 10, 54-65		12
610	Long non-coding RNAs as regulators of the endocrine system. **2015**, 11, 151-60		138
609	Correlation between IGF2BP2 gene polymorphism and the risk of breast cancer in Chinese Han women. **2015**, 69, 297-300		10
608	Vascular Complications of Diabetes Mellitus. **2015**, 1541-1593		
607	Patients with psoriasis are insulin resistant. **2015**, 72, 599-605		48
606	Rare and common genetic events in type 2 diabetes: what should biologists know?. **2015**, 21, 357-68		107
605	ATP-dependent potassium channels and type 2 diabetes mellitus. **2015**, 48, 476-82		24
604	Genetic variations in magnesium-related ion channels may affect diabetes risk among African American and Hispanic American women. **2015**, 145, 418-24		25
603	Latent autoimmune diabetes of the adult: current knowledge and uncertainty. **2015**, 32, 843-52		105
602	Genetic Variants Associated With Quantitative Glucose Homeostasis Traits Translate to Type 2 Diabetes in Mexican Americans: The GUARDIAN (Genetics Underlying Diabetes in Hispanics) Consortium. **2015**, 64, 1853-66		62
601	Proinsulin misfolding and endoplasmic reticulum stress during the development and progression of diabetes. **2015**, 42, 105-18		88

600	Elite athletes' genetic predisposition for altered risk of complex metabolic traits. **2015**, 16, 25		14
599	Association of FTO, KCNJ11, SLC30A8, and CDKN2B polymorphisms with type 2 diabetes mellitus. **2015**, 49, 103-111		6
598	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
597	Long Non-coding RNA ANRIL and Polycomb in Human Cancers and Cardiovascular Disease. **2016**, 394, 29-39		55
596	Krüppel-like factor 14 increases insulin sensitivity through activation of PI3K/Akt signal pathway. **2015**, 27, 2201-8		33
595	Characterization of the transcriptional machinery bound across the widely presumed type 2 diabetes causal variant, rs7903146, within TCF7L2. **2015**, 23, 103-9		17
594	Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk. **2015**, 241, 419-26		23
593	Molecular genetics of coronary artery disease and ischemic stroke. **2015**, 4, 4-12		1
592	The Physiological, Biochemical, and Molecular Roles of Zinc Transporters in Zinc Homeostasis and Metabolism. **2015**, 95, 749-84		493
591	Effects of IGF2BP2, KCNQ1 and GCKR polymorphisms on clinical outcome in metastatic gastric cancer treated with EOF regimen. **2015**, 16, 959-70		20
590	Structural forms of the human amylase locus and their relationships to SNPs, haplotypes and obesity. **2015**, 47, 921-5		92
589	Genetics of type 2 diabetes-pitfalls and possibilities. *Genes*, **2015**, 6, 87-123	4.2	257
588	Joint effect of CENTD2 and KCNQ1 polymorphisms on the risk of type 2 diabetes mellitus among Chinese Han population. **2015**, 407, 46-51		9
587	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
586	Functional mechanisms for type 2 diabetes-associated genetic variants. **2015**, 29, 497-501		1
585	Longevity Genes. **2015**,		2
584	Exome and whole genome sequencing in aging and longevity. **2015**, 847, 127-39		5
583	Contribution of the hypothalamus and gut to weight gain susceptibility and resistance in mice. **2015**, 225, 191-204		6

582	The genetics of type 2 diabetes. **2015**, 401-412		
581	The genetics of diabetic complications. **2015**, 11, 277-87		99
580	Genome Mapping and Genomics in Human and Non-Human Primates. **2015**,		
579	IGF2BP2/IMP2-Deficient mice resist obesity through enhanced translation of Ucp1 mRNA and Other mRNAs encoding mitochondrial proteins. **2015**, 21, 609-21		87
578	Genomics, Personalized Medicine and Oral Disease. **2015**,		1
577	The Genetics of Pediatric Obesity. **2015**, 26, 711-721		45
576	The HHEX rs1111875A/G gene polymorphism is associated with susceptibility to type 2 diabetes in the iranian population. **2015**, 49, 535-542		6
575	Genetics of Type 2 Diabetes. **2015**, 1-21		
574	Type 2 diabetes-related variants influence the risk of developing multiple myeloma: results from the IMMEnSE consortium. **2015**, 22, 545-59		10
573	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. **2015**, 47, 1415-25		292
572	Evidence of non-pancreatic beta cell-dependent roles of Tcf7l2 in the regulation of glucose metabolism in mice. *Human Molecular Genetics*, **2015**, 24, 1646-54	5.6	23
571	T2DM GWAS in the Lebanese population confirms the role of TCF7L2 and CDKAL1 in disease susceptibility. **2014**, 4, 7351		22
570	RNA epigenetics. **2015**, 165, 28-35		86
569	Quality control metrics improve repeatability and reproducibility of single-nucleotide variants derived from whole-genome sequencing. **2015**, 15, 298-309		8
568	Selective disruption of Tcf7l2 in the pancreatic □cell impairs secretory function and lowers □cell mass. *Human Molecular Genetics*, **2015**, 24, 1390-9	5.6	68
567	SLC30A8 mutations in type 2 diabetes. **2015**, 58, 31-6		73
566	The genetics of diabetic pregnancy. **2015**, 29, 102-9		1
565	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

564	Genes Associated with Increased Fasting Glucose in Patients with Schizophrenia Spectrum Disorders. **2016**, 6,		
563	Literature Reviews on Methods for Rare Variant Association Studies. **2016**, 06,		
562	Comparison of Two Meta-Analysis Methods: Inverse-Variance-Weighted Average and Weighted Sum of Z-Scores. **2016**, 14, 173-180		56
561	Genetic Susceptibility to Cardiovascular Diseases: From Mendelian Disorders to Common Variants. **2016**, 137-157		
560	Association between IGF2BP2 Polymorphisms and Type 2 Diabetes Mellitus: A Case-Control Study and Meta-Analysis. **2016**, 13,		25
559	Confirming an integrated pathology of diabetes and its complications by molecular biomarker-target network analysis. **2016**, 14, 2213-21		2
558	Lack of Association between Variants and Type 2 Diabetes in Mexican American Families. **2016**, 2016, 6463214		6
557	The Decay of Disease Association with Declining Linkage Disequilibrium: A Fine Mapping Theorem. **2016**, 7, 217		1
556	Validation of Type 2 Diabetes Risk Variants Identified by Genome-Wide Association Studies in Northern Han Chinese. **2016**, 13,		7
555	The Functions of Metallothionein and ZIP and ZnT Transporters: An Overview and Perspective. *International Journal of Molecular Sciences*, **2016**, 17, 336	6.3	221
554	CERAMIC: Case-Control Association Testing in Samples with Related Individuals, Based on Retrospective Mixed Model Analysis with Adjustment for Covariates. **2016**, 12, e1006329		11
553	KATP Channels in the Pancreas. **2016**, 199-221		0
552	Type 2 diabetes: genetic data sharing to advance complex disease research. **2016**, 17, 535-49		92
551	A Clustered Multiclass Likelihood-Ratio Ensemble Method for Family-Based Association Analysis Accounting for Phenotypic Heterogeneity. **2016**, 40, 512-9		3
550	Melatonin receptor 1B gene associated with hyperglycemia in bipolar disorder. **2016**, 26, 136-9		2
549	IMP2 axonal localization, RNA interactome, and function in the development of axon trajectories. **2016**, 143, 2753-9		12
548	Reverse geroscience: how does exposure to early diseases accelerate the age-related decline in health?. **2016**, 1386, 30-44		18
547	IMPs: an RNA-binding protein family that provides a link between stem cell maintenance in normal development and cancer. **2016**, 30, 2459-2474		132

546	Genetic Architecture of Type 2 Diabetes. **2016**, 187-204	
545	Zinc Transport Gets Its Zing Back: Double-Knockout of ZnT7 and ZnT8 Reveals the Importance of Zinc Transporters to Insulin Secretion. **2016**, 157, 4542-4544	4
544	The Trilogy of GxE: Conceptualization, Operationalization, and Application. **2016**, 1-52	1
543	Exome-wide study of ankylosing spondylitis demonstrates additional shared genetic background with inflammatory bowel disease. **2016**, 1, 16008	21
542	Genetics of Type 2 Diabetes. **2016**, 31, 203-20	42
541	Long Non-coding RNAs in Human Disease. **2016**,	3
540	The Genetics of Type 2 Diabetes and Related Traits. **2016**,	3
539	Genome-Wide Association Studies of Type 2 Diabetes. **2016**, 13-61	4
538	Physiology Insights. **2016**, 207-221	
537	Radical S-Adenosylmethionine Enzymes in Human Health and Disease. **2016**, 85, 485-514	147
536	Islet biology, the CDKN2A/B locus and type 2 diabetes risk. **2016**, 59, 1579-93	50
535	Modeling Type 2 Diabetes GWAS Candidate Gene Function in hESCs. **2016**, 19, 281-2	4
534	Diabetes mellitus. Criterios diagn□sticos y clasificaci□n. Epidemiolog□a. Etiopatogenia. Evaluaci□n inicial del paciente con diabetes. **2016**, 12, 935-946	1
533	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
532	Body mass index: Has epidemiology started to break down causal contributions to health and disease?. **2016**, 24, 1630-8	14
531	Post-Transcriptional Modifications of RNA: Impact on RNA Function and Human Health. **2016**, 91-130	3
530	Genetic markers of type 2 diabetes: Progress in genome-wide association studies and clinical application for risk prediction. **2016**, 8, 24-35	49
529	Replication of genome-wide association signals in Asian Indians with early-onset type 2 diabetes. **2016**, 53, 915-923	11

528	The Relevance of Genomic Signatures at Adhesion GPCR Loci in Humans. **2016**, 234, 179-217		13
527	Adhesion G Protein-coupled Receptors. **2016**,		7
526	Meta-Analysis of the Association of IGF2BP2 Gene rs1470579 Polymorphisms with T2DM. **2016**,		
525	Phylogenetic and promoter analysis of islet amyloid polypeptide gene causing type 2 diabetes in mammalian species. **2016**, 36, 477-489		1
524	Cross-Disorder Psychiatric Genomics. **2016**, 3, 256-263		11
523	Genetic variants associated with lean and obese type 2 diabetes in a Han Chinese population: A case-control study. **2016**, 95, e3841		19
522	Insights into islet development and biology through characterization of a human iPSC-derived endocrine pancreas model. **2016**, 8, 83-95		18
521	Genetic variants in the mTOR pathway and interaction with body size and weight gain on breast cancer risk in African-American and European American women. **2016**, 27, 965-76		13
520	Whole-genome re-sequencing for the identification of high contribution susceptibility gene variants in patients with type 2 diabetes. **2016**, 13, 3735-46		5
519	Transcription Factor 7-Like 2 (TCF7L2). **2016**, 297-316		0
518	SLC30A8: A Complex Road from Association to Function. **2016**, 379-401		1
517	Genome-Wide Association Studies of Quantitative Glycaemic Traits. **2016**, 63-89		
516	Fine-Mapping of Type 2 Diabetes Loci. **2016**, 127-151		
515	Environmental Health and Long Non-coding RNAs. **2016**, 3, 178-87		64
514	Multiple testing correction in linear mixed models. **2016**, 17, 62		44
513	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
512	Genetics of Type 2 Diabetes. **2016**, 141-157		
511	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. *Nature Communications*, **2016**, 7, 10531	17.4	99

510	Targeting Insulin-Degrading Enzyme to Treat Type 2 Diabetes Mellitus. **2016**, 27, 24-34		58
509	Assessing statistical significance in multivariable genome wide association analysis. **2016**, 32, 1990-2000		22
508	Increased Expression of the Diabetes Gene SOX4 Reduces Insulin Secretion by Impaired Fusion Pore Expansion. **2016**, 65, 1952-61		39
507	Perspectives in Polycystic Ovary Syndrome: From Hair to Eternity. **2016**, 101, 759-68		55
506	Genome-Wide DNA and Histone Modification Studies in Metabolic Disease. **2016**, 255-270		
505	Genetic and clinical variables identify predictors for chronic kidney disease in type 2 diabetes. **2016**, 89, 411-20		12
504	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. *Human Molecular Genetics*, **2016**, 25, 2070-2081	5.6	20
503	Association of SLC30A8 gene polymorphism with type 2 diabetes, evidence from 46 studies: a meta-analysis. **2016**, 53, 381-94		23
502	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
501	Recent progress in genetic and epigenetic research on type 2 diabetes. **2016**, 48, e220		92
500	The Lipogenic Effect of Insulin Revisited. **2016**, 285-295		
499	Exploiting Linkage Disequilibrium for Ultrahigh-Dimensional Genome-Wide Data with an Integrated Statistical Approach. **2016**, 202, 411-26		3
498	Hepatic De Novo Lipogenesis and Regulation of Metabolism. **2016**,		3
497	The top 100 most cited scientific reports focused on diabetes research. **2016**, 53, 13-26		29
496	A Type 1 Diabetes Genetic Risk Score Can Aid Discrimination Between Type 1 and Type 2 Diabetes in Young Adults. **2016**, 39, 337-44		141
495	Genes associated with diabetes: potential for novel therapeutic targets?. **2016**, 20, 255-67		12
494	Molecular genetics of coronary artery disease. **2016**, 61, 71-7		47
493	Genome-wide gene-gene interaction analysis for next-generation sequencing. **2016**, 24, 421-8		12

492	Type 2 Diabetes Mellitus. **2016**, 691-714.e6	4
491	Common variant within the FTO gene, rs9939609, obesity and type 2 diabetes in population of Karachi, Pakistan. **2016**, 10, 43-7	12
490	Computational analyses of type 2 diabetes-associated loci identified by genome-wide association studies. **2017**, 9, 362-377	14
489	Long noncoding RNA variations in cardiometabolic diseases. **2017**, 62, 97-104	33
488	Association of a type 2 diabetes genetic risk score with insulin secretion modulated by insulin sensitivity among Chinese Hans. **2017**, 91, 832-842	8
487	Transdisciplinary approaches enhance the production of translational knowledge. **2017**, 182, 123-134	31
486	Fat mass and obesity-associated gene variations are related to fatty liver disease in HIV-infected patients. **2017**, 18, 546-554	4
485	A Statistical Framework for Pathway and Gene Identification from Integrative Analysis. **2017**, 156, 1-17	0
484	Joker de Bruijn: Sequence Libraries to Cover All -mers Using Joker Characters. **2017**, 10229, 389-390	
483	Perinatal DNA Methylation at CDKN2A Is Associated With Offspring Bone Mass: Findings From the Southampton Women's Survey. **2017**, 32, 2030-2040	24
482	Major review: Molecular genetics of primary open-angle glaucoma. **2017**, 160, 62-84	73
481	No association detected between seven common variants in the CDKAL1 gene and gestational glycemic traits. **2017**, 34, 64-67	1
480	Using genetics to inform new therapeutics for diabetes. **2017**, 12, 159-169	
479	ANRIL Promoter DNA Methylation: A Perinatal Marker for Later Adiposity. **2017**, 19, 60-72	49
478	Association of the type 2 diabetes mellitus susceptibility gene (IGF2BP2) with schizophrenia in an Egyptian sample. **2017**, 24, 55-62	1
477	Exploring the Association Between Demographics, SLC30A8 Genotype, and Human Islet Content of Zinc, Cadmium, Copper, Iron, Manganese and Nickel. **2017**, 7, 473	25
476	MicroRNA profiling in clear cell renal cell carcinoma tissues potentially links tumorigenesis and recurrence with obesity. **2017**, 116, 77-84	30
475	Gene variants in the FTO gene are associated with adiponectin and TNF-alpha levels in gestational diabetes mellitus. **2017**, 9, 32	17

474	The rs7903146 Variant in the Gene Increases the Risk of Prediabetes/Type 2 Diabetes in Obese Adolescents by Impairing □-Cell Function and Hepatic Insulin Sensitivity. **2017**, 40, 1082-1089	34
473	Inositol phosphates and phosphoinositides activate insulin-degrading enzyme, while phosphoinositides also mediate binding to endosomes. **2017**, 114, E2826-E2835	12
472	Obstacles to Translating Genotype-Phenotype Correlates in Metabolic Disease. **2017**, 32, 42-50	2
471	Pancreatic alpha cell-selective deletion of Tcf7l2 impairs glucagon secretion and counter-regulatory responses to hypoglycaemia in mice. **2017**, 60, 1043-1050	13
470	Genome-Wide Association Study Meta-Analysis of Long-Term Average Blood Pressure in East Asians. **2017**, 10, e001527	20
469	The Pathophysiology of Hyperglycemia in Older Adults: Clinical Considerations. **2017**, 40, 444-452	66
468	Dwarfism and Altered Craniofacial Development in Rabbits Is Caused by a 12.1 kb Deletion at the HMGA2 Locus. **2017**, 205, 955-965	21
467	Prediabetes in youth - mechanisms and biomarkers. **2017**, 1, 240-248	27
466	A Loss-of-Function Splice Acceptor Variant in Is Protective for Type 2 Diabetes. **2017**, 66, 2903-2914	32
465	Zinc, Insulin and IGF-I Interplay in Aging. **2017**, 57-90	0
464	Implications of impaired zinc homeostasis in diabetic cardiomyopathy and nephropathy. **2017**, 43, 770-784	5
463	RNA sequencing of db/db mice liver identifies lncRNA H19 as a key regulator of gluconeogenesis and hepatic glucose output. **2017**, 7, 8312	32
462	Cdkal1, a type 2 diabetes susceptibility gene, regulates mitochondrial function in adipose tissue. **2017**, 6, 1212-1225	25
461	Improving power of association tests using multiple sets of imputed genotypes from distributed reference panels. **2017**, 41, 744-755	13
460	Human beta cell mass and function in diabetes: Recent advances in knowledge and technologies to understand disease pathogenesis. **2017**, 6, 943-957	215
459	Meta-analysis of gene-environment interaction exploiting gene-environment independence across multiple case-control studies. **2017**, 36, 3895-3909	1
458	ANRIL polymorphism rs1333049, a novel genetic predictor for diabetic retinopathy complication. **2017**, 14, 33-37	2
457	CDK5 Regulatory Subunit-Associated Protein 1-like 1 Negatively Regulates Adipocyte Differentiation through Activation of Wnt Signaling Pathway. **2017**, 7, 7326	6

456	AIM. **2017**,		4
455	Fusion pore in exocytosis: More than an exit gate? A -cell perspective. **2017**, 68, 45-61		10
454	A genetic stochastic process model for genome-wide joint analysis of biomarker dynamics and disease susceptibility with longitudinal data. **2017**, 41, 620-635		3
453	Concise Review: Challenges in Regenerating the Diabetic Heart: A Comprehensive Review. **2017**, 35, 2009-2026		9
452	Introduction of the DiaGene study: clinical characteristics, pathophysiology and determinants of vascular complications of type 2 diabetes. **2017**, 9, 47		11
451	Aging: Treating the Older Patient. **2017**, 23, 193-200		21
450	Cellular senescence: Implications for metabolic disease. **2017**, 455, 93-102		35
449	Primary Open-Angle Glaucoma Genetics in African Americans. **2017**, 5, 167-174		7
448	FTO Genotype and Type 2 Diabetes Mellitus: Spatial Analysis and Meta-Analysis of 62 Case-Control Studies from Different Regions. *Genes*, **2017**, 8,	4.2	22
447	Diabetes. **2017**, 245-282		1
446	Genetic Variations as Modifying Factors to Dietary Zinc Requirements-A Systematic Review. **2017**, 9,		11
445	Association of common polymorphisms with gestational diabetes mellitus in Japanese women: A case-control study. **2017**, 64, 463-475		14
444	Long Noncoding RNAs as Diagnostic and Therapeutic Targets in Type 2 Diabetes and Related Complications. *Genes*, **2017**, 8,	4.2	53
443	Meta-Analysis of the association ofIGF2BP2gene rs4402960 polymorphisms with T2DM in Asia. **2017**, 8, 02003		1
442	Type 2 Diabetes Susceptibility in the Greek-Cypriot Population: Replication of Associations with TCF7L2, FTO, HHEX, SLC30A8 and IGF2BP2 Polymorphisms. *Genes*, **2017**, 8,	4.2	15
441	Gene-Diet Interaction and Precision Nutrition in Obesity. *International Journal of Molecular Sciences* , **2017**, 18,	6.3	79
440	K Channel Mutations and Neonatal Diabetes. **2017**, 56, 2387-2393		16
439	Transcription factor 7-like 2 (TCF7L2) gene polymorphisms are strong predictorsof type 2 diabetes among nonobese diabetics in the Turkish population. **2017**, 47, 22-28		10

438	RNA Epigenetics (Epitranscriptomics). **2017**, 19-35		
437	Utilization of genetic data can improve the prediction of type 2 diabetes incidence in a Swedish cohort. *PLoS ONE*, **2017**, 12, e0180180	3.7	2
436	Association between 28 single nucleotide polymorphisms and type 2 diabetes mellitus in the Kazakh population: a case-control study. **2017**, 18, 76		13
435	Genetics and Diabetes. **2017**, 659-675		
434	Myeloma in Elderly Patients: When Less Is More and More Is More. **2017**, 37, 575-585		10
433	LncRNAs: key players and novel insights into diabetes mellitus. **2017**, 8, 71325-71341		54
432	The pathogenetic role of β-cell mitochondria in type 2 diabetes. **2018**, 236, R145-R159		46
431	Progress in defining the genetic contribution to type 2 diabetes susceptibility. **2018**, 50, 41-51		15
430	Precision medicine in diabetes prevention, classification and management. **2018**, 9, 998-1015		32
429	IAPP/amylin and β-cell failure: implication of the risk factors of type 2 diabetes. **2018**, 9, 143-157		19
428	Novel association between CDKAL1 and cholesterol efflux capacity: Replication after GWAS-based discovery. **2018**, 273, 21-27		2
427	T2D Genome-Wide Association Study Risk SNPs Impact Locus Gene Expression and Proliferation in Human Islets. **2018**, 67, 872-884		28
426	Transcriptomic alterations during ageing reflect the shift from cancer to degenerative diseases in the elderly. *Nature Communications*, **2018**, 9, 327	17.4	53
425	Physiologic Interpretation of GWAS Signals for Type 2 Diabetes. **2018**, 1706, 323-351		1
424	Association of CDKAL1 nucleotide variants with the risk of non-syndromic cleft lip with or without cleft palate. **2018**, 63, 397-406		4
423	Genetics and Genomics of Coronary Artery Disease. **2018**, 661-678		1
422	Pathogenesis and Management of Adiposity and Insulin Resistance in Polycystic Ovary Syndrome (PCOS). **2018**, 629-642		1
421	A candidate functional SNP rs7074440 in TCF7L2 alters gene expression through C-FOS in hepatocytes. **2018**, 592, 422-433		8

420	Metabolomics study on the association between nicotinamide N-methyltransferase gene polymorphisms and type 2 diabetes. **2018**, 38, 409-416	3
419	Epigenetic reprogramming during spermatogenesis and male factor infertility. **2018**, 156, R9-R21	37
418	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
417	Variants of CDKAL1 rs7754840 (G/C) and CDKN2A/2B rs10811661 (C/T) with gestational diabetes: insignificant association. **2018**, 11, 181	8
416	Design of Arab Diabetes Gene-Centric Array (ADGCA) in population with an epidemic of Type 2 Diabetes: A population specific SNP evaluation. **2018**, 663, 157-164	4
415	Genome-Wide Association Studies and Heritability Estimation in the Functional Genomics Era. **2018**, 361-425	4
414	Jointly determining significance levels of primary and replication studies by controlling the false discovery rate in two-stage genome-wide association studies. **2018**, 27, 2795-2808	1
413	A genetic variant in CDKN2A/B gene is associated with the increased risk of breast cancer. **2018**, 32,	16
412	Cellular Senescence Biomarker p16INK4a+ Cell Burden in Thigh Adipose is Associated With Poor Physical Function in Older Women. **2018**, 73, 939-945	70
411	Association of CDKN2A/CDKN2B with inflammatory bowel disease in Koreans. **2018**, 33, 887-893	6
410	Inhibition of Cdk5 Promotes □-Cell Differentiation From Ductal Progenitors. **2018**, 67, 58-70	24
409	Metabolic pathways at the crossroads of diabetes and inborn errors. **2018**, 41, 5-17	4
408	Psoriasis and the risk of diabetes: A prospective population-based cohort study. **2018**, 78, 315-322.e1	57
407	The role of cellular senescence in aging through the prism of Koch-like criteria. **2018**, 41, 18-33	27
406	Senescence and aging: Causes, consequences, and therapeutic avenues. **2018**, 217, 65-77	426
405	Genetic Approaches to the Study of Gene Variants and Their Impact on the Pathophysiology of Type 2 Diabetes. **2018**, 56, 22-55	17
404	The GAIT translational control system. **2018**, 9, e1441	28
403	Nutrient Sensing, Signaling and Ageing: The Role of IGF-1 and mTOR in Ageing and Age-Related Disease. **2018**, 90, 49-97	21

402	Periodontal, metabolic, and cardiovascular disease: Exploring the role of inflammation and mental health. **2018**, 29, 124-163		16
401	Genes associated with Type 2 Diabetes and vascular complications. **2018**, 10, 178-196		27
400	[Next generation biobanking: the challenge of data]. **2018**, 34, 849-851		0
399	Trace Elements and Minerals in Health and Longevity. **2018**,		3
398	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
397	Identifying loci affecting trait variability and detecting interactions in genome-wide association studies. **2018**, 50, 1608-1614		34
396	Association Between SLC30A8 rs13266634 Polymorphism and Risk of T2DM and IGR in Chinese Population: A Systematic Review and Meta-Analysis. *Frontiers in Endocrinology*, **2018**, 9, 564	5.7	4
395	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
394	Exome sequencing-based identification of novel type 2 diabetes risk allele loci in the Qatari population. *PLoS ONE*, **2018**, 13, e0199837	3.7	3
393	Highly specific monoclonal antibodies for allosteric inhibition and immunodetection of the human pancreatic zinc transporter ZnT8. **2018**, 293, 16206-16216		8
392	tRNA modifications and islet function. **2018**, 20 Suppl 2, 20-27		10
391	Body mass index modulates the association between CDKAL1 rs10946398 variant and type 2 diabetes among Taiwanese women. **2018**, 8, 13235		11
390	Pathophysiology of Type 2 Diabetes in Koreans. **2018**, 33, 9-16		8
389	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
388	Molecular functions and specific roles of circRNAs in the cardiovascular system. **2018**, 3, 75-98		38
387	The Roles of Insulin-Like Growth Factor 2 mRNA-Binding Protein 2 in Cancer and Cancer Stem Cells. **2018**, 2018, 4217259		61
386	High-Throughput Approaches onto Uncover (Epi)Genomic Architecture of Type 2 Diabetes. *Genes*, **2018**, 9,	4.2	10
385	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

384	FTO, GCKR, CDKAL1 and CDKN2A/B gene polymorphisms and the risk of gestational diabetes mellitus: a meta-analysis. **2018**, 298, 705-715		8
383	Mediating Effect of Diabetes Mellitus on the Association Between Chromosome 9p21.3 Locus and Myocardial Infarction Risk: A Case-Control Study in Shanghai, China. *Frontiers in Endocrinology*, **2018**, 9, 362	5.7	2
382	Long Non-Coding RNAs in Vascular Inflammation. **2018**, 5, 22		15
381	Type 2 Diabetes Mellitus and Cardiovascular Disease: Genetic and Epigenetic Links. *Frontiers in Endocrinology*, **2018**, 9, 2	5.7	138
380	Solute Carrier Family 30 Member 8 Gene 807C/T Polymorphism and Type 2 Diabetes Mellitus in the Chinese Population: A Meta-Analysis Including 6,942 Subjects. *Frontiers in Endocrinology*, **2018**, 9, 263	5.7	4
379	Genetics of Diabetes and Diabetic Complications. **2018**, 1-60		
378	Effect of smoking on the association of HHEX (rs5015480) with diabetes among Korean women and heavy smoking men. **2018**, 19, 68		0
377	From SNPs to pathways: Biological interpretation of type 2 diabetes (T2DM) genome wide association study (GWAS) results. *PLoS ONE*, **2018**, 13, e0193515	3.7	24
376	: A lncRNA at the CDKN2A/B Locus With Roles in Cancer and Metabolic Disease. *Frontiers in Endocrinology*, **2018**, 9, 405	5.7	85
375	Cohort Profile: Genetics of Diabetes Audit and Research in Tayside Scotland (GoDARTS). **2018**, 47, 380-381j		37
374	Linear isoforms of the long noncoding RNA CDKN2B-AS1 regulate the c-myc-enhancer binding factor RBMS1. **2019**, 27, 80-89		26
373	Use of a comprehensive frailty assessment to predict morbidity in patients with multiple myeloma undergoing transplant. **2019**, 10, 479-485		40
372	Statistical tests for detecting variance effects in quantitative trait studies. **2019**, 35, 200-210		16
371	RNAs and RNA-Binding Proteins in Immuno-Metabolic Homeostasis and Diseases. **2019**, 6, 106		13
370	Recent advances and perspectives in next generation sequencing application to the genetic research of type 2 diabetes. **2019**, 10, 376-395		8
369	Regulation of growth hormone biosynthesis by Cdk5 regulatory subunit associated protein 1-like 1 (CDKAL1) in pituitary adenomas. **2019**, 66, 807-816		4
368	The genetic side of type 2 diabetes - A review. **2019**, 13, 2503-2506		17
367	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

366	Insulin Sensitivity Is Associated with Lipoprotein Lipase () and Catenin Delta 2 () DNA Methylation in Peripheral White Blood Cells in Non-Diabetic Young Women. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	4
365	Genetics, adaptation to environmental changes and archaic admixture in the pathogenesis of diabetes mellitus in Indigenous Australians. **2019**, 20, 321-332		2
364	A Novel Polymorphism (rs35612982) in CDKAL1 Is a Risk Factor of Type 2 Diabetes: A Case-Control Study. **2019**, 44, 1313-1326		10
363	Association of MTHFR C677T polymorphism and type 2 diabetes mellitus (T2DM) susceptibility. **2019**, 7, e1020		8
362	A general statistic to test an optimally weighted combination of common and/or rare variants. **2019** , 43, 966-979		2
361	From Pre-Diabetes to Diabetes: Diagnosis, Treatments and Translational Research. **2019**, 55,		66
360	The Burmese cat as a genetic model of type 2 diabetes in humans. **2019**, 50, 319-325		9
359	BMI-associated gene variants in and cardiometabolic and brain disease: obesity or pleiotropy?. **2019** , 51, 311-322		6
358	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
357	Long Non-coding RNAs in Vascular Health and Disease. **2019**, 151-179		
356	Molecular Biology of Long Non-coding RNAs. **2019**,		1
355	Association of Omentin rs2274907 and FTO rs9939609 gene polymorphisms with insulin resistance in Iranian individuals with newly diagnosed type 2 diabetes. **2019**, 18, 142		16
354	Genetics of Type 2 Diabetes: A Review. **2019**, 6, 59-63		1
353	New Insights Into the Circadian Rhythm and Its Related Diseases. **2019**, 10, 682		76
352	Function and Mechanism of Long Noncoding RNAs in Adipocyte Biology. **2019**, 68, 887-896		29
351	Effects of variants of 50 genes on diabetes risk among the Chinese population born in the early 1960s. **2019**, 11, 857-868		2
350	Disease-Associated SNPs in Inflammation-Related lncRNAs. **2019**, 10, 420		41
349	Genetic, Functional, and Immunological Study of ZnT8 in Diabetes. **2019**, 2019, 1524905		5

348	Robust Reference Powered Association Test of Genome-Wide Association Studies. **2019**, 10, 319	1
347	Circadian rhythms and the molecular clock in cardiovascular biology and disease. **2019**, 16, 437-447	140
346	Co-shared genetics and possible risk gene pathway partially explain the comorbidity of schizophrenia, major depressive disorder, type 2 diabetes, and metabolic syndrome. **2019**, 180, 186-203	40
345	Zinc and its regulators in pancreas. **2019**, 27, 453-464	14
344	Type 2 Diabetes-Associated Genetic Polymorphisms as Potential Disease Predictors. **2019**, 12, 2689-2706	14
343	A Review of Type 2 Diabetes Mellitus Predisposing Genes. **2019**, 16, 52-61	12
342	An in´vivo screen for neuronal genes involved in obesity identifies Diacylglycerol kinase as a regulator of insulin secretion. **2019**, 19, 13-23	1
341	Type 2 diabetes - An unresolved disease across centuries contributing to a public health emergency. **2019**, 13, 450-453	22
340	Interaction of amylin species with transition metals and membranes. **2019**, 191, 69-76	24
339	Deciphering Cardiovascular Genomics and How They Apply to Cardiovascular Disease Prevention. **2019**, 99-111	
338	Interdisciplinary Care Model: Diabetes and Oral Health. **2019**, 47-61	2
337	Improving Imputation Accuracy by Inferring Causal Variants in Genetic Studies. **2019**, 26, 1203-1213	
336	LncRNAs in vascular biology and disease. **2019**, 114, 145-156	86
335	Linking diabetic vascular complications with LncRNAs. **2019**, 114, 139-144	22
334	Peripheral Artery Disease and Aortic Disease. **2016**, 11, 313-326	6
333	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
332	Genetic susceptibility, lifestyle intervention and glycemic changes among women with prior gestational diabetes. **2020**, 39, 2144-2150	3
331	Cattle genomics: genome projects, current status, and future applications. **2020**, 3-28	0

330	Pleiotropy in eye disease and related traits. **2020**, 315-336		1
329	Association of cyclin-dependent kinase inhibitor 2A/B with increased risk of developing breast cancer. **2020**, 235, 5141-5145		5
328	Pathophysiology of Type 2 Diabetes in Children and Adolescents. **2020**, 16, 220-229		16
327	Seeking genetic determinants of selected metabolic disorders in women aged 45-60. **2020**, 27, 407-412		0
326	The Diverse Functions of IMP2/IGF2BP2 in Metabolism. **2020**, 31, 670-679		24
325	Genome plasticity and endocrine diseases. **2020**, 211-235		
324	Analysis of the interaction effect of 48 SNPs and obesity on type 2 diabetes in Chinese Hans. **2020**, 8,		1
323	Disease-Causing Mutations and Rearrangements in Long Non-coding RNA Gene Loci. **2020**, 11, 527484		11
322	Genetic Studies of Gestational Diabetes and Glucose Metabolism in Pregnancy. **2020**, 20, 69		13
321	Intracellular and tissue specific expression of FTO protein in pig: changes with age, energy intake and metabolic status. **2020**, 10, 13029		4
320	S-adenosylmethionine tRNA modification: unexpected/unsuspected implications of former/new players. **2020**, 16, 3018-3027		2
319	Comparison of novel single nucleotide polymorphisms of zinc transporters with zinc concentration in the human blood and vaginal tissues. **2020**, 33, 323-337		1
318	Nutrient consumption-dependent association of a glucagon-like peptide-1 receptor gene polymorphism with insulin secretion. **2020**, 10, 16382		1
317	JS-MA: A Jensen-Shannon Divergence Based Method for Mapping Genome-Wide Associations on Multiple Diseases. **2020**, 11, 507038		2
316	Functional Genomics in Pancreatic □Cells: Recent Advances in Gene Deletion and Genome Editing Technologies for Diabetes Research. *Frontiers in Endocrinology*, **2020**, 11, 576632	5.7	7
315	Prevention of Diabetes and Cardiovascular Disease in Obesity. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	17
314	Secretome-Based Screening in Target Discovery. **2020**, 25, 535-551		5
313	Genetic predisposition in type 2 diabetes: A promising approach toward a personalized management of diabetes. **2020**, 98, 525-547		16

312	Drivers for the comorbidity of type 2 diabetes mellitus and epilepsy: A scoping review. **2020**, 106, 107043		5
311	Secretory Autophagy and Its Relevance in Metabolic and Degenerative Disease. *Frontiers in Endocrinology*, **2020**, 11, 266	5.7	15
310	Computational determination of human PPARG gene: SNPs and prediction of their effect on protein functions of diabetic patients. **2020**, 9, 7		7
309	A Comprehensive Genome-Wide and Phenome-Wide Examination of BMI and Obesity in a Northern Nevadan Cohort. **2020**, 10, 645-664		15
308	Understanding the Interrelationship between Education, Income, and Obesity among Adults in Saudi Arabia. **2020**, 13, 77-85		6
307	The association between HHEX single-nucleotide polymorphism rs5015480 and gestational diabetes mellitus: A meta-analysis. **2020**, 99, e19478		1
306	Systematic Review of Polygenic Risk Scores for Type 1 and Type 2 Diabetes. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	15
305	Structure/Function Analysis of human ZnT8 (SLC30A8): A Diabetes Risk Factor and Zinc Transporter. **2020**, 2, 144-155		4
304	Genetic factors for short life span associated with evolution of the loss of flight ability. **2020**, 10, 6020-6029		1
303	Insights into pancreatic islet cell dysfunction from type 2 diabetes mellitus genetics. **2020**, 16, 202-212		50
302	Lifestyle intervention in individuals with impaired glucose regulation affects Caveolin-1 expression and DNA methylation. **2020**, 9, 96-107		3
301	A Unifying Framework for Imputing Summary Statistics in Genome-Wide Association Studies. **2020**, 27, 418-428		1
300	Irp2 regulates insulin production through iron-mediated Cdkal1-catalyzed tRNA modification. *Nature Communications*, **2020**, 11, 296	17.4	28
299	Hierarchical inference for genome-wide association studies: a view on methodology with software. **2020**, 35, 1-40		5
298	The ChinaMAP analytics of deep whole genome sequences in 10,588 individuals. **2020**, 30, 717-731		60
297	E2f8 and Dlg2 genes have independent effects on impaired insulin secretion associated with hyperglycaemia. **2020**, 63, 1333-1348		5
296	The lncRNA is down-regulated in peripheral blood of patients with periodontitis. **2020**, 5, 60-66		15
295	Is there a CDKN2A-centric networkin´pancreatic ductal adenocarcinoma?. **2020**, 13, 2551-2562		4

294	Rs9939609 polymorphism of the fat mass and obesity-associated (FTO) gene and metabolic syndrome susceptibility in the Chinese population: a meta-analysis. **2020**, 69, 278-285		5
293	and are Associated with Type 2 Diabetes Mellitus in Iranian Patients. **2020**, 13, 897-906		14
292	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
291	GCN5 acetyltransferase in cellular energetic and metabolic processes. **2021**, 1864, 194626		21
290	Genome-Wide Association Analysis of Pancreatic Beta-Cell Glucose Sensitivity. **2021**, 106, 80-90		2
289	Common Variants Associated to Type 2 Diabetes in the Italian Population. **2021**, 11, 24-42		1
288	tRNA Biology in the Pathogenesis of Diabetes: Role of Genetic and Environmental Factors. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	3
287	Progressive Shifts in the Gut Microbiome Reflect Prediabetes and Diabetes Development in a Treatment-Naive Mexican Cohort. *Frontiers in Endocrinology*, **2020**, 11, 602326	5.7	2
286	Combining twin-family designs with measured genetic variants to study the causes of epigenetic variation. **2021**, 239-259		
285	Regulation of divalent metal ions to the aggregation and membrane damage of human islet amyloid polypeptide oligomers.. **2021**, 11, 12815-12825		1
284	Diet and Pro12Ala Polymorphism Interactions in Relation to Cancer Risk: A Systematic Review. **2021** , 13,		3
283	Genome-wide screening of upstream transcription factors using an expression library. **2021**, 10, 51		1
282	Diabetes Mellitus. **2021**, 814-883		1
281	Two decades since the fetal insulin hypothesis: what have we learned from genetics?. **2021**, 64, 717-726		3
280	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
279	Genetic Variations Influencing Glucose Homeostasis and Insulin Secretion and their Associations with Autism Spectrum Disorder in Kazakhstan. **2021**, 18, em274		0
278	Genome-wide screening of upstream transcription factors using an expression library. **2021**, 10, 51		3
277	All thresholds of maternal hyperglycaemia from the WHO 2013 criteria for gestational diabetes identify women with a higher genetic risk for type 2 diabetes. **2020**, 5, 175		0

276	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
275	Autocrine IGF2 programmes β-cell plasticity under conditions of increased metabolic demand. **2021**, 11, 7717		1
274	Progress in Defining the Genetic Contribution to Type 2 Diabetes in Individuals of East Asian Ancestry. **2021**, 21, 17		2
273	Assessment of genetic risk of type 2 diabetes among Pakistanis based on GWAS-implicated loci. **2021**, 783, 145563		0
272	Human Pluripotent Stem Cells Go Diabetic: A Glimpse on Monogenic Variants. *Frontiers in Endocrinology*, **2021**, 12, 648284	5.7	2
271	Kidney Disease in Diabetic Patients: From Pathophysiology to Pharmacological Aspects with a Focus on Therapeutic Inertia. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	7
270	The Impact of Variants in Four Genes: MC4R, FTO, PPARG and PPARGC1A in Overweight and Obesity in a Large Sample of the Brazilian Population. **2021**, 59, 1666-1679		1
269	Pancreatic β-cell-selective zinc transporter 8 insufficiency accelerates diabetes associated with islet amyloidosis. **2021**, 6,		3
268	Mapping pleiotropic loci using a fast-sequential testing algorithm. **2021**, 29, 1762-1773		0
267	Common genetic variation in circadian clock genes are associated with cardiovascular risk factors in an African American and Hispanic/Latino cohort. **2021**, 34, 100808		2
266	Type 2 diabetes is associated with the MTNR1B gene, a genetic bridge between circadian rhythm and glucose metabolism, in a Turkish population. **2021**, 48, 4181-4189		1
265	Insulin-like Growth Factor 2 mRNA-Binding Protein 2-a Potential Link Between Type 2 Diabetes Mellitus and Cancer. **2021**, 106, 2807-2818		5
264	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
263	RNA m6A reader IMP2/IGF2BP2 promotes pancreatic β-cell proliferation and insulin secretion by enhancing PDX1 expression. **2021**, 48, 101209		9
262	Epigenetic Regulation of the Vascular Endothelium by Angiogenic LncRNAs. **2021**, 12, 668313		2
261	Role of FOXP3 gene polymorphisms (SNPs rs3761547, rs3761549, and rs2232365) in the development of Type 2 diabetes mellitus. **2021**, 24, 101253		1
260	Non-Coding RNA as Biomarkers for Type 2 Diabetes Development and Clinical Management. *Frontiers in Endocrinology*, **2021**, 12, 630032	5.7	5
259	The role of long non-coding RNAs in the regulation of pancreatic beta cell identity. **2021**, 49, 2153-2161		1

258	Association of polymorphic loci of susceptibility to diabetes mellitus type 2 in various ethnic groups of the Russian Federation. *Diabetes Mellitus*, **2021**, 24, 262-272	1.6	0
257	The risk variant of CDKAL1 (rs7756992) impairs fasting glucose levels and insulin resistance improvements after a partial meal-replacement hypocaloric diet. **2021**,		
256	IGF-2 mRNA binding protein 2 regulates primordial germ cell development in zebrafish. **2021**, 313, 113875		0
255	Senotherapeutics: Experimental therapy of cellular senescence. **2021**, 251-284		
254	Association of type 2 diabetes mellitus and periodontal disease susceptibility with genome-wide association-identified risk variants in a Southeastern Brazilian population. *Clinical Oral Investigations*, **2021**, 25, 3873-3892	4.2	4
253	Association Between Single Nucleotide Polymorphisms in and and Type 2 Diabetes in Chinese Population. **2020**, 13, 5113-5123		4
252	Genetic Associations in Schizophrenia. 269-288		2
251	The Main Events in the History of Diabetes Mellitus. **2010**, 3-16		16
250	Pharmacogenomics of endocrine therapy in breast cancer. **2008**, 630, 220-31		14
249	Established Facts and Open Questions of Regulated Exocytosis in -Cells A Background for a Focused Systems Analysis Approach. **2011**, 25-52		1
248	Family Influences on Children Well-Being: Potential Roles of Molecular Genetics and Epigenetics. **2011**, 181-204		1
247	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
246	High-throughput SNP genotyping: combining tag SNPs and molecular beacons. **2009**, 578, 255-76		23
245	Genome-wide association studies. **2011**, 713, 89-103		3
244	Statistical and Methodological Considerations in Exercise Genomics. **2011**, 23-43		2
243	Zinc. **2018**, 99-131		2
242	Annotation, genetics and transcriptomics. **2008**, 123-136		1
241	The Main Events in the History of Diabetes Mellitus. **2017**, 3-19		1

240	DAM: A Bayesian Method for Detecting Genome-wide Associations on Multiple Diseases. **2015**, 96-107	3
239	Insulin Action in the Brain and the Pathogenesis of Alzheimer Disease. **2010**, 1-20	7
238	Wnt Signaling in Pancreatic Islets. **2014**, 1-31	1
237	Genome-Wide Association Study for Type 2 Diabetes. **2019**, 49-86	1
236	Epigenetic Basis of Oxidative Stress in Diabetic Coronary Atherosclerosis: A Shift in Focus from Genetic Prerogative. **2019**, 419-455	1
235	Type 2 Diabetes Mellitus. **2010**, 765-787	2
234	Sleep-related breathing disorders. 279-301	1
233	The association of TNF- 308G/A and -238G/A polymorphisms with type 2 diabetes mellitus: a meta-analysis. **2019**, 39,	3
232	Influence of IGF2BP2, HMG20A, and HNF1B genetic polymorphisms on the susceptibility to Type 2 diabetes mellitus in Chinese Han population. **2020**, 40,	4
231	Genetic Predictors of Obesity. **2008**, 437-460	4
230	Genetics Insights in the Relationship Between Type 2 Diabetes and Coronary Heart Disease. **2020**, 126, 1526-1548	22
229	Mechanisms by which common variants in the TCF7L2 gene increase risk of type 2 diabetes. **2007**, 117, 2155-63	574
228	Genetic and epigenetic factors are associated with expression of respiratory chain component NDUFB6 in human skeletal muscle. **2007**, 117, 3427-35	146
227	Prime suspect: the TCF7L2 gene and type 2 diabetes risk. **2007**, 117, 2077-9	37
226	Cholesterol in islet dysfunction and type 2 diabetes. **2008**, 118, 403-8	105
225	Variations in the G6PC2/ABCB11 genomic region are associated with fasting glucose levels. **2008**, 118, 2620-8	127
224	Deficit of tRNA(Lys) modification by Cdkal1 causes the development of type 2 diabetes in mice. **2011**, 121, 3598-608	173
223	The role of aging upon cell turnover. **2013**, 123, 990-5	114

222	The Regulatory and Signaling Functions of Zinc Ions in Human Cellular Physiology. **2010**, 181-212		3
221	Estimation of false discovery proportion in multiple testing: From normal to chi-squared test statistics. **2017**, 11,		1
220	Gene Polymorphism Association with Type 2 Diabetes and Related Gene-Gene and Gene-Environment Interactions in a Uyghur Population. **2016**, 22, 474-87		13
219	Extracting replicable associations across multiple studies: Empirical Bayes algorithms for controlling the false discovery rate. **2017**, 13, e1005700		7
218	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
217	HHEX_23 AA Genotype Exacerbates Effect of Diabetes on Dementia and Alzheimer Disease: A Population-Based Longitudinal Study. **2015**, 12, e1001853		6
216	Polymorphisms within novel risk loci for type 2 diabetes determine beta-cell function. *PLoS ONE*, **2007**, 2, e832	3.7	127
215	Neither replication nor simulation supports a role for the axon guidance pathway in the genetics of Parkinson's disease. *PLoS ONE*, **2008**, 3, e2707	3.7	15
214	Polymorphisms within the novel type 2 diabetes risk locus MTNR1B determine beta-cell function. *PLoS ONE*, **2008**, 3, e3962	3.7	93
213	SLC30A3 responds to glucose- and zinc variations in beta-cells and is critical for insulin production and in vivo glucose-metabolism during beta-cell stress. *PLoS ONE*, **2009**, 4, e5684	3.7	68
212	Low frequency variants in the exons only encoding isoform A of HNF1A do not contribute to susceptibility to type 2 diabetes. *PLoS ONE*, **2009**, 4, e6615	3.7	4
211	Variant near ADAMTS9 known to associate with type 2 diabetes is related to insulin resistance in offspring of type 2 diabetes patients--EUGENE2 study. *PLoS ONE*, **2009**, 4, e7236	3.7	43
210	The dopamine transporter gene, a spectrum of most common risky behaviors, and the legal status of the behaviors. *PLoS ONE*, **2010**, 5, e9352	3.7	40
209	An Environment-Wide Association Study (EWAS) on type 2 diabetes mellitus. *PLoS ONE*, **2010**, 5, e10746	3.7	372
208	Evaluation of association of HNF1B variants with diverse cancers: collaborative analysis of data from 19 genome-wide association studies. *PLoS ONE*, **2010**, 5, e10858	3.7	24
207	Type 2 diabetes susceptibility gene expression in normal or diabetic sorted human alpha and beta cells: correlations with age or BMI of islet donors. *PLoS ONE*, **2010**, 5, e11053	3.7	39
206	Case-control analysis of SNPs in GLUT4, RBP4 and STRA6: association of SNPs in STRA6 with type 2 diabetes in a South Indian population. *PLoS ONE*, **2010**, 5, e11444	3.7	41
205	Deletion of CDKAL1 affects mitochondrial ATP generation and first-phase insulin exocytosis. *PLoS ONE*, **2010**, 5, e15553	3.7	57

204	Short telomeres compromise β-cell signaling and survival. *PLoS ONE*, **2011**, 6, e17858	3.7	64
203	Novel susceptibility locus at 22q11 for diabetic nephropathy in type 1 diabetes. *PLoS ONE*, **2011**, 6, e24053	3.7	8
202	The CDKN2A G500 allele is more frequent in GBM patients with no defined telomere maintenance mechanism tumors and is associated with poorer survival. *PLoS ONE*, **2011**, 6, e26737	3.7	22
201	The KCNJ11 E23K polymorphism and progression of glycaemia in Southern Chinese: a long-term prospective study. *PLoS ONE*, **2011**, 6, e28598	3.7	8
200	The role of inflammatory pathway genetic variation on maternal metabolic phenotypes during pregnancy. *PLoS ONE*, **2012**, 7, e32958	3.7	19
199	Two isoforms of the mRNA binding protein IGF2BP2 are generated by alternative translational initiation. *PLoS ONE*, **2012**, 7, e33140	3.7	14
198	Amerind ancestry, socioeconomic status and the genetics of type 2 diabetes in a Colombian population. *PLoS ONE*, **2012**, 7, e33570	3.7	40
197	The physiological effects of deleting the mouse SLC30A8 gene encoding zinc transporter-8 are influenced by gender and genetic background. *PLoS ONE*, **2012**, 7, e40972	3.7	55
196	Technical reproducibility of genotyping SNP arrays used in genome-wide association studies. *PLoS ONE*, **2012**, 7, e44483	3.7	46
195	A single nucleotide polymorphism within DUSP9 is associated with susceptibility to type 2 diabetes in a Japanese population. *PLoS ONE*, **2012**, 7, e46263	3.7	27
194	Rare and low frequency variant stratification in the UK population: description and impact on association tests. *PLoS ONE*, **2012**, 7, e46519	3.7	22
193	Deletion of CDKAL1 affects high-fat diet-induced fat accumulation and glucose-stimulated insulin secretion in mice, indicating relevance to diabetes. *PLoS ONE*, **2012**, 7, e49055	3.7	22
192	Hematopoietically-expressed homeobox gene three widely-evaluated polymorphisms and risk for diabetes: a meta-analysis. *PLoS ONE*, **2012**, 7, e49917	3.7	13
191	Replication of type 2 diabetes candidate genes variations in three geographically unrelated Indian population groups. *PLoS ONE*, **2013**, 8, e58881	3.7	23
190	Mutations in Mll2, an H3K4 methyltransferase, result in insulin resistance and impaired glucose tolerance in mice. *PLoS ONE*, **2013**, 8, e61870	3.7	31
189	Genetic associations of type 2 diabetes with islet amyloid polypeptide processing and degrading pathways in asian populations. *PLoS ONE*, **2013**, 8, e62378	3.7	6
188	Polymorphism of 9p21.3 locus is associated with 5-year survival in high-risk patients with myocardial infarction. *PLoS ONE*, **2013**, 8, e72333	3.7	6
187	Use of net reclassification improvement (NRI) method confirms the utility of combined genetic risk score to predict type 2 diabetes. *PLoS ONE*, **2013**, 8, e83093	3.7	29

186	Familial young-onset diabetes, pre-diabetes and cardiovascular disease are associated with genetic variants of DACH1 in Chinese. *PLoS ONE*, **2014**, 9, e84770	3.7	12
185	Joint effects of known type 2 diabetes susceptibility loci in genome-wide association study of Singapore Chinese: the Singapore Chinese health study. *PLoS ONE*, **2014**, 9, e87762	3.7	14
184	Population specific impact of genetic variants in KCNJ11 gene to type 2 diabetes: a case-control and meta-analysis study. *PLoS ONE*, **2014**, 9, e107021	3.7	25
183	Zip4 mediated zinc influx stimulates insulin secretion in pancreatic beta cells. *PLoS ONE*, **2015**, 10, e0119136	3.7	23
182	Can data science inform environmental justice and community risk screening for type 2 diabetes?. *PLoS ONE*, **2015**, 10, e0121855	3.7	3
181	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. *PLoS ONE*, **2015**, 10, e0126363	3.7	9
180	Modelling the Interplay between Lifestyle Factors and Genetic Predisposition on Markers of Type 2 Diabetes Mellitus Risk. *PLoS ONE*, **2015**, 10, e0131681	3.7	5
179	Comparative Genome of GK and Wistar Rats Reveals Genetic Basis of Type 2 Diabetes. *PLoS ONE*, **2015**, 10, e0141859	3.7	11
178	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. *PLoS ONE*, **2015**, 10, e0143607	3.7	33
177	Association between the rs7903146 Polymorphism in the TCF7L2 Gene and Parameters Derived with Continuous Glucose Monitoring in Individuals without Diabetes. *PLoS ONE*, **2016**, 11, e0149992	3.7	8
176	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. *PLoS ONE*, **2016**, 11, e0154093	3.7	8
175	Association Study with 77 SNPs Confirms the Robust Role for the rs10830963/G of MTNR1B Variant and Identifies Two Novel Associations in Gestational Diabetes Mellitus Development. *PLoS ONE*, **2017**, 12, e0169781	3.7	32
174	Common and rare exonic MUC5B variants associated with type 2 diabetes in Han Chinese. *PLoS ONE* , **2017**, 12, e0173784	3.7	5
173	Genetic framework of type 2 diabetes mellitus. *Diabetes Mellitus*, **2013**, 16, 11-16	1.6	4
172	Myeloma in Elderly Patients: When Less Is More and More Is More. **2017**, 37, 575-585		18
171	Personalized Medicine. **2019**, 74, 61-70		5
170	Pathophysiological and genetic changes in the body of a pregnant with gestational diabetes. **2017**, 66, 27-36		3
169	The association analysis polymorphism of CDKAL1 and diabetic retinopathy in Chinese Han population. **2016**, 9, 707-12		12

168	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
167	Impact of diabetes-related gene polymorphisms on the clinical characteristics of type 2 diabetes Chinese Han population. **2016**, 7, 85464-85471	10
166	Mitochondrial DNA variants in the pathogenesis of type 2 diabetes - relevance of asian population studies. **2009**, 6, 237-46	18
165	Beyond the Protein-Coding Sequence: Noncoding RNAs in the Pathogenesis of Type 2 Diabetes. **2015**, 12, 260-76	7
164	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
163	The Nexus of Stem Cell-Derived Beta-Cells and Genome Engineering. **2017**, 14, 39-50	8
162	Lead Optimization Resources in Drug Discovery for Diabetes. **2019**, 19, 754-774	3
161	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
160	Genomewide Association Studies. **2008**, 225-238	3
159	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
158	Genome-wide association studies--a summary for the clinical gastroenterologist. **2009**, 15, 5377-96	12
157	Association of CDKAL1, CDKN2A/B & HHEX gene polymorphisms with type 2 diabetes mellitus in the population of Hyderabad, India. **2016**, 143, 455-63	18
156	Significance of a common variant in the CDKAL1 gene with susceptibility to type 2 diabetes mellitus in Iranian population. **2015**, 4, 45	14
155	Pharmacogenomics of Sulfonylureas 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
154	Association of gene variants with susceptibility to type 2 diabetes among Omanis. **2015**, 6, 358-66	31
153	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
152	Risk Prediction Using Genome-Wide Association Studies on Type 2 Diabetes. **2016**, 14, 138-148	9
151	Migration and DNA methylation: a comparison of methylation patterns in type 2 diabetes susceptibility genes between indians and europeans. **2013**, 2, 6	4

150	Interaction of Wnt pathway related variants with type 2 diabetes in a Chinese Han population. **2015**, 3, e1304	5
149	lncRNA-mRNA competing endogenous RNA network in IR-hepG2 cells ameliorated by APBBR decreasing ROS levels: a systematic analysis. **2020**, 8, e8604	6
148	Detecting Changepoint in Gene Expressions over Time: An Application to Childhood Obesity. **2021**, 475-488	
147	Disease-Associated Risk Variants in Are Associated with Tumor-Infiltrating Lymphocyte Presence in Primary Melanomas in the Population-Based GEM Study. **2021**, 30, 2309-2316	0
146	Robust estimates of heritable coronary disease risk in individuals with type 2 diabetes. **2021**,	1
145	Ocular expression of cyclin-dependent kinase 5 in patients with proliferative diabetic retinopathy. **2021**,	0
144	CDKN2B-AS1 participates in high glucose-induced apoptosis and fibrosis via NOTCH2 through functioning as a miR-98-5p decoy in human podocytes and renal tubular cells. **2021**, 13, 107	2
143	Pharmacogenomic Applications in Children. **2008**, 447-477	
142	p16INK4a and Stem Cell Ageing: A Telomere-Independent Process?. **2008**, 181-202	
141	Cyclin-Dependent Kinase 5 and Insulin Secretion. **2008**, 145-158	
140	Reporting and Interpreting Results. **2008**, 275-292	
139	Diabetes. **2009**, 1187-1193	
138	Data Mining in Genome Wide Association Studies. **2009**, 465-471	
137	Encyclopedia of Complexity and Systems Science. **2009**, 3964-3985	
136	Genetic Dyslipidemia. **2009**, 71-84	
135	The Genetic Basis of Diabetes. **2009**, 377-413	
134	Genetics. **2009**, 49-55	
133	Inter-Species Comparative Sequence Analysis: A Tool for Genomic Medicine. **2009**, 120-130	

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

131 Molecular Genetics of Susceptibility to Coronary Heart Disease.

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

129 Genetics of Obesity and Diabetes. **2010**, 499-521 0

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

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

126 Direct to Consumer Testing. **2010**, 191-199

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

124 Pathogenesis and Management of Adiposity and Insulin Resistance in PCOS: Prevention and Treatment of the Metabolic Disease Components. **2010**, 357-367

123 Molecular Genetics of Myocardial Infarction.

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

121 Risk Factors for Type 2 and Gestational Diabetes. **2010**, 33-64

120 Public Health Genomics of Type 1 Diabetes, Type 2 Diabetes, and Diabetic Complications. **2010**, 665-686

119 Genetic Studies of Schizophrenia. **2011**, 333-380

118 Visual integration of results from a large DNA biobank (BioVU) using synthesis-view. **2011**, 265-75 10

117 Genome-wide Association Studies of Cancers.

116 Genome-wide association studies: Where we are heading?. **2011**, 1, 23 0

115 Pharmacogenomics. **2011**, 81-93

114	Interaction Between Exercise and Genetics in Type 2 Diabetes Mellitus: An Epidemiological Perspective. **2011**, 73-100	
113	Molecular genetics of atherosclerosis and acute coronary syndromes. **2011**, 35-43	
112	DNA Variations, Impaired Insulin Secretion and Type 2 Diabetes. **2011**, 275-297	
111	Association of KCNJ11 with impaired glucose regulation in essential hypertension. **2011**, 10, 1111-9	2
110	Recent Progress in Identifying Genes Contributing to Type 2 Diabetes and Metabolic Syndrome. 106-119	
109	Pharmacogenomics and Organ Transplantation. 133-145	
108	Genetics of Childhood Obesity. **2014**, 71-91	1
107	Genetics of Birth Weight.	
106	Estimation Strategies. **2014**, 1-7	
105	Genetics of Childhood Obesity. **2013**, 1-21	
104	Vascular Complications of Diabetes Mellitus. **2014**, 1-65	
103	Genetic variants at 10q23.33 are associated with plasma lipid levels in a Chinese population. **2014**, 28, 53-8	3
102	Genetic Epidemiology of Atherosclerotic Vascular Disease. **2014**, 1-24	
101	Wnt Signaling in Pancreatic Islets. **2015**, 707-741	1
100	Mapping of Susceptibility Genes for Obesity, Type 2 Diabetes, and the Metabolic Syndrome in Human Populations. **2015**, 181-245	
99	Gene Expression Studies and Complex Diseases. **2015**, 67-83	
98	Periodontal Disease. **2015**, 145-166	
97	Genetic Epidemiology of Atherosclerotic Vascular Disease. **2015**, 1517-1539	

96	The Main Events in the History of Diabetes Mellitus. **2015**, 1-17	
95	Genetic Determinants of Type 2 Diabetes in Asians. **2015**, 2015,	6
94	Genetics of Endocrinology. **2016**, 49-68	1
93	Genetics of Type 2 Diabetes: From Candidate Genes to Genome-Wide Association Analysis. **2016**, 1-24	
92	Genome-Wide Association Data: Where Are the Standards?. 17-30	
91	Genetics of Type 2 Diabetes: From Candidate Genes to Genome-Wide Association Analysis. **2017**, 1-24	
90	Improving Imputation Accuracy by Inferring Causal Variants in Genetic Studies. **2017**, 303-317	1
89	Genetics of Type 2 Diabetes: From Candidate Genes to Genome-Wide Association Analysis. **2017**, 191-214	
88	Genetic architecture of early childhood growth phenotypes gives insights into their link with later obesity.	0
87	Myeloid-Derived Suppressor Cells in Aged Humans. **2018**, 1-12	
86	Electrical Excitability of the Endoplasmic Reticulum Membrane Drives Electrical Bursting and the Pulsatile Secretion of Insulin in a Pancreatic Beta Cell Model.	
85	Genetics of Diabetes and Diabetic Complications. **2018**, 81-139	1
84	A unifying framework for summary statistic imputation.	
83	Robust Reference Powered Association Test of genome-wide association studies.	
82	Myeloid-Derived Suppressor Cells in Aged Humans. **2019**, 733-744	
81	Long Noncoding RNAs in Cardiovascular Disease. **2019**, 199-288	0
80	Socioeconomic and Genomic Roots of Verbal Ability.	
79	A General Statistic to Test an Optimally Weighted Combination of Common and/or Rare Variants.	

78	A Comprehensive Genome-wide and Phenome-wide Examination of BMI and Obesity in a Northern Nevadan Cohort.	
77	All thresholds of maternal hyperglycaemia from the WHO 2013 criteria for gestational diabetes identify women with a higher genetic risk for type 2 diabetes.	
76	Progressive shifts in the gut microbiome reflect prediabetes and diabetes development in a treatment-naive Mexican cohort.	0
75	The Pivotal Role of Senescence in Cell Death and Aging: Where Do We Stand?. **2020**, 6, 91-101	
74	All thresholds of maternal hyperglycaemia from the WHO 2013 criteria for gestational diabetes identify women with a higher genetic risk for type 2 diabetes. **2020**, 5, 175	0
73	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
72	[illegible] **2020**, 184-191	1
71	Autophagic Dysfunction in Neurodegeneration. **2020**, 25-62	
70	Genomic Epidemiology of Human Papillomavirus (HPV), Prostate Cancer, and Diabetes. 43-75	
69	An adipocyte-specific lncRAP2 [illegible]gf2bp2 complex enhances adipogenesis and energy expenditure by stabilizing target mRNAs.	
68	All thresholds of maternal hyperglycaemia from the WHO 2013 criteria for gestational diabetes identify women with a higher genetic risk for type 2 diabetes. 5, 175	
67	Electrophoretic techniques applied to the detection and analysis of the human microsatellite DG10s478. **2007**, 18, 298-305	2
66	Genome-wide association studies: progress in identifying genetic biomarkers in common, complex diseases. **2007**, 2, 283-92	12
65	Genomic approaches to coronary artery disease. **2010**, 132, 567-78	16
64	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
63	Mining the human phenome using semantic web technologies: a case study for Type 2 Diabetes. **2012**, 2012, 699-708	8
62	Advances in genetic studies of substance abuse in China. **2013**, 25, 199-211	3
61	ANKRD7 and CYTL1 are novel risk genes for alcohol drinking behavior. **2012**, 125, 1127-34	10

60	Genetic & epigenetic approach to human obesity. **2014**, 140, 589-603		16
59	Association of Type 2 Diabetes Mellitus related SNP genotypes with altered serum adipokine levels and metabolic syndrome phenotypes. **2015**, 8, 4464-71		3
58	Correlation between polymorphism of FTO gene and type 2 diabetes mellitus in Uygur people from northwest China. **2015**, 8, 9744-50		9
57	Association of rs7754840 G/C polymorphisms in CDKAL1 with type 2 diabetes: a meta-analysis of 70141 subjects. **2015**, 8, 17392-405		9
56	The association of a genetic variant in CDKN2A/B gene and the risk of colorectal cancer. *EXCLI Journal*, **2020**, 19, 1316-1321	2.4	
55	Transcription factor 7-like 2 (TCF7L2): a culprit gene in Type 2 Diabetes Mellitus. *Diabetes Mellitus*, **2021**, 24, 371-376	1.6	
54	The roles of ANRIL polymorphisms in periodontitis: a systematic review and meta-analysis. *Clinical Oral Investigations*, **2021**, 1	4.2	0
53	The risk variant of CDKAL1 (rs7756992) impairs fasting glucose levels and insulin resistance improvements after a partial meal-replacement hypocaloric diet. *Endocrinología Diabetes Y Nutrición (English Ed)*, **2021**, 68, 548-556	0.1	
52	Metabolic Syndrome: Updates on Pathophysiology and Management in 2021.. *International Journal of Molecular Sciences*, **2022**, 23,	6.3	24
51	An adipose lncRAP2-Igf2bp2 complex enhances adipogenesis and energy expenditure by stabilizing target mRNAs.. *IScience*, **2022**, 25, 103680	6.1	0
50	Novel diabetes gene discovery through comprehensive characterization and integrative analysis of longitudinal gene expression changes.. *Human Molecular Genetics*, **2022**,	5.6	0
49	Lower miR-21/ROS/HNE levels associate with lower glycemia after habit-intervention: DIAPASON study 1-year later.. *Cardiovascular Diabetology*, **2022**, 21, 35	8.7	0
48	Insights Into Genome-Wide Association Study for Diabetes: A Bibliometric and Visual Analysis From 2001 to 2021.. *Frontiers in Endocrinology*, **2022**, 13, 817620	5.7	1
47	Association of Long Non-Coding RNA Growth Arrest-Specific 5 Genetic Variants with Diabetic Retinopathy.. *Genes*, **2022**, 13,	4.2	2
46	Association of CDKN2A/B gene polymorphisms (rs10811661 and rs2383208) with type 2 diabetes mellitus in a sample of Iraqi population. *Egyptian Journal of Medical Human Genetics*, **2022**, 23,	2	0
45	Implication of KCNJ11 and TCF7L2 gene variants for the predisposition of type 2 diabetes mellitus in West Bengal, India. *Diabetes Epidemiology and Management*, **2022**, 6, 100066		
44	Human islet amyloid polypeptide: A therapeutic target for the management of type 2 diabetes mellitus. *Journal of Pharmaceutical Analysis*, **2022**,	14	0
43	Genetic risk factors associated with gestational diabetes in a multi-ethnic population.. *PLoS ONE*, **2021**, 16, e0261137	3.7	0

42 Relationship Between Polymorphism and Type 2 Diabetes Risk in Northwestern China.. *Pharmacogenomics and Personalized Medicine*, **2021**, 14, 1731-1751 2.1

41 Image_1.tif. **2021**,

40 Image_2.tif. **2021**,

39 Image_1.TIFF. **2019**,

38 Image_2.TIFF. **2019**,

37 Image_3.TIFF. **2019**,

36 Image_4.TIFF. **2019**,

35 Table_1.XLS. **2019**,

34 Table_2.XLS. **2019**,

33 Table_3.XLS. **2019**,

32 Table_4.xls. **2019**,

31 Table_5.xls. **2019**,

30 Table_6.xls. **2019**,

29 Data_Sheet_1.PDF. **2020**,

28 table_1.DOCX. **2018**,

27 table_2.DOCX. **2018**,

26 Table_1.DOCX. **2018**,

25 Table_2.DOCX. **2018**,

24	Table_3.DOCX. **2018**,		
23	Studies on the fat mass and obesity-associated (FTO) gene and its impact on obesity-associated diseases. *Genes and Diseases*, **2022**,	6.6	0
22	Type 2 Diabetes-Related Variants Influence the Risk of Developing Prostate Cancer: A Population-Based Case-Control Study and Meta-Analysis. *Cancers*, **2022**, 14, 2376	6.6	1
21	Identification of Candidate Genes Regulating Carcass Depth and Hind Leg Circumference in Simmental Beef Cattle Using Illumina Bovine Beadchip and Next-Generation Sequencing Analyses.. *Animals*, **2022**, 12,	3.1	1
20	The IGF2BP family of RNA binding proteins links epitranscriptomics to cancer. *Seminars in Cancer Biology*, **2022**,	12.7	0
19	Inherited basis of visceral, abdominal subcutaneous and gluteofemoral fat depots. *Nature Communications*, **2022**, 13,	17.4	0
18	The role of proton in a eukaryotic zinc transporter.		
17	Unraveling the Influence of HHEX Risk Polymorphism rs7923837 on Multiple Sclerosis Pathogenesis. *International Journal of Molecular Sciences*, **2022**, 23, 7956	6.3	
16	Exposure to per- and polyfluoroalkyl substances (PFAS) and type 2 diabetes risk. 13,		1
15	Genetics of Type 2 Diabetes: Past, Present, and Future. **2022**, 14, 3201		2
14	Nontargeted and Targeted Metabolomic Profiling Reveals Novel Metabolite Biomarkers of Incident Diabetes in African Americans.		0
13	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		
12	Socioeconomic and genomic roots of verbal ability from current evidence. **2022**, 7,		0
11	Genetics of type 2 diabetes mellitus in Indian and Global Population: A Review. **2022**, 23,		0
10	Insulin, Glucose, and the Metabolic Syndrome in Cardiovascular Behavioral Medicine. **2022**, 809-831		0
9	Using Data to Improve the Management of Diabetes: The Tayside Experience.		0
8	Human T2D Associated Gene IMP2/IGF2BP2 Promotes the Commitment of Mesenchymal Stem Cells into Adipogenic Lineage.		1
7	Association between TCF7L2 polymorphism and type 2 diabetes mellitus susceptibility: a case□ontrol study among the Bangladeshi population.		0

6	Cryo-EM structure of a eukaryotic zinc transporter at a low pH suggests its Zn2+-releasing mechanism. **2023**, 215, 107926	0
5	Progress in genetics of type 2 diabetes and diabetic complications.	0
4	THE RELEVANCE OF RS6777038 AND RS6444082 OF IGF2BP2 GENE POLYMORPHISM AND TYPE 2 DIABETES MELLITUS: A CASE CONTROL STUDY. **2022**, 75, 2811-2816	0
3	CDKAL1 Drives the Maintenance of Cancer Stem-Like Cells by Assembling the eIF4F Translation Initiation Complex. 2206542	0
2	A Wrong Fate Decision in Adipose Stem Cells upon Obesity. **2023**, 12, 662	0
1	Evaluation of rs10811661 polymorphism in CDKN2A / B in colon and gastric cancer.	0