Christian Dina

List of Publications by Year
in descending order

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148 papers	32,939 citations	9234 74 h-index	7718 150 g-index
164 all docs	164 docs citations	164 times ranked	34909 citing authors

#	Article	IF	Citations
1	Genome-wide association study reveals novel genetic loci: a new polygenic risk score for mitral valve prolapse. European Heart Journal, 2022, 43, 1668-1680.	1.0	25
2	Computational estimates of annular diameter reveal genetic determinants of mitral valve function and disease. JCI Insight, 2022, 7, .	2.3	9
3	Genome-wide association analyses identify new Brugada syndrome risk loci and highlight a new mechanism of sodium channel regulation in disease susceptibility. Nature Genetics, 2022, 54, 232-239.	9.4	55
4	Familial Recurrence Patterns in Congenitally Corrected Transposition of the Great Arteries: An International Study. Circulation Genomic and Precision Medicine, 2022, 15, 101161CIRCGEN121003464.	1.6	3
5	Moment estimators of relatedness from low-depth whole-genome sequencing data. BMC Bioinformatics, 2022, 23, .	1.2	1
6	Shared genetic risk between eating disorderâ€•and substanceâ€useâ€related phenotypes: Evidence from genomeâ€wide association studies. Addiction Biology, 2021, 26, e12880.	1.4	28
7	Functionally validated SCN5A variants allow interpretation of pathogenicity and prediction of lethal events in Brugada syndrome. European Heart Journal, 2021, 42, 2854-2863.	1.0	37
8	Association of Coding Variants in Hydroxysteroid 17-beta Dehydrogenase 14 (HSD17B14) with Reduced Progression to End Stage Kidney Disease in Type 1 Diabetes. Journal of the American Society of Nephrology: JASN, 2021, 32, 2634-2651.	3.0	9
9	Genome-Wide Association Meta-Analysis Supports Genes Involved in Valve and Cardiac Development to Associate With Mitral Valve Prolapse. Circulation Genomic and Precision Medicine, 2021, 14, e003148.	1.6	7
10	Genome-wide association study of intracranial aneurysms identifies 17 risk loci and genetic overlap with clinical risk factors. Nature Genetics, 2020, 52, 1303-1313.	9.4	163
11	The genetic history of France. European Journal of Human Genetics, 2020, 28, 853-865.	1.4	15
12	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. Nature Genetics, 2019, 51, 1207-1214.	9.4	641
13	Population structure of modern-day Italians reveals patterns of ancient and archaic ancestries in Southern Europe. Science Advances, 2019, 5, eaaw3492.	4.7	53
14	Variation In Lpa And Calcific Aortic Valve Stenosis In Patients Undergoing Cardiac Surgery And Familial Risk Of Aortic Valve Microcalcification. Atherosclerosis, 2019, 287, e16-e17.	0.4	0
15	Genetic Variation in LPA, Calcific Aortic Valve Stenosis in Patients Undergoing Cardiac Surgery, and Familial Risk of Aortic Valve Microcalcification. JAMA Cardiology, 2019, 4, 620.	3.0	32
16	Primary cilia defects causing mitral valve prolapse. Science Translational Medicine, 2019, 11, .	5.8	76
17	RRAD mutation causes electrical and cytoskeletal defects in cardiomyocytes derived from a familial case of Brugada syndrome. European Heart Journal, 2019, 40, 3081-3094.	1.0	48
18	Associations Between Attention-Deficit/Hyperactivity Disorder and Various Eating Disorders: A Swedish Nationwide Population Study Using Multiple Genetically Informative Approaches. Biological Psychiatry, 2019, 86, 577-586.	0.7	43

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19	Genome-Wide Association Studyâ€“Driven Gene-Set Analyses, Genetic, and Functional Follow-Up Suggest GLIS1 as a Susceptibility Gene for Mitral Valve Prolapse. Circulation Genomic and Precision Medicine, 2019, 12, e002497.	1.6	31
20	Rare Coding Variants in ANGPTL6 Are Associated with Familial Forms of Intracranial Aneurysm. American Journal of Human Genetics, 2018, 102, 133-141.	2.6	37
21	New insights into mitral valve dystrophy: a Filamin-A genotypeâ€“phenotype and outcome study. European Heart Journal, 2018, 39, 1269-1277.	1.0	44
22	The impact of a fine-scale population stratification on rare variant association test results. PLoS ONE, 2018, 13, e0207677.	1.1	32
23	Significant Locus and Metabolic Genetic Correlations Revealed in Genome-Wide Association Study of Anorexia Nervosa. American Journal of Psychiatry, 2017, 174, 850-858.	4.0	410
24	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
25	Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. Lancet Neurology, The, 2017, 16, 898-907.	4.9	191
26	DoEstRare: A statistical test to identify local enrichments in rare genomic variants associated with disease. PLoS ONE, 2017, 12, e0179364.	1.1	7
27	Biallelic Variants in UBA5 Reveal that Disruption of the UFM1 Cascade Can Result in Early-Onset Encephalopathy. American Journal of Human Genetics, 2016, 99, 695-703.	2.6	87
28	Dysfunction of the Voltageâ€Gated K ⁺ Channel Î²2 Subunit in a Familial Case of Brugada Syndrome. Journal of the American Heart Association, 2016, 5, .	1.6	20
29	De Novo Truncating Mutations in the Kinetochore-Microtubules Attachment GeneCHAMP1Cause Syndromic Intellectual Disability. Human Mutation, 2016, 37, 354-358.	1.1	40
30	Search for Rare Copy-Number Variants in Congenital Heart Defects Identifies Novel Candidate Genes and a Potential Role for FOXC1 in Patients With Coarctation of the Aorta. Circulation: Cardiovascular Genetics, 2016, 9, 86-94.	5.1	38
31	Targeted resequencing identifies TRPM4 as a major gene predisposing to progressive familial heart block type I. International Journal of Cardiology, 2016, 207, 349-358.	0.8	62
32	Investigation of the Matrix Metalloproteinase-2 Gene in Patients with Non-Syndromic Mitral Valve Prolapse. Journal of Cardiovascular Development and Disease, 2015, 2, 176-189.	0.8	1
33	A survey about methods dedicated to epistasis detection. Frontiers in Genetics, 2015, 6, 285.	1.1	114
34	Staphylokinase and ABO group phenotype: new players inStaphylococcus aureusimplant-associated infections development. Future Microbiology, 2015, 10, 1929-1938.	1.0	6
35	Testing the burden of rare variation in arrhythmia-susceptibility genes provides new insights into molecular diagnosis for Brugada syndrome. Human Molecular Genetics, 2015, 24, 2757-2763.	1.4	130
36	Fine-scale human genetic structure in Western France. European Journal of Human Genetics, 2015, 23, 831-836.	1.4	31

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37	Mitral valve diseaseâ€"morphology and mechanisms. Nature Reviews Cardiology, 2015, 12, 689-710.	6.1	281
38	Mutations in DCHS1 cause mitral valve prolapse. Nature, 2015, 525, 109-113.	13.7	150
39	Genetic association analyses highlight biological pathways underlying mitral valve prolapse. Nature Genetics, 2015, 47, 1206-1211.	9.4	103
40	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	13.5	113
41	GAIN-OF-FUNCTION MUTATION IN THE VOLTAGE-GATED K+ CHANNEL BETA-2 SUBUNIT IS ASSOCIATED WITH BRUGADA SYNDROME. Heart Rhythm, 2014, 11, 2133.	0.3	1
42	A genome-wide association study of anorexia nervosa. Molecular Psychiatry, 2014, 19, 1085-1094.	4.1	282
43	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
44	Common variants at SCN5A-SCN10A and HEY2 are associated with Brugada syndrome, a rare disease with high risk of sudden cardiac death. Nature Genetics, 2013, 45, 1044-1049.	9.4	467
45	Genome-Wide Association Analysis Identifies 3 Common Variants Predisposing to Brugada Syndrome, a Rare Disease with High Risk of Sudden Cardiac Death. Heart Rhythm, 2013, 10, 1743-1744.	0.3	1
46	Identification of heart rateâ€"associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
47	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
48	Parental Electrocardiographic Screening Identifies a High Degree of Inheritance for Congenital and Childhood Nonimmune Isolated Atrioventricular Block. Circulation, 2012, 126, 1469-1477.	1.6	25
49	Novel association approach for variable number tandem repeats (VNTRs) identifies DOCK5 as a susceptibility gene for severe obesity. Human Molecular Genetics, 2012, 21, 3727-3738.	1.4	37
50	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
51	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
52	Multifocal Ectopic Purkinje-Related Premature Contractions. Journal of the American College of Cardiology, 2012, 60, 144-156.	1.2	156
53	Rare MTNR1B variants impairing melatonin receptor 1B function contribute to type 2 diabetes. Nature Genetics, 2012, 44, 297-301.	9.4	319
54	R222Q Nav1.5 Mutation Associated with a New SCN5A-Related Cardiac Arrhythmia. Biophysical Journal, 2012, 102, 527a.	0.2	0

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55	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
56	Common variants near TARDBP and EGR2 are associated with susceptibility to Ewing sarcoma. Nature Genetics, 2012, 44, 323-327.	9.4	160
57	Of 508 Mice and 40,000 Humans. Journal of Molecular and Cellular Cardiology, 2011, 50, 377-379.	0.9	1
58	Truncating mutations in the last exon of NOTCH2 cause a rare skeletal disorder with osteoporosis. Nature Genetics, 2011, 43, 306-308.	9.4	181
59	Genetics of Venous Thrombosis: Insights from a New Genome Wide Association Study. PLoS ONE, 2011, 6, e25581.	1.1	127
60	Visualization of Pairwise and Multilocus Linkage Disequilibrium Structure Using Latent Forests. PLoS ONE, 2011, 6, e27320.	1.1	6
61	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	9.4	591
62	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
63	Multipleâ€Cohort Genetic Association Study Reveals CXCR6 as a New Chemokine Receptor Involved in Longâ€Term Nonprogression to AIDS. Journal of Infectious Diseases, 2010, 202, 908-915.	1.9	82
64	Genetic and Functional Assessment of the Role of the rs13431652-A and rs573225-A Alleles in the G6PC2 Promoter That Are Strongly Associated With Elevated Fasting Glucose Levels. Diabetes, 2010, 59, 2662-2671.	0.3	31
65	Two New Loci for Body-Weight Regulation Identified in a Joint Analysis of Genome-Wide Association Studies for Early-Onset Extreme Obesity in French and German Study Groups. PLoS Genetics, 2010, 6, e1000916.	1.5	287
66	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
67	Genomewide Association Study of an AIDSâ€Nonprogression Cohort Emphasizes the Role Played byHLAGenes (ANRS Genomewide Association Study 02). Journal of Infectious Diseases, 2009, 199, 419-426.	1.9	220
68	The T-381C SNP in BNP gene may be modestly associated with type 2 diabetes: an updated meta-analysis in 49 279 subjects. Human Molecular Genetics, 2009, 18, 2495-2501.	1.4	30
69	G-allele of Intronic rs10830963 in MTNR1B Confers Increased Risk of Impaired Fasting Glycemia and Type 2 Diabetes Through an Impaired Glucose-Stimulated Insulin Release. Diabetes, 2009, 58, 1450-1456.	0.3	125
70	Genomewide Association Study of a Rapid Progression Cohort Identifies New Susceptibility Alleles for AIDS (ANRS Genomewide Association Study 03). Journal of Infectious Diseases, 2009, 200, 1194-1201.	1.9	99
71	Meta-Analysis of the INSIG2 Association with Obesity Including 74,345 Individuals: Does Heterogeneity of Estimates Relate to Study Design?. PLoS Genetics, 2009, 5, e1000694.	1.5	62
72	Genetic Variant in HK1 Is Associated With a Proanemic State and A1C but Not Other Glycemic Control-Related Traits. Diabetes, 2009, 58, 2687-2697.	0.3	34

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73	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	13.7	521
74	A variant near MTNR1B is associated with increased fasting plasma glucose levels and type 2 diabetes risk. Nature Genetics, 2009, 41, 89-94.	9.4	540
75	Genome-wide association study for early-onset and morbid adult obesity identifies three new risk loci in European populations. Nature Genetics, 2009, 41, 157-159.	9.4	585
76	Genetic variant near IRS1 is associated with type 2 diabetes, insulin resistance and hyperinsulinemia. Nature Genetics, 2009, 41, 1110-1115.	9.4	418
77	Replication of the association between variants in WFS1 and risk of type 2 diabetes in European populations. Diabetologia, 2008, 51, 458-463.	2.9	99
78	Individual differences in allocation of funds in the dictator game associated with length of the arginine vasopressin 1a receptor RS3 promoter region and correlation between RS3 length and hippocampal mRNA. Genes, Brain and Behavior, 2008, 7, 266-275.	1.1	303
79	Effects of TCF7L2 Polymorphisms on Obesity in European Populations. Obesity, 2008, 16, 476-482.	1.5	83
80	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
81	Common nonsynonymous variants in PCSK1 confer risk of obesity. Nature Genetics, 2008, 40, 943-945.	9.4	275
82	A Polymorphism Within the G6PC2 Gene Is Associated with Fasting Plasma Glucose Levels. Science, 2008, 320, 1085-1088.	6.0	227
83	Impact of Common Type 2 Diabetes Risk Polymorphisms in the DESIR Prospective Study. Diabetes, 2008, 57, 244-254.	0.3	146
84	Endocannabinoid receptor 1 gene variations increase risk for obesity and modulate body mass index in European populations. Human Molecular Genetics, 2008, 17, 1916-1921.	1.4	89
85	Genome-wide association scans identified CTNNBL1 as a novel gene for obesity. Human Molecular Genetics, 2008, 17, 1803-1813.	1.4	168
86	Prevalence of Melanocortin-4 Receptor Deficiency in Europeans and Their Age-Dependent Penetrance in Multigenerational Pedigrees. Diabetes, 2008, 57, 2511-2518.	0.3	229
87	New insights into the genetics of body weight. Current Opinion in Clinical Nutrition and Metabolic Care, 2008, 11, 378-384.	1.3	25
88	Comment on "A Common Genetic Variant Is Associated with Adult and Childhood Obesity". Science, 2007, 315, 187.2-187.	6.0	107
89	Variation in FTO contributes to childhood obesity and severe adult obesity. Nature Genetics, 2007, 39, 724-726.	9.4	1,390
90	A genome-wide association study identifies novel risk loci for type 2 diabetes. Nature, 2007, 445, 881-885.	13.7	2,651

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91	TCF7L2 is reproducibly associated with type 2 diabetes in various ethnic groups: a global meta-analysis. Journal of Molecular Medicine, 2007, 85, 777-782.	1.7	321
92	ACDC/Adiponectin Polymorphisms Are Associated With Severe Childhood and Adult Obesity. Diabetes, 2006, 55, 545-550.	0.3	154
93	Association of the calpain-10 gene with type 2 diabetes in Europeans: Results of pooled and meta-analyses. Molecular Genetics and Metabolism, 2006, 89, 174-184.	0.5	76
94	Epistasis Between Type 2 Diabetes Susceptibility Loci on Chromosomes 1q21-25 and 10q23-26 in Northern Europeans. Annals of Human Genetics, 2006, 70, 726-737.	0.3	20
95	Association between the arginine vasopressin 1a receptor (AVPR1a) gene and autism in a family-based study: mediation by socialization skills. Molecular Psychiatry, 2006, 11, 488-494.	4.1	217
96	Genome-wide scan for genes involved in bipolar affective disorder in 70 European families ascertained through a bipolar type I early-onset proband: supportive evidence for linkage at 3p14. Molecular Psychiatry, 2006, 11, 685-694.	4.1	68
97	Genotype-by-nutrient interactions assessed in European obese women. European Journal of Nutrition, 2006, 45, 454-462.	1.8	46
98	Genetic Polymorphisms and Weight Loss in Obesity: A Randomised Trial of Hypo-Energetic High- versus Low-Fat Diets. PLOS Clinical Trials, 2006, 1, e12.	3.5	62
99	TCF7L2 Variation Predicts Hyperglycemia Incidence in a French General Population: The Data From an Epidemiological Study on the Insulin Resistance Syndrome (DESIR) Study. Diabetes, 2006, 55, 3189-3192.	0.3	98
100	Transcription Factor TCF7L2 Genetic Study in the French Population: Expression in Human Â-Cells and Adipose Tissue and Strong Association With Type 2 Diabetes. Diabetes, 2006, 55, 2903-2908.	0.3	300
101	EIF4A2 Is a Positional Candidate Gene at the 3q27 Locus Linked to Type 2 Diabetes in French Families. Diabetes, 2006, 55, 1171-1176.	0.3	23
102	Genetic Analysis of ADIPOR1 and ADIPOR2 Candidate Polymorphisms for Type 2 Diabetes in the Caucasian Population. Diabetes, 2006, 55, 856-861.	0.3	72
103	Variants of ENPP1 are associated with childhood and adult obesity and increase the risk of glucose intolerance and type 2 diabetes. Nature Genetics, 2005, 37, 863-867.	9.4	290
104	Dopaminergic polymorphisms associated with self-report measures of human altruism: a fresh phenotype for the dopamine D4 receptor. Molecular Psychiatry, 2005, 10, 333-335.	4.1	102
105	Fine mapping of a region on chromosome 8p gives evidence for a QTL contributing to individual differences in an anxiety-related personality trait: TPQ harm avoidance. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 132B, 104-108.	1.1	23
106	Effect of common polymorphisms in the HNF4? promoter on susceptibility to type 2 diabetes in the French Caucasian population. Diabetologia, 2005, 48, 440-444.	2.9	31
107	Hypoadiponectinaemia and high risk of type 2 diabetes are associated with adiponectin-encoding (ACDC) gene promoter variants in morbid obesity: evidence for a role of ACDC in diabesity. Diabetologia, 2005, 48, 892-899.	2.9	118
108	Analysis of sequence variability in the CART gene in relation to obesity in a Caucasian population. BMC Genetics, 2005, 6, 19.	2.7	39

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109	AVPR1a and SLC6A4 Gene Polymorphisms Are Associated with Creative Dance Performance. PLoS Genetics, 2005, 1, e42.	1.5	166
110	From The Cover: Role of transcription factor KLF11 and its diabetes-associated gene variants in pancreatic beta cell function. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4807-4812.	3.3	231
111	Genome-wide Linkage Analysis for Severe Obesity in French Caucasians Finds Significant Susceptibility Locus on Chromosome 19q. Diabetes, 2004, 53, 1857-1865.	0.3	68
112	A Genome-Wide Scan for Childhood Obesity-Associated Traits in French Families Shows Significant Linkage on Chromosome 6q22.31-q23.2. Diabetes, 2004, 53, 803-811.	0.3	152
113	Polymorphisms in the Amino Acid Transporter Solute Carrier Family 6 (Neurotransmitter Transporter) Member 14 Gene Contribute to Polygenic Obesity in French Caucasians. Diabetes, 2004, 53, 2483-2486.	0.3	77
114	The adiponectin gene SNP+45 is associated with coronary artery disease in TypeÂ2 (non-insulin-dependent) diabetes mellitus. Diabetic Medicine, 2004, 21, 776-781.	1.2	93
115	VNTR Polymorphism of the Insulin Gene and Childhood Overweight in a General Population. Obesity, 2004, 12, 499-504.	4.0	16
116	Genetic study of the CD36 gene In a French diabetic population. Diabetes and Metabolism, 2004, 30, 459-463.	1.4	39
117	Does the â˜11377 promoter variant of APM1 gene contribute to the genetic risk for Type 2 diabetes mellitus in Japanese families?. Diabetologia, 2003, 46, 443-445.	2.9	61
118	PAI-1 polymorphisms modulate phenotypes associated with the metabolic syndrome in obese and diabetic Caucasian population. Diabetologia, 2003, 46, 1284-1290.	2.9	57
119	Tridimensional personality questionnaire trait of harm avoidance (anxiety proneness) is linked to a locus on chromosome 8p21. American Journal of Medical Genetics Part A, 2003, 117B, 66-69.	2.4	50
120	A meta-analysis of four European genome screens (GIFT Consortium) shows evidence for a novel region on chromosome 17p11.2-q22 linked to type 2 diabetes. Human Molecular Genetics, 2003, 12, 1865-1873.	1.4	68
121	A Genome-Wide Scan in Families With Maturity-Onset Diabetes of the Young: Evidence for Further Genetic Heterogeneity. Diabetes, 2003, 52, 872-881.	0.3	62
122	GAD2 on Chromosome 10p12 Is a Candidate Gene for Human Obesity. PLoS Biology, 2003, 1, e68.	2.6	128
123	Mutation Screening of the Urocortin Gene: Identification of New Single Nucleotide Polymorphisms and Association Studies with Obesity in French Caucasians. Journal of Clinical Endocrinology and Metabolism, 2002, 87, 867-869.	1.8	10
124	Genome-Wide Search for Type 2 Diabetes in Japanese Affected Sib-Pairs Confirms Susceptibility Genes on 3q, 15q, and 20q and Identifies Two New Candidate Loci on 7p and 11p. Diabetes, 2002, 51, 1247-1255.	0.3	229
125	Positional Candidate Gene Analysis of Lim Domain Homeobox Gene (Isl-1) on Chromosome 5q11-q13 in a French Morbidly Obese Population Suggests Indication for Association With Type 2 Diabetes. Diabetes, 2002, 51, 1640-1643.	0.3	23
126	Genetic, pharmacological and functional analysis of cholecystokinin-1 and cholecystokinin-2 receptor polymorphism in type 2 diabetes and obese patients. Pharmacogenetics and Genomics, 2002, 12, 23-30.	5.7	44

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127	A Quantitative Trait Locus Influencing Type 2 Diabetes Susceptibility Maps to a Region on 5q in an Extended French Family. Diabetes, 2002, 51, 3568-3572.	0.3	26
128	Single-nucleotide polymorphism haplotypes in the both proximal promoter and exon 3 of the APM1 gene modulate adipocyte-secreted adiponectin hormone levels and contribute to the genetic risk for type 2 diabetes in French Caucasians. Human Molecular Genetics, 2002, 11, 2607-2614.	1.4	433
129	Genetic Variation in the Gene Encoding Adiponectin Is Associated With an Increased Risk of Type 2 Diabetes in the Japanese Population. Diabetes, 2002, 51, 536-540.	0.3	668
130	A new locus for spinocerebellar ataxia (SCA21) maps to chromosome 7p21.3-p15.1. Annals of Neurology, 2002, 52, 666-670.	2.8	73
131	A genome-wide scan for coronary heart disease suggests in Indo-Mauritians a susceptibility locus on chromosome 16p13 and replicates linkage with the metabolic syndrome on 3q27. Human Molecular Genetics, 2001, 10, 2751-2765.	1.4	233
132	Naturally Occurring Mutations in the Melanocortin Receptor 3 Gene Are Not Associated with Type 2 Diabetes Mellitus in French Caucasians. Journal of Clinical Endocrinology and Metabolism, 2001, 86, 2895-2898.	1.8	39
133	The gene MAPK8IP1, encoding islet-brain-1, is a candidate for type 2 diabetes. Nature Genetics, 2000, 24, 291-295.	9.4	182
134	Linkage and association studies between the proopiomelanocortin (POMC) gene and obesity in caucasian families. Diabetologia, 2000, 43, 1554-1557.	2.9	49
135	A genetic variation in the 5 â€² flanking region of the UCP3 gene is associated with body mass index in humans in interaction with physical activity. Diabetologia, 2000, 43, 245-249.	2.9	154
136	Genomewide Search for Type 2 Diabetesâ€“Susceptibility Genes in French Whites: Evidence for a Novel Susceptibility Locus for Early-Onset Diabetes on Chromosome 3q27-qter and Independent Replication of a Type 2â€–Diabetes Locus on Chromosome 1q21â€–q24. American Journal of Human Genetics, 2000, 67, 1470-1480.	2.6	630
137	A sib-pair analysis study of 15 candidate genes in French families with morbid obesity: indication for linkage with islet 1 locus on chromosome 5q. Diabetes, 1999, 48, 398-402.	0.3	51
138	No evidence of linkage or diabetes-associated mutations in the transcription factors BETA2/NEUROD1 and PAX4 in Type II diabetes in France. Diabetologia, 1999, 42, 480-484.	2.9	36
139	Defective mutations in the insulin promoter factor-1 (IPF-1) gene in late-onset type 2 diabetes mellitus. Journal of Clinical Investigation, 1999, 104, R41-R48.	3.9	256
140	Absence of replication in the French population of the association between beta 2/NEUROD-A45T polymorphism and type 1 diabetes. Diabetes and Metabolism, 1999, 25, 516-7.	1.4	16
141	A genome-wide scan for human obesity genes reveals a major susceptibility locus on chromosome 10. Nature Genetics, 1998, 20, 304-308.	9.4	356
142	A mutation in the human leptin receptor gene causes obesity and pituitary dysfunction. Nature, 1998, 392, 398-401.	13.7	2,112
143	Genetic studies of polymorphisms in ten non-insulin-dependent diabetes mellitus candidate genes in Tamil Indians from Pondichery. Diabetes and Metabolism, 1998, 24, 244-50.	1.4	23
144	Genetic studies of the leptin receptor gene in morbidly obese French Caucasian families. Human Genetics, 1997, 100, 491-496.	1.8	48

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145	Genetic studies of neuropeptide Y and neuropeptide Y receptors Y1 and Y5 regions in morbid obesity. Diabetologia, 1997, 40, 671-675.	2.9	33
146	Empirical affected-sib-pair statistics: Two simulation strategies. Genetic Epidemiology, 1997, 14, 1073-1078.	0.6	0
147	Genetic studies of the sulfonylurea receptor gene locus in NIDDM and in morbid obesity among French Caucasians. Diabetes, 1997, 46, 688-694.	0.3	29
148	Genomic structure of the downstream part of the human FLT3 gene: exon/intron structure conservation among genes encoding receptor tyrosine kinases (RTK) of subclass III. Gene, 1994, 145, 283-288.	1.0	99