Josee Dupuis

List of Publications by Year in Descending Order

277 papers	30,851 citations	78 h-index	174 g-index
300 ext. papers	38,154 ext. citations	9.6 avg, IF	5.72 L-index

#	Paper	IF	Citations
277	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
276	Obesity Partially Mediates the Diabetogenic Effect of Lowering LDL Cholesterol. *Diabetes Care*, **2021**,	14.6	4
275	Genetic association tests in family samples for multi-category phenotypes. *BMC Genomics*, **2021**, 22, 873	4.5	0
274	Exploiting family history in aggregation unit-based genetic association tests. *European Journal of Human Genetics*, **2021**,	5.3	1
273	Detecting differentially methylated regions with multiple distinct associations. *Epigenomics*, **2021**, 13, 451-464	4.4	2
272	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
271	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. *Nature Communications*, **2021**, 12, 3505	17.4	5
270	Host and gut microbial tryptophan metabolism and type 2 diabetes: an integrative analysis of host genetics, diet, gut microbiome and circulating metabolites in cohort studies. *Gut*, **2021**,	19.2	16
269	An Integrative Genomic Strategy Identifies sRAGE as a Causal and Protective Biomarker of Lung Function. *Chest*, **2021**,	5.3	1
268	A systematic analysis of protein-altering exonic variants in chronic obstructive pulmonary disease. *American Journal of Physiology - Lung Cellular and Molecular Physiology*, **2021**, 321, L130-L143	5.8	2
267	Association of Circulating Monocyte Chemoattractant Protein-1 Levels With Cardiovascular Mortality: A Meta-analysis of Population-Based Studies. *JAMA Cardiology*, **2021**, 6, 587-592	16.2	8
266	The Association of Aging Biomarkers, Interstitial Lung Abnormalities, and Mortality. *American Journal of Respiratory and Critical Care Medicine*, **2021**, 203, 1149-1157	10.2	9
265	JEM: A joint test to estimate the effect of multiple genetic variants on DNA methylation. *Genetic Epidemiology*, **2021**, 45, 280-292	2.6	
264	Associations of Ɐ Fatty Acids With Interstitial Lung Disease and Lung Imaging Abnormalities Among Adults. *American Journal of Epidemiology*, **2021**, 190, 95-108	3.8	8
263	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
262	Sugar-Sweetened Beverage Consumption May Modify Associations Between Genetic Variants in the CHREBP (Carbohydrate Responsive Element Binding Protein) Locus and HDL-C (High-Density Lipoprotein Cholesterol) and Triglyceride Concentrations. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003288	5.2	1
261	Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits. *Nature Human Behaviour*, **2021**,	12.8	5

260	Mapping gene and gene pathways associated with coronary artery disease: a CARDIoGRAM exome and multi-ancestry UK biobank analysis. *Scientific Reports*, **2021**, 11, 16461	4.9	0
259	Anisocoria and Poor Pupil Reactivity by Quantitative Pupillometry in Patients With Intracranial Pathology. *Critical Care Medicine*, **2021**,	1.4	1
258	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. *Scientific Reports*, **2021**, 11, 19365	4.9	0
257	Approximate conditional phenotype analysis based on genome wide association summary statistics. *Scientific Reports*, **2021**, 11, 2518	4.9	3
256	Genetic analysis of biobank data: Familial history aggregation-based tests (FHAT) with application to Alzheimer's disease. *Alzheimer's and Dementia*, **2020**, 16, e038648	1.2	
255	Comparative trans-ethnic meta-analysis of whole exome sequencing variation for Alzheimer's disease (AD) in 18,402 individuals of the Alzheimer's Disease Sequencing Project (ADSP). *Alzheimer's and Dementia*, **2020**, 16, e041583	1.2	
254	Genome-wide meta-analysis of late-onset Alzheimer's disease using rare variant imputation in 65,602 subjects identifies risk loci with roles in memory, neurodevelopment, and cardiometabolic traits: The international genomics of Alzheimer's project (IGAP). *Alzheimer's and Dementia*, **2020**, 16, e044193	1.2	0
253	Assessing whole genome sequencing variation for Alzheimer's disease in 4707 individuals from the Alzheimer's Disease Sequencing Project (ADSP). *Alzheimer's and Dementia*, **2020**, 16, e045548	1.2	
252	Frequency of familial Alzheimer's disease gene mutations within the Alzheimer Disease Sequencing Project (ADSP). *Alzheimer's and Dementia*, **2020**, 16, e046203	1.2	
251	Cerebral small vessel disease genomics and its implications across the lifespan. *Nature Communications*, **2020**, 11, 6285	17.4	22
250	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. *PLoS ONE*, **2020**, 15, e0230815	3.7	4
249	The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature*, **2020**, 581, 434-443	50.4	2278
248	Transcript expression-aware annotation improves rare variant interpretation. *Nature*, **2020**, 581, 452-458	50.4	55
247	Evaluation of population stratification adjustment using genome-wide or exonic variants. *Genetic Epidemiology*, **2020**, 44, 702-716	2.6	1
246	Beverage Consumption and Longitudinal Changes in Lipoprotein Concentrations and Incident Dyslipidemia in US Adults: The Framingham Heart Study. *Journal of the American Heart Association*, **2020**, 9, e014083	6	20
245	Convex combination sequence kernel association test for rare-variant studies. *Genetic Epidemiology* , **2020**, 44, 352-367	2.6	2
244	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. *American Journal of Human Genetics*, **2020**, 106, 112-120	11	2
243	Searching for parent-of-origin effects on cardiometabolic traits in imprinted genomic regions. *European Journal of Human Genetics*, **2020**, 28, 646-655	5.3	1

242	A unified method for rare variant analysis of gene-environment interactions. *Statistics in Medicine*, **2020**, 39, 801-813	2.3	2
241	Integrative Omics Approach to Identifying Genes Associated With Atrial Fibrillation. *Circulation Research*, **2020**, 126, 350-360	15.7	21
240	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. *Nature Communications*, **2020**, 11, 5182	17.4	6
239	Interactions Between Sugar-Sweetened Beverage Consumption and Genetic Variants in the ChREBP Locus on Lipoprotein Concentrations in the UK Biobank: A Replication Study. *Current Developments in Nutrition*, **2020**, 4, 1255-1255	0.4	78
238	Associations Between Genetic Variants near the CHREBP Locus and Lipoprotein Concentrations May Be Modified by Sugar-Sweetened Beverage Consumption. *Current Developments in Nutrition*, **2020**, 4, 1256-1256	0.4	78
237	Analysis of brain region-specific co-expression networks reveals clustering of established and novel genes associated with Alzheimer disease. *Alzheimer's Research and Therapy*, **2020**, 12, 103	9	2
236	Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. *Molecular Psychiatry*, **2020**, 25, 1859-1875	15.1	106
235	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
234	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
233	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
232	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
231	Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. *American Journal of Human Genetics*, **2019**, 105, 706-718	11	22
230	Childhood Tobacco Smoke Exposure and Risk of Atrial Fibrillation in Adulthood. *Journal of the American College of Cardiology*, **2019**, 74, 1658-1664	15.1	11
229	Comparison of methods for multivariate gene-based association tests for complex diseases using common variants. *European Journal of Human Genetics*, **2019**, 27, 811-823	5.3	8
228	Mendelian Randomization Analysis of Hemoglobin A as a Risk Factor for Coronary Artery Disease. *Diabetes Care*, **2019**, 42, 1202-1208	14.6	17
227	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. *Nature Communications*, **2019**, 10, 2581	17.4	31
226	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. *Nature*, **2019**, 570, 71-76	50.4	129
225	Adipocyte hyperplasia: the primary mechanism of supraspinatus intramuscular fat accumulation after a complete rotator cuff tendon tear: a study in the rabbit. *Adipocyte*, **2019**, 8, 144-153	3.2	1

224	Quality control and integration of genotypes from two calling pipelines for whole genome sequence data in the Alzheimer's disease sequencing project. *Genomics*, **2019**, 111, 808-818	4.3	10
223	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. *Molecular Psychiatry*, **2019**, 24, 1920-1932	15.1	30
222	Potential Interplay between Dietary Saturated Fats and Genetic Variants of the NLRP3 Inflammasome to Modulate Insulin Resistance and Diabetes Risk: Insights from a Meta-Analysis of 19□05 Individuals. *Molecular Nutrition and Food Research*, **2019**, 63, e1900226	5.9	11
221	Overlap of Genetic Risk between Interstitial Lung Abnormalities and Idiopathic Pulmonary Fibrosis. *American Journal of Respiratory and Critical Care Medicine*, **2019**, 200, 1402-1413	10.2	37
220	Quality of dietary fat and genetic risk of type 2 diabetes: individual participant data meta-analysis. *BMJ, The*, **2019**, 366, l4292	5.9	23
219	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. *Scientific Reports*, **2019**, 9, 9439	4.9	3
218	Epigenome-Wide Association Study of Incident Type 2 Diabetes in a British Population: EPIC-Norfolk Study. *Diabetes*, **2019**, 68, 2315-2326	0.9	40
217	Omega-3 Fatty Acids and Genome-Wide Interaction Analyses Reveal DPP10-Pulmonary Function Association. *American Journal of Respiratory and Critical Care Medicine*, **2019**, 199, 631-642	10.2	5
216	Increased Airway Wall Thickness in Interstitial Lung Abnormalities and Idiopathic Pulmonary Fibrosis. *Annals of the American Thoracic Society*, **2019**, 16, 447-454	4.7	15
215	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
214	Transethnic Evaluation Identifies Low-Frequency Loci Associated With 25-Hydroxyvitamin D Concentrations. *Journal of Clinical Endocrinology and Metabolism*, **2018**, 103, 1380-1392	5.6	18
213	Metabolomics insights into early type 2 diabetes pathogenesis and detection in individuals with normal fasting glucose. *Diabetologia*, **2018**, 61, 1315-1324	10.3	66
212	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. *Nature Communications*, **2018**, 9, 260	17.4	174
211	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 379-384	11.5	21
210	Whole genome sequence analyses of brain imaging measures in the Framingham Study. *Neurology*, **2018**, 90, e188-e196	6.5	19
209	Sugar-sweetened beverage intake associations with fasting glucose and insulin concentrations are not modified by selected genetic variants in a ChREBP-FGF21 pathway: a meta-analysis. *Diabetologia*, **2018**, 61, 317-330	10.3	17
208	Epigenome-Wide Association Study of Soluble Tumor Necrosis Factor Receptor 2 Levels in the Framingham Heart Study. *Frontiers in Pharmacology*, **2018**, 9, 207	5.6	8
207	Heritability and genome-wide association study of diffusing capacity of the lung. *European Respiratory Journal*, **2018**, 52,	13.6	12

206	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. *Nature Communications*, **2018**, 9, 2976	17.4	45
205	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16
204	Investigation of parent-of-origin effects induced by fenofibrate treatment on triglycerides levels. *BMC Genetics*, **2018**, 19, 83	2.6	2
203	Evaluation of a phenotype imputation approach using GAW20 simulated data. *BMC Proceedings*, **2018**, 12, 56	2.3	3
202	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. *Nature Genetics*, **2018**, 50, 1505-1513	36.3	675
201	ProxECAT: Proxy External Controls Association Test. A new case-control gene region association test using allele frequencies from public controls. *PLoS Genetics*, **2018**, 14, e1007591	6	13
200	Comparison of novel and existing methods for detecting differentially methylated regions. *BMC Genetics*, **2018**, 19, 84	2.6	7
199	Meta-analysis across Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium provides evidence for an association of serum vitamin D with pulmonary function. *British Journal of Nutrition*, **2018**, 120, 1159-1170	3.6	7
198	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. *International Journal of Epidemiology*, **2017**, 46, 894-904	7.8	25
197	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. *Genome Biology*, **2017**, 18, 16	18.3	108
196	Genetic loci associated with chronic obstructive pulmonary disease overlap with loci for lung function and pulmonary fibrosis. *Nature Genetics*, **2017**, 49, 426-432	36.3	201
195	Pleural abnormalities in the Framingham Heart Study: prevalence and CT image features. *Occupational and Environmental Medicine*, **2017**, 74, 756-761	2.1	9
194	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	8.9	414
193	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes*, **2017**, 66, 2019-2032	0.9	29
192	Genetically Driven Hyperglycemia Increases Risk of Coronary Artery Disease Separately From Type 2 Diabetes. *Diabetes Care*, **2017**, 40, 687-693	14.6	34
191	MicroRNA Signature of Cigarette Smoking and Evidence for a Putative Causal Role of MicroRNAs in Smoking-Related Inflammation and Target Organ Damage. *Circulation: Cardiovascular Genetics*, **2017**, 10,		28
190	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. *PLoS Medicine*, **2017**, 14, e1002383	11.6	223
189	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. *Nature Genetics*, **2017**, 49, 1373-1384	36.3	508

188	Genome-wide association study of subclinical interstitial lung disease in MESA. *Respiratory Research* , **2017**, 18, 97	7.3	15
187	Sex-Based Genetic Association Study Identifies CELSR1 as a Possible Chronic Obstructive Pulmonary Disease Risk Locus among Women. *American Journal of Respiratory Cell and Molecular Biology*, **2017**, 56, 332-341	5.7	22
186	Heritability of Atrial Fibrillation. *Circulation: Cardiovascular Genetics*, **2017**, 10,		39
185	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
184	[O11104]: TOPMED WHOLE GENOME SEQUENCE (WGS) ASSOCIATIONS WITH BRAIN MRI MEASURES IN THE FRAMINGHAM STUDY **2017**, 13, P219-P220		
183	Structured mating: Patterns and implications. *PLoS Genetics*, **2017**, 13, e1006655	6	18
182	Identification of a novel proinsulin-associated SNP and demonstration that proinsulin is unlikely to be a causal factor in subclinical vascular remodelling using Mendelian randomisation. *Atherosclerosis*, **2017**, 266, 196-204	3.1	2
181	Peripheral Blood Transcriptomic Signatures of Fasting Glucose and Insulin Concentrations. *Diabetes* , **2016**, 65, 3794-3804	0.9	18
180	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci. *Diabetes*, **2016**, 65, 3200-11	0.9	47
179	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. *Science Translational Medicine*, **2016**, 8, 341ra76	17.5	77
178	Comparison of multiple single-nucleotide variant association tests in a meta-analysis of Genetic Analysis Workshop 19 family and unrelated data. *BMC Proceedings*, **2016**, 10, 187-191	2.3	
177	Development and Progression of Interstitial Lung Abnormalities in the Framingham Heart Study. *American Journal of Respiratory and Critical Care Medicine*, **2016**, 194, 1514-1522	10.2	147
176	Incident Type 2 Diabetes Risk is Influenced by Obesity and Diabetes in Social Contacts: a Social Network Analysis. *Journal of General Internal Medicine*, **2016**, 31, 1127-33	4	18
175	Type 2 Diabetes Prediction **2016**, 425-440		
174	Trans-ethnic Meta-analysis and Functional Annotation Illuminates the Genetic Architecture of Fasting Glucose and Insulin. *American Journal of Human Genetics*, **2016**, 99, 56-75	11	41
173	Normal thymus in adults: appearance on CT and associations with age, sex, BMI and smoking. *European Radiology*, **2016**, 26, 15-24	8	39
172	Rare variant associations with waist-to-hip ratio in European-American and African-American women from the NHLBI-Exome Sequencing Project. *European Journal of Human Genetics*, **2016**, 24, 1181-7	5.3	2
171	Galectin-3 Is Associated with Restrictive Lung Disease and Interstitial Lung Abnormalities. *American Journal of Respiratory and Critical Care Medicine*, **2016**, 194, 77-83	10.2	43

170	Genome-wide gene-environment interactions on quantitative traits using family data. *European Journal of Human Genetics*, **2016**, 24, 1022-8	5.3	1
169	Association Between Interstitial Lung Abnormalities and All-Cause Mortality. *JAMA - Journal of the American Medical Association*, **2016**, 315, 672-81	27.4	209
168	Type 2 Diabetes Genetic Predisposition, Obesity, and All-Cause Mortality Risk in the U.S.: A Multiethnic Analysis. *Diabetes Care*, **2016**, 39, 539-46	14.6	25
167	Association of the IGF1 gene with fasting insulin levels. *European Journal of Human Genetics*, **2016**, 24, 1337-43	5.3	4
166	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
165	Shared genetic susceptibility of vascular-related biomarkers with ischemic and recurrent stroke. *Neurology*, **2016**, 86, 351-9	6.5	26
164	Evaluation of power of the Illumina HumanOmni5M-4v1 BeadChip to detect risk variants for human complex diseases. *European Journal of Human Genetics*, **2016**, 24, 1029-34	5.3	4
163	Joint association analysis of a binary and a quantitative trait in family samples. *European Journal of Human Genetics*, **2016**, 25, 130-136	5.3	3
162	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
161	Robust analysis of secondary phenotypes in case-control genetic association studies. *Statistics in Medicine*, **2016**, 35, 4226-37	2.3	7
160	Evaluation of a Two-Stage Approach in Trans-Ethnic Meta-Analysis in Genome-Wide Association Studies. *Genetic Epidemiology*, **2016**, 40, 284-92	2.6	8
159	Meta-Analysis for Penalized Regression Methods with Multi-Cohort Genome-Wide Association Studies. *Human Heredity*, **2016**, 81, 142-149	1.1	1
158	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. *Genome Biology*, **2016**, 17, 255	18.3	171
157	P1-018: Rare Deleterious And Loss-of-Function Variants in OPRL1 and GAS2L2 Contribute to the Risk of Late-Onset Alzheimer□ Disease: Alzheimer□ Disease Sequencing Project Case-Control Study **2016**, 12, P406-P406		1
156	General Framework for Meta-Analysis of Haplotype Association Tests. *Genetic Epidemiology*, **2016**, 40, 244-52	2.6	
155	Directional dominance on stature and cognition in□diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
154	Gene expression markers of age-related inflammation in two human cohorts. *Experimental Gerontology*, **2015**, 70, 37-45	4.5	17
153	Identification and functional characterization of G6PC2 coding variants influencing glycemic traits define an effector transcript at the G6PC2-ABCB11 locus. *PLoS Genetics*, **2015**, 11, e1004876	6	76

152	Integrative pathway genomics of lung function and airflow obstruction. *Human Molecular Genetics*, **2015**, 24, 6836-48	5.6	20
151	Association of a 62 Variants Type 2 Diabetes Genetic Risk Score With Markers of Subclinical Atherosclerosis: A Transethnic, Multicenter Study. *Circulation: Cardiovascular Genetics*, **2015**, 8, 507-15		11
150	Pulmonary cysts identified on chest CT: are they part of aging change or of clinical significance?. *Thorax*, **2015**, 70, 1156-62	7.3	29
149	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
148	A comparison of visual and quantitative methods to identify interstitial lung abnormalities. *BMC Pulmonary Medicine*, **2015**, 15, 134	3.5	27
147	Parent-of-Origin Effects of the APOB Gene on Adiposity in Young Adults. *PLoS Genetics*, **2015**, 11, e1005673		9
146	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. *Human Molecular Genetics*, **2015**, 24, 559-71	5.6	31
145	Paraseptal emphysema: Prevalence and distribution on CT and association with interstitial lung abnormalities. *European Journal of Radiology*, **2015**, 84, 1413-8	4.7	36
144	Anterior Mediastinal Masses in the Framingham Heart Study: Prevalence and CT Image Characteristics. *European Journal of Radiology Open*, **2015**, 2, 26-31	2.6	30
143	Metabolic factors and genetic risk mediate familial type 2 diabetes risk in the Framingham Heart Study. *Diabetologia*, **2015**, 58, 988-96	10.3	10
142	Revisiting heritability accounting for shared environmental effects and maternal inheritance. *Human Genetics*, **2015**, 134, 169-79	6.3	10
141	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
140	Rare Variant Association Analysis: Beyond Collapsing Approaches **2015**, 149-167		1
139	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
138	Leveraging cross-species transcription factor binding site patterns: from diabetes risk loci to disease mechanisms. *Cell*, **2014**, 156, 343-58	56.2	96
137	Genome-wide association analysis identifies six new loci associated with forced vital capacity. *Nature Genetics*, **2014**, 46, 669-77	36.3	104
136	Rare genetic variant analysis on blood pressure in related samples. *BMC Proceedings*, **2014**, 8, S35	2.3	4
135	Large multiethnic Candidate Gene Study for C-reactive protein levels: identification of a novel association at CD36 in African Americans. *Human Genetics*, **2014**, 133, 985-95	6.3	25

134	Strategies to design and analyze targeted sequencing data: cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. *Circulation: Cardiovascular Genetics*, **2014**, 7, 335-43		15
133	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. *Lancet Diabetes and Endocrinology,the*, **2014**, 2, 719-29	18.1	250
132	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics*, **2014**, 46, 234-44	36.3	784
131	Meta-analysis of genome-wide association studies identifies two loci associated with circulating osteoprotegerin levels. *Human Molecular Genetics*, **2014**, 23, 6684-93	5.6	11
130	Whole blood gene expression and atrial fibrillation: the Framingham Heart Study. *PLoS ONE*, **2014**, 9, e96794	3.7	18
129	Incorporating gene-environment interaction in testing for association with rare genetic variants. *Human Heredity*, **2014**, 78, 81-90	1.1	22
128	Large-scale genome-wide association studies and meta-analyses of longitudinal change in adult lung function. *PLoS ONE*, **2014**, 9, e100776	3.7	42
127	Impact of type 2 diabetes susceptibility variants on quantitative glycemic traits reveals mechanistic heterogeneity. *Diabetes*, **2014**, 63, 2158-71	0.9	235
126	Genome-wide study of percent emphysema on computed tomography in the general population. The Multi-Ethnic Study of Atherosclerosis Lung/SNP Health Association Resource Study. *American Journal of Respiratory and Critical Care Medicine*, **2014**, 189, 408-18	10.2	77
125	ADAM19 and HTR4 variants and pulmonary function: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. *Circulation: Cardiovascular Genetics*, **2014**, 7, 350-8		6
124	Correction for multiple testing in a gene region. *European Journal of Human Genetics*, **2014**, 22, 414-8	5.3	29
123	Polygenic type 2 diabetes prediction at the limit of common variant detection. *Diabetes*, **2014**, 63, 2172-82	8.9	96
122	Sequence kernel association test for survival traits. *Genetic Epidemiology*, **2014**, 38, 191-7	2.6	44
121	Whole blood gene expression and interleukin-6 levels. *Genomics*, **2014**, 104, 490-5	4.3	19
120	Performance of statistical methods on CHARGE targeted sequencing data. *BMC Genetics*, **2014**, 15, 104	2.6	
119	A low-frequency variant in MAPK14 provides mechanistic evidence of a link with myeloperoxidase: a prognostic cardiovascular risk marker. *Journal of the American Heart Association*, **2014**, 3,	6	6
118	Association of levels of fasting glucose and insulin with rare variants at the chromosome 11p11.2-MADD locus: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. *Circulation: Cardiovascular Genetics*, **2014**, 7, 374-382		9
117	Pleiotropic genes for metabolic syndrome and inflammation. *Molecular Genetics and Metabolism*, **2014**, 112, 317-38	3.7	81

116	Network-guided sparse regression modeling for detection of gene-by-gene interactions. *Bioinformatics*, **2013**, 29, 1241-9	7.2	4
115	Association testing of the mitochondrial genome using pedigree data. *Genetic Epidemiology*, **2013**, 37, 239-47	2.6	6
114	Meta-analysis investigating associations between healthy diet and fasting glucose and insulin levels and modification by loci associated with glucose homeostasis in data from 15 cohorts. *American Journal of Epidemiology*, **2013**, 177, 103-15	3.8	63
113	Genome-wide study identifies two loci associated with lung function decline in mild to moderate COPD. *Human Genetics*, **2013**, 132, 79-90	6.3	39
112	Sequence kernel association test for quantitative traits in family samples. *Genetic Epidemiology*, **2013**, 37, 196-204	2.6	169
111	Common variants in and near IRS1 and subclinical cardiovascular disease in the Framingham Heart Study. *Atherosclerosis*, **2013**, 229, 149-54	3.1	9
110	MUC5B promoter polymorphism and interstitial lung abnormalities. *New England Journal of Medicine*, **2013**, 368, 2192-200	59.2	265
109	Causal relationship between obesity and vitamin D status: bi-directional Mendelian randomization analysis of multiple cohorts. *PLoS Medicine*, **2013**, 10, e1001383	11.6	592
108	Transferability and fine mapping of type 2 diabetes loci in African Americans: the Candidate Gene Association Resource Plus Study. *Diabetes*, **2013**, 62, 965-76	0.9	51
107	Mendelian randomization studies do not support a causal role for reduced circulating adiponectin levels in insulin resistance and type 2 diabetes. *Diabetes*, **2013**, 62, 3589-98	0.9	95
106	Genome-wide and gene-centric analyses of circulating myeloperoxidase levels in the charge and care consortia. *Human Molecular Genetics*, **2013**, 22, 3381-93	5.6	18
105	Lack of interaction of beta-cell-function-associated variants with hypertension on change in fasting glucose and diabetes risk: the Framingham Offspring Study. *Journal of Hypertension*, **2013**, 31, 1001-9	1.9	
104	A method of moments estimator for random effect multivariate meta-analysis. *Biometrics*, **2012**, 68, 1278-84	1.8	126
103	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics*, **2012**, 44, 981-90	36.3	1482
102	Race-ethnic differences in the association of genetic loci with HbA1c levels and mortality in U.S. adults: the third National Health and Nutrition Examination Survey (NHANES III). *BMC Medical Genetics*, **2012**, 13, 30	2.1	26
101	Impact of common variation in bone-related genes on type 2 diabetes and related traits. *Diabetes*, **2012**, 61, 2176-86	0.9	25
100	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
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5	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
4	Rare Non-coding Variation Identified by Large Scale Whole Genome Sequencing Reveals Unexplained Heritability of Type 2 Diabetes		2
3	Fine-mapping of an expanded set of type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps		18
2	Genetic discovery and translational decision support from exome sequencing of 20,791 type 2 diabetes cases and 24,440 controls from five ancestries		2
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