Josee Dupuis

List of Publications by Citations

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	The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature*, **2020**, 581, 434-443	50.4	2278
276	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics*, **2010**, 42, 105-16	36.3	1673
275	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
274	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
273	Common genetic determinants of vitamin D insufficiency: a genome-wide association study. *Lancet, The*, **2010**, 376, 180-8	40	1183
272	Common variants at 30 loci contribute to polygenic dyslipidemia. *Nature Genetics*, **2009**, 41, 56-65	36.3	1095
271	A mutation in the LDL receptor-related protein 5 gene results in the autosomal dominant high-bone-mass trait. *American Journal of Human Genetics*, **2002**, 70, 11-9	11	1076
270	Association of the ADAM33 gene with asthma and bronchial hyperresponsiveness. *Nature*, **2002**, 418, 426-30	50.4	879
269	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
268	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
267	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
266	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
265	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. *Nature Genetics*, **2012**, 44, 659-69	36.3	615
264	Genotype score in addition to common risk factors for prediction of type 2 diabetes. *New England Journal of Medicine*, **2008**, 359, 2208-19	59.2	608
263	Causal relationship between obesity and vitamin D status: bi-directional Mendelian randomization analysis of multiple cohorts. *PLoS Medicine*, **2013**, 10, e1001383	11.6	592
262	Variants in MTNR1B influence fasting glucose levels. *Nature Genetics*, **2009**, 41, 77-81	36.3	584
261	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. *Nature Genetics*, **2010**, 42, 142-8	36.3	527

260	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
259	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	8.2	414
258	Meta-analysis of genome-wide association studies in >80 000 subjects identifies multiple loci for C-reactive protein levels. *Circulation*, **2011**, 123, 731-8	16.7	395
257	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	6	326
256	Common variants at 10 genomic loci influence hemoglobin A[C) levels via glycemic and nonglycemic pathways. *Diabetes*, **2010**, 59, 3229-39	0.9	314
255	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
254	Genome-wide association identifies nine common variants associated with fasting proinsulin levels and provides new insights into the pathophysiology of type 2 diabetes. *Diabetes*, **2011**, 60, 2624-34	0.9	285
253	Identifying SNPs predictive of phenotype using random forests. *Genetic Epidemiology*, **2005**, 28, 171-82	2.6	267
252	MUC5B promoter polymorphism and interstitial lung abnormalities. *New England Journal of Medicine*, **2013**, 368, 2192-200	59.2	265
251	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
250	Impact of type 2 diabetes susceptibility variants on quantitative glycemic traits reveals mechanistic heterogeneity. *Diabetes*, **2014**, 63, 2158-71	0.9	235
249	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
248	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
247	Detailed physiologic characterization reveals diverse mechanisms for novel genetic Loci regulating glucose and insulin metabolism in humans. *Diabetes*, **2010**, 59, 1266-75	0.9	211
246	Association Between Interstitial Lung Abnormalities and All-Cause Mortality. *JAMA - Journal of the American Medical Association*, **2016**, 315, 672-81	27.4	209
245	NRXN3 is a novel locus for waist circumference: a genome-wide association study from the CHARGE Consortium. *PLoS Genetics*, **2009**, 5, e1000539	6	203
244	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
243	Statistical methods for mapping quantitative trait loci from a dense set of markers. *Genetics*, **1999**, 151, 373-86	4	201

242	Genome-wide association with bone mass and geometry in the Framingham Heart Study. *BMC Medical Genetics*, **2007**, 8 Suppl 1, S14	2.1	200
241	Atrial fibrillation: current knowledge and future directions in epidemiology and genomics. *Circulation*, **2011**, 124, 1982-93	16.7	197
240	Large-scale genomic studies reveal central role of ABO in sP-selectin and sICAM-1 levels. *Human Molecular Genetics*, **2010**, 19, 1863-72	5.6	186
239	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
238	Genome-wide association scan identifies candidate polymorphisms associated with differential response to anti-TNF treatment in rheumatoid arthritis. *Molecular Medicine*, **2008**, 14, 575-81	6.2	172
237	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. *Genome Biology*, **2016**, 17, 255	18.3	171
236	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
235	Sequence kernel association test for quantitative traits in family samples. *Genetic Epidemiology*, **2013**, 37, 196-204	2.6	169
234	Large scale replication and meta-analysis of variants on chromosome 4q25 associated with atrial fibrillation. *European Heart Journal*, **2009**, 30, 813-9	9.5	165
233	Genetic variants at 2q24 are associated with susceptibility to type 2 diabetes. *Human Molecular Genetics*, **2010**, 19, 2706-15	5.6	164
232	Stratifying type 2 diabetes cases by BMI identifies genetic risk variants in LAMA1 and enrichment for risk variants in lean compared to obese cases. *PLoS Genetics*, **2012**, 8, e1002741	6	162
231	The Framingham Heart Study 100K SNP genome-wide association study resource: overview of 17 phenotype working group reports. *BMC Medical Genetics*, **2007**, 8 Suppl 1, S1	2.1	152
230	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
229	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
228	Genetic risk reclassification for type 2 diabetes by age below or above 50 years using 40 type 2 diabetes risk single nucleotide polymorphisms. *Diabetes Care*, **2011**, 34, 121-5	14.6	145
227	Poor performance of bootstrap confidence intervals for the location of a quantitative trait locus. *Genetics*, **2006**, 174, 481-9	4	144
226	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
225	Genome-wide association studies identify CHRNA5/3 and HTR4 in the development of airflow obstruction. *American Journal of Respiratory and Critical Care Medicine*, **2012**, 186, 622-32	10.2	131

224	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. *Nature*, **2019**, 570, 71-76	50.4	129
223	A genome-wide association study reveals variants in ARL15 that influence adiponectin levels. *PLoS Genetics*, **2009**, 5, e1000768	6	129
222	Common variants in the adiponectin gene (ADIPOQ) associated with plasma adiponectin levels, type 2 diabetes, and diabetes-related quantitative traits: the Framingham Offspring Study. *Diabetes*, **2008**, 57, 3353-9	0.9	129
221	Clear detection of ADIPOQ locus as the major gene for plasma adiponectin: results of genome-wide association analyses including 4659 European individuals. *Atherosclerosis*, **2010**, 208, 412-20	3.1	128
220	Genome-wide association to body mass index and waist circumference: the Framingham Heart Study 100K project. *BMC Medical Genetics*, **2007**, 8 Suppl 1, S18	2.1	128
219	A method of moments estimator for random effect multivariate meta-analysis. *Biometrics*, **2012**, 68, 1278-84	1.8	126
218	Meta-analysis of gene-environment interaction: joint estimation of SNP and SNP environment regression coefficients. *Genetic Epidemiology*, **2011**, 35, 11-8	2.6	121
217	Relations of inflammatory biomarkers and common genetic variants with arterial stiffness and wave reflection. *Hypertension*, **2008**, 51, 1651-7	8.5	120
216	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
215	Interactions of dietary whole-grain intake with fasting glucose- and insulin-related genetic loci in individuals of European descent: a meta-analysis of 14 cohort studies. *Diabetes Care*, **2010**, 33, 2684-91	14.6	112
214	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. *Genome Biology*, **2017**, 18, 16	18.3	108
213	Genome-wide joint meta-analysis of SNP and SNP-by-smoking interaction identifies novel loci for pulmonary function. *PLoS Genetics*, **2012**, 8, e1003098	6	108
212	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
211	Genome-wide association analysis identifies six new loci associated with forced vital capacity. *Nature Genetics*, **2014**, 46, 669-77	36.3	104
210	Genetic variation at the low-density lipoprotein receptor-related protein 5 (LRP5) locus modulates Wnt signaling and the relationship of physical activity with bone mineral density in men. *Bone*, **2007** , 40, 587-96	4.7	99
209	Leveraging cross-species transcription factor binding site patterns: from diabetes risk loci to disease mechanisms. *Cell*, **2014**, 156, 343-58	56.2	96
208	Polygenic type 2 diabetes prediction at the limit of common variant detection. *Diabetes*, **2014**, 63, 2172-82	8.9	96
207	Duffy antigen receptor for chemokines (Darc) polymorphism regulates circulating concentrations of monocyte chemoattractant protein-1 and other inflammatory mediators. *Blood*, **2010**, 115, 5289-99	2.2	96

206	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
205	Genome-wide association with select biomarker traits in the Framingham Heart Study. *BMC Medical Genetics*, **2007**, 8 Suppl 1, S11	2.1	94
204	Genome scan of systemic biomarkers of vascular inflammation in the Framingham Heart Study: evidence for susceptibility loci on 1q. *Atherosclerosis*, **2005**, 182, 307-14	3.1	91
203	Pleiotropic genes for metabolic syndrome and inflammation. *Molecular Genetics and Metabolism*, **2014**, 112, 317-38	3.7	81
202	Total zinc intake may modify the glucose-raising effect of a zinc transporter (SLC30A8) variant: a 14-cohort meta-analysis. *Diabetes*, **2011**, 60, 2407-16	0.9	81
201	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
200	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
199	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
198	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
197	Association of variants in RETN with plasma resistin levels and diabetes-related traits in the Framingham Offspring Study. *Diabetes*, **2009**, 58, 750-6	0.9	77
196	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
195	Eight genetic loci associated with variation in lipoprotein-associated phospholipase A2 mass and activity and coronary heart disease: meta-analysis of genome-wide association studies from five community-based studies. *European Heart Journal*, **2012**, 33, 238-51	9.5	75
194	A 100K genome-wide association scan for diabetes and related traits in the Framingham Heart Study: replication and integration with other genome-wide datasets. *Diabetes*, **2007**, 56, 3063-74	0.9	74
193	Genome-wide association with diabetes-related traits in the Framingham Heart Study. *BMC Medical Genetics*, **2007**, 8 Suppl 1, S16	2.1	72
192	Metabolomics insights into early type 2 diabetes pathogenesis and detection in individuals with normal fasting glucose. *Diabetologia*, **2018**, 61, 1315-1324	10.3	66
191	Genome-wide association analysis of soluble ICAM-1 concentration reveals novel associations at the NFKBIK, PNPLA3, RELA, and SH2B3 loci. *PLoS Genetics*, **2011**, 7, e1001374	6	65
190	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
189	Association of variation at the ABO locus with circulating levels of soluble intercellular adhesion molecule-1, soluble P-selectin, and soluble E-selectin: a meta-analysis. *Circulation: Cardiovascular Genetics*, **2011**, 4, 681-6		59

188	Transcript expression-aware annotation improves rare variant interpretation. *Nature*, **2020**, 581, 452-458	50.4	55
187	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
186	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
185	The relation of genetic and environmental factors to systemic inflammatory biomarker concentrations. *Circulation: Cardiovascular Genetics*, **2009**, 2, 229-37		47
184	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. *Nature Communications*, **2018**, 9, 2976	17.4	45
183	Sequence kernel association test for survival traits. *Genetic Epidemiology*, **2014**, 38, 191-7	2.6	44
182	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
181	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
180	Large-scale genome-wide association studies and meta-analyses of longitudinal change in adult lung function. *PLoS ONE*, **2014**, 9, e100776	3.7	42
179	Peptidoglycan recognition proteins Pglyrp3 and Pglyrp4 are encoded from the epidermal differentiation complex and are candidate genes for the Psors4 locus on chromosome 1q21. *Human Genetics*, **2006**, 119, 113-25	6.3	42
178	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
177	Mapping complex traits using Random Forests. *BMC Genetics*, **2003**, 4 Suppl 1, S64	2.6	41
176	Epigenome-Wide Association Study of Incident Type 2 Diabetes in a British Population: EPIC-Norfolk Study. *Diabetes*, **2019**, 68, 2315-2326	0.9	40
175	Normal thymus in adults: appearance on CT and associations with age, sex, BMI and smoking. *European Radiology*, **2016**, 26, 15-24	8	39
174	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
173	Heritability of Atrial Fibrillation. *Circulation: Cardiovascular Genetics*, **2017**, 10,		39
172	Haplotype structure of the ENPP1 Gene and Nominal Association of the K121Q missense single nucleotide polymorphism with glycemic traits in the Framingham Heart Study. *Diabetes*, **2008**, 57, 1971-7	9.9	39
171	The insulin gene variable number tandem repeat and risk of type 2 diabetes in a population-based sample of families and unrelated men and women. *Journal of Clinical Endocrinology and Metabolism*, **2005**, 90, 1137-43	5.6	39

170	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
169	Paraseptal emphysema: Prevalence and distribution on CT and association with interstitial lung abnormalities. *European Journal of Radiology*, **2015**, 84, 1413-8	4.7	36
168	Genetically Driven Hyperglycemia Increases Risk of Coronary Artery Disease Separately From Type 2 Diabetes. *Diabetes Care*, **2017**, 40, 687-693	14.6	34
167	The type 2 deiodinase (DIO2) A/G polymorphism is not associated with glycemic traits: the Framingham Heart Study. *Thyroid*, **2007**, 17, 199-202	6.2	32
166	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. *Nature Communications*, **2019**, 10, 2581	17.4	31
165	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. *Human Molecular Genetics*, **2015**, 24, 559-71	5.6	31
164	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
163	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
162	Genome-wide association study evaluating lipoprotein-associated phospholipase A2 mass and activity at baseline and after rosuvastatin therapy. *Circulation: Cardiovascular Genetics*, **2012**, 5, 676-85		30
161	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
160	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
159	Pulmonary cysts identified on chest CT: are they part of aging change or of clinical significance?. *Thorax*, **2015**, 70, 1156-62	7.3	29
158	Correction for multiple testing in a gene region. *European Journal of Human Genetics*, **2014**, 22, 414-8	5.3	29
157	Clinical and genetic factors associated with lipoprotein-associated phospholipase A2 in the Framingham Heart Study. *Atherosclerosis*, **2009**, 204, 601-7	3.1	29
156	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
155	A comparison of visual and quantitative methods to identify interstitial lung abnormalities. *BMC Pulmonary Medicine*, **2015**, 15, 134	3.5	27
154	Shared genetic susceptibility of vascular-related biomarkers with ischemic and recurrent stroke. *Neurology*, **2016**, 86, 351-9	6.5	26
153	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

152	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. *International Journal of Epidemiology*, **2017**, 46, 894-904	7.8	25
151	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
150	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
149	Impact of common variation in bone-related genes on type 2 diabetes and related traits. *Diabetes*, **2012**, 61, 2176-86	0.9	25
148	PAI-1 Gene 4G/5G polymorphism and risk of type 2 diabetes in a population-based sample. *Obesity*, **2006**, 14, 753-8	8	24
147	Quality of dietary fat and genetic risk of type 2 diabetes: individual participant data meta-analysis. *BMJ, The*, **2019**, 366, l4292	5.9	23
146	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
145	Cerebral small vessel disease genomics and its implications across the lifespan. *Nature Communications*, **2020**, 11, 6285	17.4	22
144	Incorporating gene-environment interaction in testing for association with rare genetic variants. *Human Heredity*, **2014**, 78, 81-90	1.1	22
143	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
142	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
141	Diurnal variation of serum alanine transaminase activity in chronic liver disease. *Hepatology*, **1998**, 28, 1724-5	11.2	22
140	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
139	Variants in the CNR1 and the FAAH genes and adiposity traits in the community. *Obesity*, **2009**, 17, 755-60	8	21
138	No interactions between previously associated 2-hour glucose gene variants and physical activity or BMI on 2-hour glucose levels. *Diabetes*, **2012**, 61, 1291-6	0.9	21
137	Integrative Omics Approach to Identifying Genes Associated With Atrial Fibrillation. *Circulation Research*, **2020**, 126, 350-360	15.7	21
136	Integrative pathway genomics of lung function and airflow obstruction. *Human Molecular Genetics*, **2015**, 24, 6836-48	5.6	20
135	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

134	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
133	Whole genome sequence analyses of brain imaging measures in the Framingham Study. *Neurology*, **2018**, 90, e188-e196	6.5	19
132	Whole blood gene expression and interleukin-6 levels. *Genomics*, **2014**, 104, 490-5	4.3	19
131	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
130	Peripheral Blood Transcriptomic Signatures of Fasting Glucose and Insulin Concentrations. *Diabetes* , **2016**, 65, 3794-3804	0.9	18
129	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
128	Whole blood gene expression and atrial fibrillation: the Framingham Heart Study. *PLoS ONE*, **2014**, 9, e96794	3.7	18
127	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
126	Racial/ethnic differences in association of fasting glucose-associated genomic loci with fasting glucose, HOMA-B, and impaired fasting glucose in the U.S. adult population. *Diabetes Care*, **2010**, 33, 2370-7	14.6	18
125	United states research published in major surgical journals is decreasing. *Annals of Surgery*, **1995**, 222, 263-6; discussion 266-9	7.8	18
124	Structured mating: Patterns and implications. *PLoS Genetics*, **2017**, 13, e1006655	6	18
123	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
122	Mendelian Randomization Analysis of Hemoglobin A as a Risk Factor for Coronary Artery Disease. *Diabetes Care*, **2019**, 42, 1202-1208	14.6	17
121	Gene expression markers of age-related inflammation in two human cohorts. *Experimental Gerontology*, **2015**, 70, 37-45	4.5	17
120	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
119	Identification of novel type 2 diabetes candidate genes involved in the crosstalk between the mitochondrial and the insulin signaling systems. *PLoS Genetics*, **2012**, 8, e1003046	6	17
118	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16
117	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

116	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
115	Genome-wide association study of subclinical interstitial lung disease in MESA. *Respiratory Research* , **2017**, 18, 97	7.3	15
114	Interpreting results of large-scale genetic association studies: separating gold from fool's gold. *JAMA - Journal of the American Medical Association*, **2007**, 297, 529-31	27.4	15
113	Expectation maximization algorithm based haplotype relative risk (EM-HRR): test of linkage disequilibrium using incomplete case-parents trios. *Human Heredity*, **2005**, 59, 125-35	1.1	15
112	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
111	Refined QTLs of osteoporosis-related traits by linkage analysis with genome-wide SNPs: Framingham SHARe. *Bone*, **2010**, 46, 1114-21	4.7	14
110	Handling linkage disequilibrium in qualitative trait linkage analysis using dense SNPs: a two-step strategy. *BMC Genetics*, **2009**, 10, 44	2.6	14
109	Variants at the endocannabinoid receptor CB1 gene (CNR1) and insulin sensitivity, type 2 diabetes, and coronary heart disease. *Obesity*, **2011**, 19, 2031-7	8	13
108	Exo-proofreading, a versatile SNP scoring technology. *Genome Research*, **2003**, 13, 925-31	9.7	13
107	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
106	Heritability and genome-wide association study of diffusing capacity of the lung. *European Respiratory Journal*, **2018**, 52,	13.6	12
105	Clinical correlates, heritability, and genetic linkage of circulating CD40 ligand in the Framingham Offspring Study. *American Heart Journal*, **2008**, 156, 1003-1009.e1	4.9	12
104	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
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