Josee Dupuis

List of Publications by Year in descending order

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281 papers	43,102 citations	5268 83 h-index	2684 193 g-index
300 all docs	300 docs citations	300 times ranked	52151 citing authors

#	Article	IF	Citations
1	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	27.8	6,140
2	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
3	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	21.4	1,748
4	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
5	Common genetic determinants of vitamin D insufficiency: a genome-wide association study. Lancet, The, 2010, 376, 180-188.	13.7	1,385
6	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.	21.4	1,331
7	Common variants at 30 loci contribute to polygenic dyslipidemia. Nature Genetics, 2009, 41, 56-65.	21.4	1,234
8	A Mutation in the LDL Receptorâ€“Related Protein 5 Gene Results in the Autosomal Dominant Highâ€“Bone-Mass Trait. American Journal of Human Genetics, 2002, 70, 11-19.	6.2	1,196
9	Association of the ADAM33 gene with asthma and bronchial hyperresponsiveness. Nature, 2002, 418, 426-430.	27.8	1,025
10	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
11	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
12	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
13	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	21.4	762
14	Causal Relationship between Obesity and Vitamin D Status: Bi-Directional Mendelian Randomization Analysis of Multiple Cohorts. PLoS Medicine, 2013, 10, e1001383.	8.4	753
15	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
16	Genotype Score in Addition to Common Risk Factors for Prediction of Type 2 Diabetes. New England Journal of Medicine, 2008, 359, 2208-2219.	27.0	696
17	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	21.4	662
18	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615

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19	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	21.4	591
20	Meta-Analysis of Genome-Wide Association Studies in >80 000 Subjects Identifies Multiple Loci for C-Reactive Protein Levels. Circulation, 2011, 123, 731-738.	1.6	461
21	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.	3.5	419
22	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.6	387
23	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
24	MUC5B Promoter Polymorphism and Interstitial Lung Abnormalities. New England Journal of Medicine, 2013, 368, 2192-2200.	27.0	358
25	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
26	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.	8.4	341
27	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
28	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, 2624-2634.	0.6	335
29	Association Between Interstitial Lung Abnormalities and All-Cause Mortality. JAMA - Journal of the American Medical Association, 2016, 315, 672.	7.4	333
30	Identifying SNPs predictive of phenotype using random forests. Genetic Epidemiology, 2005, 28, 171-182.	1.3	321
31	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2014, 2, 719-729.	11.4	319
32	Genetic loci associated with chronic obstructive pulmonary disease overlap with loci for lung function and pulmonary fibrosis. Nature Genetics, 2017, 49, 426-432.	21.4	306
33	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. Diabetes, 2014, 63, 2158-2171.	0.6	297
34	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. Nature Communications, 2018, 9, 260.	12.8	295
35	Statistical Methods for Mapping Quantitative Trait Loci From a Dense Set of Markers. Genetics, 1999, 151, 373-386.	2.9	266
36	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	8.8	251

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37	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
38	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
39	Detailed Physiologic Characterization Reveals Diverse Mechanisms for Novel Genetic Loci Regulating Glucose and Insulin Metabolism in Humans. Diabetes, 2010, 59, 1266-1275.	0.6	237
40	Large-scale genomic studies reveal central role of ABO in sP-selectin and sICAM-1 levels. Human Molecular Genetics, 2010, 19, 1863-1872.	2.9	233
41	Development and Progression of Interstitial Lung Abnormalities in the Framingham Heart Study. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 1514-1522.	5.6	233
42	Genome-wide association with bone mass and geometry in the Framingham Heart Study. BMC Medical Genetics, 2007, 8, S14.	2.1	232
43	NRXN3 Is a Novel Locus for Waist Circumference: A Genome-Wide Association Study from the CHARGE Consortium. PLoS Genetics, 2009, 5, e1000539.	3.5	230
44	Atrial Fibrillation. Circulation, 2011, 124, 1982-1993.	1.6	225
45	Genome-Wide Association Scan Identifies Candidate Polymorphisms Associated with Differential Response to Anti-TNF Treatment in Rheumatoid Arthritis. Molecular Medicine, 2008, 14, 575-581.	4.4	199
46	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197
47	Large scale replication and meta-analysis of variants on chromosome 4q25 associated with atrial fibrillation. European Heart Journal, 2008, 30, 813-819.	2.2	193
48	Sequence Kernel Association Test for Quantitative Traits in Family Samples. Genetic Epidemiology, 2013, 37, 196-204.	1.3	193
49	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
50	Whole exome sequencing study identifies novel rare and common Alzheimerâ€™s-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	7.9	191
51	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.	3.5	190
52	Poor Performance of Bootstrap Confidence Intervals for the Location of a Quantitative Trait Locus. Genetics, 2006, 174, 481-489.	2.9	184
53	Genetic variants at 2q24 are associated with susceptibility to type 2 diabetes. Human Molecular Genetics, 2010, 19, 2706-2715.	2.9	178
54	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173

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55	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
56	The Framingham Heart Study 100K SNP genome-wide association study resource: overview of 17 phenotype working group reports. BMC Medical Genetics, 2007, 8, S1.	2.1	169
57	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, 121-125.	8.6	165
58	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, 622-632.	5.6	164
59	A Method of Moments Estimator for Random Effect Multivariate Metaâ€Analysis. Biometrics, 2012, 68, 1278-1284.	1.4	159
60	Meta-analysis of gene-environment interaction: joint estimation of SNP and SNP Ã— environment regression coefficients. Genetic Epidemiology, 2011, 35, 11-18.	1.3	158
61	Genome-wide association to body mass index and waist circumference: the Framingham Heart Study 100K project. BMC Medical Genetics, 2007, 8, S18.	2.1	154
62	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. Genome Biology, 2017, 18, 16.	8.8	151
63	A Genome-Wide Association Study Reveals Variants in ARL15 that Influence Adiponectin Levels. PLoS Genetics, 2009, 5, e1000768.	3.5	148
64	Common Variants in the Adiponectin Gene (ADIPOQ) Associated With Plasma Adiponectin Levels, Type 2 Diabetes, and Diabetes-Related Quantitative Traits. Diabetes, 2008, 57, 3353-3359.	0.6	147
65	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, 412-420.	0.8	146
66	Transcript expression-aware annotation improves rare variant interpretation. Nature, 2020, 581, 452-458.	27.8	142
67	Relations of Inflammatory Biomarkers and Common Genetic Variants With Arterial Stiffness and Wave Reflection. Hypertension, 2008, 51, 1651-1657.	2.7	141
68	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
69	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. PLoS Genetics, 2012, 8, e1003098.	3.5	130
70	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, 2684-2691.	8.6	127
71	Polygenic Type 2 Diabetes Prediction at the Limit of Common Variant Detection. Diabetes, 2014, 63, 2172-2182.	0.6	127
72	Mendelian Randomization Studies Do Not Support a Causal Role for Reduced Circulating Adiponectin Levels in Insulin Resistance and Type 2 Diabetes. Diabetes, 2013, 62, 3589-3598.	0.6	116

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73	Duffy antigen receptor for chemokines (Darc) polymorphism regulates circulating concentrations of monocyte chemoattractant protein-1 and other inflammatory mediators. Blood, 2010, 115, 5289-5299.	1.4	113
74	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	28.9	113
75	Genome-wide association with select biomarker traits in the Framingham Heart Study. BMC Medical Genetics, 2007, 8, S11.	2.1	111
76	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, 587-596.	2.9	107
77	Association of Variants in RETN With Plasma Resistin Levels and Diabetes-Related Traits in the Framingham Offspring Study. Diabetes, 2009, 58, 750-756.	0.6	107
78	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	1.1	107
79	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	12.4	100
80	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, 2022, 71, 1095-1105.	12.1	98
81	Genome scan of systemic biomarkers of vascular inflammation in the Framingham Heart Study: Evidence for susceptibility loci on 1q. Atherosclerosis, 2005, 182, 307-314.	0.8	96
82	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.	3.5	95
83	Metabolomics insights into early type 2 diabetes pathogenesis and detection in individuals with normal fasting glucose. Diabetologia, 2018, 61, 1315-1324.	6.3	93
84	Total Zinc Intake May Modify the Glucose-Raising Effect of a Zinc Transporter (SLC30A8) Variant: A 14-Cohort Meta-analysis. Diabetes, 2011, 60, 2407-2416.	0.6	91
85	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, 238-251.	2.2	89
86	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	12.8	89
87	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, 3063-3074.	0.6	87
88	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, 408-418.	5.6	87
89	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
90	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	12.8	85

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91	Genome-wide association with diabetes-related traits in the Framingham Heart Study. BMC Medical Genetics, 2007, 8, S16.	2.1	80
92	Association of Variation at the ABO Locus With Circulating Levels of Soluble Intercellular Adhesion Molecule-1, Soluble P-selectin, and Soluble E-selectin. Circulation: Cardiovascular Genetics, 2011, 4, 681-686.	5.1	77
93	Overlap of Genetic Risk between Interstitial Lung Abnormalities and Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 1402-1413.	5.6	77
94	Epigenome-Wide Association Study of Incident Type 2 Diabetes in a British Population: EPIC-Norfolk Study. Diabetes, 2019, 68, 2315-2326.	0.6	77
95	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.	3.5	76
96	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, 103-115.	3.4	74
97	Heritability of Atrial Fibrillation. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	72
98	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci. Diabetes, 2016, 65, 3200-3211.	0.6	67
99	Galectin-3 Is Associated with Restrictive Lung Disease and Interstitial Lung Abnormalities. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 77-83.	5.6	66
100	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, 2581.	12.8	62
101	Transferability and Fine Mapping of Type 2 Diabetes Loci in African Americans. Diabetes, 2013, 62, 965-976.	0.6	59
102	The Relation of Genetic and Environmental Factors to Systemic Inflammatory Biomarker Concentrations. Circulation: Cardiovascular Genetics, 2009, 2, 229-237.	5.1	58
103	Sequence Kernel Association Test for Survival Traits. Genetic Epidemiology, 2014, 38, 191-197.	1.3	58
104	Normal thymus in adults: appearance on CT and associations with age, sex, BMI and smoking. European Radiology, 2016, 26, 15-24.	4.5	57
105	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	6.2	55
106	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. PLoS ONE, 2014, 9, e100776.	2.5	52
107	Mapping complex traits using Random Forests. BMC Genetics, 2003, 4, S64.	2.7	50
108	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	12.8	49

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109	Pulmonary cysts identified on chest CT: are they part of aging change or of clinical significance?. Thorax, 2015, 70, 1156-1162.	5.6	48
110	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
111	Anterior mediastinal masses in the Framingham Heart Study: Prevalence and CT image characteristics. European Journal of Radiology Open, 2015, 2, 26-31.	1.6	46
112	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, 113-125.	3.8	45
113	Genome-wide study identifies two loci associated with lung function decline in mild to moderate COPD. Human Genetics, 2013, 132, 79-90.	3.8	45
114	Genetically Driven Hyperglycemia Increases Risk of Coronary Artery Disease Separately From Type 2 Diabetes. Diabetes Care, 2017, 40, 687-693.	8.6	45
115	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, .	5.1	45
116	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, 1137-1143.	3.6	44
117	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.	7.9	44
118	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.	6.2	44
119	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, 1971-1977.	0.6	42
120	Paraseptal emphysema: Prevalence and distribution on CT and association with interstitial lung abnormalities. European Journal of Radiology, 2015, 84, 1413-1418.	2.6	42
121	Integrative Omics Approach to Identifying Genes Associated With Atrial Fibrillation. Circulation Research, 2020, 126, 350-360.	4.5	41
122	Correction for multiple testing in a gene region. European Journal of Human Genetics, 2014, 22, 414-418.	2.8	39
123	A comparison of visual and quantitative methods to identify interstitial lung abnormalities. BMC Pulmonary Medicine, 2015, 15, 134.	2.0	39
124	Type 2 Diabetes Genetic Predisposition, Obesity, and All-Cause Mortality Risk in the U.S.: A Multiethnic Analysis. Diabetes Care, 2016, 39, 539-546.	8.6	38
125	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.	3.7	38
126	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	36

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127	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571.	2.9	36
128	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	1.9	36
129	Incorporating Gene-Environment Interaction in Testing for Association with Rare Genetic Variants. Human Heredity, 2014, 78, 81-90.	0.8	35
130	Association of Circulating Monocyte Chemoattractant Proteinâ€“1 Levels With Cardiovascular Mortality. JAMA Cardiology, 2021, 6, 587.	6.1	35
131	The Association of Aging Biomarkers, Interstitial Lung Abnormalities, and Mortality. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 1149-1157.	5.6	35
132	The Type 2 Deiodinase (DIO2) A/G Polymorphism Is Not Associated with Glycemic Traits: The Framingham Heart Study. Thyroid, 2007, 17, 199-202.	4.5	34
133	Clinical and genetic factors associated with lipoprotein-associated phospholipase A2 in the Framingham Heart Study. Atherosclerosis, 2009, 204, 601-607.	0.8	34
134	Whole genome sequence analyses of brain imaging measures in the Framingham Study. Neurology, 2018, 90, e188-e196.	1.1	34
135	Genome-Wide Association Study Evaluating Lipoprotein-Associated Phospholipase A ₂ Mass and Activity at Baseline and After Rosuvastatin Therapy. Circulation: Cardiovascular Genetics, 2012, 5, 676-685.	5.1	33
136	Shared genetic susceptibility of vascular-related biomarkers with ischemic and recurrent stroke. Neurology, 2016, 86, 351-359.	1.1	33
137	Transethnic Evaluation Identifies Low-Frequency Loci Associated With 25-Hydroxyvitamin D Concentrations. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 1380-1392.	3.6	33
138	Mendelian Randomization Analysis of Hemoglobin A1c as a Risk Factor for Coronary Artery Disease. Diabetes Care, 2019, 42, 1202-1208.	8.6	33
139	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.	6.3	32
140	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	12.8	32
141	Impact of Common Variation in Bone-Related Genes on Type 2 Diabetes and Related Traits. Diabetes, 2012, 61, 2176-2186.	0.6	31
142	Large multiethnic Candidate Gene Study for C-reactive protein levels: identification of a novel association at CD36 in African Americans. Human Genetics, 2014, 133, 985-995.	3.8	31
143	Genome-wide association study of subclinical interstitial lung disease in MESA. Respiratory Research, 2017, 18, 97.	3.6	31
144	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31

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145	Diurnal variation of serum alanine transaminase activity in chronic liver disease. Hepatology, 1998, 28, 1724-1725.	7.3	29
146	Variants in the CNR1 and the FAAH Genes and Adiposity Traits in the Community. Obesity, 2009, 17, 755-760.	3.0	29
147	Structured mating: Patterns and implications. PLoS Genetics, 2017, 13, e1006655.	3.5	29
148	Type 2 Diabetes Partitioned Polygenic Scores Associate With Disease Outcomes in 454,193 Individuals Across 13 Cohorts. Diabetes Care, 2022, 45, 674-683.	8.6	29
149	PAI-1 Gene 4G/5G Polymorphism and Risk of Type 2 Diabetes in a Population-based Sample*. Obesity, 2006, 14, 753-758.	3.0	28
150	Integrative pathway genomics of lung function and airflow obstruction. Human Molecular Genetics, 2015, 24, 6836-6848.	2.9	28
151	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.	2.9	28
152	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.	7.1	28
153	Quality of dietary fat and genetic risk of type 2 diabetes: individual participant data meta-analysis. BMJ: British Medical Journal, 2019, 366, l4292.	2.3	28
154	Childhood Tobacco Smoke Exposure and Risk of Atrial Fibrillation in Adulthood. Journal of the American College of Cardiology, 2019, 74, 1658-1664.	2.8	27
155	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.	2.9	26
156	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, 1127-1133.	2.6	25
157	Whole blood gene expression and interleukin-6 levels. Genomics, 2014, 104, 490-495.	2.9	24
158	Comparison of methods for multivariate gene-based association tests for complex diseases using common variants. European Journal of Human Genetics, 2019, 27, 811-823.	2.8	24
159	United States Research Published in Major Surgical Journals Is Decreasing. Annals of Surgery, 1995, 222, 263-269.	4.2	23
160	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.	3.5	23
161	No Interactions Between Previously Associated 2-Hour Glucose Gene Variants and Physical Activity or BMI on 2-Hour Glucose Levels. Diabetes, 2012, 61, 1291-1296.	0.6	23
162	Whole Blood Gene Expression and Atrial Fibrillation: The Framingham Heart Study. PLoS ONE, 2014, 9, e96794.	2.5	23

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163	Gene expression markers of age-related inflammation in two human cohorts. Experimental Gerontology, 2015, 70, 37-45.	2.8	23
164	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.	3.5	23
165	Genome-wide and gene-centric analyses of circulating myeloperoxidase levels in the charge and care consortia. Human Molecular Genetics, 2013, 22, 3381-3393.	2.9	22
166	Peripheral Blood Transcriptomic Signatures of Fasting Glucose and Insulin Concentrations. Diabetes, 2016, 65, 3794-3804.	0.6	22
167	Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits. Nature Human Behaviour, 2022, 6, 155-163.	12.0	22
168	Interpreting Results of Large-Scale Genetic Association Studies. JAMA - Journal of the American Medical Association, 2007, 297, 529.	7.4	21
169	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	2.9	21
170	Racial/Ethnic Differences in Association of Fasting Glucoseâ€“Associated Genomic Loci With Fasting Glucose, HOMA-B, and Impaired Fasting Glucose in the U.S. Adult Population. Diabetes Care, 2010, 33, 2370-2377.	8.6	20
171	Increased Airway Wall Thickness in Interstitial Lung Abnormalities and Idiopathic Pulmonary Fibrosis. Annals of the American Thoracic Society, 2019, 16, 447-454.	3.2	20
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