

Inga Prokopenko

List of Publications by Year in descending order

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Version: 2024-02-01

160
papers

52,330
citations

4658

85
h-index

4885

168
g-index

181
all docs

181
docs citations

181
times ranked

48345
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
2	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	21.4	2,634
3	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	21.4	1,982
4	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	27.8	1,855
5	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	21.4	1,818
6	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	27.8	1,789
7	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	21.4	1,748
8	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. <i>Nature Genetics</i> , 2008, 40, 638-645.	21.4	1,683
9	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010, 42, 579-589.	21.4	1,631
10	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. <i>Nature Genetics</i> , 2009, 41, 25-34.	21.4	1,572
11	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328
12	Common variants near MC4R are associated with fat mass, weight and risk of obesity. <i>Nature Genetics</i> , 2008, 40, 768-775.	21.4	1,179
13	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	21.4	959
14	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	27.8	952
15	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	21.4	836
16	Identification of seven loci affecting mean telomere length and their association with disease. <i>Nature Genetics</i> , 2013, 45, 422-427.	21.4	808
17	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycaemic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	21.4	762
18	Large-scale association analyses identify new loci influencing glycaemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012, 44, 991-1005.	21.4	746

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19	Genome-wide association analysis identifies 20 loci that influence adult height. <i>Nature Genetics</i> , 2008, 40, 575-583.	21.4	742
20	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. <i>Nature</i> , 2010, 464, 713-720.	27.8	737
21	New loci associated with kidney function and chronic kidney disease. <i>Nature Genetics</i> , 2010, 42, 376-384.	21.4	710
22	Biological interpretation of genome-wide association studies using predicted gene functions. <i>Nature Communications</i> , 2015, 6, 5890.	12.8	706
23	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	21.4	675
24	Variants in MTNR1B influence fasting glucose levels. <i>Nature Genetics</i> , 2009, 41, 77-81.	21.4	662
25	Sequence variants at CHRN3, CHRNA6 and CYP2A6 affect smoking behavior. <i>Nature Genetics</i> , 2010, 42, 448-453.	21.4	649
26	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	0.6	615
27	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. <i>Nature Genetics</i> , 2010, 42, 142-148.	21.4	591
28	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	21.4	578
29	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011, 43, 1131-1138.	21.4	501
30	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2011, 43, 984-989.	21.4	481
31	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. <i>PLoS Genetics</i> , 2009, 5, e1000508.	3.5	453
32	The MetaboChip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. <i>PLoS Genetics</i> , 2012, 8, e1002793.	3.5	448
33	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. <i>PLoS Genetics</i> , 2012, 8, e1002607.	3.5	419
34	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	12.8	412
35	Genome-wide associations for birth weight and correlations with adult disease. <i>Nature</i> , 2016, 538, 248-252.	27.8	406
36	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019, 51, 804-814.	21.4	402

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37	New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , 2011, 480, 201-208.	27.8	401
38	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. <i>Diabetes</i> , 2010, 59, 3229-3239.	0.6	387
39	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	27.8	383
40	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	3.5	371
41	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	21.4	365
42	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. <i>PLoS Medicine</i> , 2017, 14, e1002383.	8.4	341
43	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
44	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. <i>Diabetes</i> , 2011, 60, 2624-2634.	0.6	335
45	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	3.5	331
46	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	27.8	320
47	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015, 47, 589-597.	21.4	310
48	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. <i>Diabetes</i> , 2014, 63, 2158-2171.	0.6	297
49	Plasma Protein Biomarkers for Depression and Schizophrenia by Multi Analyte Profiling of Case-Control Collections. <i>PLoS ONE</i> , 2010, 5, e9166.	2.5	294
50	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. <i>Nature Genetics</i> , 2013, 45, 76-82.	21.4	293
51	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. <i>PLoS Genetics</i> , 2010, 6, e1000916.	3.5	287
52	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	21.4	284
53	Identification of rare sequence variation underlying heritable pulmonary arterial hypertension. <i>Nature Communications</i> , 2018, 9, 1416.	12.8	279
54	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7119-7124.	7.1	258

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55	Genetic loci influencing kidney function and chronic kidney disease. <i>Nature Genetics</i> , 2010, 42, 373-375.	21.4	246
56	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	12.8	245
57	Detailed Physiologic Characterization Reveals Diverse Mechanisms for Novel Genetic Loci Regulating Glucose and Insulin Metabolism in Humans. <i>Diabetes</i> , 2010, 59, 1266-1275.	0.6	237
58	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656.	7.9	235
59	Type 2 diabetes: new genes, new understanding. <i>Trends in Genetics</i> , 2008, 24, 613-621.	6.7	229
60	Variants in <i>ADCY5</i> and near <i>CCNL1</i> are associated with fetal growth and birth weight. <i>Nature Genetics</i> , 2010, 42, 430-435.	21.4	223
61	Integrated Genetic and Epigenetic Analysis Identifies Haplotype-Specific Methylation in the <i>FTO</i> Type 2 Diabetes and Obesity Susceptibility Locus. <i>PLoS ONE</i> , 2010, 5, e14040.	2.5	215
62	<i>CUBN</i> Is a Gene Locus for Albuminuria. <i>Journal of the American Society of Nephrology: JASN</i> , 2011, 22, 555-570.	6.1	208
63	Human pancreatic islet three-dimensional chromatin architecture provides insights into the genetics of type 2 diabetes. <i>Nature Genetics</i> , 2019, 51, 1137-1148.	21.4	208
64	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. <i>PLoS ONE</i> , 2012, 7, e29202.	2.5	197
65	Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in <i>LAMA1</i> and Enrichment for Risk Variants in Lean Compared to Obese Cases. <i>PLoS Genetics</i> , 2012, 8, e1002741.	3.5	190
66	Genome-wide association and longitudinal analyses reveal genetic loci linking pubertal height growth, pubertal timing and childhood adiposity. <i>Human Molecular Genetics</i> , 2013, 22, 2735-2747.	2.9	188
67	Abdominal Aortic Aneurysm Is Associated with a Variant in Low-Density Lipoprotein Receptor-Related Protein 1. <i>American Journal of Human Genetics</i> , 2011, 89, 619-627.	6.2	185
68	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. <i>PLoS Medicine</i> , 2013, 10, e1001474.	8.4	178
69	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	27.8	173
70	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. <i>Human Molecular Genetics</i> , 2011, 20, 2273-2284.	2.9	168
71	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. <i>PLoS Genetics</i> , 2012, 8, e1002584.	3.5	166
72	A Central Role for <i>GRB10</i> in Regulation of Islet Function in Man. <i>PLoS Genetics</i> , 2014, 10, e1004235.	3.5	164

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73	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
74	A Genome-Wide Association Meta-Analysis of Circulating Sex Hormoneâ€“Binding Globulin Reveals Multiple Loci Implicated in Sex Steroid Hormone Regulation. PLoS Genetics, 2012, 8, e1002805.	3.5	151
75	A Genome-Wide Association Study Reveals Variants in ARL15 that Influence Adiponectin Levels. PLoS Genetics, 2009, 5, e1000768.	3.5	148
76	Common variants at 12q15 and 12q24 are associated with infant head circumference. Nature Genetics, 2012, 44, 532-538.	21.4	130
77	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
78	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	1.9	123
79	Genetic determinants of risk in pulmonary arterial hypertension: international genome-wide association studies and meta-analysis. Lancet Respiratory Medicine, the, 2019, 7, 227-238.	10.7	122
80	Sequence variants at CYP1A1â€“CYP1A2 and AHR associate with coffee consumption. Human Molecular Genetics, 2011, 20, 2071-2077.	2.9	114
81	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	28.9	113
82	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	1.1	107
83	Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113.	3.5	106
84	Association of Genetic Loci With Glucose Levels in Childhood and Adolescence. Diabetes, 2011, 60, 1805-1812.	0.6	103
85	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
86	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
87	Genomics of body fat percentage may contribute to sex bias in anorexia nervosa. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 428-438.	1.7	87
88	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
89	CWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. Science Advances, 2019, 5, eaaw3095.	10.3	86
90	Genome-wide association study of primary tooth eruption identifies pleiotropic loci associated with height and craniofacial distances. Human Molecular Genetics, 2013, 22, 3807-3817.	2.9	84

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91	Genomewide meta-analysis identifies loci associated with IGF and IGFBP levels with impact on age-related traits. <i>Aging Cell</i> , 2016, 15, 811-824.	6.7	83
92	Association of FTO variants with BMI and fat mass in the self-contained population of Sorbs in Germany. <i>European Journal of Human Genetics</i> , 2010, 18, 104-110.	2.8	81
93	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. <i>PLoS Genetics</i> , 2014, 10, e1004508.	3.5	80
94	Characterization of GDF2 Mutations and Levels of BMP9 and BMP10 in Pulmonary Arterial Hypertension. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 201, 575-585.	5.6	80
95	Evidence of Inbreeding Depression on Human Height. <i>PLoS Genetics</i> , 2012, 8, e1002655.	3.5	79
96	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2021, 5, 59-70.	12.0	79
97	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. <i>PLoS Genetics</i> , 2015, 11, e1005230.	3.5	77
98	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. <i>American Journal of Epidemiology</i> , 2013, 177, 103-115.	3.4	74
99	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	12.8	74
100	Revisiting the Thrifty Gene Hypothesis via 65 Loci Associated with Susceptibility to Type 2 Diabetes. <i>American Journal of Human Genetics</i> , 2014, 94, 176-185.	6.2	72
101	Genome-wide enrichment analysis between endometriosis and obesity-related traits reveals novel susceptibility loci. <i>Human Molecular Genetics</i> , 2015, 24, 1185-1199.	2.9	71
102	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci. <i>Diabetes</i> , 2016, 65, 3200-3211.	0.6	67
103	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. <i>Human Molecular Genetics</i> , 2012, 21, 5329-5343.	2.9	64
104	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. <i>Diabetes</i> , 2015, 64, 1841-1852.	0.6	63
105	Evidence for three genetic loci involved in both anorexia nervosa risk and variation of body mass index. <i>Molecular Psychiatry</i> , 2017, 22, 192-201.	7.9	63
106	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. <i>American Journal of Human Genetics</i> , 2013, 93, 236-248.	6.2	60
107	Genetic Determinants of Circulating Estrogen Levels and Evidence of a Causal Effect of Estradiol on Bone Density in Men. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 991-1004.	3.6	60
108	Genetic correlations of psychiatric traits with body composition and glycemic traits are sex- and age-dependent. <i>Nature Communications</i> , 2019, 10, 5765.	12.8	59

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109	Obesity-susceptibility loci have a limited influence on birth weight: a meta-analysis of up to 28,219 individuals. <i>American Journal of Clinical Nutrition</i> , 2011, 93, 851-860.	4.7	58
110	Family history of depression is associated with younger age of onset in patients with recurrent depression. <i>Psychological Medicine</i> , 2008, 38, 641-649.	4.5	53
111	A common biological basis of obesity and nicotine addiction. <i>Translational Psychiatry</i> , 2013, 3, e308-e308.	4.8	51
112	Higher Magnesium Intake Is Associated with Lower Fasting Glucose and Insulin, with No Evidence of Interaction with Select Genetic Loci, in a Meta-Analysis of 15 CHARGE Consortium Studies. <i>Journal of Nutrition</i> , 2013, 143, 345-353.	2.9	47
113	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	0.6	47
114	Whole-Blood RNA Profiles Associated with Pulmonary Arterial Hypertension and Clinical Outcome. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 586-594.	5.6	45
115	miRNAs Identify Shared Pathways in Alzheimer's and Parkinson's Diseases. <i>Trends in Molecular Medicine</i> , 2019, 25, 662-672.	6.7	44
116	Expression of Phosphofruktokinase in Skeletal Muscle Is Influenced by Genetic Variation and Associated With Insulin Sensitivity. <i>Diabetes</i> , 2014, 63, 1154-1165.	0.6	41
117	Insights into the Genetic Susceptibility to Type 2 Diabetes from Genome-Wide Association Studies of Glycaemic Traits. <i>Current Diabetes Reports</i> , 2014, 14, 551.	4.2	38
118	The use of polygenic risk scores in pre-implantation genetic testing: an unproven, unethical practice. <i>European Journal of Human Genetics</i> , 2022, 30, 493-495.	2.8	38
119	Association between the <i>ACCN1</i> Gene and Multiple Sclerosis in Central East Sardinia. <i>PLoS ONE</i> , 2007, 2, e480.	2.5	36
120	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2013, 24, 2105-2117.	6.1	33
121	Genome Wide Meta-analysis Highlights the Role of Genetic Variation in <i>RARRES2</i> in the Regulation of Circulating Serum Chemerin. <i>PLoS Genetics</i> , 2014, 10, e1004854.	3.5	31
122	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	5.3	31
123	Linkage Disequilibrium Mapping of the Replicated Type 2 Diabetes Linkage Signal on Chromosome 1q. <i>Diabetes</i> , 2009, 58, 1704-1709.	0.6	30
124	A Genome-Wide Screen for Interactions Reveals a New Locus on 4p15 Modifying the Effect of Waist-to-Hip Ratio on Total Cholesterol. <i>PLoS Genetics</i> , 2011, 7, e1002333.	3.5	29
125	Harmonising and linking biomedical and clinical data across disparate data archives to enable integrative cross-biobank research. <i>European Journal of Human Genetics</i> , 2016, 24, 521-528.	2.8	27
126	Mendelian randomisation analysis of red cell distribution width in pulmonary arterial hypertension. <i>European Respiratory Journal</i> , 2020, 55, 1901486.	6.7	26

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127	SCOPA and META-SCOPA: software for the analysis and aggregation of genome-wide association studies of multiple correlated phenotypes. <i>BMC Bioinformatics</i> , 2017, 18, 25.	2.6	25
128	Genome-Wide Association Study Identifies Two Novel Regions at 11p15.5-p13 and 1p31 with Major Impact on Acute-Phase Serum Amyloid A. <i>PLoS Genetics</i> , 2010, 6, e1001213.	3.5	24
129	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. <i>American Journal of Human Genetics</i> , 2014, 94, 710-720.	6.2	24
130	No Interactions Between Previously Associated 2-Hour Glucose Gene Variants and Physical Activity or BMI on 2-Hour Glucose Levels. <i>Diabetes</i> , 2012, 61, 1291-1296.	0.6	23
131	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. <i>American Journal of Human Genetics</i> , 2016, 98, 857-868.	6.2	21
132	Multiple sclerosis recurrence risk for siblings in an isolated population of Central Sardinia, Italy. <i>Genetic Epidemiology</i> , 2002, 22, 265-271.	1.3	19
133	Exploring the role of genetic confounding in the association between maternal and offspring body mass index: evidence from three birth cohorts. <i>International Journal of Epidemiology</i> , 2020, 49, 233-243.	1.9	18
134	MARV: a tool for genome-wide multi-phenotype analysis of rare variants. <i>BMC Bioinformatics</i> , 2017, 18, 110.	2.6	17
135	A rare-variant test for high-dimensional data. <i>European Journal of Human Genetics</i> , 2017, 25, 988-994.	2.8	15
136	Genome-wide meta-analysis identifies novel determinants of circulating serum progranulin. <i>Human Molecular Genetics</i> , 2018, 27, 546-558.	2.9	15
137	SAIL—a software system for sample and phenotype availability across biobanks and cohorts. <i>Bioinformatics</i> , 2011, 27, 589-591.	4.1	14
138	Alzheimer's disease pathology explains association between dementia with Lewy bodies and APOE ϵ ₄ /TOMM40 long poly ϵ ₃ repeat allele variants. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , 2019, 5, 814-824.	3.7	14
139	Risk for Relatives of Patients with Multiple Sclerosis in Central Sardinia, Italy. <i>Neuroepidemiology</i> , 2003, 22, 290-296.	2.3	13
140	A new strategy for enhancing imputation quality of rare variants from next-generation sequencing data via combining SNP and exome chip data. <i>BMC Genomics</i> , 2015, 16, 1109.	2.8	13
141	<i>Bifidobacterium</i> Is Enriched in Gut Microbiome of Kashmiri Women with Polycystic Ovary Syndrome. <i>Genes</i> , 2022, 13, 379.	2.4	13
142	Understanding the complexity of glycaemic health: systematic bio-psychosocial modelling of fasting glucose in middle-age adults; a DynaHEALTH study. <i>International Journal of Obesity</i> , 2019, 43, 1181-1192.	3.4	11
143	Cohort Profile: The DynaHEALTH consortium — a European consortium for a life-course bio-psychosocial model of healthy ageing of glucose homeostasis. <i>International Journal of Epidemiology</i> , 2019, 48, 1051-1051k.	1.9	10
144	Relationship between glucose homeostasis and obesity in early life—a study of Italian children and adolescents. <i>Human Molecular Genetics</i> , 2022, 31, 816-826.	2.9	10

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145	Prevalence and Regional Distribution of Autoantibodies Against GAD65Ab in a European Population Without Diabetes: The EPIC-InterAct Study. <i>Diabetes Care</i> , 2015, 38, e114-e115.	8.6	8
146	Genome-Wide Association Studies of Type 2 Diabetes. , 2016, , 13-61.		8
147	Associations between TOMM40 Poly-T Repeat Variants and Dementia in Cases with Parkinsonism. <i>Journal of Parkinson's Disease</i> , 2016, 6, 99-108.	2.8	6
148	Heterogeneous Effects of Calorie Content and Nutritional Components Underlie Dietary Influence on Pancreatic Cancer Susceptibility. <i>Cell Reports</i> , 2020, 32, 107880.	6.4	6
149	Risk of Recurrent Pregnancy Loss in the Ukrainian Population Using a Combined Effect of Genetic Variants: A Case-Control Study. <i>Genes</i> , 2021, 12, 64.	2.4	6
150	Functional Effects In Silico Prediction for Androgen Receptor Ligand-Binding Domain Novel I836S Mutation. <i>Life</i> , 2021, 11, 659.	2.4	6
151	The Role of the European Society of Human Genetics in Delivering Genomic Education. <i>Frontiers in Genetics</i> , 2021, 12, 693952.	2.3	6
152	LongITools: Dynamic longitudinal exposome trajectories in cardiovascular and metabolic noncommunicable diseases. <i>Environmental Epidemiology</i> , 2022, 6, e184.	3.0	6
153	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. <i>Scientific Reports</i> , 2019, 9, 9439.	3.3	5
154	Understanding the cumulative risk of maternal prenatal biopsychosocial factors on birth weight: a DynaHEALTH study on two birth cohorts. <i>Journal of Epidemiology and Community Health</i> , 2020, 74, jech-2019-213154.	3.7	5
155	Measurement invariance testing of the patient health questionnaire-9 (PHQ-9) across people with and without diabetes mellitus from the NHANES, EMHS and UK Biobank datasets. <i>Journal of Affective Disorders</i> , 2021, 292, 311-318.	4.1	5
156	Multilocus associations of inflammatory genes with the risk of type 1 diabetes. <i>Gene</i> , 2019, 707, 1-8.	2.2	4
157	Expression Quantitative Trait Locus Mapping in Pulmonary Arterial Hypertension. <i>Genes</i> , 2020, 11, 1247.	2.4	3
158	The TAD-pathway for GWAS signals. <i>European Journal of Human Genetics</i> , 2017, 25, 1179-1180.	2.8	2
159	1A.11. <i>Journal of Hypertension</i> , 2015, 33, e3-e4.	0.5	1
160	A meta-analysis of Italian and Estonian individuals shows an effect of common variants in HMGCR on blood apoB levels. <i>Biomarkers in Medicine</i> , 2019, 13, 931-940.	1.4	0