

Cecilia M Lindgren

List of PR Articles by Year in descending order

Source: [//exaly.com/author-pdf/4743154/publications.pdf](https://exaly.com/author-pdf/4743154/publications.pdf)

Version: 2025-02-01

203

PR articles

62,146

PR citations

1597

92

PR h-index

1403

198

g-index

234

documents

87267

doc citations

1135

108

h-index

87415

citing authors

#	ARTICLE	IF	PR CITATIONS
1	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. <i>Nature Genetics</i> , 2022, 54, 18-29.	26.1	130
2	Making sense of the linear genome, gene function and TADs. <i>Epigenetics and Chromatin</i> , 2022, 15, .	3.3	41
3	Obesity and risk of female reproductive conditions: A Mendelian randomisation study. <i>PLoS Medicine</i> , 2022, 19, e1003679.	8.5	149
4	Evidence From Men for Ovary-independent Effects of Genetic Risk Factors for Polycystic Ovary Syndrome. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, e1577-e1587.	4.2	32
5	Multi-ancestry genome-wide association study of gestational diabetes mellitus highlights genetic links with type 2 diabetes. <i>Human Molecular Genetics</i> , 2022, 31, 3377-3391.	3.0	104
6	Broad-spectrum Antidote Discovery by Untangling the Reactivation Mechanism of Nerve-agent-inhibited Acetylcholinesterase. <i>Chemistry - A European Journal</i> , 2022, 28, .	3.4	7
7	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	26.1	616
8	Transcriptome and fatty-acid signatures of adipocyte hypertrophy and its non-invasive MR-based characterization in human adipose tissue. <i>EBioMedicine</i> , 2022, 79, 104020.	9.9	43
9	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. <i>Kidney International</i> , 2022, 102, 624-639.	5.0	46
10	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022, 5, .	4.4	31
11	Sex Differences in the Risk of Coronary Heart Disease Associated With Type 2 Diabetes: A Mendelian Randomization Analysis. <i>Diabetes Care</i> , 2021, 44, 556-562.	6.5	32
12	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, .	13.9	132
13	A regulatory variant at 3q21.1 confers an increased pleiotropic risk for hyperglycemia and altered bone mineral density. <i>Cell Metabolism</i> , 2021, 33, 615-628.e13.	26.2	42
14	Colocalization analysis of polycystic ovary syndrome to identify potential disease-mediating genes and proteins. <i>European Journal of Human Genetics</i> , 2021, 29, 1446-1454.	3.2	20
15	The trans-ancestral genomic architecture of glycemc traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	26.1	650
16	A distribution-centered approach for analyzing human adipocyte size estimates and their association with obesity-related traits and mitochondrial function. <i>International Journal of Obesity</i> , 2021, 45, 2108-2117.	3.2	27
17	Linking the <i>FTO</i> obesity rs1421085 variant circuitry to cellular, metabolic, and organismal phenotypes in vivo. <i>Science Advances</i> , 2021, 7, .	11.0	32
18	The genomics of heart failure: design and rationale of the HERMES consortium. <i>ESC Heart Failure</i> , 2021, 8, 5531-5541.	3.3	21

#	ARTICLE	IF	PR CITATIONS
19	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020, 11, .	13.9	745
20	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, 1918-1936.	4.2	54
21	A brief history of human disease genetics. <i>Nature</i> , 2020, 577, 179-189.	38.7	642
22	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148.	17.7	609
23	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020, 52, 1314-1332.	26.1	167
24	The genetic architecture of sporadic and multiple consecutive miscarriage. <i>Nature Communications</i> , 2020, 11, .	13.9	97
25	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. <i>Diabetes</i> , 2020, 69, 2806-2818.	4.4	52
26	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits. <i>PLoS Computational Biology</i> , 2020, 16, e1008044.	3.1	31
27	Corrigendum to "Genome-wide association study of adipocyte lipolysis in the GENetics of adipocyte lipolysis (GENiAL) cohort" [Molecular Metabolism 34 (2020) 85-96]. <i>Molecular Metabolism</i> , 2020, 41, 101072.	6.0	0
28	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, .	13.9	105
29	Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics. <i>Science Translational Medicine</i> , 2020, 12, .	12.7	101
30	Genome-wide association study of adipocyte lipolysis in the GENetics of adipocyte lipolysis (GENiAL) cohort. <i>Molecular Metabolism</i> , 2020, 34, 85-96.	6.0	15
31	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2020, 5, 59-70.	10.5	126
32	Genome-wide Study Identifies Association between HLA-B*55:01 and Self-Reported Penicillin Allergy. <i>American Journal of Human Genetics</i> , 2020, 107, 612-621.	6.5	54
33	Disentangling the genetics of lean mass. <i>American Journal of Clinical Nutrition</i> , 2019, 109, 276-287.	4.9	47
34	Causal relationships between obesity and the leading causes of death in women and men. <i>PLoS Genetics</i> , 2019, 15, e1008405.	3.3	158
35	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, .	13.9	207
36	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. <i>American Journal of Human Genetics</i> , 2019, 105, 15-28.	6.5	23

#	ARTICLE	IF	PR CITATIONS
37	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	26.1	796
38	MicroRNA-196a links human body fat distribution to adipose tissue extracellular matrix composition. <i>EBioMedicine</i> , 2019, 44, 467-475.	9.9	30
39	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	26.1	106
40	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. <i>Nature Communications</i> , 2019, 10, .	13.9	136
41	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. <i>Journal of the American College of Cardiology</i> , 2019, 73, 58-66.	2.4	180
42	Cerebrospinal fluid lactate and neurological outcome after subarachnoid haemorrhage. <i>Journal of Clinical Neuroscience</i> , 2019, 60, 63-67.	1.6	7
43	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry. <i>Human Molecular Genetics</i> , 2019, 28, 166-174.	3.0	1,111
44	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	26.1	429
45	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. <i>Nature Communications</i> , 2018, 9, .	13.9	66
46	Dynamics Determine Signaling in a Multicomponent System Associated with Rheumatoid Arthritis. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 4774-4790.	5.6	5
47	A genome-wide association study of IgM antibody against phosphorylcholine: shared genetics and phenotypic relationship to chronic lymphocytic leukemia. <i>Human Molecular Genetics</i> , 2018, 27, 1809-1818.	3.0	6
48	A Partial Loss-of-Function Variant in <i>AKT2</i> Is Associated With Reduced Insulin-Mediated Glucose Uptake in Multiple Insulin-Sensitive Tissues: A Genotype-Based Callback Positron Emission Tomography Study. <i>Diabetes</i> , 2018, 67, 334-342.	4.4	43
49	GWAS identifies 14 loci for device-measured physical activity and sleep duration. <i>Nature Communications</i> , 2018, 9, .	13.9	335
50	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. <i>PLoS Genetics</i> , 2018, 14, e1007813.	3.3	472
51	Genome-Wide Association Studies of Estimated Fatty Acid Desaturase Activity in Serum and Adipose Tissue in Elderly Individuals: Associations with Insulin Sensitivity. <i>Nutrients</i> , 2018, 10, 1791.	4.7	28
52	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018, 50, 1505-1513.	26.1	1,673
53	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	6.5	416
54	Noncovalent Inhibitors of Mosquito Acetylcholinesterase 1 with Resistance-Breaking Potency. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 10545-10557.	5.6	20

#	ARTICLE	IF	PR CITATIONS
55	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	26.1	1,300
56	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. <i>Nature Genetics</i> , 2018, 51, 51-62.	26.1	431
57	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018, 50, 524-537.	26.1	1,550
58	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	26.1	573
59	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	38.7	612
60	Sexual dimorphisms in genetic loci linked to body fat distribution. <i>Bioscience Reports</i> , 2017, 37, .	4.0	74
61	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, .	13.9	198
62	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. <i>Nature Communications</i> , 2017, 8, .	13.9	114
63	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 865-884.	6.5	171
64	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	4.4	717
65	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.	4.4	51
66	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475,000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	3.9	52
67	The genetic underpinnings of body fat distribution. <i>Expert Review of Endocrinology and Metabolism</i> , 2017, 12, 417-427.	3.1	3
68	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017, 8, .	13.9	168
69	Variability of genome-wide DNA methylation and mRNA expression profiles in reproductive and endocrine disease related tissues. <i>Epigenetics</i> , 2017, 12, 897-908.	3.1	40
70	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. <i>Nature Communications</i> , 2017, 8, .	13.9	192
71	Genetic and methylation variation in the <i>CYP2B6</i> gene is related to circulating p,de levels in a population-based sample. <i>Environment International</i> , 2017, 98, 212-218.	10.3	8
72	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, .	5.7	36

#	ARTICLE	IF	PR CITATIONS
73	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2017, 50, 26-41.	26.1	387
74	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017, 127, 1798-1812.	10.7	126
75	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	3.3	181
76	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. <i>PLoS Genetics</i> , 2017, 13, e1006706.	3.3	336
77	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. <i>PLoS Genetics</i> , 2017, 13, e1006812.	3.3	30
78	Leptin levels after subarachnoid haemorrhage are gender dependent. <i>SpringerPlus</i> , 2016, 5, .	1.5	1
79	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	38.7	1,051
80	Mosaic Loss of Chromosome Y in Blood Is Associated with Alzheimer Disease. <i>American Journal of Human Genetics</i> , 2016, 98, 1208-1219.	6.5	238
81	Ovarian Physiology and GWAS: Biobanks, Biology, and Beyond. <i>Trends in Endocrinology and Metabolism</i> , 2016, 27, 516-528.	8.8	10
82	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , The, 2016, 15, 695-707.	18.4	153
83	Obesity â€• On or Off?. <i>New England Journal of Medicine</i> , 2016, 374, 1486-1488.	43.7	7
84	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.	6.5	24
85	Imprinted Genes and Imprinting Control Regions Show Predominant Intermediate Methylation in Adult Somatic Tissues. <i>Epigenomics</i> , 2016, 8, 789-799.	2.3	46
86	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. <i>American Journal of Human Genetics</i> , 2016, 99, 636-646.	6.5	72
87	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, .	13.9	90
88	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	26.1	298
89	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies <i>BCL2</i> and <i>FAM19A2</i> as Novel Insulin Sensitivity Loci. <i>Diabetes</i> , 2016, 65, 3200-3211.	4.4	76
90	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. <i>Scientific Reports</i> , 2016, 6, .	3.5	30

#	ARTICLE	IF	PR CITATIONS
91	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	26.1	323
92	The influence of menstrual cycle and endometriosis on endometrial methylome. <i>Clinical Epigenetics</i> , 2016, 8, .	4.0	65
93	Genome-wide DNA methylation study identifies genes associated with the cardiovascular biomarker GDF-15. <i>Human Molecular Genetics</i> , 2016, 25, 817-827.	3.0	35
94	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, .	13.9	278
95	Testing the role of predicted gene knockouts in human anthropometric trait variation. <i>Human Molecular Genetics</i> , 2016, 25, 2082-2092.	3.0	11
96	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, .	13.9	173
97	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.	3.3	393
98	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. <i>PLoS Genetics</i> , 2015, 11, e1005230.	3.3	84
99	Robust Linear Models for Cis-eQTL Analysis. <i>PLoS ONE</i> , 2015, 10, e0127882.	2.4	8
100	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. <i>Journal of Clinical Investigation</i> , 2015, 125, 1739-1751.	10.7	111
101	Insights into the Genetic Susceptibility to Type 2 Diabetes from Genome-Wide Association Studies of Obesity-Related Traits. <i>Current Diabetes Reports</i> , 2015, 15, .	5.4	51
102	Hydroxyethylene isosteres introduced in type II collagen fragments substantially alter the structure and dynamics of class II MHC A^q/glycopeptide complexes. <i>Organic and Biomolecular Chemistry</i> , 2015, 13, 6203-6216.	2.6	6
103	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	38.7	1,561
104	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	38.7	4,431
105	CWAS-identified loci for coronary heart disease are associated with intima-media thickness and plaque presence at the carotid artery bulb. <i>Atherosclerosis</i> , 2015, 239, 304-310.	1.6	33
106	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015, 6, .	13.9	186
107	Mouse-Human Experimental Epigenetic Analysis Unmasks Dietary Targets and Genetic Liability for Diabetic Phenotypes. <i>Cell Metabolism</i> , 2015, 21, 138-149.	26.2	107
108	Blood Metabolomic Predictors of 1-Year Outcome in Subarachnoid Hemorrhage. <i>Neurocritical Care</i> , 2015, 23, 225-232.	2.8	9

#	ARTICLE	IF	PR CITATIONS
109	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. <i>PLoS Genetics</i> , 2015, 11, e1004876.	3.3	108
110	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015, 47, 589-597.	26.1	347
111	Genome-wide association study of plasma levels of polychlorinated biphenyls disclose an association with the CYP2B6 gene in a population-based sample. <i>Environmental Research</i> , 2015, 140, 95-101.	7.9	15
112	Genome-wide enrichment analysis between endometriosis and obesity-related traits reveals novel susceptibility loci. <i>Human Molecular Genetics</i> , 2015, 24, 1185-1199.	3.0	78
113	Genome-wide association study of toxic metals and trace elements reveals novel associations. <i>Human Molecular Genetics</i> , 2015, 24, 4739-4745.	3.0	138
114	Genome-wide association of polycystic ovary syndrome implicates alterations in gonadotropin secretion in European ancestry populations. <i>Nature Communications</i> , 2015, 6, .	13.9	374
115	A comprehensive 1000 Genomesâ€‘based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015, 47, 1121-1130.	26.1	2,461
116	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	26.1	408
117	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. <i>PLoS ONE</i> , 2014, 9, e100776.	2.4	57
118	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. <i>PLoS Genetics</i> , 2014, 10, e1004494.	3.3	387
119	Genome Wide Association Identifies Common Variants at the SERPINA6/SERPINA1 Locus Influencing Plasma Cortisol and Corticosteroid Binding Globulin. <i>PLoS Genetics</i> , 2014, 10, e1004474.	3.3	130
120	Rare variants in <i>PPARG</i> with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13127-13132.	7.6	167
121	Here and now â€‘ there and then: Narrative time and space in intercountry adopteesâ€™ stories about background, origin and roots. <i>Qualitative Social Work</i> , 2014, 13, 539-554.	1.5	8
122	ADMA Levels and Arginine/ADMA Ratios Reflect Severity of Disease and Extent of Inflammation After Subarachnoid Hemorrhage. <i>Neurocritical Care</i> , 2014, 21, 91-101.	2.8	18
123	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 2014, 94, 233-245.	6.5	205
124	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	26.1	1,965
125	Genetic variation in the CYP2B6 Gene is related to circulating 2,2â€™,4,4â€™-tetrabromodiphenyl ether (BDE-47) concentrations: an observational population-based study. <i>Environmental Health</i> , 2014, 13, .	5.5	12
126	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.	26.1	1,030

#	ARTICLE	IF	PR CITATIONS
127	Expression of Phosphofructokinase in Skeletal Muscle Is Influenced by Genetic Variation and Associated With Insulin Sensitivity. <i>Diabetes</i> , 2014, 63, 1154-1165.	4.4	45
128	Genetic variation in the CYP1A1 gene is related to circulating PCB118 levels in a population-based sample. <i>Environmental Research</i> , 2014, 133, 135-140.	7.9	15
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.	6.5	26
130	Benefits of statistical molecular design, covariance analysis, and reference models in QSAR: a case study on acetylcholinesterase. <i>Journal of Computer-Aided Molecular Design</i> , 2014, 29, 199-215.	2.5	19
131	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2014, 20, 647-656.	8.4	266
132	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.	6.5	65
133	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	26.1	2,993
134	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.	26.1	645
135	Insights Into the Molecular Mechanism for Type 2 Diabetes Susceptibility at the <i>KCNQ1</i> Locus From Temporal Changes in Imprinting Status in Human Islets. <i>Diabetes</i> , 2013, 62, 987-992.	4.4	118
136	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.	3.3	416
137	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. <i>PLoS Medicine</i> , 2013, 10, e1001474.	8.5	192
138	Assessing association between protein truncating variants and quantitative traits. <i>Bioinformatics</i> , 2013, 29, 2419-2426.	4.8	16
139	The Presence of Methylation Quantitative Trait Loci Indicates a Direct Genetic Influence on the Level of DNA Methylation in Adipose Tissue. <i>PLoS ONE</i> , 2013, 8, e55923.	2.4	87
140	Evaluation of the genetic overlap between osteoarthritis with body mass index and height using genome-wide association scan data. <i>Annals of the Rheumatic Diseases</i> , 2013, 72, 935-941.	12.4	54
141	Mendelian Randomization Studies Do Not Support a Causal Role for Reduced Circulating Adiponectin Levels in Insulin Resistance and Type 2 Diabetes. <i>Diabetes</i> , 2013, 62, 3589-3598.	4.4	121
142	Contribution of 32 GWAS-Identified Common Variants to Severe Obesity in European Adults Referred for Bariatric Surgery. <i>PLoS ONE</i> , 2013, 8, e70735.	2.4	41
143	The miRNA Profile of Human Pancreatic Islets and Beta-Cells and Relationship to Type 2 Diabetes Pathogenesis. <i>PLoS ONE</i> , 2013, 8, e55272.	2.4	191
144	Extent, Causes, and Consequences of Small RNA Expression Variation in Human Adipose Tissue. <i>PLoS Genetics</i> , 2012, 8, e1002704.	3.3	52

#	ARTICLE	IF	PR CITATIONS
145	The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. <i>PLoS Genetics</i> , 2012, 8, e1002793.	3.3	462
146	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.	3.3	453
147	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012, 44, 991-1005.	26.1	803
148	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	26.1	1,863
149	Clinical and Genetic Correlates of Growth Differentiation Factor 15 in the Community. <i>Clinical Chemistry</i> , 2012, 58, 1582-1591.	1.1	127
150	Coexpression Network Analysis in Abdominal and Gluteal Adipose Tissue Reveals Regulatory Genetic Loci for Metabolic Syndrome and Related Phenotypes. <i>PLoS Genetics</i> , 2012, 8, e1002505.	3.3	57
151	Mapping cis- and trans-regulatory effects across multiple tissues in twins. <i>Nature Genetics</i> , 2012, 44, 1084-1089.	26.1	734
152	Frequency of Non-convulsive Seizures and Non-convulsive Status Epilepticus in Subarachnoid Hemorrhage Patients in Need of Controlled Ventilation and Sedation. <i>Neurocritical Care</i> , 2012, 17, 367-373.	2.8	27
153	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. <i>PLoS ONE</i> , 2012, 7, e29202.	2.4	204
154	Genetics and epigenetics of obesity. <i>Maturitas</i> , 2011, 69, 41-49.	3.1	269
155	MicroRNA Expression in Abdominal and Gluteal Adipose Tissue Is Associated with mRNA Expression Levels and Partly Genetically Driven. <i>PLoS ONE</i> , 2011, 6, e27338.	2.4	46
156	Obesity: is Type II diabetes a foregone conclusion or further dependent on genetic susceptibility?. <i>Diabetes Management</i> , 2011, 1, 413-422.	0.3	0
157	The Architecture of Gene Regulatory Variation across Multiple Human Tissues: The MuTHER Study. <i>PLoS Genetics</i> , 2011, 7, e1002003.	3.3	396
158	The Use of Genome-Wide eQTL Associations in Lymphoblastoid Cell Lines to Identify Novel Genetic Pathways Involved in Complex Traits. <i>PLoS ONE</i> , 2011, 6, e22070.	2.4	36
159	The Genetics of Obesity. <i>Current Diabetes Reports</i> , 2010, 10, 498-505.	5.4	212
160	Variability of gene expression profiles in human blood and lymphoblastoid cell lines. <i>BMC Genomics</i> , 2010, 11, 96.	3.3	81
161	A powerful approach to sub-phenotype analysis in population-based genetic association studies. <i>Genetic Epidemiology</i> , 2010, 34, 335-343.	3.1	55
162	Meta-analysis of sex-specific genome-wide association studies. <i>Genetic Epidemiology</i> , 2010, 34, 846-853.	3.1	110

#	ARTICLE	IF	PR CITATIONS
163	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.	38.7	764
164	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010, 42, 579-589.	26.1	1,700
165	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.	26.1	899
166	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	26.1	2,774
167	Integrated Genetic and Epigenetic Analysis Identifies Haplotype-Specific Methylation in the FTO Type 2 Diabetes and Obesity Susceptibility Locus. <i>PLoS ONE</i> , 2010, 5, e14040.	2.4	225
168	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. <i>Human Molecular Genetics</i> , 2010, 19, 535-544.	3.0	202
169	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	26.1	2,098
170	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. <i>PLoS Genetics</i> , 2009, 5, e1000508.	3.3	466
171	Meta-Analysis of the INSIG2 Association with Obesity Including 74,345 Individuals: Does Heterogeneity of Estimates Relate to Study Design?. <i>PLoS Genetics</i> , 2009, 5, e1000694.	3.3	63
172	Type 2 Diabetes Risk Alleles Are Associated With Reduced Size at Birth. <i>Diabetes</i> , 2009, 58, 1428-1433.	4.4	136
173	MicroRNA-125a is over-expressed in insulin target tissues in a spontaneous rat model of Type 2 Diabetes. <i>BMC Medical Genomics</i> , 2009, 2, .	1.8	107
174	Identification of MAMDC1 as a Candidate Susceptibility Gene for Systemic Lupus Erythematosus (SLE). <i>PLoS ONE</i> , 2009, 4, e8037.	2.4	15
175	Population substructure in Finland and Sweden revealed by the use of spatial coordinates and a small number of unlinked autosomal SNPs. <i>BMC Genetics</i> , 2008, 9, .	2.9	34
176	Genome-wide association analysis identifies 20 loci that influence adult height. <i>Nature Genetics</i> , 2008, 40, 575-583.	26.1	777
177	Type 2 diabetes: new genes, new understanding. <i>Trends in Genetics</i> , 2008, 24, 613-621.	9.9	231
178	Restriction Site-Specific Methylation Studies of Imprinted Genes with Quantitative Real-Time PCR. <i>Clinical Chemistry</i> , 2008, 54, 491-499.	1.1	32
179	Mechanisms of Disease: genetic insights into the etiology of type 2 diabetes and obesity. <i>Nature Clinical Practice Endocrinology and Metabolism</i> , 2008, 4, 156-163.	6.1	47
180	Interactions between Glutathione S-Transferase P1, Tumor Necrosis Factor, and Traffic-Related Air Pollution for Development of Childhood Allergic Disease. <i>Environmental Health Perspectives</i> , 2008, 116, 1077-1084.	8.8	120

#	ARTICLE	IF	PR CITATIONS
181	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. <i>Nature Genetics</i> , 2008, 41, 25-34.	26.1	1,628
182	Lack of Association between Neuropeptide S Receptor 1 Gene (NPSR1) and Eczema in Five European Populations. <i>Acta Dermato-Venereologica</i> , 2008, 89, 115-121.	1.9	4
183	The human GIMAP5 gene has a common polyadenylation polymorphism increasing risk to systemic lupus erythematosus. <i>Journal of Medical Genetics</i> , 2007, 44, 314-321.	3.9	79
184	Large-Scale Zygosity Testing Using Single Nucleotide Polymorphisms. <i>Twin Research and Human Genetics</i> , 2007, 10, 604-625.	0.8	116
185	Neuropeptide S Receptor 1 Gene Polymorphism Is Associated With Susceptibility to Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2007, 133, 808-817.	1.0	93
186	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. <i>Nature Genetics</i> , 2007, 39, 1329-1337.	26.1	1,341
187	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. <i>Nature</i> , 2007, 447, 661-678.	38.7	9,233
188	G protein-coupled receptor for asthma susceptibility associates with respiratory distress syndrome. <i>Annals of Medicine</i> , 2006, 38, 357-366.	4.1	31
189	Strong Genetic Evidence of DCDC2 as a Susceptibility Gene for Dyslexia. <i>American Journal of Human Genetics</i> , 2006, 78, 52-62.	6.5	216
190	Liver X receptor gene polymorphisms and adipose tissue expression levels in obesity. <i>Pharmacogenetics and Genomics</i> , 2006, 16, 881-889.	1.3	54
191	Association analysis of the LAG3 and CD4 genes in multiple sclerosis in two independent populations. <i>Journal of Neuroimmunology</i> , 2006, 180, 193-198.	2.4	16
192	Variation in DNA Repair Genes ERCC2, XRCC1, and XRCC3 and Risk of Follicular Lymphoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 258-265.	1.2	61
193	MHC2TA is associated with differential MHC molecule expression and susceptibility to rheumatoid arthritis, multiple sclerosis and myocardial infarction. <i>Nature Genetics</i> , 2005, 37, 486-494.	26.1	288
194	Haplotype construction of the FRDA gene and evaluation of its role in type II diabetes. <i>European Journal of Human Genetics</i> , 2005, 13, 849-855.	3.2	10
195	Absence of Association Between Asthma and High Serum Immunoglobulin E Associated GPRA Haplotypes and Adult Atopic Dermatitis. <i>Journal of Investigative Dermatology</i> , 2005, 125, 399-401.	2.3	23
196	Haplotypes of G Protein-coupled Receptor 154 Are Associated with Childhood Allergy and Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2005, 171, 1089-1095.	12.2	111
197	The genetics of autoimmunity. <i>BioEssays</i> , 2004, 26, 1363-1364.	2.2	0
198	PGC-1-responsive genes involved in oxidative phosphorylation are coordinately downregulated in human diabetes. <i>Nature Genetics</i> , 2003, 34, 267-273.	26.1	9,797

#	ARTICLE	IF	PR CITATIONS
199	A genome wide scan for early onset primary hypertension in Scandinavians. Human Molecular Genetics, 2003, 12, 2077-2081.	3.0	40
200	A meta-analysis of four European genome screens (GIFT Consortium) shows evidence for a novel region on chromosome 17p11.2-q22 linked to type 2 diabetes. Human Molecular Genetics, 2003, 12, 1865-1873.	3.0	70
201	Genomewide Linkage Analysis of Stature in Multiple Populations Reveals Several Regions with Evidence of Linkage to Adult Height. American Journal of Human Genetics, 2001, 69, 106-116.	6.5	178
202	The Genetics of Type 2 Diabetes. , 2001, 11, 178-187.		17
203	Large-scale meta-analysis highlights the hypothalamicâ€“pituitaryâ€“gonadal axis in the genetic regulation of menstrual cycle length. Human Molecular Genetics, 0, , .	3.0	24