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List of Articles by Year in descending order

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107

PR articles

37,164

PR citations

8894

70

PR h-index

32680

99

g-index

110

documents

43796

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10986

72

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53847

citing authors

#	ARTICLE	IF	CITATIONS
1	Adipose tissue eQTL meta-analysis highlights the contribution of allelic heterogeneity to gene expression regulation and cardiometabolic traits. <i>Nature Genetics</i> , 2025, 57, 180-192.	25.2	15
2	Assessing the potential causal effects of 1099 plasma metabolites on 2099 binary disease endpoints. <i>Nature Communications</i> , 2025, 16, .	13.7	2
3	Extensive differential gene expression and regulation by sex in human skeletal muscle. <i>Cell Genomics</i> , 2025, 5, 100915.	6.8	9
4	Loci for insulin processing and secretion provide insight into type 2 diabetes risk. <i>American Journal of Human Genetics</i> , 2023, 110, 284-299.	6.5	35
5	Genome-wide association study and functional characterization identifies candidate genes for insulin-stimulated glucose uptake. <i>Nature Genetics</i> , 2023, 55, 973-983.	25.2	61
6	GWAS of random glucose in 476,326 individuals provide insights into diabetes pathophysiology, complications and treatment stratification. <i>Nature Genetics</i> , 2023, 55, 1448-1461.	25.2	73
7	Genetic insights into resting heart rate and its role in cardiovascular disease. <i>Nature Communications</i> , 2023, 14, .	13.7	25
8	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. <i>Nature Communications</i> , 2022, 13, .	13.7	159
9	ACE2 expression in adipose tissue is associated with cardio-metabolic risk factors and cell type composition—implications for COVID-19. <i>International Journal of Obesity</i> , 2022, 46, 1478-1486.	3.0	35
10	Genome-wide association analyses of physical activity and sedentary behavior provide insights into underlying mechanisms and roles in disease prevention. <i>Nature Genetics</i> , 2022, 54, 1332-1344.	25.2	196
11	Integrating transcriptomics, metabolomics, and GWAS helps reveal molecular mechanisms for metabolite levels and disease risk. <i>American Journal of Human Genetics</i> , 2022, 109, 1727-1741.	6.5	52
12	A saturated map of common genetic variants associated with human height. <i>Nature</i> , 2022, 610, 704-712.	37.9	687
13	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, .	13.7	132
14	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 5239-5250.	7.8	18
15	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	37.9	845
16	Adiponectin GWAS loci harboring extensive allelic heterogeneity exhibit distinct molecular consequences. <i>PLoS Genetics</i> , 2020, 16, e1009019.	3.2	14
17	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. <i>Nature Human Behaviour</i> , 2019, 3, 950-961.	9.1	90
18	Exome sequencing of Finnish isolates enhances rare-variant association power. <i>Nature</i> , 2019, 572, 323-328.	37.9	189

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19	Colocalization of GWAS and eQTL signals at loci with multiple signals identifies additional candidate genes for body fat distribution. <i>Human Molecular Genetics</i> , 2019, 28, 4161-4172.	2.9	57
20	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. <i>American Journal of Human Genetics</i> , 2019, 105, 773-787.	6.5	70
21	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	3.3	110
22	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, .	13.7	84
23	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.	37.9	303
24	Integrative analysis of gene expression, DNA methylation, physiological traits, and genetic variation in human skeletal muscle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10883-10888.	7.5	149
25	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	25.2	133
26	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	25.2	106
27	Identification of seven novel loci associated with amino acid levels using single-variant and gene-based tests in 8545 Finnish men from the METSIM study. <i>Human Molecular Genetics</i> , 2018, 27, 1664-1674.	2.9	36
28	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	6.5	156
29	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	25.2	1,300
30	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	2.3	114
31	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	37.9	612
32	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 428-443.	6.5	172
33	A Genome-Wide Association Study of IVGTT-Based Measures of First-Phase Insulin Secretion Refines the Underlying Physiology of Type 2 Diabetes Variants. <i>Diabetes</i> , 2017, 66, 2296-2309.	4.2	113
34	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, .	13.7	198
35	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	4.2	717
36	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	4.2	51

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37	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	25.2	543
38	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017, 70, .	6.6	143
39	A Type 2 Diabetes-Associated Functional Regulatory Variant in a Pancreatic Islet Enhancer at the ADCY5 Locus. <i>Diabetes</i> , 2017, 66, 2521-2530.	4.2	65
40	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, .	5.7	36
41	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.	8.1	400
42	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.	25.2	387
43	Novel association of TM6SF2 rs58542926 genotype with increased serum tyrosine levels and decreased apoB-100 particles in Finns. <i>Journal of Lipid Research</i> , 2017, 58, 1471-1481.	3.7	54
44	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	3.2	181
45	Common, low-frequency, and rare genetic variants associated with lipoprotein subclasses and triglyceride measures in Finnish men from the METSIM study. <i>PLoS Genetics</i> , 2017, 13, e1007079.	3.2	57
46	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	37.9	1,051
47	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. <i>Nature Communications</i> , 2016, 7, .	13.7	135
48	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, .	13.7	90
49	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	25.2	298
50	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	25.2	410
51	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.	4.2	76
52	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, .	13.7	278
53	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.	3.2	393
54	Multiple Hepatic Regulatory Variants at the GALNT2 GWAS Locus Associated with High-Density Lipoprotein Cholesterol. <i>American Journal of Human Genetics</i> , 2015, 97, 801-815.	6.5	55

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55	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	37.9	1,561
56	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	37.9	4,431
57	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	37.9	198
58	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.	3.2	108
59	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	25.2	408
60	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. <i>Diabetes</i> , 2014, 63, 2158-2171.	4.2	333
61	A Central Role for GRB10 in Regulation of Islet Function in Man. <i>PLoS Genetics</i> , 2014, 10, e1004235.	3.2	173
62	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	25.2	1,965
63	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.	25.2	1,030
64	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	25.2	2,993
65	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 1345-1352.	25.2	833
66	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.	25.2	645
67	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	25.2	308
68	Trans-Ethnic Fine-Mapping of Lipid Loci Identifies Population-Specific Signals and Allelic Heterogeneity That Increases the Trait Variance Explained. <i>PLoS Genetics</i> , 2013, 9, e1003379.	3.2	114
69	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.	3.2	416
70	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.	4.2	121
71	The MetaboChip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. <i>PLoS Genetics</i> , 2012, 8, e1002793.	3.2	462
72	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.	25.2	803

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73	Genome-wide meta-analysis of common variant differences between men and women. <i>Human Molecular Genetics</i> , 2012, 21, 4805-4815.	2.9	38
74	Estimating Hepatic Glucokinase Activity Using a Simple Model of Lactate Kinetics. <i>Diabetes Care</i> , 2012, 35, 1015-1020.	6.2	22
75	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	37.9	426
76	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	25.2	826
77	Exome array analysis identifies new loci and low-frequency variants influencing insulin processing and secretion. <i>Nature Genetics</i> , 2012, 45, 197-201.	25.2	262
78	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.	4.2	352
79	Effects of 34 Risk Loci for Type 2 Diabetes or Hyperglycemia on Lipoprotein Subclasses and Their Composition in 6,580 Nondiabetic Finnish Men. <i>Diabetes</i> , 2011, 60, 1608-1616.	4.2	82
80	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	25.2	421
81	Fine Mapping of Five Loci Associated with Low-Density Lipoprotein Cholesterol Detects Variants That Double the Explained Heritability. <i>PLoS Genetics</i> , 2011, 7, e1002198.	3.2	140
82	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	37.9	1,875
83	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. <i>Nature Genetics</i> , 2010, 42, 142-148.	25.2	617
84	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010, 42, 579-589.	25.2	1,700
85	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.	25.2	899
86	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	25.2	2,774
87	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	25.2	2,098
88	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. <i>PLoS Genetics</i> , 2009, 5, e1000508.	3.2	466
89	The T-381C SNP in BNP gene may be modestly associated with type 2 diabetes: an updated meta-analysis in 49 279 subjects. <i>Human Molecular Genetics</i> , 2009, 18, 2495-2501.	2.9	32
90	Genome-wide association study identifies eight loci associated with blood pressure. <i>Nature Genetics</i> , 2009, 41, 666-676.	25.2	1,142

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91	Association of 18 Confirmed Susceptibility Loci for Type 2 Diabetes With Indices of Insulin Release, Proinsulin Conversion, and Insulin Sensitivity in 5,327 Nondiabetic Finnish Men. <i>Diabetes</i> , 2009, 58, 2129-2136.	4.2	163
92	Identification of ten loci associated with height highlights new biological pathways in human growth. <i>Nature Genetics</i> , 2008, 40, 584-591.	25.2	546
93	Common variants in the GDF5-UQCC region are associated with variation in human height. <i>Nature Genetics</i> , 2008, 40, 198-203.	25.2	387
94	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. <i>Nature Genetics</i> , 2008, 40, 161-169.	25.2	1,547
95	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.	25.2	1,736
96	Common variant in MTNR1B associated with increased risk of type 2 diabetes and impaired early insulin secretion. <i>Nature Genetics</i> , 2008, 41, 82-88.	25.2	689
97	Variants in MTNR1B influence fasting glucose levels. <i>Nature Genetics</i> , 2008, 41, 77-81.	25.2	697
98	Common variants at 30 loci contribute to polygenic dyslipidemia. <i>Nature Genetics</i> , 2008, 41, 56-65.	25.2	1,291
99	Tag SNP selection for Finnish individuals based on the CEPH Utah HapMap database. <i>Genetic Epidemiology</i> , 2006, 30, 180-190.	3.1	54
100	Mitochondrial polymorphisms and susceptibility to type 2 diabetes-related traits in Finns. <i>Human Genetics</i> , 2005, 118, 245-254.	2.9	76
101	A Large Set of Finnish Affected Sibling Pair Families With Type 2 Diabetes Suggests Susceptibility Loci on Chromosomes 6, 11, and 14. <i>Diabetes</i> , 2004, 53, 821-829.	4.2	76
102	Title is missing!. , 0, .		3
103	Title is missing!. , 0, .		2
104	Title is missing!. , 0, .		3
105	Title is missing!. , 0, .		2
106	Title is missing!. , 0, .		1
107	Polygenic prediction of body mass index and obesity through the life course and across ancestries. <i>Nature Medicine</i> , 0, 31, 3151-3168.	33.0	10