Markku Laakso

List of Publications by Year
in descending order

324 papers	87,880 citations	1877 105 h-index	498 275 g-index
352 all docs	352 docs citations	352 times ranked	97160 citing authors

#	Article	IF	Citations
1	Subcutaneous adipose tissue splice quantitative trait loci reveal differences in isoform usage associated with cardiometabolic traits. American Journal of Human Genetics, 2022, 109, 66-80.	2.6	13
2	Metabolite Signature of Physical Activity and the Risk of Type 2 Diabetes in 7271 Men. Metabolites, 2022, 12, 69.	1.3	8
3	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	2.6	24
4	Multiparametric platform for profiling lipid trafficking in human leukocytes. Cell Reports Methods, 2022, 2, 100166.	1.4	3
5	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. Nature Communications, 2022, 13, 1644.	5.8	63
6	Effects of age, amyloid, sex, and APOE Îµ4 on the CSF proteome in normal cognition. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2022, 14, e12286.	1.2	4
7	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
8	Metabolite Signature in the Carriers of Pathogenic Genetic Variants for Cardiomyopathy: A Population-Based METSIM Study. Metabolites, 2022, 12, 437.	1.3	1
9	ACE2 expression in adipose tissue is associated with cardio-metabolic risk factors and cell type compositionâ€"implications for COVID-19. International Journal of Obesity, 2022, 46, 1478-1486.	1.6	18
10	Long-range chromosomal interactions increase and mark repressed gene expression during adipogenesis. Epigenetics, 2022, 17, 1849-1862.	1.3	1
11	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
12	Metabolite Signature of Albuminuria Involves Amino Acid Pathways in 8661 Finnish Men Without Diabetes. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 143-152.	1.8	5
13	Novel biomarkers associated with incident heart failure in 10Â106 Finnish men. ESC Heart Failure, 2021, 8, 605-614.	1.4	5
14	Genome-Wide Association Analysis of Pancreatic Beta-Cell Glucose Sensitivity. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 80-90.	1.8	5
15	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87
16	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	9.4	676
17	Insulin Resistance Is Associated With Enhanced Brain Glucose Uptake During Euglycemic Hyperinsulinemia: A Large-Scale PET Cohort. Diabetes Care, 2021, 44, 788-794.	4.3	31
18	Machine Learning Reveals Time-Varying Microbial Predictors with Complex Effects on Glucose Regulation. MSystems, 2021, 6, .	1.7	13

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19	n-3 Fatty Acid Biomarkers and Incident Type 2 Diabetes: An Individual Participant-Level Pooling Project of 20 Prospective Cohort Studies. Diabetes Care, 2021, 44, 1133-1142.	4.3	50
20	The FADS1 Genotype Modifies Metabolic Responses to the Linoleic Acid and Alphaâ€linolenic Acid Containing Plant Oilsâ€“Genotype Based Randomized Trial FADSDIET2. Molecular Nutrition and Food Research, 2021, 65, e2001004.	1.5	13
21	Association of structural variation with cardiometabolic traits in Finns. American Journal of Human Genetics, 2021, 108, 583-596.	2.6	22
22	Blood n-3 fatty acid levels and total and cause-specific mortality from 17 prospective studies. Nature Communications, 2021, 12, 2329.	5.8	132
23	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
24	Mitochondrial genome copy number measured by DNA sequencing in human blood is strongly associated with metabolic traits via cell-type composition differences. Human Genomics, 2021, 15, 34.	1.4	7
25	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	5.8	49
26	Profiles of Glucose Metabolism in Different Prediabetes Phenotypes, Classified by Fasting Glycemia, 2-Hour OGTT, Glycated Hemoglobin, and 1-Hour OGTT: An IMI DIRECT Study. Diabetes, 2021, 70, 2092-2106.	0.3	17
27	Identification of TBX15 as an adipose master trans regulator of abdominal obesity genes. Genome Medicine, 2021, 13, 123.	3.6	23
28	The Association of 9 Amino Acids With Cardiovascular Events in Finnish Men in a 12-Year Follow-up Study. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 3448-3454.	1.8	22
29	Effect of lifestyle intervention on the risk of incident diabetes in individuals with impaired fasting glucose and low or high genetic risk for the development of type 2 diabetes in men: a T2D-GENE trial. Food and Nutrition Research, 2021, 65, .	1.2	6
30	Sex-specific genetic regulation of adipose mitochondria and metabolic syndrome by Ndufv2. Nature Metabolism, 2021, 3, 1552-1568.	5.1	32
31	Molecular epidemiology of hereditary ataxia in Finland. BMC Neurology, 2021, 21, 382.	0.8	11
32	Chromatin accessibility and gene expression during adipocyte differentiation identify context-dependent effects at cardiometabolic GWAS loci. PLoS Genetics, 2021, 17, e1009865.	1.5	9
33	The â€œCommon Soil Hypothesisâ€•Revisitedâ€”Risk Factors for Type 2 Diabetes and Cardiovascular Disease. Metabolites, 2021, 11, 691.	1.3	17
34	Glycogen metabolism links glucose homeostasis to thermogenesis in adipocytes. Nature, 2021, 599, 296-301.	13.7	36
35	FADS1 rs174550 genotype and high linoleic acid diet modify plasma PUFA phospholipids in a dietary intervention study. European Journal of Nutrition, 2021, , 1.	1.8	1
36	Interaction of Diet/Lifestyle Intervention and TCF7L2 Genotype on Glycemic Control and Adiposity among Overweight or Obese Adults: Big Data from Seven Randomized Controlled Trials Worldwide. Health Data Science, 2021, 2021, .	1.1	0

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37	Elevated circulating follistatin associates with an increased risk of type 2 diabetes. Nature Communications, 2021, 12, 6486.	5.8	31
38	SUR1-E1506K mutation impairs glucose tolerance and promotes vulnerable atherosclerotic plaque phenotype in hypercholesterolemic mice. PLoS ONE, 2021, 16, e0258408.	1.1	1
39	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
40	The association between diabetes and Alzheimerâ€™s disease pathophysiology. Alzheimer's and Dementia, 2021, 17, .	0.4	0
41	Generation of a human induced pluripotent stem cell line (UEFi003-A) carrying heterozygous A673T variant in amyloid precursor protein associated with a reduced risk of Alzheimerâ€™s disease. Stem Cell Research, 2020, 48, 101968.	0.3	5
42	RIPK1 gene variants associate with obesity in humans and can be therapeutically silenced to reduce obesity in mice. Nature Metabolism, 2020, 2, 1113-1125.	5.1	34
43	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
44	Whole blood co-expression modules associate with metabolic traits and type 2 diabetes: an IMI-DIRECT study. Genome Medicine, 2020, 12, 109.	3.6	8
45	Estrogen receptor Î± controls metabolism in white and brown adipocytes by regulating Polg1 and mitochondrial remodeling. Science Translational Medicine, 2020, 12, .	5.8	64
46	The causal effect of obesity on prediabetes and insulin resistance reveals the important role of adipose tissue in insulin resistance. PLoS Genetics, 2020, 16, e1009018.	1.5	29
47	Fgr kinase is required for proinflammatory macrophage activation during diet-induced obesity. Nature Metabolism, 2020, 2, 974-988.	5.1	40
48	Adiponectin GWAS loci harboring extensive allelic heterogeneity exhibit distinct molecular consequences. PLoS Genetics, 2020, 16, e1009019.	1.5	11
49	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. Circulation Genomic and Precision Medicine, 2020, 13, e002769.	1.6	5
50	Association Analysis and Meta-Analysis of Multi-Allelic Variants for Large-Scale Sequence Data. Genes, 2020, 11, 586.	1.0	3
51	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	13.7	6,140
52	Transcript expression-aware annotation improves rare variant interpretation. Nature, 2020, 581, 452-458.	13.7	142
53	Fatty acids in the de novo lipogenesis pathway and incidence of type 2 diabetes: A pooled analysis of prospective cohort studies. PLoS Medicine, 2020, 17, e1003102.	3.9	38
54	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts. PLoS Medicine, 2020, 17, e1003149.	3.9	47

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55	Clinical and Genetic Characterization of 153 Patients with Persistent or Transient Congenital Hyperinsulinism. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e1686-e1694.	1.8	11
56	Efficient Estimation and Applications of Cross-Validated Genetic Predictions to Polygenic Risk Scores and Linear Mixed Models. Journal of Computational Biology, 2020, 27, 599-612.	0.8	19
57	The role of physical activity in metabolic homeostasis before and after the onset of type 2 diabetes: an IMI DIRECT study. Diabetologia, 2020, 63, 744-756.	2.9	12
58	Microbiota-Related Metabolites and the Risk of Type 2 Diabetes. Diabetes Care, 2020, 43, 1319-1325.	4.3	83
59	Post-load glucose subgroups and associated metabolic traits in individuals with type 2 diabetes: An IMI-DIRECT study. PLoS ONE, 2020, 15, e0242360.	1.1	7
60	Simvastatin profoundly impairs energy metabolism in primary human muscle cells. Endocrine Connections, 2020, 9, 1103-1113.	0.8	0
61	Simvastatin profoundly impairs energy metabolism in primary human muscle cells. Endocrine Connections, 2020, 9, 1103-1113.	0.8	5
62	Title is missing!. , 2020, 16, e1009018.		0
63	Title is missing!. , 2020, 16, e1009018.		0
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73	An intronic variant in the GCKR gene is associated with multiple lipids. Scientific Reports, 2019, 9, 10240.	1.6	32
74	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	6.2	75
75	Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.	13.7	161
76	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	2.2	38
77	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
78	Colocalization of GWAS and eQTL signals at loci with multiple signals identifies additional candidate genes for body fat distribution. Human Molecular Genetics, 2019, 28, 4161-4172.	1.4	41
79	A comprehensive study of metabolite genetics reveals strong pleiotropy and heterogeneity across time and context. Nature Communications, 2019, 10, 4788.	5.8	59
80	Biomarkers for type 2 diabetes. Molecular Metabolism, 2019, 27, S139-S146.	3.0	106
81	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. American Journal of Human Genetics, 2019, 105, 773-787.	2.6	45
82	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
83	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	5.8	64
84	Discovery of biomarkers for glycaemic deterioration before and after the onset of type 2 diabetes: descriptive characteristics of the epidemiological studies within the IMI DIRECT Consortium. Diabetologia, 2019, 62, 1601-1615.	2.9	22
85	Open Chromatin Profiling in Adipose Tissue Marks Genomic Regions with Functional Roles in Cardiometabolic Traits. G3: Genes, Genomes, Genetics, 2019, 9, 2521-2533.	0.8	19
86	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	2.6	21
87	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
88	Reverse geneâ€“environment interaction approach to identify variants influencing body-mass index in humans. Nature Metabolism, 2019, 1, 630-642.	5.1	14
89	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
90	Integrative analysis of gene expression, DNA methylation, physiological traits, and genetic variation in human skeletal muscle. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10883-10888.	3.3	114

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91	Genetic Determinants of Circulating Glycine Levels and Risk of Coronary Artery Disease. Journal of the American Heart Association, 2019, 8, e011922.	1.6	20
92	Nine Amino Acids Are Associated With Decreased Insulin Secretion and Elevated Glucose Levels in a 7.4-Year Follow-up Study of 5,181 Finnish Men. Diabetes, 2019, 68, 1353-1358.	0.3	109
93	Reverse GWAS: Using genetics to identify and model phenotypic subtypes. PLoS Genetics, 2019, 15, e1008009.	1.5	34
94	Biomarkers of Dietary Omega-6 Fatty Acids and Incident Cardiovascular Disease and Mortality. Circulation, 2019, 139, 2422-2436.	1.6	199
95	Associations of circulating very-long-chain saturated fatty acids and incident type 2 diabetes: a pooled analysis of prospective cohort studies. American Journal of Clinical Nutrition, 2019, 109, 1216-1223.	2.2	39
96	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	1.4	31
97	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	9.4	112
98	Circulating RNAs as predictive markers for the progression of type 2 diabetes. Journal of Cellular and Molecular Medicine, 2019, 23, 2753-2768.	1.6	19
99	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
100	Genetic basis and outcome in a nationwide study of Finnish patients with hypertrophic cardiomyopathy. ESC Heart Failure, 2019, 6, 436-445.	1.4	26
101	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	9.4	328
102	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. Nature Genetics, 2019, 51, 237-244.	9.4	1,307
103	Inflammatory response to dietary linoleic acid depends on FADS1 genotype. American Journal of Clinical Nutrition, 2019, 109, 165-175.	2.2	44
104	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	0.7	69
105	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. Human Molecular Genetics, 2018, 27, 1664-1674.	1.4	30
106	Integration of human adipocyte chromosomal interactions with adipose gene expression prioritizes obesity-related genes from GWAS. Nature Communications, 2018, 9, 1512.	5.8	75
107	A Common Type 2 Diabetes Risk Variant Potentiates Activity of an Evolutionarily Conserved Islet Stretch Enhancer and Increases C2CD4A and C2CD4B Expression. American Journal of Human Genetics, 2018, 102, 620-635.	2.6	47
108	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356

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109	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. Nature Genetics, 2018, 50, 572-580.	9.4	143
110	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	2.6	123
111	Elevated Plasma Levels of 3-Hydroxyisobutyric Acid Are Associated With Incident Type 2 Diabetes. EBioMedicine, 2018, 27, 151-155.	2.7	53
112	A Strategy for Discovery of Endocrine Interactions with Application to Whole-Body Metabolism. Cell Metabolism, 2018, 27, 1138-1155.e6.	7.2	58
113	Epigenome-wide association in adipose tissue from the METSIM cohort. Human Molecular Genetics, 2018, 27, 1830-1846.	1.4	38
114	Role of osteopontin and its regulation in pancreatic islet. Biochemical and Biophysical Research Communications, 2018, 495, 1426-1431.	1.0	8
115	A Partial Loss-of-Function Variant in AKT2 Is Associated With Reduced Insulin-Mediated Glucose Uptake in Multiple Insulin-Sensitive Tissues: A Genotype-Based Callback Positron Emission Tomography Study. Diabetes, 2018, 67, 334-342.	0.3	37
116	Systems Genetics Approach to Biomarker Discovery: GPNMB and Heart Failure in Mice and Humans. G3: Genes, Genomes, Genetics, 2018, 8, 3499-3506.	0.8	14
117	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.	9.4	1,331
118	Type 2 diabetes genetic loci informed by multi-trait associations point to disease mechanisms and subtypes: A soft clustering analysis. PLoS Medicine, 2018, 15, e1002654.	3.9	373
119	Phenotype-Specific Enrichment of Mendelian Disorder Genes near GWAS Regions across 62 Complex Traits. American Journal of Human Genetics, 2018, 103, 535-552.	2.6	90
120	Fatty acid biomarkers of dairy fat consumption and incidence of type 2 diabetes: A pooled analysis of prospective cohort studies. PLoS Medicine, 2018, 15, e1002670.	3.9	143
121	Functional Variant in the GCKR Gene Affects Lactate Levels Differentially in the Fasting State and During Hyperglycemia. Scientific Reports, 2018, 8, 15989.	1.6	5
122	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
123	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
124	Generation of a human induced pluripotent stem cell line from a patient with a rare A673T variant in amyloid precursor protein gene that reduces the risk for Alzheimer's disease. Stem Cell Research, 2018, 30, 96-99.	0.3	9
125	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. American Journal of Human Genetics, 2018, 102, 1204-1211.	2.6	102
126	Interactions between genetic variation and cellular environment in skeletal muscle gene expression. PLoS ONE, 2018, 13, e0195788.	1.1	18

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127	Structural Immaturity of Human iPSC-Derived Cardiomyocytes: In Silico Investigation of Effects on Function and Disease Modeling. Frontiers in Physiology, 2018, 9, 80.	1.3	110
128	Novel electrocardiographic features in carriers of hypertrophic cardiomyopathy causing sarcomeric mutations. Journal of Electrocardiology, 2018, 51, 983-989.	0.4	3
129	Proper conditional analysis in the presence of missing data: Application to large scale meta-analysis of tobacco use phenotypes. PLoS Genetics, 2018, 14, e1007452.	1.5	18
130	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
131	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
132	Short adult stature predicts impaired beta-cell function, insulin resistance, glycemia and type 2 diabetes in Finnish men. Journal of Clinical Endocrinology and Metabolism, 2017, 102, jc.2016-2933.	1.8	32
133	The Metabolic Syndrome in Men study: a resource for studies of metabolic and cardiovascular diseases. Journal of Lipid Research, 2017, 58, 481-493.	2.0	147
134	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
135	Diabetes Secondary to Treatment with Statins. Current Diabetes Reports, 2017, 17, 10.	1.7	46
136	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. American Journal of Human Genetics, 2017, 100, 428-443.	2.6	141
137	Relationships between gut microbiota, plasma metabolites, and metabolic syndrome traits in the METSIM cohort. Genome Biology, 2017, 18, 70.	3.8	245
138	A Genome-Wide Association Study of IVGTT-Based Measures of First-Phase Insulin Secretion Refines the Underlying Physiology of Type 2 Diabetes Variants. Diabetes, 2017, 66, 2296-2309.	0.3	102
139	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	5.8	169
140	The influence of insulin resistance on cerebrospinal fluid and plasma biomarkers of Alzheimerâ€™s pathology. Alzheimer's Research and Therapy, 2017, 9, 31.	3.0	36
141	The TMAO-Producing Enzyme Flavin-Containing Monooxygenase 3 Regulates Obesity and the Beiging of White Adipose Tissue. Cell Reports, 2017, 19, 2451-2461.	2.9	194
142	Acute detachment of hexokinase II from mitochondria modestly increases oxygen consumption of the intact mouse heart. Metabolism: Clinical and Experimental, 2017, 72, 66-74.	1.5	15
143	Decreased plasma Î²â€amyloid in the Alzheimer's disease <scp>APP</scp><scp>A</scp>673<scp>T</scp> variant carriers. Annals of Neurology, 2017, 82, 128-132.	2.8	39
144	Genetic risk scores in the prediction of plasma glucose, impaired insulin secretion, insulin resistance and incident type 2 diabetes in the METSIM study. Diabetologia, 2017, 60, 1722-1730.	2.9	26

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145	A nationwide study on parathyroid carcinoma. Acta OncolÃ³gica, 2017, 56, 991-1003.	0.8	84
146	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	3.0	39
147	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
148	Omega-6 fatty acid biomarkers and incident type 2 diabetes: pooled analysis of individual-level data for 39â€˜740 adults from 20 prospective cohort studies. Lancet Diabetes and Endocrinology,the, 2017, 5, 965-974.	5.5	213
149	Heterozygous RFX6 protein truncating variants are associated with MODY with reduced penetrance. Nature Communications, 2017, 8, 888.	5.8	95
150	A genomic exploration identifies mechanisms that may explain adverse cardiovascular effects of COX-2 inhibitors. Scientific Reports, 2017, 7, 10252.	1.6	16
151	Differential Associations of Inflammatory Markers With Insulin Sensitivity and Secretion: The Prospective METSIM Study. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 3600-3609.	1.8	52
152	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
153	Trans-ancestry Fine Mapping and Molecular Assays Identify Regulatory Variants at the ANGPTL8 HDL-C GWAS Locus. G3: Genes, Genomes, Genetics, 2017, 7, 3217-3227.	0.8	19
154	Plasma Mannose Levels Are Associated with Incident Type 2 Diabetes and Cardiovascular Disease. Cell Metabolism, 2017, 26, 281-283.	7.2	85
155	Family-specific aggregation of lipid GWAS variants confers the susceptibility to familial hypercholesterolemia in a large Austrian family. Atherosclerosis, 2017, 264, 58-66.	0.4	6
156	A Type 2 Diabetesâ€“Associated Functional Regulatory Variant in a Pancreatic Islet Enhancer at the ADCY5 Locus. Diabetes, 2017, 66, 2521-2530.	0.3	54
157	Plant-derived compounds strigolactone GR24 and pinosylvin activate SIRT1 and enhance glucose uptake in rat skeletal muscle cells. Scientific Reports, 2017, 7, 17606.	1.6	24
158	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
159	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.	3.9	341
160	Identification and characterization of a FOXA2-regulated transcriptional enhancer at a type 2 diabetes intronic locus that controls GCKR expression in liver cells. Genome Medicine, 2017, 9, 63.	3.6	21
161	Novel association of TM6SF2 rs58542926 genotype with increased serum tyrosine levels and decreased apoB-100 particles in Finns. Journal of Lipid Research, 2017, 58, 1471-1481.	2.0	49
162	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158

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163	Common, low-frequency, and rare genetic variants associated with lipoprotein subclasses and triglyceride measures in Finnish men from the METSIM study. PLoS Genetics, 2017, 13, e1007079.	1.5	49
164	Genomic correlates of glatiramer acetate adverse cardiovascular effects lead to a novel locus mediating coronary risk. PLoS ONE, 2017, 12, e0182999.	1.1	5
165	Glucose-Dependent Insulinotropic Polypeptide Stimulates Osteopontin Expression in the Vasculature via Endothelin-1 and CREB. Diabetes, 2016, 65, 239-254.	0.3	41
166	Finnish Diabetes Risk Score Is Associated with Impaired Insulin Secretion and Insulin Sensitivity, Drug-Treated Hypertension and Cardiovascular Disease: A Follow-Up Study of the METSIM Cohort. PLoS ONE, 2016, 11, e0166584.	1.1	16
167	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
168	Geneâ€diet interaction of a common FADS1 variant with marine polyunsaturated fatty acids for fatty acid composition in plasma and erythrocytes among men. Molecular Nutrition and Food Research, 2016, 60, 381-389.	1.5	22
169	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. Nature Communications, 2016, 7, 11764.	5.8	114
170	Genetics of Type 2 Diabetes. Endocrine Development, 2016, 31, 203-220.	1.3	59
171	Regulation of alternative splicing in human obesity loci. Obesity, 2016, 24, 2033-2037.	1.5	11
172	Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291.	13.7	9,051
173	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74
174	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
175	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
176	Detection of Novel Gene Variants Associated with Congenital Hypothyroidism in a Finnish Patient Cohort. Thyroid, 2016, 26, 1215-1224.	2.4	63
177	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.	0.3	67
178	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	5.8	100
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