PÃ¤ivi Pajukanta

List of Publications by Year
in descending order

95 papers	8,362 citations	117625 34 h-index	53230 85 g-index
100 all docs	100 docs citations	100 times ranked	13294 citing authors

#	Article	IF	Citations
1	Identification of 90 NAFLD GWAS loci and establishment of NAFLD PRS and causal role of NAFLD in coronary artery disease. Human Genetics and Genomics Advances, 2022, 3, 100056.	1.7	10
2	Fast estimation of genetic correlation for biobank-scale data. American Journal of Human Genetics, 2022, 109, 24-32.	6.2	11
3	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.	6.2	13
4	Human liver single nucleus and singleÂcell RNA sequencing identify a hepatocellular carcinoma-associated cell-type affecting survival. Genome Medicine, 2022, 14, 50.	8.2	27
5	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.	3.4	18
6	Hyperinsulinemia Is Highly Associated With Markers of Hepatocytic Senescence in Two Independent Cohorts. Diabetes, 2022, 71, 1929-1936.	0.6	11
7	Long-range chromosomal interactions increase and mark repressed gene expression during adipogenesis. Epigenetics, 2022, 17, 1849-1862.	2.7	1
8	Serum aromatic and branchedâ€chain amino acids associated with NASH demonstrate divergent associations with serum lipids. Liver International, 2021, 41, 754-763.	3.9	23
9	Further evidence supporting a potential role for ADH1B in obesity. Scientific Reports, 2021, 11, 1932.	3.3	11
10	Differential Mitochondrial Gene Expression in Adipose Tissue Following Weight Loss Induced by Diet or Bariatric Surgery. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 1312-1324.	3.6	13
11	Integrative analysis of liver-specific non-coding regulatory SNPs associated with the risk of coronary artery disease. American Journal of Human Genetics, 2021, 108, 411-430.	6.2	20
12	Molecular pathways behind acquired obesity: Adipose tissue and skeletal muscle multiomics in monozygotic twin pairs discordant for BMI. Cell Reports Medicine, 2021, 2, 100226.	6.5	31
13	Identification of TBX15 as an adipose master trans regulator of abdominal obesity genes. Genome Medicine, 2021, 13, 123.	8.2	23
14	Electrical impedance tomography for non-invasive identification of fatty liver infiltrate in overweight individuals. Scientific Reports, 2021, 11, 19859.	3.3	6
15	Indole-3-Propionic Acid, a Gut-Derived Tryptophan Metabolite, Associates with Hepatic Fibrosis. Nutrients, 2021, 13, 3509.	4.1	25
16	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
17	Î²2-spectrin (SPTBN1) as a therapeutic target for diet-induced liver disease and preventing cancer development. Science Translational Medicine, 2021, 13, eabk2267.	12.4	23
18	RIPK1 gene variants associate with obesity in humans and can be therapeutically silenced to reduce obesity in mice. Nature Metabolism, 2020, 2, 1113-1125.	11.9	34

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19	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.	3.5	29
20	Adiponectin GWAS loci harboring extensive allelic heterogeneity exhibit distinct molecular consequences. PLoS Genetics, 2020, 16, e1009019.	3.5	11
21	Enhancing droplet-based single-nucleus RNA-seq resolution using the semi-supervised machine learning classifier DIEM. Scientific Reports, 2020, 10, 11019.	3.3	64
22	Accurate estimation of cell composition in bulk expression through robust integration of single-cell information. Nature Communications, 2020, 11, 1971.	12.8	200
23	Title is missing!. , 2020, 16, e1009018.		0
24	Title is missing!. , 2020, 16, e1009018.		0
25	Title is missing!. , 2020, 16, e1009018.		0
26	Title is missing!. , 2020, 16, e1009018.		0
27	Title is missing!. , 2020, 16, e1009018.		0
28	Title is missing!. , 2020, 16, e1009018.		0
29	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.	2.9	41
30	Novel Lipid Long Intervening Noncoding RNA, Oligodendrocyte Maturationâ€Associated Long Intergenic Noncoding RNA, Regulates the Liver Steatosis Gene Stearoylâ€Coenzyme A Desaturase As an Enhancer RNA. Hepatology Communications, 2019, 3, 1356-1372.	4.3	28
31	A comprehensive study of metabolite genetics reveals strong pleiotropy and heterogeneity across time and context. Nature Communications, 2019, 10, 4788.	12.8	59
32	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. American Journal of Human Genetics, 2019, 105, 773-787.	6.2	45
33	Reverse geneâ€“environment interaction approach to identify variants influencing body-mass index in humans. Nature Metabolism, 2019, 1, 630-642.	11.9	14
34	Reverse GWAS: Using genetics to identify and model phenotypic subtypes. PLoS Genetics, 2019, 15, e1008009.	3.5	34
35	Genetic and environmental perturbations lead to regulatory decoherence. ELife, 2019, 8, .	6.0	34
36	Integration of human adipocyte chromosomal interactions with adipose gene expression prioritizes obesity-related genes from GWAS. Nature Communications, 2018, 9, 1512.	12.8	75

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37	ASElux: an ultra-fast and accurate allelic reads counter. Bioinformatics, 2018, 34, 1313-1320.	4.1	13
38	Phenotype-Specific Enrichment of Mendelian Disorder Genes near GWAS Regions across 62 Complex Traits. American Journal of Human Genetics, 2018, 103, 535-552.	6.2	90
39	Genomics and Systems Biology Approaches in the Study of Lipid Disorders. Revista De Investigacion Clinica, 2018, 70, 217-223.	0.4	6
40	The Metabolic Syndrome in Men study: a resource for studies of metabolic and cardiovascular diseases. Journal of Lipid Research, 2017, 58, 481-493.	4.2	147
41	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. American Journal of Human Genetics, 2017, 100, 428-443.	6.2	141
42	Family-specific aggregation of lipid GWAS variants confers the susceptibility to familial hypercholesterolemia in a large Austrian family. Atherosclerosis, 2017, 264, 58-66.	0.8	6
43	Genetic analysis of hyperemesis gravidarum reveals association with intracellular calcium release channel (RYR2). Molecular and Cellular Endocrinology, 2017, 439, 308-316.	3.2	22
44	The Contribution of GWAS Loci in Familial Dyslipidemias. PLoS Genetics, 2016, 12, e1006078.	3.5	48
45	Regulation of alternative splicing in human obesity loci. Obesity, 2016, 24, 2033-2037.	3.0	11
46	Molecular Characterization of the Lipid Genome-Wide Association Study Signal on Chromosome 18q11.2 Implicates HNF4A-Mediated Regulation of the TMEM241 Gene. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 1350-1355.	2.4	10
47	Integrative approaches for large-scale transcriptome-wide association studies. Nature Genetics, 2016, 48, 245-252.	21.4	1,618
48	An integrated, ontology-driven approach to constructing observational databases for research. Journal of Biomedical Informatics, 2015, 55, 132-142.	4.3	16
49	Familial hypercholesterolaemia in children and adolescents: gaining decades of life by optimizing detection and treatment. European Heart Journal, 2015, 36, 2425-2437.	2.2	644
50	Remote Ischemic Conditioning Alters Methylation and Expression of Cell Cycle Genes in Aneurysmal Subarachnoid Hemorrhage. Stroke, 2015, 46, 2445-2451.	2.0	25
51	Amerindian-specific regions under positive selection harbour new lipid variants in Latinos. Nature Communications, 2014, 5, 3983.	12.8	81
52	Homozygous familial hypercholesterolaemia: new insights and guidance for clinicians to improve detection and clinical management. A position paper from the Consensus Panel on Familial Hypercholesterolaemia of the European Atherosclerosis Society. European Heart Journal, 2014, 35, 2146-2157.	2.2	835
53	The WWOX Gene Modulates High-Density Lipoprotein and Lipid Metabolism. Circulation: Cardiovascular Genetics, 2014, 7, 491-504.	5.1	49
54	Genetic and environmental determinants of the susceptibility of Amerindian derived populations for having hypertriglyceridemia. Metabolism: Clinical and Experimental, 2014, 63, 887-894.	3.4	29

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55	The polygenic nature of hypertriglyceridaemia: implications for definition, diagnosis, and management. Lancet Diabetes and Endocrinology,the, 2014, 2, 655-666.	11.4	473
56	New Directions in Networks and Systems Approaches to Cardiovascular Disease. Current Genetic Medicine Reports, 2013, 1, 15-20.	1.9	0
57	Genomic study in Mexicans identifies a new locus for triglycerides and refines European lipid loci. Journal of Medical Genetics, 2013, 50, 298-308.	3.2	116
58	Exome Sequencing Identifies 2 Rare Variants for Low High-Density Lipoprotein Cholesterol in an Extended Family. Circulation: Cardiovascular Genetics, 2012, 5, 538-546.	5.1	17
59	Hyperglycemia and a Common Variant of GCKR Are Associated With the Levels of Eight Amino Acids in 9,369 Finnish Men. Diabetes, 2012, 61, 1895-1902.	0.6	251
60	Adipose Co-expression networks across Finns and Mexicans identify novel triglyceride-associated genes. BMC Medical Genomics, 2012, 5, 61.	1.5	33
61	A nonsynonymous SNP within PCDH15 is associated with lipid traits in familial combined hyperlipidemia. Human Genetics, 2010, 127, 83-89.	3.8	23
62	Fine mapping and association studies of a high-density lipoprotein cholesterol linkage region on chromosome 16 in French-Canadian subjects. European Journal of Human Genetics, 2010, 18, 342-347.	2.8	15
63	Leena Peltonen-Palotie (1952-2010) A renaissance woman of science. Clinical Genetics, 2010, 78, 409-410.	2.0	0
64	Upstream transcription factor 1 influences plasma lipid and metabolic traits in mice. Human Molecular Genetics, 2010, 19, 597-608.	2.9	30
65	Identification of Two Common Variants Contributing to Serum Apolipoprotein B Levels in Mexicans. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 353-359.	2.4	11
66	Genetic causes of high and low serum HDL-cholesterol. Journal of Lipid Research, 2010, 51, 2032-2057.	4.2	172
67	Galanin Preproprotein Is Associated With Elevated Plasma Triglycerides. Arteriosclerosis, Thrombosis, and Vascular Biology, 2009, 29, 147-152.	2.4	27
68	A Systems Genetics Approach Implicates USF1, FADS3, and Other Causal Candidate Genes for Familial Combined Hyperlipidemia. PLoS Genetics, 2009, 5, e1000642.	3.5	168
69	Genetic Variation at the Proprotein Convertase Subtilisin/Kexin Type 5 Gene Modulates High-Density Lipoprotein Cholesterol Levels. Circulation: Cardiovascular Genetics, 2009, 2, 467-475.	5.1	33
70	WW-Domain-Containing Oxidoreductase Is Associated with Low Plasma HDL-C Levels. American Journal of Human Genetics, 2008, 83, 180-192.	6.2	54
71	Merging microsatellite data: enhanced methodology and software to combine genotype data for linkage and association analysis. BMC Bioinformatics, 2008, 9, 317.	2.6	5
72	USF1 Contributes to High Serum Lipid Levels in Dutch FCHL Families and U.S. Whites With Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2007, 27, 2222-2227.	2.4	35

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73	Unraveling the complex genetics of familial combined hyperlipidemia. Annals of Medicine, 2006, 38, 337-351.	3.8	29
74	Familial combined hyperlipidemia: upstream transcription factor 1 and beyond. Current Opinion in Lipidology, 2006, 17, 101-109.	2.7	38
75	Risk Alleles of USF1 Gene Predict Cardiovascular Disease of Women in Two Prospective Studies. PLoS Genetics, 2006, 2, e69.	3.5	51
76	Common Hepatic Nuclear Factor-4Â Variants Are Associated With High Serum Lipid Levels and the Metabolic Syndrome. Diabetes, 2006, 55, 1970-1977.	0.6	60
77	Evidence for a Gene Influencing High-Density Lipoprotein Cholesterol on Chromosome 4q31.21. Arteriosclerosis, Thrombosis, and Vascular Biology, 2006, 26, 392-397.	2.4	18
78	USF1 and dyslipidemias: converging evidence for a functional intronic variant. Human Molecular Genetics, 2005, 14, 2595-2605.	2.9	78
79	Familial Combined Hyperlipidemia in Mexicans. Arteriosclerosis, Thrombosis, and Vascular Biology, 2005, 25, 1985-1991.	2.4	66
80	Association Testing in a Linked Region Using Large Pedigrees. American Journal of Human Genetics, 2005, 76, 538-542.	6.2	25
81	Association of theAPOLIPOPROTEIN A1/C3/A4/A5Gene Cluster With Triglyceride Levels and LDL Particle Size in Familial Combined Hyperlipidemia. Circulation Research, 2004, 94, 993-999.	4.5	92
82	Locus for quantitative HDL-cholesterol on chromosome 10q in Finnish families with dyslipidemia. Journal of Lipid Research, 2004, 45, 1876-1884.	4.2	22
83	Familial combined hyperlipidemia is associated with upstream transcription factor 1 (USF1). Nature Genetics, 2004, 36, 371-376.	21.4	295
84	GENETICS OF ATHEROSCLEROSIS. Annual Review of Genomics and Human Genetics, 2004, 5, 189-218.	6.2	265
85	Do DNA sequence variants in ABCA1 contribute to HDL cholesterol levels in the general population?. Journal of Clinical Investigation, 2004, 114, 1244-1247.	8.2	8
86	Do DNA sequence variants in ABCA1 contribute to HDL cholesterol levels in the general population?. Journal of Clinical Investigation, 2004, 114, 1244-1247.	8.2	7
87	Combined Analysis of Genome Scans of Dutch and Finnish Families Reveals a Susceptibility Locus for High-Density Lipoprotein Cholesterol on Chromosome 16q. American Journal of Human Genetics, 2003, 72, 903-917.	6.2	89
88	Locus for Elevated Apolipoprotein B Levels on Chromosome 1p31 in Families With Familial Combined Hyperlipidemia. Circulation Research, 2002, 90, 926-931.	4.5	46
89	A candidate gene study in low HDL-cholesterol families provides evidence for the involvement of the APOA2 gene and the APOA1C3A4 gene cluster. Atherosclerosis, 2002, 164, 103-111.	0.8	17
90	Genome Scans Provide Evidence for Low-HDL-C Loci on Chromosomes 8q23, 16q24.1-24.2, and 20q13.11 in Finnish Families. American Journal of Human Genetics, 2002, 70, 1333-1340.	6.2	91

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91	Quantitative-Trait-Locus Analysis of Body-Mass Index and of Stature, by Combined Analysis of Genome Scans of Five Finnish Study Groups. American Journal of Human Genetics, 2001, 69, 117-123.	6.2	111
92	Fine mapping of Hyplip1 and the human homolog, a potential locus for FCHL. Mammalian Genome, 2001, 12, 238-245.	2.2	17
93	Genetics of familial combined hyperlipidemia. Current Atherosclerosis Reports, 1999, 1, 79-86.	4.8	9
94	Genomewide Scan for Familial Combined Hyperlipidemia Genes in Finnish Families, Suggesting Multiple Susceptibility Loci Influencing Triglyceride, Cholesterol, and Apolipoprotein B Levels. American Journal of Human Genetics, 1999, 64, 1453-1463.	6.2	137
95	Linkage of familial combined hyperlipidaemia to chromosome 1q21â€“q23. Nature Genetics, 1998, 18, 369-373.	21.4	241