Gina M Peloso

List of Publications by Year
in descending order

98 papers	30,863 citations	41339 49 h-index	40976 93 g-index
108 all docs	108 docs citations	108 times ranked	48689 citing authors

#	Article	IF	Citations
1	Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291.	27.8	9,051
2	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
3	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
4	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	13.7	1,937
5	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
6	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	27.0	936
7	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
8	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. Journal of the American College of Cardiology, 2016, 67, 2578-2589.	2.8	723
9	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
10	Exome Sequencing,ANGPTL3Mutations, and Familial Combined Hypolipidemia. New England Journal of Medicine, 2010, 363, 2220-2227.	27.0	640
11	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	581
12	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
13	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. Nature Genetics, 2018, 50, 1514-1523.	21.4	497
14	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
15	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	12.6	438
16	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	27.0	427
17	Inactivating Mutations in NPC1L1 and Protection from Coronary Heart Disease. New England Journal of Medicine, 2014, 371, 2072-2082.	27.0	386
18	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353

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19	Forty-Three Loci Associated with Plasma Lipoprotein Size, Concentration, and Cholesterol Content in Genome-Wide Analysis. PLoS Genetics, 2009, 5, e1000730.	3.5	300
20	A genome-wide association study for blood lipid phenotypes in the Framingham Heart Study. BMC Medical Genetics, 2007, 8, S17.	2.1	289
21	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. American Journal of Human Genetics, 2014, 94, 223-232.	6.2	287
22	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
23	Best Practices and Joint Calling of the HumanExome BeadChip: The CHARGE Consortium. PLoS ONE, 2013, 8, e68095.	2.5	219
24	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
25	Prospective functional classification of all possible missense variants in PPARG. Nature Genetics, 2016, 48, 1570-1575.	21.4	210
26	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
27	Phenotypic Characterization of GeneticallyÂLowered Human Lipoprotein(a) Levels. Journal of the American College of Cardiology, 2016, 68, 2761-2772.	2.8	186
28	Association of Low-Density Lipoprotein Cholesterolâ€“Related Genetic Variants With Aortic Valve Calcium and Incident Aortic Stenosis. JAMA - Journal of the American Medical Association, 2014, 312, 1764.	7.4	184
29	Meta-analysis of gene-level tests for rare variant association. Nature Genetics, 2014, 46, 200-204.	21.4	178
30	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
31	Long-Term Cardiovascular Risk inÂWomenÂWith Hypertension DuringÂPregnancy. Journal of the American College of Cardiology, 2019, 74, 2743-2754.	2.8	169
32	Association of Sickle Cell Trait With Chronic Kidney Disease and Albuminuria in African Americans. JAMA - Journal of the American Medical Association, 2014, 312, 2115.	7.4	167
33	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. JAMA - Journal of the American Medical Association, 2017, 317, 937.	7.4	148
34	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146
35	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	12.8	140
36	Exome chip meta-analysis identifies novel loci and East Asianâ€“specific coding variants that contribute to lipid levels and coronary artery disease. Nature Genetics, 2017, 49, 1722-1730.	21.4	129

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37	Loss of Function of GALNT2 Lowers High-Density Lipoproteins in Humans, Nonhuman Primates, and Rodents. Cell Metabolism, 2016, 24, 234-245.	16.2	103
38	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	12.4	100
39	Recurring exon deletions in the HP (haptoglobin) gene contribute to lower blood cholesterol levels. Nature Genetics, 2016, 48, 359-366.	21.4	93
40	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
41	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	12.6	89
42	A human APOC3 missense variant and monoclonal antibody accelerate apoC-III clearance and lower triglyceride-rich lipoprotein levels. Nature Medicine, 2017, 23, 1086-1094.	30.7	88
43	Common genetic variation in multiple metabolic pathways influences susceptibility to low HDL-cholesterol and coronary heart disease. Journal of Lipid Research, 2010, 51, 3524-3532.	4.2	87
44	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
45	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. Nature Communications, 2018, 9, 2606.	12.8	79
46	Multi-ancestry fine mapping implicates OAS1 splicing in risk of severe COVID-19. Nature Genetics, 2022, 54, 125-127.	21.4	75
47	Protein-Truncating Variants at the Cholesteryl Ester Transfer Protein Gene and Risk for Coronary Heart Disease. Circulation Research, 2017, 121, 81-88.	4.5	68
48	Phenotypic extremes in rare variant study designs. European Journal of Human Genetics, 2016, 24, 924-930.	2.8	65
49	Rare Protein-Truncating Variants in APOB , Lower Low-Density Lipoprotein Cholesterol, and Protection Against Coronary Heart Disease. Circulation Genomic and Precision Medicine, 2019, 12, e002376.	3.6	57
50	Aggregate penetrance of genomic variants for actionable disorders in European and African Americans. Science Translational Medicine, 2016, 8, 364ra151.	12.4	55
51	Systematic Cell-Based Phenotyping of Missense Alleles Empowers Rare Variant Association Studies: A Case for LDLR and Myocardial Infarction. PLoS Genetics, 2015, 11, e1004855.	3.5	50
52	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
53	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. American Journal of Human Genetics, 2016, 99, 481-488.	6.2	45
54	HeterozygousABCG5Gene Deficiency and Risk of Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2020, 13, 417-423.	3.6	45

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55	Beverage Consumption and Longitudinal Changes in Lipoprotein Concentrations and Incident Dyslipidemia in US Adults: The Framingham Heart Study. Journal of the American Heart Association, 2020, 9, e014083.	3.7	38
56	Cardiovascular health, genetic risk, and risk of dementia in the Framingham Heart Study. Neurology, 2020, 95, e1341-e1350.	1.1	37
57	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
58	Genetic variants inCETPincrease risk of intracerebral hemorrhage. Annals of Neurology, 2016, 80, 730-740.	5.3	33
59	Multiple Associated Variants Increase the Heritability Explained for Plasma Lipids and Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2014, 7, 583-587.	5.1	29
60	Structured mating: Patterns and implications. PLoS Genetics, 2017, 13, e1006655.	3.5	29
61	Genetic Variation in Cardiometabolic Traits and Medication Targets and the Risk of Hypertensive Disorders of Pregnancy. Circulation, 2020, 142, 711-713.	1.6	27
62	Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk. Atherosclerosis, 2015, 241, 419-426.	0.8	26
63	Association of Triglyceride-Related Genetic Variants With MitralÂAnnularÂCalcification. Journal of the American College of Cardiology, 2017, 69, 2941-2948.	2.8	25
64	New Sequencing technologies help revealing unexpected mutations in Autosomal Dominant Hypercholesterolemia. Scientific Reports, 2018, 8, 1943.	3.3	25
65	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.	6.2	24
66	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
67	Twoâ€Sample Multivariable Mendelian Randomization Analysis Using R. Current Protocols, 2021, 1, e335.	2.9	17
68	Choice of population structure informative principal components for adjustment in a case-control study. BMC Genetics, 2011, 12, 64.	2.7	15
69	Targeted exonic sequencing of GWAS loci in the high extremes of the plasma lipids distribution. Atherosclerosis, 2016, 250, 63-68.	0.8	11
70	Lipoprotein(a) and Coronary Artery Disease Risk Without a Family History of Heart Disease. Journal of the American Heart Association, 2021, 10, e017470.	3.7	10
71	A null mutation in ANGPTL8 does not associate with either plasma glucose or type 2 diabetes in humans. BMC Endocrine Disorders, 2016, 16, 7.	2.2	9
72	Insights from population-based analyses of plasma lipids across the allele frequency spectrum. Current Opinion in Genetics and Development, 2018, 50, 1-6.	3.3	9

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73	Genetic Loci Associated With COVID-19 Positivity and Hospitalization in White, Black, and Hispanic Veterans of the VA Million Veteran Program. Frontiers in Genetics, 2021, 12, 777076.	2.3	9
74	Association of Exome Sequences With Cardiovascular Traits Among Blacks in the Jackson Heart Study. Circulation: Cardiovascular Genetics, 2016, 9, 368-374.	5.1	8
75	EDEM3 Modulates Plasma Triglyceride Level through Its Regulation of LRP1 Expression. IScience, 2020, 23, 100973.	4.1	8
76	Sugar-Sweetened Beverage Consumption May Modify Associations Between Genetic Variants in the CHREBP (Carbohydrate Responsive Element Binding Protein) Locus and HDL-C (High-Density Lipoprotein) Tj ETQq0 0 0 rgBT /Overlock 1 e003288.	3.6	8
77	Robust, flexible, and scalable tests for Hardyâ€“Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	2.9	6
78	Genetic Interaction with Plasma Lipids on Alzheimerâ€™s Disease in the Framingham Heart Study. Journal of Alzheimer's Disease, 2018, 66, 1275-1282.	2.6	5
79	Evaluation of a phenotype imputation approach using GAW20 simulated data. BMC Proceedings, 2018, 12, 56.	1.6	5
80	Genome-wide association study for multiple phenotype analysis. BMC Proceedings, 2018, 12, 55.	1.6	5
81	Searching for parent-of-origin effects on cardiometabolic traits in imprinted genomic regions. European Journal of Human Genetics, 2020, 28, 646-655.	2.8	5
82	Exploiting family history in aggregation unit-based genetic association tests. European Journal of Human Genetics, 2022, 30, 1355-1362.	2.8	4
83	Evaluation of methods accounting for population structure with pedigree data and continuous outcomes. Genetic Epidemiology, 2011, 35, n/a-n/a.	1.3	3
84	Observational and Genetic Associations of Resting Heart Rate With Aortic Valve Calcium. American Journal of Cardiology, 2018, 121, 1246-1252.	1.6	3
85	Evaluation of population stratification adjustment using genomeâ€wide or exonic variants. Genetic Epidemiology, 2020, 44, 702-716.	1.3	3
86	Genetically elevated highâ€density lipoprotein cholesterol through the cholesteryl ester transfer protein gene does not associate with risk of Alzheimer's disease. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2018, 10, 595-598.	2.4	2
87	History of Suicide Attempts and COVID-19 Infection in Veterans with Schizophrenia or Schizoaffective Disorder: Moderating Effects of Age and Body Mass Index. Complex Psychiatry, 2022, 8, 28-34.	0.9	2
88	Genome-wide and phenome-wide analysis of ideal cardiovascular health in the VA Million Veteran Program. PLoS ONE, 2022, 17, e0267900.	2.5	2
89	Family history aggregation unit-based tests to detect rare genetic variant associations with application to the Framingham Heart Study. American Journal of Human Genetics, 2022, 109, 738-749.	6.2	1
90	P2â€111: INTERACTION BETWEEN ALZHEIMER'S DISEASE GENETIC RISK SCORE AND MIDLIFE PLASMA LIPID LEVELS ON ALZHEIMER â€™S DISEASE IN THE FRAMINGHAM HEART STUDY. Alzheimer's and Dementia, 2018, 14, P711.	0.8	0

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91	Beverage Consumption and Longitudinal Changes in Lipid Concentrations and Incident Dyslipidemia in U.S. Adults: The Framingham Heart Study (P18-017-19). Current Developments in Nutrition, 2019, 3, nzz039.P18-017-19.	0.3	0
92	Interactions Between Sugar-Sweetened Beverage Consumption and Genetic Variants in the ChREBP Locus on Lipoprotein Concentrations in the UK Biobank: A Replication Study. Current Developments in Nutrition, 2020, 4, nzaa058_013.	0.3	0
93	Associations Between Genetic Variants near the CHREBP Locus and Lipoprotein Concentrations May Be Modified by Sugar-Sweetened Beverage Consumption. Current Developments in Nutrition, 2020, 4, nzaa058_014.	0.3	0
94	Genetic analysis of biobank data: Familial history aggregationâ€based tests (FHAT) with application to Alzheimer's disease. Alzheimer's and Dementia, 2020, 16, e038648.	0.8	0
95	Comparative transâ€ethnic metaâ€analysis of whole exome sequencing variation for Alzheimerâ€™s disease (AD) in 18,402 individuals of the Alzheimerâ€™s Disease Sequencing Project (ADSP). Alzheimer's and Dementia, 2020, 16, e041583.	0.8	0
96	Assessing whole genome sequencing variation for Alzheimerâ€™s disease in 4707 individuals from the Alzheimerâ€™s Disease Sequencing Project (ADSP). Alzheimer's and Dementia, 2020, 16, e045548.	0.8	0
97	Frequency of familial Alzheimerâ€™s disease gene mutations within the Alzheimer Disease Sequencing Project (ADSP). Alzheimer's and Dementia, 2020, 16, e046203.	0.8	0
98	Whole genome sequencing analysis of cognitively Wellderly individuals identifies potential protective genetic variants for Alzheimer's disease.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e054917.	0.8	0