L Adrienne Cupples

List of Publications by Year in Descending Order

642 papers	80,729 citations	138 h-index	266 g-index
679 ext. papers	93,451 ext. citations	9.1 avg, IF	6.84 L-index

#	Paper	IF	Citations
642	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed.. *Cell Genomics*, **2022**, 2, 100084-100084		1
641	Sociodemographic Patterns of Exposure to Civil Aircraft Noise in the United States.. *Environmental Health Perspectives*, **2022**, 130, 27009	8.4	1
640	Rare coding variants in RCN3 are associated with blood pressure.. *BMC Genomics*, **2022**, 23, 148	4.5	
639	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data.. *Nature Genetics*, **2022**,	36.3	6
638	Meta-analysis of genome-wide association studies identifies ancestry-specific associations underlying circulating total tau levels.. *Communications Biology*, **2022**, 5, 336	6.7	0
637	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential.. *Science Advances*, **2022**, 8, eabl6579	14.3	3
636	Lymphocyte activation gene-3-associated protein networks are associated with HDL-cholesterol and mortality in the Trans-omics for Precision Medicine program.. *Communications Biology*, **2022**, 5, 362	6.7	0
635	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
634	Association of Clonal Hematopoiesis with Chronic Obstructive Pulmonary Disease. *Blood*, **2021**,	2.2	5
633	Association of mitochondrial DNA copy number with cardiometabolic diseases.. *Cell Genomics*, **2021**, 1,		1
632	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. *Nature Genetics*, **2021**, 53, 1504-1516	36.3	7
631	Small Dense Low-Density Lipoprotein Cholesterol Is the Most Atherogenic Lipoprotein Parameter in the Prospective Framingham Offspring Study. *Journal of the American Heart Association*, **2021**, 10, e019140	6	20
630	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. *American Journal of Human Genetics*, **2021**, 108, 564-582	11	7
629	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nature Communications*, **2021**, 12, 2182	17.4	5
628	A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. *American Journal of Epidemiology*, **2021**, 190, 1977-1992	3.8	3
627	Genetic variants modify the associations of concentrations of methylmalonic acid, vitamin B-12, vitamin B-6, and folate with bone mineral density. *American Journal of Clinical Nutrition*, **2021**, 114, 578-587	7	3
626	Genome sequencing unveils a regulatory landscape of platelet reactivity. *Nature Communications*, **2021**, 12, 3626	17.4	6

625	Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. *Nature Communications*, **2021**, 12, 3506	17.4	
624	Exome sequence association study of levels and longitudinal change of cardiovascular risk factor phenotypes in European Americans and African Americans from the Atherosclerosis Risk in Communities Study. *Genetic Epidemiology*, **2021**, 45, 651-663	2.6	0
623	Proteomic Signatures of Lifestyle Risk Factors for Cardiovascular Disease: A Cross-Sectional Analysis of the Plasma Proteome in the Framingham Heart Study. *Journal of the American Heart Association*, **2021**, 10, e018020	6	3
622	Revisiting methods for modeling longitudinal and survival data: Framingham Heart Study. *BMC Medical Research Methodology*, **2021**, 21, 29	4.7	1
621	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*, **2021**, 590, 290-299	50.4	268
620	BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. *Human Genetics and Genomics Advances*, **2021**, 2,	0.8	1
619	Identification of novel and rare variants associated with handgrip strength using whole genome sequence data from the NHLBI Trans-Omics in Precision Medicine (TOPMed) Program. *PLoS ONE*, **2021**, 16, e0253611	3.7	1
618	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. *Genome Medicine*, **2021**, 13, 136	14.4	3
617	Presence and transmission of mitochondrial heteroplasmic mutations in human populations of European and African ancestry. *Mitochondrion*, **2021**, 60, 33-42	4.9	0
616	Lifestyle Risk Score: handling missingness of individual lifestyle components in meta-analysis of gene-by-lifestyle interactions. *European Journal of Human Genetics*, **2021**, 29, 839-850	5.3	
615	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002772	5.2	8
614	Disclosing genetic risk for Alzheimer's dementia to individuals with mild cognitive impairment. *Alzheimer's and Dementia: Translational Research and Clinical Interventions*, **2020**, 6, e12002	6	9
613	Searching for parent-of-origin effects on cardiometabolic traits in imprinted genomic regions. *European Journal of Human Genetics*, **2020**, 28, 646-655	5.3	1
612	Genome-wide meta-analysis of variant-by-diuretic interactions as modulators of lipid traits in persons of European and African ancestry. *Pharmacogenomics Journal*, **2020**, 20, 482-493	3.5	1
611	Statin-induced LDL cholesterol response and type 2 diabetes: a bidirectional two-sample Mendelian randomization study. *Pharmacogenomics Journal*, **2020**, 20, 462-470	3.5	7
610	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. *Nature Communications*, **2020**, 11, 5182	17.4	6
609	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature*, **2020**, 586, 763-768	50.4	127
608	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	36.3	33

607	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. *Nature Communications*, **2020**, 11, 6417	17.4	17
606	Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. *Molecular Psychiatry*, **2020**, 25, 1859-1875	15.1	106
605	Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. *American Journal of Human Genetics*, **2019**, 105, 706-718	11	22
604	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39
603	A fully adjusted two-stage procedure for rank-normalization in genetic association studies. *Genetic Epidemiology*, **2019**, 43, 263-275	2.6	29
602	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. *Nature Communications*, **2019**, 10, 376	17.4	41
601	Direct Versus Calculated LDL Cholesterol and C-Reactive Protein in Cardiovascular Disease Risk Assessment in the Framingham Offspring Study. *Clinical Chemistry*, **2019**, 65, 1102-1114	5.5	5
600	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. *Human Molecular Genetics*, **2019**, 28, 2615-2633	5.6	14
599	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. *Nature Genetics*, **2019**, 51, 636-648	36.3	59
598	Quality control and integration of genotypes from two calling pipelines for whole genome sequence data in the Alzheimer's disease sequencing project. *Genomics*, **2019**, 111, 808-818	4.3	10
597	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. *Molecular Psychiatry*, **2019**, 24, 1920-1932	15.1	30
596	GENERATING SURVIVAL TIMES WITH TIME-VARYING COVARIATES USING THE LAMBERT W FUNCTION. *Communications in Statistics Part B: Simulation and Computation*, **2019**, 2019,	0.6	1
595	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. *Nature Communications*, **2019**, 10, 5121	17.4	31
594	Integrating genetic, transcriptional, and biological information provides insights into obesity. *International Journal of Obesity*, **2019**, 43, 457-467	5.5	3
593	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A tau, immunity and lipid processing. *Nature Genetics*, **2019**, 51, 414-430	36.3	917
592	Revisit Population-based and Family-based Genotype Imputation. *Scientific Reports*, **2019**, 9, 1800	4.9	2
591	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. *PLoS Genetics*, **2019**, 15, e1008500	6	90
590	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. *American Journal of Human Genetics*, **2019**, 104, 260-274	11	43

589	A Longitudinal Study of Trunk Muscle Properties and Severity of Thoracic Kyphosis in Women and Men: The Framingham Study. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2019**, 74, 420-427	6.4	21
588	A longitudinal study of disc height narrowing and facet joint osteoarthritis at the thoracic and lumbar spine, evaluated by computed tomography: the Framingham Study. *Spine Journal*, **2018**, 18, 2065-2073	4	18
587	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. *Nature Communications*, **2018**, 9, 260	17.4	174
586	Whole genome sequence analyses of brain imaging measures in the Framingham Study. *Neurology*, **2018**, 90, e188-e196	6.5	19
585	Lower Lean Mass Measured by Dual-Energy X-ray Absorptiometry (DXA) is Not Associated with Increased Risk of Hip Fracture in Women: The Framingham Osteoporosis Study. *Calcified Tissue International*, **2018**, 103, 16-23	3.9	13
584	Large-scale pharmacogenomic study of sulfonylureas and the QT, JT and QRS intervals: CHARGE Pharmacogenomics Working Group. *Pharmacogenomics Journal*, **2018**, 18, 127-135	3.5	9
583	A randomized controlled trial of disclosing genetic risk information for Alzheimer disease via telephone. *Genetics in Medicine*, **2018**, 20, 132-141	8.1	27
582	Pharmacogenomics study of thiazide diuretics and QT interval in multi-ethnic populations: the cohorts for heart and aging research in genomic epidemiology. *Pharmacogenomics Journal*, **2018**, 18, 215-226	3.5	2
581	Sugar-sweetened beverage intake associations with fasting glucose and insulin concentrations are not modified by selected genetic variants in a ChREBP-FGF21 pathway: a meta-analysis. *Diabetologia*, **2018**, 61, 317-330	10.3	17
580	Genome-Wide Interactions with Dairy Intake for Body Mass Index in Adults of European Descent. *Molecular Nutrition and Food Research*, **2018**, 62, 1700347	5.9	5
579	Diabetes and Deficits in Cortical Bone Density, Microarchitecture, and Bone Size: Framingham HR-pQCT Study. *Journal of Bone and Mineral Research*, **2018**, 33, 54-62	6.3	96
578	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. *Nature Communications*, **2018**, 9, 2606	17.4	53
577	A fine-mapping study of central obesity loci incorporating functional annotation and imputation. *European Journal of Human Genetics*, **2018**, 26, 1369-1377	5.3	4
576	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. *Nature Communications*, **2018**, 9, 3391	17.4	90
575	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. *PLoS ONE*, **2018**, 13, e0198166	3.7	31
574	Association of Obesity With Mortality Over 24 Years of Weight History: Findings From the Framingham Heart Study. *JAMA Network Open*, **2018**, 1, e184587	10.4	67
573	Do changes in DNA methylation mediate or interact with SNP variation? A pharmacoepigenetic analysis. *BMC Genetics*, **2018**, 19, 70	2.6	6
572	Common Coding Variants in Are Associated With the Nav1.8 Late Current and Cardiac Conduction. *Circulation Genomic and Precision Medicine*, **2018**, 11, e001663	5.2	14

571	A high throughput, functional screen of human Body Mass Index GWAS loci using tissue-specific RNAi Drosophila melanogaster crosses. *PLoS Genetics*, **2018**, 14, e1007222	6	14
570	Common variants associated with changes in levels of circulating free fatty acids after administration of glucose-insulin-potassium (GIK) therapy in the IMMEDIATE trial. *Pharmacogenomics Journal*, **2017**, 17, 76-83	3.5	5
569	A genome-wide interaction analysis of tricyclic/tetracyclic antidepressants and RR and QT intervals: a pharmacogenomics study from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. *Journal of Medical Genetics*, **2017**, 54, 313-323	5.8	5
568	Epigenetic Patterns in Blood Associated With Lipid Traits Predict Incident Coronary Heart Disease Events and Are Enriched for Results From Genome-Wide Association Studies. *Circulation: Cardiovascular Genetics*, **2017**, 10,		72
567	Cardiovascular disease prevalence and insulin resistance in the Kyushu-Okinawa Population Study and the Framingham Offspring Study. *Journal of Clinical Lipidology*, **2017**, 11, 348-356	4.9	10
566	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. *Nature Communications*, **2017**, 8, 14977	17.4	105
565	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. *Nature Genetics*, **2017**, 49, 125-130	36.3	80
564	Multiancestry Study of Gene-Lifestyle Interactions for Cardiovascular Traits in 610 475 Individuals From 124 Cohorts: Design and Rationale. *Circulation: Cardiovascular Genetics*, **2017**, 10,		30
563	Association of Triglyceride-Related Genetic Variants With Mitral Annular Calcification. *Journal of the American College of Cardiology*, **2017**, 69, 2941-2948	15.1	16
562	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. *American Journal of Human Genetics*, **2017**, 100, 51-63	11	30
561	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. *Nature Genetics*, **2017**, 49, 1560-1563	36.3	68
560	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
559	Genome-wide association meta-analysis of fish and EPA+DHA consumption in 17 US and European cohorts. *PLoS ONE*, **2017**, 12, e0186456	3.7	15
558	Genetic assessment of age-associated Alzheimer disease risk: Development and validation of a polygenic hazard score. *PLoS Medicine*, **2017**, 14, e1002258	11.6	209
557	Whole exome sequencing in the Framingham Heart Study identifies rare variation in HYAL2 that influences platelet aggregation. *Thrombosis and Haemostasis*, **2017**, 117, 1083-1092	7	9
556	Thoracic Kyphosis and Physical Function: The Framingham Study. *Journal of the American Geriatrics Society*, **2017**, 65, 2257-2264	5.6	15
555	Genome-wide association and functional studies identify a role for matrix Gla protein in osteoarthritis of the hand. *Annals of the Rheumatic Diseases*, **2017**, 76, 2046-2053	2.4	42
554	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. *Nature Genetics*, **2017**, 49, 1373-1384	36.3	508

553	Loss-of-Function Variants, Low-Density Lipoprotein Cholesterol, and Risk of Coronary Heart Disease and Stroke: Data From 9 Studies of Blacks and Whites. *Circulation: Cardiovascular Genetics*, **2017**, 10, e001632		39
552	Visceral Adipose Tissue Is Associated With Bone Microarchitecture in the Framingham Osteoporosis Study. *Journal of Bone and Mineral Research*, **2017**, 32, 143-150	6.3	37
551	Heritability and Genetic Correlations for Bone Microarchitecture: The Framingham Study Families. *Journal of Bone and Mineral Research*, **2017**, 32, 106-114	6.3	21
550	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
549	Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. *PLoS Genetics*, **2017**, 13, e1006719	6	60
548	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. *PLoS Genetics*, **2017**, 13, e1006812	6	13
547	Approaches to detect genetic effects that differ between two strata in genome-wide meta-analyses: Recommendations based on a systematic evaluation. *PLoS ONE*, **2017**, 12, e0181038	3.7	14
546	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. *Circulation: Cardiovascular Genetics*, **2016**, 9, 511-520		34
545	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
544	Rooted in risk: genetic predisposition for low-density lipoprotein cholesterol level associates with diminished low-density lipoprotein cholesterol response to statin treatment. *Pharmacogenomics*, **2016**, 17, 1621-1628	2.6	8
543	Targeted sequencing of genome wide significant loci associated with bone mineral density (BMD) reveals significant novel and rare variants: the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) targeted sequencing study. *Human Molecular Genetics*, **2016**, 25, 5234-5243	5.6	6
542	Ethnic Differences in Glucose Homeostasis Markers between the Kyushu-Okinawa Population Study and the Framingham Offspring Study. *Scientific Reports*, **2016**, 6, 36725	4.9	8
541	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. *Science Translational Medicine*, **2016**, 8, 341ra76	17.5	77
540	Imputing rare variants in families using a two-stage approach. *BMC Proceedings*, **2016**, 10, 209-214	2.3	4
539	Rare variant associations with waist-to-hip ratio in European-American and African-American women from the NHLBI-Exome Sequencing Project. *European Journal of Human Genetics*, **2016**, 24, 1181-7	5.3	2
538	Genome-wide gene-environment interactions on quantitative traits using family data. *European Journal of Human Genetics*, **2016**, 24, 1022-8	5.3	1
537	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
536	Evaluation of power of the Illumina HumanOmni5M-4v1 BeadChip to detect risk variants for human complex diseases. *European Journal of Human Genetics*, **2016**, 24, 1029-34	5.3	4

535	Discovery of Genetic Variation on Chromosome 5q22 Associated with Mortality in Heart Failure. *PLoS Genetics*, **2016**, 12, e1006034	6	26
534	Whole Exome Sequencing in Atrial Fibrillation. *PLoS Genetics*, **2016**, 12, e1006284	6	24
533	Genome-Wide Association Study for Incident Myocardial Infarction and Coronary Heart Disease in Prospective Cohort Studies: The CHARGE Consortium. *PLoS ONE*, **2016**, 11, e0144997	3.7	53
532	An Empirical Comparison of Joint and Stratified Frameworks for Studying G E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Gene-Lifestyle Interactions Working Group. *Genetic Epidemiology*, **2016**, 40, 404-15	2.6	15
531	Robust analysis of secondary phenotypes in case-control genetic association studies. *Statistics in Medicine*, **2016**, 35, 4226-37	2.3	7
530	Evaluation of a Two-Stage Approach in Trans-Ethnic Meta-Analysis in Genome-Wide Association Studies. *Genetic Epidemiology*, **2016**, 40, 284-92	2.6	8
529	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. *Journal of Medical Genetics*, **2016**, 53, 835-845	5.8	28
528	Meta-analysis of 49 549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in ANGPTL4 determining fasting TG levels. *Journal of Medical Genetics*, **2016**, 53, 441-9	5.8	27
527	O1-09-04: Identification of Whole Exome Sequencing Variants Associated with Late-Onset Alzheimer N Disease in the Cohorts for Heart and Aging Research in Genomic Epidemiology (Charge) Consortium **2016**, 12, P197-P198		
526	A comparison of time dependent Cox regression, pooled logistic regression and cross sectional pooling with simulations and an application to the Framingham Heart Study. *BMC Medical Research Methodology*, **2016**, 16, 148	4.7	30
525	Disclosing Pleiotropic Effects During Genetic Risk Assessment for Alzheimer Disease: A Randomized Trial. *Annals of Internal Medicine*, **2016**, 164, 155-63	8	26
524	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. *Journal of the American College of Cardiology*, **2016**, 67, 2578-89	15.1	458
523	Genetic loci associated with ideal cardiovascular health: A meta-analysis of genome-wide association studies. *American Heart Journal*, **2016**, 175, 112-20	4.9	17
522	A genetic risk score is associated with statin-induced low-density lipoprotein cholesterol lowering. *Pharmacogenomics*, **2016**, 17, 583-91	2.6	8
521	Novel Genetic Variants Associated With Increased Vertebral Volumetric BMD, Reduced Vertebral Fracture Risk, and Increased Expression of SLC1A3 and EPHB2. *Journal of Bone and Mineral Research*, **2016**, 31, 2085-2097	6.3	33
520	Heritability of Thoracic Spine Curvature and Genetic Correlations With Other Spine Traits: The Framingham Study. *Journal of Bone and Mineral Research*, **2016**, 31, 2077-2084	6.3	18
519	Integromic analysis of genetic variation and gene expression identifies networks for cardiovascular disease phenotypes. *Circulation*, **2015**, 131, 536-49	16.7	46
518	Genetic variation at glucose and insulin trait loci and response to glucose-insulin-potassium (GIK) therapy: the IMMEDIATE trial. *Pharmacogenomics Journal*, **2015**, 15, 55-62	3.5	6

517	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
516	Analysis of loss-of-function variants and 20 risk factor phenotypes in 8,554 individuals identifies loci influencing chronic disease. *Nature Genetics*, **2015**, 47, 640-2	36.3	39
515	Genetic modifiers of response to glucose-insulin-potassium (GIK) infusion in acute coronary syndromes and associations with clinical outcomes in the IMMEDIATE trial. *Pharmacogenomics Journal*, **2015**, 15, 488-95	3.5	7
514	Rare and Coding Region Genetic Variants Associated With Risk of Ischemic Stroke: The NHLBI Exome Sequence Project. *JAMA Neurology*, **2015**, 72, 781-8	17.2	37
513	Genome of The Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. *Nature Communications*, **2015**, 6, 6065	17.4	32
512	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. *Nature*, **2015**, 526, 112-7	50.4	308
511	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
510	Consumption of meat is associated with higher fasting glucose and insulin concentrations regardless of glucose and insulin genetic risk scores: a meta-analysis of 50,345 Caucasians. *American Journal of Clinical Nutrition*, **2015**, 102, 1266-78	7	51
509	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. *Nature*, **2015**, 518, 102-6	50.4	463
508	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. *Molecular Psychiatry*, **2015**, 20, 647-656	15.1	167
507	Fine mapping the region reveals a common intronic insertion associated to HDL-C. *Npj Aging and Mechanisms of Disease*, **2015**, 1, 15011	5.5	5
506	QCT Volumetric Bone Mineral Density and Vascular and Valvular Calcification: The Framingham Study. *Journal of Bone and Mineral Research*, **2015**, 30, 1767-74	6.3	29
505	Generalized estimating equations for genome-wide association studies using longitudinal phenotype data. *Statistics in Medicine*, **2015**, 34, 118-30	2.3	31
504	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. *PLoS Genetics*, **2015**, 11, e1005378	6	220
503	Drug-Gene Interactions of Antihypertensive Medications and Risk of Incident Cardiovascular Disease: A Pharmacogenomics Study from the CHARGE Consortium. *PLoS ONE*, **2015**, 10, e0140496	3.7	12
502	Factors affecting recall of different types of personal genetic information about Alzheimer's disease risk: the REVEAL study. *Public Health Genomics*, **2015**, 18, 78-86	1.9	4
501	Gene dietary pattern interactions in obesity: analysis of up to 68 317 adults of European ancestry. *Human Molecular Genetics*, **2015**, 24, 4728-38	5.6	68
500	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920

499	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
498	Revisiting heritability accounting for shared environmental effects and maternal inheritance. *Human Genetics*, **2015**, 134, 169-79	6.3	10
497	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
496	A randomized noninferiority trial of condensed protocols for genetic risk disclosure of Alzheimer's disease. *Alzheimer's and Dementia*, **2015**, 11, 1222-30	1.2	24
495	Population genomic analysis of 962 whole genome sequences of humans reveals natural selection in non-coding regions. *PLoS ONE*, **2015**, 10, e0121644	3.7	12
494	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, 223-32	11	233
493	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
492	Multi-ethnic fine-mapping of 14 central adiposity loci. *Human Molecular Genetics*, **2014**, 23, 4738-44	5.6	38
491	Comparing baseline and longitudinal measures in association studies. *BMC Proceedings*, **2014**, 8, S84	2.3	2
490	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
489	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. *BMJ, The*, **2014**, 349, g4164	5.9	406
488	Sequencing of SCN5A identifies rare and common variants associated with cardiac conduction: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. *Circulation: Cardiovascular Genetics*, **2014**, 7, 365-73		7
487	Trans-ethnic meta-analysis of white blood cell phenotypes. *Human Molecular Genetics*, **2014**, 23, 6944-60	5.6	45
486	Meta-analysis of loci associated with age at natural menopause in African-American women. *Human Molecular Genetics*, **2014**, 23, 3327-42	5.6	44
485	Loss-of-function mutations in APOC3, triglycerides, and coronary disease. *New England Journal of Medicine*, **2014**, 371, 22-31	59.2	721
484	Meta-analysis identifies loci affecting levels of the potential osteoarthritis biomarkers sCOMP and uCTX-II with genome wide significance. *Journal of Medical Genetics*, **2014**, 51, 596-604	5.8	15
483	Sequencing of 2 subclinical atherosclerosis candidate regions in 3669 individuals: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. *Circulation: Cardiovascular Genetics*, **2014**, 7, 359-64		11
482	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. *Nature Communications*, **2014**, 5, 5068	17.4	160

481	A genome-wide copy number association study of osteoporotic fractures points to the 6p25.1 locus. *Journal of Medical Genetics*, **2014**, 51, 122-31	5.8	32
480	Trends in the association of parental history of obesity over 60 years. *Obesity*, **2014**, 22, 919-24	8	12
479	Sequence kernel association test for survival traits. *Genetic Epidemiology*, **2014**, 38, 191-7	2.6	44
478	FTO genetic variants, dietary intake and body mass index: insights from 177,330 individuals. *Human Molecular Genetics*, **2014**, 23, 6961-72	5.6	120
477	Vertebral size, bone density, and strength in men and women matched for age and areal spine BMD. *Journal of Bone and Mineral Research*, **2014**, 29, 562-9	6.3	30
476	Performance of statistical methods on CHARGE targeted sequencing data. *BMC Genetics*, **2014**, 15, 104	2.6	
475	Association of low-density lipoprotein cholesterol-related genetic variants with aortic valve calcium and incident aortic stenosis. *JAMA - Journal of the American Medical Association*, **2014**, 312, 1764-71	27.4	134
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4	Rare coding variants in 35 genes associate with circulating lipid levels □ multi-ancestry analysis of 170,000 exomes		2
3	Multi-ancestry analysis of gene-sleep interactions in 126,926 individuals identifies multiple novel blood lipid loci that contribute to our understanding of sleep-associated adverse blood lipid profile		1
2	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program		68
1	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations		2