Nancy L Heard-Costa

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

57 papers	14,408 citations	37 h-index	64 g-index
64 ext. papers	17,319 ext. citations	15.7 avg, IF	3.91 L-index

#	Paper	IF	Citations
57	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
56	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
55	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
54	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
53	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
52	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. *Nature Genetics*, **2010**, 42, 949-60	36.3	724
51	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
50	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. *Nature Genetics*, **2011**, 43, 1131-8	36.3	415
49	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
48	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
47	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics*, **2013**, 9, e1003500	6	277
46	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
45	NRXN3 is a novel locus for waist circumference: a genome-wide association study from the CHARGE Consortium. *PLoS Genetics*, **2009**, 5, e1000539	6	203
44	Genetic variation in white matter hyperintensity volume in the Framingham Study. *Stroke*, **2004**, 35, 1609-13	6.7	203
43	Genome-wide association for abdominal subcutaneous and visceral adipose reveals a novel locus for visceral fat in women. *PLoS Genetics*, **2012**, 8, e1002695	6	199
42	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
41	The Framingham Heart Study 100K SNP genome-wide association study resource: overview of 17 phenotype working group reports. *BMC Medical Genetics*, **2007**, 8 Suppl 1, S1	2.1	152

40	Framingham Heart Study 100K project: genome-wide associations for cardiovascular disease outcomes. *BMC Medical Genetics*, **2007**, 8 Suppl 1, S5	2.1	139
39	Genomewide linkage analysis of body mass index across 28 years of the Framingham Heart Study. *American Journal of Human Genetics*, **2002**, 71, 1044-50	11	135
38	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. *Nature*, **2019**, 570, 71-76	50.4	129
37	Genome-wide association to body mass index and waist circumference: the Framingham Heart Study 100K project. *BMC Medical Genetics*, **2007**, 8 Suppl 1, S18	2.1	128
36	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
35	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. *Genome Biology*, **2017**, 18, 16	18.3	108
34	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
33	Genome-wide analysis of BMI in adolescents and young adults reveals additional insight into the effects of genetic loci over the life course. *Human Molecular Genetics*, **2013**, 22, 3597-607	5.6	103
32	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
31	Polymorphisms in the insulin-degrading enzyme gene are associated with type 2 diabetes in men from the NHLBI Framingham Heart Study. *Diabetes*, **2003**, 52, 1562-7	0.9	89
30	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
29	Genomewide linkage analysis to presbycusis in the Framingham Heart Study. *JAMA Otolaryngology*, **2003**, 129, 285-9		69
28	Genome-wide scan for white matter hyperintensity: the Framingham Heart Study. *Stroke*, **2006**, 37, 77-81	6.7	61
27	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
26	Genetics Analysis Workshop 16 Problem 2: the Framingham Heart Study data. *BMC Proceedings*, **2009**, 3 Suppl 7, S3	2.3	45
25	Sequence kernel association test for survival traits. *Genetic Epidemiology*, **2014**, 38, 191-7	2.6	44
24	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
23	Genome-wide association of pericardial fat identifies a unique locus for ectopic fat. *PLoS Genetics*, **2012**, 8, e1002705	6	42

22	Evidence for a gene influencing serum bilirubin on chromosome 2q telomere: a genomewide scan in the Framingham study. *American Journal of Human Genetics*, **2003**, 72, 1029-34	11	42
21	Genome-wide linkage to chromosome 6 for waist circumference in the Framingham Heart Study. *Diabetes*, **2004**, 53, 1399-402	0.9	41
20	Heritability, linkage, and genetic associations of exercise treadmill test responses. *Circulation*, **2007** , 115, 2917-24	16.7	32
19	Limits of fine-mapping a quantitative trait. *Genetic Epidemiology*, **2003**, 24, 99-106	2.6	31
18	Genomewide linkage analysis of weight change in the Framingham Heart Study. *Journal of Clinical Endocrinology and Metabolism*, **2005**, 90, 3197-201	5.6	30
17	De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 2560-2569	11.5	29
16	Linkage and association with pulmonary function measures on chromosome 6q27 in the Framingham Heart Study. *Human Molecular Genetics*, **2003**, 12, 2745-51	5.6	29
15	Gene-centric meta-analyses for central adiposity traits in up to 57 412 individuals of European descent confirm known loci and reveal several novel associations. *Human Molecular Genetics*, **2014**, 23, 2498-510	5.6	22
14	Sex and age specific effects of chromosomal regions linked to body mass index in the Framingham Study. *BMC Genetics*, **2006**, 7, 7	2.6	18
13	Genome-wide association meta-analysis identifies five novel loci for age-related hearing impairment. *Scientific Reports*, **2019**, 9, 15192	4.9	14
12	Trends in the association of parental history of obesity over 60 years. *Obesity*, **2014**, 22, 919-24	8	12
11	Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. *Human Molecular Genetics*, **2014**, 23, 6607-15	5.6	11
10	Sequence variation in TMEM18 in association with body mass index: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. *Circulation: Cardiovascular Genetics*, **2014**, 7, 344-9		5
9	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 874-893	11	5
8	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. *Nature Communications*, **2021**, 12, 3505	17.4	5
7	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
6	Integrating genetic, transcriptional, and biological information provides insights into obesity. *International Journal of Obesity*, **2019**, 43, 457-467	5.5	3
5	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

4	Consistency of linkage results across exams and methods in the Framingham Heart Study. *BMC Genetics*, **2003**, 4 Suppl 1, S30	2.6	2
3	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. *Stroke*, **2021**, STROKEAHA120031792	6.7	2
2	Revisit Population-based and Family-based Genotype Imputation. *Scientific Reports*, **2019**, 9, 1800	4.9	2
1	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 1836-1851	11	1