

Nancy L Heard-Costa

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

18,937
citations

87888

38
h-index

118850

62
g-index

64
all docs

64
docs citations

64
times ranked

26190
citing authors

#	ARTICLE	IF	CITATIONS
1	Rare coding variants in 35 genes associate with circulating lipid levelsâ€”A multi-ancestry analysis of 170,000 exomes. <i>American Journal of Human Genetics</i> , 2022, 109, 81-96.	6.2	24
2	Genome-wide association meta-analysis identifies 48 risk variants and highlights the role of the stria vascularis in hearing loss. <i>American Journal of Human Genetics</i> , 2022, 109, 1077-1091.	6.2	27
3	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021, 108, 874-893.	6.2	28
4	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. <i>Nature Communications</i> , 2021, 12, 3505.	12.8	49
5	Hearing Function: Identification of New Candidate Genes Further Explaining the Complexity of This Sensory Ability. <i>Genes</i> , 2021, 12, 1228.	2.4	1
6	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021, 108, 1836-1851.	6.2	14
7	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. <i>Stroke</i> , 2021, , STROKEAHA120031792.	2.0	16
8	De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2560-2569.	7.1	71
9	Genome-wide association meta-analysis identifies five novel loci for age-related hearing impairment. <i>Scientific Reports</i> , 2019, 9, 15192.	3.3	32
10	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.	27.8	248
11	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	21.4	89
12	Revisit Population-based and Family-based Genotype Imputation. <i>Scientific Reports</i> , 2019, 9, 1800.	3.3	4
13	Integrating genetic, transcriptional, and biological information provides insights into obesity. <i>International Journal of Obesity</i> , 2019, 43, 457-467.	3.4	8
14	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	21.4	286
15	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. <i>Genome Biology</i> , 2017, 18, 16.	8.8	151
16	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
17	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	12.8	169
18	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. <i>Nature Genetics</i> , 2017, 49, 125-130.	21.4	116

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19	Genome-wide physical activity interactions in adiposity • A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
20	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
21	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, 1181-1187.	2.8	5
22	Evaluation of power of the Illumina HumanOmni5M-4v1 BeadChip to detect risk variants for human complex diseases. European Journal of Human Genetics, 2016, 24, 1029-1034.	2.8	7
23	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.	3.5	331
24	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
25	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
26	Directional dominance on stature and cognition in diverse human populations. Nature, 2015, 523, 459-462.	27.8	173
27	Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. Human Molecular Genetics, 2014, 23, 6607-6615.	2.9	14
28	Trends in the association of parental history of obesity over 60 years. Obesity, 2014, 22, 919-924.	3.0	15
29	Sequence Kernel Association Test for Survival Traits. Genetic Epidemiology, 2014, 38, 191-197.	1.3	58
30	Sequence Variation in <i>TMEM18</i> in Association With Body Mass Index. Circulation: Cardiovascular Genetics, 2014, 7, 344-349.	5.1	8
31	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, 2498-2510.	2.9	28
32	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
33	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
34	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, 3597-3607.	2.9	116
35	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
36	Genome-Wide Association of Pericardial Fat Identifies a Unique Locus for Ectopic Fat. PLoS Genetics, 2012, 8, e1002705.	3.5	48

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37	Genome-Wide Association for Abdominal Subcutaneous and Visceral Adipose Reveals a Novel Locus for Visceral Fat in Women. <i>PLoS Genetics</i> , 2012, 8, e1002695.	3.5	245
38	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	27.8	383
39	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011, 43, 1131-1138.	21.4	501
40	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	27.8	1,789
41	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	21.4	836
42	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	21.4	2,634
43	NRXN3 Is a Novel Locus for Waist Circumference: A Genome-Wide Association Study from the CHARGE Consortium. <i>PLoS Genetics</i> , 2009, 5, e1000539.	3.5	230
44	Genetics Analysis Workshop 16 Problem 2: the Framingham Heart Study data. <i>BMC Proceedings</i> , 2009, 3, S3.	1.6	80
45	Heritability, Linkage, and Genetic Associations of Exercise Treadmill Test Responses. <i>Circulation</i> , 2007, 115, 2917-2924.	1.6	34
46	The Framingham Heart Study 100K SNP genome-wide association study resource: overview of 17 phenotype working group reports. <i>BMC Medical Genetics</i> , 2007, 8, S1.	2.1	169
47	Genome-wide association to body mass index and waist circumference: the Framingham Heart Study 100K project. <i>BMC Medical Genetics</i> , 2007, 8, S18.	2.1	154
48	Framingham Heart Study 100K project: genome-wide associations for cardiovascular disease outcomes. <i>BMC Medical Genetics</i> , 2007, 8, S5.	2.1	155
49	Sex and age specific effects of chromosomal regions linked to body mass index in the Framingham Study. <i>BMC Genetics</i> , 2006, 7, 7.	2.7	21
50	Genome-Wide Scan for White Matter Hyperintensity. <i>Stroke</i> , 2006, 37, 77-81.	2.0	67
51	Genomewide Linkage Analysis of Weight Change in the Framingham Heart Study. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2005, 90, 3197-3201.	3.6	35
52	Genetic Variation in White Matter Hyperintensity Volume in the Framingham Study. <i>Stroke</i> , 2004, 35, 1609-1613.	2.0	251
53	Genome-Wide Linkage to Chromosome 6 for Waist Circumference in the Framingham Heart Study. <i>Diabetes</i> , 2004, 53, 1399-1402.	0.6	44
54	Limits of fine-mapping a quantitative trait. <i>Genetic Epidemiology</i> , 2003, 24, 99-106.	1.3	37

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55	Consistency of linkage results across exams and methods in the Framingham Heart Study. <i>BMC Genetics</i> , 2003, 4, S30.	2.7	2
56	Evidence for a Gene Influencing Serum Bilirubin on Chromosome 2q Telomere: A Genomewide Scan in the Framingham Study. <i>American Journal of Human Genetics</i> , 2003, 72, 1029-1034.	6.2	50
57	Linkage and association with pulmonary function measures on chromosome 6q27 in the Framingham Heart Study. <i>Human Molecular Genetics</i> , 2003, 12, 2745-2751.	2.9	34
58	Polymorphisms in the Insulin-Degrading Enzyme Gene Are Associated With Type 2 Diabetes in Men From the NHLBI Framingham Heart Study. <i>Diabetes</i> , 2003, 52, 1562-1567.	0.6	100
59	Genomewide Linkage Analysis to Presbycusis in the Framingham Heart Study. <i>JAMA Otolaryngology</i> , 2003, 129, 285.	1.2	81
60	Genomewide Linkage Analysis of Body Mass Index across 28 Years of the Framingham Heart Study. <i>American Journal of Human Genetics</i> , 2002, 71, 1044-1050.	6.2	144