

Nancy L Heard-Costa

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2265077/publications.pdf>

Version: 2024-02-01

60
papers

18,937
citations

87723

38
h-index

118652

62
g-index

64
all docs

64
docs citations

64
times ranked

26190
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
2	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	9.4	2,634
3	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
4	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	13.7	1,789
5	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
6	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.	9.4	836
7	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	9.4	578
8	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544
9	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011, 43, 1131-1138.	9.4	501
10	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	13.7	383
11	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	1.5	371
12	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	1.5	331
13	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.	9.4	286
14	Genetic Variation in White Matter Hyperintensity Volume in the Framingham Study. <i>Stroke</i> , 2004, 35, 1609-1613.	1.0	251
15	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.	13.7	248
16	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.	1.5	245
17	NRXN3 Is a Novel Locus for Waist Circumference: A Genome-Wide Association Study from the CHARGE Consortium. <i>PLoS Genetics</i> , 2009, 5, e1000539.	1.5	230
18	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173

#	ARTICLE	IF	CITATIONS
19	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
20	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.	5.8	169
21	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	1.5	158
22	Framingham Heart Study 100K project: genome-wide associations for cardiovascular disease outcomes. <i>BMC Medical Genetics</i> , 2007, 8, S5.	2.1	155
23	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
24	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. <i>Genome Biology</i> , 2017, 18, 16.	3.8	151
25	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.	2.6	144
26	Genome-wide analysis of BMI in adolescents and young adults reveals additional insight into the effects of genetic loci over the life course. <i>Human Molecular Genetics</i> , 2013, 22, 3597-3607.	1.4	116
27	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.	9.4	116
28	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.	0.3	100
29	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	9.4	89
30	Genomewide Linkage Analysis to Presbycusis in the Framingham Heart Study. <i>JAMA Otolaryngology</i> , 2003, 129, 285.	1.5	81
31	Genetics Analysis Workshop 16 Problem 2: the Framingham Heart Study data. <i>BMC Proceedings</i> , 2009, 3, S3.	1.8	80
32	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	5.8	74
33	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.	3.3	71
34	Genome-Wide Scan for White Matter Hyperintensity. <i>Stroke</i> , 2006, 37, 77-81.	1.0	67
35	Sequence Kernel Association Test for Survival Traits. <i>Genetic Epidemiology</i> , 2014, 38, 191-197.	0.6	58
36	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.	2.6	50

#	ARTICLE	IF	CITATIONS
37	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. <i>Nature Communications</i> , 2021, 12, 3505.	5.8	49
38	Genome-Wide Association of Pericardial Fat Identifies a Unique Locus for Ectopic Fat. <i>PLoS Genetics</i> , 2012, 8, e1002705.	1.5	48
39	Genome-Wide Linkage to Chromosome 6 for Waist Circumference in the Framingham Heart Study. <i>Diabetes</i> , 2004, 53, 1399-1402.	0.3	44
40	Limits of fine-mapping a quantitative trait. <i>Genetic Epidemiology</i> , 2003, 24, 99-106.	0.6	37
41	Genomewide Linkage Analysis of Weight Change in the Framingham Heart Study. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2005, 90, 3197-3201.	1.8	35
42	Linkage and association with pulmonary function measures on chromosome 6q27 in the Framingham Heart Study. <i>Human Molecular Genetics</i> , 2003, 12, 2745-2751.	1.4	34
43	Heritability, Linkage, and Genetic Associations of Exercise Treadmill Test Responses. <i>Circulation</i> , 2007, 115, 2917-2924.	1.6	34
44	Genome-wide association meta-analysis identifies five novel loci for age-related hearing impairment. <i>Scientific Reports</i> , 2019, 9, 15192.	1.6	32
45	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. <i>Human Molecular Genetics</i> , 2014, 23, 2498-2510.	1.4	28
46	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.	2.6	28
47	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.	2.6	27
48	Rare coding variants in 35 genes associate with circulating lipid levels—A multi-ancestry analysis of 170,000 exomes. <i>American Journal of Human Genetics</i> , 2022, 109, 81-96.	2.6	24
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	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.	1.0	16
51	Trends in the association of parental history of obesity over 60 years. <i>Obesity</i> , 2014, 22, 919-924.	1.5	15
52	Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. <i>Human Molecular Genetics</i> , 2014, 23, 6607-6615.	1.4	14
53	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.	2.6	14
54	Sequence Variation in <i>TMEM18</i> in Association With Body Mass Index. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 344-349.	5.1	8

#	ARTICLE	IF	CITATIONS
55	Integrating genetic, transcriptional, and biological information provides insights into obesity. <i>International Journal of Obesity</i> , 2019, 43, 457-467.	1.6	8
56	Evaluation of power of the Illumina HumanOmni5M-4v1 BeadChip to detect risk variants for human complex diseases. <i>European Journal of Human Genetics</i> , 2016, 24, 1029-1034.	1.4	7
57	Rare variant associations with waist-to-hip ratio in European-American and African-American women from the NHLBI-Exome Sequencing Project. <i>European Journal of Human Genetics</i> , 2016, 24, 1181-1187.	1.4	5
58	Revisit Population-based and Family-based Genotype Imputation. <i>Scientific Reports</i> , 2019, 9, 1800.	1.6	4
59	Consistency of linkage results across exams and methods in the Framingham Heart Study. <i>BMC Genetics</i> , 2003, 4, S30.	2.7	2
60	Hearing Function: Identification of New Candidate Genes Further Explaining the Complexity of This Sensory Ability. <i>Genes</i> , 2021, 12, 1228.	1.0	1