

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

87888

38
h-index

118850

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. | 27.8 | 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. | 21.4 | 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. | 21.4 | 1,818 |
| 4 | Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838. | 27.8 | 1,789 |
| 5 | New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196. | 27.8 | 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. | 21.4 | 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. | 21.4 | 578 |
| 8 | Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190. | 27.8 | 544 |
| 9 | Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011, 43, 1131-1138. | 21.4 | 501 |
| 10 | FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272. | 27.8 | 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. | 3.5 | 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. | 3.5 | 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. | 21.4 | 286 |
| 14 | Genetic Variation in White Matter Hyperintensity Volume in the Framingham Study. <i>Stroke</i> , 2004, 35, 1609-1613. | 2.0 | 251 |
| 15 | Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76. | 27.8 | 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. | 3.5 | 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. | 3.5 | 230 |
| 18 | Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462. | 27.8 | 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. | 12.8 | 169 |
| 21 | Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528. | 3.5 | 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. | 8.8 | 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. | 6.2 | 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. | 2.9 | 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. | 21.4 | 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. | 0.6 | 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. | 21.4 | 89 |
| 30 | Genomewide Linkage Analysis to Presbycusis in the Framingham Heart Study. <i>JAMA Otolaryngology</i> , 2003, 129, 285. | 1.2 | 81 |
| 31 | Genetics Analysis Workshop 16 Problem 2: the Framingham Heart Study data. <i>BMC Proceedings</i> , 2009, 3, S3. | 1.6 | 80 |
| 32 | A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357. | 12.8 | 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. | 7.1 | 71 |
| 34 | Genome-Wide Scan for White Matter Hyperintensity. <i>Stroke</i> , 2006, 37, 77-81. | 2.0 | 67 |
| 35 | Sequence Kernel Association Test for Survival Traits. <i>Genetic Epidemiology</i> , 2014, 38, 191-197. | 1.3 | 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. | 6.2 | 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. | 12.8 | 49 |
| 38 | Genome-Wide Association of Pericardial Fat Identifies a Unique Locus for Ectopic Fat. <i>PLoS Genetics</i> , 2012, 8, e1002705. | 3.5 | 48 |
| 39 | Genome-Wide Linkage to Chromosome 6 for Waist Circumference in the Framingham Heart Study. <i>Diabetes</i> , 2004, 53, 1399-1402. | 0.6 | 44 |
| 40 | Limits of fine-mapping a quantitative trait. <i>Genetic Epidemiology</i> , 2003, 24, 99-106. | 1.3 | 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. | 3.6 | 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. | 2.9 | 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. | 3.3 | 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. | 2.9 | 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. | 6.2 | 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. | 6.2 | 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. | 6.2 | 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. | 2.0 | 16 |
| 51 | Trends in the association of parental history of obesity over 60 years. <i>Obesity</i> , 2014, 22, 919-924. | 3.0 | 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. | 2.9 | 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. | 6.2 | 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. | 3.4 | 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. | 2.8 | 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. | 2.8 | 5 |
| 58 | Revisit Population-based and Family-based Genotype Imputation. <i>Scientific Reports</i> , 2019, 9, 1800. | 3.3 | 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. | 2.4 | 1 |