# Lucia A Hindorff

List of Publications by Year
in descending order



| | | | |
|---|---|---|---|
| 52 papers | 16,698 citations | 218592 26 h-index | 206029 48 g-index |
| 55 all docs | 55 docs citations | 55 times ranked | 30360 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | US private payersâ€™ perspectives on insurance coverage for genome sequencing versus exome sequencing: A study by the Clinical Sequencing Evidence-Generating Research Consortium (CSER). Genetics in Medicine, 2022, 24, 238-244. | 1.1 | 6 |
| 2 | Predicted gene expression in ancestrally diverse populations leads to discovery of susceptibility loci for lifestyle and cardiometabolic traits. American Journal of Human Genetics, 2022, 109, 669-679. | 2.6 | 5 |
| 3 | Multi-ethnic genome-wide association analyses of white blood cell and platelet traits in the Population Architecture using Genomics and Epidemiology (PAGE) study. BMC Genomics, 2021, 22, 432. | 1.2 | 6 |
| 4 | Examining access to care in clinical genomic research and medicine: Experiences from the CSER Consortium. Journal of Clinical and Translational Science, 2021, 5, e193. | 0.3 | 21 |
| 5 | Sequencing-based genome-wide association studies reporting standards. Cell Genomics, 2021, 1, 100005. | 3.0 | 17 |
| 6 | Variant Classification Concordance using the ACMG-AMP Variant Interpretation Guidelines across Nine Genomic Implementation Research Studies. American Journal of Human Genetics, 2020, 107, 932-941. | 2.6 | 51 |
| 7 | Lessons learned about harmonizing survey measures for the CSER consortium. Journal of Clinical and Translational Science, 2020, 4, 537-546. | 0.3 | 16 |
| 8 | Clinical Genetics Lacks Standard Definitions and Protocols for the Collection and Use of Diversity Measures. American Journal of Human Genetics, 2020, 107, 72-82. | 2.6 | 52 |
| 9 | Ancestry-specific associations identified in genome-wide combined-phenotype study of red blood cell traits emphasize benefits of diversity in genomics. BMC Genomics, 2020, 21, 228. | 1.2 | 19 |
| 10 | Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. PLoS Genetics, 2020, 16, e1008684. | 1.5 | 17 |
| 11 | Multi-Ethnic Genome-Wide Association Study of Decomposed Cardioelectric Phenotypes Illustrates Strategies to Identify and Characterize Evidence of Shared Genetic Effects for Complex Traits. Circulation Genomic and Precision Medicine, 2020, 13, e002680. | 1.6 | 4 |
| 12 | Title is missing!. , 2020, 16, e1008684. | | 0 |
| 13 | Title is missing!. , 2020, 16, e1008684. | | 0 |
| 14 | Title is missing!. , 2020, 16, e1008684. | | 0 |
| 15 | Title is missing!. , 2020, 16, e1008684. | | 0 |
| 16 | Title is missing!. , 2020, 16, e1008684. | | 0 |
| 17 | Title is missing!. , 2020, 16, e1008684. | | 0 |
| 18 | Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518. | 13.7 | 679 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | The Genomic Medicine Integrative Research Framework: A Conceptual Framework for Conducting Genomic Medicine Research. American Journal of Human Genetics, 2019, 104, 1088-1096. | 2.6 | 35 |
| 20 | The NHGRI-EBI GWAS Catalog of published genome-wide association studies, targeted arrays and summary statistics 2019. Nucleic Acids Research, 2019, 47, D1005-D1012. | 6.5 | 3,179 |
| 21 | Secondary findings from clinical genomic sequencing: prevalence, patient perspectives, family history assessment, and health-care costs from a multisite study. Genetics in Medicine, 2019, 21, 1100-1110. | 1.1 | 111 |
| 22 | Anticipated responses of early adopter genetic specialists and nongenetic specialists to unsolicited genomic secondary findings. Genetics in Medicine, 2018, 20, 1186-1195. | 1.1 | 11 |
| 23 | Characterizing reduced coverage regions through comparison of exome and genome sequencing data across 10 centers. Genetics in Medicine, 2018, 20, 855-866. | 1.1 | 22 |
| 24 | Enhancing diversity to reduce health information disparities and build an evidence base for genomic medicine. Personalized Medicine, 2018, 15, 403-412. | 0.8 | 39 |
| 25 | The Clinical Sequencing Evidence-Generating Research Consortium: Integrating Genomic Sequencing in Diverse and Medically Underserved Populations. American Journal of Human Genetics, 2018, 103, 319-327. | 2.6 | 122 |
| 26 | The genetic underpinnings of variation in ages at menarche and natural menopause among women from the multi-ethnic Population Architecture using Genomics and Epidemiology (PAGE) Study: A trans-ethnic meta-analysis. PLoS ONE, 2018, 13, e0200486. | 1.1 | 25 |
| 27 | Generalization and fine mapping of red blood cell trait genetic associations to multiâ€ethnic populations: The PAGE study. American Journal of Hematology, 2018, 93, 1061-1073. | 2.0 | 5 |
| 28 | A standardized framework for representation of ancestry data in genomics studies, with application to the NHGRI-EBI GWAS Catalog. Genome Biology, 2018, 19, 21. | 3.8 | 159 |
| 29 | Discovery, fine-mapping, and conditional analyses of genetic variants associated with C-reactive protein in multiethnic populations using the Metabochip in the Population Architecture using Genomics and Epidemiology (PAGE) study. Human Molecular Genetics, 2018, 27, 2940-2953. | 1.4 | 16 |
| 30 | Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. Human Genetics, 2017, 136, 771-800. | 1.8 | 31 |
| 31 | Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977. | 5.8 | 169 |
| 32 | Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119. | 9.4 | 260 |
| 33 | A survey of current practices for genomic sequencing test interpretation and reporting processes in US laboratories. Genetics in Medicine, 2017, 19, 575-582. | 1.1 | 68 |
| 34 | The new NHGRI-EBI Catalog of published genome-wide association studies (GWAS Catalog). Nucleic Acids Research, 2017, 45, D896-D901. | 6.5 | 1,932 |
| 35 | Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528. | 1.5 | 158 |
| 36 | Variant Discovery and Fine Mapping of Genetic Loci Associated with Blood Pressure Traits in Hispanics and African Americans. PLoS ONE, 2016, 11, e0164132. | 1.1 | 24 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. American Journal of Human Genetics, 2016, 98, 1051-1066. | 2.6 | 137 |
| 38 | Recommendations for the integration of genomics into clinical practice. Genetics in Medicine, 2016, 18, 1075-1084. | 1.1 | 125 |
| 39 | Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array. PLoS ONE, 2016, 11, e0167758. | 1.1 | 72 |
| 40 | Pleiotropic and Sex-Specific Effects of Cancer GWAS SNPs on Melanoma Risk in the Population Architecture Using Genomics and Epidemiology (PAGE) Study. PLoS ONE, 2015, 10, e0120491. | 1.1 | 19 |
| 41 | Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206. | 13.7 | 3,823 |
| 42 | Pleiotropy of Cancer Susceptibility Variants on the Risk of Non-Hodgkin Lymphoma: The PAGE Consortium. PLoS ONE, 2014, 9, e89791. | 1.1 | 16 |
| 43 | The NHGRI GWAS Catalog, a curated resource of SNP-trait associations. Nucleic Acids Research, 2014, 42, D1001-D1006. | 6.5 | 2,608 |
| 44 | Replication of Associations between GWAS SNPs and Melanoma Risk in the Population Architecture Using Genomics and Epidemiology (PAGE) Study. Journal of Investigative Dermatology, 2014, 134, 2049-2052. | 0.3 | 21 |
| 45 | Association of Cancer Susceptibility Variants with Risk of Multiple Primary Cancers: The Population Architecture using Genomics and Epidemiology Study. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2568-2578. | 1.1 | 23 |
| 46 | Phenome-wide association studies demonstrating pleiotropy of genetic variants within FTO with and without adjustment for body mass index. Frontiers in Genetics, 2014, 5, 250. | 1.1 | 66 |
| 47 | Phenotypeâ€“Genotype Integrator (PheGenI): synthesizing genome-wide association study (GWAS) data with existing genomic resources. European Journal of Human Genetics, 2014, 22, 144-147. | 1.4 | 207 |
| 48 | Genetic Determinants of Age-Related Macular Degeneration in Diverse Populations From the PAGE Study. Investigative Ophthalmology and Visual Science, 2014, 55, 6839-6850. | 3.3 | 59 |
| 49 | Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186. | 9.4 | 1,818 |
| 50 | Prospective Associations of Coronary Heart Disease Loci in African Americans Using the MetaboChip: The PAGE Study. PLoS ONE, 2014, 9, e113203. | 1.1 | 27 |
| 51 | Generalization and Dilution of Association Results from European GWAS in Populations of Non-European Ancestry: The PAGE Study. PLoS Biology, 2013, 11, e1001661. | 2.6 | 235 |
| 52 | The Next PAGE in Understanding Complex Traits: Design for the Analysis of Population Architecture Using Genetics and Epidemiology (PAGE) Study. American Journal of Epidemiology, 2011, 174, 849-859. | 1.6 | 161 |