Resource Summary Report

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Cohorts for Heart and Aging Research in Genomic Epidemiology

RRID:SCR_004034
Type: Tool

Proper Citation

Cohorts for Heart and Aging Research in Genomic Epidemiology (RRID:SCR_004034)

Resource Information

URL: http://www.chargeconsortium.com/

Proper Citation: Cohorts for Heart and Aging Research in Genomic Epidemiology (RRID:SCR_004034)

Description: Consortium formed to facilitate genome-wide association study meta-analyses and replication opportunities among multiple large and well-phenotyped longitudinal cohort studies. A bibliography of CHARGE publications is available. Its founding member cohorts include: * Age, Gene, Environment, Susceptibility Study -- Reykjavik * Atherosclerosis Risk in Communities Study * Cardiovascular Health Study * Framingham Heart Study * Rotterdam Study Additional core cohorts include: * Coronary Artery Risk Development in Young Adults * Family Heart Study * Health, Aging, and Body Composition Study * Jackson Heart Study * Multi-Ethnic Study of Atherosclerosis

Abbreviations: CHARGE Consortium, CHARGE

Resource Type: organization portal, portal, bibliography, data or information resource, consortium

Defining Citation: PMID:20031568

Keywords: genome-wide association study, genomic, epidemiology, phenotype, longitudinal

Related Condition: Aging, Heart disease

Funding:

Resource Name: Cohorts for Heart and Aging Research in Genomic Epidemiology

Resource ID: SCR_004034

Alternate IDs: nlx_158460

Record Creation Time: 20220129T080222+0000

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Ratings and Alerts

No rating or validation information has been found for Cohorts for Heart and Aging Research in Genomic Epidemiology.

No alerts have been found for Cohorts for Heart and Aging Research in Genomic Epidemiology.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 17 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Robinson GE, et al. (2024) The genomic case against genetic determinism. PLoS biology, 22(2), e3002510.

Kasher M, et al. (2022) Understanding the complex genetic architecture connecting rheumatoid arthritis, osteoporosis and inflammation: discovering causal pathways. Human molecular genetics, 31(16), 2810.

Zhang T, et al. (2021) The associations of plasma phospholipid arachidonic acid with cardiovascular diseases: A Mendelian randomization study. EBioMedicine, 63, 103189.

Xu B, et al. (2021) Effect of n-3 polyunsaturated fatty acids on ischemic heart disease and cardiometabolic risk factors: a two-sample Mendelian randomization study. BMC cardiovascular disorders, 21(1), 532.

Lee KS, et al. (2021) A genome wide association study for lung function in the Korean population using an exome array. The Korean journal of internal medicine, 36(Suppl 1), S142.

Strawbridge RJ, et al. (2020) Carotid Intima-Media Thickness: Novel Loci, Sex-Specific Effects, and Genetic Correlations With Obesity and Glucometabolic Traits in UK Biobank. Arteriosclerosis, thrombosis, and vascular biology, 40(2), 446.

Moore JH, et al. (2019) Artificial Intelligence Based Approaches to Identify Molecular Determinants of Exceptional Health and Life Span-An Interdisciplinary Workshop at the National Institute on Aging. Frontiers in artificial intelligence, 2, 12.

Schork NJ, et al. (2018) Report: NIA workshop on translating genetic variants associated with longevity into drug targets. GeroScience, 40(5-6), 523.

Carnero-Montoro E, et al. (2018) Epigenome-wide association studies for systemic autoimmune diseases: The road behind and the road ahead. Clinical immunology (Orlando, Fla.), 196, 21.

Heeney C, et al. (2017) Balancing the local and the universal in maintaining ethical access to a genomics biobank. BMC medical ethics, 18(1), 80.

Reijnders MRF, et al. (2017) Variation in a range of mTOR-related genes associates with intracranial volume and intellectual disability. Nature communications, 8(1), 1052.

Bomba L, et al. (2017) The impact of rare and low-frequency genetic variants in common disease. Genome biology, 18(1), 77.

Xu M, et al. (2017) Mutations in the Spliceosome Component CWC27 Cause Retinal Degeneration with or without Additional Developmental Anomalies. American journal of human genetics, 100(4), 592.

Smith JG, et al. (2017) Molecular Epidemiology of Heart Failure: Translational Challenges and Opportunities. JACC. Basic to translational science, 2(6), 757.

Thompson PM, et al. (2017) ENIGMA and the individual: Predicting factors that affect the brain in 35 countries worldwide. NeuroImage, 145(Pt B), 389.

Auer PL, et al. (2016) Guidelines for Large-Scale Sequence-Based Complex Trait Association Studies: Lessons Learned from the NHLBI Exome Sequencing Project. American journal of human genetics, 99(4), 791.

Nowak C, et al. (2016) Effect of Insulin Resistance on Monounsaturated Fatty Acid Levels: A Multi-cohort Non-targeted Metabolomics and Mendelian Randomization Study. PLoS genetics, 12(10), e1006379.