Resource Summary Report

Generated by RRID on May 15, 2025

deCODE genetics

RRID:SCR_003334
Type: Tool

Proper Citation

deCODE genetics (RRID:SCR_003334)

Resource Information

URL: http://www.decode.com/

Proper Citation: deCODE genetics (RRID:SCR_003334)

Description: A biopharmaceutical company applying its discoveries in human genetics to develop drugs and diagnostics for common diseases. They specialize in gene discovery - their population approach and resources have enabled them to isolate key genes contributing to major public health challenges from cardiovascular disease to cancer. The company's genotyping capacity is now one of the highest in the world. They have a large population-based biobank containing whole blood and DNA samples with extensive relevant phenotypic information from around 120.000 Icelanders. In the company's work in more than 50 disease projects, their statistical and informatics departments have established themselves in data processing and analysis. deCODE genetics is widely recognized as a center of excellence in genetic research.

Abbreviations: deCODE

Synonyms: Islensk Erfdagreining EHF, Islensk Erfdagreining

Resource Type: commercial organization

Keywords: biopharmaceutical, genetics, drug, diagnostic, genotyping, phenotype, data processing, analysis, genetic variant, risk factor, genome, blood, dna, biobank, single nucleotide polymorphism

Related Condition: Schizophrenia, Cardiovascular disease, Cancer, Type 2 diabetes, Atrial fibrillation, Heart attack

Funding:

Resource Name: deCODE genetics

Resource ID: SCR_003334

Alternate IDs: nif-0000-31959, ISNI: 0000 0004 0618 6889, grid.421812.c, Wikidata: Q493712

Alternate URLs: https://ror.org/04dzdm737

Record Creation Time: 20220129T080218+0000

Record Last Update: 20250420T014140+0000

Ratings and Alerts

No rating or validation information has been found for deCODE genetics.

No alerts have been found for deCODE genetics.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 48 mentions in open access literature.

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

Lv R, et al. (2025) Investigating causal relationships between plasma proteins and lung adenocarcinoma: result from proteomics and Mendelian randomization study. Discover oncology, 16(1), 42.

Hu M, et al. (2025) Identifying Key Biomarkers Related to Immune Response in the Progression of Diabetic Kidney Disease: Mendelian Randomization Combined With Comprehensive Transcriptomics and Single-Cell Sequencing Analysis. Journal of inflammation research, 18, 949.

Malomane DK, et al. (2025) Patterns of population structure and genetic variation within the Saudi Arabian population. bioRxiv : the preprint server for biology.

Fan W, et al. (2025) Mendelian randomization analysis of plasma proteins reveals potential novel tumor markers for gastric cancer. Scientific reports, 15(1), 3537.

Li J, et al. (2024) Proteome-wide Mendelian randomization identifies potential therapeutic targets for nonalcoholic fatty liver diseases. Scientific reports, 14(1), 11814.

Xu H, et al. (2024) Exploring the causal effect of complement and IgA nephropathy-a Mendelian randomization study. Renal failure, 46(2), 2436632.

Olafsdottir TA, et al. (2024) Sequence variants influencing the regulation of serum IgG subclass levels. Nature communications, 15(1), 8054.

Saevarsdottir S, et al. (2024) Start codon variant in LAG3 is associated with decreased LAG-3 expression and increased risk of autoimmune thyroid disease. Nature communications, 15(1), 5748.

Pahlevan Kakhki M, et al. (2024) A genetic-epigenetic interplay at 1q21.1 locus underlies CHD1L-mediated vulnerability to primary progressive multiple sclerosis. Nature communications, 15(1), 6419.

Yu K, et al. (2024) Integrated analyses of single-cell transcriptome and Mendelian randomization reveal the protective role of FCRL3 in multiple sclerosis. Frontiers in immunology, 15, 1428962.

Song J, et al. (2024) Identifying new biomarkers and potential therapeutic targets for breast cancer through the integration of human plasma proteomics: a Mendelian randomization study and colocalization analysis. Frontiers in endocrinology, 15, 1449668.

Liu X, et al. (2024) Integrative genomic analysis of RNA-modification-single nucleotide polymorphisms associated with kidney function. Heliyon, 10(20), e38815.

Zhang W, et al. (2024) Bidirectional relationship between type 2 diabetes mellitus and coronary artery disease: Prospective cohort study and genetic analyses. Chinese medical journal, 137(5), 577.

Li H, et al. (2024) Proteome-wide Mendelian randomization identifies causal plasma proteins in lung cancer. iScience, 27(2), 108985.

Ding Y, et al. (2024) The critical involvement of monocytes/macrophages in the pathogenesis of primary Sjögren's syndrome: New evidence from Mendelian randomization and single-cell sequencing. Heliyon, 10(20), e39130.

Williams AT, et al. (2023) Genome-wide association study of thyroid-stimulating hormone highlights new genes, pathways and associations with thyroid disease. Nature communications, 14(1), 6713.

Ko YK, et al. (2022) New Drug Development and Clinical Trial Design by Applying Genomic Information Management. Pharmaceutics, 14(8).

David S, et al. (2022) COVID-19: impact on Public Health and hypothesis-driven investigations on genetic susceptibility and severity. Immunogenetics, 74(4), 381.

Grasso C, et al. (2022) Association Study between Polymorphisms in DNA Methylation-Related Genes and Testicular Germ Cell Tumor Risk. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 31(9), 1769.

Shahab-Movahed Z, et al. (2021) Distal Renal Tubular Acidosis in an Iranian Patient with Hereditary Spherocytosis. Iranian biomedical journal, 25(5), 359.