Resource Summary Report

Generated by kravitz2 on Jul 31, 2026

Common Metabolic Diseases Knowledge Portal

RRID:SCR_020937
Type: Tool

Proper Citation

Common Metabolic Diseases Knowledge Portal (RRID:SCR_020937)

Resource Information

URL: https://hugeamp.org

Proper Citation: Common Metabolic Diseases Knowledge Portal (RRID:SCR_020937)

Description: Portal enables browsing, searching, and analysis of human genetic information linked to common metabolic diseases and traits, while protecting integrity and confidentiality of underlying data. Aggregates and analyzes genetic association results, epigenomic annotations, and results of computational prediction methods to provide data, visualizations, and tools in open access portal.

Abbreviations: CMDKP

Resource Type: service resource, data repository, disease-related portal, portal, topical portal, data or information resource, database, storage service resource

Keywords: Analyzes genetic association results, aggregates genetic association results, epigenomic annotations, genetic data, epigenomic data

Related Condition: Metabolic diseases, Type 1 diabetes, Type 2 diabetes, Cardiovascular disease, Cerebrovascular disease, Sleep disorder, Circadian disorder, Diabetes

Funding: Accelerating Medicines Partnership

Availability: Free, Available for download, Freely available

Resource Name: Common Metabolic Diseases Knowledge Portal

Resource ID: SCR_020937

Record Creation Time: 20220129T080352+0000

Record Last Update: 20260731T043048+0000

Ratings and Alerts

No rating or validation information has been found for Common Metabolic Diseases Knowledge Portal.

No alerts have been found for Common Metabolic Diseases Knowledge Portal.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 49 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Michalek DA, et al. (2026) HLA-focused type 1 diabetes genetic risk prediction in populations of diverse ancestry. Diabetologia, 69(1), 146.

Park J, et al. (2026) A robust pleiotropy method with applications to lipid traits and to inflammatory bowel disease subtypes with sample overlap. HGG advances, 7(1), 100501.

Michalek DA, et al. (2025) HLA-focused type 1 diabetes genetic risk prediction in populations of diverse ancestry. medRxiv : the preprint server for health sciences.

Breunig M, et al. (2025) PPDPF is not a key regulator of human pancreas development. PLoS genetics, 21(4), e1011657.

Li JH, et al. (2025) Common genetic variants near SLC2A2 and glycemic response to glimepiride in the GRADE comparative effectiveness clinical trial. medRxiv : the preprint server for health sciences.

Van de Velde S, et al. (2025) Med14 phosphorylation shapes genomic response to GLP-1 Agonist. bioRxiv : the preprint server for biology.

Carty JRE, et al. (2025) Amygdala-liver signalling orchestrates glycaemic responses to stress. Nature.

Tsang CH, et al. (2025) Identification and molecular characterization of missense mutations in orphan G protein-coupled receptor GPR61 occurring in severe obesity. Molecular pharmacology, 107(4), 100026.

Mogire RM, et al. (2025) OSBPL11 is an African-specific locus associated with 25-hydroxyvitamin D concentrations and cardiometabolic health. medRxiv : the preprint server for health sciences.

Zhou F, et al. (2025) Improved genetic discovery and fine-mapping resolution through multivariate latent factor analysis of high-dimensional traits. Cell genomics, 5(5), 100847.

Auger C, et al. (2025) Mitochondrial control of fuel switching via carnitine biosynthesis. bioRxiv : the preprint server for biology.

Zhong S, et al. (2025) The impact of leisure sedentary behaviors on risk of chronic kidney disease, diabetes, and related complications: Mendelian randomization study. Renal failure, 47(1), 2479177.

Rouby NE, et al. (2025) Genome-wide associations with metabolic syndrome among UK Biobank participants reporting use of second-generation antipsychotics. Pharmacotherapy, 45(8), 476.

Chen HH, et al. (2025) Multiomics reveal key inflammatory drivers of severe obesity: IL4R, LILRA5, and OSM. Cell genomics, 5(3), 100784.

Ferraretti G, et al. (2025) Convergent evolution of complex adaptive traits modulates angiogenesis in high-altitude Andean and Himalayan human populations. Communications biology, 8(1), 377.

Wendland Z, et al. (2025) A genome-wide association study of hidradenitis suppurativa from the VA's Million Veteran Program. medRxiv : the preprint server for health sciences.

Neupane KR, et al. (2025) Impaired Chylomicron Secretion Results in Reduced Body Fat and Increased Intestinal Fatty Acid Oxidation by Activation of Autophagy. bioRxiv : the preprint server for biology.

Rios Coronado PE, et al. (2025) CXCL12 drives natural variation in coronary artery anatomy across diverse populations. Cell, 188(7), 1784.

Yuan S, et al. (2025) CYB5R4 sustains endothelial proliferation and ischemia-induced angiogenesis by maintaining RRM2-dependent nucleotide balance. bioRxiv : the preprint server for biology.

Lin S, et al. (2024) TargetGene: a comprehensive database of cell-type-specific target genes for genetic variants. Nucleic acids research, 52(D1), D1072.