

Resource Summary Report

Generated by ASWG on Aug 31, 2026

KI Biobank - BROAD

RRID:SCR_005916

Type: Tool

Proper Citation

KI Biobank - BROAD (RRID:SCR_005916)

Resource Information

URL: <http://ki.se/en/meb/broad>

Proper Citation: KI Biobank - BROAD (RRID:SCR_005916)

Description: The study will collect 1,500 cases with schizophrenia and 1,500 well-matched controls ascertained via high-quality Swedish national hospitalization and population registries. Both cases and controls will be population-based and of Scandinavian ancestry. Types of samples * EDTA whole blood * DNA Number of donors: 10 820 (June 2010)

Abbreviations: KI Biobank - BROAD

Resource Type: biomaterial supply resource, material resource

Keywords: matched control, psychiatric disease, population

Related Condition: Schizophrenia, Normal control

Resource Name: KI Biobank - BROAD

Resource ID: SCR_005916

Alternate IDs: nlx_149508

Old URLs: <http://ki.se/ki/jsp/polopoly.jsp?d=29350&a=24110&l=en>

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260829T183047+0000

Ratings and Alerts

No rating or validation information has been found for KI Biobank - BROAD.

No alerts have been found for KI Biobank - BROAD.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [ASWG](#) .

McCutchan G, et al. (2023) Assessing, updating and utilising primary care smoking records for lung cancer screening. BMC pulmonary medicine, 23(1), 445.

Joshi S, et al. (2017) TEAD transcription factors are required for normal primary myoblast differentiation in vitro and muscle regeneration in vivo. PLoS genetics, 13(2), e1006600.

Markham LW, et al. (2017) GRMD cardiac and skeletal muscle metabolism gene profiles are distinct. BMC medical genomics, 10(1), 21.

Martianov I, et al. (2016) TRF2 is recruited to the pre-initiation complex as a testis-specific subunit of TFIIA/ALF to promote haploid cell gene expression. Scientific reports, 6, 32069.

Du H, et al. (2015) The Evolutionary History of R2R3-MYB Proteins Across 50 Eukaryotes: New Insights Into Subfamily Classification and Expansion. Scientific reports, 5, 11037.

Bihani T, et al. (2015) Resistance to everolimus driven by epigenetic regulation of MYC in ER+ breast cancers. Oncotarget, 6(4), 2407.

Berg A, et al. (2015) Molecular profiling of endometrial carcinoma precursor, primary and metastatic lesions suggests different targets for treatment in obese compared to non-obese patients. Oncotarget, 6(2), 1327.

Riesenberg S, et al. (2015) MITF and c-Jun antagonism interconnects melanoma dedifferentiation with pro-inflammatory cytokine responsiveness and myeloid cell recruitment. Nature communications, 6, 8755.

Böhne A, et al. (2014) Comparative transcriptomics in East African cichlids reveals sex- and species-specific expression and new candidates for sex differentiation in fishes. Genome biology and evolution, 6(9), 2567.

Bonnet A, et al. (2013) An overview of gene expression dynamics during early ovarian folliculogenesis: specificity of follicular compartments and bi-directional dialog. BMC genomics, 14, 904.