

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

METABRIC

RRID:SCR_028351

Type: Tool

Proper Citation

METABRIC (RRID:SCR_028351)

Resource Information

URL: <https://ega-archive.org/studies/EGAS00000000083>

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Description: Molecular Taxonomy of the Breast Cancer International Consortium (METABRIC) is a landmark study and dataset comprising primary breast tumour samples with detailed genomic, transcriptomic, and clinical data. It identified ten distinct "integrative clusters" (IntClust) based on copy number aberrations and gene expression, revealing new, clinically relevant subtypes with varying prognoses.

Synonyms: Molecular Taxonomy of the Breast Cancer International Consortium (METABRIC)

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

Keywords: European Genome-phenome Archive, breast cancer, primary breast tumour samples, genomic data, transcriptomic data, clinical data,

Availability: Free, Freely available,

Resource Name: METABRIC

Resource ID: SCR_028351

Record Creation Time: 20260430T063406+0000

Record Last Update: 20260905T133610+0000

Ratings and Alerts

No rating or validation information has been found for METABRIC.

No alerts have been found for METABRIC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Wang Z, et al. (2026) Podoplanin-defined tumour plasticity and CCR7-mediated lymphatic metastasis in triple-negative breast cancer. British journal of cancer, 134(12), 1730.

Ingebriktsen LM, et al. (2024) Elevated expression of Aurora-A/AURKA in breast cancer associates with younger age and aggressive features. Breast cancer research : BCR, 26(1), 126.

Wiecek AJ, et al. (2023) Genomic hallmarks and therapeutic implications of G0 cell cycle arrest in cancer. Genome biology, 24(1), 128.

Lee JV, et al. (2022) Combinatorial immunotherapies overcome MYC-driven immune evasion in triple negative breast cancer. Nature communications, 13(1), 3671.

Islam MM, et al. (2022) Differential Private Deep Learning Models for Analyzing Breast Cancer Omics Data. Frontiers in oncology, 12, 879607.

King L, et al. (2022) GNOSIS: an R Shiny app supporting cancer genomics survival analysis with cBioPortal. HRB open research, 5, 8.

Di Benedetto C, et al. (2022) NSMCE2, a novel super-enhancer-regulated gene, is linked to poor prognosis and therapy resistance in breast cancer. BMC cancer, 22(1), 1056.

He Q, et al. (2021) Mining immune-related genes with prognostic value in the tumor microenvironment of breast invasive ductal carcinoma. Medicine, 100(17), e25715.