

Resource Summary Report

Generated by [nidm-terms](#) on Sep 21, 2026

Glioma Molecular Dignostic Initiatives

RRID:SCR_003329

Type: Tool

Proper Citation

Glioma Molecular Dignostic Initiatives (RRID:SCR_003329)

Resource Information

URL: <http://caintegrator-info.nci.nih.gov/rembrandt>

Proper Citation: Glioma Molecular Dignostic Initiatives (RRID:SCR_003329)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on April 28,2023. An initiative to develop a molecular classification schema that is both clinically and biologically meaningful, based on gene expression and genomic data from tumors (Gliomas) of patients who will be prospectively followed through natural history and treatment phase of their illness. The study will also explore gene expression profiles to determine the responsiveness of the patients and correlate with discrete chromosomal abnormalities. The initiative was designed to obtain a large amount of molecular data on DNA and RNA of freshly collected tumor samples that were collected, processed and analyzed in a standardized fashion to allow for large-scale cross sample analysis. The sample collection is accompanied by careful and prospective clinical data acquisition, allowing a variety of matched molecular and clinical data permitting a wide variety of analyses. GMDI has accrued fresh frozen tumors in the retrospective phase (all from the Henry Ford Hospital, without germline DNA) and fresh frozen tumors in the prospective phase (from a variety of institutions). In addition to characterizing the samples from patients enrolled in GMDI, the microarray group has generated genomic-scale analyses of the many human and canine glioma initiating cells/glioma stem cells (GIC/GSC) lines, as well as many canine and murine normal neural stem cell (NSC) lines produced in laboratory.

Abbreviations: GMDI

Synonyms: Glioma Molecular Diagnostic Initiative: Characterizing Brain Tumor Data

Resource Type: controlled vocabulary, data or information resource, data repository, narrative resource, service resource, standard specification, storage service resource

Keywords: molecular neuroanatomy resource, molecular data, clinical data, genomic analyses, genomics, gene, expression array, snp array, gene expression, microarray, glioma initiating cell, glioma stem cell, protein, glioma, molecular, diagnostic, dna, rna,

tumor, tissue, blood, plasma, data repository

Related Condition: Glioma, Brain cancer, Brain tumor

Funding: NCI

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Glioma Molecular Dignostic Initiatives

Resource ID: SCR_003329

Alternate IDs: nif-0000-31950

Alternate URLs:

http://search.engrant.com/project/NxvG9G/the_glioma_molecular_diagnostic_initiative_characterizin

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260919T195017+0000

Ratings and Alerts

No rating or validation information has been found for Glioma Molecular Dignostic Initiatives.

No alerts have been found for Glioma Molecular Dignostic Initiatives.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Liu Z, et al. (2025) Focal adhesion in the tumour metastasis: from molecular mechanisms to therapeutic targets. Biomarker research, 13(1), 38.

Xiao Z, et al. (2023) Prognosis and clinical features analysis of EMT-related signature and tumor Immune microenvironment in glioma. Journal of medical biochemistry, 42(1), 122.

Ma W, et al. (2022) LRRFIP1, an epigenetically regulated gene, is a prognostic biomarker and predicts malignant phenotypes of glioma. CNS neuroscience & therapeutics, 28(6), 873.

Wang G, et al. (2022) Angiogenesis-Related Gene Signature-Derived Risk Score for Glioblastoma: Prospects for Predicting Prognosis and Immune Heterogeneity in Glioblastoma. Frontiers in cell and developmental biology, 10, 778286.

Wang X, et al. (2022) The copper-associated protein STEAP2 correlated with glioma prognosis and immune infiltration. *Frontiers in cellular neuroscience*, 16, 944682.

Zhang Z, et al. (2019) PLK4 is a determinant of temozolomide sensitivity through phosphorylation of IKBKE in glioblastoma. *Cancer letters*, 443, 91.

Zeng F, et al. (2019) RELB: A novel prognostic marker for glioblastoma as identified by population-based analysis. *Oncology letters*, 18(1), 386.

Wang KY, et al. (2019) Molecular and clinical characterization of TMEM71 expression at the transcriptional level in glioma. *CNS neuroscience & therapeutics*, 25(9), 965.

Zhang Y, et al. (2018) ADAR3 expression is an independent prognostic factor in lower-grade diffuse gliomas and positively correlated with the editing level of GRIA2Q607R. *Cancer cell international*, 18, 196.

Lee SY, et al. (2017) CD133 Regulates IL-1?? Signaling and Neutrophil Recruitment in Glioblastoma. *Molecules and cells*, 40(7), 515.

Eun K, et al. (2017) A cell-autonomous positive-signaling circuit associated with the PDGF-NO-ID4-regulatory axis in glioblastoma cells. *Biochemical and biophysical research communications*, 486(2), 564.

Sun L, et al. (2016) KIF23 is an independent prognostic biomarker in glioma, transcriptionally regulated by TCF-4. *Oncotarget*, 7(17), 24646.

Li MY, et al. (2016) Low c-Met expression levels are prognostic for and predict the benefits of temozolomide chemotherapy in malignant gliomas. *Scientific reports*, 6, 21141.

Kim JK, et al. (2014) Tumoral RANKL activates astrocytes that promote glioma cell invasion through cytokine signaling. *Cancer letters*, 353(2), 194.

Liu Y, et al. (2014) Multidimensional analysis of gene expression reveals TGFB1I1-induced EMT contributes to malignant progression of astrocytomas. *Oncotarget*, 5(24), 12593.

Martino-Echarri E, et al. (2014) Relevance of IGFBP2 proteolysis in glioma and contribution of the extracellular protease ADAMTS1. *Oncotarget*, 5(12), 4295.

Bozdag S, et al. (2013) Age-specific signatures of glioblastoma at the genomic, genetic, and epigenetic levels. *PloS one*, 8(4), e62982.

Baysan M, et al. (2012) G-cimp status prediction of glioblastoma samples using mRNA expression data. *PloS one*, 7(11), e47839.

Kim M, et al. (2011) An informatics framework for testing data integrity and correctness of federated biomedical databases. *AMIA Joint Summits on Translational Science proceedings. AMIA Joint Summits on Translational Science*, 2011, 22.

Smits M, et al. (2010) miR-101 is down-regulated in glioblastoma resulting in EZH2-induced proliferation, migration, and angiogenesis. *Oncotarget*, 1(8), 710.