

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

GBMatch_CNN - GBMPredictor

RRID:SCR_025316

Type: Tool

Proper Citation

GBMatch_CNN - GBMPredictor (RRID:SCR_025316)

Resource Information

URL: https://github.com/tovaroe/GBMatch_CNN/

Proper Citation: GBMatch_CNN - GBMPredictor (RRID:SCR_025316)

Description: Software tool for predicting TS and risk from glioblastoma whole slide images. Used to predict risk scores and transcriptional subtypes from whole slide images of glioblastomas.

Resource Type: source code, software application, software resource

Keywords: Histology, predicting TS, glioblastoma whole slide images, predict risk scores, predict transcriptional subtypes, whole slide images, glioblastomas,

Availability: Free, Available for download, Freely available

Resource Name: GBMatch_CNN - GBMPredictor

Resource ID: SCR_025316

License: GNU GPL v3

Record Creation Time: 20240511T053259+0000

Record Last Update: 20260815T042934+0000

Ratings and Alerts

No rating or validation information has been found for GBMatch_CNN - GBMPredictor.

No alerts have been found for GBMatch_CNN - GBMPredictor.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Roetzer-Pejrimovsky T, et al. (2024) Deep learning links localized digital pathology phenotypes with transcriptional subtype and patient outcome in glioblastoma. GigaScience, 13.