

Ivy Glioblastoma Atlas Project (Ivy GAP)

Summary

This data collection consists of MRI/CT scan data for brain tumor patients that form the cohort for the resource Ivy Glioblastoma Atlas Project (Ivy GAP). There are 390 studies for 39 patients that include pre-surgery, post-surgery and follow up scans. The Ivy GAP is a collaborative partnership between the [Ben and Catherine Ivy Foundation](#), which generously provided the financial support, the [Allen Institute for Brain Science](#), and the [Ben and Catherine Ivy Center for Advanced Brain Tumor Treatment](#). The goal of the project is to provide online resources to scientists and physicians dedicated to the development of innovative treatments and diagnostics that will enhance the quality of life and survival of patients with brain cancer.

These resources represent an unprecedented platform for exploring the anatomic and genetic basis of glioblastoma at the cellular and molecular levels. In addition to the DICOM images in TCIA there are two interactive databases linked together by de-identified tumor specimen numbers to facilitate comparisons across data modalities:

1. [Ivy Glioblastoma Atlas Project](#) - An open/public database providing in situ hybridization (ISH) and RNA sequencing (RNA-Seq) data, which map gene expression across the anatomic structures and putative cancer stem cell clusters in glioblastoma. The associated histological dataset is annotated and is suitable for neuropathological examination.
2. [Ivy GAP Clinical and Genomic Database](#) - A database offering detailed clinical, genomic, and expression array data sets that are designed to elucidate the pathways involved in glioblastoma development and progression. This database requires registration for access.

The Ivy GAP is described in the resource paper: Puchalski RB, Shah N, ...Foltz GD. An anatomic transcriptional atlas of human glioblastoma. *Science* 360, 660-663 (2018). doi:10.1126/science.aaf2666.

For scientific or other inquiries about this dataset, please [contact the TCIA Helpdesk](#).

Data Access

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Click the **Download** button to save a ".tcia" manifest file to your computer, which you must open with the [NBIA Data Retriever](#). Click the **Search** button to open our Data Portal, where you can browse the data collection and/or download a subset of its contents.

Data Type	Download all or Query/Filter
Images (DICOM, 130.4GB)	 
Summary ISH, RNA, gene expression and clinical data	
Detailed clinical, genomic, and expression array data	

Click the Versions tab for more info about data releases.

Third Party Analyses of this Dataset

TCIA encourages the community to [publish your analyses of our datasets](#). Below is a list of such third party analyses published using this Collection:

- [SDTM datasets of clinical data and measurements for selected cancer collections to TCIA](#)
- [Multi-Institutional Paired Expert Segmentations and Radiomic Features of the Ivy GAP Dataset](#)

Detailed Description

Detailed Description

Collection Statistics	
Modalities	MR
Number of Participants	39
Number of Studies	390
Number of Series	5223
Number of Images	846743
Image Size (GB)	130.4

Supporting Documentation

In addition to the DICOM images in TCIA there are two additional databases linked together by de-identified tumor specimen numbers to facilitate comparisons across data modalities:

1. The [Ivy Glioblastoma Atlas Project web site](#) includes the following data:
 - a. [ISH](#): Image data at cellular resolution of *in situ* hybridization (ISH) tissue sections and adjacent hematoxylin and eosin (H&E)-stained sections annotated for anatomic structures
 - i. **Anatomic Structures ISH Survey**: Primary screen of 8 tumors with probes for 343 genes enriched in glioblastoma.
 - ii. **Anatomic Structures ISH for Enriched Genes**: Subsequent screen of 29 tumors with probes for 37 genes enriched in glioblastoma structures identified in Anatomic Structures RNA-Seq Study (see below).
 - iii. **Cancer Stem Cells ISH Survey**: Primary screen of 16 tumors with probes for 55 genes enriched in putative cancer stem cells, resulting in a 20 probe reference set, which was then used in an extensive screen of 42 tumors.
 - iv. **Cancer Stem Cells ISH for Enriched Genes**: Subsequent screen of 37 tumors with probes for 76 genes enriched in clusters of putative cancer stem cells identified in the Cancer Stem Cells RNA-Seq Study (see below).
 - b. [RNA-Seq](#): RNA sequencing data for anatomic structures identified in the Anatomic Structures ISH Survey and putative cancer stem cell clusters isolated by laser microdissection
 - i. **Anatomic Structures RNA-Seq**: Screen of 5 structures (Leading Edge, Infiltrating Tumor, Cellular Tumor, Microvascular Proliferation, and Pseudopalisading Cells Around Necrosis) identified by H&E staining. A total of 122 RNA samples were generated from 10 tumors.
 - ii. **Cancer Stem Cells RNA-Seq**: Screen of 35 clusters of putative cancer stem cells identified by ISH with a 17 reference probe subset (validated in the Cancer Stem Cells ISH Survey). A total of 148 RNA samples were generated from 34 tumors.
 - c. [Specimen Metadata](#): De-identified clinical data for each patient and tumor.
2. The [Ivy GAP Clinical and Genomic Database](#) contains detailed clinical information including pathology images, genomic data, and prospectively collected outcomes data. This site requires separate registration.

Citations & Data Usage Policy

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Users of this data must abide by the [TCIA Data Usage Policy](#) and the [Creative Commons Attribution 3.0 Unported License](#) under which it has been published. Attribution should include references to the following citations:

Data Citation

Shah, N., Feng, X., Lankerovich, M., Puchalski, R. B., & Keogh, B. (2016). **Data from Ivy GAP [Data set]**. The Cancer Imaging Archive. <https://doi.org/10.7937/K9/TCIA.2016.XLWAN6NL>

Publication Citation

Puchalski RB, Shah N, Miller J, Dalley R, Nomura SR, Yoon J-G, Smith KA, Lankerovich M, Bertagnolli D, Bickley K, Boe AF, Brouner K, Butler S, Caldejon S, Chapin M, Datta S, Dee N, Desta T, Dolbear T, Dotson N, Ebbert A, Feng D, Feng X, Fisher M, Gee G, Goldy J, Gourley L, Gregor BW, Gu G, Hejazinia N, Hohmann J, Hothi P, Howard R, Joines K, Kriedberg A, Kuan L, Lau C, Lee F, Lee H, Lemon T, Long F, Mastan N, Mott E, Murthy C, Ngo K, Olson E, Reding M, Riley Z, Rosen D, Sandman D, Shapovalova N, Slaughterbeck CR, Sodt A, Stockdale G, Szafer A, Wakeman W, Wohnoutka PE, White SJ, Marsh D, Rostomily RC, Ng L, Dang C, Jones A, Keogh B, Gittleman HR, Barnholtz-Sloan JS, Cimino PJ, Uppin MS, Keene CD, Farrokhi FR, Lathia JD, Berens ME, Iavarone A, Bernard A, Lein E, Phillips JW, Rostad SW, Cobbs C, Hawrylycz MJ, Foltz GD. (2018). **An anatomic transcriptional atlas of human glioblastoma**. *Science*, 360(6389), 660–663. <https://doi.org/10.1126/science.aaf2666>

TCIA Citation

Clark, K., Vendt, B., Smith, K., Freymann, J., Kirby, J., Koppel, P., Moore, S., Phillips, S., Maffitt, D., Pringle, M., Tarbox, L., & Prior, F. (2013). **The Cancer Imaging Archive (TCIA): Maintaining and Operating a Public Information Repository**. *Journal of Digital Imaging*, 26(6), 1045–1057. <https://doi.org/10.1007/s10278-013-9622-7>



Other Publications Using This Data

TCIA maintains [a list of publications](#) that leverage our data. At this time, we are not aware of any publications based on this data. If you have a publication you'd like to add, please [contact the TCIA Helpdesk](#).

Altmetrics

Versions

Version 1 (Current): Updated 2016/12/30

Data Type	Download all or Query/Filter
Images (DICOM, 130.4GB)	 
Summary ISH, RNA, gene expression and clinical data	
Detailed clinical, genomic, and expression array data	

