

HOW TO ACCESS OPEN-ACCESS TARGET DATA

Open access data are verified and interpreted data that cannot be used to identify individual patients. These types of data can be analyzed, for example, to make correlations between expression of genomic variants in molecular subtypes and clinical outcomes. Most researchers may find open access data sufficient in fulfilling their research needs.

Instructions for how to download open access data:

1. Go to the TARGET Data Matrix by clicking this link:
http://target.nci.nih.gov/dataMatrix/TARGET_DataMatrix.html
2. Click on any link in the Matrix labeled “Open” to download data.

HOW TO ACCESS PROTECTED TARGET DATA

Controlled access data are tumor/patient information and unverified or raw molecular data that pose significant probability of patient re-identification. Examples include raw sequencing files and specific phenotype or genotype data for each case. These types of data can be used to perform sophisticated bioinformatics analyses. Data Use Certification, or approval, is required to access and download. Users must apply for Data Use Certification through the database of Genotypes and Phenotypes (dbGaP) and must agree to the data use limitations of TARGET.

Instructions for how to download controlled access data:

1. Apply for Access to Controlled TARGET Data through dbGaP.

dbGaP video tutorial: <https://www.youtube.com/watch?v=-3tUBeKbP5c>

- a. Login to dbGaP website using eRA Commons account (<https://dbgap.ncbi.nlm.nih.gov/aa/wga.cgi?page=login>).
 - i. If you do not have an eRA Commons account, register for one on the dbGaP authorization page
- b. Create a new research project page to fill out data access request
 - i. Input project information and datasets you wish to access
 - ii. Add any other required information
- c. Review and agree to Data Use Limitations of TARGET

- d. Attach any required documents (e.g., IRB form)
 - e. Review and submit request
 - f. The signing official will need to accredit your request
 - g. Users can track approval status on the dbGaP project page
2. Upon approval, dbGaP sends email notification of approval to new user and NCI database security managers.
3. Approved users may access raw sequence files by visiting the following locations (an eRA Commons account is required):
 - a. NCBI SRA (<http://www.ncbi.nlm.nih.gov/Traces/sra/sra.cgi>) – Next generation sequencing files (e.g., BAM)
 - b. NCBI Trace Archive (http://www.ncbi.nlm.nih.gov/Traces/trace.cgi?view=list_arrivals) – Sanger files
 - c. UCSC Cancer Genomics Hub (<https://cghub.ucsc.edu/>) – Addition of next generation sequencing files (e.g., BAM) in progress
4. Approved users may access all controlled data (excluding raw sequence files) through the NCI Data Coordinating Center (DCC). Approved users receive an email from the NCI database security managers containing a link to download the data at the NCI DCC and NCI-issued user account information (for extramural investigators only).
 - a. Intramural investigators must use HHS account credentials to download data
 - b. Extramural investigators must use NCI-issued account credentials to download data
 - c. The links to access this controlled data are also provided via the TARGET Data Matrix (http://target.nci.nih.gov/dataMatrix/TARGET_DataMatrix.html). Same user account credentials are required
5. To maintain user accounts for data access, users must renew accounts regularly. Review the following account-specific information:
 - a. NCI-issued account –
 - i. Register/login at <http://password.nci.nih.gov/>
 - ii. Expiration date is every 60 days
 - iii. Problems? Email ncicbiit@mail.nih.gov or call 240-276-5541
 - b. eRA Commons account –
 - i. Register/login at <https://dbgap.ncbi.nlm.nih.gov/aa/wga.cgi?page=login>
 - ii. Expiration date is every 90 days
 - iii. Problems? http://era.nih.gov/commons/faq_commons.cfm

6. Approved users must renew or close-out a project in dbGaP annually.
 - a. Learn how to renew a project:
<http://www.youtube.com/watch?v=PG9D5mUouXg>
 - b. Learn how to close out a project:
<http://www.youtube.com/watch?v=i85gl937ZPA>