

Manual Library File Installation

This guide outlines how to manually install library files required for use in Applied Biosystems microarray instrument and analysis software.

GeneChip™ Command Console (GCC)

The GCC library files for processing arrays can be downloaded from thermofisher.com. Navigate to the specific Array's product page, then go to the Support Files section, as shown in the Axiom Genome-Wide Chicken Array example below.

Support Files

-  [Current NetAffx Annotation Files: Axiom_GW_GT_Chicken Annotations, CSV Format, Release 35](#)
-  [Current NetAffx Annotation Files: Axiom_GW_GT_Chicken Annotations, SQLite Format, Release 35](#)
-  [Library Files: AGCC 3.x Axiom® Genome Wide Chicken GeneTitan MC library files](#)

GeneTitan™ Instrument

The library file zip package is installed using the **GeneTitan Library File Installer**. Do not unzip the GCC library file package. For detailed instructions, refer to the GeneChip Command Console User Guide (P/N 702569).

GCS3000 Instrument

The library files for the GCS3000 instrument come in two different types of ZIP packages. If the ZIP file name contains "AGCC" then unzip the contents and double click on the enclosed EXE installer and follow the directions provided. Otherwise, this library package is a legacy format and requires the use of the Library File Importer. Do not unzip the contents of this file. For detailed instructions, refer to the GeneChip Command Console User Guide (P/N 702569).

Microarray Analysis Software for Axiom, Reproductive Health, and Transcriptome Arrays

1. Go to thermofisher.com.
2. Navigate to the specific Array's product page, then go to the Support Files section.
3. Locate, then download the library zip package.
4. From the software's **Preferences** window, note the Library folder's location/path.
5. Navigate to the Library folder, then create a new sub-folder inside it. Do not create a sub-folder inside any existing sub-folder(s).
6. Unzip the library zip file package into your new Library sub-folder.

AxAS users

- For multi-species designs, each species must be in its own sub-folder.
- Do not create a sub-folder inside a sub-folder.

RHAS users

- Annotation files (NetAffxGenomicAnnotation files) are updated quarterly. Contact Technical Support for the most recent annotation file.

<https://www.thermofisher.com/us/en/home/technical-resources/contact-us.html>

Chromosome Analysis Suite (ChAS)

1. Go to thermofisher.com.
2. Navigate to the Chromosome Analysis Suite software page.

The XON library files associated with ChAS v4.3 are shown in the example below.

ChAS 4.3 Library

 [CytoScan XON Array Analysis Files hg19.r7 Part 1](#)

 [CytoScan XON Array Analysis Files hg19.r7 Part 2](#)

 [CytoScan XON Array Analysis Files hg38.r7 Part 1](#)

 [CytoScan XON Array Analysis Files hg38.r7 Part 2](#)

3. Locate, then download the appropriate library zip package(s).
4. Unzip the package(s) directly into the C:\Affymetrix\ChAS\Library folder. Do not create a sub-folder inside this Library folder.

Note: To locate the library files associated with a previous ChAS software release, navigate to the specific Microarray's product page, then download and install its library package(s). Annotation files (NetAffxGenomicAnnotation files) are updated quarterly. Contact Technical Support for the most recent annotation file.

<https://www.thermofisher.com/us/en/home/technical-resources/contact-us.html>