

# What's new for caArray

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## Highlights of caArray 2.5.0 released in July, 2012

- User enhancements
  - Improved large data support
    - Large datasets can now be imported together – it is no longer necessary to split large imports into smaller subsets.
    - Large datasets can be uploaded easily via multiple file selection, drag and drop. (not supported in Internet Explorer)
  - Audit logging of sample and data additions and deletions
  - Ability to restrict access to samples based on sample characteristics
  - Support for automatic refresh of experiments from caIntegrator by providing information about sample and data changes.
  - Ability to configure single sign-on between caArray and caIntegrator.
- Technical enhancements
  - Improved file storage: Uploaded files are now stored on the file system instead of in the database.
  - A plugin architecture allowing the user community to develop and deploy parsers for new data types easily.
  - Major technology upgrades: Jboss 5.1, Java 6, caGrid v1.5, Struts 2.3.1.5, and NCI build-and-deploy infrastructure (NCI Nexus repository, AntHill Pro 3, BDALite).

For more information refer to the [Release Notes](#).

## Highlights of caArray 2.4.1 released on 10/3/2011

- The 2.4.1 release ([caArray 2.4.1 Release Note](#)) addresses the following issues:
  - Visibility into the queue of import and validation jobs, and where your job is in relation to other jobs in the system. Ability to cancel a queued job.
  - Search for experiments by publication author or PubMed ID.
  - Organisms are now restricted to terms from the NCBI Taxonomy.
  - Bug fix to allow proper import of Agilent array design files where the chromosome name is not in a strictly numeric or X/Y format.
  - The installer no longer depends on an internet connection.
  - Fix to bug where experiments with multiple array designs may cause copy number data to get imported as "Imported (Not Parsed)".

## Highlights of caArray 2.4.0.2 released on 2/17/2011

- The 2.4.0.2 release ([caArray 2.4.0.2 Release Note](#)) addresses the following issues with the 2.4.0 release:
  - Fixes an error which causes copy number data to not parse.
  - Addresses issues recently found with 2.4.0 installers.

## Highlights of caArray 2.4.0.1 released on 1/6/2011

- The 2.4.0.1 release addresses the following issues with the 2.4.0 release:
  - Fixes occasional out-of-memory errors with the parsers.
  - Addresses null pointer exception in the upgrade installer.
  - Adds probe name validation to the data file parsers.
  - Adds a security patch to Struts 2.1.x.
  - Correctly validates Genepix GAL array designs with non-integer block header information.

## Highlights of caArray 2.4.0 released on 9/21/2010

- This release represents a feature release of the caArray 2 software. Highlights of caArray 2.4.0 are:
  - Agilent raw TXT for aCGH, expression and miRNA assays
  - Agilent GEML/XML array designs
- **Nimblegen pair Report TXT (raw and normalized)**
- **Nimblegen NDF array designs**
  - Illumina Sample Probe Profile TXT
  - Illumina genotyping processed data matrix TXT
  - Illumina BGX/TXT array designs
  - Affymetrix CEL and CHP in AGCC/Calvin formats in addition to the GCOS formats
  - Affymetrix CNCHP copy number data (CN4 and CN5)
  - Copy Number data in a prescribed MAGE-TAB Data Matrix format.

- If you have copy number data that is not in the caArray-prescribed Copy Number MAGE-TAB Data Matrix format, we provide a conversion utility. The conversion utility is found inside the cn2magetab.jar file, and is invoked from the command line. Please see the README\_copy\_number\_conversion.txt for more details on its operation.

## What's New in caArray - Archive

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