

## Welcome to the Molecular Analysis Tools Knowledge Center

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### Mission and Scope

The caBIG® Molecular Analysis Tools Knowledge Center is an NCI-supported entity led by the Columbia University Herbert Irving Comprehensive Cancer Center with The Broad Institute of MIT and Harvard. The Knowledge Center provides a centralized, authoritative repository of knowledge, information, and web-based support to facilitate the deployment and ongoing development of caBIG® tools, standards, and infrastructure in the molecular analysis domain. Key services provided by the Knowledge Center include:

- Providing domain expertise on using the supported tools to carry out molecular analysis
- Posting up-to-date installation packages for related tools
- Maintaining technical and end-user documentation
- Fostering open source development of caBIG® tools by the community
- Collecting and monitoring defect reports, feature requests, and end-user requirements

### Alert for first-time visitors

If you want to post in the forum or add entries into the defect tracking/feature request system, please create a free account at [http://wikiutils.nci.nih.gov/KC\\_signup](http://wikiutils.nci.nih.gov/KC_signup).

Upon receiving your account credentials, you can post messages to the forums. To receive email notification when responses to your posts are made, simply click the "subscribe forum" or "subscribe topic" link at the bottom of the page.

If you have been using various email lists for the tools below, please be advised that forums hosted by this knowledge center will gradually become the main vehicle for your comments and questions on the tools. The email lists will be used mainly for announcements in the near future. Thank you for your understanding and support. Please let us know your thoughts and experience with this new channel of communication so that we can make it better.

## Learn About and Access Tools

The following software tools are currently supported by the Molecular Analysis Tools Knowledge Center. Links are provided to helpful resources including a summary tool landing page (provides an overview of the tool with links to resources), links to wiki pages (with additional information about the tool), forums (to post questions or comments), a bug tracker and feature request system, and the developer's code repository.

### ***caArray***

caArray is an open-source microarray data management system which is accessible both via the web and programmatically. caArray guides the annotation and exchange of array data using a federated model of local installations whose results are shareable across the cancer Biomedical Informatics Grid (caBIG®).

[About caArray](#) | [What's new](#) | [Download caArray](#) | [Questions and comments](#) | [Submit defects/feature requests](#) | [Open-source development](#)

### ***caIntegrator***

caIntegrator provides a database schema and associated programming framework that can be used to build applications integrating genomic and clinical data. It provides researchers with the ability to perform ad hoc querying and reporting across multiple domains. It currently powers several genomics/clinical applications: caGWAS, CMA, CGEMS, I-SPY, and Rembrandt.

[About caIntegrator](#) | [What's new](#) | [Download caIntegrator](#) | [Questions and comments](#) | [Submit defects/feature requests](#) | [Open-source development](#)

### ***geWorkbench***

geWorkbench (genomics Workbench) is a Java-based open-source platform for integrated genomics. Using a component architecture it allows individually developed plug-ins to be configured into complex bioinformatic applications. At present there are more than 50 available plug-ins supporting the visualization and analysis of gene expression and sequence data.

[About geWorkbench](#) | [What's new](#) | [Download geWorkbench](#) | [Questions and comments](#) | [Submit defects/feature requests](#) | [Open-source development](#)

## **GenePattern**

GenePattern combines a powerful scientific workflow platform with more than 90 computational and visualization tools for the analysis of genomic data.

[About GenePattern](#) | [What's new](#) | [Download GenePattern](#) | [Questions and comments](#) | [Submit defects/feature requests](#) | [Open-source development](#)

## **Integration of Tools**

There are extensive integration among caArray, caIntegrator, geWorkbench, and GenePattern. For example, geWorkbench can retrieve microarray data directly from caArray hosted at NCI. GenePattern is also connected to caArray for data retrieval. caIntegrator uses GenePattern as one of its data analysis services. Instead of developing all data analysis modules independently, geWorkbench and GenePattern each can invoke several modules of the other party to provide a comprehensive data analysis platform. To learn how to use these tools together, please check out corresponding tool's wiki pages as well as the forums ([End Users forum](#) and [Developers forum](#)) dedicated to the integration of these tools.

## **Visit Domain Level Knowledge Center Forum**

[Molecular Analysis Tools Domain Forum](#). This forum is for visitors to submit questions and comments that are beyond the scope of any specific tool, but that are within the domain addressed by the Knowledge Center. What questions or comments do you have that extend beyond the coverage of the existing caBIG® tool set? Write your thoughts in this forum, so that they can be answered by the Knowledge Center Team and/or brought to appropriate stakeholder groups such as the Integrative Cancer Research (ICR) workspace.

## **Related Links**

- Link to [ICR Workspace Page](#) (On caBIG® Community Website)
- Link to [caBIG® Support Service Provider Listing](#)
- Link to [caBIG® Community Website](#)