

# caLIMS v2: a next generation cancer Laboratory Information Management System designed for caBIG® Interoperability

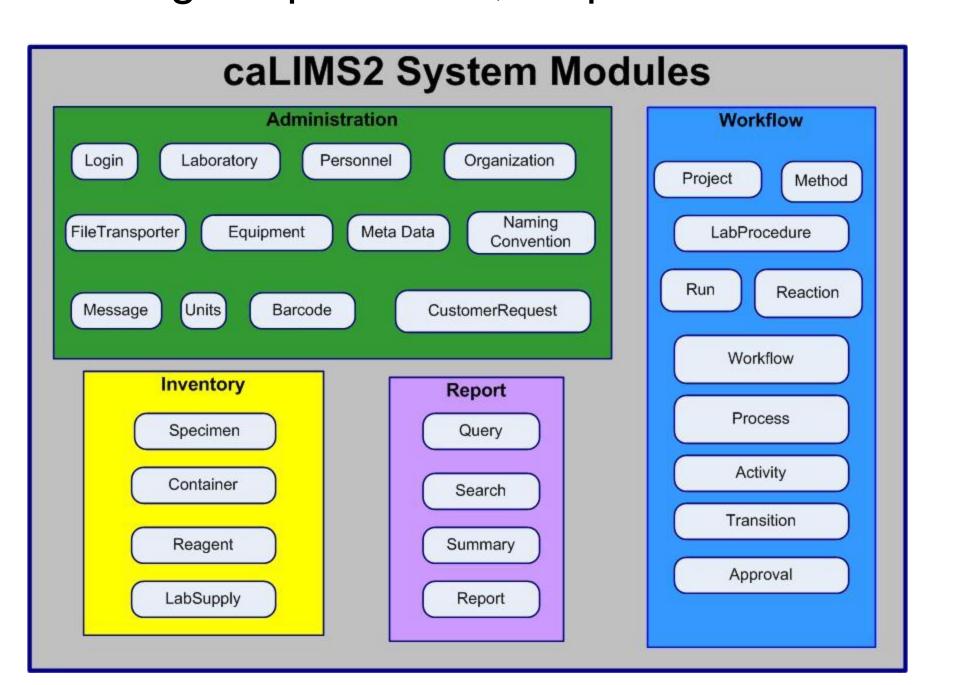


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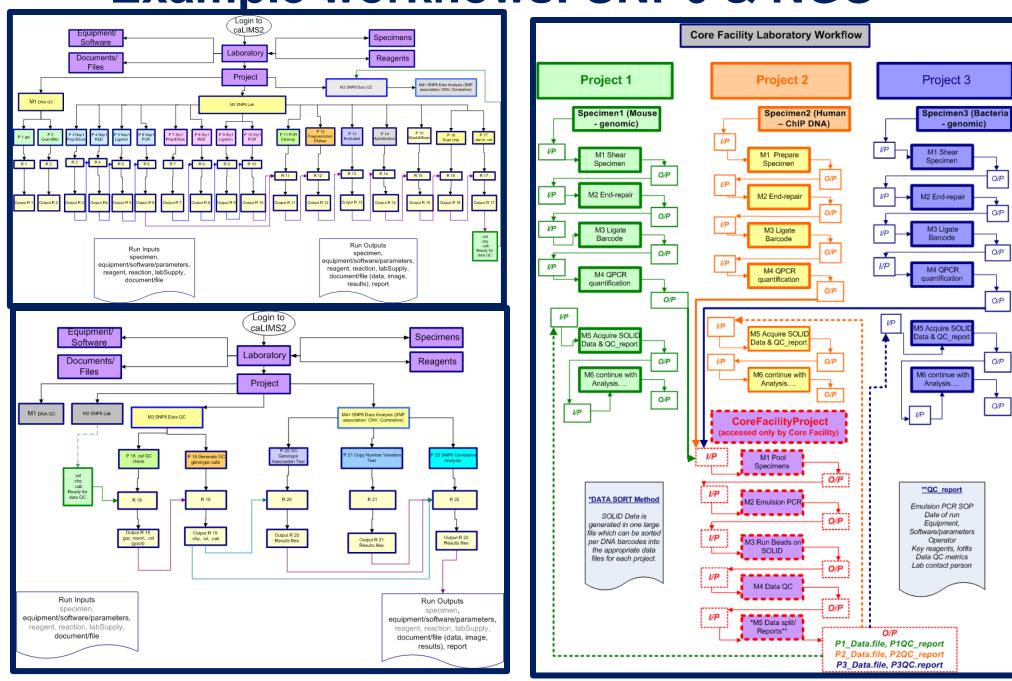
1) NCI Laboratory of Population Genetics, 2) Moxie Informatics

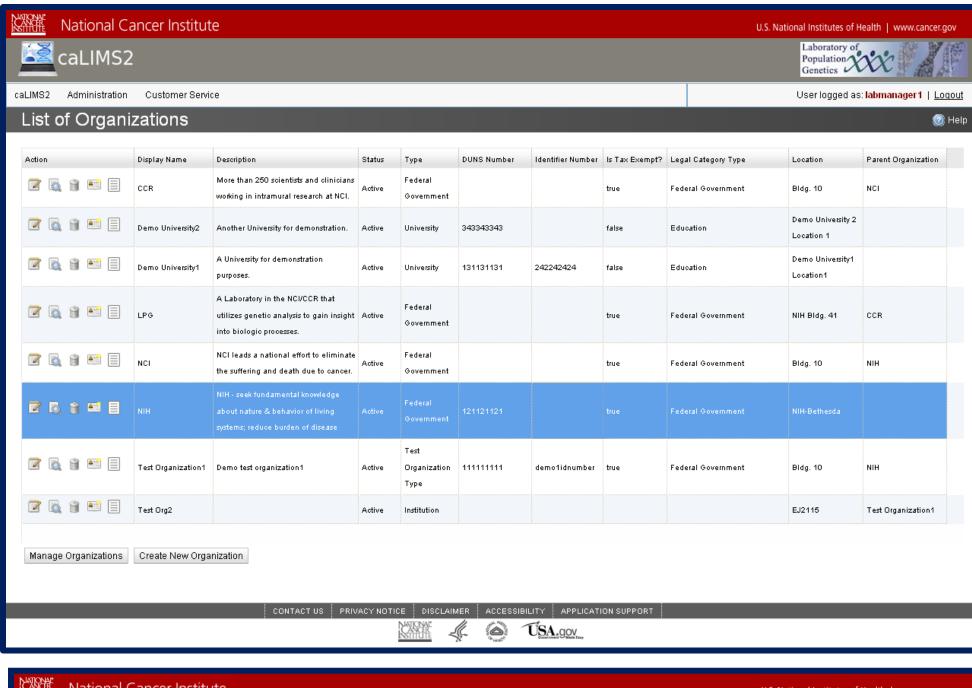
## Background

caLIMS v2 is a web-based Laboratory Information Management System designed according to caBIG® principles to support Life Sciences research laboratories and core facilities. caLIMS v2 completes the caBIG® bench to bed model by bridging the gap between biospecimen repositories, data repositories and analysis tools. The application is designed to allow easy customization by users and to facilitate integration with laboratory equipment, analytical tools and data sources. caLIMS v2 will help further translational cancer research through the organization of laboratory data and metadata, and the appropriate sharing and dissemination of the data to support subsequent analyses.



#### **Example workflows: SNP6 & NGS**





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### Features of caLIMS v2

- Open source, consortium-based development
- caBIG<sup>®</sup> integration
- Security management via CSM/UPT/GAARDS
- Generic Experiment Method model supports multiple lab domains (genomics, proteomics, nanomaterial, etc.)
- Platform and database independence
- Customizable UI layer
- Laboratory Workflow management exchange/share template workflows using Experiment Method Service
- FileTransporter module import/export/associate files
- Support for research laboratories and core facilities
- Not cancer specific supports other disease research

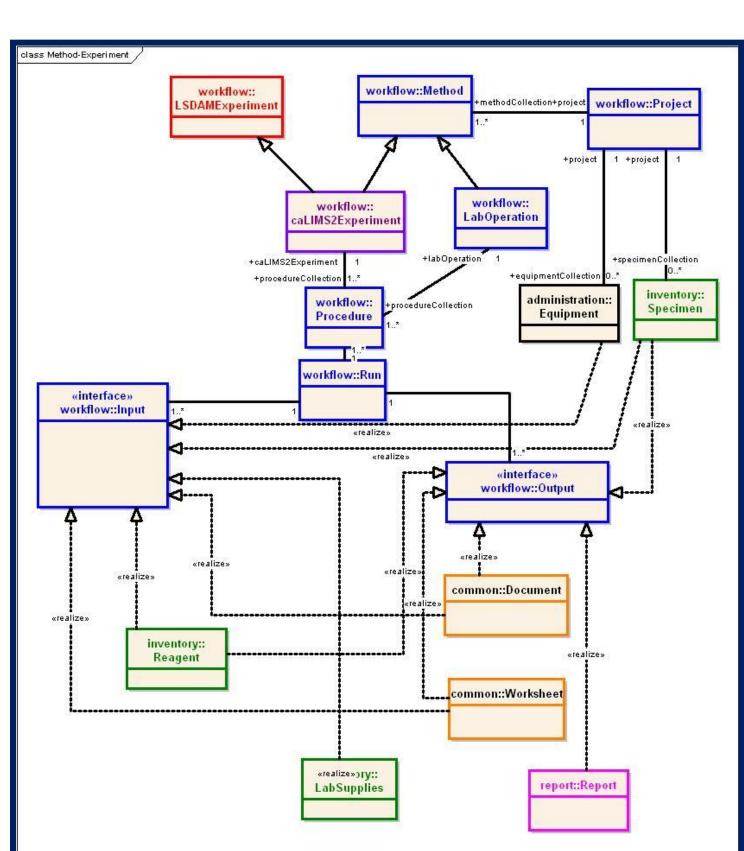
## **Equipment Service**

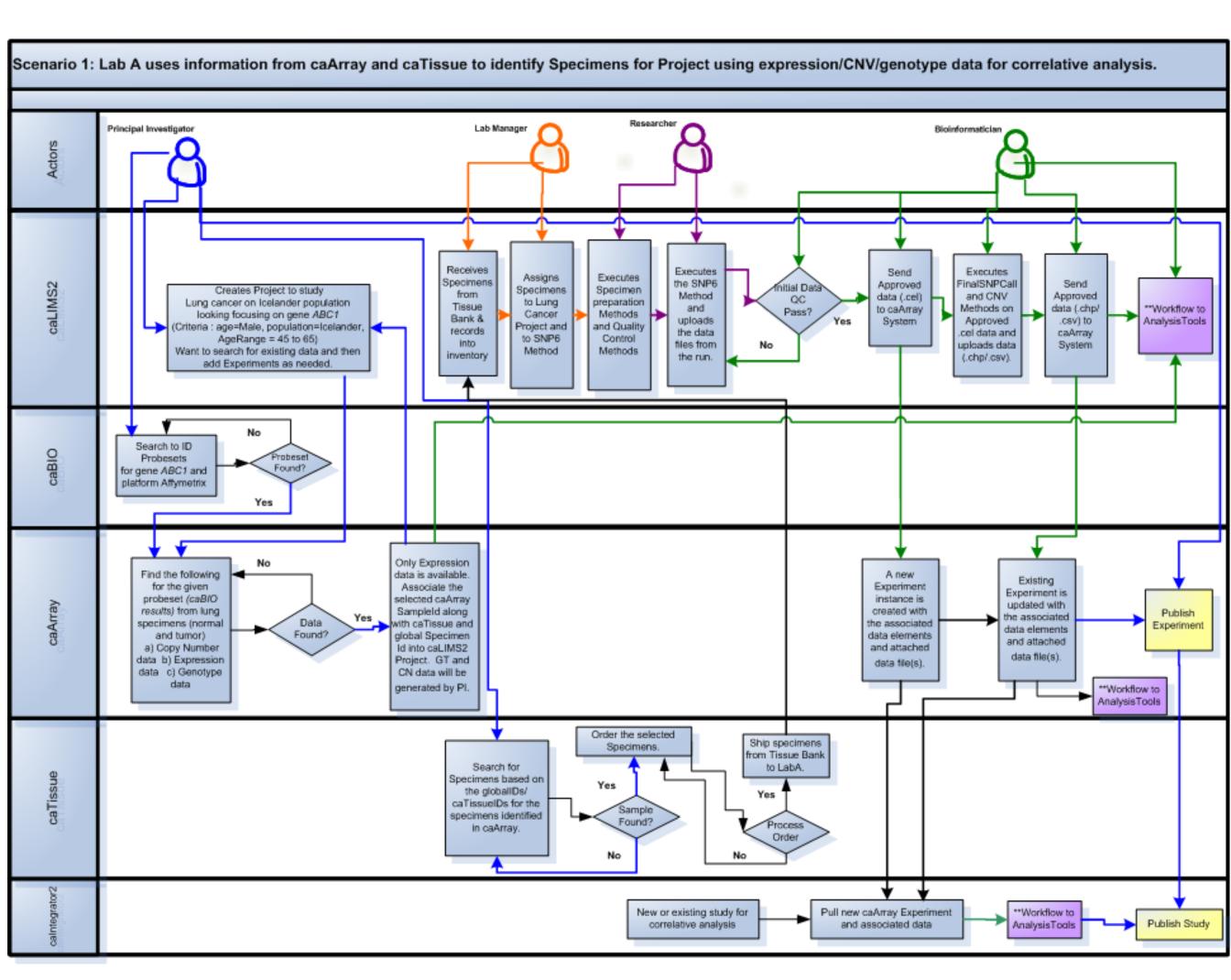
- Registration of equipment type
- manufacturer, model,
   associated software (operating,
- firmware, collection, data management/analysis)
  •Definition of user defined input
- parametersFunctional platforms supported
- and their expected Input(s), Output(s), and Parameters
- Query Equipment (standard and advanced)

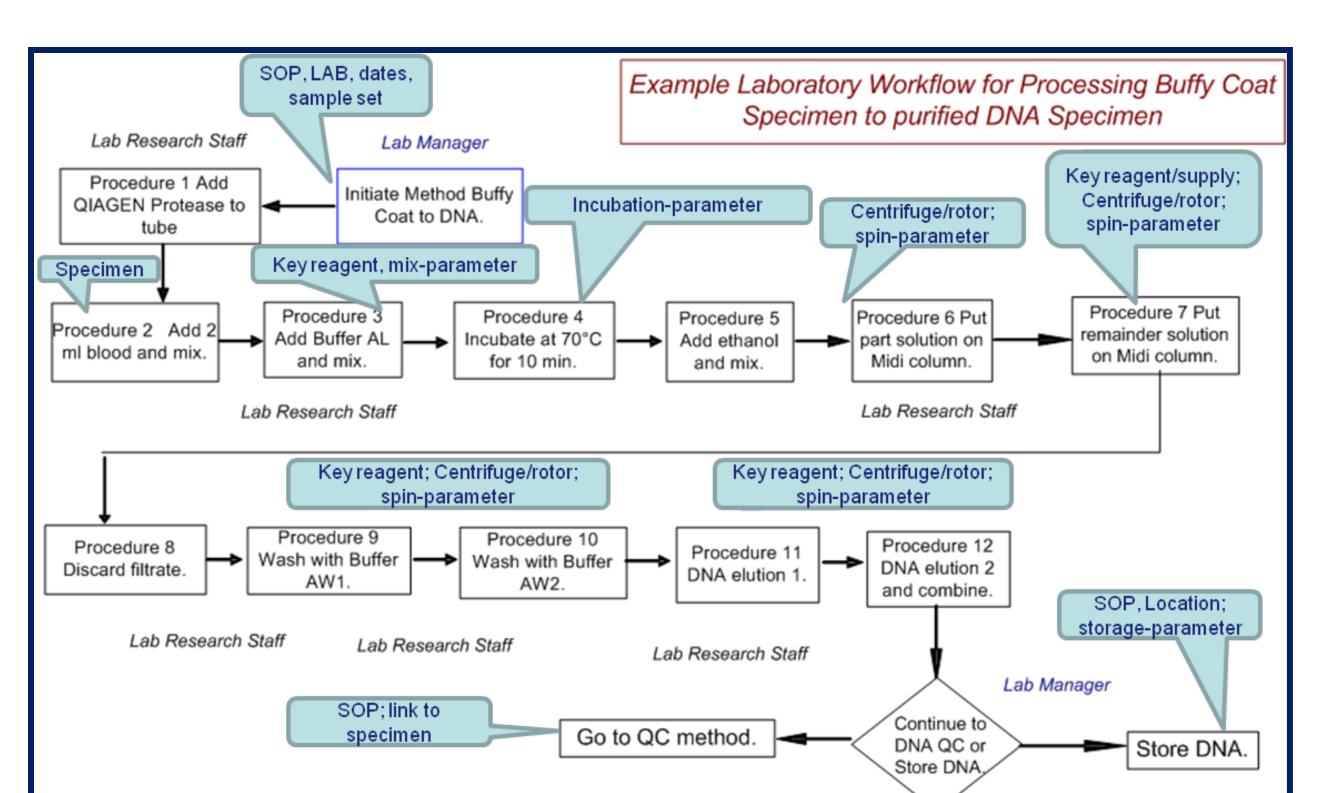
## SOP (Experiment Method) Service

- Create SOP (Experiment Method )by
- Defining Method and Procedure(s)
- •Defining expected Input(s),
  Parameter(s), and Output(s)
- typesReference to associated
- Equipment serviceQuery Experiment Method

(standard and advanced)





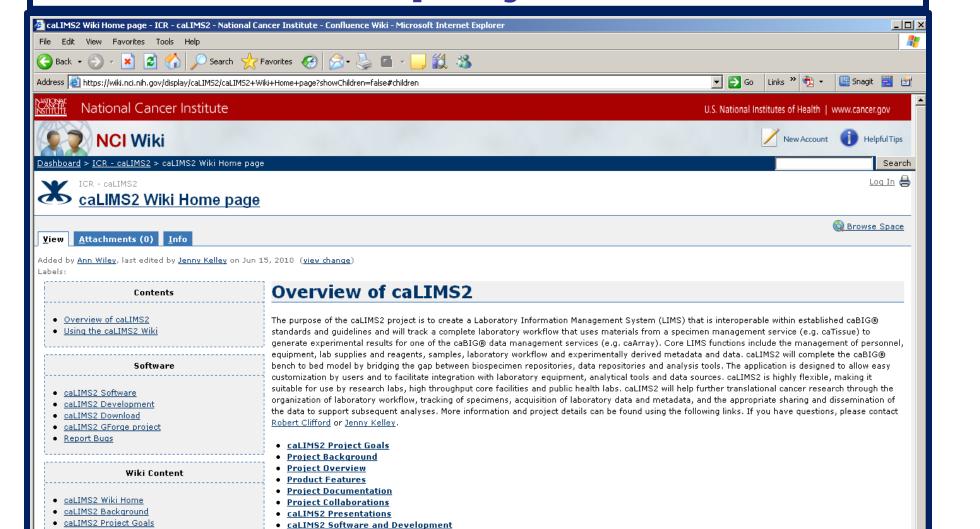


## Use Case: Integrating caLIMS v2 with caBIG® Services and Applications

- A Principal Investigator wants to participate in a collaborative study involving the relationship of gene ABC1 and lung cancer susceptibility in men age 45 – 65. The PI is particularly interested in a population from Iceland.
- PI plans to use multiple data types (copy number, genotype, gene expression) in a new form of correlative analysis and wants to take advantage of existing data and specimen resources.
- PI obtains appropriate tissue specimens by searching caTissue and contacting Biorepository.
- PI obtains pre-existing gene expression data from caArray and generates new genotype and copy number data in her laboratory.
- PI programmatically submits final data to the caArray repository.
- PI publishes paper and makes caArray data available to public.

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caLIMS v2 project wiki site



This is the wiki home page of calims2 (Cancer Laboratory Information Management System 2). Project team members may edit this page and add more

• caLIMS2 Development Working Grou

Using the caLIMS2 Wiki

caLIMS2 Features

caLIMS2 Software

• caLIMS2 Communication
• NCI LIMS Consortium

calIMS2 Community Input

caLIMS2 Documentation
 caLIMS2 Collaborations
 caLIMS2 Presentations

### NCI CBIIT LIMS Consortium

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