

Organization of Sample Storage using Starlims in the RWTH cBMB

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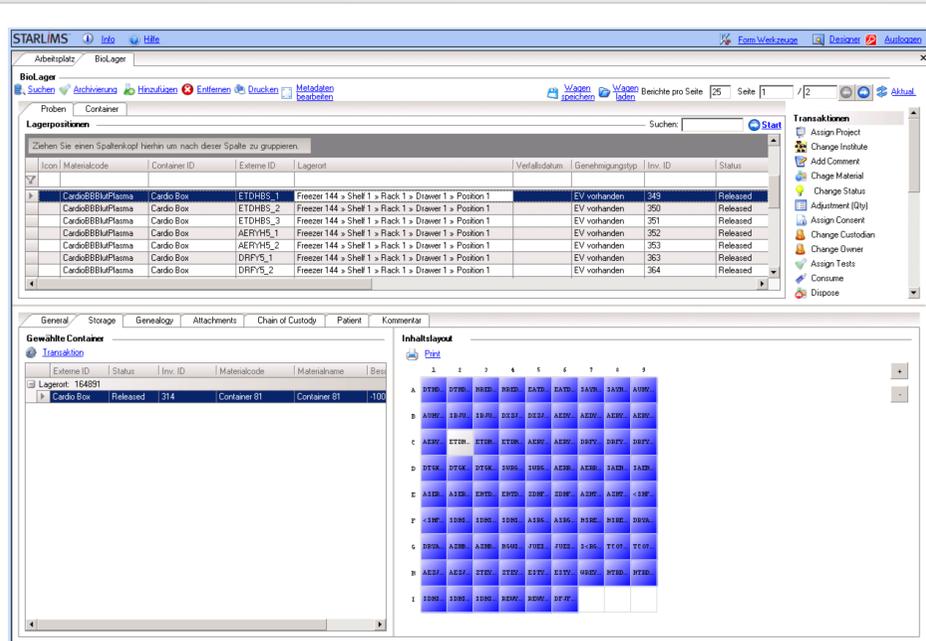
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Starlims

Starlims is a commercial browser-based Laboratory Information Management System (LIMS), deployed in RWTH cBMB in 2011 to manage organizational sample data. The archiving workflow has been revised and new features have been added to improve the sample archiving process in the biobank.

BioRepository

The BioRepository module has been selected as a central Starlims component in RWTH cBMB for sample archiving. The following sample data is stored in BioRepository: labID, number of aliquots, submitting institute and project, storage location, position in container, archiving and pick dates, additional sample specific data.



BioRepository: main sample data grid, list of available transactions, container grid displaying sample position.

Sample Management

BioRepository transactions are used to move or dispose samples and to update sample data. All transactions are logged, which helps to track sample history from reception till disposal and view all changes performed by users.

New transactions have been developed by our team to edit specimen attributes like material type, institute or labID. Flexible storage location management is provided by the Location Manager module, which is used to configure freezer structure, specify environment conditions and display sample position in locations hierarchy.

Metadata

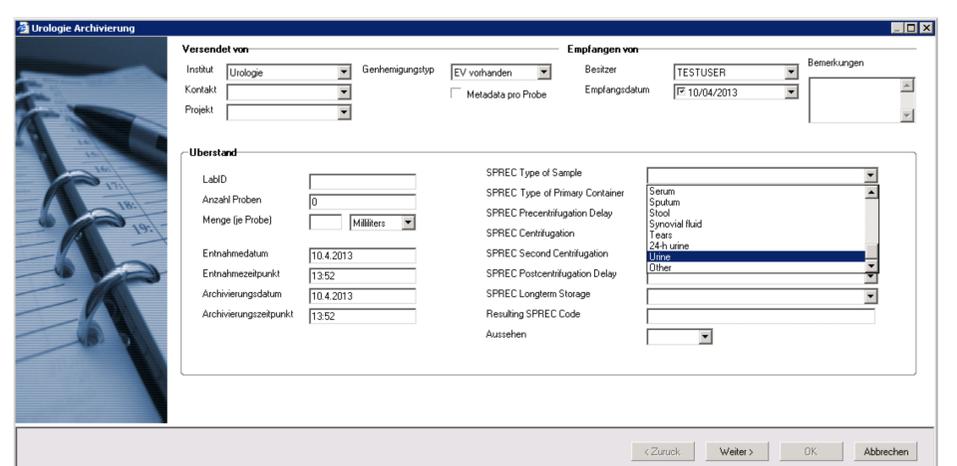
Metadata is used to expand BioRepository sample information with arbitrary number of user-defined parameters. Metadata fields and layout are configured using templates, so that each sample gets specific set of metadata attributes depending on material (e.g. tissue type, serum appearance) or project (e.g. EFACTS container ID). Metadata may also include SPREC codes and other process related data.

Sample Archiving

BioRepository has been enhanced to conform with the RWTH cBMB laboratory archiving workflow. The customized sample archiving interfaces correspond to the most common types of sample deliveries, varying in project, material, submitting organization and metadata set. Entering specimen parameters, editing metadata and positioning sample in container is performed atomically. Most of the data fields are prepopulated with default values, thus reducing the number of repeated actions in most cases.

Here are some examples:

- New wizard for the EFACTS project helps to facilitate the archiving of samples, which arrive in large batches. Submission consists in entering container IDs in metadata, whereas all other parameters are predefined.
- Samples from the Clinic of Urology, including supernatant, sediment, EDTA blood and serum can be submitted in one interface, thus avoiding redundant data entries. (see picture below).
- The generic sample archiving interface can be used to archive specimens of arbitrary material types or projects.



Sample archiving interface for the Clinic of Urology