2020-07-29

MISO LIMS Training

Introduction



Agenda

- Introduction
 - MISO LIMS
 - Navigation
 - Entering Data
 - Getting Help
 - Projects
- Samples
- Libraries
- Sequencing

MISO LIMS

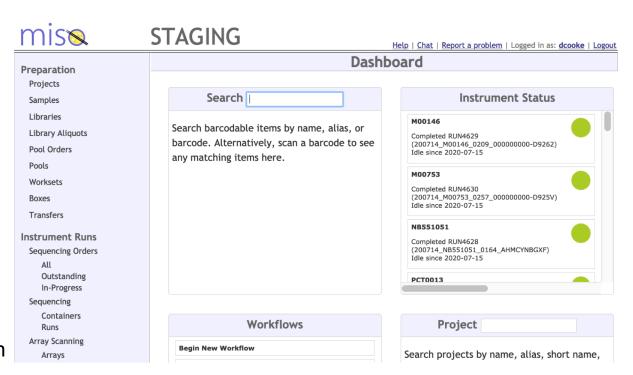
- Laboratory Information Management System for next-generation sequencing centres
- Created by Earlham Institute (formerly TGAC)
- Developed by Ontario Institute for Cancer Research since 2015
 - Ongoing new features still being added
- Track all lab processes from sample receipt to sequencing

MISO LIMS

- Sample receipt and wet lab work
- Library receipt or preparation
- Pooling
- Sequencing
- Quality Control
- Location tracking
 - Barcoding
 - Tube storage
 - Freezers
 - Transfers receipt, internal, and distribution
- Orders communicating requirements between teams

Navigating MISO

- Home Page
 - Widgets
 - Navigation Menu
 - Preparation
 - Instrument Runs
 - Tools
 - Misc
 - Institute Defaults
 - ENA
 - User Administration



List Pages



Working with Tables

- Bulk entry in MISO is done using a table interface similar to Excel and other spreadsheet software
- Tables have import and export features
 - Can work in spreadsheet software outside of MISO
- In some cases, the bulk table does not include all information
 - Check the individual item page

Bulk Pages

Create Libraries

Save

Quick Help 0

Fill Box	es by Rov	/ Fill E	Boxes by Colum	n Check	QCs Sort	Import Export							
	Name	Alias	Sample Type	Project	Subproject	Sci. Name	External Name	Identity Alias	Donor Sex	Consent	Sample Class	Tissue Origin	Tissue
1			GENOMIC ▼	DEMO ▼	•	Homo sapiens ▼		▼	Unknown ▼	This Project ▼	gDNA (aliquot)	▼	
2			GENOMIC ▼	DEMO ▼	▼	Homo sapiens ▼		▼	Unknown ▼	This Project ▼	gDNA (aliquot)	▼	
3			GENOMIC ▼	DEMO ▼	•	Homo sapiens ▼		▼	Unknown ▼	This Project ▼	gDNA (aliquot)	▼	
4			GENOMIC ▼	DEMO ▼	▼	Homo sapiens ▼		▼	Unknown ▼	This Project ▼	gDNA (aliquot)	▼	
5			GENOMIC ▼	DEMO ▼	▼	Homo sapiens ▼		▼	Unknown ▼	This Project ▼	gDNA (aliquot)	▼	
6			GENOMIC ▼	DEMO ▼	▼	Homo sapiens ▼		▼	Unknown ▼	This Project ▼	gDNA (aliquot)	▼	
7			GENOMIC ▼	DEMO ▼	▼	Homo sapiens ▼		▼	Unknown ▼	This Project ▼	gDNA (aliquot)	▼	
8			GENOMIC ▼	DEMO ▼	▼	Homo sapiens ▼		▼	Unknown ▼	This Project ▼	gDNA (aliquot)	▼	
9			GENOMIC ▼	DEMO ▼	▼	Homo sapiens ▼		▼	Unknown ▼	This Project ▼	gDNA (aliquot)	▼	
10			GENOMIC ▼	DEMO ▼	▼	Homo sapiens ▼		▼	Unknown ▼	This Project ▼	gDNA (aliquot)	▼	
11			GENOMIC ▼	DEMO ▼	▼	Homo sapiens ▼		▼	Unknown ▼	This Project ▼	gDNA (aliquot)	▼	
12			GENOMIC ▼	DEMO ▼	▼	Homo sapiens ▼		▼	Unknown ▼	This Project ▼	gDNA (aliquot)	▼	

Edit Pages

Edit Sample Save Previous Sample SAM268249 Home DEMO Quick Help 0 **Sample Information** Sample ID: 268250 Project:* DEMO Name: SAM268250 Alias:* DEMO_0001_Pa_P_nn_1-1_D_S1 Description: Matrix Barcode: Date of Receipt: YYYY-MM-DD Requisition ID: Scientific Name:* Homo sapiens Sample Type:* **GENOMIC** QC Status: Ready QC Status Note: Discarded:

Edit Pages (Continued)



Working with Boxes

- Samples, libraries, library aliquots, and pools can be stored in barcoded tubes
- These tubes are stored in boxes
- Boxes are usually stored in freezers
- Boxes may also represent plates which do not have a barcode for each well
- The Box Contents diagram in MISO allows you to select and work with one or many box positions to choose or modify what is stored in the box
- The VisionMate scanner can be used to scan all of the tubes at once to quickly fill a box in MISO

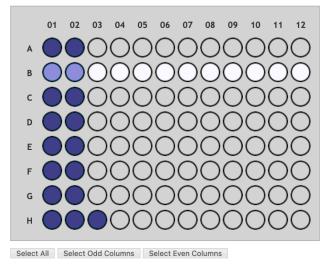


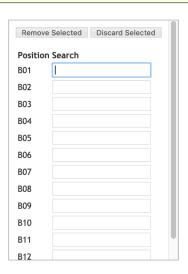
Edit Box Page

Contents

Options ▼

Hold down Ctrl (Windows, Linux) or Command (Mac) to select multiple positions. Click a row or column header to select the entire row or column.





Print Barcodes by Position	Edit 1	Make aliquots	Print Barcode(s)	Download	Parents	Children	Add QCs	Edit Q	Cs A	dd to W	/orkset	
Attach Files Transfer												
Show 96 🗘 entries	List all I	Box Content	h:									
Position	_	Element Name \$				Element Alias						<
B01		<u>LIB39970</u>				CPTRG_0111_Ov_M_PE_60702_EX						
B02		<u>LIB39978</u>				CPTRG_0118_Ov_M_PE_60710_EX						
Showing 1 to 2 of 2 entries (fi			Last	Next	1 Pr	revious	First					

Getting Help

- Links in Header
 - Help User Manual
 - Chat Gitter
 - Report a problem
- Quick Help
- Help Bubbles ??



Projects

- Represent a sequencing effort toward a particular goal
- Grouping of samples, libraries, sequencer runs, and other related items
- Samples belong to a project. Most other items are related indirectly through samples
 - Libraries and library aliquots belong to the project of the parent sample
 - Pools and runs may contain items from multiple projects
- Edit Project page shows all related items

Exercise

Complete the following tutorials using Chrome or Firefox:

- Tutorial 3: Working with Boxes
- Tutorial 4: Working with Tables
- Tutorial 5: Project Coordination

https://miso-lims.github.io/walkthroughs/

Note: These are the OICR walkthroughs. Other labs may have an alternate site.



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