Baobab LIMS Documentation

Release 1.3

SANBI(UWC)

Aug 23, 2018

Contents

1 Installing **3**
- 1.1 Plone installation . . . 3
- 1.2 Install Baobab LIMS . . . 4
- 1.3 Test your installation . . . 5

2 Setup Manual **7**
- 2.1 Introduction to Baobab LIMS . . . 7
- 2.2 Install your Baobab distribution . . . 8
- 2.3 Change the Baobab Theme . . . 9
- 2.4 Your Baobab distribution . . . 12

3 Baobab LIMS User manual **31**
- 3.1 Plone Configuration . . . 32
- 3.2 Baobab LIMS Configuration . . . 34
- 3.3 Add client . . . 35
- 3.4 Add project . . . 36
- 3.5 Projects . . . 38
- 3.6 Kits . . . 39
- 3.7 Shipments . . . 40
- 3.8 Biospecimens . . . 42
- 3.9 Performing an analysis request . . . 43

Baobab LIMS is an open-source laboratory information management system (LIMS) software that will ensure that researchers can track the lifecycle of a biospecimen in the laboratory from receipt to storage and reuse. This software ensures that sufficient metadata is captured..

An open source LIMS for human Biobanks. Baobab is a common name given to nine tree species in different countries in the world, mostly in Africa. Baobab LIMS written in Plone, a python framework known for its robustness, and inherits some modules from Bika LIMS.

The code is open source, and available on GitHub.

The main documentation for the site is organized into a couple sections:

- user-docs
- feature-docs
- about-docs

Information about development is also available:

- dev-docs
- design-docs

This website covers project information for BaobabLIMS such as the changelog, contribution guidelines, development roadmap, news/blog, and so forth. Detailed usage and API documentation can be found at our code documentation site, docs.fabfile.org.

Please see the navigation sidebar to the left to begin.

CHAPTER 1

Installing

1.1 Plone installation

Here we describe how to install Plone onto the Ubuntu Linux System. For an installation in a different operating system, check the Plone online documentation, here. The installation process requires users to have root priveledges and a basic knowledge of the Linux command lines using Terminal. If you are not familiar with a UNIX operating system, read this tutorial Linux shell tutorial. Please note that a single line must be completed at a time.

1.1.1 Plone dependencies

‘‘Plone‘‘ framework requires the installation of additional system packages. Without these packages available in your system, Plone will not compile.

```
$ sudo apt-get install build-essential gcc python-dev git-core
libffi-dev
```

```
$ sudo apt-get install libpcre3 libpcre3-dev autoconf libtool
pkg-config
```

```
$ sudo apt-get install zlib1g-dev libssl-dev libexpat1-dev libxslt1.1
```

```
$ sudo apt-get install gnuplot libcairo2 libpango1.0-0
libgdk-pixbuf2.0-0
```

1.1.2 Download Plone 4.3 Unified Installer

The Baobab LIMS is implemented and tested with Plone 4.3.11, a version released in 2016-09-12. You can download Plone 4.3.x by visiting the Plone site. Select and click on the Unified installer of your choice or use ‘‘wget‘‘ command line in your terminal with the path to the Plone version to install. Only Plone 4.3.11 can be used.

```
$ wget --no-check-certificate https://launchpad.net/plone/4.3/4.3.11/
+download/Plone-4.3.11-r1-UnifiedInstaller.tgz
```

If the download has been done from the Plone site, the installer would be located in the ‘‘~/Downloads‘‘ directory. If the second option used i.e, the wget command line, the installer should be downloaded into the current directory.

1.1.3 Install Ploner

To continue the installation, in the terminal, change directory to the folder containing the downloaded file then run the following command line to unpack the archive file.

```
$ tar -xf Plone-4.3.11-r1-UnifiedInstaller.tgz
```

Change to the extracted folder in the terminal.

```
$ cd Plone-4.3.11-r1-UnifiedInstaller
```

Run the following command to install Plone

```
$ ./install.sh --target=/usr/local/Plone --build-python zeo
```

```
$ ./install.sh --target=/home/ubuntu/Plone --build-python zeo
```

where `--target` parameter is used to specify the path to the installation folder, `--build` python will add and build Python package in your system, (this is optional if Python already exist) and finally zeo option will install Plone as a Client-Server application. Plone requires Python2.7 in order to operate. Run ./install.sh –help to obtain the full list of the available parameters and their meaning.

1.2 Install Baobab LIMS

In the new folder created ‘‘/usr/local/Plone‘‘ , another folder named zeocluster can be found. This folder contains the configuration file, buildout.cfg. Find in the configuration file, and in the section starting with eggs=, add bika.lims and baobab.lims to the existing entries.

Note: Bika LIMS is a dependency that Baobab LIMS needs to function. Some of modules in Baobab LIMS reference modules in Bika LIMS.

```
$ eggs =
    Plone
    Pillow
    bika.lims
    baobab.lims
```

Add to the section developer = the path to your version of Baobab LIMS and BIKA LIMS that should be already downloaded into your local machine. By convention it is preferable to put the source code in zeocluster/src of your Plone installation folder.

Add to the section developer = the path to your version of Baobab LIMS and BIKA LIMS that should be already downloaded into your local machine. By convention it is preferable to put the source code in ‘‘zeocluster/src‘‘ of your Plone installation folder.

```
$ developer =
    src/baobab.lims
    src/bika.lims
```

Use git clone or fork this project to have your own copy in your local machine. For developers, any change in your source code that you judge interesting and useful for the community please create a `Pull` request and let us know if you want to become a collaborator in the Baobab LIMS project.

Links below; Bika labs Baobab LIMS

Save the file, and run `bin/buildout -n`. Buildout will download and install all the declared dependencies.

If you installed ‘‘Plone‘‘ as a root user i.e., using sudo, you should run the buildout command line with the user plone_buildout, this user is automatically created during the Plone installation:

```
$ sudo -u plone_buildout bin/buildout
```

Warning: If you encounter the `packages not found` issue, add the following line, issue related to this: https://github.com/BaobabLims/baobab.lims/issues/55

```
index = https://pypi.python.org/simple/
```

Add the above line in the `[buildout]` section.

1.3 Test your installation

First, you will need to start the zeoserver (this is the database process).

```
$ bin/zeoserver start
```

To start a Plone client in debug mode, run this command:

```
$ bin/client1 fg
```

If you installed Plone as a root user, you will need to use the following commands instead:

```
$ sudo -u plone_daemon bin/zeoserver start
```

```
$ sudo -u plone_daemon bin/client1 fg
```

Note: any error messages, and take corrective action if required. If no errors are encountered, you can press Control+C to exit.

In your preferred browser, Firefox or google chrome, run ‘http://localhost:8080/’_ and start working with Baobab LIMS. Enjoy it!

If installed on a remote server, an IP address (of the server) is associated with the use of LIMS eg: https://192.168.1.1:8080/

In production mode, other important tools need to be installed and configured, like `Supervisorctl` and nginx. The following article details the process to follow to add those tools cited before.

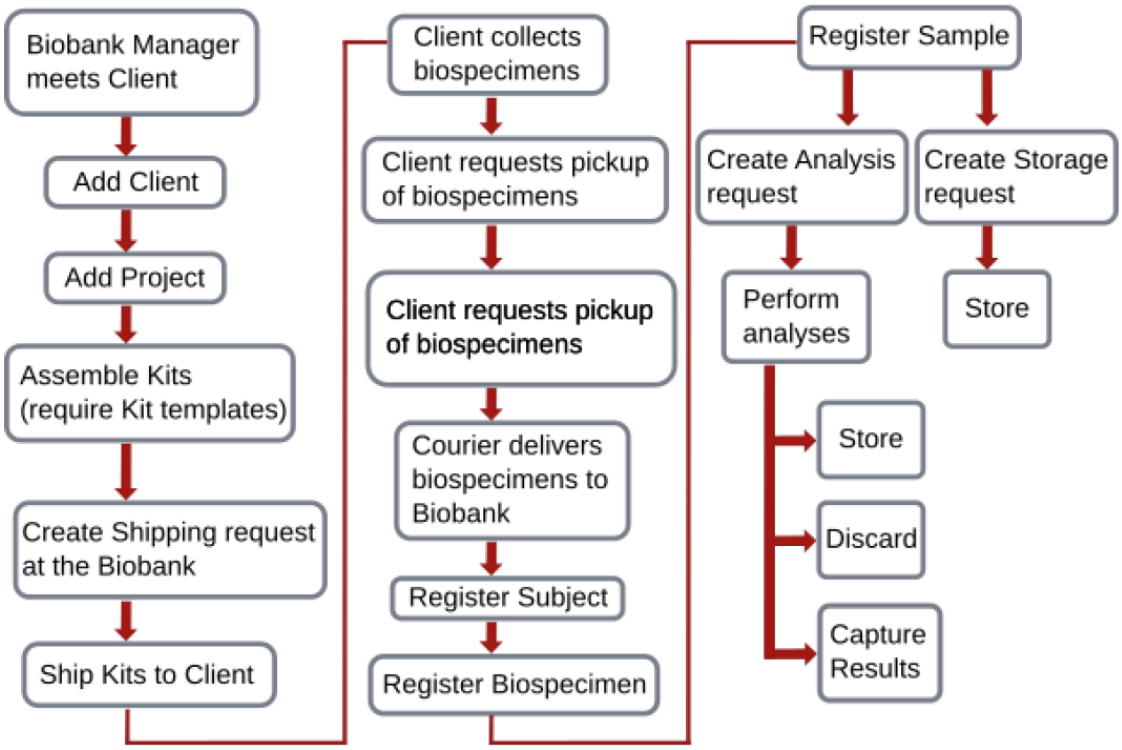
CHAPTER 2

Setup Manual

2.1 Introduction to Baobab LIMS

Baobab LIMS is a Laboratory Information Management System (LIMS) designed for the collection, processing and storage of human biospecimens. The system was designed a priori using the Standard operating procedures (SOPs) of the NHLS-Stellenbosch University Biobank. Baobab LIMS comprises modules for biospecimen kit assembly, biospecimen shipping, storage management, analysis requests, reporting and invoicing. Current developed SOPs define the biobanking activities of the Biobank and in an effort to extend the usability of the system, collaborations which incorporate SOPs generated by other Biobanking facilities, are ongoing. The figure demonstrates the workflow of the current system, deduced from SOPs.

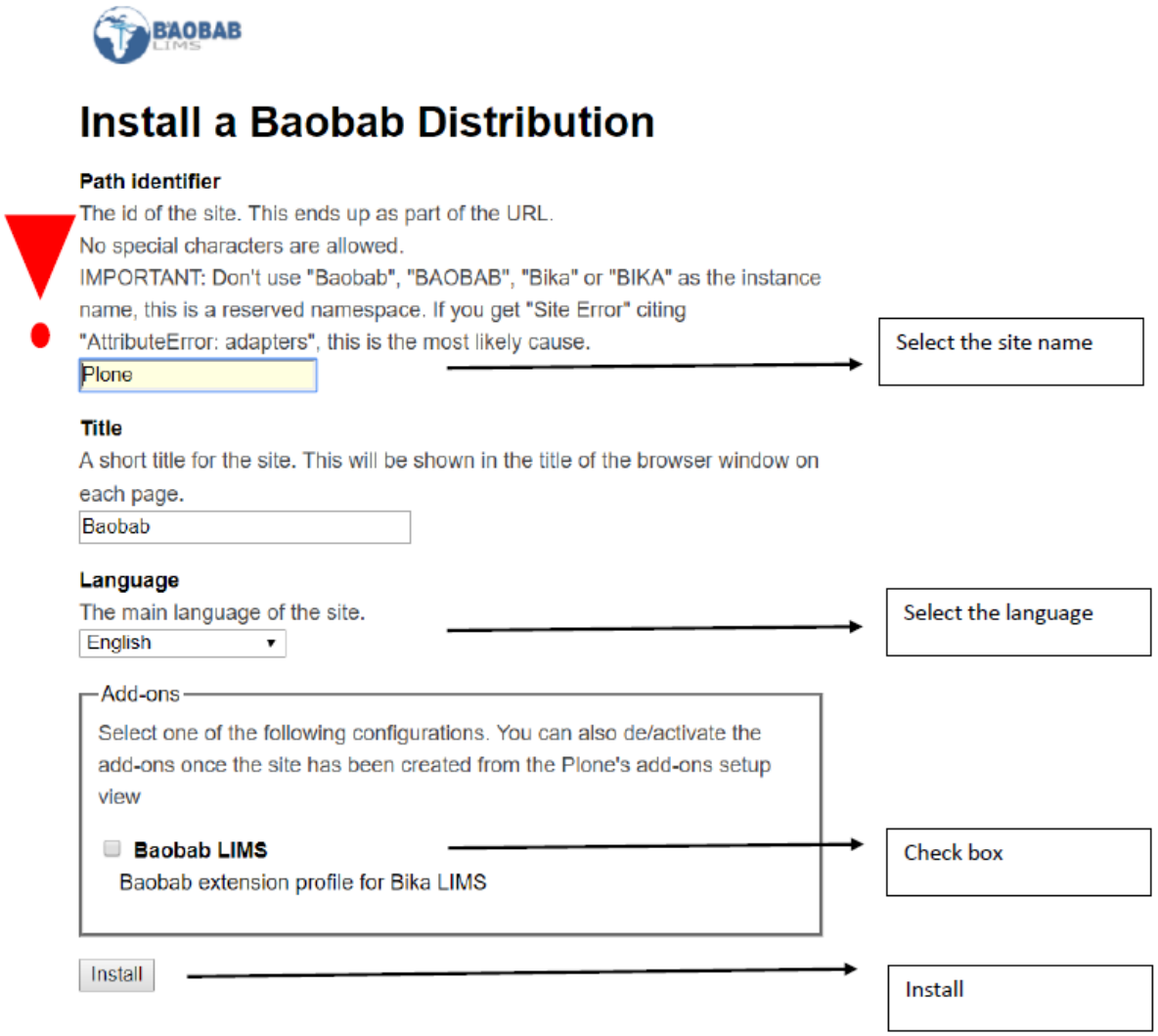
Baobab LIMS is both Free and Open Source with some modules being inherited from Bika LIMS. Furthermore, Baobab LIMS can be customized to the specific needs of your laboratory.



For more additional resources, use the following link to github, or read the parer here

2.2 Install your Baobab distribution

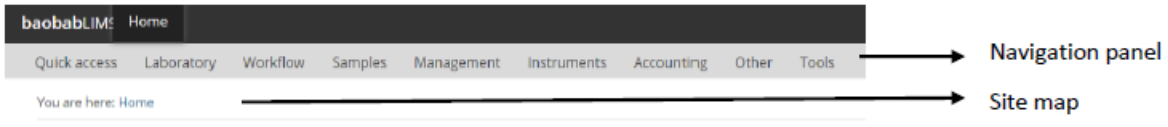
Go to https://<server IP address>/manage_main Select 'Add Plone site'



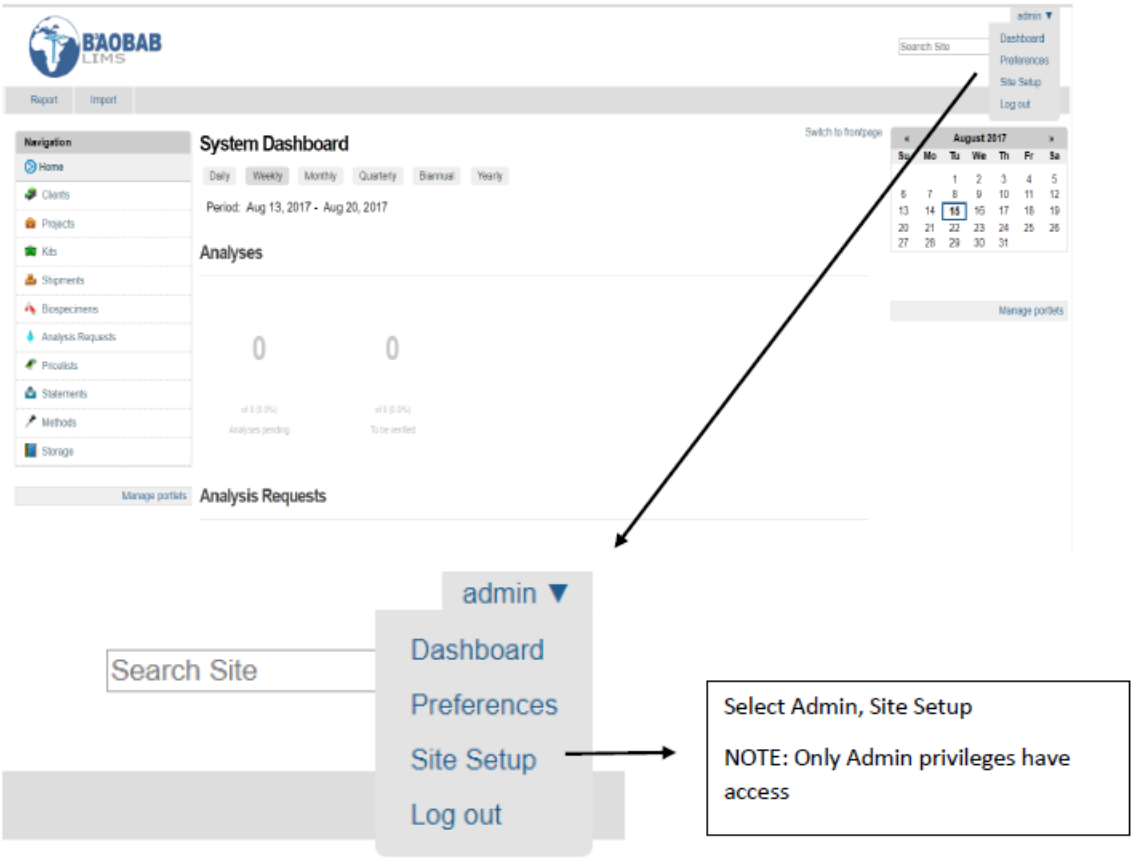
Warning: It is important that you do not use “baobab”, “BAOBAB”, “BIKA” or “bika” in your instance name. This is a reserved namespace and a “site error” will occur

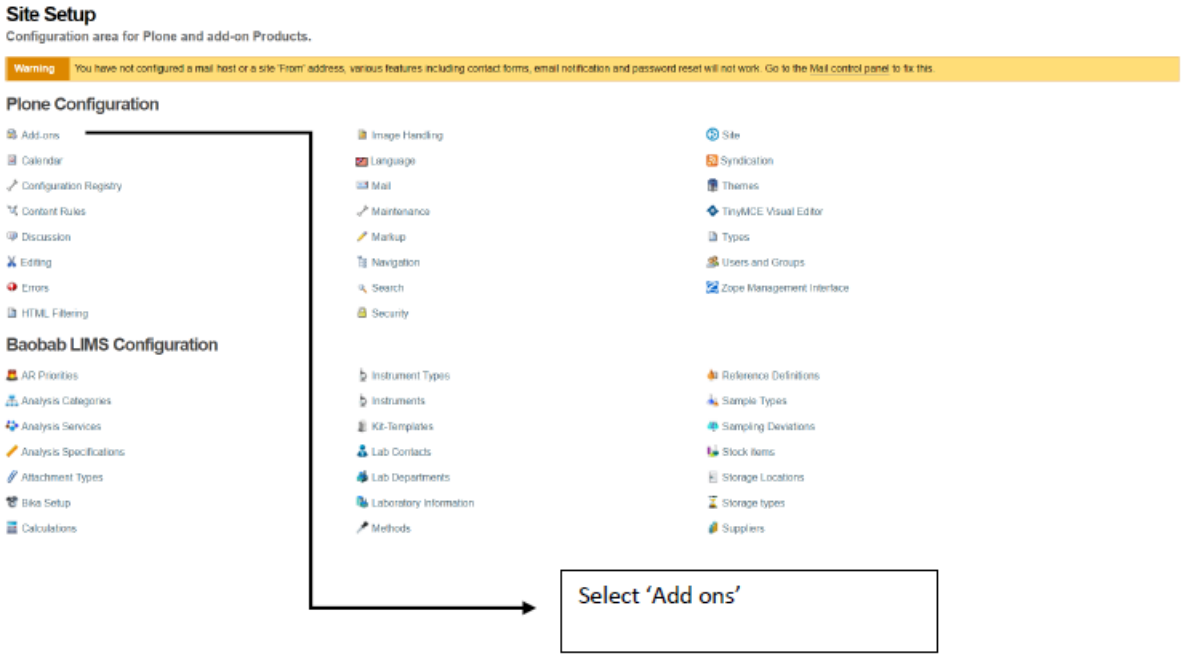
2.3 Change the Baobab Theme

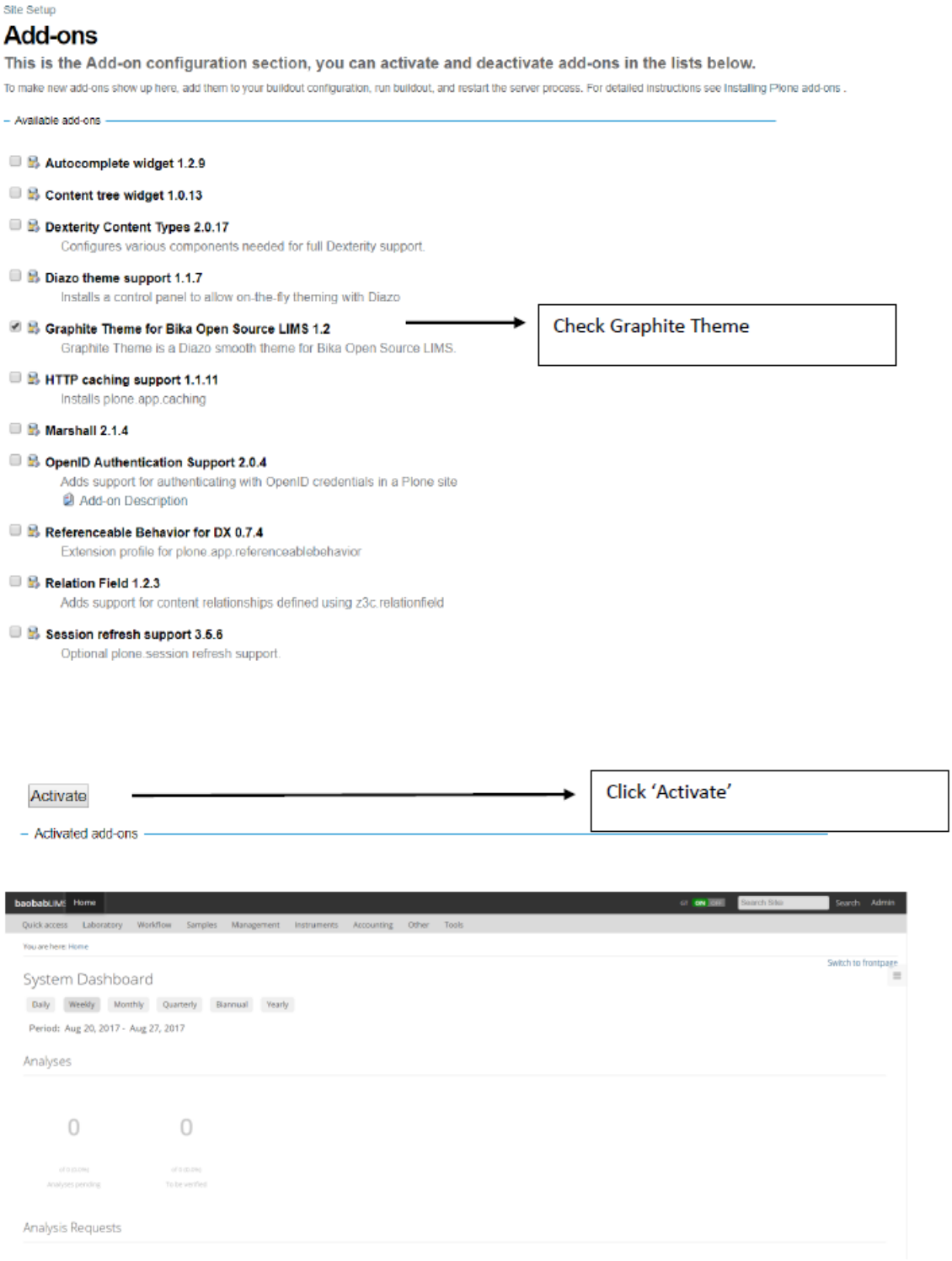
The Baobab theme can be changed to the graphite theme. The graphite theme has an easy access navigation panel at the top of the page and a site map.



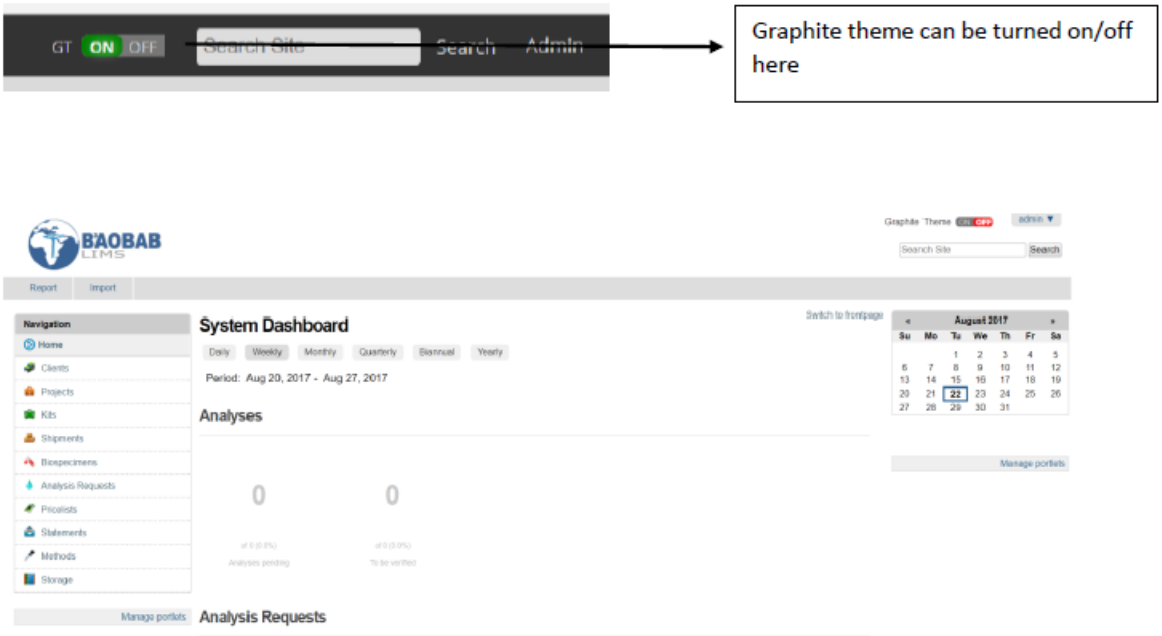
Follow the instructions below to change your theme;


admin ▼
Search Site
Dashboard
Preferences
Site Setup
Log out
Select Admin, Site Setup
NOTE: Only Admin privileges have access


Site Setup
Configuration area for Plone and add-on Products.
Warning
Plone Configuration
Add-ons
Baobab LIMS Configuration
Select 'Add ons'



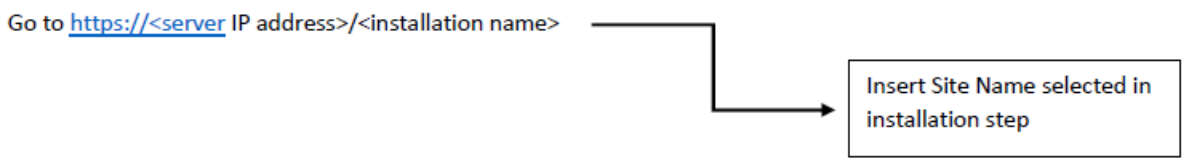
The figure above represents the homepage of the Graphite theme.



The figure above represents the homepage if the graphite theme has been disabled.

2.4 Your Baobab distribution

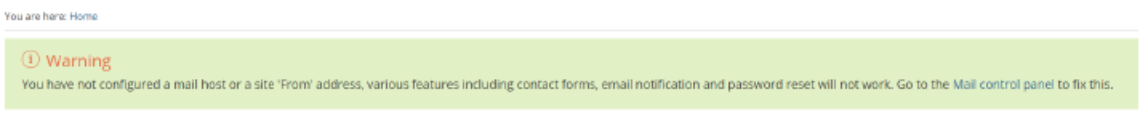
With your installation complete, you can now set up your site. Baobab LIMS requires that your site is set up before you can start to manage clients and projects and certain compulsory information is required for each step and is indicated by a red square or asterix. As such, we recommend that you follow this setup section in a stepwise manner.



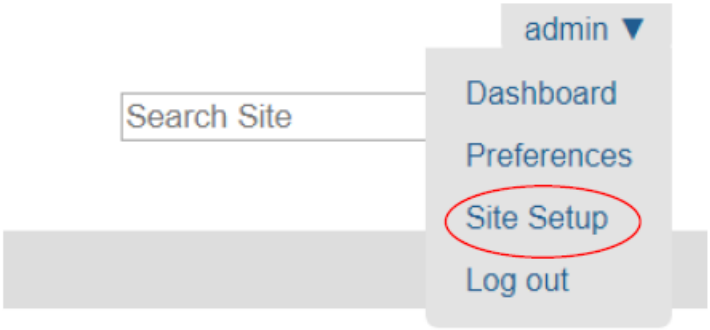
This will open the homepage for your distribution.

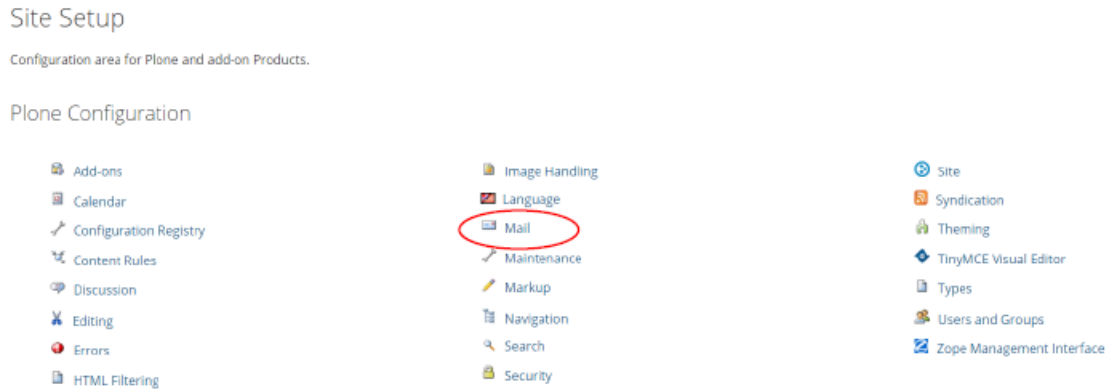
2.4.1 Set up your mail settings

As the administrator for the site, the mail settings will need to be configured, the page will display the following error.

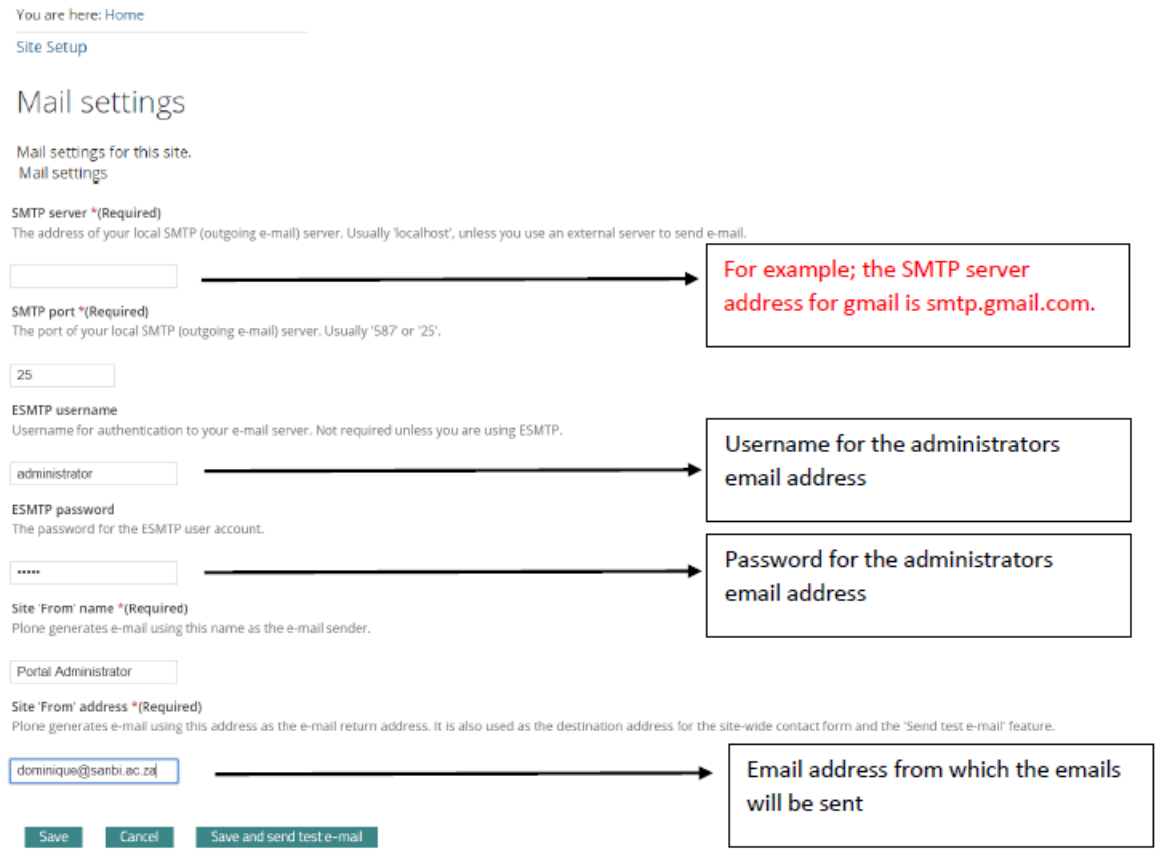


To set up the mail settings select the 'Mail control panel' link in the error message. Alternatively, go to 'site setup' and select the 'Mail' tab.

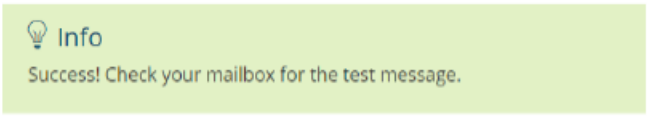


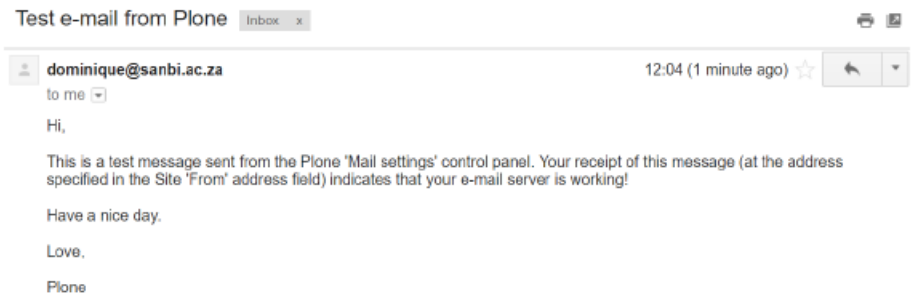


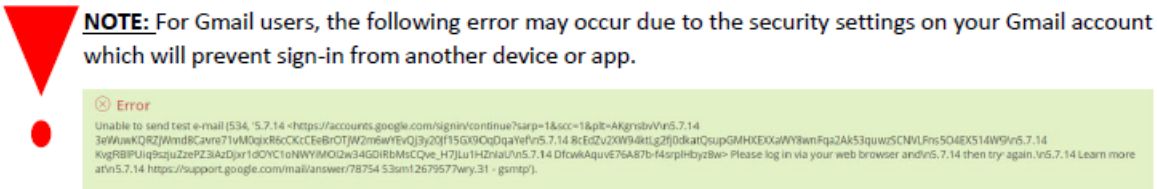
You will be automatically directed to the 'Mail settings' page where you will be required to enter the SMTP server address and will be able to set the administrator username and password. Ensure that all the required fields are completed and select 'save and send test email'.



Following successful set-up, you will receive an email confirming that the email server is working.



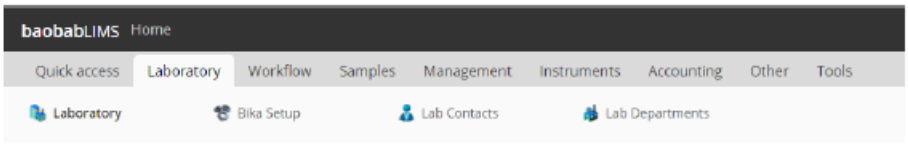




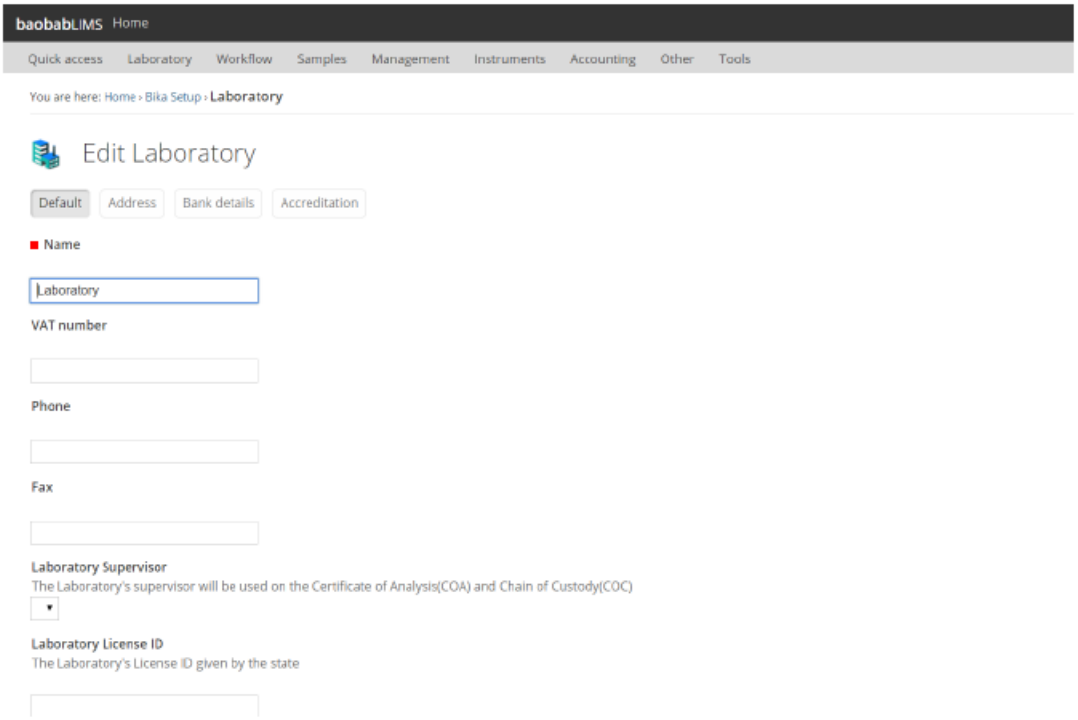
Please ensure that your Gmail settings permit the site to access your account. Use the following `link` to understand more;

2.4.2 Set up your laboratory

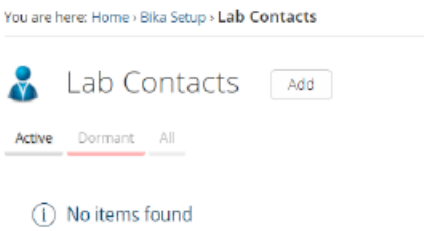
Mouse over the 'Laboratory' Tab and select 'Laboratory'



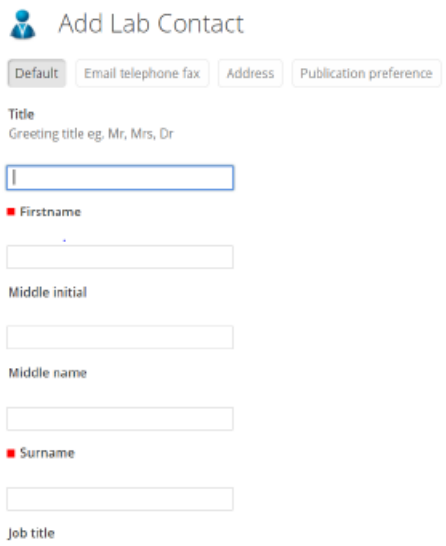
Enter the details of the laboratory and press 'save'. Compulsory fields are indicated by a red square.



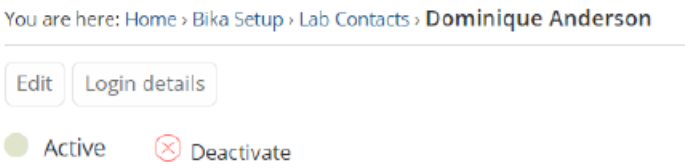
Mouse over 'Laboratory' and select 'Lab Contacts' Add a lab contact by selecting the 'add' button



Enter the details of the lab contact and press 'save'. Compulsory fields are indicated by a red square Select the 'email, telephone, fax' tab, enter the email address of the lab contact and press 'save'.

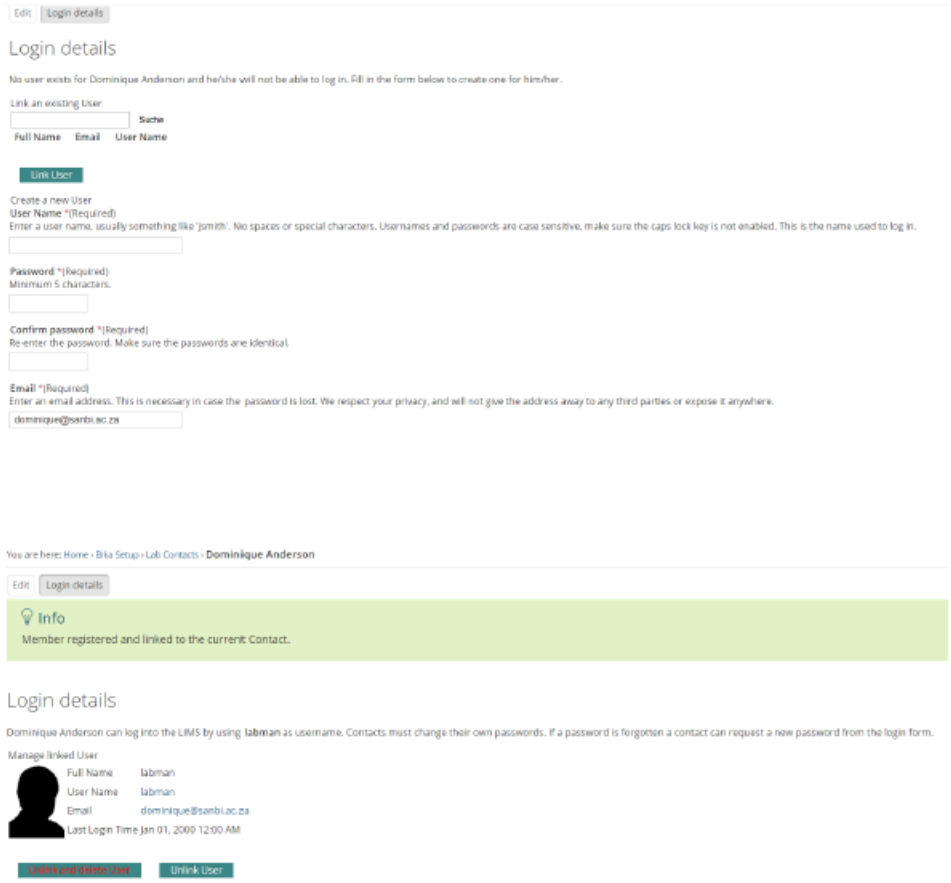


Select 'Login details'

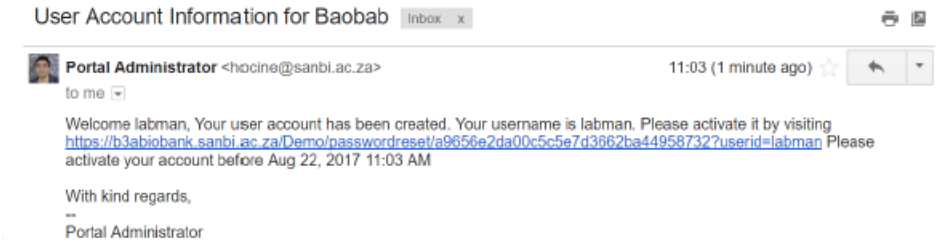


Enter the details of the user and press 'save'

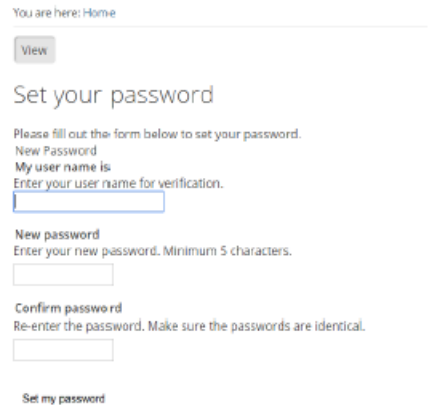
An email will be sent to the users email address



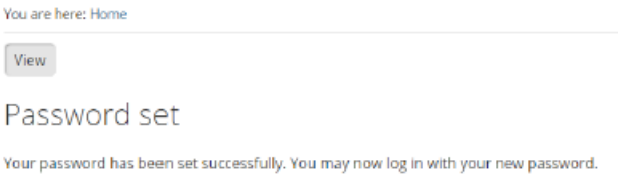
An email will be sent to the users email address



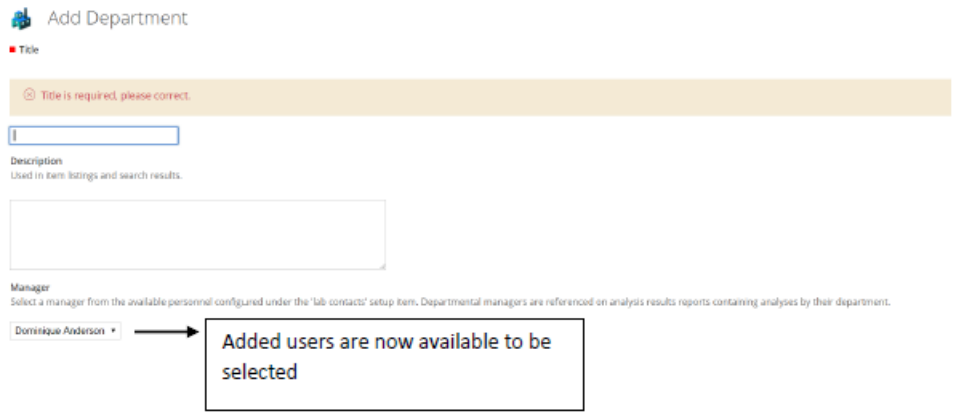
Select the link to activate the account and change the password



Set the new password and the user will now be able to login

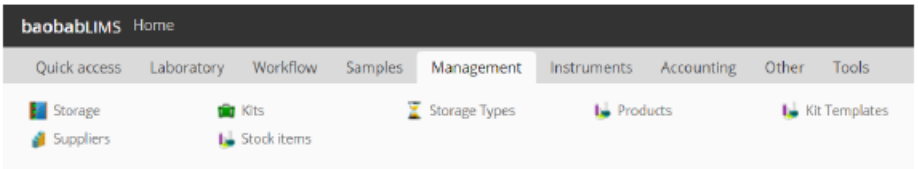


Mouse over 'Laboratory' and select 'Lab Departments' Add a lab department by selecting the 'add' button. Compulsory fields are indicated by a red square.

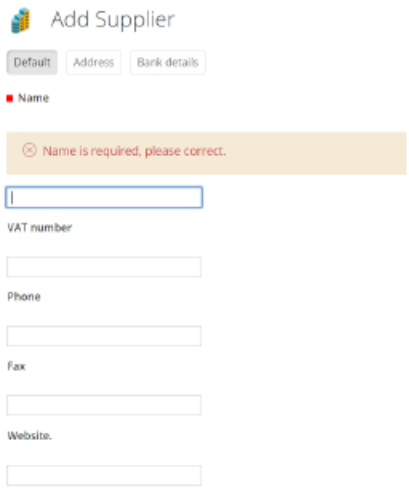


2.4.3 Set up your suppliers

Mouse over the 'management' tab and select 'Suppliers'

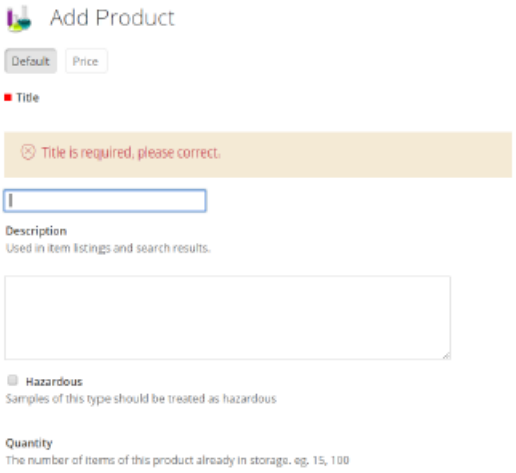


Add a supplier by using the 'Add' button Enter the details of the supplier and press the 'save' . Compulsory fields are indicated by a red square.



Once a supplier has been added, contacts, instruments and inventory orders associated with the supplier can be added. Note that products belonging to the supplier must be added using the 'Products' tab.

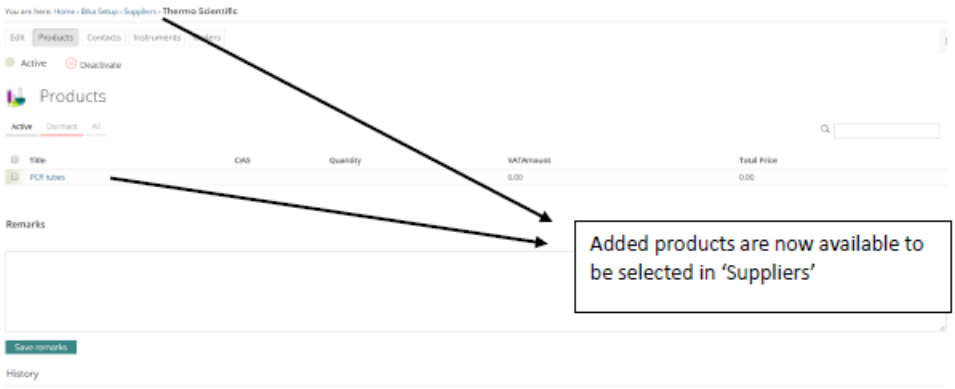
Mouse over the 'management' tab and select 'Products' Add a product by using the 'Add' button



Enter the details of the product and press the 'save' . The suppliers which you added in the previous step will be available from the drop down menu.

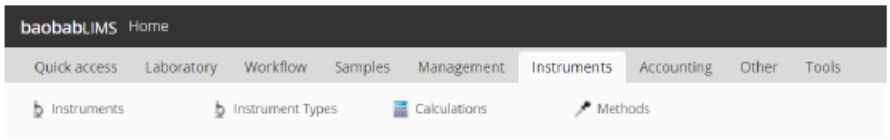
Compulsory fields are indicated by a red square.

Once products associated to suppliers have been added, the products are now available to be selected in the 'Suppliers' tab.

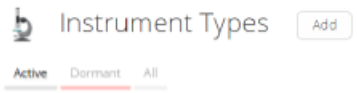


2.4.4 Set up your instruments

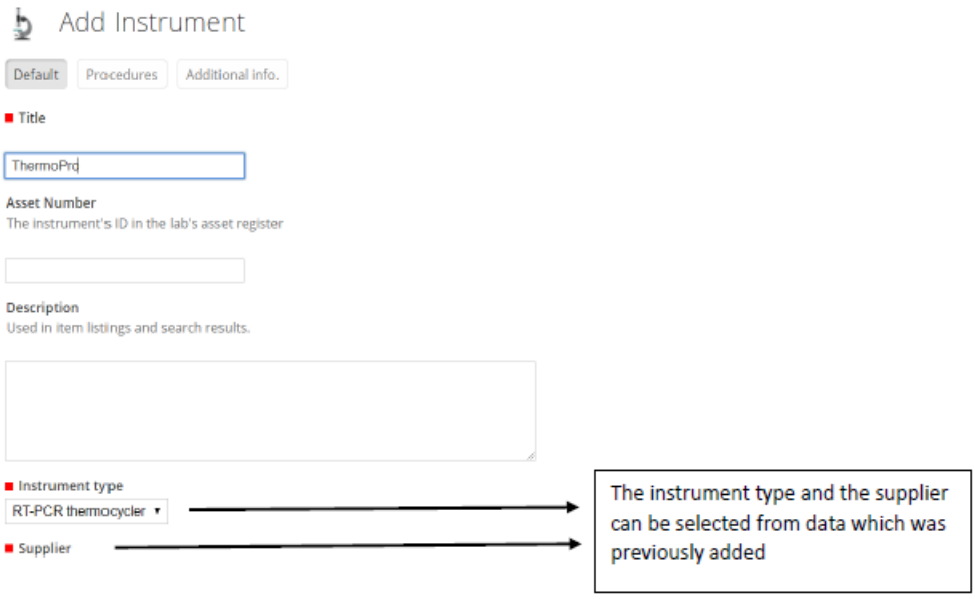
Mouse over the 'Instruments' tab and select 'Instrument types'



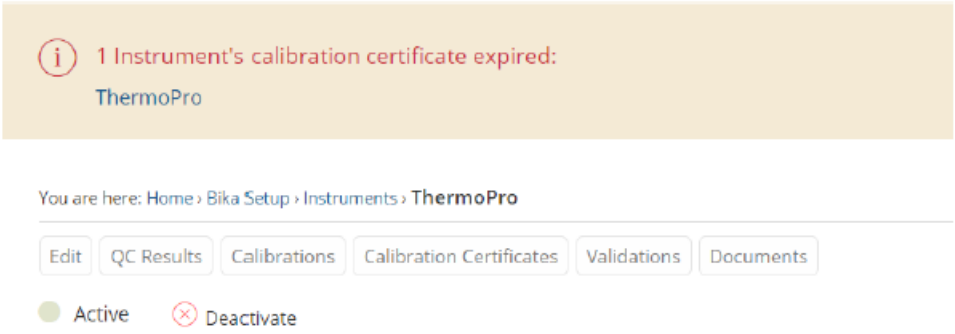
Add an instrument type by using the 'Add' button



Enter the details of the instrument type and press the 'save' . Compulsory fields are indicated by a red square. Once instrument types have been added, select the 'Instruments' tab. Add an instrument using the 'Add' button. Enter the details of the instrument and press 'save'. Compulsory fields are indicated by a red square.



Once an instrument has been added, a notification of expired calibration certification will appear and additional tabs will become available for editing.

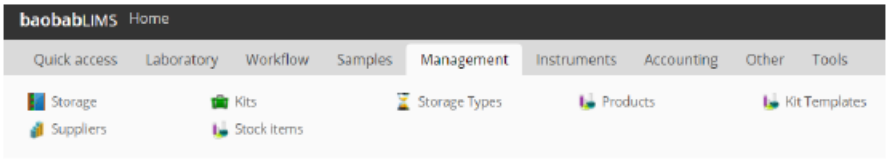


Select the 'Calibration Certificates' tab and add a certification specifically related to the instrument using the 'Add' button. Enter the details of an instruments calibration and press 'save'. Compulsory fields are indicated by a red square.

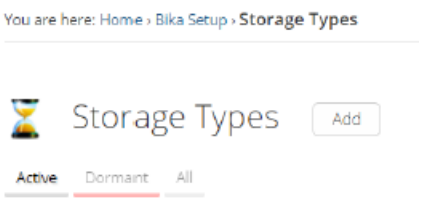
If the calibration dates are current, the notification which occurred, will automatically be removed

2.4.5 Set up your storage types

Mouse over the 'Management' tab and select 'Storage Types'



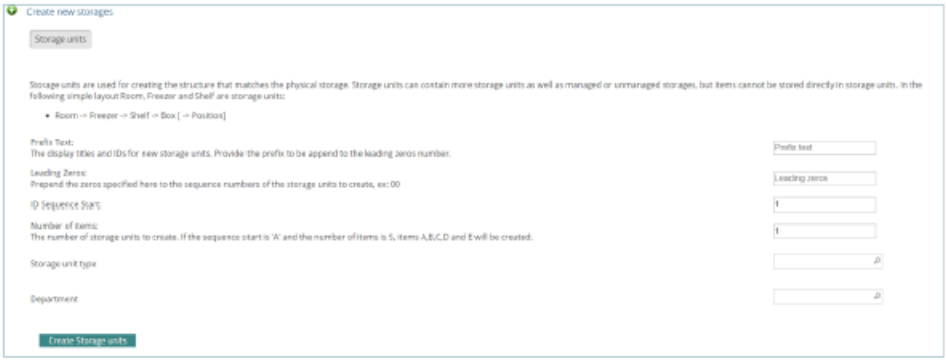
Add a storage type by using the 'Add' button



Enter the details of the storage type (e.g. a freezer) and press the 'save'. Compulsory fields are indicated by a red square.

2.4.6 Set up your storage

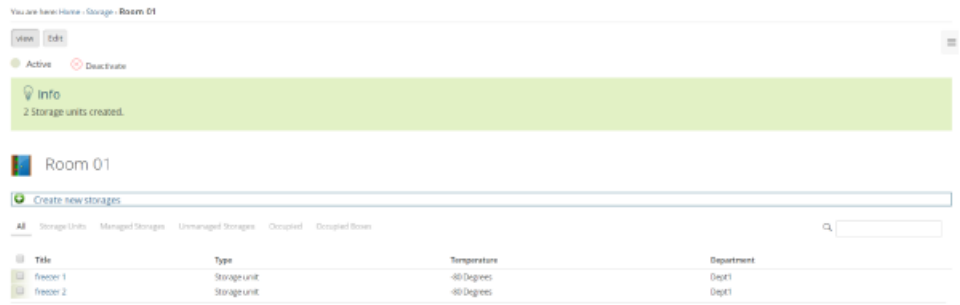
Mouse over the 'Management' tab and select 'Storage'



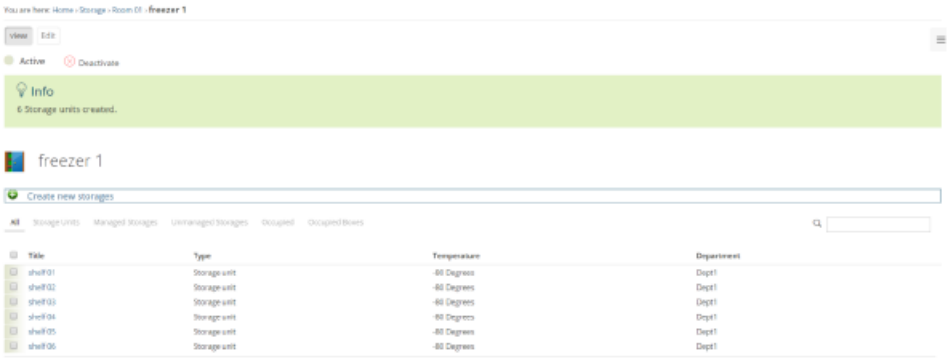
Prefix text: such as room, shelf, box Leading zeros: denotes the prefix number ID sequence start: the number on which the prefix should start Number of items: How many units with the prefix must be created Storage unit type: become available once defined in the 'Storage types' (This is only applicable at the level below a room eg: a freezer) Department: becomes available once defined in the 'departments' section in 'set up your laboratory' Enter the details of the storage and press 'create storage units'

Once a storage has been created, the storage unit can be selected and a hierarchical storage system can be created for each unit. Example: Room > Freezer > Shelf > Box > Position

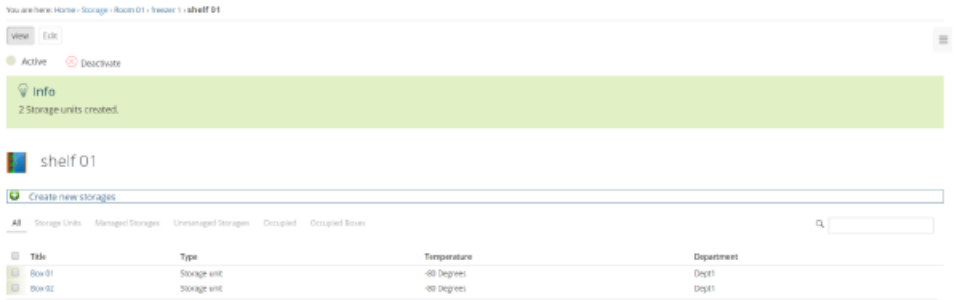
Select the 'Room' initially created. Enter the details of a new storage unit and press 'create storage unit'



Select a freezer storage unit that has been created. Enter the details of a new storage unit and press 'create storage unit'



Select a shelf storage unit that has been created. Enter the details of a new storage unit and press 'create storage unit'



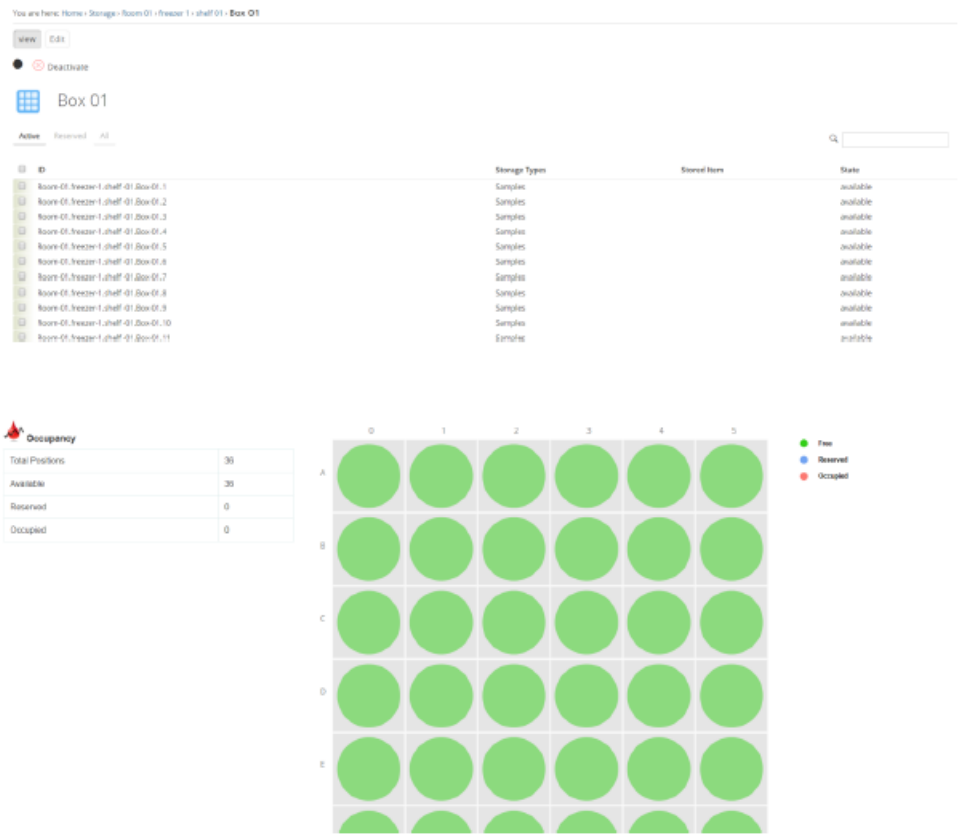
At each level of a storage unit creating, space can be managed (ie. Spaces are assigned) or unmanaged (ie. Spaces are not allocated prior to storage).

2.4.7 Managed storage

Managed storage is used specifically for the storage maintenance of biospecimens. The process of creating managed storage is as follows;

Navigate to the storage unit created in the previous step and select the 'managed storage' tab.

Enter the details required to create managed storage and press 'create storage'. By selecting the created storage unit, a list of created positions will be shown. In addition, a graphical display is available.



By selecting a storage unit (a position within a box), the item may be reserved. When the item is reserved, the state of the item will change and this change will also be reflected in the graphical representation.

The storage position can be freed by selecting the position and pressing ‘liberate’.

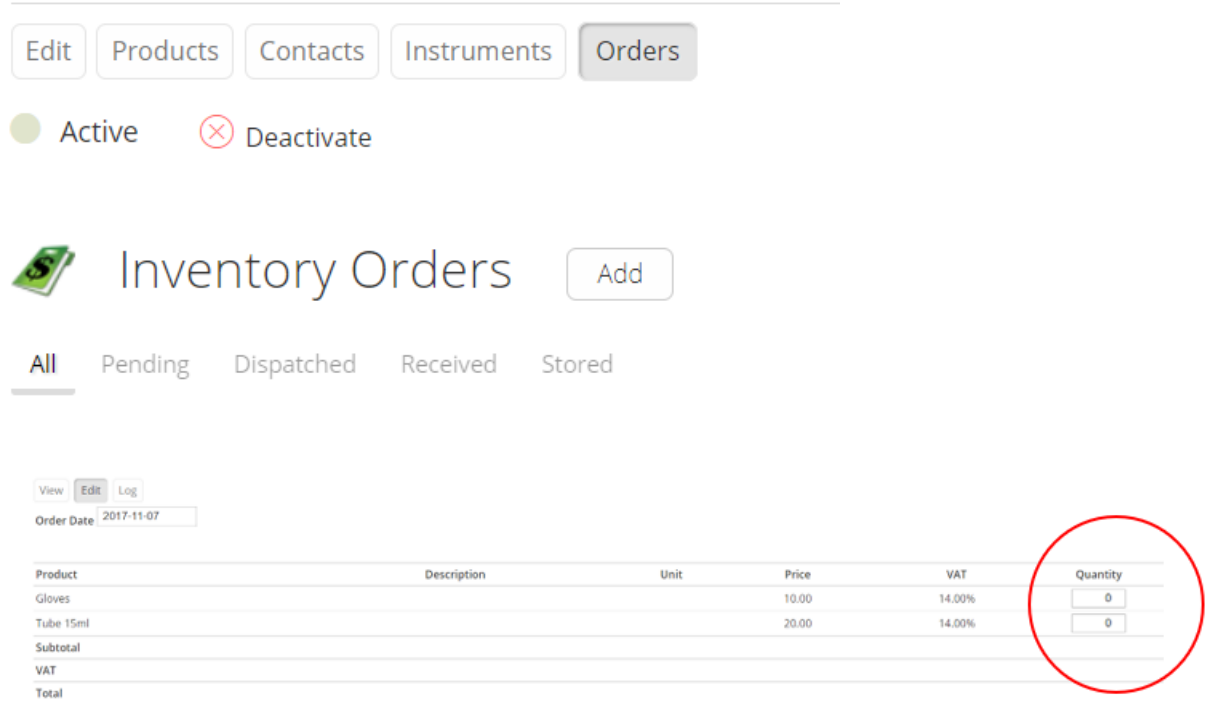
2.4.8 Unmanaged storage

Unmanaged storage refers to locations for items such as inventory stock items that will be used in kit assembly. The process of creating unmanaged storage is as follows;

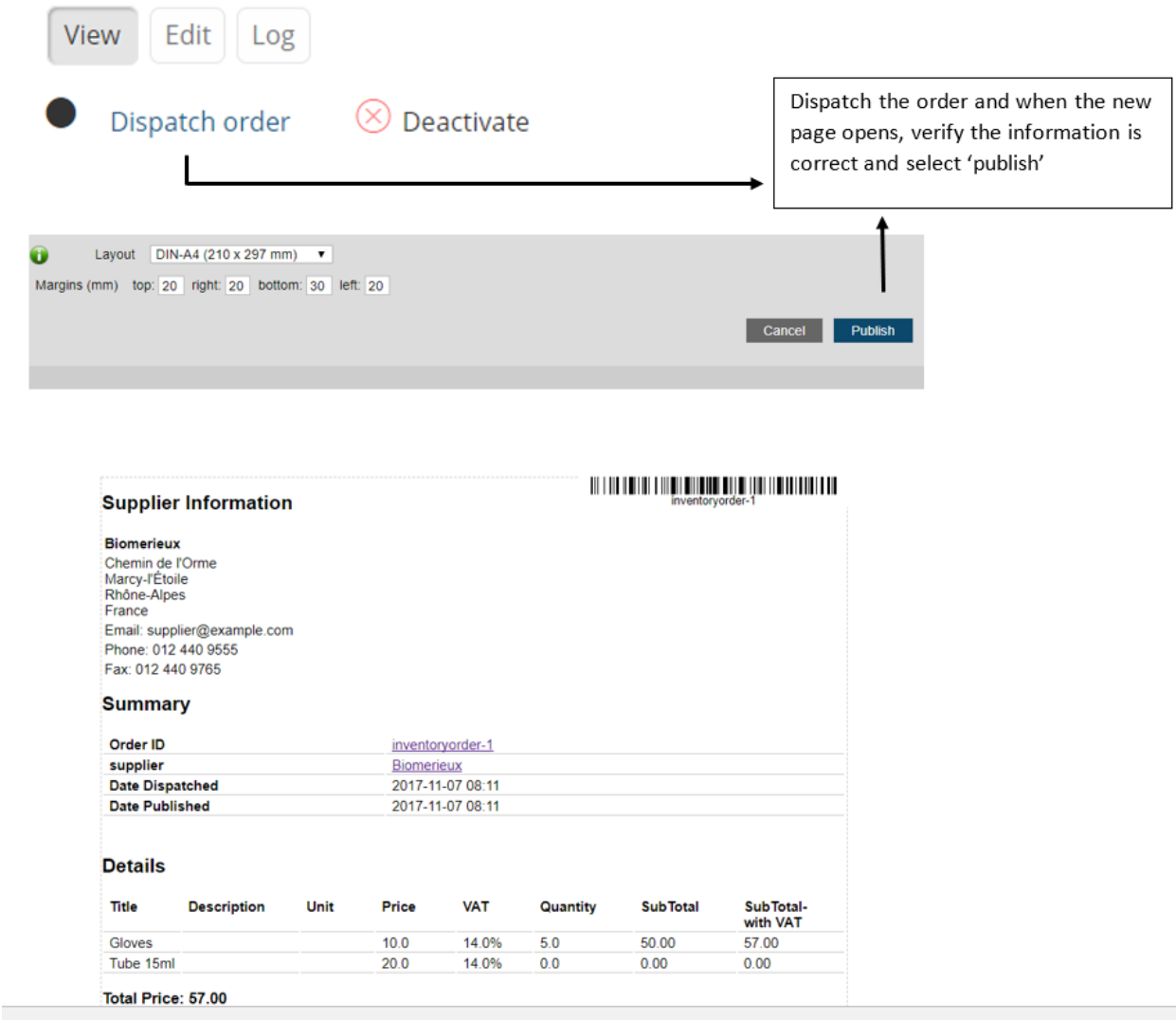
Navigate to the storage unit created previously and select the 'add new storage' button. Navigate to the 'unmanaged storage' tab and enter the details of the storage. In the example below, Room01 contains 3 shelves for storage of inventory items. The shelves are labeled from 1 to 3 and will contain stock items.

2.4.9 Set up your stock items for unmanaged storage

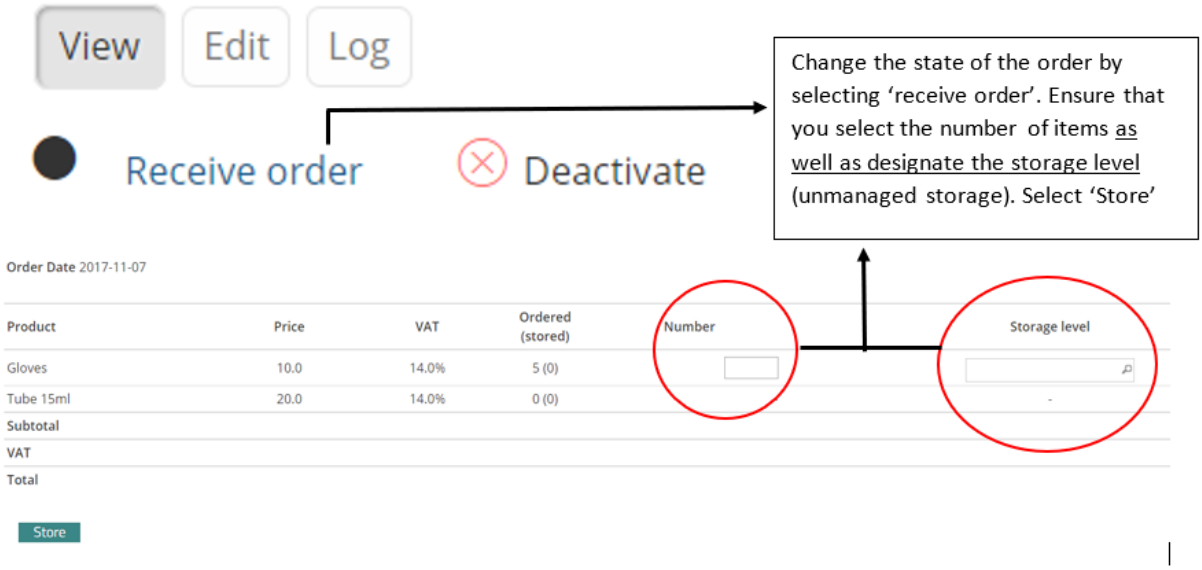
Go to 'Suppliers' and navigate to the 'Orders' tab. Select 'Add' and enter a quantity which you would like to order and press 'save'.



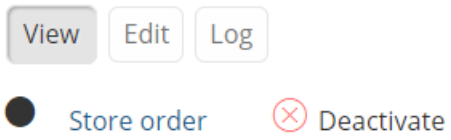
Select 'Dispatch the order' and wait to 'publish', which opens in a new tab.



Once published and you have received the order, you can change the state of the order to 'receive order'.

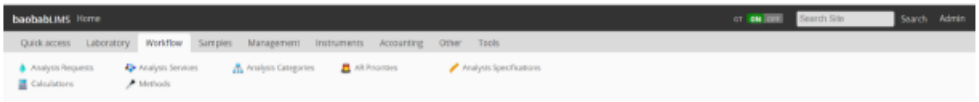


Now you can change the state of the item by selecting 'store order'

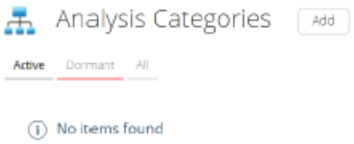


2.4.10 Set up your analysis category

Mouse over the 'Workflow' tab and select 'Analysis category'



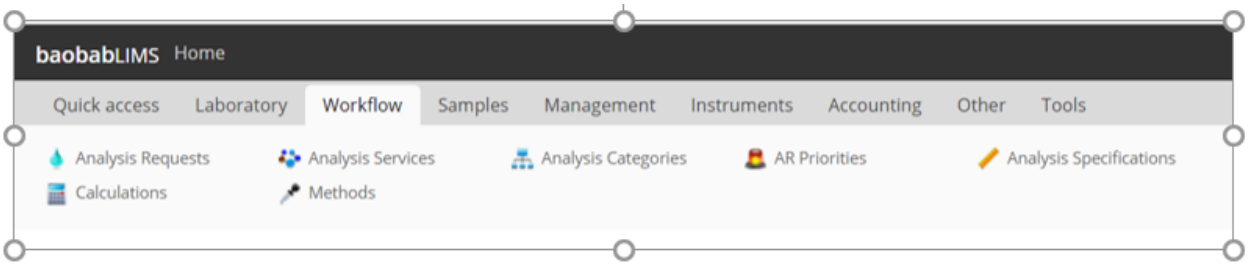
Add an analysis category by using the 'Add' button



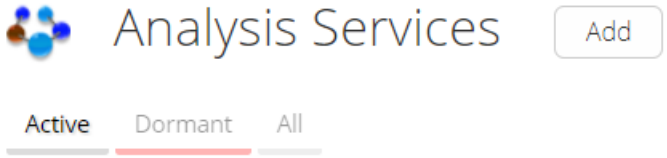
Enter the details of the analysis category and press the 'save'. Compulsory fields are indicated by a red square.

2.4.11 Set up your Analysis services

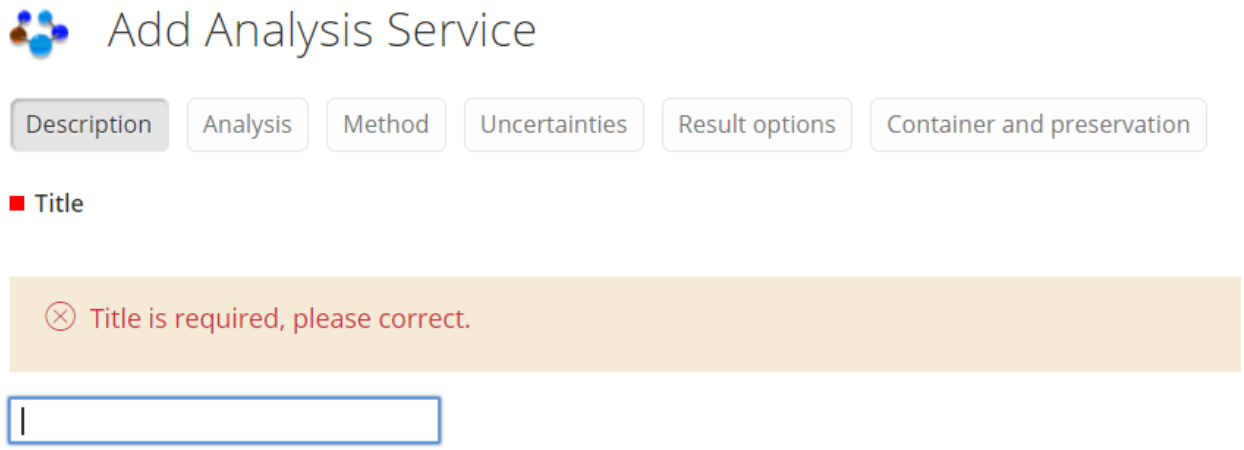
Navigate to the 'Workflow' tab and select 'Analysis services'.



Add an analysis service by using the 'Add' button



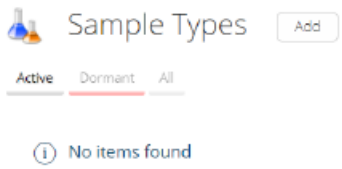
Enter any details related to your analysis services and press 'save' Compulsory fields are indicated by a red square.



2.4.12 Set up your Samples

Mouse over the 'Samples' tab and select 'Sample Types'

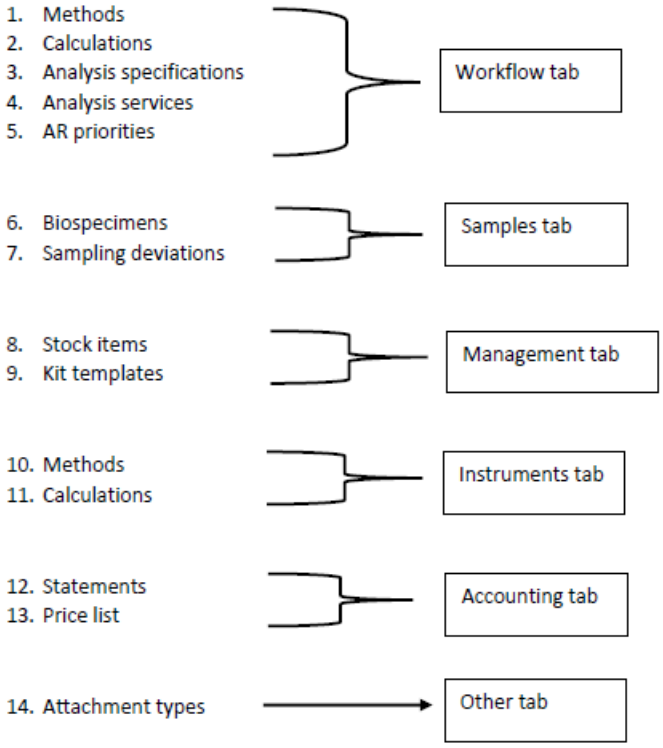
Add a sample type by using the 'Add' button



Enter the details of the sample type and press the 'save'. Compulsory fields are indicated by a red square.

2.4.13 Set up your other parameters

Once all the above categories have been set up, all other categories can be set up. These can be managed by simply selecting the category and adding information using the 'Add' button. Enter details related to the category and press the 'save' button. Compulsory fields are indicated by a red square.



CHAPTER 3

Baobab LIMS User manual

This manual will guide you through the process of creating projects and the associated data related to projects. This manual is for use FOLLOWING the setup of your lab (see 'SETUP' manual).

Warning: Please make use of the user manual following the setup of your site

3.1 Plone Configuration

Tab	Function
Add-ons	For Plone, available add-ons can be activated or deactivated according to desired preferences. To add new add-ons that will be reflected in the Add-ons tab, modules will need to be added to the build-out configuration in the terminal. Build-out must be run and the server restarted in order for changes to be reflected. Detailed instructions may be found using the hyperlink, Installing Plone add-ons.
Calendar	Calendar settings can be managed using this tab. To update settings, save changes and return to the dashboard.
Configuration registry	Records managed by the configuration registry are tabulated here. Records can be obtained using a prefix or a filtered search and edited accordingly.
Content rules	Content rules will automatically perform actions on the content when a defined trigger occurs. Content rules can be added and following definitions, they can be assigned to a folder .
Discussion settings	Discussion settings can be modified using this tab. Not all discussion related settings are located here and in order to enable comments for a specific type, or enable moderation workflow for comments, use the 'Types' tab.
Editing settings	General editing settings
Errors	Logs the errors or exceptions which have recently occurred. A user may select how many logs are kept and if the logs should be copied to Zope event log files.
HTML filtering	HTML tags which may be considered as security risks can be tagged using Plone filters.
Image handling	These settings allow for image handling and scaling.
Languages	Interface language and content translation settings.

Mail	Email related settings for the site.
Maintenance	Zope server and Baobab site maintenance options.
Markup	When editing content, these settings enable the user to control which mark-ups are available.
Navigation	Navigation settings allow the user to control navigation construction on the users site. To control the display of the navigation tree, the 'manage portlet' tab is used.
Search	The user can define the search settings for the site.
Security	Multiple options for control of the security settings for the site are found here.
Site	Site-wide settings.
Themes	The look and feel of the site can be modified using these settings.
TinyMCE visual settings	These settings are used to alter the TinyMCE Wysiwyg HTML editor.
Users and Groups	Plone configuration allows for the addition of Users or Groups in the Users and Groups tab. An individual user may be added or removed, or the specific details of a user, modified accordingly, in this section. Furthermore, a user can be linked to a specified group and the privileges of that particular group can be managed. Users overview provides a list of currently registered users on the system. Users are assigned a role which is inherited from membership and occurs when a new user is added to a specified group upon initial registration. By selecting a specific user, personal information, personal preferences and group membership can be edited accordingly. Group membership can also be updated in the 'overview' page. The 'Groups' tab provides a tabulated list of collections of users. Selecting a group from the Group Name provides information on the members assigned to the group, group properties, group portlets and the group dashboard.
Zope management interface	These settings are for use by administrators.

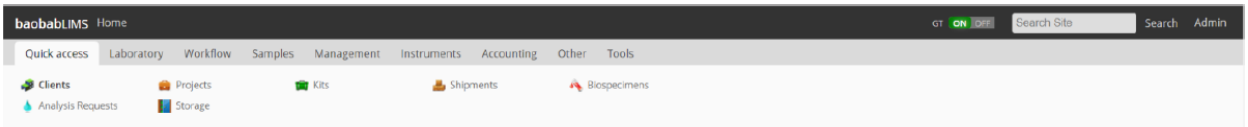
3.2 Baobab LIMS Configuration

AR priorities	All analysis requests are listed in this section. The priority status of an analysis request can be added or changed by selecting the 'Add' button.
Analysis categories	Various analysis tools utilized by the laboratory can be described and categorized.
Analysis services	Analysis services provided by the laboratory are listed in this section. New analysis services can be added by selecting the 'Add' button. A number of options exist to define the analysis service and includes the description, analysis specification, methodology (including assigned instrumentation), uncertainties, result options, and container/preservation information.
Analysis specification	Specifications relating to the results of an analysis service are listed in this section. By selecting the 'Add' button, specifications relating to a sample type and the related analysis service can be defined.
Attachment types	Attachment types are defined.
Bika setup	The Bika setup tab allows for changes to be made in the security, accounting, results report and analyses. In the accounting tab, currency, levy, vat and member discounts can be adjusted accordingly. Result report formats can be set up using the Results reports tab and formats related to the Analysis can be modified in the Analyses tab. Stickers can be automatically printed when new analysis reports or sample records are created by selecting 'register' in the stickers tab. Similarly, stickers can be printed when analysis reports or samples are received by selecting the 'receive' option. The format of the sticker can also be adjusted accordingly in this tab. In the ID server tag, the configuration of ID's for content items can be formatted. The storage tab allows the user to set the costing of sample storage depending on the storage required.
Calculations	Calculation formula related to tests and analysis can be defined, edited and maintained.
Instrument location	Add, manage or remove locations for instruments.
Instrument types	Instrument types are listed in this section. New instrument types can be added and defined by selecting the 'add' button.
Instruments	The laboratory list of instruments and equipment is listed in this section. By selecting the 'Add' button, new instruments can be added. Detailed information relating to the piece of equipment such as the serial number, supplier and model number can be included. In addition, in-house calibration and maintenance procedures can be included. Other related additional information can be captured and this includes instrument location, and certification documentation.
Kit templates	Current kits that are loaded onto the system are displayed here. New kit templates can be added by selecting the 'add' button which allows the user to define the kit according

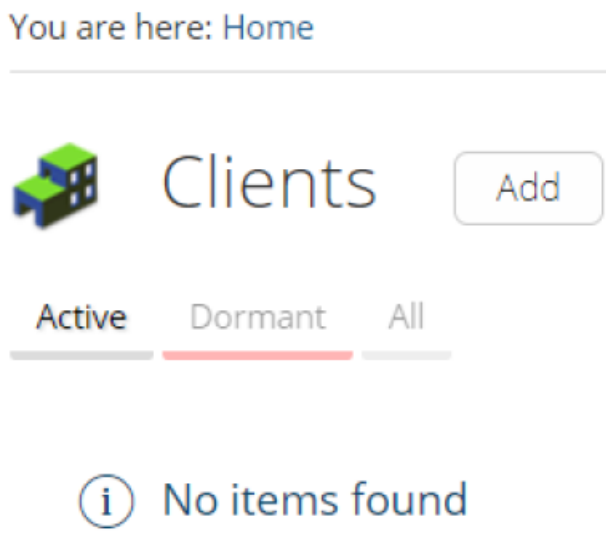
	to components and costing. For components to be selected, these products need to be registered in the 'products' section.
Lab contacts	Laboratory staff information can be added, edited and maintained.
Lab departments	Laboratory departments and corresponding manager contacts can be added, edited and maintained.
Laboratory information	Information related to the specific laboratory including registration, accreditation and address can be added, edited and maintained.
Methods	Methods associated to analysis of a sample are listed in this section. By selecting the 'Add' button, new analysis methods can be added and various parameters described. In addition, associated method documentation and SOPs can be uploaded.
Products	Consumable information, specification and suppliers can be added, edited and maintained.
Reference definitions	Reference definitions or sample types used for QC testing can be added, edited and maintained.
Sample conditions	Conditions for a specific sample type can be added, edited and maintained.
Sample types	Samples and their corresponding descriptors are listed in this section. By selecting the 'Add' button, new sample types can be added to the list. In addition, the types of analysis or services related to the sample type can be defined and are grouped into analysis categories.
Stock items	Inventory stock items are displayed in this section. New inventory products can be added by selecting the 'Add' button and defined according to the storage location, invoice number, batch ID, date received, date opened, expiry and details of the receiving individual.
Storage location	The storage location describes the physical location of a storage type and is listed in this section. New storage locations can be added by selecting the 'Add' button and can be defined using multiple descriptors.
Storage types	The storage types refer to the storage system used for sample storage. Storage systems are displayed in this section and new storage can be added and defined by selecting the 'add' button.
Suppliers	Suppliers that are defined in the system are listed here and new suppliers can be added by selecting the 'Add' button. Information linked to each supplier, such as company registration, website, banking details and contact details can be defined.

3.3 Add client

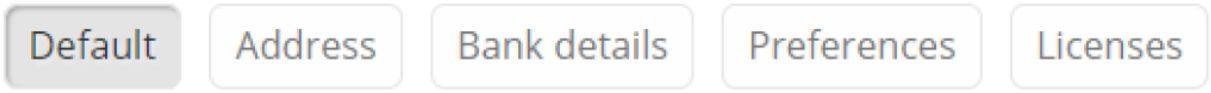
Mouse over 'quick access' and selecting the 'Clients' tab. All added clients are listed in this section.



Add a client by selecting the 'Add' button. Enter the details of the client and press the 'save' button. Compulsory fields are indicated by a red square.

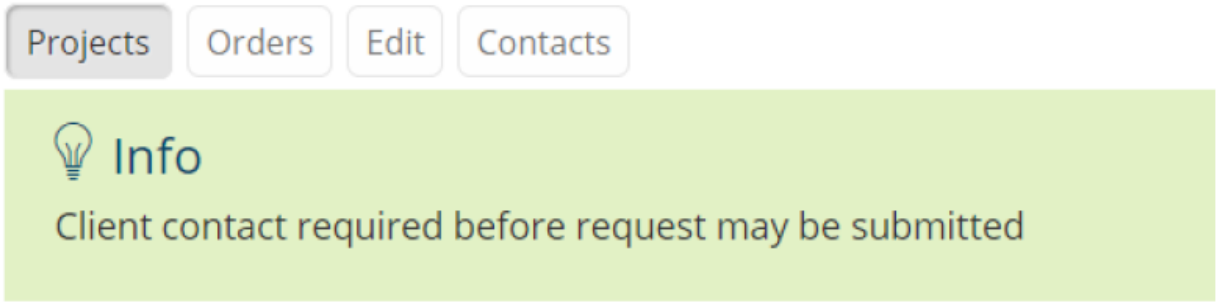


Client information includes address, bank details, preferences and licenses and can be added by selecting the required tab and entering the information.

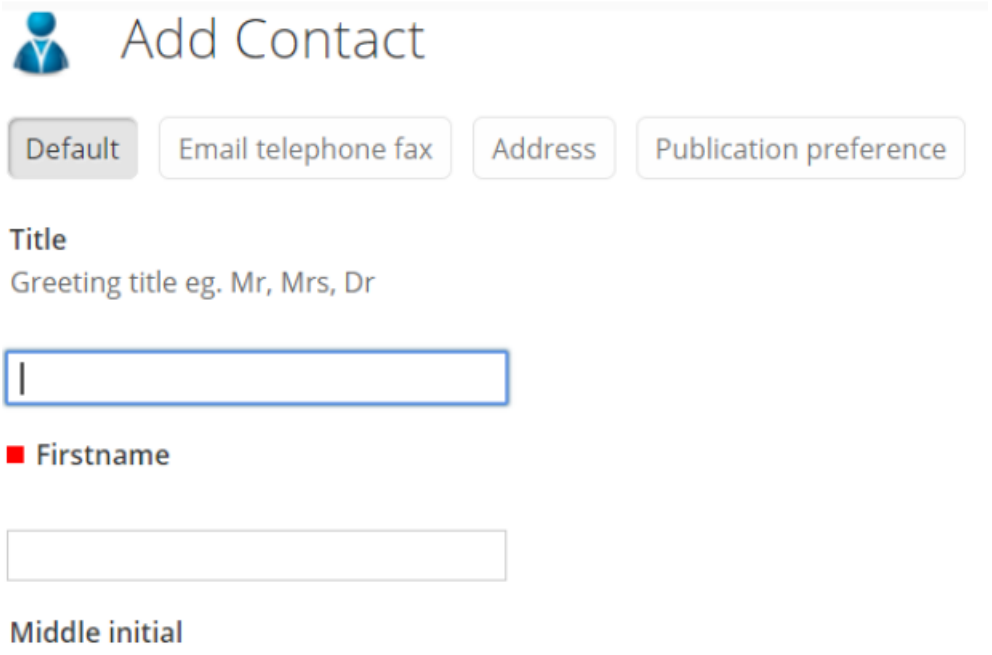


3.4 Add project

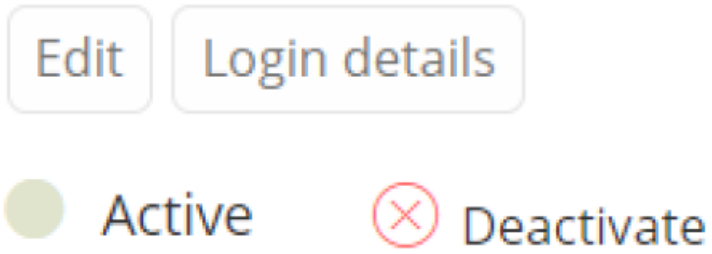
In the clients list, select the client of interest which will automatically take you to the 'projects' page. A notification may appear requesting for client contact information to be submitted.



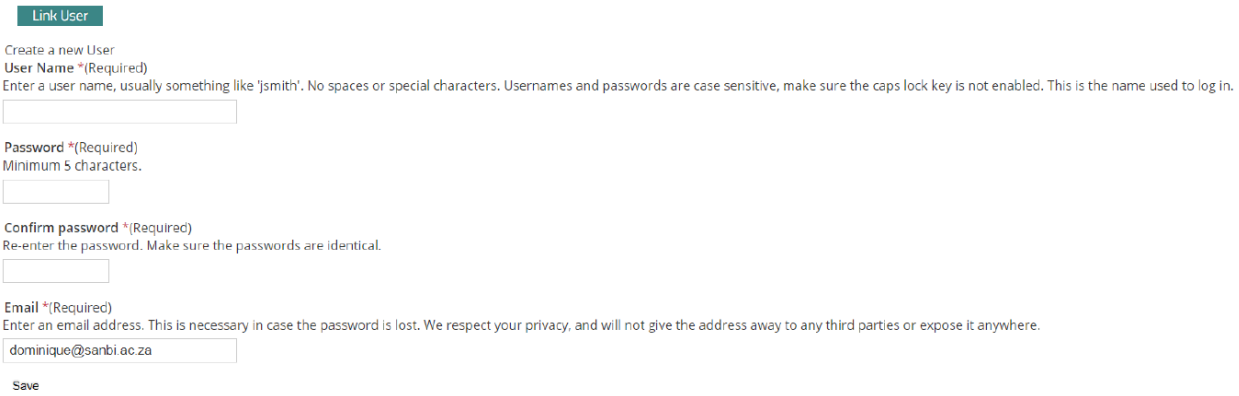
Proceed to the 'Contacts' tab above the notification and select the 'add' button. Enter the details and press the 'save' button. Compulsory fields are indicated by a red square.



By adding a client contact details, the login details of the contact can be edited by navigating to the 'Login details' tab.

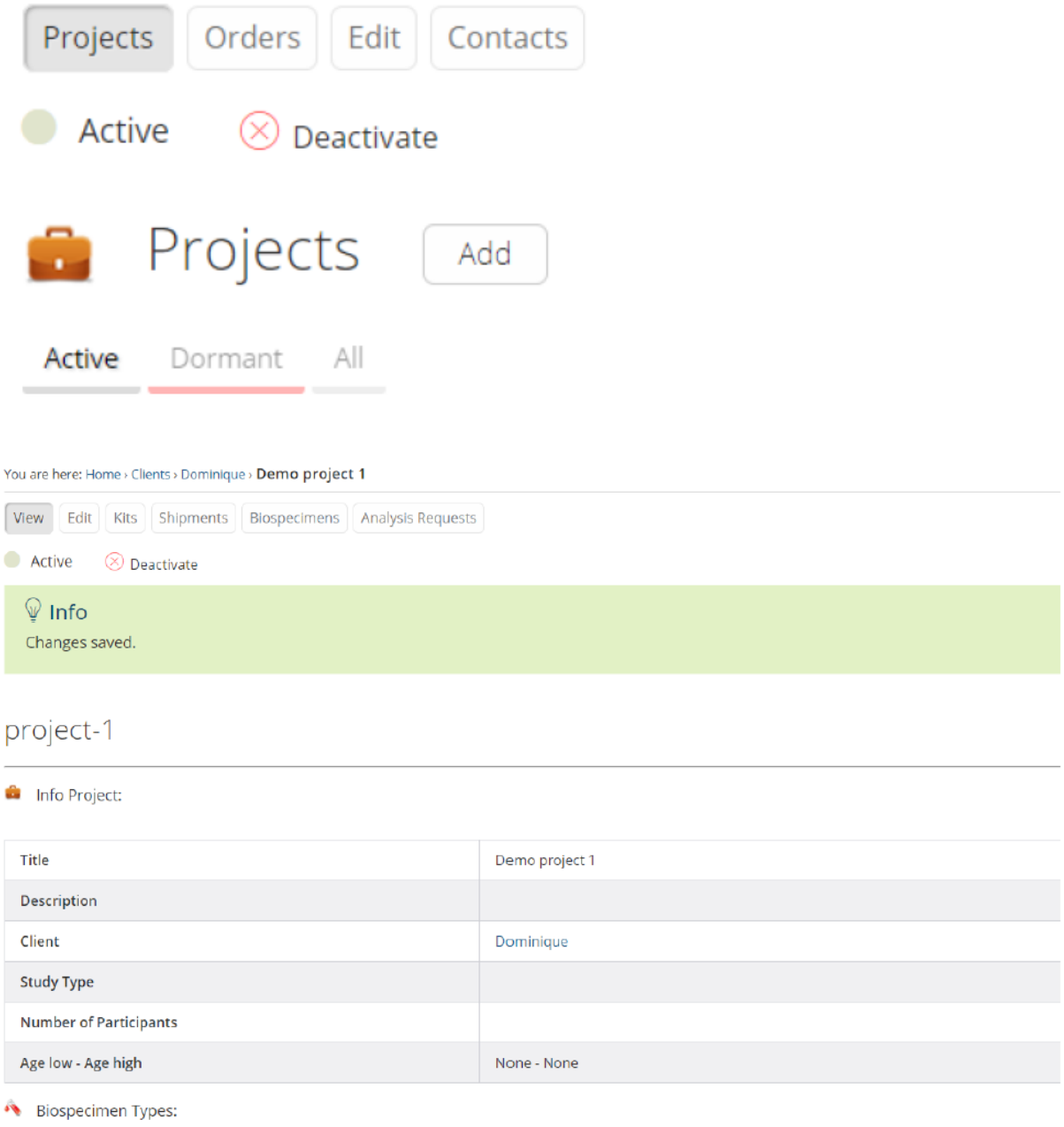


The login details for the Client contact can be added and the once saved, the client will receive an email indicating the username and password. The client can login to the LIMS site using these details, but will have limited access to modules on the site (as stipulated by the user role). User roles can be defined by the administrator in the `plone configuration` under the tab `Users and Groups`.



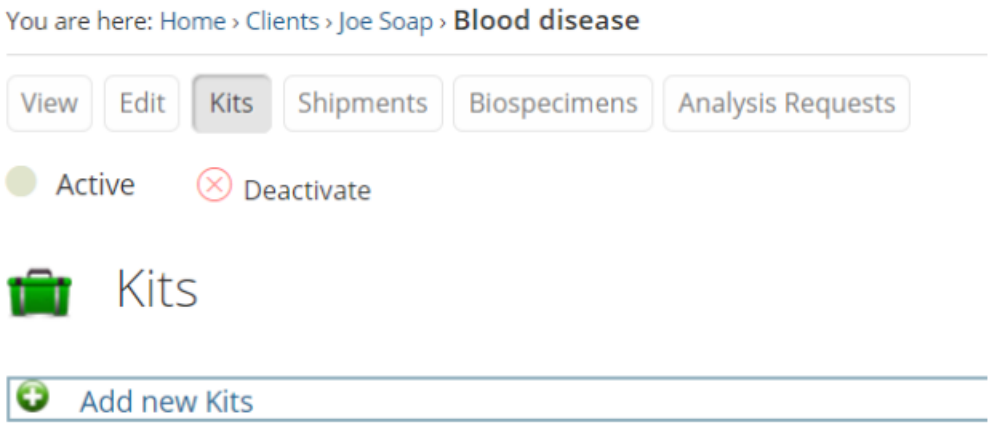
3.5 Projects

The Biobank user can now be directed to the 'projects' page for the specific client. Add a project by selecting the 'Add' button and enter the details of the project. Compulsory fields are indicated by a red square. The user will be automatically directed to the created project page where tabs for kits, shipments, biospecimens and analysis requests can be selected, and items can be added or viewed.

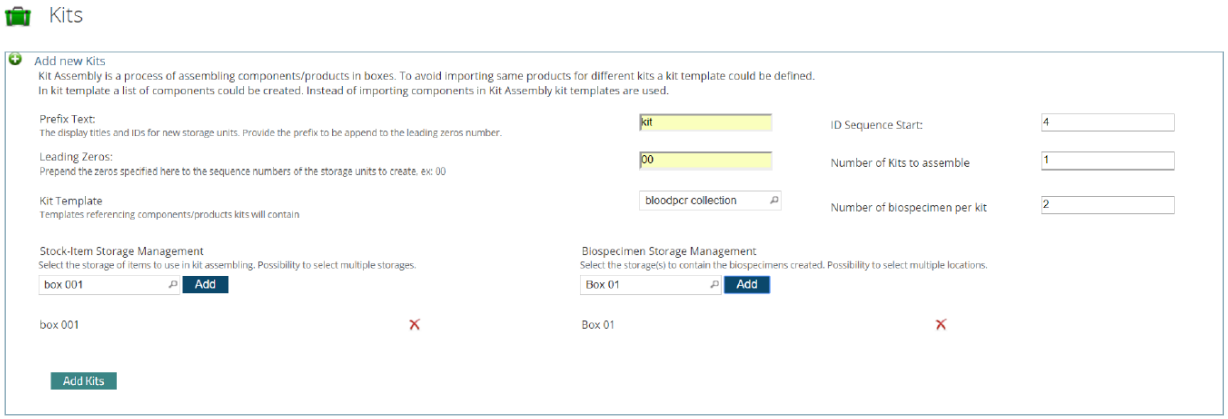


3.6 Kits

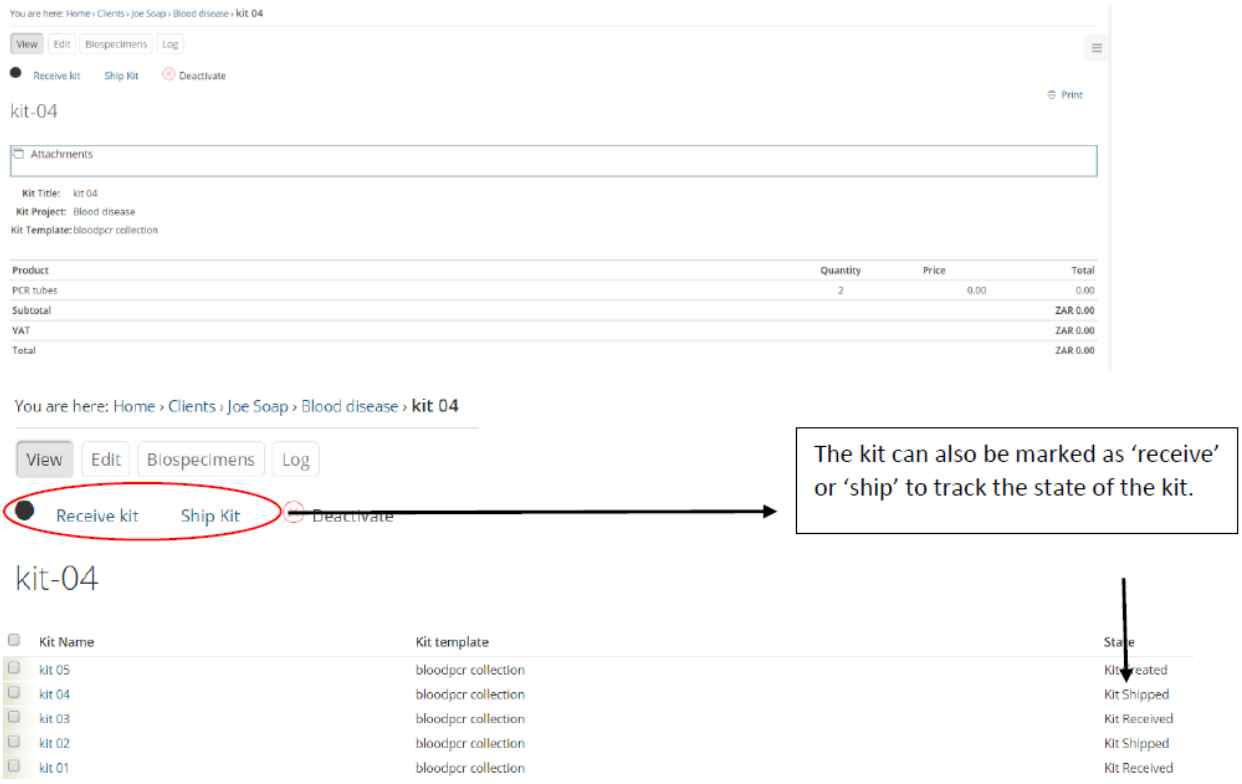
In the 'Kits' tab, select 'add new kits'.



The page will be generated allowing the user to add kits accordingly. In the `example` below, prefix text 'kit' is used. There will be 1 kit with 3 already generated, therefore, the next kit will start from the next number in sequence i.e. 4. According to the kit template generated, each kit will contain 2 biospecimens. The stock item to be used will be selected from an unmanaged storage which was generated, and the storage will be selected from a managed storage unit which was previously generated.

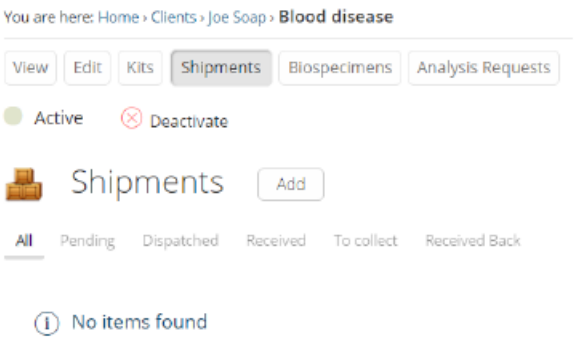


By selecting the kit which has been added, details of the kit can be visualized.

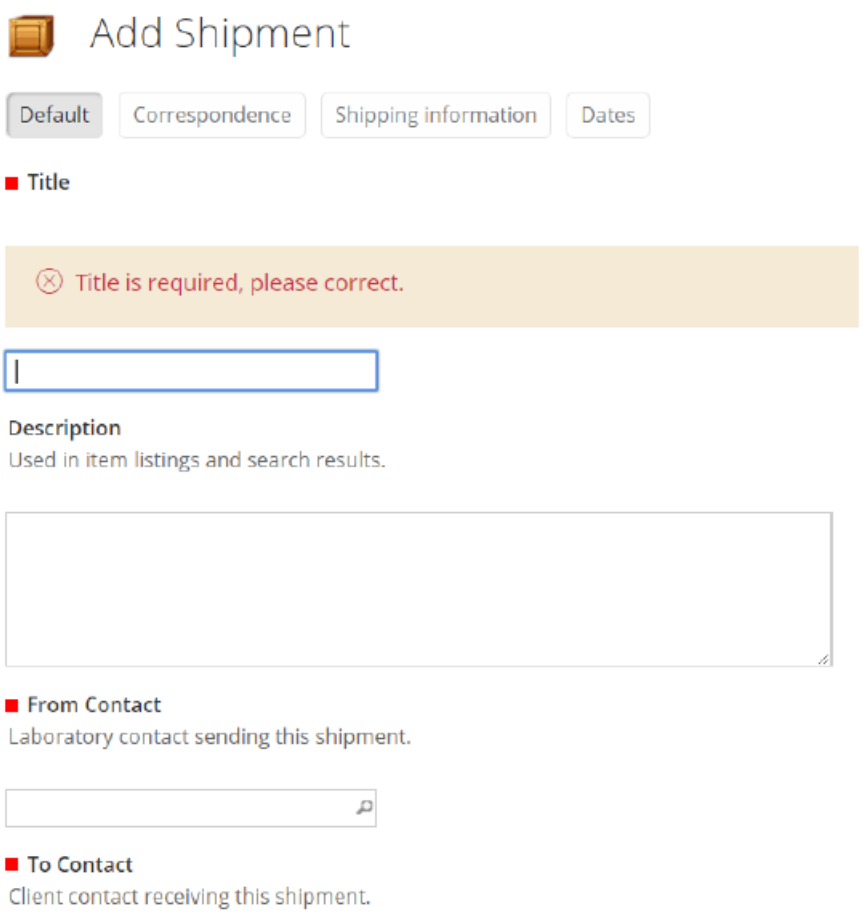


3.7 Shipments

Add a shipment by selecting the 'Add' button and enter the details of the shipment. Compulsory fields are indicated by



Note: Compulsory fields are also present in the 'correspondence' tab and need to be entered to continue.



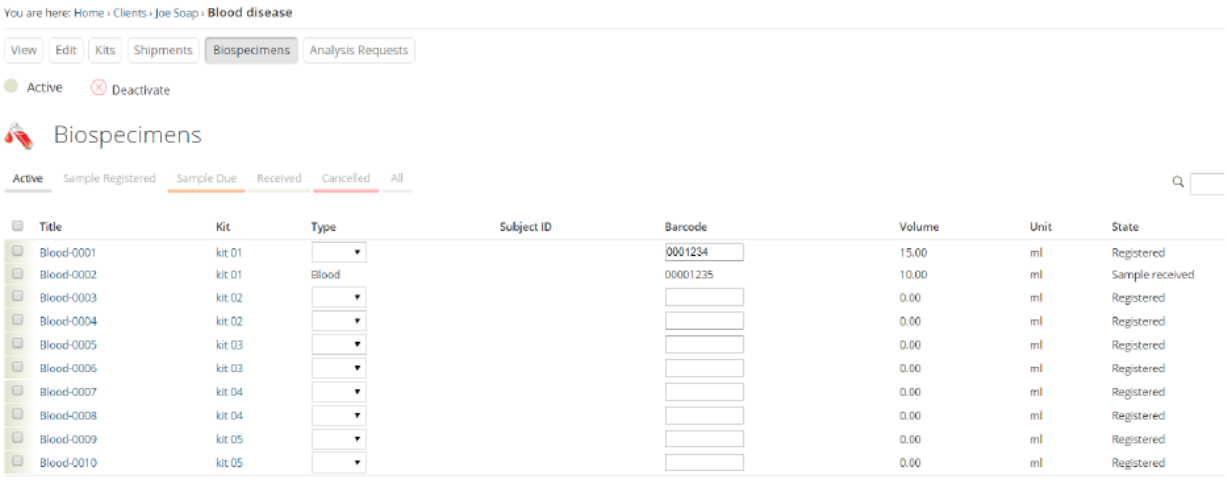
The process for shipments is as follows;

1. The Biobank selects 'dispatch' (an email is sent to client to inform them that a shipment has been dispatched)
2. The client logs in with his/her username and password and selects `projects < shipments < shipment# < and ' receive'`
3. Client fills the tubes with samples
4. Client selects 'collect' and an email is sent back to the biobank. The Biobank then arranges for the courier to now collect shipment
5. The Biobank checks their shipments and selects 'receive back'. An email will be sent to the client informing the client that the kit has been received back at the Biobank.
6. The Biobank selects the specific kit and changes the state of the kit by selecting 'receive kit'
7. The Biobank unpacks and checks kit contents and selects 'process kit'
8. The Biobank examines the biospecimens in the kit and adds subject ID, volume and other relevant details
9. The Biobank then selects 'receive sample'
10. The sample is now in storage

Note: barcodes can be scanned in if a scanner is available.

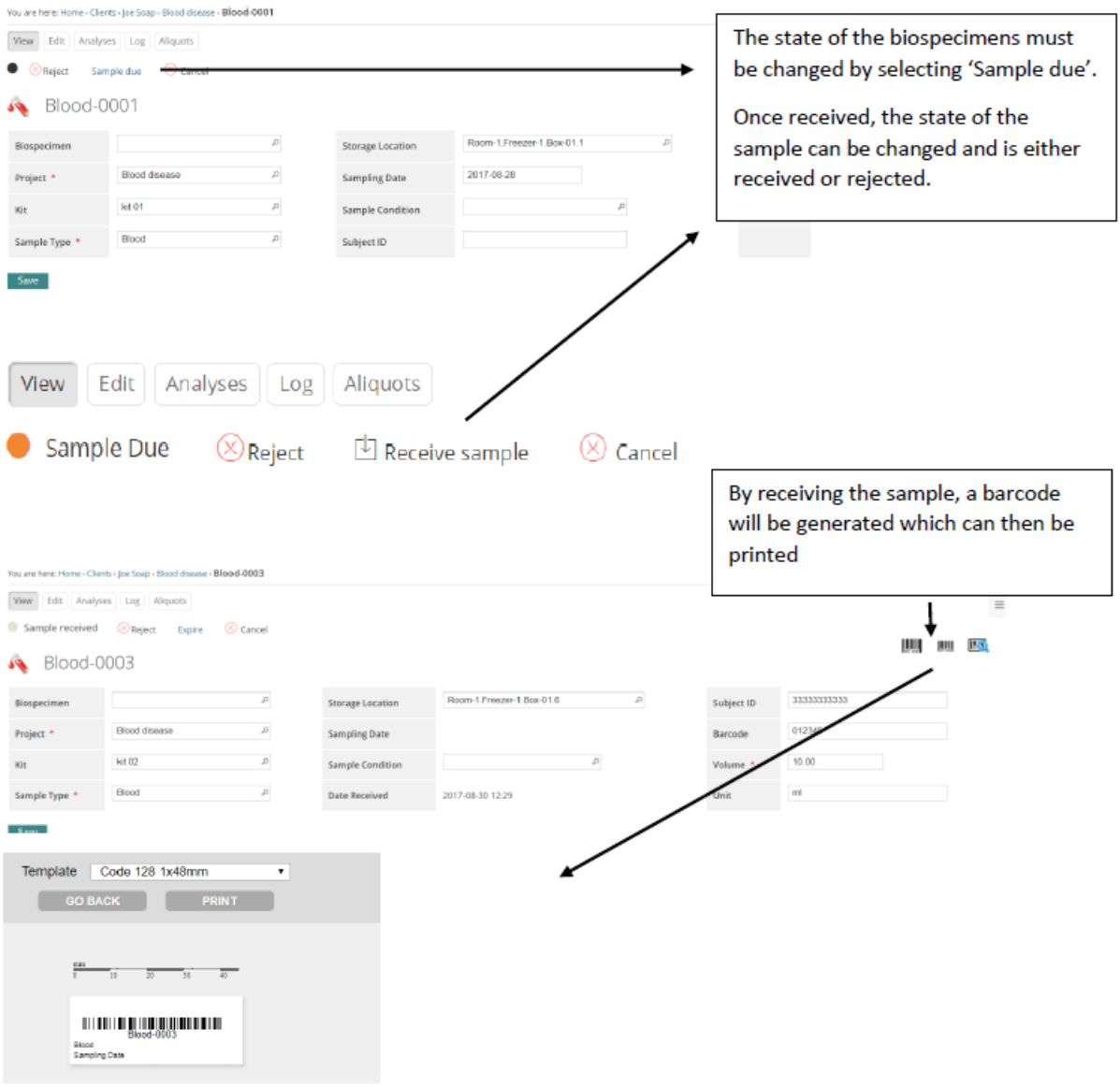
3.8 Biospecimens

Biospecimens associated with the project can be viewed in this tab and are generated automatically when a kit is created from a template.



Title	Kit	Type	Subject ID	Barcode	Volume	Unit	State
Blood-0001	kit 01			0001234	15.00	ml	Registered
Blood-0002	kit 01	Blood		00001235	10.00	ml	Sample received
Blood-0003	kit 02				0.00	ml	Registered
Blood-0004	kit 02				0.00	ml	Registered
Blood-0005	kit 03				0.00	ml	Registered
Blood-0006	kit 03				0.00	ml	Registered
Blood-0007	kit 04				0.00	ml	Registered
Blood-0008	kit 04				0.00	ml	Registered
Blood-0009	kit 05				0.00	ml	Registered
Blood-0010	kit 05				0.00	ml	Registered

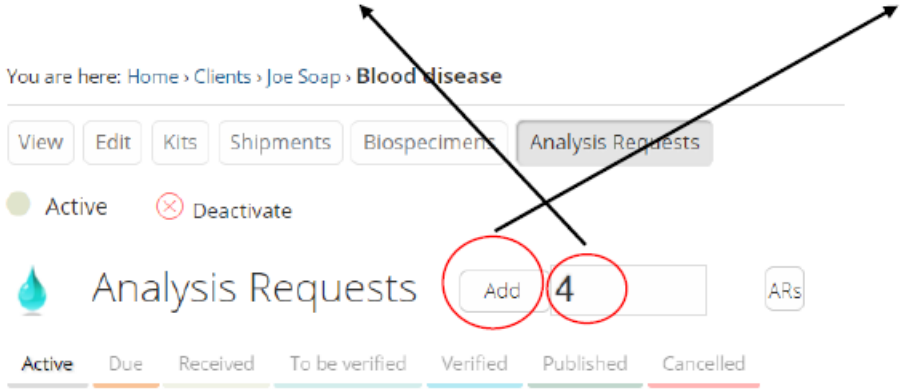
By selecting the biospecimen, the parameters of the specimen can be established, such as, barcode, volume, sample condition etc.

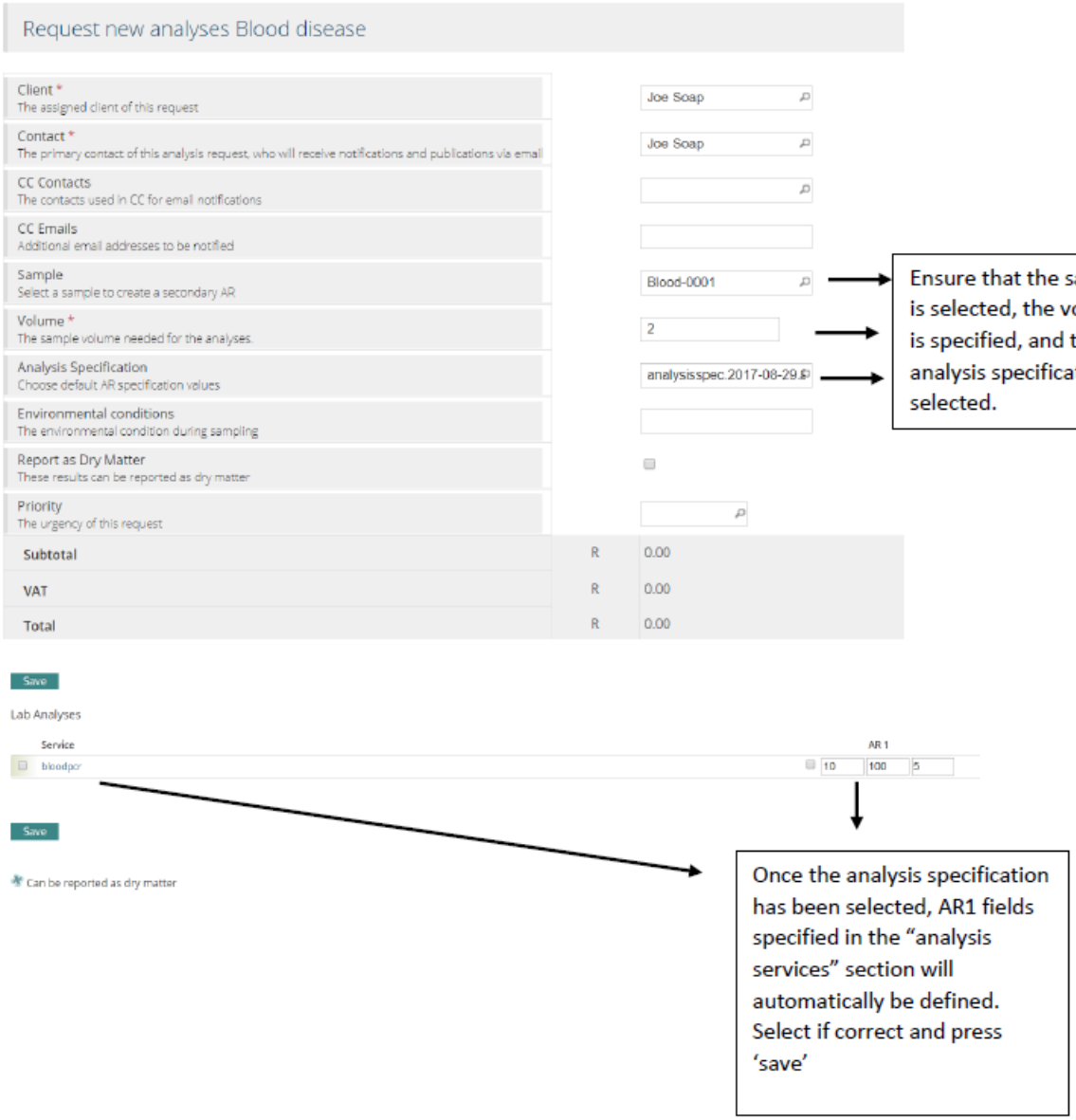


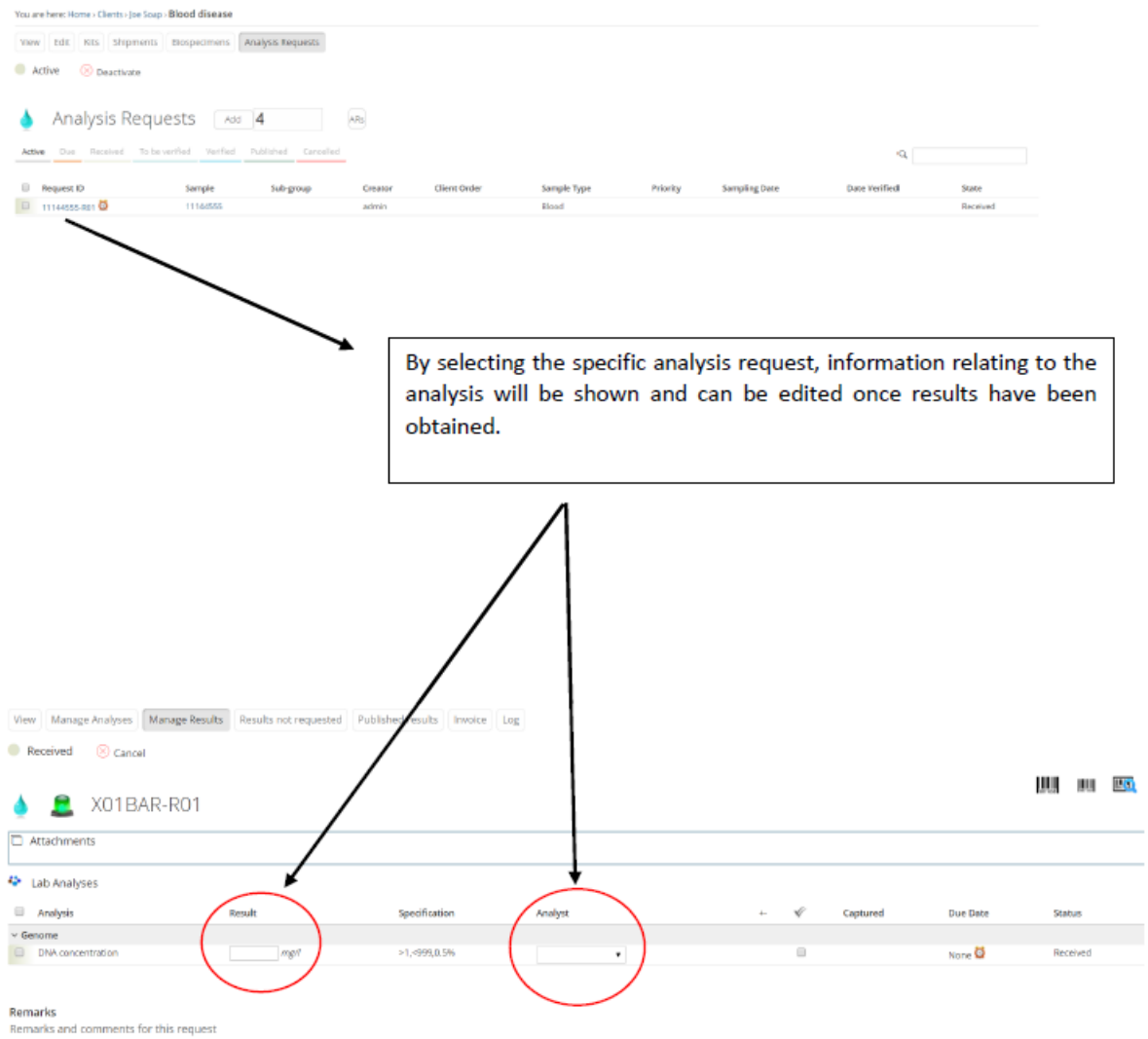
3.9 Performing an analysis request

If your biobank can perform an analysis for a client, ensure that you have selected the analyses service to be provided for the project. To do this, select the 'edit' tab in the project and select the service to be performed.

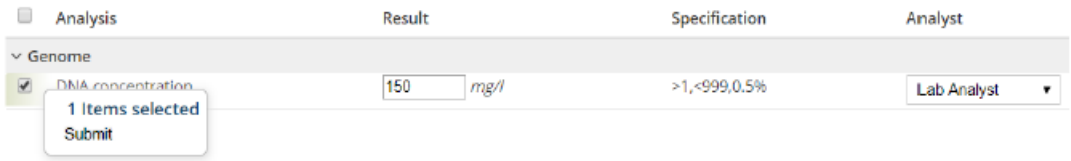
The user can now select the number of Analysis requests and create them by using the 'Add' button.



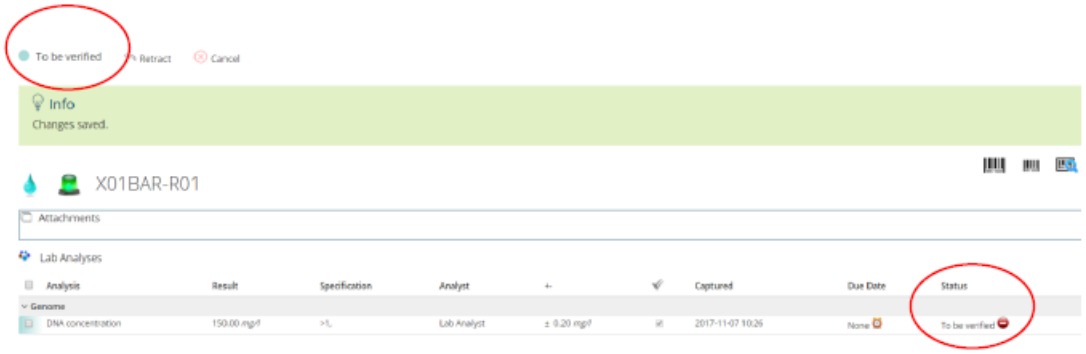

Request new analyses Blood disease
Client *
The assigned client of this request
Joe Soap
Contact *
The primary contact of this analysis request, who will receive notifications and publications via email
Joe Soap
CC Contacts
The contacts used in CC for email notifications
CC Emails
Additional email addresses to be notified
Sample
Select a sample to create a secondary AR
Blood-0001
Volume *
The sample volume needed for the analyses
2
Analysis Specification
Choose default AR specification values
analysisspec-2017-08-29
Environmental conditions
The environmental condition during sampling
Report as Dry Matter
These results can be reported as dry matter
Priority
The urgency of this request
Subtotal R 0.00
VAT R 0.00
Total R 0.00
Ensure that the sample is selected, the volume is specified, and the analysis specification is selected.
Save
Lab Analyses
Service
AR 1
bloodpcr
10
100
5
Save
Can be reported as dry matter
Once the analysis specification has been selected, AR1 fields specified in the “analysis services” section will automatically be defined. Select if correct and press ‘save’



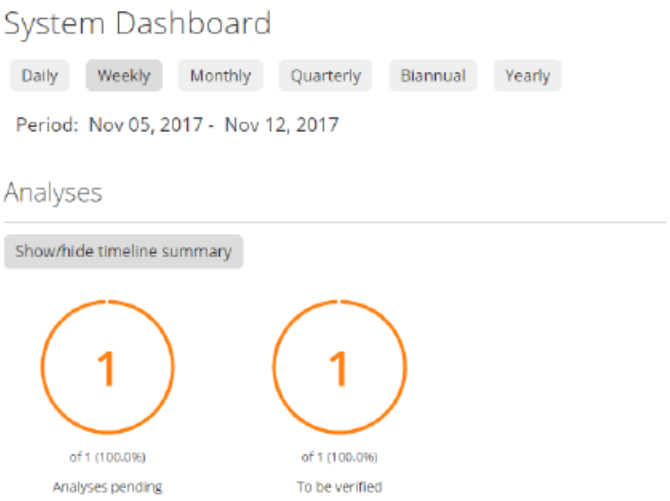
Once the results and the analyst have been selected, the analysis can be submitted by selecting 'submit'.



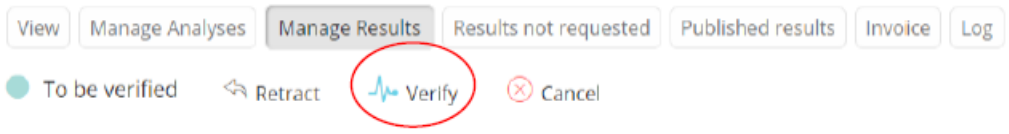
The status of the analysis request will change as the result will need to be verified by another analyst with verification permissions.

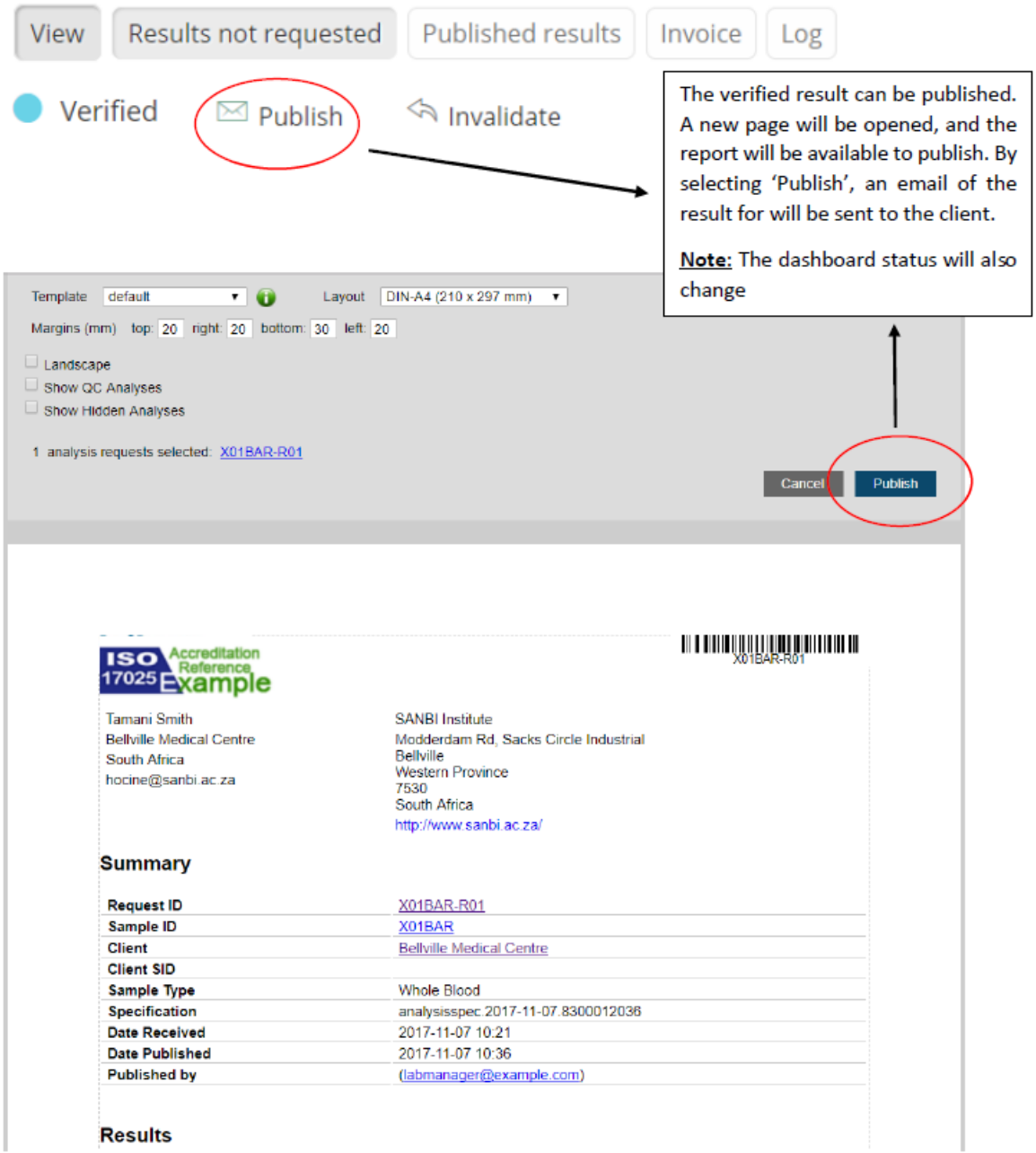


Note: The system dashboard will indicate that an analysis is pending and needs to be verified.

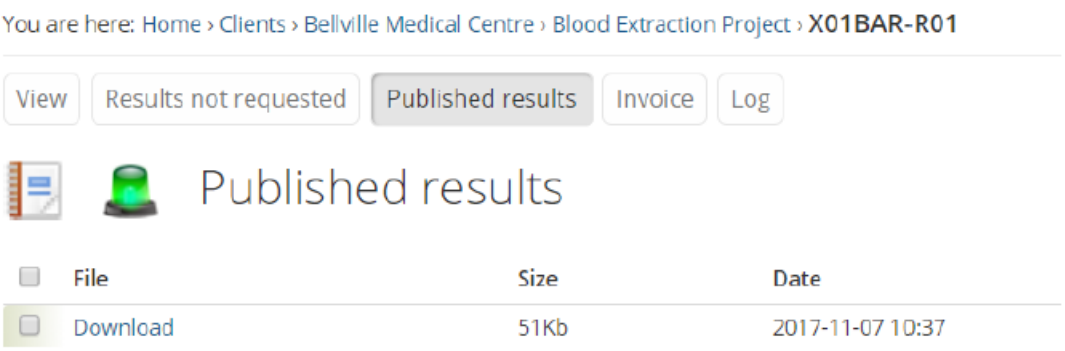


The analyst with verification permission can log in with their username and password and navigate to the analysis request and select 'Verify'.





Published results can be emailed to the Client and can also be downloaded by navigating to the Analysis request and selecting the 'Published results' tab.


You are here: Home › Clients › Bellville Medical Centre › Blood Extraction Project › X01BAR-R01
View
Results not requested
Published results
Invoice
Log
Published results
File
Size
Date
Download
51Kb
2017-11-07 10:37