



**Ramaciotti Centre
for Genomics**

dnaLIMS User guide

June 2018

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1. Setting up a login account

- Go to <http://sequencing.ramaciotti.unsw.edu.au/>
- Follow the link to 'Create login account for dnaLIMS' and set up a login name and password for yourself. Please ensure that you complete all of the required information.
- Select the 'Validate Form' button and then 'Submit'.
 - **Affiliation:** The type of facility where you work, make sure you select 'UNSW' if you are using internal account code for payment.
 - **Discipline:** The field of your research.
 - **PI (primary investigator):** this is your supervisor (or yourself where relevant).
- Make sure you fill in the 'Billing Information' and 'Shipping Information' sections.
- Changes can be made using the 'Change User Profile' link on the User Tools page.

Ramaciotti Centre for Genomics
www.ramaciotti.unsw.edu.au

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Phone: 02 9385 1237
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Login Information * Required Fields.

Login Name *
Password *
Re-Type Password *

First Name *
Last Name *
Email Address *

Affiliation
Select the Affiliation Type then PI before filling in Contact Info.

Affiliation * --Select--
Discipline * --Select--
PI * Last First
(Do not add Ph.D., Dr., or Mr. etc.)
PI Email *

Contact Information

Billing Information (Accounts Payable)

Name *
Institution *
Dept.
Address *
Address 2
City *
State or Territory * --Select--
Postal Code *
Phone * Ext.
Fax
Email *

Shipping Information

Name
Institution
Dept.
Address 1
Address 2
City
State or Territory --Select--
Postal Code
Phone Ext.
Fax
Email

Copy Billing to Shipping
Copy Shipping to Billing
Clear Billing
Clear Shipping

When creating your login information, do not use the following characters: < > / ; ' =

Cancel Clear Validate Form Submit

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2. Submitting samples

All sequencing and fragment analysis requests will only be accepted using dnaLIMS.

- Go to <http://sequencing.ramaciotti.unsw.edu.au/>

- Click '**Login to dnaLIMS**' – login and this will take you to the dnaLIMS User Tools page.
- There are two formats for sample submissions, small batch size submissions using individual 1.5mL microfuge tubes or large batch submissions (>40 samples) using specified 96-well plates.
- For small batch size submissions, sample names for individual samples submission can be entered via the '**Enter Individual DNA Sequencing Requests**' or by uploading a completed excel template downloadable via '**Upload and Import DNA Tube File**' links.
- For large batch size submissions, sample names can be entered by uploading a completed excel template downloadable via the '**Upload and Import DNA File**' or '**Upload and Import Fragment Analysis File**' links.
- Please note that Fragment Analysis is only available as plate submissions.



The screenshot shows the dnaLIMS user interface. At the top, there are navigation links for 'Logout', 'Store', 'DNA', and 'dnaLIMS'. On the right, there are links for 'NCBI Blast' and 'Google'. The main content area is divided into three columns: 'Sequencing', 'User Profile', and 'Resources'. The 'Sequencing' column is highlighted with a red rounded rectangle and contains links for 'Enter Individual DNA Sequencing Requests', 'Upload and Import DNA Tube File', 'Upload and Import DNA Plate File', 'View Your Requests', 'Display Order Summary', 'Download DNA Results', 'Enter Individual Fragment Analysis Requests', 'Upload and Import Fragment Analysis File', and 'Download Fragment Analysis Results'. The 'User Profile' column contains links for 'Change Your Email', 'Change Your Password', and 'Change Your Profile'. The 'Resources' column contains links for 'Contact Info.', 'Sample Preparation Guidelines', 'Instructions to activate Java', 'Supported Browsers', 'Learn More', and 'Bottom of Page'.

*** Sequencing guide and sample preparation information downloadable on our website ***

2.1 Using 'Enter Individual DNA Sequencing Requests'

- Click the 'Enter Individual DNA Sequencing Requests'.
 - Make sure you select the correct 'Sequencing Type'.
 - Enter number of samples and then 'Submit'.

Enter the Number of Reactions to Create Sequencing Requests For:



Select the Sequencing Type: User_Prep ▾

Core_prep = sequencing reaction and clean up service, submit purified templates and primers.
User_prep = electrophoresis service only, submit dried purified post-sequencing reaction products.

Dried samples should be submitted in either 1.5mL microfuge tubes or in 96 well AB3730 trays.
The minimum number of samples that must be submitted in trays is 40 for a half plate (odd columns) or 80 for a full plate.
Less than this will result in being billed for the entire 48 or 96 wells



- Fill in the required details on the DNA Sequencing form. It is essential that you enter the correct billing information for the order.
 - Users paying with UNSW accounts please enter the full code (Fund-Department-Project). For example: G1123-BABS-PS12345.
 - Users not paying with UNSW accounts, please enter a valid Purchase Order number or billing reference.
 - Incorrect billing information leading to reissuing of invoice might incur administration surcharge.
- You can fill in the form line by line or use the fill, clear, and toggle buttons to help fill in the sample names on your form.
 - For example: For samples named AB1-AB10, enter AB, click on index, enter the number “1” and it will automatically populate the template name boxes with the correct numbering. Sample names are limited to 15 characters consisting only of letters, numbers, and hyphens. Use the drop-down options where available if appropriate.

User_Prep Request Form
Sequencing by User.

UNSW Fund Number:	(Fund - Dept - Project) <-- Fields (G1123 - BABS - PS12345) <-- Example <input type="text"/> - <input type="text"/> - <input type="text"/>
Principal Investigator:	Ramaciotti Centre
Dye Chemistry:	BigDye_V3.1 ▾
EXOSAPIT cleanup:	no ▾ Will result in additional \$2.00 charge per reaction.
Comments to Lab:	<input type="text"/>

No Validation response means all required fields are filled in.

By clicking on the **Submit** button you are agreeing to the terms and conditions as listed on the [Ramaciotti website](#).

Sample Name	Template Information		
	Name	Type	Size bp
	Index	Fill	Clear
1	<input type="text"/>	Select ▾	<input type="text"/>
2	<input type="text"/>	Select ▾	<input type="text"/>
3	<input type="text"/>	Select ▾	<input type="text"/>
4	<input type="text"/>	Select ▾	<input type="text"/>
5	<input type="text"/>	Select ▾	<input type="text"/>
6	<input type="text"/>	Select ▾	<input type="text"/>

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- Press ‘**Validate Table**’ and then ‘**Submit**’ to submit your sample request. Record your order number. Label the samples with the order number and consecutive sample number. The specific sample names can be written on the **side of the tubes** if desired.
- Follow our sequencing guide on our website for detail on sample preparation.

2.2 Using ‘Upload and Import DNA Tube File’



Import requests from electronic spreadsheets.

Right click to Download this [Sequencing Template 96 Well](#) to your PC.
 Edit the template file with the program Excel. I.e. Open Excel first then the file from within Excel.
 No spaces or illegal characters allowed. Allowable characters include: a - z, A - Z, 0 - 9, and hyphens.
 Save the edits to a Tab delimited file with a .txt extension on your PC.
 Use the Choose File button to select the modified template for uploading and importing.
Do Not have Duplicate Sample and Primer name pairs on multiple lines in the import file.

Core_prep = sequencing reaction and clean up service, submit purified templates and primers.
 User_prep = electrophoresis service only, submit dried purified post-sequencing reaction products.

Fund Number:	(Fund - Dept - Project) <-- Fields (G1123 - BABS - PS12345) <-- Example
Principal Investigator:	Ramaciotti Centre
Service Request:	<input type="button" value="User Prep"/> <input checked="" type="button" value="Core Prep"/>
DNA Type:	-- Select --
DNA Conc:	
Primer:	-- Select --
Primer Conc:	3.2
Dye Chemistry:	BigDye_V3.1
EXOSAPIT cleanup:	<input type="checkbox"/> no <input checked="" type="checkbox"/> Will result in an additional \$2.00 charge per reaction. ONLY use for Core_Prep service.



Comments:

Select the Browse or Choose File button to locate the upload file.

Upload File:

After selecting the file, click the Submit button to upload the file.

By clicking on the Submit button you are agreeing to the terms and conditions as listed on the [Ramaciotti website](#).

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- Select 'Upload and Import DNA Tube File'.
- Download the Excel template and fill in the sample names.
- Make sure you select the correct 'Service Request'.
- Fill in the required details on the DNA Sequencing form. It is essential that you enter the correct billing information for the order.
 - Users paying with UNSW accounts please enter the full code (Fund-Department-Project). For example: G1123-BABS-PS12345.
 - Users not paying with UNSW accounts, please enter a valid Purchase Order number or billing reference.
 - Incorrect billing information leading to reissuing of invoice might incur administration surcharge.
- Attach the file.
- Press 'Submit' to submit your order. Record your order number. Label the samples with the order number and consecutive sample number. The specific sample names can be written on the **side of the tubes** if desired.
- Follow our sequencing guide on our website for detail on sample preparation.

2.3 Using "Upload and Import DNA Plate File"

- Select 'Upload and Import DNA Plate File'
- Download the Excel template and fill in the sample names.
- Make sure you select the correct 'Service Request'.



- Fill in the required details on the DNA Sequencing form. It is essential that you enter the correct billing information for the order.
 - Users paying with UNSW accounts please enter the full code (Fund-Department-Project). For example: GI123-BABS-PS12345.
 - Users not paying with UNSW accounts, please enter a valid Purchase Order number or billing reference.
 - Incorrect billing information leading to reissuing of invoice might incur administration surcharge.
- Attach the file.
- Press **'Submit'** to submit your order. Record your order number. Label the samples with the order number and consecutive sample number. The specific sample names can be written on the **side of the tubes** if desired.
- Follow our sequencing guide on our website for detail on sample preparation.

Right click to Download this [Sequencing Template 96 Well](#) to your PC.
 Edit the template file with the program Excel, i.e. Open Excel first then the file from within Excel.
 No spaces or illegal characters allowed. Allowable characters include: a - z, A - Z, 0 - 9, and hyphens.
 Save the edits to a Tab delimited file with a .txt extension on your PC.
 Use the Choose File button to select the modified template for uploading and importing.
Do Not have Duplicate Sample and Primer name pairs on multiple lines in the import file.

Plate-User_Prep = Does not include either EXOSAPIT or Bead cleanup.
 Plate-User_PrepPlus = Automatically includes Bead cleanup.

Plate-Core_Prep = Optional EXOSAPIT or Bead cleanup.

Plate-Core_PrepBead40 = Automatically includes Bead cleanup for plates of 40+ samples.
 Plate-Core_PrepBead96 = Automatically includes Bead cleanup for plates of 96 samples.

Fund Number:	(Fund - Dept - Project) <-- Fields (GI123 - BABS - PS12345) <-- Example <input type="text"/> - <input type="text"/> - <input type="text"/>
Principal Investigator:	Ramaciotti Centre
Service Request:	<div style="border: 1px solid black; padding: 2px;"> Plate-User_Prep Plate-User_PrepPlus ---- Plate-Core_Prep ---- Plate-Core_PrepBead40 Plate-Core_PrepBead96 ---- Project_PCR2DIR </div>
DNA Type:	Plate-Core_Prep ----
DNA Conc:	Plate-Core_PrepBead40 Plate-Core_PrepBead96 ----
Primer:	<input type="text"/>
Primer Conc:	Project_PCR2DIR 3.2 <input type="text"/>
Dye Chemistry:	BigDye_V3.1 <input type="button" value="v"/>
EXOSAPIT cleanup:	no <input type="button" value="v"/> Will result in an additional \$2.00 charge per reaction. ONLY use for Plate-Core_Prep service. Choose Exo or Bead, but not both.
Bead cleanup:	no <input type="button" value="v"/> Will result in an additional \$3.95 charge per reaction. ONLY use for Plate-Core_Prep service. Choose Exo or Bead, but not both.
Comments:	<input type="text"/>

Select the Browse or Choose File button to locate the upload file.

Upload File:

After selecting the file, click the Submit button to upload the file.

By clicking on the Submit button you are agreeing to the terms and conditions as listed on the [Ramaciotti website](#).

2.4 Using “Upload and Import Fragment Analysis File”

- Select ‘**Upload and Import Fragment Analysis File**’
- Download the Excel template and fill in the sample names.
- Make sure you select the correct ‘**Service Request**’.
- Fill in the required details on the DNA Sequencing form. It is essential that you enter the correct billing information for the order.
 - Users paying with UNSW accounts please enter the full code (Fund-Department-Project). For example: GI123-BABS-PS12345.
 - Users not paying with UNSW accounts, please enter a valid Purchase Order number or billing reference.
 - Incorrect billing information leading to reissuing of invoice might incur administration surcharge.
- Attach the file.
- Press ‘**Submit**’ to submit your order. Record your order number. Label the samples with the order number and consecutive sample number. The specific sample names can be written on the **side of the tubes** if desired.
- Follow our sequencing guide on our website for detail on sample preparation.

Import requests from electronic spreadsheets.

Right click to Download this [Fragment Analysis Template 96](#) to your PC.
Edit the template file with the program Excel, i.e. Open Excel first then the file from within Excel.
No spaces or illegal characters allowed. Allowable characters include: a - z, A - Z, 0 - 9, and hyphens.
Save the edits to a Tab delimited file with a .txt extension on your PC.
Use the Choose File button to select the modified template for uploading and importing.
Do Not have Duplicate Sample and Primer name pairs on multiple lines in the import file.

Fund Number:	(Fund - Dept - Project) <-- Fields (GI123 - BABS - PS12345) <-- Example <input type="text"/> - <input type="text"/> - <input type="text"/>
Principal Investigator:	Ramaciotti Centre
Service Request:	<input type="text" value="Plate-FA"/>
Std Needed:	<input type="text" value="LIZ500"/> LIZ is Size Standard
Dye present in Sample:	<input type="checkbox"/> 6-FAM <input type="checkbox"/> VIC <input type="checkbox"/> NED <input type="checkbox"/> PET <input type="checkbox"/> OTHER Enter the Dye Name in the Comments box if OTHER is checked.
Comments:	<input type="text"/>

Select the Browse or Choose File button to locate the upload file.

Upload File: Browse...

After selecting the file, click the Submit button to upload the file.

By clicking on the Submit button you are agreeing to the terms and conditions as listed on the [Ramaciotti website](#).

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3. Viewing sequencing requests

- View or delete your sequencing requests by Request or Order number by clicking on "**View your requests**". Select the appropriate options.
 - You can view the length of the queue by choosing the "**queue length**" link.
- Press '**Submit**' after making your choice.

Search the Sequencing Request Queue.

Request = 1 reaction.
Order = all reactions requested at one time.

To view ALL your requests in the queue. Select Submit
To view a Specific Order. Select an Order Number below then Submit.

Requisition or Order Number:

Search by Request Number

View All Requests in the Queue

View Request

Delete Request

Search Your Orders

View Order

Order#	#_Samples	Order_Date
18326	4	Aug 24 2016
18102	96	Jun 30 2016
17941	1	Jun 1 2016
17619	8	Mar 21 2016
14901	32	Aug 29 2014
14861	32	Aug 22 2014
10980	16	Nov 15 2012
8482	8	Oct 12 2011
4812	2	Jul 21 2010
4505	1	Jun 25 2010

Delete Order

Queue Length

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4. Retrieving sequencing results

- You can access your files via dnaLIMS. Choose '**Download DNA Results**' or '**Download Fragment Analysis Results**' from the User Tools page.
- Select your order number and press '**Submit**'. Follow the instructions to download individual files or all trace/sequence files in one go. If you download all files together, they will need to be unzipped.
- The following files are available to download:
 - Raw trace (.ab1 file)
 - Raw, unfiltered basecall sequence (.seq file)
 - Text file of you sequence
 - FASTA Sequence
 - System QC score of the sequence
- You can view the chromatogram via JAVA online using the '**View**' option.



Download DNA Sequencing Results

Clear Submit

If your Order Number search displays an empty table, please use the Plate Number Search. Or manually type in the Order Number, click the radio button, then click Submit. Please use the Plate Number search when retrieving reruns, Thank You.

Order Number Search

<input type="radio"/> Order Number <input type="text"/> <input type="button" value="Submit"/> [View Phred Data]	<table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="text-align: left;">Order#</th> <th style="text-align: left;"># Samples</th> <th style="text-align: left;">Date</th> </tr> </thead> <tbody> <tr><td>18326</td><td>4</td><td>Aug 29 2016</td></tr> <tr><td>18102</td><td>96</td><td>Jun 30 2016</td></tr> <tr><td>17941</td><td>1</td><td>Jun 7 2016</td></tr> <tr><td>17619</td><td>8</td><td>Mar 24 2016</td></tr> <tr><td>14901</td><td>32</td><td>Sep 2 2014</td></tr> <tr><td>14861</td><td>32</td><td>Aug 27 2014</td></tr> <tr><td>14861</td><td>32</td><td>Aug 25 2014</td></tr> <tr><td>11203</td><td>6</td><td>Jan 3 2013</td></tr> <tr><td>11204</td><td>48</td><td>Jan 3 2013</td></tr> <tr><td>10980</td><td>16</td><td>Nov 19 2012</td></tr> </tbody> </table>	Order#	# Samples	Date	18326	4	Aug 29 2016	18102	96	Jun 30 2016	17941	1	Jun 7 2016	17619	8	Mar 24 2016	14901	32	Sep 2 2014	14861	32	Aug 27 2014	14861	32	Aug 25 2014	11203	6	Jan 3 2013	11204	48	Jan 3 2013	10980	16	Nov 19 2012
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14861	32	Aug 27 2014																																
14861	32	Aug 25 2014																																
11203	6	Jan 3 2013																																
11204	48	Jan 3 2013																																
10980	16	Nov 19 2012																																

Plate Number Search

<input checked="" type="radio"/> Plate Number <input type="text" value="6087"/> <input type="button" value="Submit"/> [View Phred Data]	<table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="text-align: left;">Plate</th> <th style="text-align: left;">Date</th> </tr> </thead> <tbody> <tr style="background-color: #e0e0e0;"><td>6087</td><td>Aug 31 2016</td></tr> <tr><td>6081</td><td>Aug 29 2016</td></tr> <tr><td>6079</td><td>Aug 29 2016</td></tr> <tr><td>6073</td><td>Aug 24 2016</td></tr> <tr><td>6068</td><td>Aug 24 2016</td></tr> <tr><td>6067</td><td>Aug 19 2016</td></tr> <tr><td>6066</td><td>Aug 17 2016</td></tr> <tr><td>6064</td><td>Aug 16 2016</td></tr> <tr><td>6063</td><td>Aug 11 2016</td></tr> <tr><td>6059</td><td>Aug 9 2016</td></tr> </tbody> </table>	Plate	Date	6087	Aug 31 2016	6081	Aug 29 2016	6079	Aug 29 2016	6073	Aug 24 2016	6068	Aug 24 2016	6067	Aug 19 2016	6066	Aug 17 2016	6064	Aug 16 2016	6063	Aug 11 2016	6059	Aug 9 2016
Plate	Date																						
6087	Aug 31 2016																						
6081	Aug 29 2016																						
6079	Aug 29 2016																						
6073	Aug 24 2016																						
6068	Aug 24 2016																						
6067	Aug 19 2016																						
6066	Aug 17 2016																						
6064	Aug 16 2016																						
6063	Aug 11 2016																						
6059	Aug 9 2016																						

Do Not use this form to download Fragment Analysis Results.
Order Number Search: Select a drop box entry to download results from your Order.
Sample Sheet Search: Select a drop box entry to download your results from your samples processed in this Sample Sheet.

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Download Sequencing Results [Bottom of Page](#)

Use top table to download all the files together and use the bottom table to download individual files. Check comment column of bottom table for individual sample status such as re-runs etc.

➔

Sequencer Output		Phred Output			
Text	Trace	Fasta	Qual	Phred	SCF
Text	Chromat	fasta	qual	phred	

To download individual files:
Mac: Hold down Control Key, Click Mouse. Select Save Linked File As...
PC: Right Mouse Click, Save Link As...

Plate Number: 6087

Select Order# link to compose then send an email message to that user.
 Rows in grey are checked in to be rerun.

Order + email	Req#	Download	View	SeqId	WID	Sample	Primer	Investigator	UID	Date	Phred Q20	Comments
cs	413162	Text Chromat	View	6087-1	A1	pGem	CP2	koyal,jason	1368	Aug 29 2016	phd qual 1027 fasta	Results Available

There are 1 samples.

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[dnaLIMS Menu](#)

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5. Store

All consumables and reagents must now be purchased through the dnaLIMS Store module. **The discounted prices listed are for our sequencing customers only, surplus (20%) will be applied on consumable purchases from non-sequencing customers.**

- Select the 'Login to dnaLIMS' link and login choosing the 'Stores' LIMS. This will take you to the dnaLIMS User Tools page.
- Select 'Place a New Order' and then choose the quantity of each item you would like to order.
 - Make sure you include a unit of delivery if you are not picking the order up in person.
 - Standard collection hours are 2pm-4pm Monday to Friday, please contact us before dropping in other times to make sure the order is ready for collection.
- Next press 'Step 2: Preview Order' to review your selection(s).
 - Enter either your PO number or UNSW account code (Fund-Dept-Project).
- When completed, press 'Place Order' to place your order. You may wish to print this page for your records.
- Order will be available for in-person collection on the next business day. For orders via delivery, you will receive an email when your order is dispatched.

The screenshot shows the dnaLIMS Store module interface. At the top left is the Ramaciotti Centre for Genomics logo and name. At the top right is contact information for the centre. Below the header is a navigation bar with tabs for 'Store', 'DNA', and 'dnaLIMS'. A red arrow points to the 'Store' tab. The main content area is divided into three columns: 'Sequencing', 'User Profile', and 'Resources'. The 'Sequencing' column contains links for entering and downloading DNA and Fragment Analysis requests. The 'User Profile' column contains links for changing email, password, profile, and viewing PI-Group results. The 'Resources' column contains links for contact info, sample preparation guidelines, and instructions to activate Java.

