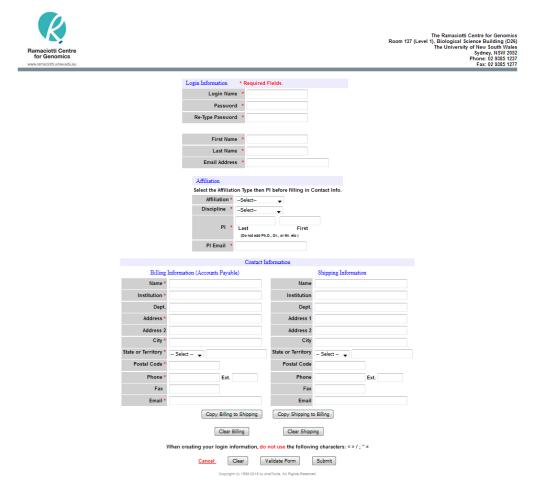# dnaLIMS User guide

June 2018

Contents

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**'.

  o **Affiliation**: The type of facility where you work, make sure you select '**UNSW**' if you are using internal account code for payment.

  o **Discipline**: The field of your research.

  o **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.

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 <u>individual</u> 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.

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

2.1 Using 'Enter Individual DNA Sequencing Requests'

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

- 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.

- 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.

- 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'

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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.
  - o Users paying with UNSW accounts please enter the full code (Fund-Department-Project). For example: GI123-BABS-PS12345.
  - o Users not paying with UNSW accounts, please enter a valid Purchase Order number or billing reference.
  - o 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'**.

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- 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
	[ ] - [ ] - [ ]
Principal Investigator:	**Ramaciotti Centre**
Service Request:	Plate-User_Prep
	Plate-User_PrepPlus

	Plate-Core_Prep
DNA Type:	----
DNA Conc:	Plate-Core_PrepBead40
	Plate-Core_PrepBead96
Primer:	----
	Project_PCR2DIR
Primer Conc:	3.2
Dye Chemistry:	BigDye_V3.1 ✓
EXOSAPIT cleanup:	no ✓ 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 ✓ 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: [   ]

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.

[Clear]   [Submit]

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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**
	[ ] - [ ] - [ ]
Principal Investigator:	**Ramaciotti Centre**
Service Request:	Plate-FA ▾
Std Needed:	LIZ500 ▾ **LIZ is Size Standard**
Dye present in Sample:	☐ 6-FAM ☐ VIC ☐ NED ☐ PET ☐ OTHER
	Enter the Dye Name in the Comments box if OTHER is checked.

Comments: [   ]

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.**

[Clear]   [Submit]

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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.

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.

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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.
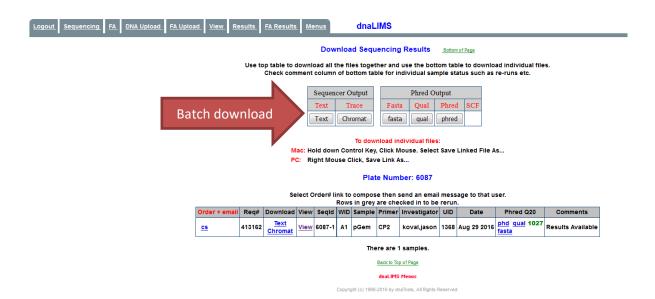Please use the Plate Number search when retrieving reruns, Thank You.**

Order Number Search

○ **Order Number**	Order#	#_Samples	Date
	18326	4	Aug 29 2016
	18102	96	Jun 30 2016
[Submit]	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
[View Phred Data]	11204	48	Jan 3 2013
	10980	16	Nov 19 2012

Plate Number Search

● **Plate Number**	Plate	Date
6087	6087	Aug 31 2016
	6081	Aug 29 2016
[Submit]	6079	Aug 29 2016
	6073	Aug 24 2016
	6068	Aug 24 2016
	6067	Aug 19 2016
	6066	Aug 17 2016
	6064	Aug 16 2016
[View Phred Data]	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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| Logout | Sequencing | FA | DNA Upload | FA Upload | View | Results | FA Results | Menus | **dnaLIMS** |

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.

Batch download →

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	koval,jason	1368	Aug 29 2016	phd qual 1027 fasta	Results Available

There are 1 samples.

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dnaLIMS Menus

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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.