GMG Sample Submission Portal - Client Instructions

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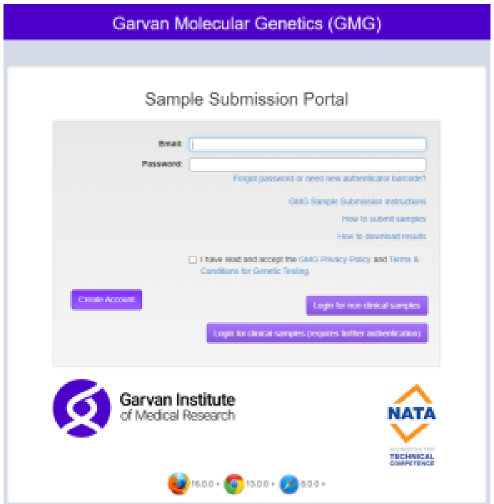
Original Author	Pavel Bitter	**Date of Last Review/Edit**	10 Oct 2022
Original Date of Creation	27 Oct 2016	**Last Changes Made**	Transferred to Confluence

Create account procedure

Navigate to our Sample Submission Portal (MSSS) which is located on the Garvan Institute server at https://gmg-submit.gimr.garvan.org.au/#/login.



☐ I have read and accept the GMG Privacy Policy and Terms & Conditions for Genetic Testing.

Figure 1: GMG Sample Submission Portal landing page

Click on the button 'Create Account', once clicked a new popup window will appear and all information for the new account that is to be created must be entered, see Figure 2. In the box 'Register' under Account Details there are two fields 'Client Details' and 'Billing Details'. If the details for 'Client details' are filled in the button 'Same as Client Details' can be clicked to transfer the data from the client details field to the billing details field.

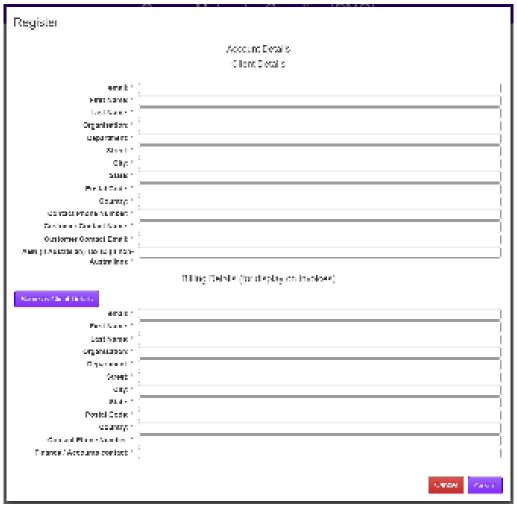
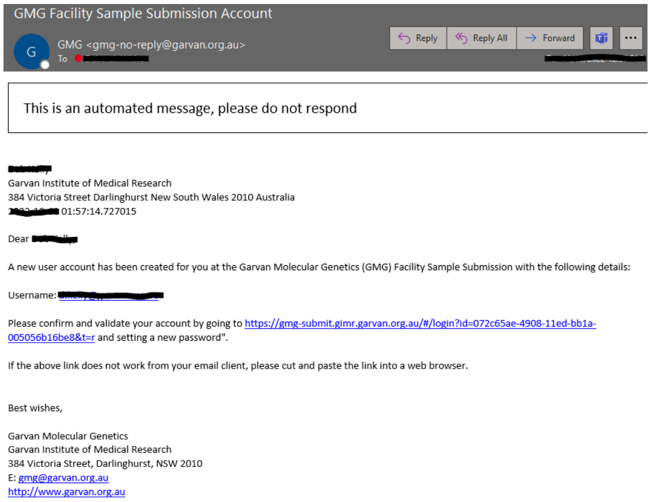


Figure 2: Registering new client page ('Create Account')

Once all fields marked with an asterisks (*) have been entered and either the billing information is entered or the 'Same as Client details' button was clicked, click the button 'Create' for the information to be saved and the popup window to close.

Confirmation email

The software will then send an account validation email to your nominated email address, see Figure 3 for an example. This email contains a link to validate the account and email address. If the link in the email is clicked a popup window opens, see Figure 4.



GMG Facility Sample Submission Account

GMG <gmg-no-reply@garvan.org.au>
To [redacted]

[redacted]

This is an automated message, please do not respond

[redacted]
Garvan Institute of Medical Research
384 Victoria Street Darlinghurst New South Wales 2010 Australia
[redacted] 01:57:14.727015

Dear [redacted]

A new user account has been created for you at the Garvan Molecular Genetics (GMG) Facility Sample Submission with the following details:

Username: [redacted]

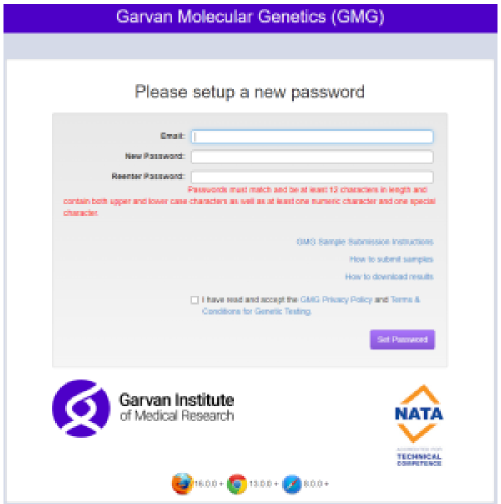
Please confirm and validate your account by going to https://gmg-submit.gimr.garvan.org.au/#/login?id=072c65ae-4908-11ed-bb1a-005056b16be8&t=r and setting a new password".

If the above link does not work from your email client, please cut and paste the link into a web browser.

Best wishes,

Garvan Molecular Genetics
Garvan Institute of Medical Research
384 Victoria Street, Darlinghurst, NSW 2010
E: gmg@garvan.org.au
http://www.garvan.org.au

Figure 3: Example of account validation email sent by the software



Passwords must match and be at least 12 characters in length and contain both upper and lower case characters as well as at least one numeric character and one special character.

☐ I have read and accept the GMG Privacy Policy and Terms & Conditions for Genetic Testing.

Figure 4: Popup window if link in validation email is clicked

In this popup window you need to enter your email address and you can set a new password in the field 'New Password'. In the field 'Re-enter Password' the new password must be re-entered. Finally, the box called 'I have read and accept the GMG Privacy and Terms & Conditions' must be ticked and the button 'Set Password' clicked.

Login with new password

In the login screen you need to enter the account linked email address in the field 'Email', see Figure 1. The password that set in the account setup procedure needs to be entered in the field 'Password'. The box 'I have read and accept the GMG Privacy Policy and Terms & Conditions for Genetic Testing' must be ticked and the button 'Login for non clinical samples' or 'Logon for clinical samples (requires further authentication)', depending on the type of samples being submitted, needs to be clicked.

Two step authentication

After the successful entry of the email address and password there will be a new popup window shown in Figure 5.

Figure 5: Two step authentication screen with barcode

You need to download on your phone or tablet an application called 'Authenticator' from Apple’s App Store or Google’s Play Store. Once installed on your phone or tablet the barcode shown on the screen needs to be scanned with the phone’s camera, see Figure 6.

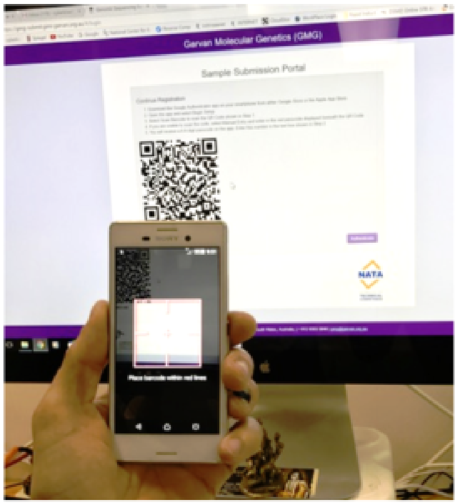
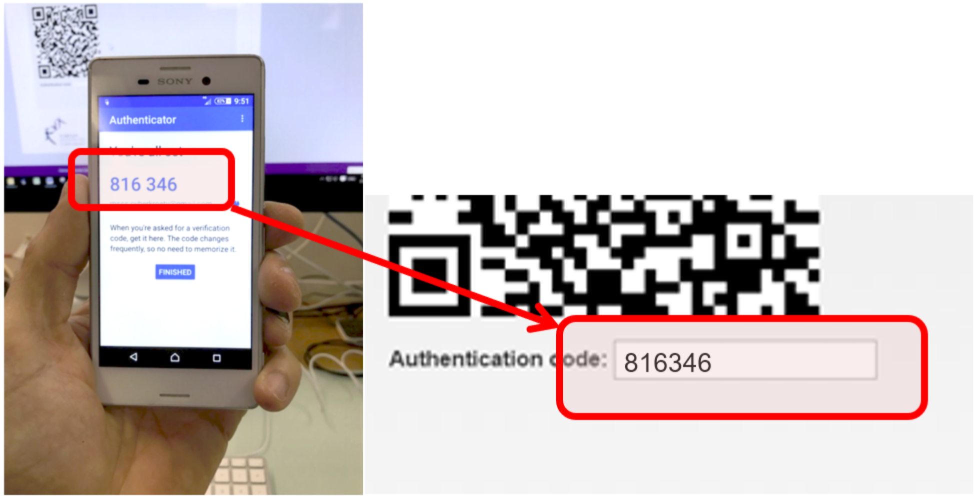


Figure 6: Authenticator software on phone scanning the barcode displayed on MSSS

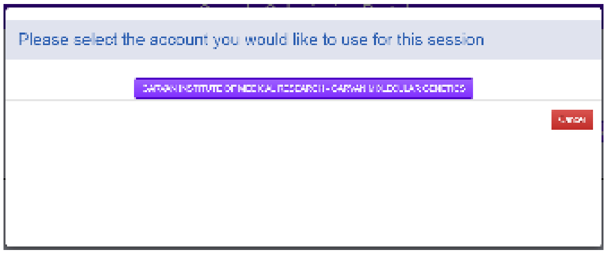
As soon as the barcode is recognised by the Authenticator software it will show a MSSS software specific code on the display of the phone, see Figure 7.



Authentication code: 816346

Figure 7: Entering the Authentication Code from the Authenticator software into MSSS

Once this 6 digit code is entered into the field 'Authentication Code' the button 'Authenticate' can be clicked. If the code matches the code the MSSS expects the next window shown on the screen will be for you to select which account you wish to use, it will list all account you are a user of and accounts that you have a proxy over, see Figure 8. If the authentication fails there will be an error message and you will need to repeat the process. The most likely reason for a failed authentication is that the authenticator code is timed out. Each authenticator password refreshes after 30sec. There is a little icon on your phone's screen indicating how much time of the 30sec is left for this code to be active.



Please select the account you would like to use for this session

Figure 8: Account selection screen MSSS software

Submitting samples on MSSS

Attention, when submitting samples to our service you will need a Purchase Order number and enter this number into the corresponding filed of your submission. We cannot process your samples without a purchase order number, please contact your financial department to generate a PO for your submission. We can generate an official quotation for your submission if needed.

Once successfully logged on the first screen shown is the account home screen of the software, see Figure 9.

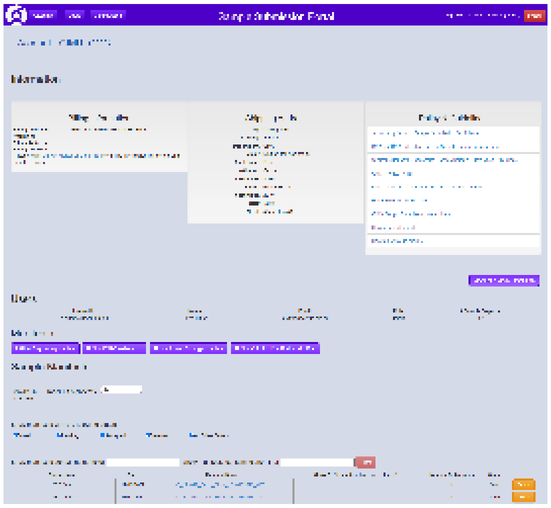


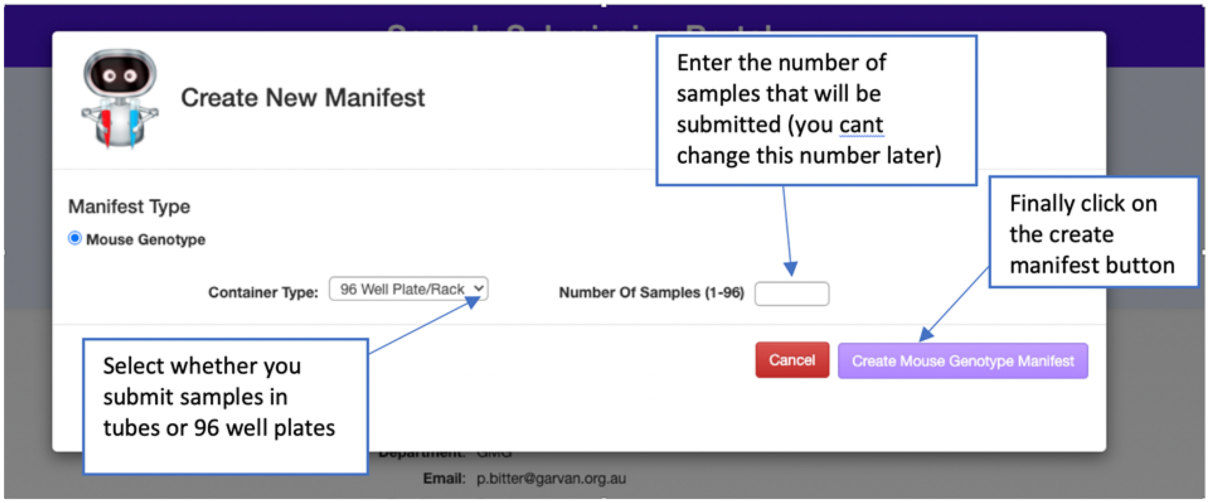
Figure 9: Example of an account home screen

New Mouse Genotyping manifest

Samples are submitted in 'Manifests'. Manifests are the virtual entities which contain the sample information and establish a collection of one to many samples that are treated as a unity in processing, progression, resulting and billing.

Creating a new manifest

By clicking on the button 'New Mouse Genotype Manifest' a popup window will appear that looks like Figure 10



Create New Manifest

Manifest Type

● Mouse Genotype

Container Type: 96 Well Plate/Rack

Number Of Samples (1-96)

Enter the number of samples that will be submitted (you cant change this number later)

Finally click on the create manifest button

Select whether you submit samples in tubes or 96 well plates

Email: p.bitter@garvan.org.au

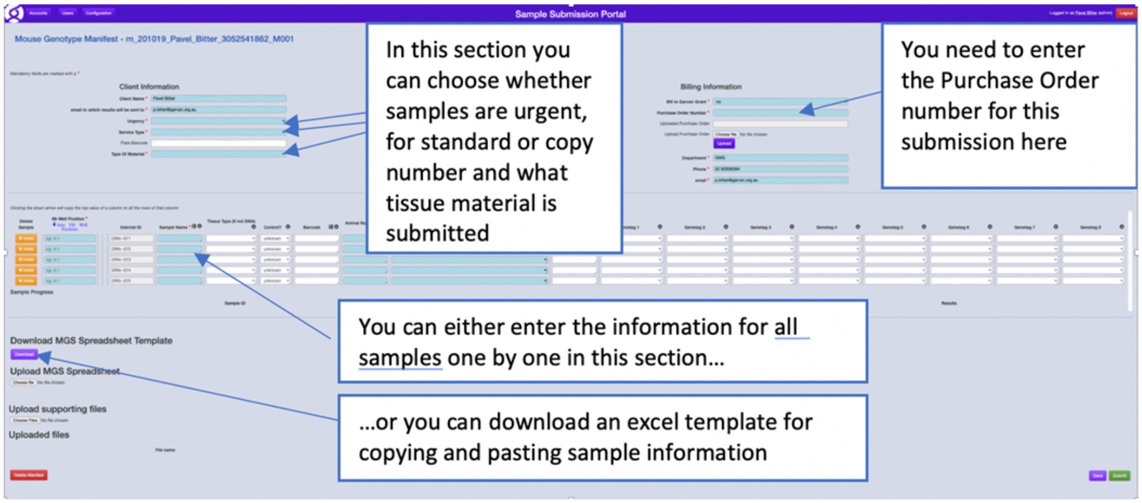
Figure 10: Popup window to define sample numbers of new manifest

Select whether you submit samples in tubes or plates and enter the amount of samples that will be submitted (Attention: you cannot change this number in the next window and cannot go back). Click on the button 'Create Mouse Genotype Manifest' to close this window.

Filling in the manifest information

If samples are urgent you can select from a dropdown menu to prioritise these samples (Attention: 2x service fees apply). You can also select from a dropdown menu whether these samples are for copy number analysis, standard genotyping or pathogen screening (Helicobacter, Corynebacterium etc). And you can select from another dropdown menu what tissue material these samples are (tail, ear, paws, swabs), see Figure 11. Please enter a valid Purchase Order number, most financial departments do not accept our invoices if you do not provide a valid Purchase Order number for this service request. Please contact your financial department and ask to create a Purchase Order number. They may need a quotation which we can provide or you generate a standing Purchase Order number that covers a certain dollar amount against which we invoice until it is used up.

In the section for the sample information you can either enter the information for each sample manually or you can download a template onto your desktop. When you work with the downloaded template you can copy and paste sample information from another Excel sheet or csv file. This method is preferable for many samples that are submitted.



In this section you can choose whether samples are urgent, for standard or copy number and what tissue material is submitted

You need to enter the Purchase Order number for this submission here

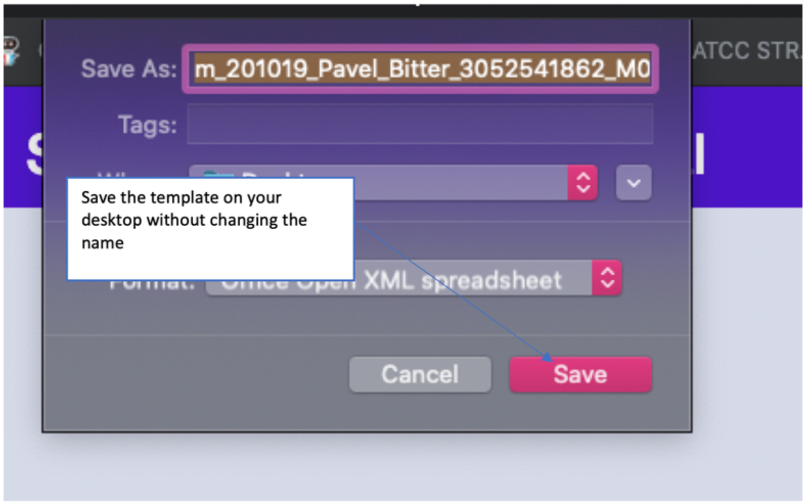
You can either enter the information for all samples one by one in this section…

…or you can download an excel template for copying and pasting sample information

Figure 11: Filling in the Manifest or downloading a template file

Downloading the template

Click on the button 'Download' to save a template file on the desktop. There will be a popup window asking you where you want to save the template file, see Figure 12. Please don't change the name of the template file, as the system will only recognise this name when you re-upload.


Save As: m_201019_Pavel_Bitter_3052541862_M0

Tags:

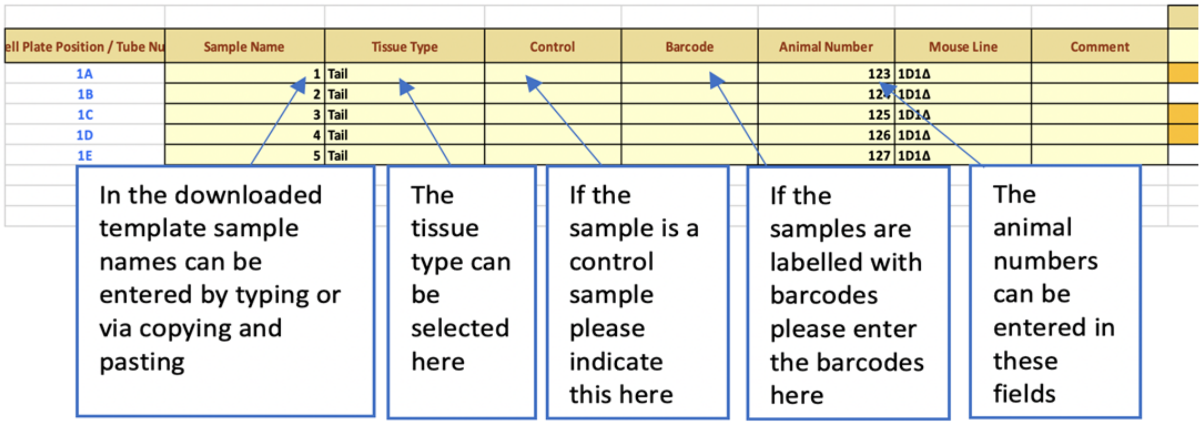
Format: Office Open XML spreadsheet

Save the template on your desktop without changing the name

Figure 12: Saving the template file onto your desktop

Filling in the template file

Open the template file. In the column 'Sample Name' type the sample names or copy and paste the sample names. The column 'Tissue Type' is a dropdown menu and you can select the tissue type and fill down for all samples. In the column 'Control' you can indicate whether this submitted sample is a control sample of known genotype, you can select from the dropdown menu. In the column 'Barcode' enter the barcode of the sample if tubes are labelled with barcodes. In the column 'Animal Number' enter the animal number the sample has in your system, see Figure 13.



ell Plate Position / Tube Nu	Sample Name	Tissue Type	Control	Barcode	Animal Number	Mouse Line	Comment
1A	1	Tail			123	1D1Δ	
1B	2	Tail			124	1D1Δ	
1C	3	Tail			125	1D1Δ	
1D	4	Tail			126	1D1Δ	
1E	5	Tail			127	1D1Δ	

In the downloaded template sample names can be entered by typing or via copying and pasting

The tissue type can be selected here

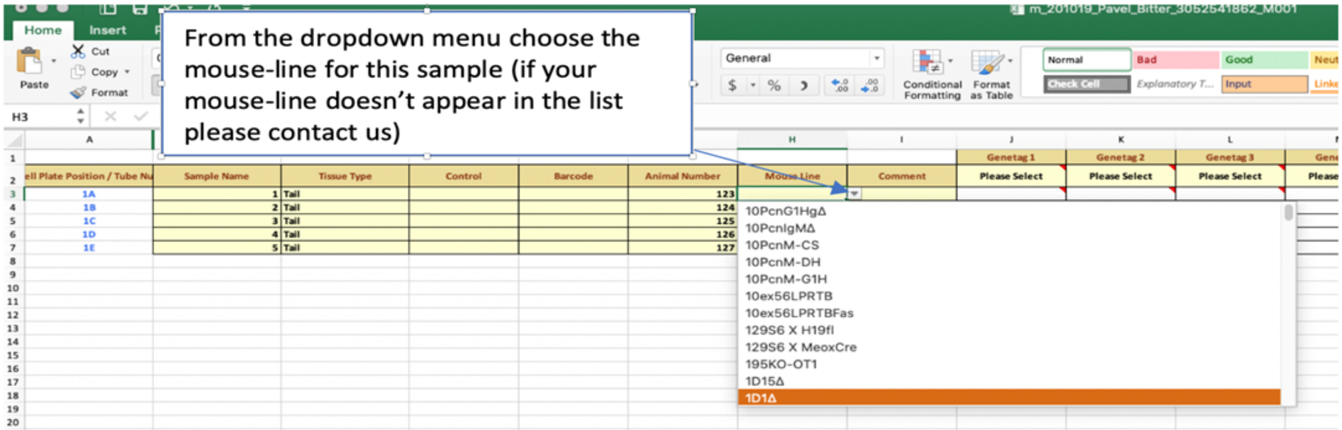
If the sample is a control sample please indicate this here

If the samples are labelled with barcodes please enter the barcodes here

The animal numbers can be entered in these fields

Figure 13: Filling in sample information in the template

Select the mouse-line for each sample from the dropdown menu, see Figure 14. All your established mouse lines will be listed. If the mouse-line does not appear that means it has yet not been established with us, please contact us on gmg@garvan.org.au.

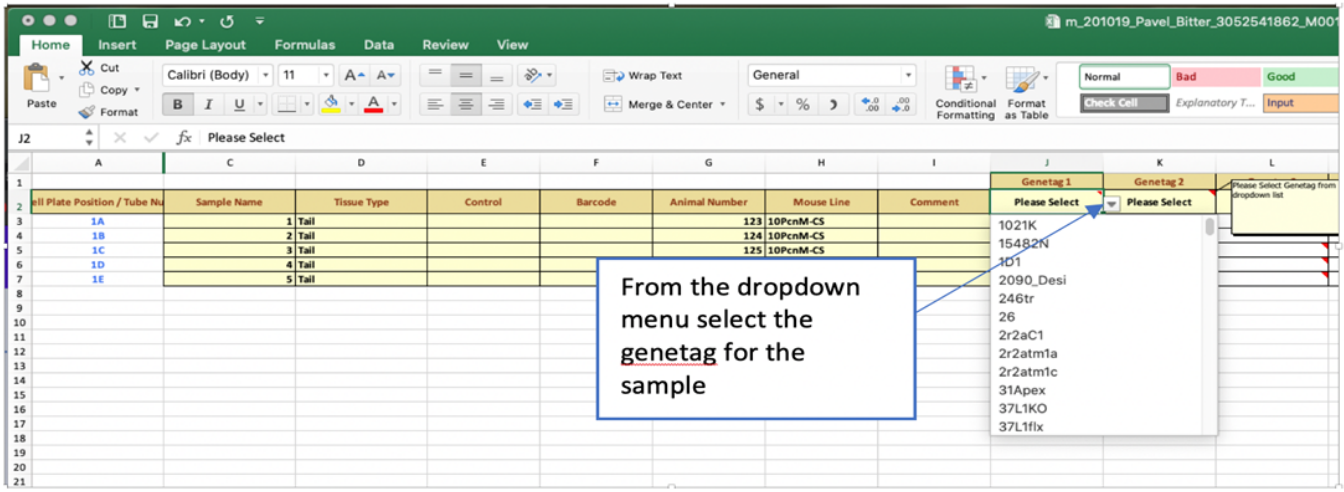


From the dropdown menu choose the mouse-line for this sample (if your mouse-line doesn't appear in the list please contact us)

ell Plate Position / Tube Nu	Sample Name	Tissue Type	Control	Barcode	Animal Number	Mouse Line	Comment	Genetag 1	Genetag 2	Genetag 3
								Please Select	Please Select	Please Select
1A	1	Tail			123					
1B	2	Tail			124					
1C	3	Tail			125					
1D	4	Tail			126					
1E	5	Tail			127					

Figure 14: Selecting the mouse-line for each sample

Select the genetag for each sample from the dropdown menu, see Figure 15. All your established genetags will be listed. If the genetag does not appear that means it has yet not been established with us, please contact us on gmg@garvan.org.au. Please make sure the genetag is established with the selected mouse-line otherwise there will be an error when uploading.

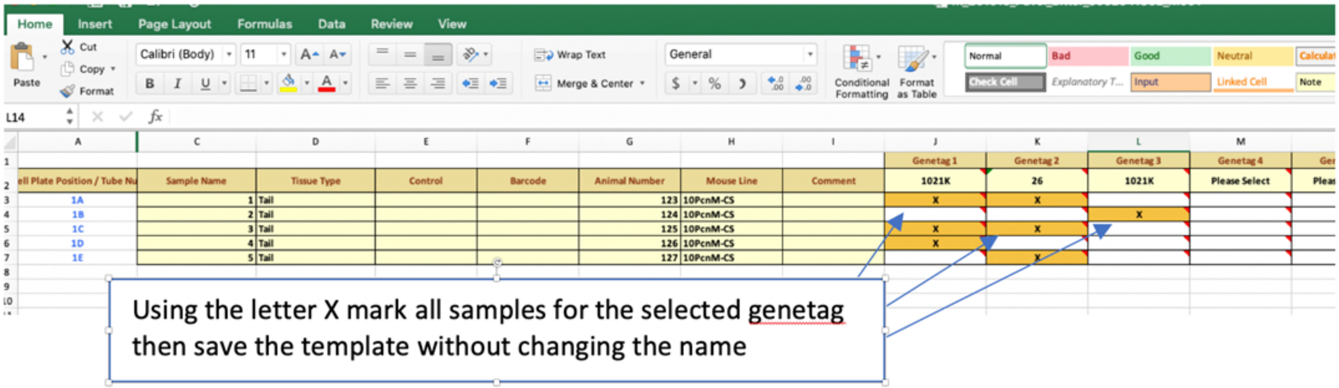


ell Plate Position / Tube Nu	Sample Name	Tissue Type	Control	Barcode	Animal Number	Mouse Line	Comment	Genetag 1	Genetag 2
								Please Select	Please Select
1A	1	Tail			123	10PcnM-CS			
1B	2	Tail			124	10PcnM-CS			
1C	3	Tail			125	10PcnM-CS			
1D	4	Tail							
1E	5	Tail							

From the dropdown menu select the genetag for the sample

Figure 15: Selecting the genetag for each sample

Marking the Genetags for each sample with the letter 'X' for all samples where this Genetag applies, see Figure 16.



	A	C	D	E	F	G	H	I	J	K	L	M
1									Genetag 1	Genetag 2	Genetag 3	Genetag 4
2	ell Plate Position / Tube Nu	Sample Name	Tissue Type	Control	Barcode	Animal Number	Mouse Line	Comment	1021K	26	1021K	Please Select
3	1A	1	Tail			123	10PcnM-CS		X	X		
4	1B	2	Tail			124	10PcnM-CS				X	
5	1C	3	Tail			125	10PcnM-CS		X	X		
6	1D	4	Tail			126	10PcnM-CS		X			
7	1E	5	Tail			127	10PcnM-CS			X		

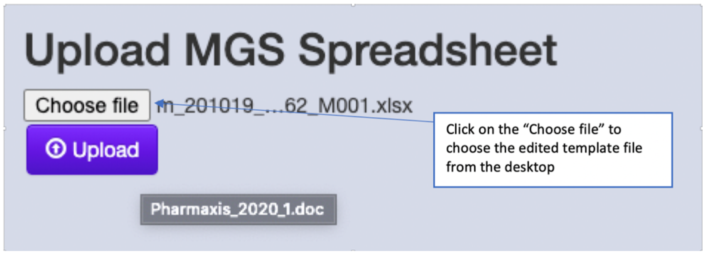
Using the letter X mark all samples for the selected genetag then save the template without changing the name

Figure 16: Marking samples with X to apply Genetags

Save the Manifest by clicking on the 'Save' button in the menu (without changing the name of the file).

Uploading the edited template file

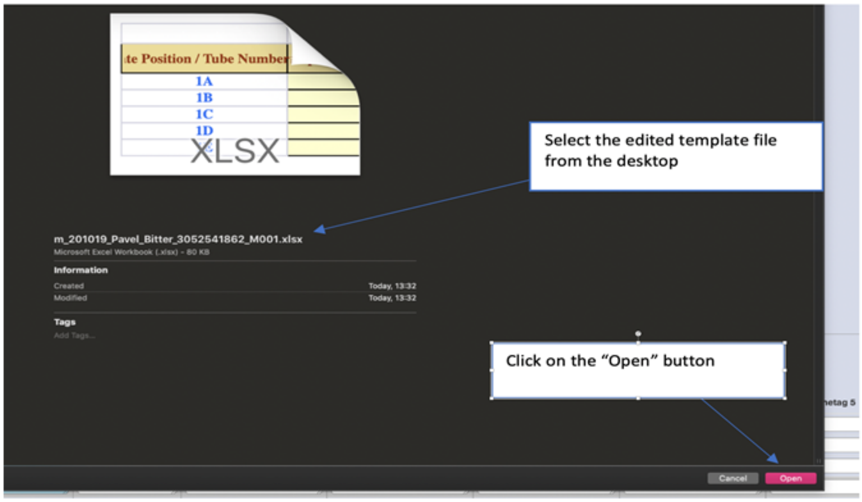
In the Portal use the button 'Choose file' to upload the edited template file, see Figure 17. There will be a popup window, see Figure 18, in which you confirm by clicking the button 'Open'.



Upload MGS Spreadsheet

Click on the "Choose file" to choose the edited template file from the desktop

Figure 17: Choose File button to upload edited template file



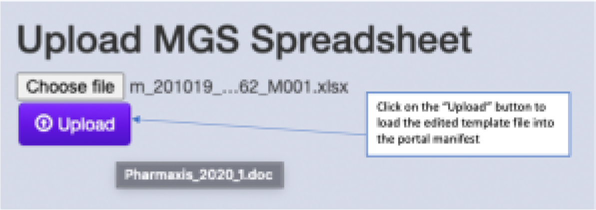
m_201019_Pavel_Bitter_3052541862_M001.xlsx
Microsoft Excel Workbook (.xlsx) - 80 KB
Information
Created Today, 13:32
Modified Today, 13:32

Select the edited template file from the desktop

Click on the "Open" button

Figure 18: Click on Open to upload the edited template file

Use the Upload button in the Portal to upload the edited template file, see Figure 19.



Click on the "Upload" button to load the edited template file into the portal manifest

Figure 19: Clicking on the button 'Upload' to upload the edited template file

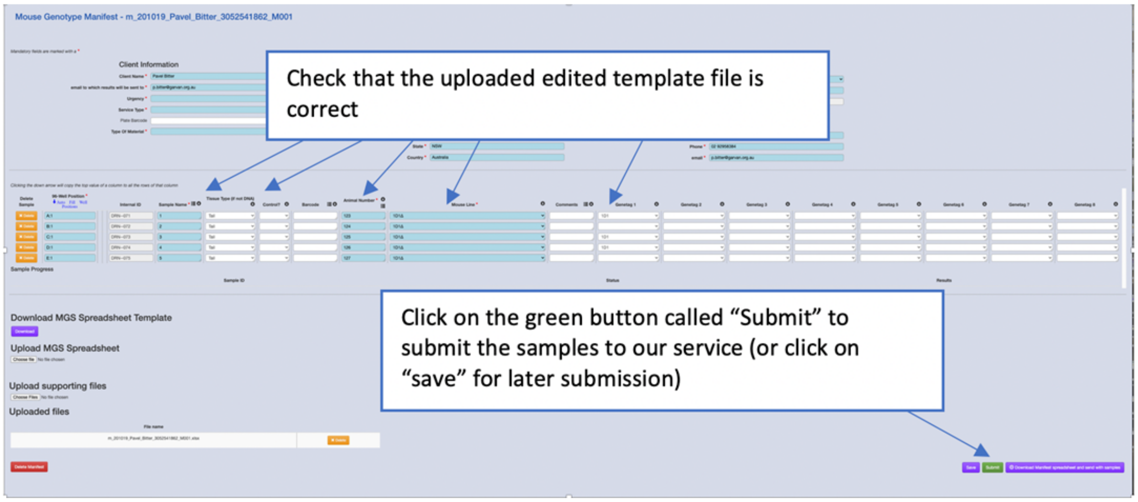
Confirm the upload by clicking on the button 'Close', see Figure 20.

File m_201019_Pavel_Bitter_3052541862_M001.xlsx uploaded.

In the confirmation window for the successful upload click on the button called "Close"

Figure 20: Confirm the upload by clicking on 'Close'

Check the correct upload and click on the button 'Save' for later submission or 'Submit' for immediate submission of these samples to our service, see Figur 21.

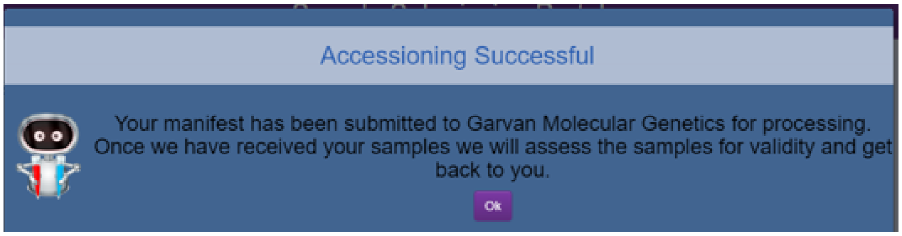


Check that the uploaded edited template file is correct

Click on the green button called "Submit" to submit the samples to our service (or click on "save" for later submission)

Figure 21: Submit samples by clicking on the button called 'Submit'

After submission the edited template file will be checked and if there are no errors it will be accepted, there will be a completed action confirmation popup window, see Figure 22. This window is closed by clicking on the button 'Ok'.



Your manifest has been submitted to Garvan Molecular Genetics for processing. Once we have received your samples we will assess the samples for validity and get back to you.

Figure 22: Popup window after submission

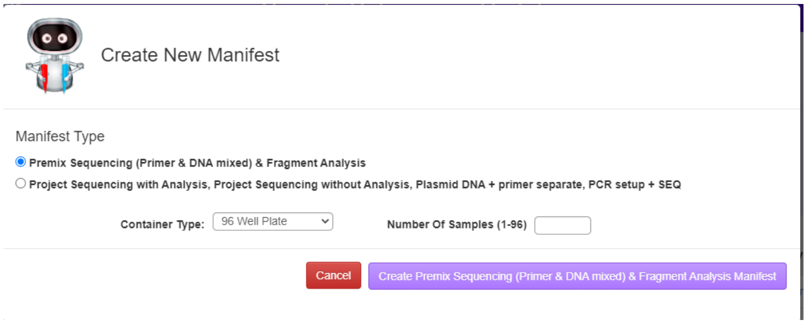
New Sequencing Manifest

By clicking on the button 'New Sequencing Manifest' a new manifest for the Sequencing and Fragment Analysis services is generated. There are 2 service modules you can choose from, see :

- Premix (Primer & DNA mixed) & Fragment Analysis

- Project Sequencing with Analysis, Project Sequencing without Analysis, Plasmid + primer separate, PCR setup + SEQ

By clicking on the buttons 'Premix (Primer & DNA mixed) & Fragment Analysis' or 'Project Sequencing with Analysis, Project Sequencing without Analysis, Plasmid + primer separate, PCR setup + SEQ' you can choose the module. In the field 'Number of Samples' the number of samples to be submitted can be entered. After selecting the module you need to click on the button 'Create'.



Create New Manifest

Manifest Type

● **Premix Sequencing (Primer & DNA mixed) & Fragment Analysis**

○ **Project Sequencing with Analysis, Project Sequencing without Analysis, Plasmid DNA + primer separate, PCR setup + SEQ**

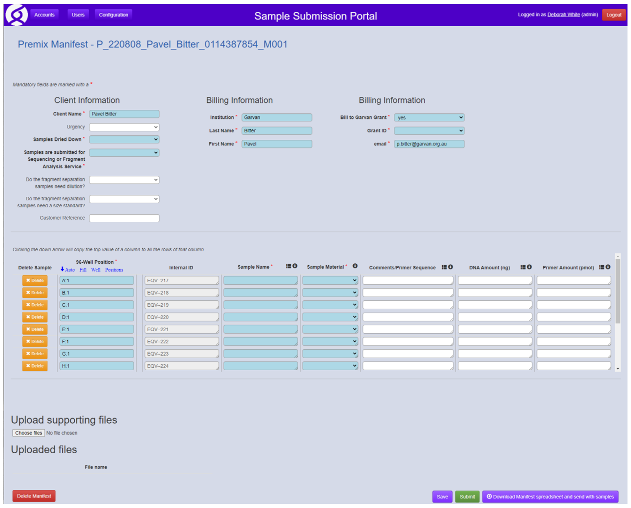
Container Type: 96 Well Plate

Number Of Samples (1-96)

Figure 23: Popup Window to select the module for creating the manifest

Premix SEQ & Fragment Analysis Module

After the module 'Premix (Primer & DNA mixed) & Fragment Analysis' has been selected and the create button was clicked a new window appears, see Figure 24



Premix Manifest - P_220808_Pavel_Bitter_0114387854_M001

*Mandatory fields are marked with a **

Client Information

Client Name *: Pavel Bitter

Urgency:

Samples Dried Down *:

Samples are submitted for Sequencing or Fragment Analysis Service *:

Do the fragment separation samples need dilution?:

Do the fragment separation samples need a size standard?:

Customer Reference:

Billing Information

Institution *: Garvan

Last Name *: Bitter

First Name *: Pavel

Billing Information

Bill to Garvan Grant *: yes

Grant ID *:

email *: p.bitter@garvan.org.au

Clicking the down arrow will copy the top value of a column to all the rows of that column

Delete Sample	96-Well Position *	Internal ID	Sample Name *	Sample Material *	Comments/Primer Sequence	DNA Amount (ng)	Primer Amount (pmol)
✖ Delete	A:1	EQV--217					
✖ Delete	B:1	EQV--218					
✖ Delete	C:1	EQV--219					
✖ Delete	D:1	EQV--220					
✖ Delete	E:1	EQV--221					
✖ Delete	F:1	EQV--222					
✖ Delete	G:1	EQV--223					
✖ Delete	H:1	EQV--224					

Upload supporting files

No file chosen

Uploaded files

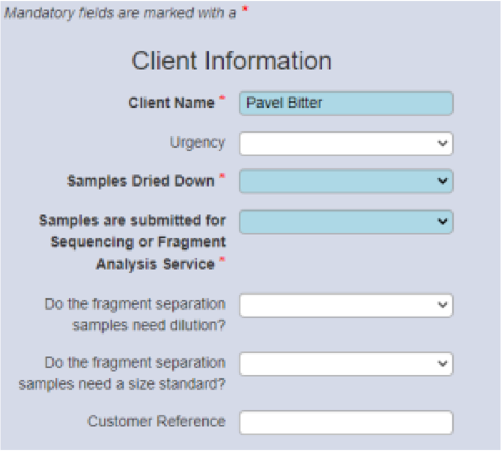
File name

Figure 24: Premix SEQ & Fragment Analysis manifest screen

The fields for Billing Information should be prefilled by the software, please check they are still current. The Purchase Order number for this submission MUST be entered in the field for Purchase Order.

Overall manifest settings

The Client Information field has the Name prefilled but certain fields need to be updated using drop down menus, see Figure 25. If you are sending urgent samples you can choose between 24h and 8h urgency levels in the drop down menu in the field 'Urgency'. The field 'Samples dried down' is a mandatory field and must be filled in by the client, the options are 'Yes' or 'No' from the drop down menu. The next field down is 'Samples are submitted Sequencing or Fragment Analysis Service' and is also mandatory, the options are either 'Sequencing Service' or 'Fragment Analysis Service'. The fields 'Do the fragment separation samples need dilution?' and 'Do the fragment separation samples need a size standard?' have the options 'Yes' or 'No' from the drop down menu. The field 'Customer Reference' you can enter any information you would like to associate with the manifest.


Mandatory fields are marked with a *

Client Information

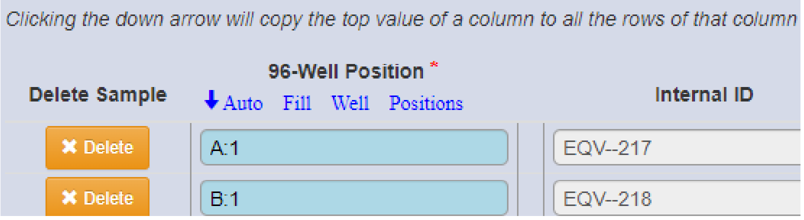
Client Name *	Pavel Bitter
Urgency	
Samples Dried Down *	
Samples are submitted for Sequencing or Fragment Analysis Service *	
Do the fragment separation samples need dilution?	
Do the fragment separation samples need a size standard?	
Customer Reference	

Figure 25: Premix SEQ & Fragment Analysis screen Client fields that need client input2

Filling in sample information

Sample positions

There are two options for entering the location of the sample in the submission, Strip of tubes or the 96x well plate. If a 96x well plate is used the blue arrow can be clicked and the software will automatically fill the location for the number of samples selected, see Filling in sample positions 1. If you have a different way of submitting samples (other than the autofill position) the autofill can be overwritten or sample locations can be entered manually in the format 'letter:number' for example A:1, A:2, A:3 etc or A:1, B:1, C:1 etc. All fields must be entered, meaning no sample can be without location information in the correct format.


Clicking the down arrow will copy the top value of a column to all the rows of that column

Delete Sample	96-Well Position * ↓Auto Fill Well Positions	Internal ID
✖ Delete	A:1	EQV--217
✖ Delete	B:1	EQV--218

Filling in sample positions 1:

If you have submitted your samples in strips the location of the samples in the strips can be entered in the second column called 'Strip Position'. Using the red 'Auto Fill' down button will prefill the fields for each sample. If you have a different way of submitting samples (other than the autofill position) the autofill can be overwritten or sample locations can be entered manually in the format 'SX:Y' where X = strip number and Y= sample number; for example S1: 1, S1:2, S1:3 etc or S2:1, S2:2, S2:3 etc. All fields must be entered, meaning no sample can be without location information in the correct format.

Sample names

Sample names are mandatory and can be entered in the fields under the heading called 'Sample Name'. The rules for sample names are that they must contain more than 1 letter or number and no special characters can be used like ,.::”+=@$%^&*()<>?! or hyphen. The only permitted character is an underscore (_). All samples need to have a name, names can be repetitive. Samples can also be copied and pasted from excel sheets by clicking on the little table button, see below, 'Table button', see Figure 26. A popup window will appear, see Figure 27, and sample names can be copied from any source file into this window. Clicking on the button 'Save will apply the sample names into the sample name fields of the software.

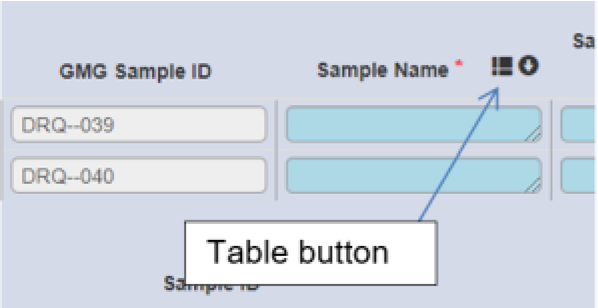

GMG Sample ID	Sample Name *
DRQ--039	
DRQ--040	

Figure 26: Filling in sample names

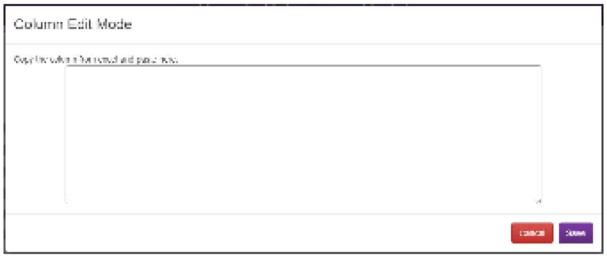


Figure 27: Sample name input via Excel copy and paste input

Sample material

Sample material is a mandatory field and is selected from the dropdown menu, the options are 'Plasmid', 'PCR product' and 'Other', see Figure 28

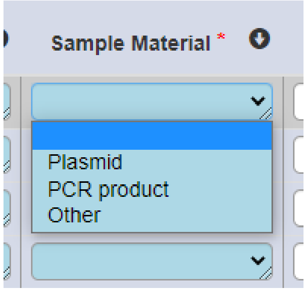


Figure 28: Filling in sample material

Optional fields

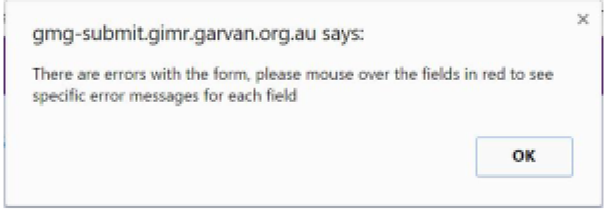
You can enter more information like 'Comments', 'Primer Sequence', 'DNA Amount' or 'Primer amount'. These fields are not mandatory and the information will be associated to the submitted sample.

Submitting the manifest

You can submit your manifest by clicking on the button 'Submit', see Figure 24 If there is no error in the manifest the submission will be confirmed by a popup window displayed in Figure 22 This window can be confirmed by clicking on the button 'Ok'.

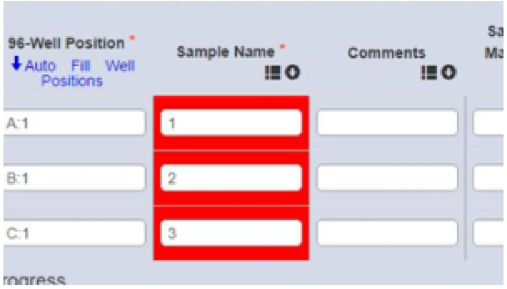
Error message when submitting

If there are errors in the manifest there will be a popup window as shown in Figure 29. After the button 'Ok' was clicked the popup window disappears and the Premix SEQ & Fragment Analysis screen shows the manifest with the fields in which the error occurred in red, see Figure 30. After correcting the errors you can click the button 'Submit' again.


gmg-submit.gimr.garvan.org.au says:

There are errors with the form, please mouse over the fields in red to see specific error messages for each field

Figure 29: Premix SEQ & Fragment Analysis screen error popup window

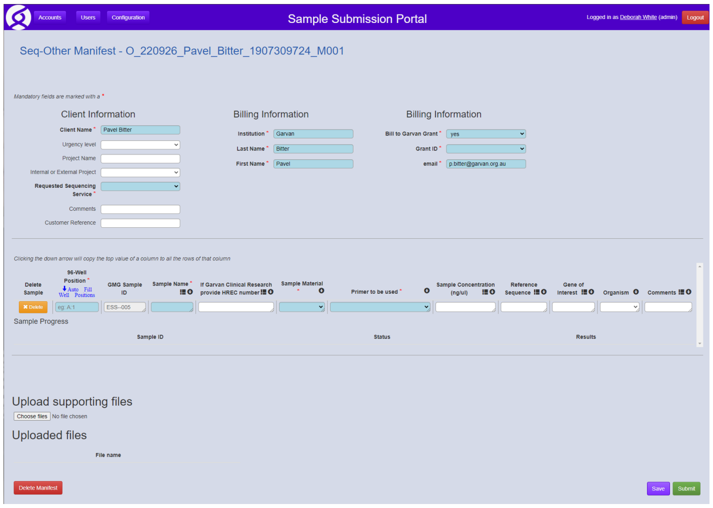


96-Well Position * ↓Auto Fill Well Positions	Sample Name *	Comments
A:1	1	
B:1	2	
C:1	3	

Figure 30: Premix SEQ & Fragment Analysis screen with errors highlighted red

Project Sequencing with Analysis, Project Sequencing without Analysis, Plasmid + primer separate, PCR setup + SEQ

After the module 'Project Sequencing with Analysis, Project Sequencing without Analysis, Plasmid + primer separate, PCR setup + SEQ' has been selected and the create button clicked a new window will appear, see Figure 31.



Seq-Other Manifest - O_220926_Pavel_Bitter_1907309724_M001

*Mandatory fields are marked with a **

Client Information

Client Name * Pavel Bitter
Urgency level
Project Name
Internal or External Project
Requested Sequencing Service *
Comments
Customer Reference

Billing Information

Institution * Garvan
Last Name * Bitter
First Name * Pavel

Billing Information

Bill to Garvan Grant * yes
Grant ID *
email * p.bitter@garvan.org.au

Clicking the down arrow will copy the top value of a column to all the rows of that column

Delete Sample	96-Well Position * ↓Auto Fill Well Positions	GMG Sample ID	Sample Name *	If Garvan Clinical Research provide HREC number	Sample Material *	Primer to be used *	Sample Concentration (ng/ul)	Reference Sequence	Gene of Interest	Organism	Comments
✖ Delete	eg: A:1	ESS--005									

Sample Progress

Sample ID	Status	Results

Upload supporting files

No file chosen

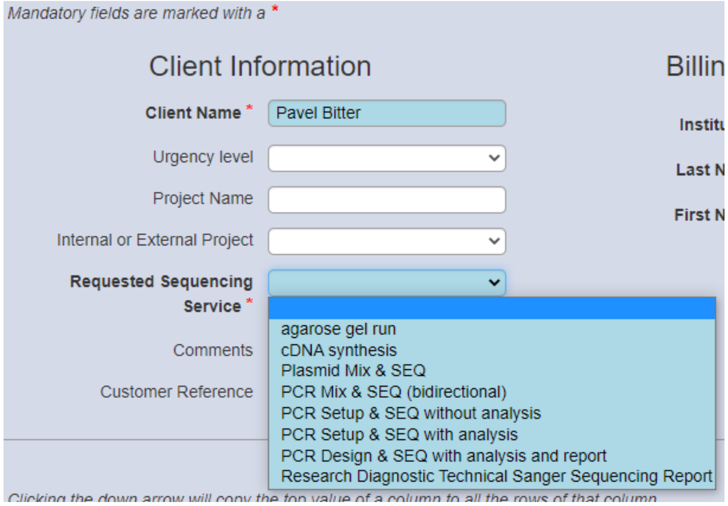
Uploaded files

File name

Figure 31: Project Sequencing with Analysis, Project Sequencing without Analysis, Plasmid + primer separate, PCR setup + SEQ sample submission screen

The fields for Billing Information should be prefilled by the software. Please fill in your Purchase Order for this manifest, this is crucial for our invoicing process.

Fill in the overall manifest selection fields by using the drop down menus, see Figure 32



*Mandatory fields are marked with a **

Client Information

Client Name * Pavel Bitter
Urgency level
Project Name
Internal or External Project
Requested Sequencing Service *
Comments
Customer Reference

agarose gel run
cDNA synthesis
Plasmid Mix & SEQ
PCR Mix & SEQ (bidirectional)
PCR Setup & SEQ without analysis
PCR Setup & SEQ with analysis
PCR Design & SEQ with analysis and report
Research Diagnostic Technical Sanger Sequencing Report

Clicking the down arrow will copy the top value of a column to all the rows of that column

Figure 32: Overall Manifest selections

If your samples are urgent you can choose between '8 working days - 2x price' or '4 working days - 4x price' urgency levels in the drop down menu in the field 'Urgency'. The field 'Project name' can be filled with a project or reference name of your choice. The next field down is 'Internal or External Project'. with the options 'internal' or 'external' which can be selected from the dropdown menu. The next field down 'Requested Sequencing Service' and is a mandatory field. The options are:

- agarose gel run
- cDNA synthesis
- Plasmid Mix & SEQ
- PCR Mix & SEQ (bidirectional)
- PCR Setup & SEQ without analysis
- PCR Setup & SEQ with analysis
- PCR Design & SEQ with analysis and report
- Research Diagnostic Technical Sanger Sequencing Report

One of these modules needs to be selected, please see our webpage at https://www.garvan.org.au/research/capabilities/molecular-genetics/shop for more information regarding prices and the service items included for each selection option. The next fields are 'Comments' and 'Customer Reference' you can enter comments that may be relevant for the project you are submitting and will be good to know for the operator and in regards to analysis or billing.

Filling in sample information

Sample positions

See Sample positions

Sample names

See Sample names

Sample material

Sample material is a mandatory field and is selected from the dropdown menu, the options are 'Blood', 'Cells', 'Buffy Coat', 'DNA', 'cDNA', 'Tissue', etc. The arrow down can be used to fill the entire column with the selected sample material of the first field, see Figure 33

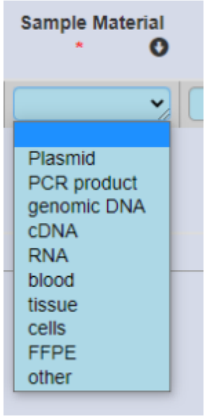


Figure 33: Sample material drop-down list

Primer to be used

You have to enter the primer that you want to be used with the submitted samples in the field 'Primer to be used'. This is a mandatory field. There are several options to choose from in the dropdown menu:

- to be ordered by GMG according to sequence given in Comments field
- submitted with sample
- to be designed by GMG from your submitted SEQ file
- 2_Primer_AOX_3'_Rev
- 3_Primer_3_AOX_5'_For
- 4_Primer_BGH_Reverse
- 5_Primer_CMV_For (-50)
- 6_Primer_CMV_Forward
- 1_Primer_M13_For (-47)
- 8_Primer_M13_For (-20)
- 7_Primer_M13_Rev (distant)

- 9_Primer_M13_Rev(17mer)
- 10_Primer_pA (-120)
- 11_Primer_pET_Rev
- 12_Primer_pGAP_For
- 13_Primer_pGL_RV_pr3
- 14_Primer_pGL_pr2_R
- 23_Primer_pGEX_For
- 24_Primer_pGEX_Rev
- 25_Primer_pET_3'
- 15_Primer_puc_U1
- 16_Primer_puc_U2
- 18_Primer_Primer_ori
- 17_Primer_Revers_A
- 19_Primer_SP6
- 20_Primer_T3_Promoter
- 21_Primer_T7
- 22_Primer_T7_Terminator

The black down arrow can be used to fill the entire column with the selected sample material of the first field.

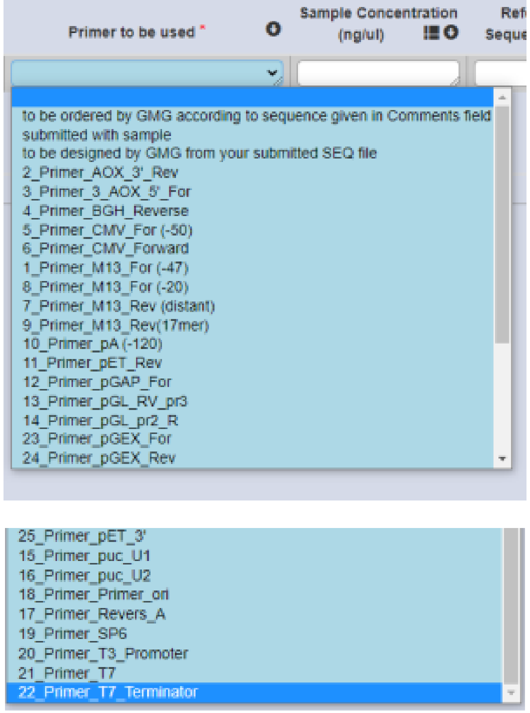


Figure 34: Primer to be used drop-down list

Optional fields

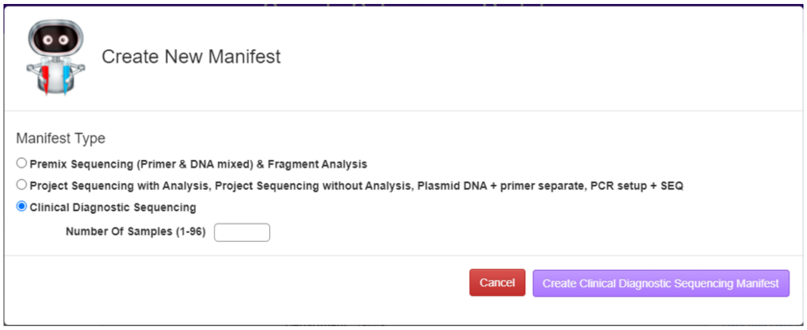
You can enter further information about your samples in the non-mandatory fields such as; 'If Clinical Research provide HREC number', 'Sample Concentration (ng/µL)', 'Reference Sequence', 'Gene of Interest', 'Organism' and 'Comments'. The down arrow can be used to fill the entire column with the information entered into the first box.

Submitting the manifest

See Submitting the manifest

Clinical Diagnostic Sequencing Service Module

For submission of Clinical Diagnostic samples you need to logon with two step authentication, please use the 'Login for clinical samples (requires further authentication)' option. You will need the google authenticator on your phone installed and enter the two step authentication code, see Two step authentication. In the popup screen select Clinical Diagnostic Sequencing, then click on 'Create Clinical Diagnostic Sequencing Manifest', see Figure 35



Create New Manifest

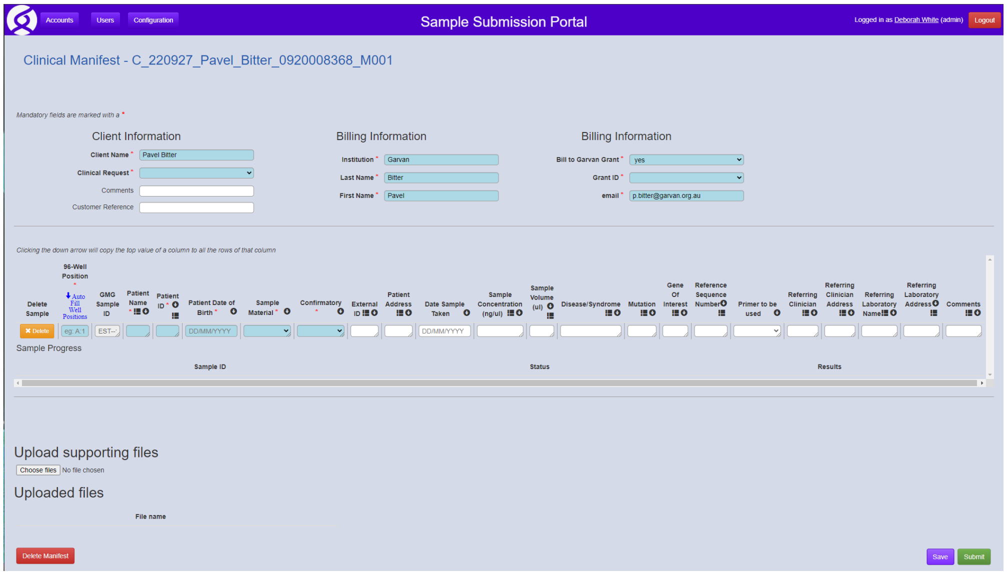
Manifest Type

○ Premix Sequencing (Primer & DNA mixed) & Fragment Analysis
○ Project Sequencing with Analysis, Project Sequencing without Analysis, Plasmid DNA + primer separate, PCR setup + SEQ
● Clinical Diagnostic Sequencing

Number Of Samples (1-96)

Figure 35: Create new manifest - Clinical Diagnostic Sequencing

After clicking 'Create' the new manifest window will open, see Figure 36



Clinical Manifest - C_220927_Pavel_Bitter_0920008368_M001

Mandatory fields are marked with a *

Client Information

Client Name * Pavel Bitter
Clinical Request *
Comments
Customer Reference

Billing Information

Institution * Garvan
Last Name * Bitter
First Name * Pavel

Billing Information

Bill to Garvan Grant * yes
Grant ID *
email * p.bitter@garvan.org.au

Clicking the down arrow will copy the top value of a column to all the rows of that column

Figure 36: New clinical sequencing manifest

The fields for Billing Information should be prefilled by the software. Please check and advise gmg@garvan.org.au if changes need to be made. Please enter the Purchase Order number for this sample submission, this is crucial for our invoicing process. In the field 'Clinical Request' select from the dropdown menu the option 'Clinical Diagnostic SEQ with Technical Report'.

Filling in sample information

Sample positions

See Sample positions

Patient name and Patient ID

You have to enter the name of the patient(s) in the field(s) under the heading called 'Patient Name'. You must enter the Patient ID of the samples they are sending in the field 'Patient ID'. These are mandatory fields. The rules for sample names are that they must contain more than 1 letter or number and no special characters can be used like ,.::"+=@$%^&*()<>?! or hyphen. The only permitted character is an underscore (_). All samples need to have a name, names can be repetitive. Samples can also be copied and pasted from excel sheets by clicking on the little table button, see below, 'Table button', see Figure 37.

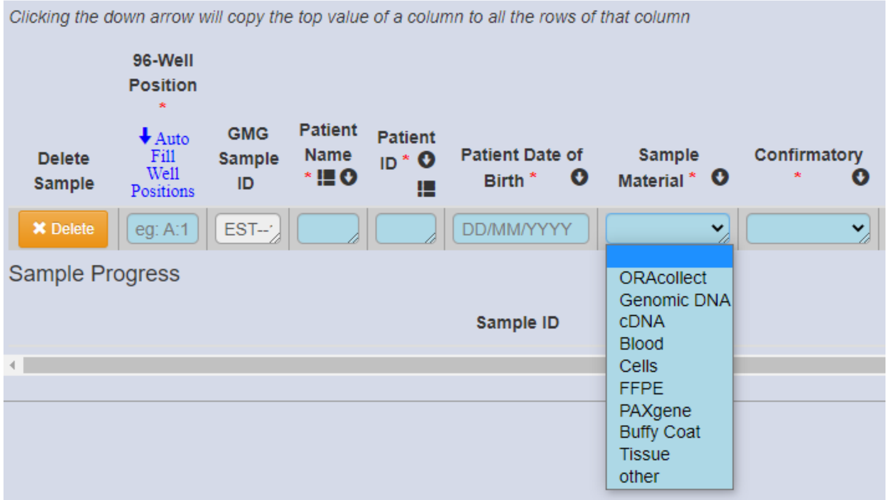

Clicking the down arrow will copy the top value of a column to all the rows of that column

Figure 37: Clinical sequencing manifest - mandatory fields

Patient date of birth

You have to enter the Date of Birth of the patient for the sample they are sending in the field 'Patient Date of Birth'. This is a mandatory field. The date of birth of the patient can either be entered by typing the date of birth in the field in the format DD/MM/YYYY, i.e. for a patient with a date of birth on the 2nd of August 2000 the correct entry would be '02/08/2000' or the entry can be done via a pop-down calendar, see Figure 37. Navigation in the calendar window occurs with the left and right arrows for selection of the month and year and by clicking on the number of the day for selection of the day.

Sample material

Clients have to enter the material of the samples they are sending in the field 'Sample Material'. This is a mandatory field. There are several options to choose from in the dropdown menu like 'Blood', 'Cells', 'Buffy Coat', 'cDNA', 'Tissue', etc. The down arrow can be used to fill the entire column with the selected sample material of the first field, see drop-down list in Figure 37.

Confirmatory

You have to confirm that the sample submission is for confirmatory testing not predictive testing. Therefore in the drop down menu for the field 'Confirmatory' there is only one selection, 'Yes'. This field is mandatory and you need to select this option to legally state that this is a confirmatory diagnostic submission. The down arrow can be used to fill the entire column with the selected sample material of the first field, see Figure 37.

Optional fields

You can enter further information about your samples in the non-mandatory fields such as; 'External ID', 'Patient Address', 'Date Sample Taken', 'Sample Concentration (ng/µL)', 'Sample Volume (µL)', 'Disease/Syndrome', 'Mutation', 'Gene of Interest', 'Reference Sequence Number', Primer to be used', 'Referring Clinician', 'Referring Laboratory Name', 'Referring Laboratory Address' and 'Comments'. The arrow down can be used to fill the entire column with the selected sample material of the first field, see Figure 38

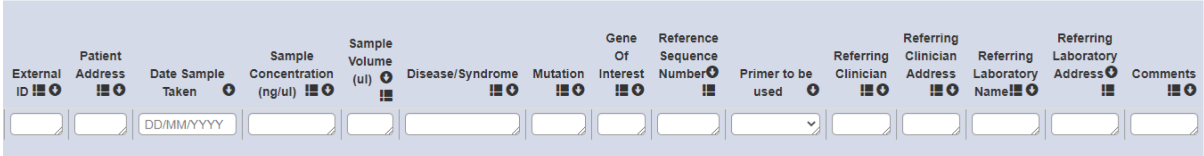


Figure 38: Clinical sequencing manifest - Non-mandatory fields

Submitting the manifest

See Submitting the manifest

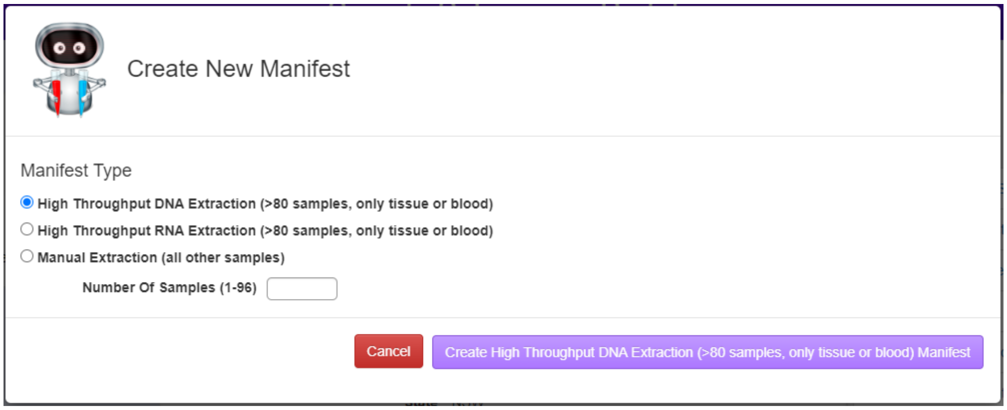
New Nucleic Acid Extraction Manifest

By clicking on the button 'New DNA/RNA Manifest' a new manifest for the Nucleic Acid Extraction Service is generated. There are 3 service modules the client can choose from:

- High Throughput DNA Extraction
- High Throughput RNA Extraction

- Manual Extraction

After clicking the button 'New DNA/RNA Manifest' a popup window will appear that looks like Figure 39



Create New Manifest

Manifest Type

● High Throughput DNA Extraction (>80 samples, only tissue or blood)
○ High Throughput RNA Extraction (>80 samples, only tissue or blood)
○ Manual Extraction (all other samples)

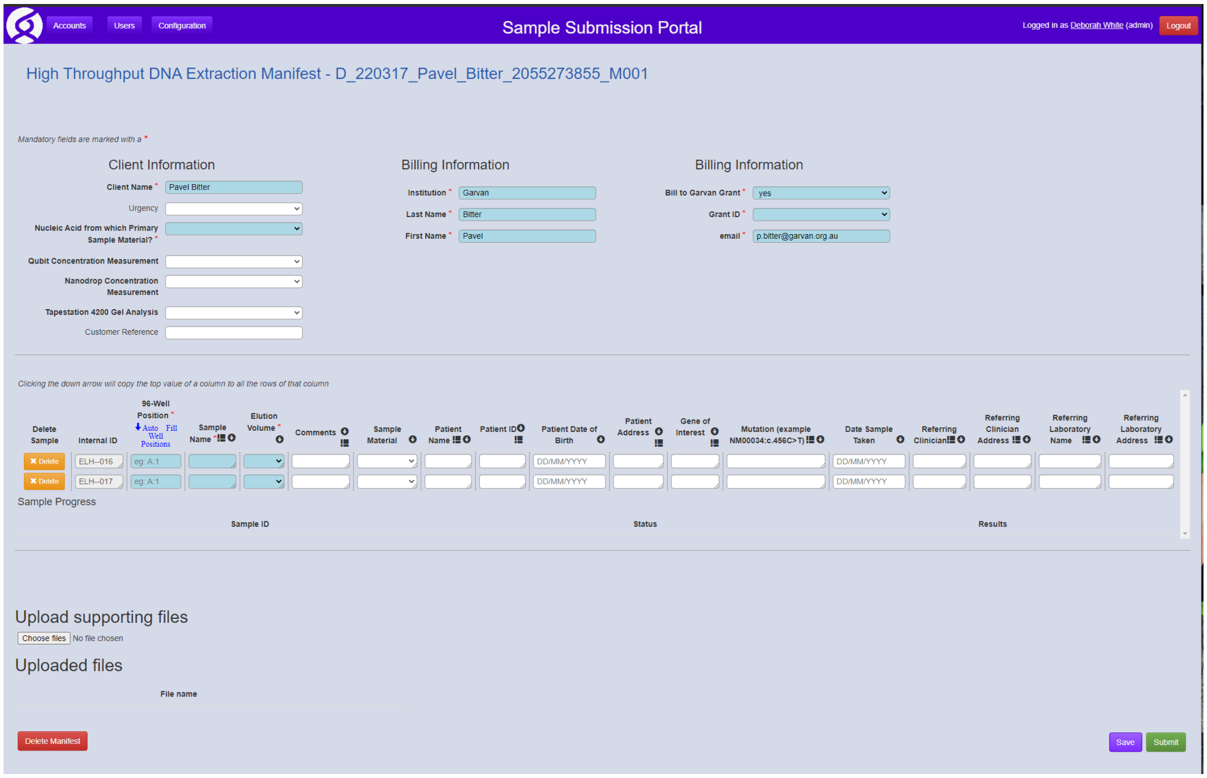
Number Of Samples (1-96)

Figure 39: Popup Window to select the module for creating a manifest

By clicking on the buttons called 'High Throughput DNA Extraction' or 'High Throughput RNA Extraction' or 'Manual Extraction' you can choose the module that is right for you. In the field 'Number of Samples' the number of samples to be submitted can be entered. After selecting the module you need to click on the button 'Create'.

High Throughput DNA Extraction Module

After the module 'High Throughput DNA Extraction' has been selected and the 'Create' button was clicked a new window appears, see Figure 40.



High Throughput DNA Extraction Manifest - D_220317_Pavel_Bitter_2055273855_M001

Mandatory fields are marked with a *

Client Information

Client Name *: Pavel Bitter
Urgency:
Nucleic Acid from which Primary Sample Material? *:
Qubit Concentration Measurement:
Nanodrop Concentration Measurement:
Tapestation 4200 Gel Analysis:
Customer Reference:

Billing Information

Institution *: Garvan
Last Name *: Bitter
First Name *: Pavel

Billing Information

Bill to Garvan Grant *: yes
Grant ID *:
email *: p.bitter@garvan.org.au

Clicking the down arrow will copy the top value of a column to all the rows of that column

Delete Sample	Internal ID	96-Well Position * ↓Auto Fill Well Positions	Sample Name *	Elution Volume *	Comments	Sample Material	Patient Name	Patient ID	Patient Date of Birth	Patient Address	Gene of Interest	Mutation (example NM00034:c.456C>T)	Date Sample Taken	Referring Clinician	Referring Clinician Address	Referring Laboratory Name	Referring Laboratory Address
✖ Delete	ELH--016	eg: A:1							DD/MM/YYYY				DD/MM/YYYY				
✖ Delete	ELH--017	eg: A:1							DD/MM/YYYY				DD/MM/YYYY				

Sample Progress

Sample ID	Status	Results

Upload supporting files

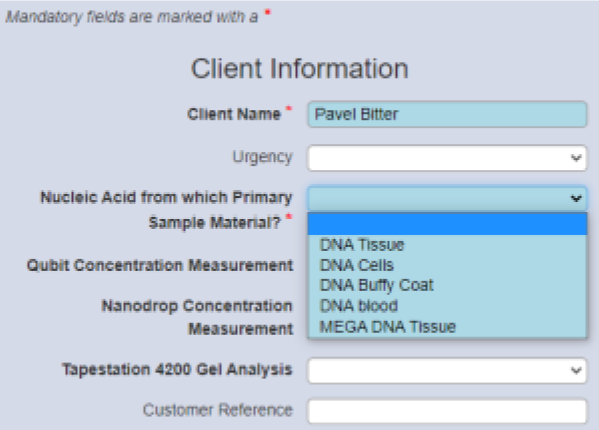
Choose files No file chosen

Uploaded files

File name

Figure 40: High Throughput DNA Extraction sample submission screen

The fields for Billing Information should be prefilled by the software. Please check and advise gmg@garvan.org.au if changes need to be made. Please enter the Purchase Order number for this sample submission, this is crucial for our invoicing process. The Client Information field has the name prefilled but certain fields need to be updated using drop down menus, see Figure 41. If your samples are urgent you can choose between 5days and 3days urgency levels in the drop down menu in the field 'Urgency'. The field 'Nucleic Acid from which Primary Sample Material' is a mandatory field. The options are 'DNA Tissue', 'DNA Cells', 'DNA Buffy Coat', 'DNA Blood' or 'MEGA DNA Tissue'. The next fields 'Qubit Concentration Measurement', 'Nanodrop Concentration Measurement' and 'Tapestation 4200 Gel Analysis' are not mandatory. The options are 'Yes' or 'No' from the drop down menus. The field 'Customer Reference' you can enter comments that may be relevant for the project you are submitting.



Mandatory fields are marked with a *

Client Information

Client Name * Pavel Bitter

Urgency

Nucleic Acid from which Primary Sample Material? *

- DNA Tissue
- DNA Cells
- DNA Buffy Coat
- DNA blood
- MEGA DNA Tissue

Qubit Concentration Measurement

Nanodrop Concentration Measurement

Tapestation 4200 Gel Analysis

Customer Reference

Figure 41: High Throughput DNA Extraction Client Information fields

Filling in sample information

Sample positions

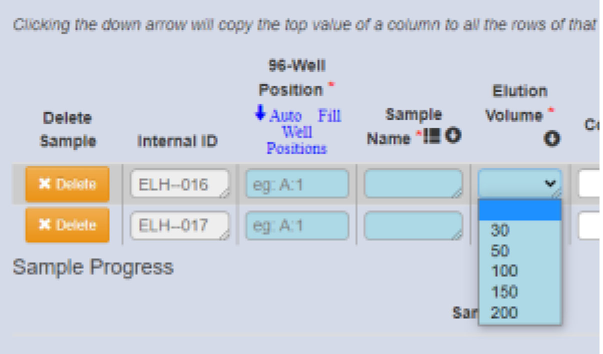
See Sample positions

Sample names

See Sample names

Elution volume

Select the 'Elution Volume' in µL that you would like for you samples from the drop-down list. The options are; 30, 50, 100, 150, 200, see Figure 42



Clicking the down arrow will copy the top value of a column to all the rows of that

Delete Sample	Internal ID	96-Well Position *	Sample Name *	Elution Volume *
✖ Delete	ELH–016	eg: A:1		
✖ Delete	ELH–017	eg: A:1		

- 30
- 50
- 100
- 150
- 200

Sample Progress

Figure 42: High Throughput DNA Extraction - mandatory fields

Optional fields

You can enter further information about your samples in the non-mandatory fields such as; 'Comments', 'Sample Material', 'Patient Name', 'Patient ID', 'Patient Date of Birth', 'Patient Address', 'Gene of Interest', 'Mutation (example NM000.4:c.456C>T)', 'Date Sample Taken', 'Referring Clinician', 'Referring Clinician Address', 'Referring Laboratory Name' and 'Referring Laboratory Address'. The arrow down can be used to fill the entire column with the selected sample material of the first field, see Figure 43.

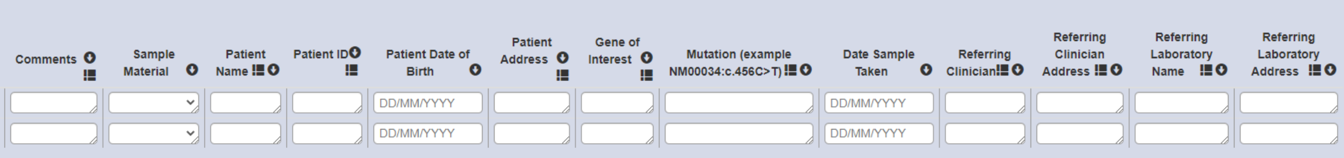


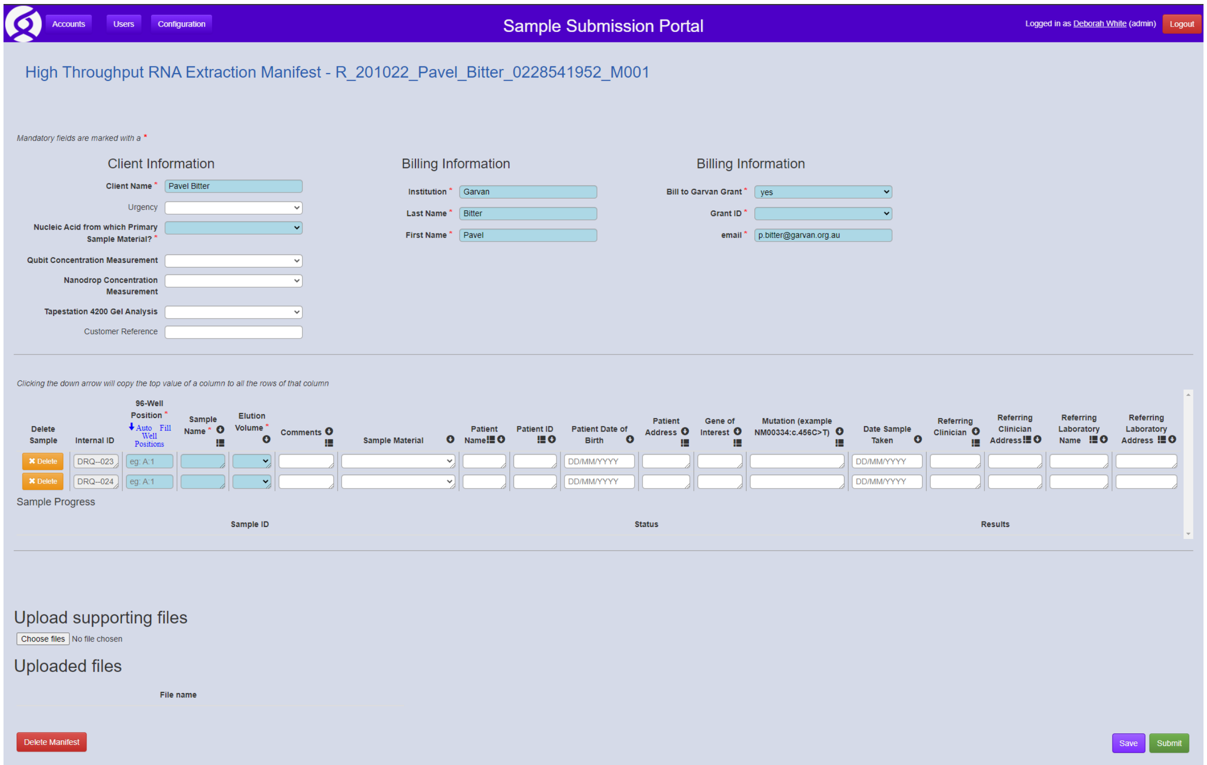
Figure 43: High throughput DNA manifest - Non-mandatory fields

Submitting the manifest

See Submitting the manifest

High Throughput RNA Extraction Module

After the module 'High Throughput RNA Extraction' has been selected and the 'Create' button clicked a new window appears, see Figure 44.



High Throughput RNA Extraction Manifest - R_201022_Pavel_Bitter_0228541952_M001

*Mandatory fields are marked with a **

Client Information

Client Name *: Pavel Bitter
Urgency:
Nucleic Acid from which Primary Sample Material? *:
Qubit Concentration Measurement:
Nanodrop Concentration Measurement:
Tapestation 4200 Gel Analysis:
Customer Reference:

Billing Information

Institution *: Garvan
Last Name *: Bitter
First Name *: Pavel

Billing Information

Bill to Garvan Grant *: yes
Grant ID *:
email *: p.bitter@garvan.org.au

Clicking the down arrow will copy the top value of a column to all the rows of that column

Delete Sample	Internal ID	96-Well Position * Auto Fill Well Positions	Sample Name *	Elution Volume *	Comments	Sample Material	Patient Name	Patient ID	Patient Date of Birth	Patient Address	Gene of Interest	Mutation (example NM00334:c.456C>T)	Date Sample Taken	Referring Clinician	Referring Clinician Address	Referring Laboratory Name	Referring Laboratory Address
✖ Delete	DRQ--023	eg: A:1							DD/MM/YYYY				DD/MM/YYYY				
✖ Delete	DRQ--024	eg: A:1							DD/MM/YYYY				DD/MM/YYYY				

Sample Progress

Sample ID	Status	Results

Upload supporting files

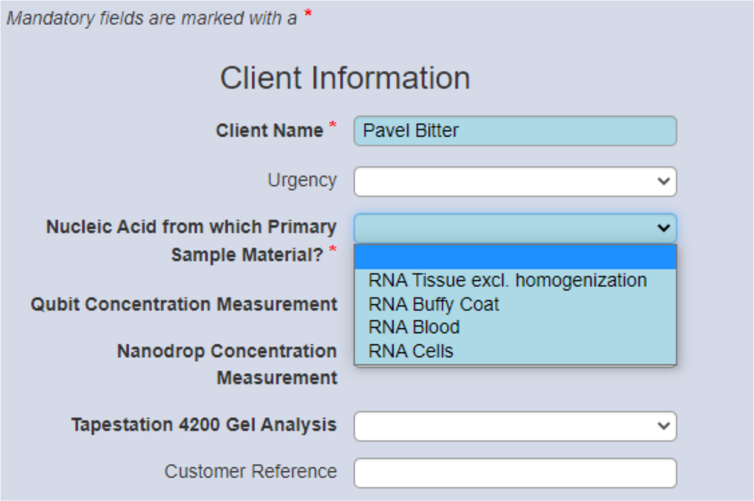
Choose files No file chosen

Uploaded files

File name

Figure 44: High Throughput RNA Extraction sample submission screen

The fields for Billing Information should be prefilled by the software. Please check and advise gmg@garvan.org.au if changes need to be made. Please enter the Purchase Order number for this sample submission, this is crucial for our invoicing process. The Client Information field has the name prefilled but certain fields need to be updated using drop down menus, see Figure 45. If your samples are urgent you can choose between 5days and 3days urgency levels in the drop down menu in the field 'Urgency'. The field 'Nucleic Acid from which Primary Sample Material' is a mandatory field. The options are 'RNA Tissue excl. homogenization', 'RNA Buffy Coat', 'RNA Blood' or 'RNA Cells'. The next fields 'Qubit Concentration Measurement', 'Nanodrop Concentration Measurement' and 'Tapestation 4200 Gel Analysis' are not mandatory. The options are 'Yes' or 'No' from the drop down menus. The field 'Customer Reference' you can enter comments that may be relevant for the project you are submitting.


*Mandatory fields are marked with a **

Client Information

Client Name * Pavel Bitter

Urgency

Nucleic Acid from which Primary Sample Material? *

Qubit Concentration Measurement

Nanodrop Concentration Measurement

Tapestation 4200 Gel Analysis

Customer Reference

Figure 45: High Throughput RNA Extraction Client Information fields

Filling in sample information

Sample positions

See Sample positions

Sample names

See Sample names

Elution Volume

See Elution volume

Optional fields

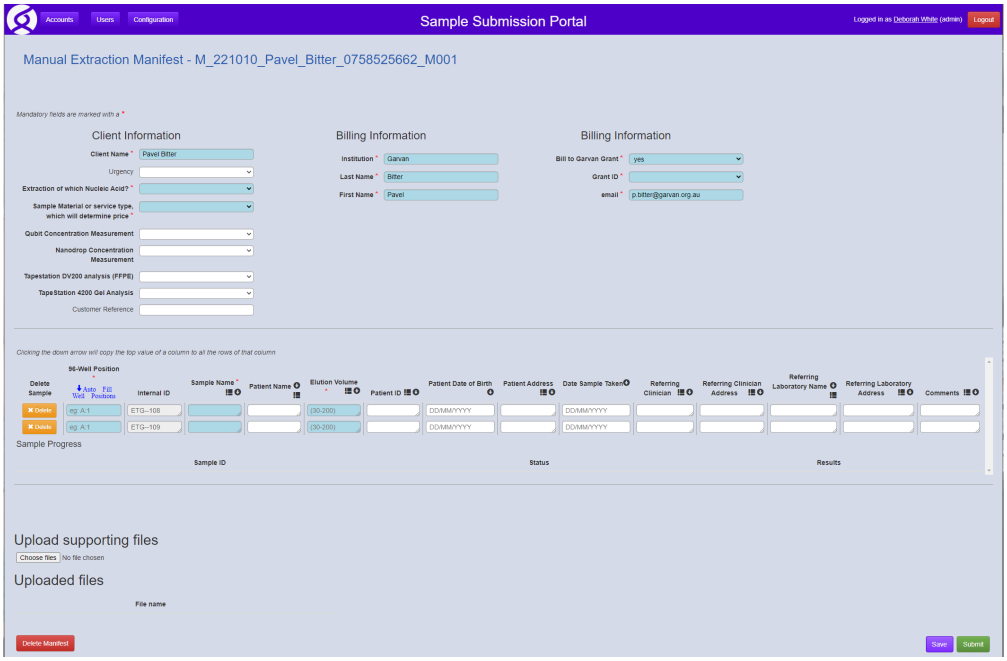
See Optional fields

Submitting the manifest

See Submitting the manifest

Manual Extraction Module

After the module 'Manual Extraction' has been selected and the 'Create' button clicked a new window appears, see Figure 46.



Manual Extraction Manifest - M_221010_Pavel_Bitter_0758525662_M001

Mandatory fields are marked with a *

Client Information

Client Name * Pavel Bitter
Urgency
Extraction of which Nucleic Acid? *
Sample Material or service type, which will determine price *
Qubit Concentration Measurement
Nanodrop Concentration Measurement
Tapestation DV200 analysis (FFPE)
TapeStation 4200 Gel Analysis
Customer Reference

Billing Information

Institution * Garvan
Last Name * Bitter
First Name * Pavel

Billing Information

Bill to Garvan Grant * yes
Grant ID *
email * p.bitter@garvan.org.au

Clicking the down arrow will copy the top value of a column to all the rows of that column

Delete Sample	96-Well Position * ↓Auto Well Fill Positions	Internal ID	Sample Name *	Patient Name	Elution Volume *	Patient ID	Patient Date of Birth	Patient Address	Date Sample Taken	Referring Clinician	Referring Clinician Address	Referring Laboratory Name	Referring Laboratory Address	Comments
✖ Delete	eg: A:1	ETG--108			(30-200)		DD/MM/YYYY		DD/MM/YYYY					
✖ Delete	eg: A:1	ETG--109			(30-200)		DD/MM/YYYY		DD/MM/YYYY					

Sample Progress

Sample ID	Status	Results

Upload supporting files

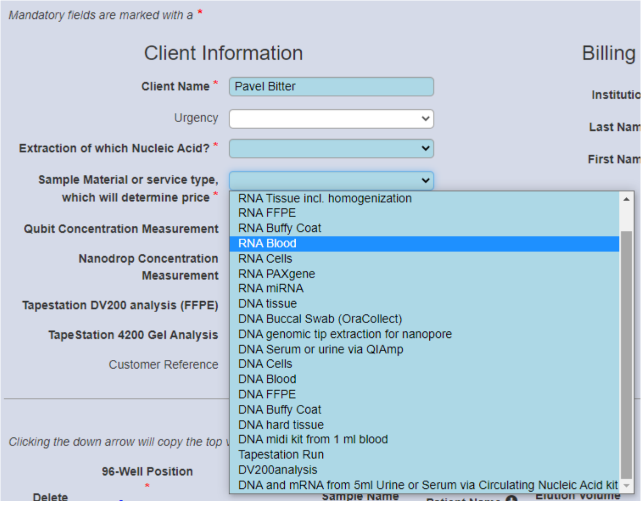
Choose files No file chosen

Uploaded files

File name

Figure 46: Manual Extraction sample submission screen

The fields for Billing Information should be prefilled by the software. Please check and advise gmg@garvan.org.au if changes need to be made. Please enter the Purchase Order number for this sample submission, this is crucial for our invoicing process. The Client Information field has the name prefilled but certain fields need to be updated using drop down menus, see Figure 47. If your samples are urgent you can choose between 48h and 24h urgency levels in the drop down menu in the field 'Urgency'. The field 'Extraction of which Nucleic Acid?' is a mandatory field, the options are 'DNA' or 'RNA'. The field 'Sample Material or service type, which will determine price' is a mandatory field. The options are 'RNA Tissue excl. homogenization', 'RNA Tissue incl. homogenization', 'RNA FFPE', 'RNA Buffy Coat', 'RNA Blood', 'RNA Cells', 'RNA PAXgene', 'RNA miRNA', 'DNA tissue', 'DNA Buccal Swab (OraCollect)', 'DNA genomic tip extraction for nanopore', 'DNA serum or urine via QIAmp', 'DNA Cells', 'DNA Blood', 'DNA FFPE', 'DNA Buffy Coat', 'DNA hard tissue', 'DNA midi kit from 1 ml blood', 'Tapestation Run', 'DV200analysis' or 'DNA and mRNA from 5ml Urine or Serum via Circulating Nucleic Acid kit'. The next fields 'Qubit Concentration Measurement', 'Nanodrop Concentration Measurement', 'Tapestation DV200 analysis (FFPE)' and 'Tapestation 4200 Gel Analysis' are not mandatory. The options are 'Yes' or 'No' from the drop down menus. The field 'Customer Reference' you can enter comments that may be relevant for the project you are submitting.


Mandatory fields are marked with a *

Client Information

Client Name * Pavel Bitter
Urgency
Extraction of which Nucleic Acid? *
Sample Material or service type, which will determine price *
Qubit Concentration Measurement
Nanodrop Concentration Measurement
Tapestation DV200 analysis (FFPE)
TapeStation 4200 Gel Analysis
Customer Reference

Figure 47: Manual Extraction Client Information fields

Filling in sample information

Sample positions

See Sample positions

Sample names

See Sample names

Elution Volume

See Elution volume

Optional fields

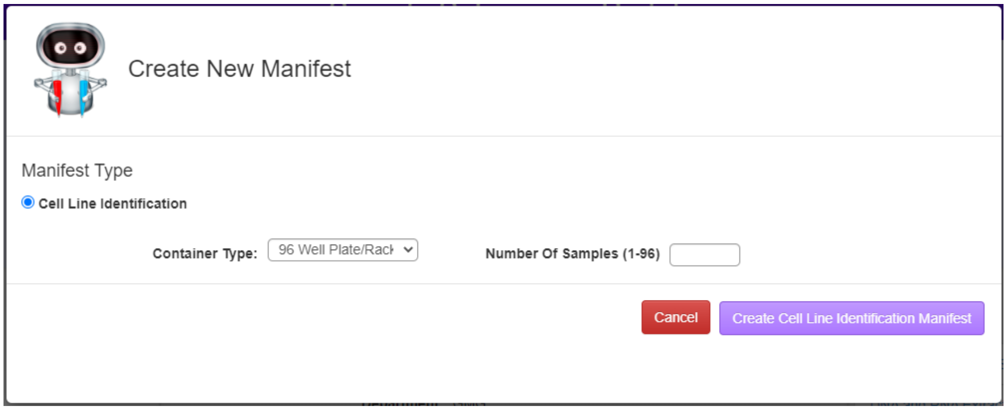
See Optional fields

Submitting the manifest

See Submitting the manifest

New Cell Line Identification Manifest

By clicking on the button 'New Cell Line Identification Manifest' a new manifest for the Cell Line Identification Service is generated. A popup window will appear that looks like Figure 48.



Create New Manifest

Manifest Type

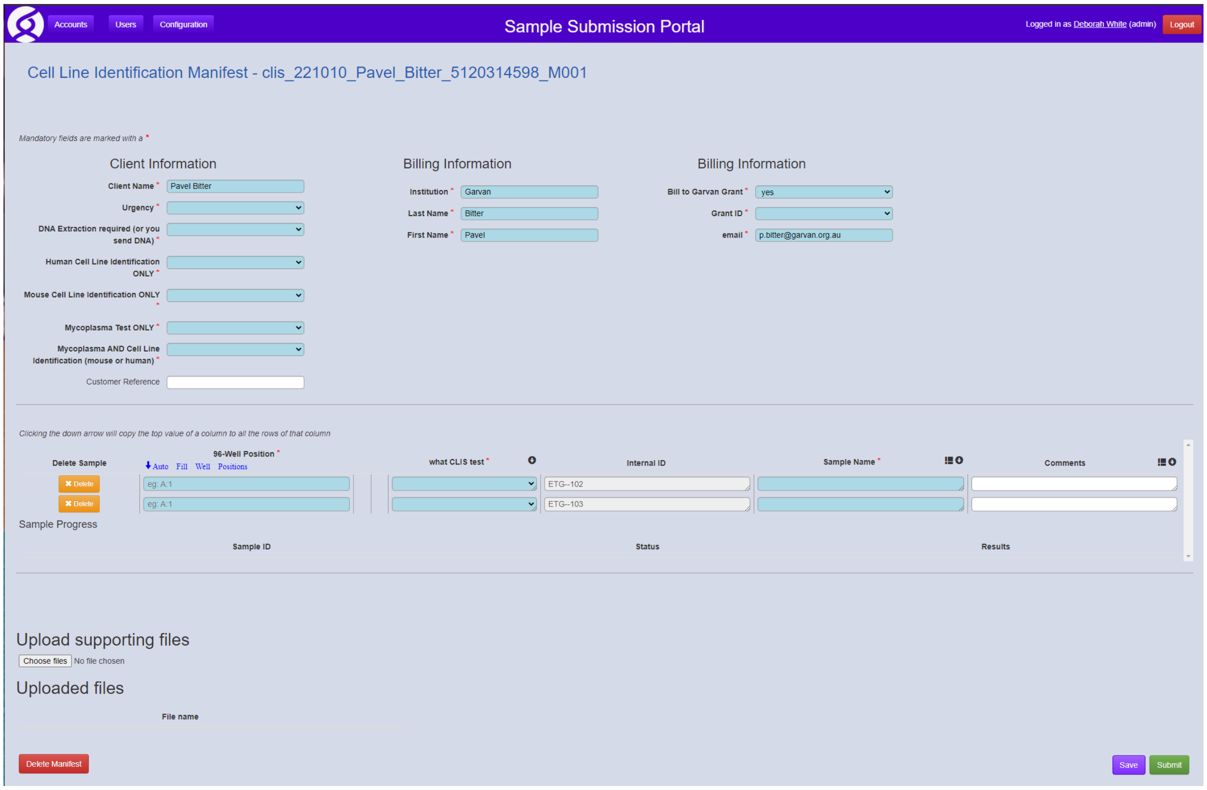
● Cell Line Identification

Container Type: 96 Well Plate/Rack

Number Of Samples (1-96)

Figure 48: Popup Window to select the module for creating a manifest

In the field 'Container Type' choose from the option of 96 well plate (for submitting more than 50 samples) or Single Tubes (for submitting less than 50 samples). In the field 'Number of Samples' the number of samples to be submitted can be entered. Click on the button 'Create' and the manifest screen will open, see Figure 49



Sample Submission Portal

Logged in as Deborah White (admin)

Cell Line Identification Manifest - clis_221010_Pavel_Bitter_5120314598_M001

Mandatory fields are marked with a *

Client Information

Client Name *: Pavel Bitter
Urgency *:
DNA Extraction required (or you send DNA) *:
Human Cell Line Identification ONLY *:
Mouse Cell Line Identification ONLY *:
Mycoplasma Test ONLY *:
Mycoplasma AND Cell Line Identification (mouse or human) *:
Customer Reference:

Billing Information

Institution *: Garvan
Last Name *: Bitter
First Name *: Pavel

Billing Information

Bill to Garvan Grant *: yes
Grant ID *:
email *: p.bitter@garvan.org.au

Clicking the down arrow will copy the top value of a column to all the rows of that column

Delete Sample	96-Well Position * Auto Fill Well Positions	what CLIS test *	Internal ID	Sample Name *	Comments
Delete	eg: A:1		ETG--102		
Delete	eg: A:1		ETG--103		

Sample Progress

Sample ID	Status	Results

Upload supporting files

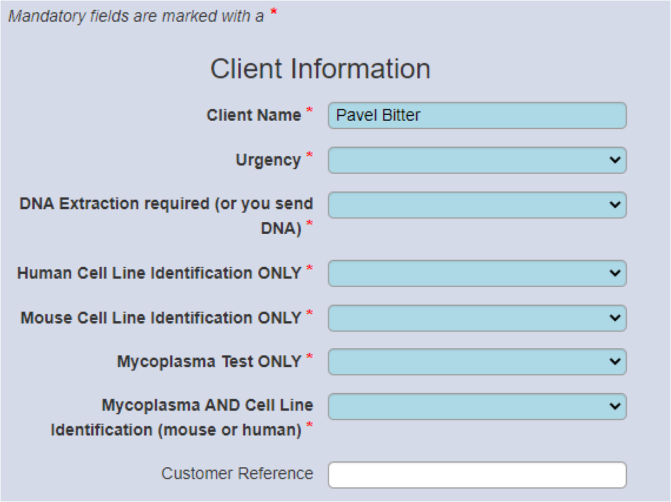
Choose files No file chosen

Uploaded files

File name

Figure 49: New Cell Line Identification manifest

The fields for Billing Information should be prefilled by the software. Please check and advise gmg@garvan.org.au if changes need to be made. Please enter the Purchase Order number for this sample submission, this is crucial for our invoicing process. The Client Information field has the name prefilled but certain fields need to be updated using drop down menus, see Figure 50. If your samples are urgent in the 'Urgency' drop-down menu choose to prioritise these samples (Attention: 2x service fees apply). The fields 'DNA Extraction required (or you send DNA)', 'Human Cell Line Identification ONLY', 'Mouse Cell Line Identification ONLY', 'Mycoplasma Test ONLY', or 'Mycoplasma AND Cell Line Identification (human or mouse)' the options are 'Yes' or 'No' from the drop down menus. The field 'Customer Reference' you can enter comments that may be relevant for the project you are submitting.



Mandatory fields are marked with a *

Client Information

Client Name *: Pavel Bitter
Urgency *:
DNA Extraction required (or you send DNA) *:
Human Cell Line Identification ONLY *:
Mouse Cell Line Identification ONLY *:
Mycoplasma Test ONLY *:
Mycoplasma AND Cell Line Identification (mouse or human) *:
Customer Reference:

Figure 50: Overall Manifest selection options

Filling in sample information

Sample positions

See Sample positions

Sample names

See Sample names

What CLIS test

Select from the drop-down menu which type of test is to be preformed, the options are 'human CLIS' or 'mouse CLIS'

Optional fields

You can enter further information about your samples in the non-mandatory field 'Comments', '

Submitting the manifest

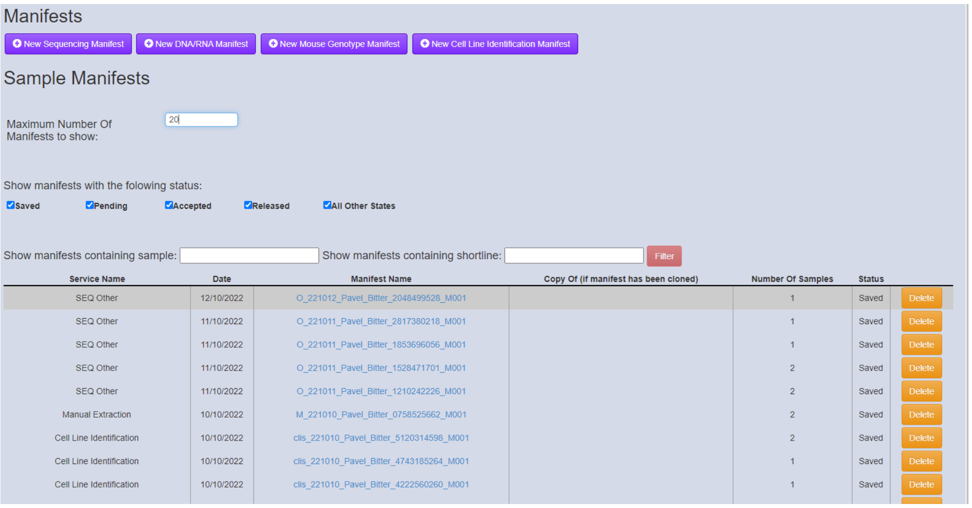
See Submitting the manifest

Manifest management

You can view the status of your submitted sample manifests on the 'Home' screen. Sample Manifests are shown in the lower half of the screen as either 'Saved', 'Pending', 'Accepted' or 'Released'.

Saved and Pending manifests

Saved Manifests have been saved but not submitted, see Figure 51 for an example. These manifests can be reopened by clicking on the manifest and then you can continue completing the manifest and either save for a later submission or submit for these manifests to become a status 'Pending' manifest. As soon as the saved manifest is submitted it appears in GMG’s sample management software. Saved and Pending manifests can be deleted with the button 'Delete'. If you choose to click on the delete button a popup window will appear, see Figure 52 In the popup window the action of deleting a manifest can be either confirmed by clicking the button 'Delete' or cancelled by clicking the button 'Cancel'. After clicking either one of these two options the popup window will disappear.



Manifests

Sample Manifests

Maximum Number Of Manifests to show: 20

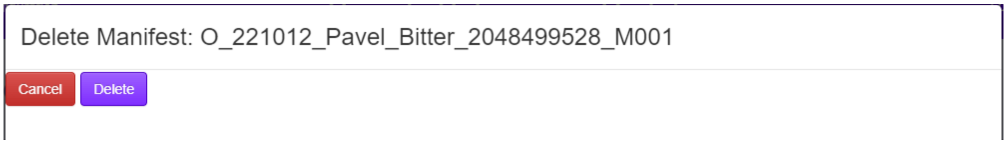
Show manifests with the folowing status:

☑Saved ☑Pending ☑Accepted ☑Released ☑All Other States

Show manifests containing sample: Show manifests containing shortline:

Service Name	Date	Manifest Name	Copy Of (if manifest has been cloned)	Number Of Samples	Status	
SEQ Other	12/10/2022	O_221012_Pavel_Bitter_2048499528_M001		1	Saved	Delete
SEQ Other	11/10/2022	O_221011_Pavel_Bitter_2817380218_M001		1	Saved	Delete
SEQ Other	11/10/2022	O_221011_Pavel_Bitter_1853696056_M001		1	Saved	Delete
SEQ Other	11/10/2022	O_221011_Pavel_Bitter_1528471701_M001		2	Saved	Delete
SEQ Other	11/10/2022	O_221011_Pavel_Bitter_1210242226_M001		2	Saved	Delete
Manual Extraction	10/10/2022	M_221010_Pavel_Bitter_0758525662_M001		2	Saved	Delete
Cell Line Identification	10/10/2022	clis_221010_Pavel_Bitter_5120314598_M001		2	Saved	Delete
Cell Line Identification	10/10/2022	clis_221010_Pavel_Bitter_4743185264_M001		1	Saved	Delete
Cell Line Identification	10/10/2022	clis_221010_Pavel_Bitter_4222560260_M001		1	Saved	Delete

Figure 51: Sample Submission Portal Home Screen

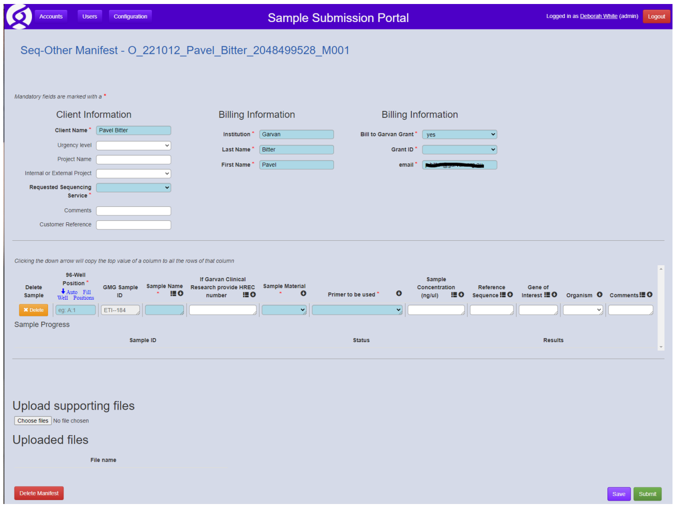


Delete Manifest: O_221012_Pavel_Bitter_2048499528_M001

Figure 52: Delete Popup Window

Accepted and Released manifests

Accepted, Released and Other State Manifests can only be viewed, these manifests are completed and cannot be altered after their completion. If the manifest link is clicked on the manifest will open and show its content, see figure 25 for an example.



Seq-Other Manifest - O_221012_Pavel_Bitter_2048499528_M001

*Mandatory fields are marked with a **

Client Information

Client Name *: Pavel Bitter
Urgency level:
Project Name:
Internal or External Project:
Requested Sequencing Service *:
Comments:
Customer Reference:

Billing Information

Institution *: Garvan
Last Name *: Bitter
First Name *: Pavel

Billing Information

Bill to Garvan Grant *: yes
Grant ID *:
email *: [redacted]

Clicking the down arrow will copy the top value of a column to all the rows of that column

Delete Sample	96-Well Position * Auto Well Fill Positions	GMG Sample ID	Sample Name *	If Garvan Clinical Research provide HREC number	Sample Material *	Primer to be used *	Sample Concentration (ng/ul)	Reference Sequence	Gene of Interest	Organism	Comments
✖ Delete	eg: A:1	ETI--184									

Sample Progress

Sample ID	Status	Results

Upload supporting files

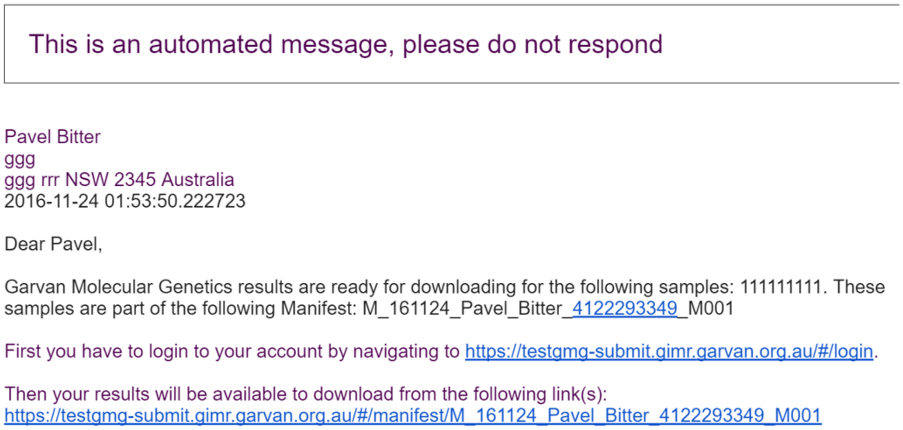
Uploaded files

File name

Figure 53: Example Manifest that was opened after a release status update

Download of results for submitted samples

Once manifests have been progressed in MSSS to the status of 'Released' the software will send an automatic email to your nominated email address defined in your account, see Figure 54 for an example email. In this email there is a link that enables you to download the results for the submitted samples as a ZIP file. You have to login into your account first and THEN you can download the data via the link in the email. If you click the link directly without logging in first the software will take you to the login screen. The email also contains the technical report according to NATA requirements as an attachment.



This is an automated message, please do not respond

Pavel Bitter
ggg
ggg rrr NSW 2345 Australia
2016-11-24 01:53:50.222723

Dear Pavel,

Garvan Molecular Genetics results are ready for downloading for the following samples: 111111111. These samples are part of the following Manifest: M_161124_Pavel_Bitter_4122293349_M001

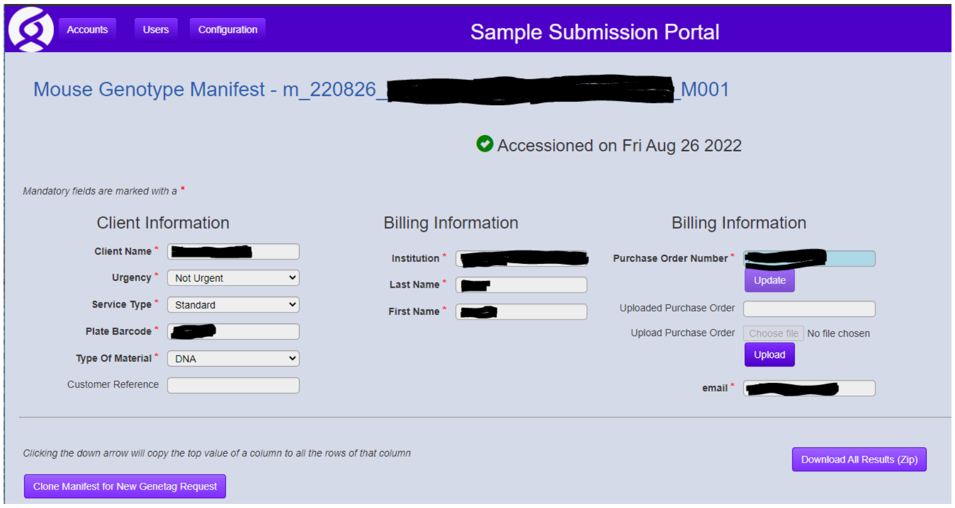
First you have to login to your account by navigating to https://testgmg-submit.gimr.garvan.org.au/#/login.

Then your results will be available to download from the following link(s):
https://testgmg-submit.gimr.garvan.org.au/#/manifest/M_161124_Pavel_Bitter_4122293349_M001

Figure 54: Automatic email for released manifests

Downloading results directly from MSSS

Sample manifests are shown in the Home screen of the sample submission portal as 'Released' you can click on the manifest link to access the manifest to download the results. When the manifest is opened the screen shows the information for the results and also contains a button 'Download All Results (zip)', see Figure 55.



Mouse Genotype Manifest - m_220826_[redacted]_M001

Accessioned on Fri Aug 26 2022

*Mandatory fields are marked with a **

Client Information

Client Name *: [redacted]
Urgency *: Not Urgent
Service Type *: Standard
Plate Barcode *: [redacted]
Type Of Material *: DNA
Customer Reference:

Billing Information

Institution *: [redacted]
Last Name *: [redacted]
First Name *: [redacted]

Billing Information

Purchase Order Number *: [redacted]
Uploaded Purchase Order:
Upload Purchase Order: No file chosen
email *: [redacted]

Clicking the down arrow will copy the top value of a column to all the rows of that column

Figure 55: Manifest screen with button 'Download All Results (zip)'

If this button is clicked the software will create a ZIP folder in your download folder on the C: drive of your computer, in this ZIP folder are the actual result files. These results will also be sent to your nominated email addresses that are stored in our database. Please email gmg@garvan.org.au for a change in email addresses to which result emails shall be sent to. Also email gmg@garvan.org.au for changes in the billing information.

Sending Samples to GMG

Please use the below address to send samples to us. The samples should be sent in a padded envelope with Australia Mail or by courier:

For Australia Mail

Attn. Pavel Bitter

Garvan Institute

GMG/ Level 8

384 Victoria Street

Darlinghurst, NSW 2010

For Couriers

Attn. Pavel Bitter

Garvan Institute

Loading Dock

West Street (off Burton Street)

Darlinghurst, NSW 2010

Dock times: 8am to 4pm

Loading Dock Phone: 02 9295 8640

Alternatively you can drop off your samples in our sample reception fridge located on level 8 behind the lifts.

Contact us

We have an all encompassing webpage, please have a look at:

https://www.garvan.org.au/research/capabilities/molecular-genetics

Garvan Molecular Genetics

Telephone: 02 92958384

Email: gmg@garvan.org.au

Pavel Bitter (Molecular Genetics Facility Manager)

Email: p.bitter@garvan.org.au

Pricing information

Please find our current pricing information on our webpage at https://www.garvan.org.au/research/capabilities/molecular-genetics/shop

Garvan Molecular Genetics Terms and Conditions

Our Terms and Conditions apply to all services provided by GMG, a service of the Garvan Institute of Medical Research, on request from Specialists or Researchers. The obligation of GMG to perform the Services is conditional on acceptance of a Request and the samples which need to pass acceptance to the service. On acceptance of the Request, GMG will perform the Services in accordance with our Terms and Conditions.