

---

## Guide on Bio Basic Asia Pacific Customer Portal

---

1. Log in to <https://customerportal.biobasic-asia.com/>
2. For first time user, please click on 'Register' on the top right corner of the webpage.



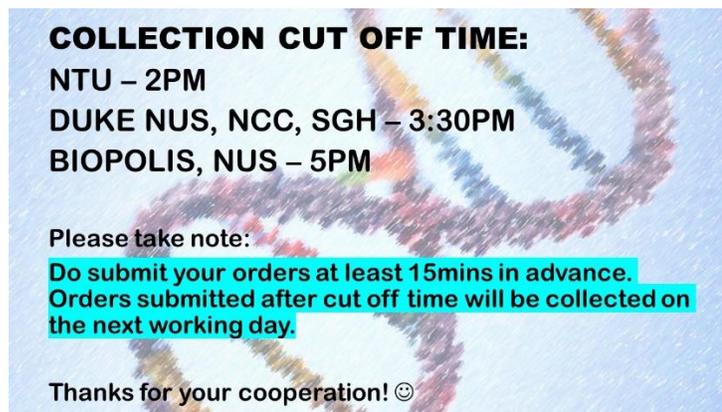
3. Provide us with the email address you would like to register with a password.
  - If errors occur upon registration, e.g. it shows that your email has been taken, please approach us via [sg-sequencing@biobasic-asia.com](mailto:sg-sequencing@biobasic-asia.com) or +65 6928 9042.

4. You may click on "Forgot your password" to reset your password if you have already



registered but forgotten your password.

5. Please kindly take note of the sample collection hours.

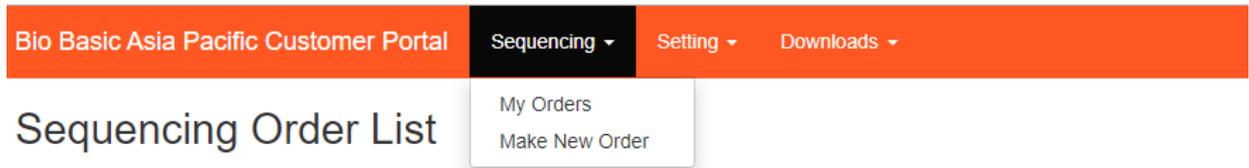


\*2pm cut off hour is for NTU main campus.

For other locations, we will arrange the collection specially.

## Order Submission

1. Proceed to the **'Sequencing'** tab & **Make New Order**.



2. Next, input a short description of your samples and the billing package to use.

### Create Sequencing Order

A screenshot of the 'Create Sequencing Order' form. The form has a progress bar at the top with four steps: 'Essentials' (active), 'Samples', 'Your Contact', and 'Summary'. The main content area contains the following text and form elements:

This order will be under your account **admin@biobasic.com**

Provide a short title for today's samples?

This helps you differentiate orders. e.g., *Results for experiment AX01*

Which billing package to use?

Loaded from last order. If this is the first time, please contact our sales to confirm

Previous Next

- If you are unsure about your package ID, please contact our sales representative or drop us an email at [sg-sequencing@biobasic-asia.com](mailto:sg-sequencing@biobasic-asia.com)
3. Next, sequencing sample details can be uploaded either using **Excel File** or **Manual Input**

**For MANUAL INPUT,**

1. Fill up the mandatory fields as per stated. More details of the sample via the optional fields is highly recommended.

Manual Input ×

---

**Mandatory fields:**

Process Method	DNA Type	Sample Type	Primer
<input type="text" value="Standard"/>	<input type="text" value="PCR"/>	<input type="text" value="Water"/>	<input type="text" value="Custom"/>

**Optional fields:**

Total Size(bp)	Template Conc(ng/ul)	Template Amount(μl)
<input type="text"/>	<input type="text"/>	<input type="text"/>
Primer Conc (μM)	Primer Amount (μl)	Tm (°C)
<input type="text"/>	<input type="text"/>	<input type="text"/>

GC rich     Repeats     Poly ATCG

---

Use the above settings to fill  samples

2. You may generate more than 1 sample at a time, and do so more than once.

Use the above settings to fill  samples

**For INPUT USING EXCEL FILE,**

1. You may download the **Bio Basic Sequencing Form Template**.

Upload a Excel Template File ×

Don't have the template file? [Download here](#)

Select filled Excel file

2. Proceed to fill up the necessary details of your samples.
  - Under “Primer Name”, please note that each reaction requires **1 primer only** in sanger sequencing reaction setup. If the sample requires sequencing with more than 1 primer, please create separate reactions. You may refer to the examples below:

Example of **correct** sample detail:

<b>Sample Information</b>						
No	Type of Service	Sample Name	DNA Type	Sample Type	Primer Type	Primer Name
1	Standard	Sample 1	PCR	Water	Custom	27F
2	Standard	Sample 1	PCR	Water	Custom	1492R
3						

Example of **incorrect** sample detail:

<b>Sample Information</b>						
No	Type of Service	Sample Name	DNA Type	Sample Type	Primer Type	Primer Name
1	Standard	Sample 1	PCR	Water	Custom	27F and 1492R
2						

3. Upload the file by clicking on '**Select filled Excel file**'.
4. Please note that each excel file is limited to 96 samples. If you have more than 96 samples to key in, please save the additional sample information in another Excel file.

- It is important to remind our team if there is any special information regarding this order. E.g. presence of hairpin structure in the DNA, re-use of previously submitted DNA/primer, arrangement of collection on another day etc. **Please state such information under remarks.**
- Next, update your contact information. For first time user, **please fill up the address and complete as much as possible to facilitate the sample collection.**

How to fill the contact information?

[Load from previous saved list](#) [Fill a new address](#)

Which lab are you in?

Organization/Institute/School Name	PI/Lab/Group Name
<input type="text" value="BioBasic Asia Pacific"/> <small>e.g., National University of Singapore</small>	<input type="text" value="BioBasic"/> <small>e.g., Prof. Tan</small>

How do we collect your samples?

Contact Person	Mobile	Phone	Email (For multiple: a@a.com, b@b.com)
<input type="text" value="BioBasic"/>	<input type="text" value="00000000"/> <small>For SMS notification</small>	<input type="text" value="00000000"/>	<input type="text" value="admin@biobasic.com, sg-sequencing@biobasic."/>

Collection Address

[Previous](#) [Next](#)

- Under “Email”, you may save multiple email addresses here ( as indicated in the orange box in the image above). **Notification will be sent to these email addresses when results are ready.**

8. In this order summary, kindly double check the information you have created. Do click the box of **"I want to save contact used here for future use"** so you do not have to re-enter the contact information for the next sample.

### Create Sequencing Order

Essentials Samples Your Contact **Summary**

#### ORDER SUMMARY

Organization/Institute/School Name BioBasic Asia Pacific		PI/Lab/Group Name BioBasic	
Contact Person BioBasic	Mobile 00000000	Phone 00000000	Email admin@biobasic.com, sg-sequencing@biobasic.com
Collection Address 25 Bukit Batok Crescent, Elitist 04-06, Singapore 658066			

#	Sample Name	Process Method	DNA type	Sample type	Primer	Total Size(bp)	Template Conc (ng/ul)	Template Amount (ul)	Primer Conc (uM)	Primer Amount (ul)	Tm (°C)	GC rich Repeats Poly/ATCG
1	Sample 1	Standard	PCR	Water	Universal 27F	1500	50	10				<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/>
2	Sample 1	Standard	PCR	Water	Universal 1492R	1500	50	10				<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/>

Remarks (Max 500)

If the above details are correct, please click "Submit" to confirm this order.

I want to save contact used here for future use

9. Once submitted, you may print the **Sample Sequencing Collection Form** and attached it **to the sample** you are sending in for sequencing.

10. Under “Saved Contacts”, you can save multiple contact information. For future order submission, you can easily select your preferred contact person or whichever email that you would like to receive the result notification. **Please note that these emails are for notification and contact purposes only. There is only one login email for each account.**

Bio Basic Asia Pacific Customer Portal   Sequencing ▾   **Setting ▾**   Downloads ▾   Hello admin@biobasic.com!   Log out

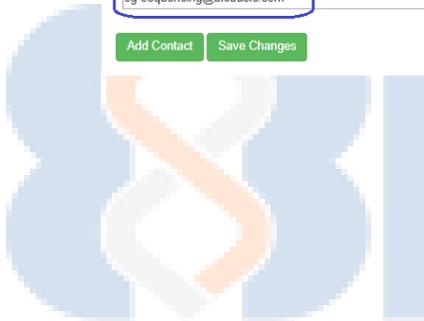
Saved Contacts

### Edit Contacts

These information can help to fill your order quickly.

<b>Organization</b> BioBasic APAC	<b>Person</b> Admin	<b>Phone</b> 00000000	<b>Address</b> 25 Bukit Batok Crescent, Ellitist 04-06, Singapore 658066	<a href="#">Delete</a>
<b>ResearchGroup</b> BioBasic APAC		<b>Mobile</b> 00000000		
<b>Emails (a@a.com, b@b.com)</b> admin@biobasic.com				
<b>Organization</b> BioBasic APAC	<b>Person</b> Sequencing team	<b>Phone</b> 00000000	<b>Address</b> 25 Bukit Batok Crescent, Ellitist 04-06, Singapore 658066	<a href="#">Delete</a>
<b>ResearchGroup</b> BioBasic APAC		<b>Mobile</b> 00000000		
<b>Emails (a@a.com, b@b.com)</b> sg-sequencing@biobasic.com				

[Add Contact](#)   [Save Changes](#)



**BIO BASIC**  
Quality-Affordable Research

## Updating your password

1. Click on your login email on the top right corner



2. Click on "Password" to change the password by providing you current password and the new password.

## Manage your account

Change your account settings

Profile

Password

Two-factor authentication

Change password

Current password

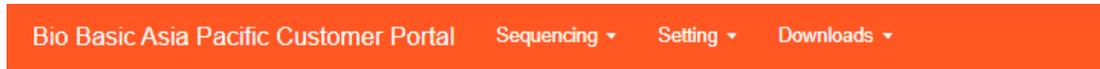
New password

Confirm new password

Update password

## Downloading Sequencing Results

1. Log in to <https://customerportal.biobasic-asia.com/Account/Login>
2. Your sequencing order will be listed on the main page.
3. You may click on the Order ID to check on the updates and status of your samples that you send in.



### Sequencing Order List

OrderID	Created	Title	Status	Collection
110918	2019-09-25	Standard sequencing	Finished ✓	Collected

1

4. Scroll down to check if results are uploaded.
5. Once results are ready, under **"Files available for downloading"**, results will be uploaded in zipped format. Click on it for downloading.

Sequencing Order No: 110918

Order Status:  Confirmed  Processing  Finished

Title	Sample Count	Created	Collection
Standard sequencing	10	2019-09-25 17:55:06	Collected
Organization / Lab		Contact Person	Phone/Mobile
Email			
Address			

SampleID	Sample Name	Process Method	DNA type	Primer	QC Fail Remarks	Status
110918001	W1F	Standard	PCR	Universal:ITS4		Finished
110918002	W2F	Standard	PCR	Universal:ITS4		Finished
110918003	W4F	Standard	PCR	Universal:ITS4		Finished
110918004	W5F	Standard	PCR	Universal:ITS4		Finished
110918005	W6F	Standard	PCR	Universal:ITS4		Finished
110918006	W7F	Standard	PCR	Universal:ITS4		Finished
110918007	W8F	Standard	PCR	Universal:ITS4		Finished
110918008	W9F	Standard	PCR	Universal:ITS4		Finished
110918009	W9F 2	Standard	PCR	Universal:ITS4		Finished
110918010	W10F	Standard	PCR	Universal:ITS4		Finished
Remarks						



Files available for downloading:  
[110918\\_20190926232309.zip](#)  
[110918\\_20190930031220.zip](#)

## Frequently Asked Questions

Q: Can I change my sample or primer name after the order is submitted?

A: Yes, you can do so while the order status is still being “confirmed”.

Q: What if I want to add more reactions to my current order?

A: Unfortunately, once the order is submitted, total number of reaction is unchangeable. In this case, please kindly submit a new order online.

Q: Can I use old samples/primers for a new order?

A: Please kindly check with our sequencing team before proceeding to submit a new order. If the samples are submitted more than a week, it is highly advisable to prepare fresh samples for sequencing.

Q: Can I re-sequence my sample with another primer for free?

A: For sequencing with a different primer, it is considered as a new request, thus a new order is needed and chargeable.

Q: The sequencing result I obtained is not desirable, can I request a re-run?

A: The team will usually perform a re-run if we believe that the result can be improved. Else, kindly inform us which reaction(s) you wish to be re-run.

Q: I have provided more than then the required concentration but was informed that the concentration was low. Why is this so?

A: We estimate the quantity of the sample received via gel electrophoresis and comparing it to a known standard, which is a very accurate method. If you have diluted the samples before sending to us, you might want to send the stock without dilution to us.

Q: When can I expect to receive the sequencing results?

A: We strive to upload the results within 24 hours. Usually most results will be available before noon the next working day. However, depending on amount of orders we received, they might be uploaded later during the day. If you require the results urgently, kindly contact us so we can expediate it.

Q: Do you have any special protocol for sequencing templates with hairpin structures, with high GC content or other difficult regions?

A: You may indicate on the order form if the template is GC rich, or has repetitive regions. You may also write in the remarks section if they contain known secondary structures such as with shRNA sample. The team will use an appropriate protocol for them.

Q: The concentration of my samples is below the requirement, how will this affect the results?

A: As sanger sequencing is a linear process, samples that have lower concentration will have lower quality reads and a shorter readable length. Sequencing are also very likely to fail altogether. Hence it is highly advisable to prepare samples with optimal concentration.

Q: Why does it take a re-run to produce good result sometimes?

A: The re-run allows us to use a more suitable protocol for any issues discovered during the initial run. Sometimes better results are obtained in the second run whereby further optimization is performed. Hence, it is important to provide us with information such as presence of hairpin loop in the sequencing template, GC-rich region, or sample with low concentration etc, so that the team can take note and adopt an appropriate protocol in the first run.