

FAQ

1. I am a new customer. How do I set up an account?

On our homepage you will see a "Register" link to set up a new account in the upper right-hand corner. Clicking on this link will allow you to enter your name and other details. After registration, you will be provided with a User ID and Password, using which you can login to your account. You are ready to submit your first order.

2. What is the average read length expected with one sample and a single primer?

Template quality will affect length of read. Average read length is 500 bp, but could be as much as 650-750 bp.

3. What size primers should I design?

Primers should be between 18-25 bases long.

4. What T_m value should primers have?

Primers should fall within the range of T_m values 55-65°C

5. I want to have my template sample read using both the forward and reverse primers. How do I indicate this on the order form?

Please use the same sample ID twice on the order form and enlist the respective forward and reverse primers against it. Thus, there would be two line items. You can submit the sample in just one tube as per our sample submission guidelines.

6. What is the minimum size of DNA fragment that you can sequence?

Ideally DNA templates should be 100bp and above. With our optimized running protocol and module, we can sequence DNA templates as small as 90-100bp, but this will be subjected to the DNA template quality and the priming efficiency of its sequencing primer.

7. Can you sequence PCR products labeled with FAM, ROX or SyBR Green dyes?

We cannot sequence FAM- and ROX-labeled Samples. Fluorescence from the dyes will interfere with the sequencing results.

8. How long will my DNA template and sequencing primers be kept? How can I reuse them for my next order?

We will only keep DNA templates and sequencing primers for 1 week upon receiving them. Please indicate in the order form if you would like us to keep your DNA templates or sequencing primers for further sequencing reactions. A nominal fee will apply for storing your DNA templates or sequencing primers in our laboratories.

9. Should I resuspend template in TE or H₂O?

H₂O is better. EDTA in TE can cause poor quality or failed reactions.

10. When will I get my sequence if I submit samples in individual tubes?

The turnaround time for individual tubes is 1-3 days depending on if the sample needs to be repeated. Most sequences are returned within 1-2 days from when we receive the sample.

11. What are the software that can be used to view the result?

The result files contain .ab1 files, trimmed FASTA files (Quality Sequence only) and Chromatogram files (PDF format). To view raw data, open the .ab1 files using the free software FINCHTV.

12. I do not see the sequence of my primer in the sequence data. Was there a problem with my sequencing reaction?

There was no problem with your sequencing reaction. The sequence of the primer is not expected to be returned in the sequence data; furthermore, you will also notice that the initial 20-40 bases following the 3' end of the primer are not determined accurately due to poor resolution. This is consistent with the behaviour expected with Sanger method of sequencing. However, the sequence of the primer is typically determined by using a primer to sequence the complimentary strand. By assembling the two reads, a consensus sequence can be generated that includes segments corresponding to both the primer sequences.