

Amplicon-seq sample requirements

Note that the user is responsible for the results in case the samples submitted do not match the specifications below.

- Amplicon-seq samples should be submitted as PCR reactions, no purification required, at 25 ul.
- Samples should be submitted as follows:
 - in 1.7 ml Eppendorf tubes (<12 samples) or in PCR strip/96 well plate with an aluminum seal (>12 samples).
 - Tubes must be clearly marked with a serial number on the top and the side of the tube (not sample name), corresponding to the sample's number in the Sample Information Form. In the matching electronic sample information form, write the number and a meaningful name (this name will be used as the sample name in your fastq files and subsequent data analysis). Ensure that the number on the tube is identical to the serial number of the sample in the electronic Sample Submission Form.
 - Arrange samples in the correct order in a box. We cannot accept samples in plastic bags or randomly place on ice. Mark the box with your name and date.
- An electronic **Sample Submission Form** should be filled out and sent by email to linde@technion.ac.il.
 - It is important to **accurately** fill out the Sample Submission Form. The information on the form is obligatory and the ATGC will process the samples according to this information.
 - It is important to indicate the amplicon size **including the length of the primers!**
 - Please indicate under Remarks if a sample has a **low concentration** or **non-specific PCR products**.

Recommendations-

1. We recommend performing amplicon validation prior to sending your samples. The amplicon should be a single fragment at the expected length. There is no size-selection during library prep and all fragments in the sample will be sequenced (which will reduce the coverage of the target amplicon).