

# Sample Submission Guide for Next-Generation Sequencing

at the joint **Biomedical Sequencing Facility (BSF)** of the **Medical University of Vienna**  
and the **CeMM Research Center for Molecular Medicine** of the Austrian Academy of Sciences

This guide will help you prepare your samples for submission to our next-generation sequencing services. Before submitting your samples, please ensure that they meet the sample submission criteria listed below.

## Submission

Before you plan to submit samples or libraries for next-generation sequencing, please contact us via [bsf@cemm.oeaw.ac.at](mailto:bsf@cemm.oeaw.ac.at). Our offered scientific consulting and sequencing services, latest submission documents and price lists are available at the BSF webpage (<http://www.biomedical-sequencing.at/>).

## Documents needed for the submission

- *Sample annotation sheet*: Providing sufficient background for sequencing and data processing
- *Sequencing authorization form*: Authorizing the BSF to perform the requested sequencing services

## Sample labeling

Importantly, samples should be clearly labelled with permanent marker pen or adhesive labels that will withstand freezing. Sample names should be simple with up to 8 alpha-numeric characters. Avoid using names such as A, B, C, etc. or 1, 2, 3, etc. The sample annotation sheet provides an opportunity to correlate sample labels on tubes with more meaningful sample names for bioinformatics analysis. Please remember that sample names will be used for file names, appear in gene lists and plots so the shorter and more meaningful they are the better. Samples are accepted in 1.5 ml or 2 ml DNase- and RNase-free LoBind microcentrifuge tubes. If you plan to submit your samples in a 96-well format please contact us and request for a 96-well sample submission kit.

## Sample requirements

Before you start a library preparation for Illumina sequencing systems please review pooling guidelines for balanced adapter index combinations. All samples submitted for next-generation sequencing analysis will be quantified and evaluated for quality measures. Please follow our minimum requirements for sample submission listed below with an additional sample overhead for quality control. **You are always encouraged to provide more material for sequencing** than the minimal requested amount since it may significantly increase the chance of obtaining high-quality results. Please discuss with us up-front if these amounts are not feasible for a specific experiment. All concentration measurements should be assessed using a fluorometric quantitation assay such as Qubit® or PicoGreen®.

	Minimal amount	Minimal concentration	Minimal volume	Storage buffer
<b>User provided sequencing libraries</b>	50 ng	5 ng/µl	10 µl	10 mM Tris-Cl, pH 8.5
<b>DNA samples for library preparation</b>				
Whole genome sequencing	1000 ng	50 ng/µl	20 µl	10 mM Tris-Cl, pH 8.5
Exome sequencing	50 ng	10 ng/µl	5 µl	10 mM Tris-Cl, pH 8.5
ChIP-seq library preparation	5 ng	0,5 ng/µl	10 µl	10 mM Tris-Cl, pH 8.5
<b>RNA samples for library preparation</b>				
Stranded mRNA-seq (poly-A enrichment)	100 ng	10 ng/µl	10 µl	nuclease free water
Transcription fingerprinting 3' RNA-seq	500 ng	100 ng/µl	5 µl	nuclease free water
Single cell RNA-seq			please inquire	

## Sample delivery

Arrange the samples in the same order as on the sample annotation sheet in a cryo storage box or similar. Before sample submission, please always contact us via [bsf@cemm.oeaw.ac.at](mailto:bsf@cemm.oeaw.ac.at) and select from one of the following options:

### *Option 1: In-person delivery*

Please arrange an appointment via [bsf@cemm.oeaw.ac.at](mailto:bsf@cemm.oeaw.ac.at). User-provided sequencing libraries should be delivered on ice, while it is particularly critical to deliver DNA or RNA samples for library preparation on dry ice.

### *Option 2: Delivery via express mail or courier*

Please contact us in advance when you are planning to send the samples or libraries by express mail or courier and please use the fastest service available. Samples should always be sent on dry ice to minimize degradation. Make sure you supply sufficient dry ice for the whole transport including unexpected delays. Insulate and seal the package carefully to minimize thawing. Please send the parcel at the beginning of the week to avoid an over-weekend delivery. To avoid delays in customs, please describe the contents accurately: i.e. purified DNA dissolved in 10 mM Tris-Cl, for research purpose only. The commercial invoice should state a value of 0 (or lowest amount possible).

Please send to the following address:

Biomedical Sequencing Facility (BSF)  
CeMM Research Center for Molecular Medicine  
of the Austrian Academy of Sciences

Lazarettgasse 14, AKH BT 25.3  
1090 Vienna, Austria

## Data storage after receiving next-generation sequencing data

The BSF will provide the raw sequence data as unaligned BAM files or provide pre-analysed data sets for standard protocols (e.g. RNA-seq, ChIP-seq, variant calling, etc.) via the BSF web site. It is important to understand that you are responsible for storing your data and that you need to copy your data sets from the BSF web server in time. We are happy to assist in packing the data in a suitable format – GNU Tape archive format (Tar) compressed with GNU Zip – for convenient transfer and long-term archival at your institution.