# **HOW TO ORDER**

## **Sequencing Guidelines**

- Download Sequencing Order form
- Fill out the Sequencing Order form following Order form guidelines
- Download Electronic Sample Sheet (ESS)
- Fill out the ESS following ESS guidelines
- Send completed ESS to gsf@uantwerpen.vib.be
- Include a printout of the filled out Sequencing Order form and ESS with the order
- Prepare your samples following the Sample submission guidelines strictly
- Sent the order to:

## **VIB Neuromics Support Facility**

Universiteit Antwerpen, Campus Drie Eiken Building V, Room V1.16 Universiteitsplein 1 B-2610 Wilrijk Belgium

## Order form guidelines

#### • A complete order must contain following information:

- o Order Reference
- o Date
- Valid Invoice Address
- Valid Delivery Address
- Signature
- Valid set of options
- Correct number of reactions and pricing information

#### • Remarks:

- Order Reference: fill out the Purchase Order number of your administration in "Order Reference. Client"
- Delivery Address: the email address specified will be used for email order confirmation and to send the sequencing data.
- Options:

## Time Schedule:

- Normal: Up to five business days from confirmation of order to data delivery (normally within 48 h)
- Prior: Orders with priority arriving before 3pm are immediately processed on the same day after confirmation of order and quality checked and sent immediately after sequencing (from confirmation to data normally within 24h)

If the full order fails, sequencing will be repeated once to exclude errors in our experimental procedures.

# Read Length:

- Short Run: 750 bp read max, on average 550 bases.
  Recommended for sequencing PCR and short templates.
- Long Run: 1000 bp read max, on average 800 bases.
  Recommended for plasmid and long template sequencing.
- For good quality data, minimum length of the template above 120 bases is recommended.
- Please keep in mind that one order CANNOT contain two different "Read Length" options. An order is either "Short Run" or "Long Run".

# **ESS** guidelines

#### General

- Use one line per sequence.
- o Fill in all needed information.
- The columns "Template" and "Primer" are combined to constitute sequence filename.
  This combination should be shorter than 20 characters; additional characters will be removed automatically in the filename.

# • Column "ID/Well":

- This column is obligatory.
- ID stands for "Identifier"

For templates delivered in tubes, specify unique number in the column "ID/WELL" starting from 1 (1, 2, 3...) for every template in an order. This ID number should be clearly written also on the template tubes.

 For templates delivered in a 96-well plate, specify well locations in the column "ID/WELL". If more than 1 plate is delivered, also indicate the plate name which is unique to every plate.

## Column "Template" :

- This column is obligatory
- o Name of the template, will be used in the filename.
- Only use the following characters: numbers (0-9), letters (a-zA-Z), hyphen (-), dot (.), underscore (\_). So no space ( ) or other characters like (\ , / ? !\*)

#### • Column "Primer":

- This column is obligatory
- o Name of the primer, will be used in the filename.
- Only use the following characters: numbers (0-9), letters (a-zA-Z), hyphen (-), dot (.), underscore (\_). So no space ( ) or other characters like (\ , / ? !\*)

# • Column "Sample Type" :

This column is obligatory

- o Indicate whether your template is a PCR fragment or a Plasmid.
- Column "Purification by NSF" :
  - Indicate how the NSF has to clean your template. Leave empty if no purification is needed.
- Column "Template Length" :
  - o This column is obligatory for PCR fragments.
  - o Indicate the size of your PCR fragment.
- Column "Template %GC" :
  - o Indicate the GC percentage of the sequence if it is known. In case the GC content is more than 65%, a special sequencing protocol is needed. Please enquire for this option.

# Sample submission guidelines

- All template plates and tubes should be labeled with unique number (tubes) or identifier (plates). All primer aliquots should be clearly and unmistakably marked with unique ID, identical to the column 'primer' in ESS.
- Concentration :
  - Sequencing primer : 5 pmol/μl.
  - Purified templates :
    - Plasmid DNA : 50 ng/μl
    - PCR products < 1 kb : 20 ng/μl</li>
    - PCR products > 1 kb : 100 ng/μl
- Volume: for both, primer and template, supply at least 10  $\mu$ l for each sequencing reaction that needs to be performed with the combination.