

| Client                                   |  | Invoice Department  |  |
|--|--|---------------------|--|
| Name of sender:                          |  | Administrator:      |  |
| Institute / Company:                     |  | Invoice department: |  |
| Department:                              |  | Invoice address:    |  |
| Shipment address:                        |  | Zip/City:           |  |
| Zip/City:                                |  | Country:            |  |
| Country:                                 |  | e-mail address:     |  |
| e-mail address:                          |  | Phone number:       |  |
| Phone number:                            |  | VAT #:              |  |
| Fax number:                              |  | Your order #:       |  |
| Other contact person:<br>e-mail address: |  | Quotation #:        |  |
|  |  | Year contract #:    |  |

## ORDER (please use the sample sheet)

### CRITERIA FOR SIRNA SEQUENCING (PRODUCT# BC-150):

- **Forward and reverse combi run:** siRNA inserts will be sequenced using standard conditions and under conditions for GC-rich and hairpin regions. Both a forward and reverse short run (max 500 nt.) will be performed. On request the resulting sequences will be assembled into a contig sequence. Please therefore provide us with the expected sequence (on disk or by email) so we can compare it to the resulting contig.
- Please note that certain siRNA inserts are almost impossible to read through, due to high stability of the hairpin structure. In these cases, 50% setup costs will be charged instead of the full price.

## RESULTS (I would like to receive my results as following)

|   |   |
|---|---|
| <input type="checkbox"/> <b>e-mail only (free of charge)</b><br><br><input type="checkbox"/> PGP encrypted (requires key) | <input type="checkbox"/> <b>regular mail including:</b><br><i>(see pricelist for additional costs)</i><br><br><input type="checkbox"/> files on CD (BC-111)<br><input type="checkbox"/> prints of sequence and peak-plot (BC-112)<br><input type="checkbox"/> preliminary results by e-mail (no charge) |
|---|---|

|   |  |
|---|--|
| <b>I accept the general terms and conditions of BaseClear*</b><br><br><b>Name</b> : _____<br><br><b>Signature</b> : _____<br><br><b>Date</b> : __ / __ / ____ | <i>To be filled out by BaseClear:</i><br><br><b>Project Code</b> : _____<br><br><b>Date of registration</b> : __ / __ / ____ |
|---|--|

\*Our General Terms and Conditions apply to all projects BaseClear carries out and can be downloaded from our website ([www.baseclear.com/labservices/terms\\_conditions](http://www.baseclear.com/labservices/terms_conditions)).

## **SAMPLES**

### **Purified plasmid**

Only deliver column purified DNA, dissolved in water or 10mM Tris (pH8.0). Please note that DNA samples should be **free of EDTA and ethanol** since trace amounts of these compounds will inhibit the sequence reaction. Dilute your DNA samples a minimum of **20 ng/µl per kb** of plasmid DNA, or **2 ng/µl per 100bp** of PCR product. We use approximately 2-5 µl per reaction and ask you to submit a **minimum of 30 µl**.

### **Bacteria**

Send in petri-dishes with single E.coli colonies or agar stab cultures. Do not send more than two samples per petridish to avoid cross contamination, and seal both petri dishes and stab vials properly with parafilm. Glycerol stocks should be sent in on dry ice to preserve cell viability. Costs associated with plasmid isolation can be found under product #201a/b.

When sending in gmo samples Dutch legislation requires that they fall within the scope of our license for handling GMO's. In order to be able to check this and in order to fulfill the necessary safety requirements we ask to submit

#### Dutch license holders:

- the IG number of your license, including article and part number under which the GMO that you are sending in is constructed,
- the containment class (ML-I, ML-II).

#### Clients from abroad:

- the containment class (ML-I, ML-II),
- the species name of the organism the sequence is derived from or by indicating in more general terms that the organism is:
  - a mammal, including human, or a plant grown for consumption;
  - a micro-organism listed on "Bijlage 1" or Appendix A of the Dutch Order of GMO, 1998 (these lists can be found at [vrom.nl/ggovergunningverlening](http://vrom.nl/ggovergunningverlening)).

When the sequence is derived from unidentified organisms or is claimed confidential, the description of the organism used in your license may help. Please indicate this accordingly on the order form together with details about antibiotic resistance and copy number. For further details please review the sample and shipping requirements on our website [www.baseclear.com](http://www.baseclear.com).

## **PRIMERS**

Universal primers will be provided free of charge by BaseClear (e.g. MF, MR, Sp6, T7, T3, pRS primers). For a complete list of standard primers, please visit our website [www.baseclear.com](http://www.baseclear.com).

You may also send in your own primers with the order. Please note the following requirements:

- Design primers using a primer design program like Primer Premier or Oligo.
- Make primers 18 to 24 bases long and with a **Tm ≥ 55 °C**.
- Dissolve your primers in water to 10 pmol/µl and send in a **minimum of 30µl**.

In case you want BaseClear to synthesize your primers please download and include the primer orderform with your sequence order. On request, we can also design custom primers. Please provide us with the target sequence in both electronic and printed format and clearly mark where primers should be designed (product #500)

## **REFERENCE SEQUENCE**

In order to compare the final contig sequence to the expected sequence of your siRNA insert, please enclose a disk with your order containing the reference sequence(s) in FASTA format. Alternatively, you may email the sequence to [dna@baseclear.com](mailto:dna@baseclear.com). Please indicate the name of the reference sequence that should be used for each sample on the samplesheet.

## **TERMS OF DELIVERY**

The siRNA Sequencing service includes the quality and quantity check of incoming DNA samples. In case samples do not pass our quality control, we will notify you before continuing with sequencing. All sequencing results are analysed by PHRED, and poor sequence runs that do not meet our quality standards are reviewed manually. Failed runs are repeated once at no additional cost.

Sequencing results are assembled into a contig sequence that is compared to the expected sequence as provided by the client. Please note that read-length of the resulting sequences is dependent on factors like quality and quantity of template and primer, but also relies on the stability of the siRNA hairpin structure. In case no sequence can be obtained, setup costs will be charged.

Whenever due to client mistakes additional work has been performed and/or extra costs have been made, BaseClear has the right to charge the client for that costs.

|                                | Sample Name | Please leave this column empty | Sample-type:<br>Pur. Plasmid (D)<br><br>Bacteria (B), see also the 3 next coloms | Number of IG-license, article and part | Organism where the insert is derived from | Class:<br><br>ML-I/<br>ML-II | Antibiotic Resistance or conc. (ug/ul) | Fragment length (bp) | Vector name | Sequence with primer (name): | Standard / Included with order Client specific (in-house)<br>To be synthesized (submit primer order form)<br>To be designed | Conc. (pmol/μl) |
|--------------------------------|-------------|--------------------------------|--|--|---|------------------------------|--|----------------------|-------------|------------------------------|---|-----------------|
| 1                              |             |                                |  |  |   |                              |  |                      |             |                              |   |                 |
| 2                              |             |                                |  |  |   |                              |  |                      |             |                              |   |                 |
| 3                              |             |                                |  |  |   |                              |  |                      |             |                              |   |                 |
| 4                              |             |                                |  |  |   |                              |  |                      |             |                              |   |                 |
| 5                              |             |                                |  |  |   |                              |  |                      |             |                              |   |                 |
| 6                              |             |                                |  |  |   |                              |  |                      |             |                              |   |                 |
| 7                              |             |                                |  |  |   |                              |  |                      |             |                              |   |                 |
| 8                              |             |                                |  |  |   |                              |  |                      |             |                              |   |                 |
| 9                              |             |                                |  |  |   |                              |  |                      |             |                              |   |                 |
| 10                             |             |                                |  |  |   |                              |  |                      |             |                              |   |                 |
| Total number of primers : ____ |             |                                |  |  |   |                              |  |                      |             |                              |   |                 |