DNA SEQUENCE SUBMISSION FORM – INTERNAL

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**NAME:**  **DATE:**

**PI/SUPERVISOR:** **TELEPHONE #:**

**E-MAIL:**  **ROOM #:**  **ACCOUNT NUMBER: (please fill out the entire MOSAIC CHARTFIELD STRING)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Fund(2)** | **Account(6)** | **Department(5)** | **Project(8) or Program(5)** | **PC Bus.Unit(5) (for Projects only)** |
| **Example:** 85 | 600001 | 10999 | 20099999 | RFHSC |
|  |  |  |  |  |

**Editing request\*\***  with **($15.00)** without **($7.50)**

RESULTS E-mailed Text file ABI file

Printouts Yes

**Special Consideration:** 1) higher than 65% **GC** content **(add DMSO)**  YES 2) Secondary Structure **(hairpin protocol)**  YES ($9.00 per rxn, 1 to 2 additional **days)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| # | **Name of DNA**  **(max 8 characters)** | **Name of PRIMER** (max 8 characters) | **#** | **Name of DNA** (max 8 characters) | **Name of PRIMER** (max 8 characters) |
| 1 |  |  | 9 |  |  |
| 2 |  |  | 10 |  |  |
| 3 |  |  | 11 |  |  |
| 4 |  |  | 12 |  |  |
| 5 |  |  | 13 |  |  |
| 6 |  |  | 14 |  |  |
| 7 |  |  | 15 |  |  |
| 8 |  |  | 16 |  |  |

# DNA & Primer - should be suspended in Water or 0.1x Elution buffer. We require 5μl of DNA and 5μl primer per reaction.

**Primer concentration: 1 picomole/μl = [1 μM]**

**DNA concentration: 1ng/μl per 100 bases**

# DNA Concentration – because sequencing is unidirectional the *number of copies of your template* in the sample becomes very important, too little DNA will result in no-signal. Too much DNA can result in a short read or a smear or no signal. Note that the input concentration should be based on the TOTAL size of the template DNA in the sample; e.g. give us 5μl @ 30 ng/μl if your plasmid + insert is 3 kb. UV absorbance–based quantification is not always accurate! Better methods are Qubit Fluorometric or gel-based quantification.

**Please indicate your TOTAL template size**

**ds DNA approx. size**

**PCR products approx. size**

**\*\***Editing is the correction of miscalled bases. These problems generally occur at the beginning and end of the sequence but can occur anywhere.

**Note** – you require the ABI file and the correct computer software to do your own editing.

**Sample Storage:** we keep the DNA samples and primers for one month after they have been processed.

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