DNA SEQUENCE SUBMISSION FORM – EXTERNAL

Phone: (905) 525-9140 ext. 27048 E-mail: mobixlab@mcmaster.ca https://healthsci.mcmaster.ca/mobix/services/sequencing

NAME:_____ **DATE:**_____

SUPERVISOR:_____ **TELEPHONE # ( )**_____**EXT.**_____

E-MAIL ADDRESS:_____ **PO#**_____

EDITING REQUEST** ☐ **WITH ($18)** ☐ **WITHOUT($12)**
E-MAIL RESULTS ☐ TEXT FILE ☐ ABI FILE

MAILING ADDRESS **BILLING ADDRESS** (if different from mailing)

SPECIAL CONSIDERATION: 1) higher than 65% **GC** content **(add DMSO)** ☐ YES
2) Secondary Structure **(hairpin protocol)** ☐ YES ($14.00 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.