

# DNA SEQUENCE SUBMISSION FORM – EXTERNAL

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NAME: \_\_\_\_\_

DATE: \_\_\_\_\_

SUPERVISOR: \_\_\_\_\_

TELEPHONE # (    ) \_\_\_\_\_ EXT. \_\_\_\_\_

E-MAIL ADDRESS: \_\_\_\_\_

PO# \_\_\_\_\_

EDITING REQUEST\*\*  WITH (\$18)  WITHOUT(\$10)  
 E-MAIL RESULTS  TEXT FILE  ABI FILE  
 MAIL PRINTOUTS (COURIER CHARGES APPLY)  YES

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.