

**Microarray Core Facility Sample Submission Form**

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*Center for Functional Genomics*  
*University at Albany*  
*East Campus, Room 328*  
*One Discovery Drive*  
*Rensselaer, NY 12144-2345*

Principal Investigator\*: \_\_\_\_\_ Date\*: \_\_\_\_\_

Institution\*: \_\_\_\_\_

Lab. Contact Person\*: \_\_\_\_\_ Contact Phone\*: \_\_\_\_\_

Contact E-mail: \_\_\_\_\_ Contact Fax\*: \_\_\_\_\_

Grant No\*.: \_\_\_\_\_ [or] P.O. No\*.: \_\_\_\_\_

**\*All fields need to be filled out**

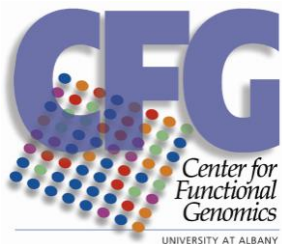
**Project Title\*:** \_\_\_\_\_

RNA information:										
Sample Number	Sample Name (AB1, AB2 etc)	RNA type (total, mRNA, IP, cRNA)	Sample Description (include any treatment details, indicate controls)	Conc. (µg/µL)	Total Amount	A <sub>260</sub> /A <sub>280</sub> Ratio	Organism	Source Tissue/Cells	RNA Isolation Method	Microarray type (from Table I)
1										
2										
3										
4										
5										
6										
7										
8										
9										
10										
11										
12										

The minimum amount of material necessary varies from 50 ng – 50 ug depending on the microarray type. Please refer to Table I next page to determine starting amount RNA for each array type. OD 260/280 ratios must be between 1.8 - 2.1 for each sample. Each sample should be provided in a single 1.5 mL microfuge tube with the initials of the Principle Investigator and a sample number written on the top. Samples that do not meet the above criteria may be assessed an additional RNA set up fee or returned unprocessed. Samples will be assayed for RNA quality by Agilent BioAnalyzer prior to microarray analysis. Investigators are responsible for all costs associated with failed or poor quality reactions caused by poor RNA samples.

**Initials** \_\_\_\_\_

**I have read and understand the above policies**



**Table I**

<b>Microarray type</b>	<b>Starting amount</b>
<b>Affymetrix 3' expression</b>	2 ug
<b>Affymetrix 3' expression (small sample prep)</b>	50 ng
<b>Affymetrix Whole Transcript – GENE ST</b>	150 ng
<b>Affymetrix Whole Transcript – EXON ST</b>	1.5 ug
<b>Nugen pico amplification</b>	10 pg
<b>Affymetrix Tiling</b>	3.5 ug
<b>Ambion mirVana (microRNA)</b>	50 ug
<b>Agilent microRNA</b>	150 ng
<b>Agilent Expression</b>	1 ug
<b>Nimblegen Expression</b>	1 ug
<b>Eppendorf</b>	5 ug

**Table II**

<b>Comparison Instructions</b>	<b>Baseline (ex. AB1)</b>	<b>Experimental (ex.AB2)</b>
<b>Pair 1</b>		
<b>Pair 2</b>		
<b>Pair 3</b>		
<b>Pair 4</b>		
<b>Pair 5</b>		
<b>Pair 6</b>		
<b>Pair 7</b>		
<b>Pair 8</b>		
<b>Pair 9</b>		
<b>Pair 10</b>		
<b>Pair 11</b>		
<b>Pair 12</b>		

**Special Instructions**

**CFG Microarray Facility use only:**

Customer ID#

Array ID #

Date Rec'd

Rec'd by: