CAP-DSC PLATE SET-UP

NAME OF USER: Sally Johnston in Dr. Brown's lab
DATE of SAMPLE DELIVERY: September 8, 2011
SCAN RATE: 2 degrees per minute
BUFFER: B1 = 10 mM Hepes, 50 mM NaCl, 50 mM Glycine, 1mM TCEP, pH 7.5; B2 = bla, bla, and so on
VOLUME IN WELL: 400 microliters
ACCOUNT NUMBER FOR BILLING: 305290435…

	1	2	3	4	5	6	7	8	9	10	11	12
A	B1	B1	B1	P1	B2	B2	B2	P2	B3	B3	B3	P3
B	B4	B4	B4	P4	C	C	W	W				
C												
D												
E												
F												
G												
H												

INSTRUCTIONS:

we'd like to point out that we will do 2 repeat scans of your buffer but it is not absolutely necessary to include a buffer-buffer run with each protein if all proteins have used the same buffer. After each protein we include a contrad clean and we have found that an additional buffer-buffer run is unnecessary.

- PROVIDE THE CORE WITH A COPY OF YOUR PLATE SET-UP WITH SAMPLE PLATE. ALL INFORMATION IN RED IS REQUIRED.
- IT IS NOT NECESSARY TO INFORM CORE WHAT PROTEINS YOU ARE RUNNING BUT THE BUFFER COMPOSITION IS NEEDED.
- KEEP A RECORD OF WHAT YOU LOAD INTO EACH WELL BECAUSE THE RESULTING DSC DATA FILES FOR YOUR DSC RUNS WILL BE NAMED B1-4, OR P1-P4, DEPENDING ON WHETHER THEY ARE BUFFER-BUFFER RUNS OR BUFFER-PROTEIN RUNS.

--Shown above is a hypothetical experimental set-up for 4 different protein samples (P1-P4) dissolved in 4 different buffers (B1-B4). **You must load in the order shown**. **Don't leave empty wells.** All sample runs require loading of two wells - one for buffer (e.g., B1) and one for the protein (e.g., P1), which are loaded into the DSC reference and sample cells, respectively. For each different buffer used, the first pair of samples in the experimental run must be the buffer baseline (e.g., B1 against B1) followed by the protein run (B1 against P1). At the end of your run, there will always be two additional control runs and you should include in your sample plate these four additional wells: two loaded with 10% contrad detergent (denoted by C – this is a contrad-contrad run) and two loaded with deionized water (denoted by W). The contrad and water will be provided by the core only.

--We recommend a scan rate of 2 degrees per minute and this will be the default unless the user requests otherwise.

--The default loading volume for the plate is 400 microliters. Don't deviate from this without discussion with Core.

--Please provide the buffer composition in case there is an incompatibility with the cells.

Your sample plate will have a little sample remaining in each well, which you may use for protein concentration determination, if necessary (there is a little dilution of sample during loading; <~10% may occur). Save your plate and reuse next time.