**Utilizing Metabolomics to Understand Novel Anti-Desmoid Tumor Drugs**

Cells were homogenized on the MagNA Lyzer, with two 30-sec cycles at 2000 rpm, resting in a -20 °C chilling block for 1 min in between pulses, and centrifuged samples at 16,000 rcf for 4 min. The cell lysate was transferred to a new 2 mL Lo-Bind Eppendorf tubes, with the final cell count approximately 10x10^6 cells for each sample. Of the twenty cell lysate samples, six samples had sufficient volume for study samples and to be included in an analytical quality control (QC) total pool. Aliquots from these cell lysate samples were combined, divided into three total pool aliquots, and processed identically to the cell lysate study samples. All study and pool samples were lyophilized to dryness and reconstituted in a 0.2M phosphate buffer, pH 7.4, in D2O with 10% Chenomx ISTD.

1H NMR spectra of cellular extracts were acquired on a Bruker Avance III 700 MHz spectrometer (located at the David H. Murdock Research Institute at Kannapolis, NC, USA) using a 5 mm cryogenically cooled ATMA inverse probe and ambient temperature of 25 °C. A noesypr-1d pulse sequence was used for data acquisition. For each sample 64 transients were collected into 65 k data points using a spectral width of 12.0227 ppm, 2s relaxation delay, 100 ms mixing time and an acquisition time of 3.89 s per FID. The water resonance was suppressed using resonance irradiation during the relaxation delay. Spectra were zero filled, and Fourier transformed after exponential multiplication with line broadening factor of 0.5. Phase and baseline of the spectra were manually corrected for each spectrum. Spectra were referenced internally to the DSS signal. The quality of each NMR spectrum was assessed for the level of noise and alignment of identified markers. Spectra were assessed for missing data and underwent quality checks.