



# VCU

## Office of Research and Innovation **spotlights...**

August 2015

### Chemical & Proteomic Mass Spectrometry Core Facility

The Chemical and Proteomic Mass Spectrometry Core Facility is available to help meet your mass analysis needs. The core is equipped for basic mass measurement of small and large molecules as well as proteomics experiments, ranging from simple protein identification to identifications of proteins in complex mixtures, analysis of post-translational modifications and quantifications via iTRAQ labeling. Instrumentation is state-of-the-art, with most purchased within the last two years. Software for data analysis yields proteomics analyses using the Scaffold program.

The core is excited to introduce the newest instrument – the **Synapt G2Si** from Waters Corporation. This instrument combines the best of dynamic range, sensitivity, accurate mass and rapid acquisition rates.

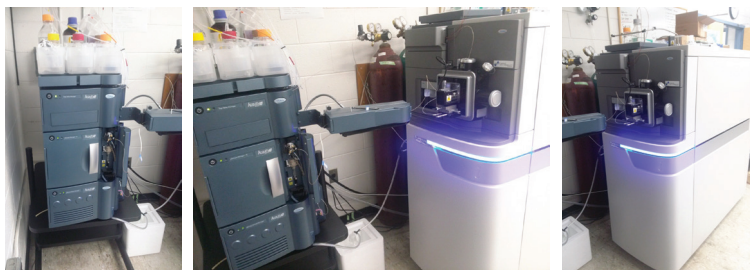
#### WHY USE THE SYNAPT G2Si?

**Increased Sensitivity** – As detectors get better and better, the available sensitivity increases. Compared to our older instruments, the Synapt G2Si has approximately a 10x increase in sensitivity. This means that less sample is required for analyses.

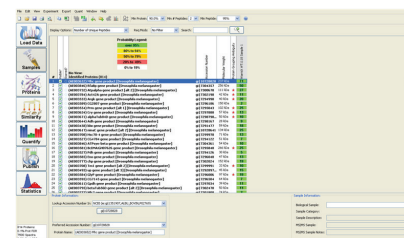
**Better Dynamic Range** – In complex proteomics experiments, often the proteins of greatest abundance are also those of least interest. The most interesting chemistry and biology may happen in the proteins with the fewest number of copies. Because of the Synapt's fundamentally different fragmentation process, the dynamic range of this instrument is greatly expanded, so we are more likely to detect those low-level proteins even in the noise of high-level proteins.

**Ion Mobility** – This technique can be used to separate species which may have similar or the same molecular weight, but a different collisional cross-section. The ion mobility portion of the instrument can also serve as another dimension of separation, which allows for even greater drill-down through extremely complex mixtures.

**Superior Chromatography** – The amazing reproducibility of chromatography afforded by the M-Class UPLC system allows for label-free comparison of relative abundance between samples. While we were previously limited to labeling samples with isobaric mass tags for comparison of protein abundance, we can now perform the same analyses with no labeling. This removes the potential for false results which can arise from fragmentation of coeluting labeled species in complex mixtures.



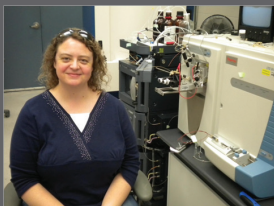
#### RESULTS



Sample Scaffold file of a MudPIT run. Over 800 proteins were detected in 9 SCX fractionations. Investigators receive this list of proteins detected and peptides detected for each protein. Samples are run against species-specific databases, if one exists, or against NCBI's non-redundant database.



Double-clicking on a particular protein shows all the peptides detected within that protein. Investigators can view a map of where the peptides are within the protein sequence, view the fragmentation spectra, look at the probability scores, and more.



**Contact Us!** We offer a wide range of mass spectrometric services, from basic mass measurement to complex proteome analyses. We encourage investigators to contact the Mass Spec Core regarding their experimental needs, so that we can discuss how to get the best results for you.

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For more information, please visit <http://www.chemistry.vcu.edu/research/spect.html>