

## FACILITIES & OTHER RESOURCES (updated on 08-19-2020)

### Laboratory

The **Emory Integrated Proteomics Core** (EIPC, <https://www.cores.emory.edu/eipc/index.html>) is located in 525 Whitehead Biomedical Research Building with 1200 square feet of dedicated wet-lab space.

### Clinical

N/A

### Animal

N/A

### Computer

The Emory Integrated Proteomics Core (EIPC) has multiple search engine platforms including Sequest, Mascot, and Byonics. A Sage-N Sorcerer2 IDA is located in-house and currently runs SorcererSequest and Scaffold. The Mascot, Proteome Discoverer 2.0, and Byonic platforms are licensed on a computing cluster in collaboration with the Emory Integrated Computing Core. All personnel have access to high-end workstations capable of processing both raw and post-analyzed data.

### Office

The EIPC has 200 sq ft of dedicated office adjacent to the laboratory space on the 5th floor of the Whitehead Biomedical Research Building, which provides for computational services, meeting customers, and weekly EIPC team meetings.

### Other

The **Emory Integrated Proteomics Core (EIPC)**, currently directed by Dr. Nicholas T. Seyfried, provides protein analytical services by cutting-edge mass spectrometry (MS). The EIPC has 200 sq ft of dedicated office adjacent to the laboratory space on the 5th floor of the Whitehead Biomedical Research Building, which provides for computational services, meeting customers, and weekly EIPC team meetings. EIPC houses several mass spectrometers—hybrid quadrupole-orbitrap including a Q-Exactive, and a Q-Exactive HF-X; tribrid mass spectrometers including two Orbitrap Fusion, and an Orbitrap Fusion Lumos; and a TSQ Altis triple-stage quadrupole (see major equipment). Each instrument is coupled with an autosampler and HPLC system. The system allows automated capillary LC-MS/MS runs for top-down, middle-down and bottom-up analyses with high resolution. These mass spectrometers are capable of detecting peptides at subfemtomolar level, identifying hundreds to thousands of proteins in complex mixtures, mapping posttranslational modification sites, and quantifying proteins based on label-free methods or different labeling strategies (e.g. TMT and SILAC). The nanoACQUITY UltraPerformance LC System is designed for nano-scale, capillary, and narrow-bore separations to attain the highest chromatographic resolution, sensitivity, and reproducibility. Both qualitative and quantitative projects benefit from the added pressure capacity (up to 10,000 psi); sensitivity is increased several folds with the use of sub-2  $\mu\text{m}$  chromatographic resins and retention time reproducibility enables label-free quantitative approaches. The core has also established the electrostatic repulsion hydrophilic interaction chromatography (ERLIC) that utilizes both hydrophilic interaction and electrostatic forces on an Agilent 1100 HPLC.

The computational platform is capable of performing sophisticated data analyses, including database search (i.e. matching MS/MS spectra to peptide sequences), data filtering (i.e. removing false positive matches), statistical inference, as well as data storage, presentation and distribution. EIPC has multiple search engine platforms including Sequest, Mascot, and Byonics. A Sage-N Sorcerer2 IDA is located in-house and currently runs SorcererSequest and Scaffold. The Mascot, Proteome Discoverer 2.0, and Byonic platforms are licensed on a computing cluster in collaboration with the Emory Integrated Computing Core. Numerous computational tools have also been developed for high throughput data processing. All personnel have access to high-end workstations capable of processing both raw and post-analyzed data.