## FACILITIES & OTHER RESOURCES (updated on 01-30-2025)

#### Laboratory

The *Emory Integrated Proteomics Core* (EIPC, <a href="https://www.cores.emory.edu/eipc/index.html">https://www.cores.emory.edu/eipc/index.html</a>) is located in 525 Whitehead Biomedical Research Building.

# **Clinical**

N/A

#### Animal

N/A

## **Computer**

The Emory Integrated Proteomics Core (EIPC) has multiple search engine platforms including Maxquant and Proteome Discoverer. All personnel have access to high-end workstations capable of processing both raw and post-analyzed data.

## Office

The EIPC has office space on the 4th floor of the Rollins Research Center, 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). EIPC houses several mass spectrometers— Q Exactive HF-X Hybrid Quadrupole-Orbitrap mass spectrometer and Orbitrap Fusion Lumos Mass Spectrometer with Electron Transfer Dissociation (ETD) (see major equipment). Each instrument is coupled with an autosampler and HPLC system. The system allows automated capillary LC-MS/MS runs for 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).

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 MaxQuant and Proteome Discoverer. All personnel have access to high-end workstations capable of processing both raw and post-analyzed data.