EINSTEIN PROTEOMICS CORE – RESOURCES

Laboratory: The Proteomics Core at Einstein has recently been renovated thanks to a remarkable investment of the School. This includes instrumentation and lab renovation (completed in May 2019). The 1,700 sq. ft. of lab space were completely renovated in an area corresponding to the previous Laboratory of Macromolecular Analysis and Proteomics (LMAP) of the Albert Einstein College of Medicine. Walls, ceiling, floor and entrances were redesigned to improve working conditions (lights, noise, open space), to include a dedicated room for cell culture and a separate space for noisy equipment like liquid handlers, SpeedVac and -80°C freezer. The lab is also already equipped with all the necessary instrumentation for being fully operative; most of the equipment was purchased new this year.

Mass Spectrometry Resources: The Core has all the instruments placed in dedicated rooms with internal temperature and humidity control to maintain calibration. The equipment includes a Thermo Orbitrap Velos, a Thermo LTQ, an Agilent Triple Quadrupole and a state-of-the-art MALDI Ultraflex (Bruker) for imaging mass spectrometry. The Core is also equipped with a TriVersa NanoMate for automated direct injection of samples for projects not requiring liquid chromatography, e.g. high-throughput analyses. All mass spectrometers are coupled with liquid chromatographers. The Orbitrap Velos is specifically coupled with nano-liquid chromatography for sub-femtomole sensitivity. The Core has also offline HPLCs for sample fractionation and purification using size-exclusion chromatography, HILIC and high pH.

Computational Resources: The Core has exclusive access to a state-of-the-art new server for computational work. This server includes a Node (32 cores, 512GB of RAM, and 10TB space), a Storage Unit (350TB space) and a Graphics Processing Unit to exploit state-of-the-art spectra identification of unknown post-translational modifications, i.e. by graphically matching spectra libraries with acquired data. The server has installed professional software for proteomics analysis, including the latest Proteome Discoverer (Thermo Scientific), Mascot (Matrix Science) and Scaffold (Proteome Software). All lab members are equipped with PCs that have direct access via Internet with the server and the mass spectrometers.

Personnel: The Proteomics Core at Einstein has officially three members working in the lab: an Operations Director, a Principal Associate and a Bioinformatician.