SCIENTIFIC SEMINAR

Félix Elortza

CIC bioGUNE

New advances in proteomic analyses

At Proteomics Platform have been settling different methodologies to improve our proteomic analysis performance in terms of sensitivity, throughput, and quality standards. We are all aware that in biomedicine and many basic research projects starting with less material is more. Biopsies can be smaller, required cell amount can be less and therefore experiments can be cheaper, etc. By applying the so called SP3 digestion method we are now able to digest very scarce starting material samples being our proven limit the human oocyte analysis. In proteomics one of the most demanded outcomes is to identify as much as possible proteins, detect which ones are differentially expressed and to quantify these differences. We have been working to implement the Dia-NN (Data Independent Acquisition-Neural Network) method within our pipeline. Overall, this method helps identifying more peptides and quantifying more proteins in complex mixtures. Finally, increasing throughput is also a needed to face some biomedical studies. We have settled a microtiter like PVDF based approach to reduce, alkylate and perform the tryptic digestion over 96x4 samples in 2-3 days of work. These improvements, together with the EVOSEP One chromatographer couple on-line to a TIMS Tof Pro mass spectrometer, make our pipelines capable to tackle high sensitivity and high throughput projects. Different examples of projects where these methods have been applied will be shown.

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MEMBER OF BASQUE RESEARCH & TECHNOLOGY ALLIANCE

EXCELENCIA SEVERO OCHOA

Friday, April 28
Atrio 800
12.00H

BRTA
BASQUE RESEARCH & TECHNOLOGY ALLIANCE