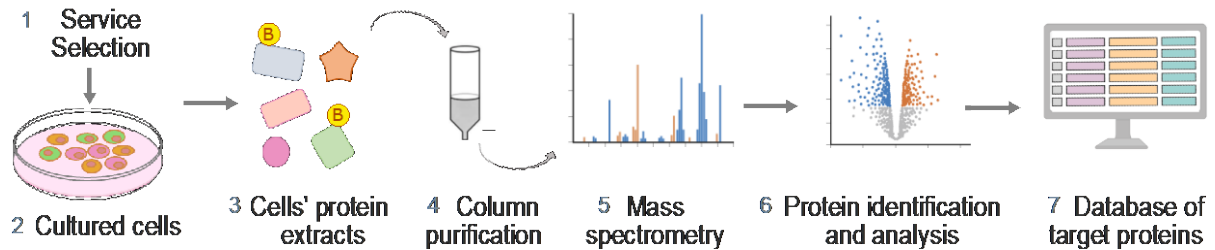


TARGET IDENTIFICATION ANALYSIS

We aim to analyze protein-protein interactions and modifications by ubiquitin (Ub) and ubiquitin-like proteins (UbLs). We use tools such as BioE3, UbL-ID, BioUbL, Molecular Traps (TUBES, SUBES) and TurboID, coupled to label-free quantitative proteomics.



The service will 1) assess needs and propose best approach among the offered technologies, 2) conduct the necessary experiments in transfected cultured cells, 3) follow the required treatments for each strategy and collect cell extracts, 4) isolate modified proteins by affinity chromatography, 5) identify isolated proteins using liquid chromatography – mass spectrometry, 6) provide bioinformatic analysis, and 7) if appropriate, archive data into dedicated databases.

> BioE3

Identification of bona-fide targets of E3 ligases of the ubiquitin family.

- To find specific bona-fide targets of E3s of interest (RING, HECT, CRL).
- To study changes in E3s specificity in upon cell chemical treatments.
- To find neosubstrates of E3s upon treatments with degraders (i.e. molecular glues in targeted protein degradation).

> Interactors

Identification of proximal interactors by proteomics.

- To find interactors in close proximity of a protein of interest.
- To study changes in proximal interactors due to chemical treatments.
- To provide additional validation for weak or dynamic interactions.

> Molecular Traps

Isolation of endogenous proteins modified by the ubiquitin family (ubiquitin and SUMO)

- To isolate proteins modified by the ubiquitin family from cultured cells and in vitro.
- To isolate modified by the ubiquitin family from animal or human tissues organs.
- To discriminate among different types of ubiquitin chains (K63, K48).

> UbL-ID

Identification of interactors of proteins modified by the ubiquitin family.

- To identify interactors of your protein of interest when UbL-modified.
- To compare interactors of a given protein with modifications by different UbLs.

> BioUbL

General identification of proteins modified by the ubiquitin family.

- To identify proteins modified by UbLs of interest in cultured cells.
- To identify proteins modified by UbLs of interest in vivo.

CONTACT

More information:

<https://www.rosabariolab.es/zbiox.php>



For specific needs, please contact our [Technology Transfer Manager](#) or rbarrio@cicbiogune.es or jsutherland@cicbiogune.es