

Mission: To provide a complete platform for the identification and quantification of proteins using mass spectrometry

Technologies

Pipelines for sample preparation from tissue/cells/IPs

- Diagenode Bioruptor
- Precellys 24 tissue homogenizer
- Covaris sonicator



State-of-the-art nano UPLC peptide separation coupled to Mass spectrometry (LC-MS/MS)

- 2 x Waters NanoAcuity UPLC
- Thermo Orbitrap Fusion Lumos Tribrid
- Thermo Orbitrap Exploris 480



Offline HPLC - high pH peptide separation and fraction collection

- Agilent 1260

Liquid handling – sample prep automation, phospho-enrichment

- Agilent BRAVO



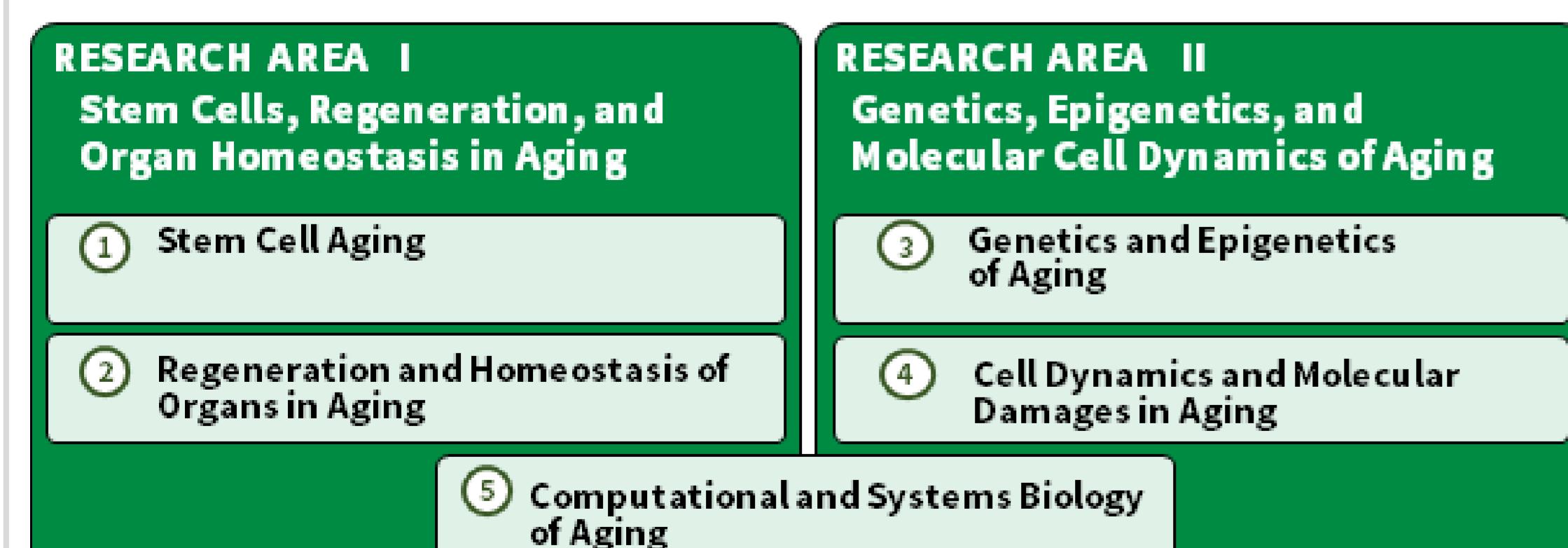
Software and Bioinformatics tools

- Matrix Science Mascot server
- Thermo Proteome Discoverer
- MaxQuant
- Biognosys Spectronaut/SpectroMine/SpectroDive/Quic
- Proteome Science Scaffold
- Bioinformatics Solutions Inc. PEAKS
- Multiple in-house written procedures based on R/Bioconductor
- Isobarquant

Services

- Method development for sample preparation and protein extraction from different biological matrices
- Optimized chromatographic separation of peptides offline (high pH) and online (low pH) with MS
- Usage or development of optimized MS methods for both label-free Data Directed Acquisition (DDA) and isobaric labelling quantification (eg for TMT-labelled samples (Tandem Mass Tags)) and Data Independent Acquisition (DIA) for multi-condition comparisons label-free
- Performing full proteomic experiments for facility users
- Providing training to allow users to process samples and data
- Performing data analysis and reporting results to facility users
- Full collaborators for projects from experimental design, optimization and contributing to manuscripts

Usage

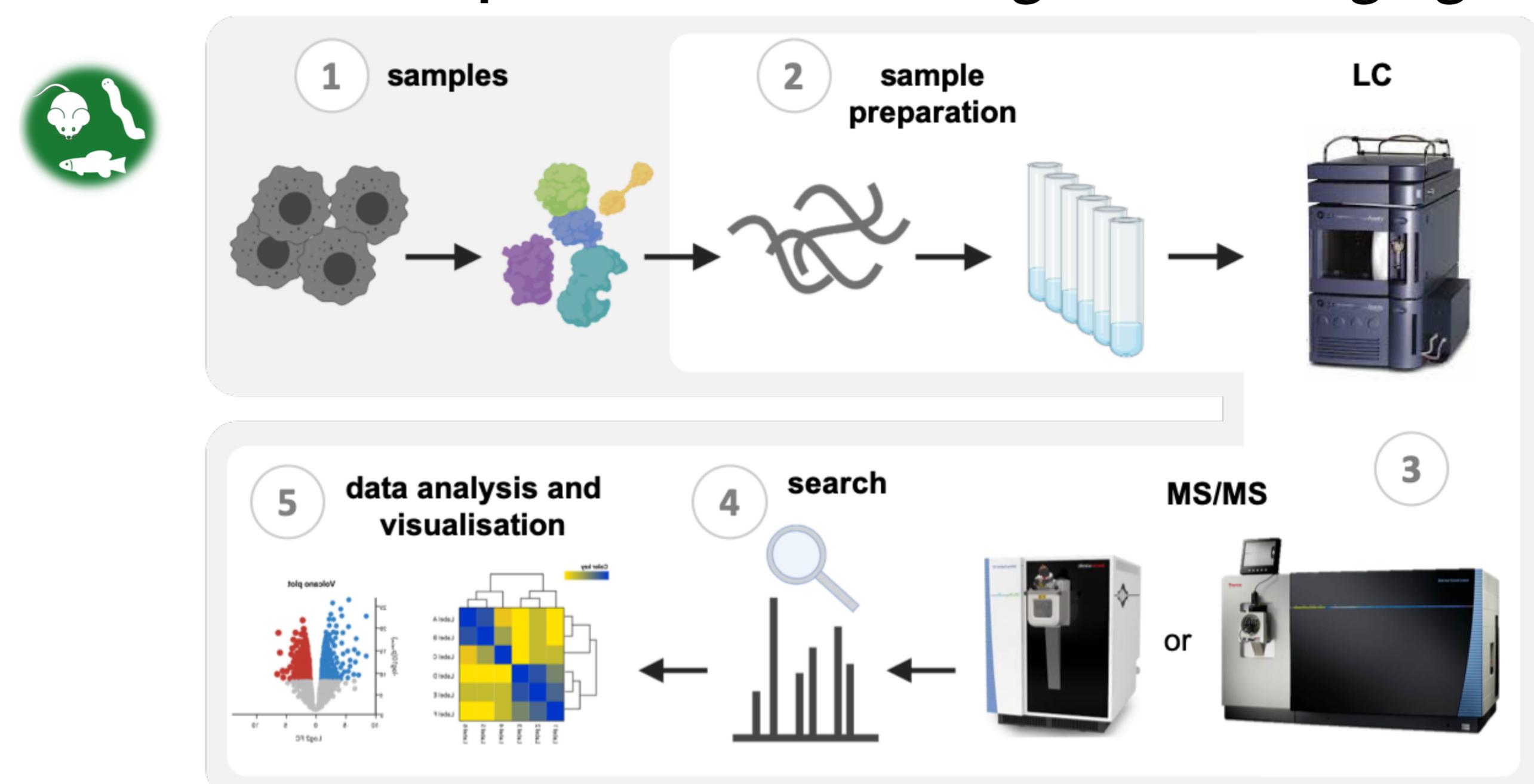


- Working with groups across all internal research areas
- Over 70 projects in 2018

- Collaborating/working on projects with external users (over 30 projects in 2018)

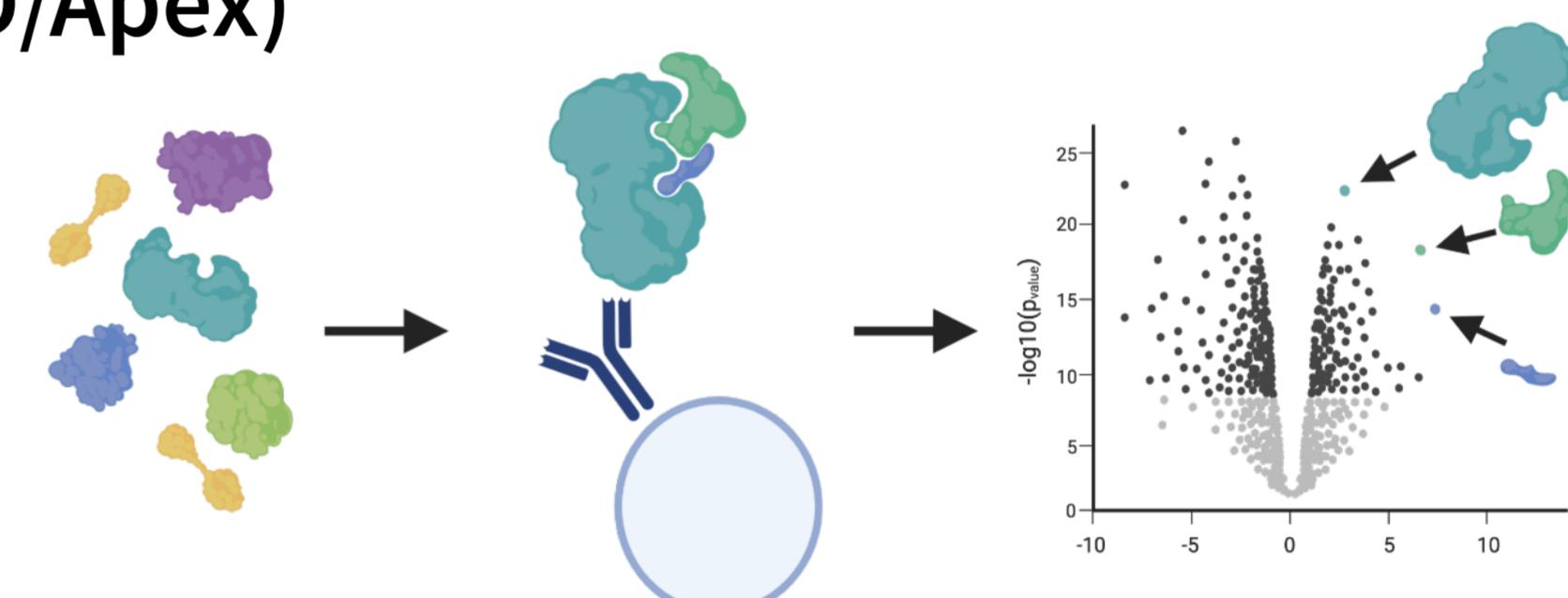
Project Types

Proteome profiles of model organisms in aging

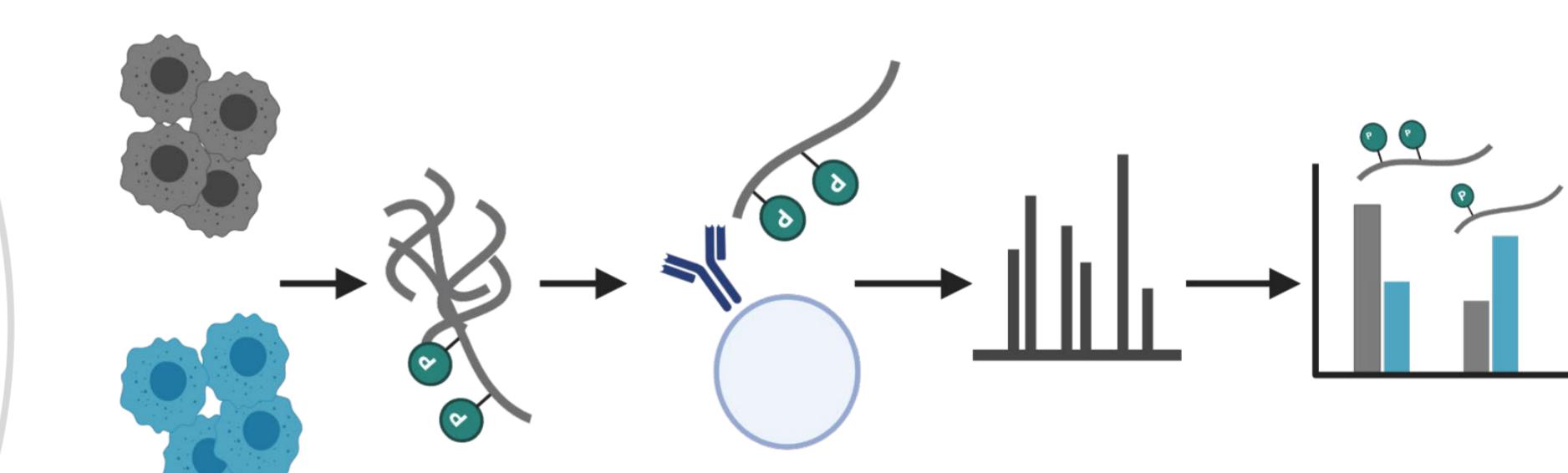


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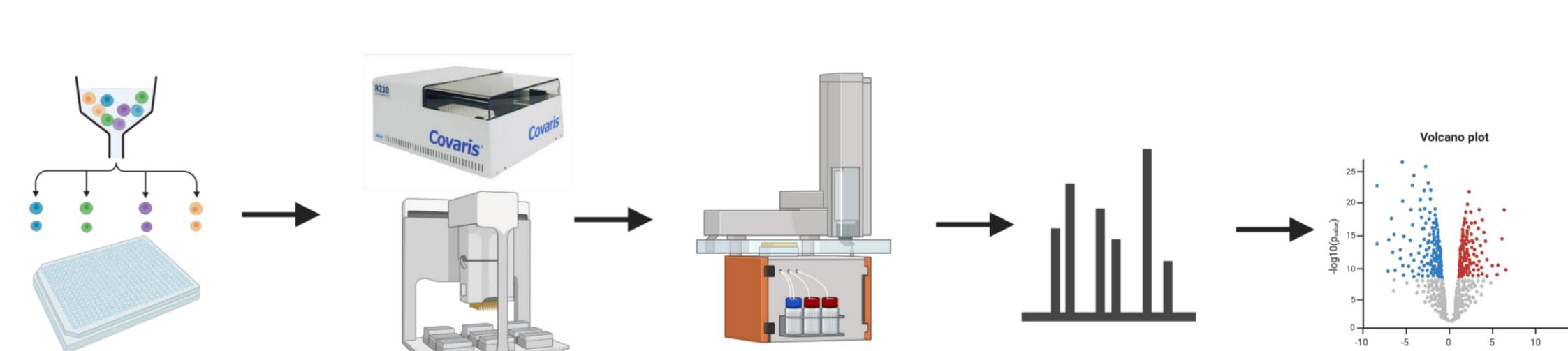
Protein-protein interactions (GFP-Trap, proximity ligation Bio-ID/Apex)



Post-translational modification enrichment and quantification strategies



Low input, high throughput proteomics analysis



Selected Publications

E. Kelmer Sacramento*, J. Kirkpatrick*, M. Mazzetto*, S. Di Sanzo, C. Caterino, M. Sanguanini, N. Papaevgeniou, M. Lefaki, D. Childs, S. Bagnoli, E. Terzibasi Tozzini, A. Bartolome, N. Romanov, M. Baumgart, W. Huber, N. Chondrogianni, M. Vendruscolo, A. Cellerino#, and A. Ori#, "Reduced proteasome activity in the aging brain results in ribosome stoichiometry loss and aggregation," *bioRxiv*, p. 577478, Mar. 2019.

J. Muntel*, J. Kirkpatrick*, R. Bruderer, T. Huang, O. Vitek, A. Ori#, and L. Reiter#, "Comparison of Protein Quantification in a Complex Background by DIA and TMT Workflows with Fixed Instrument Time," *J. Proteome Res.*, vol. 18, no. 3, pp. 1340–1351, Mar. 2019.

L. Ombrato, E. Nolan, I. Kurelac, A. Mavousian, V.L. Bridgeman, I. Heinze, P. Chakravarty, S. Horswell, E. Gonzalez-Gualda, G. Matacchione, A. Weston, J. Kirkpatrick, E. Husain, V. Speirs, L. Collinson, A. Ori, J.-H. Lee, I. Malanchi, "Metastatic-niche labelling reveals parenchymal cells with stem features," *Nature*, vol. 572, no. 7771, pp. 603–608, Aug. 2019.

G. Wyant*, M. Abu-Remaileh*, E. Frenkel, N. Laqtom, V. Dharamdasani, I. Heinze, A. Ori#, and D. Sabatini#, "NUFIP1 is a ribosome receptor for starvation-induced ribophagy," *Science*, vol. 360, no. 6390, pp. 751–758, 2018.

I. Heinze*, M. Bens*, E. Calzia*, S. Holtze, O. Dakhovnik, A. Sahm, J. M. Kirkpatrick, K. Szafranski, N. Romanov, S. N. Sama, K. Holzer, S. Singer, M. Ermolaeva, M. Platzer#, T. Hildebrandt#, and A. Ori#, "Species comparison of liver proteomes reveals links to naked mole-rat longevity and human aging," *BMC Biol.*, vol. 16, no. 1, pp. 1–18, 2018.

