The Proteomics Resource Center

http://inside.rockefeller.edu/proteomics/ or http://rockefeller.edu/proteomics/ P: 212-327-8446

Introduction

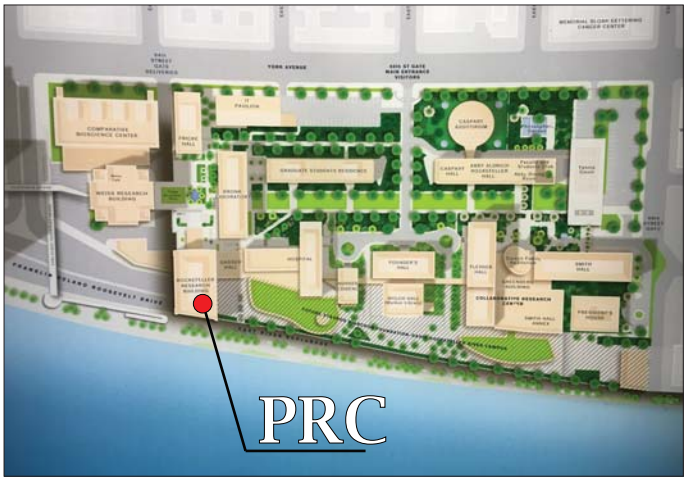
The Proteomics Resource Center (PRC) at The Rockefeller University offers analysis and synthesis of biomolecules for The Rockefeller University community on a subsidized, cost-recovery basis. Based on capacity the Center is also available to other academic institutions.

The primary goal of the Center is to extend the limits of sensitivity and broaden the range of available analytical technologies. Therefore, basic research within the Center is performed to further the development of methodologies.

The Centers' expertise is to identify, characterize and quantitate proteins, peptides and other molecules - for example metabolites and drugs – by liquid chromatography and mass spectrometry. The Center also offers peptide synthesis which includes single peptides with or without modifications and/or stable isotope labeled residues, as well as peptides for arrays.

Selected instruments housed in the Center are available for walk-up use.

The PRC is located on The Rockefeller University campus in the Rockefeller Research Building RRB157.



The Proteomics Resource Center (PRC) is located on the first floor of the RRB - marked by red dot.

A Vision for a Proteomics Resource

Proteomics is defined as *the large-scale study of proteins, particularly their structures and functions.*

For many years I found that the name of our Center: *"The Proteomics Resource Center"* was imprecise. Imprecise because, our main focus is analytical chemistry as it is applied to the identification and quantitation of small molecules, peptides and proteins - as well as peptide synthesis.

But I am beginning to see this a little differently because, though we, the Center, do not decide why and when to begin a proteomics experiment, we are very often very much involved in the design of proteomics experiments. With more than 500 projects per year a large amount of valuable experimental knowledge related to mass spectrometry based proteomics, small molecules/metabolomics and peptide synthesis exists in the Center. This knowledge allows us

The scientists of the Proteomics Resource Center. From left to right: Henry, Joe, Caitlin, Justine, Henrik, Susan & Milica

to provide a *boutique-style proteomics experience* where we tailor experiments and analysis to a particular question. I find that this is the best way to approach questions that needs to be answered by proteomic - and we are excited when we can share our experience to help design sound experiments!

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I like to see our Center as a *melting pot* for mass spectrometry-based proteomics experiments and a place where we, the Center, have the ability to not only share our experience but also act as *matchmakers* between our users - when appropriate and possible – all in the name of collaborative science.

Henrik Molina, Ph.D., Director,
Research Assistant, Professor

Typical Requests

- Exosome profiling [1]
- Co-immunoprecipitations [2]
- Targeted quantitation [3]
- SILAC based quantitation [4]
- Characterization of cyclic peptides[5]
- Nucleoside analysis [6]
- Method development [7]
- Post translational Modifications [8]
- Protein complex characterization [9]
- Epitope mapping peptide library [10]

References

1. Hoshino, A., et al., *Tumour exosome integrins determine organotropic metastasis.* Nature, 2015. **527**(7578): p. 329-35.
2. Halberg, N., et al., *PITPNC1 Recruits RAB1B to the Golgi Network to Drive Malignant Secretion.* Cancer Cell, 2016. **29**(3): p. 339-53.
3. Simon, D.J., et al., *Axon Degeneration Gated by Retrograde Activation of Somatic Pro-apoptotic Signaling.* cell, 2016.
4. Maze, I., et al., *Critical Role of Histone Turnover in Neuronal Transcription and Plasticity.* Neuron, 2015. **87**(1): p. 77-94.
5. Biggins, J.B., et al., *The chemical arsenal of Burkholderia pseudomallei is essential for pathogenicity.* J Am Chem Soc, 2014. **136**(26): p. 9484-90.
6. Zhu, X., et al., *Role of Tet1/3 Genes and Chromatin Remodeling Genes in Cerebellar Circuit Formation.* Neuron, 2015.
7. Bunkenborg, J., et al., *Covalent perturbation as a tool for validation of identifications and PTM mapping applied to bovine alpha-crystallin.* Proteomics, 2015.
8. Tang, Z., et al., *SET1 and p300 Act Synergistically, through Coupled Histone Modifications, in Transcriptional Activation by p53.* Cell, 2013. **154**(2): p. 297-310.
9. Chaker-Margot, M., et al., *Stage-specific assembly events of the 6-MDa small-subunit processome initiate eukaryotic ribosome biogenesis.* Nat Struct Mol Biol, 2015.
10. Neubert, K., et al., *Antigen Delivery to CD11c+CD8- Dendritic Cells Induces Protective Immune Responses against Experimental Melanoma in Mice In Vivo.* J Immunol, 2014. **192**(12): p. 5830-8.

Key metrics (2017) for the Proteomics Resource Center at The Rockefeller University

6 mass spectrometers (MS) coupled to HPLC

190+ users

Median turn-around time for proteomics/peptides: 8/28 days

15 co-authored publicatons and 18 acknowledgedments

Suggested readings

Fields, G.B. & Noble, R.L. *Solid phase peptide synthesis utilizing 9-fluorenylmethoxycarbonyl amino acids.* International Journal of Peptide and Protein Research 35, 161-214 (1990).

Bantscheff, M. et al. *Quantitative mass spectrometry in proteomics: critical review update from 2007 to the present.* Analytical and Bioanalytical chemistry 404, 939-965 (2012).

Acknowledgments

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