MCP GRAPHICAL ABSTRACTS—GUIDELINES

The graphical abstract is an image that is displayed on the first page of the article PDF, along with “In Brief” and “Highlights.” It will also be prominently displayed online on the MCP website in both the Table of Contents and the article page view.
The graphical abstract is intended to be the first landing page for readers to give them an immediate impression of the primary message of the paper. It is designed to help readers easily identify papers that are most relevant to their research interests.

Technical Requirements
Size: The submitted image should be square in size with a minimum of 996 × 996 pixels (h × w) at 300 dpi or 1659 × 1659 pixels (h × w) at 500 dpi.
Font: Arial, 12–16 points. Smaller fonts will not be legible.
Preferred file types: TIFF, EPS, PDF or MS Office files.
Content: The graphical abstract should consist of one single panel; you may reuse elements from figures in the paper.

The graphical abstract should:
- Consist of one single panel diagram
- Preferably be a new figure not included in the paper itself; we would accept an adapted figure from the paper as long as it captures all the salient points of a graphical abstract
- Have a clear direction, start and end, “reading” from top-to-bottom or left-to-right
- Provide a visual indication of the biological context of the results depicted (subcellular location, tissue or cell type, species, etc.)
- Emphasize the new findings from the current paper without including excess details from previous literature
- Avoid the inclusion of features that are more speculative (unless the speculative nature can be made apparent visually)
- Not include data items of any type; all the content should be in a graphical form
- Use simple labels
- Keep text to a minimum
- Highlight one process or make one point clear
- Be free of distracting and cluttering elements
- Use colors effectively to enhance the graphical abstract both aesthetically and by directing the reader’s attention to focal points of interest

Please see examples of what we deem as good graphical abstracts in the following pages.

References
1. Burlingame, A.L., Carr, S.A., Gingras, A.C. (2018) Gaining an easy visual grasp on MCP content. *Mol. Cell Proteomics* **17**, 1259-1260

Quantitative Proteomics Links the LRRC59 Interactome to mRNA Translation on the ER Membrane

Authors

Molly M. Hannigan, Alyson M. Hoffman, J. Will Thompson, Tianli Zheng, and Christopher V. Nicchitta

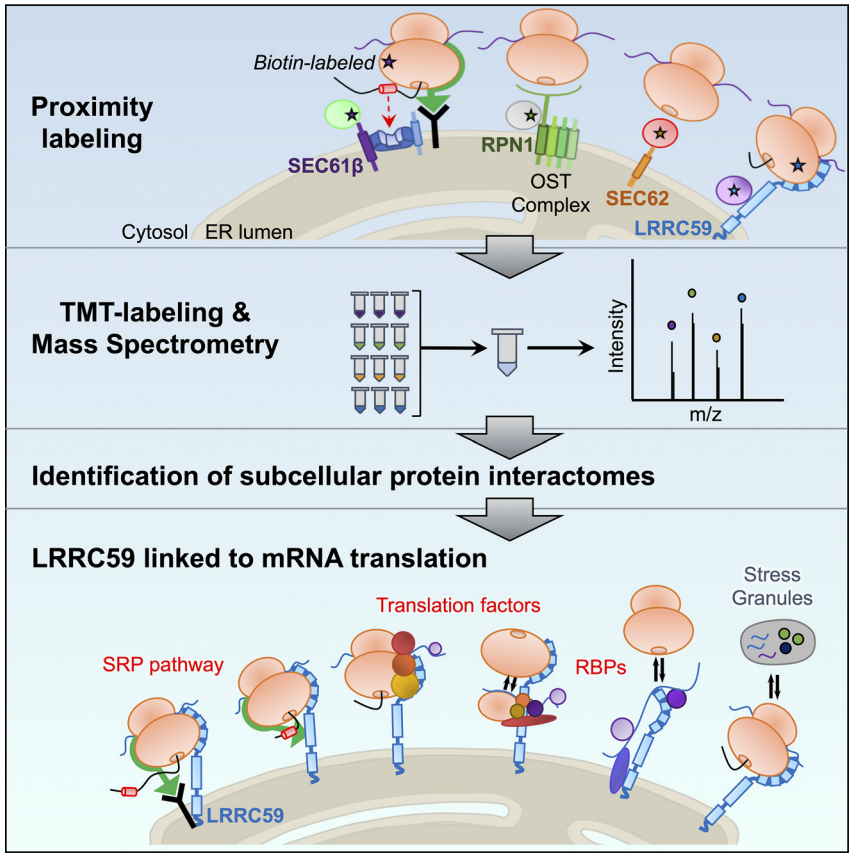
Correspondence

christopher.nicchitta@duke.edu

In Brief

Hannigan et al. characterize the protein interactomes of four candidate ER ribosome-binding proteins, providing evidence that ER-bound ribosomes reside in distinct molecular environments. Their data link SEC62 to ER redox regulation and chaperone trafficking, and suggest a new role for LRRC59 in the regulation of mRNA translation.

Graphical Abstract



Highlights

- Identification of subcellular protein interactomes via proximity labeling and quantitative multiplexed proteomics.
- SEC61β and RPN1 interactomes overlap with translocon-associated protein networks.
- SEC62 interacts with redox-linked proteins and ER luminal chaperones.
- LRRC59 directly interacts with mRNA translation factors and SRP machinery on the ER.

Hannigan et al., 2020, Mol Cell Proteomics *19(11)*, 1826–1849
November 2020

https://doi.org/10.1074/mcp.RA120.002228

Radiosensitization by Kinase Inhibition Revealed by Phosphoproteomic Analysis of Pancreatic Cancer Cells

Authors

Svenja Wiechmann, Elena Saupp, Daniela Schilling, Stephanie Heinzlmeir, Günter Schneider, Roland M. Schmid, Stephanie E. Combs, Bernhard Kuster, and Sophie Dobiasch

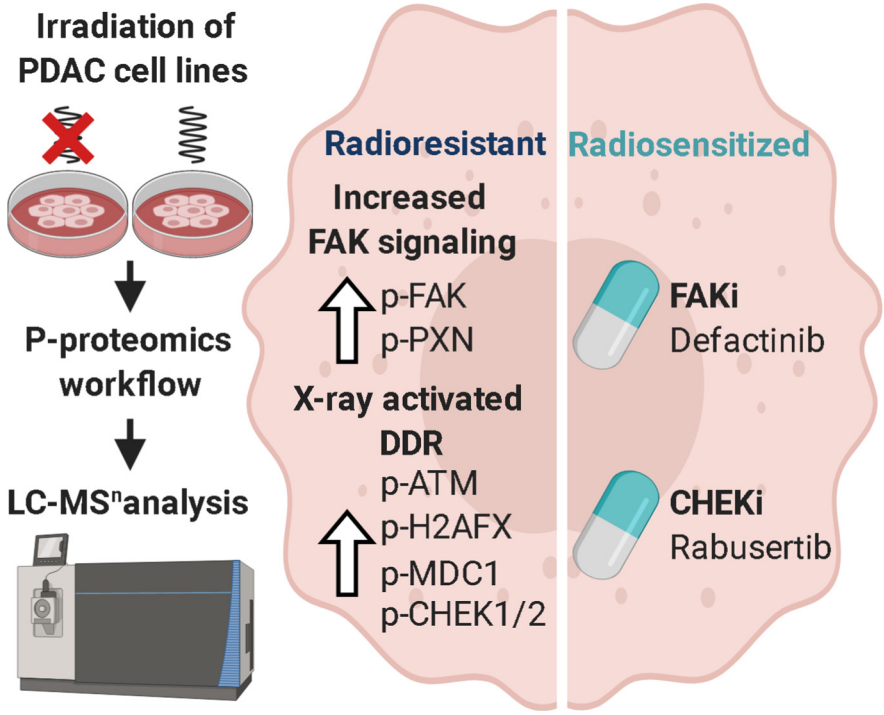
Correspondence

Sophie.Dobiasch@tum.de

In Brief

The proteomes and phosphoproteomes of radiosensitive and radioresistant PDAC cell lines were analyzed. Irrespective of the sensitivity of the cells, the phosphorylation-based radiation-responsive signaling network featured known DDR proteins and novel ATM substrates. Radioresistant cells displayed significant expression levels of apoptotic proteins, including NQO1, and elevated phosphorylation levels of proteins involved in actin dynamics and FAK activity. Sensitization of former resistant PDAC cells toward radiation was realized by pharmacological inhibition of FAK and CHEK by Defactinib and Rabusertib.

Graphical Abstract



Highlights

- Proteomes and phosphoproteomes of radiosensitive and radioresistant PDAC cell lines.
- Common activation of DDR is proven by ATM activity on known and novel substrates.
- Resistant cells bear raised NQO1 expression, actin dynamics including FAK activity.
- Inhibitors of CHEK Rabusertib and FAK Defactinib radiosensitize PDAC cells.

Wiechmann et al., 2020, Mol Cell Proteomics *19(10),* 1649–1663
October 2020 © 2020 Wiechmann et al. Published by The American Society for Biochemistry and Molecular Biology, Inc.
https://doi.org/10.1074/mcp.RA120.002046

Multisample Mass Spectrometry-Based Approach for Discovering Injury Markers in Chronic Kidney Disease

Authors

Ji Eun Kim, Dohyun Han, Jin Seon Jeong, Jong Joo Moon, Hyun Kyung Moon, Sunhwa Lee, Yong Chul Kim, Kyung Don Yoo, Jae Wook Lee, Dong Ki Kim, Young Joo Kwon, Yon Su Kim, and Seung Hee Yang

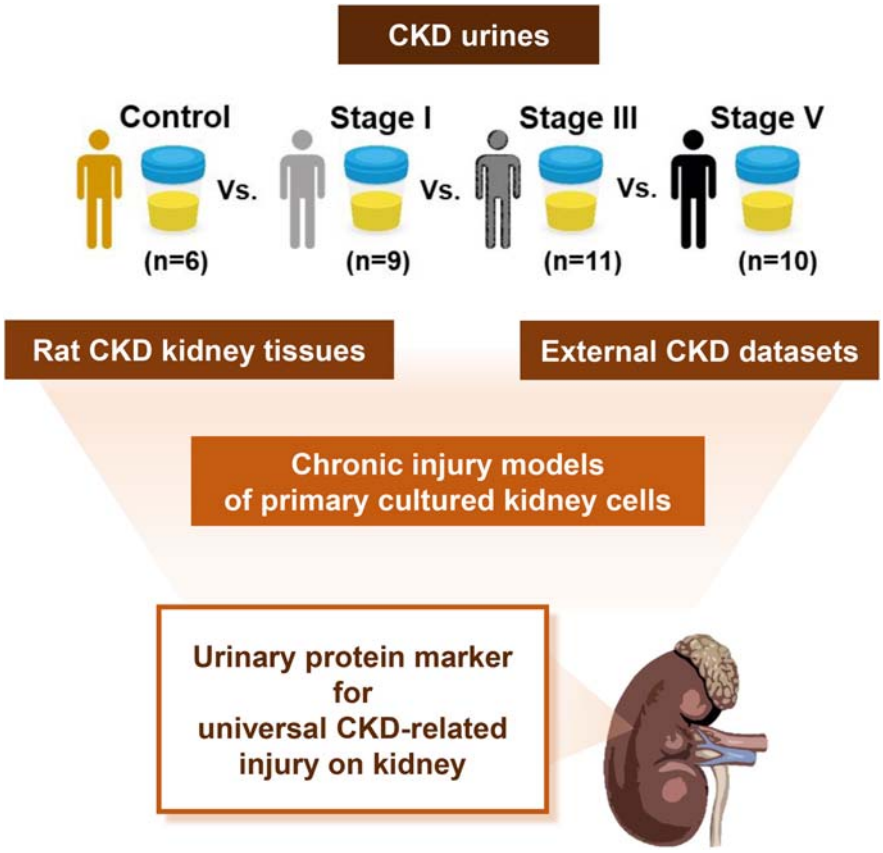
Correspondence

ysh5794@gmail.com

In Brief

The key renal-expressed proteins including protein S and galectin-1 associated with CKD stages were determined by applying quantitative MS-based proteomics using multiple types of samples. The discovered proteins represent potential markers of chronic kidney injury related to renal hypoxia and candidate contributors to CKD pathophysiology.

Graphical Abstract



Highlights

- This study aimed to specify chronic kidney injury markers through proteomics
- Ten putative candidate proteins were found to increase with chronic kidney injury
- Galectin-1 and protein S were elevated in glomeruli and tubules after chronic injury
- Galectin-1 also showed an inverse correlation with renal function

2021, Mol Cell Proteomics *20*, 100037

https://doi.org/10.1074/mcp.RA120.002159

HIGD2A is Required for Assembly of the COX3 Module of Human Mitochondrial Complex IV

Authors

Daniella H. Hock, Boris Reljic, Ching-Seng Ang, Linden Muellner-Wong, Hayley S. Mountford, Alison G. Compton, Michael T. Ryan, David R. Thorburn, and David A. Stroud

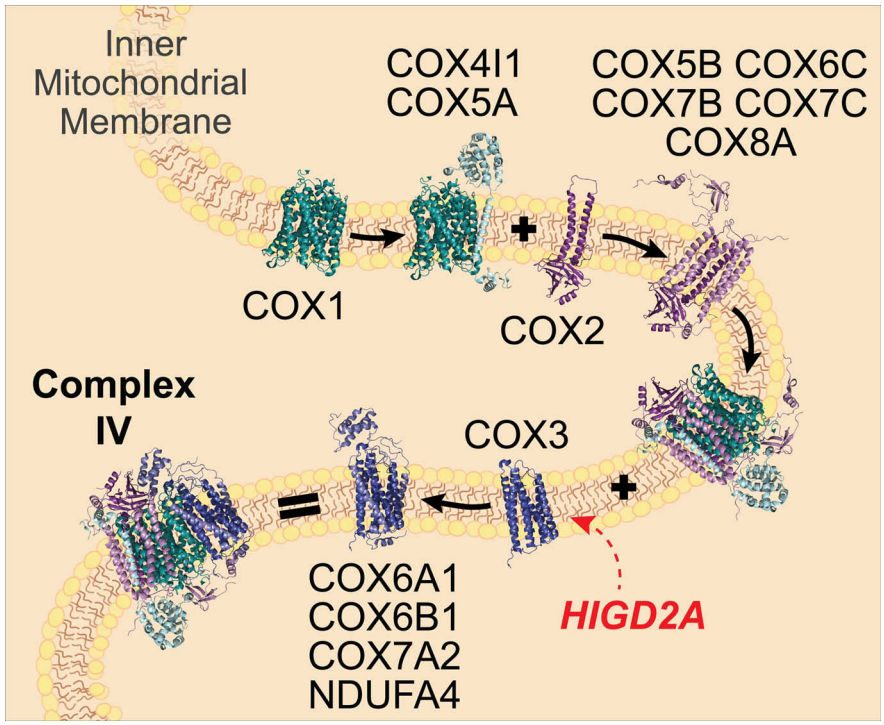
Correspondence

david.stroud@unimelb.edu.au

In Brief

Assembly factors play a critical role in the biogenesis of mitochondrial respiratory chain complexes, some of which are present in large structures known as supercomplexes. Various assembly factors have been proposed as required for supercomplex assembly, including HIGD2A. We used quantitative proteomics and gene editing to clarify the function of human HIGD2A, revealing it to be a classical assembly factor required for biogenesis of mitochondrial DNA encoded COX3, a subunit of complex IV.

Graphical Abstract



Highlights

- Quantitative proteomics reveals HIGD2A is required for assembly of the COX3 module.
- Pulse-SILAC demonstrates that HIGD2A is involved in COX3 biogenesis.
- Supercomplexes in HIGD2A knockout cells are depleted of COX3.
- HIGD2A is the first assembly factor identified for the COX3 module of Complex IV.

Hock et al., 2020, Mol Cell Proteomics *19(7)*, 1145–1160

https://doi.org/10.1074/mcp.RA120.002076

Arginine in *C9ORF72* Dipolypeptides Mediates Promiscuous Proteome Binding and Multiple Modes of Toxicity

Authors

Mona Radwan, Ching-Seng Ang, Angelique R. Ormsby, Dezerae Cox, James C. Daly, Gavin E. Reid, and Danny M. Hatters

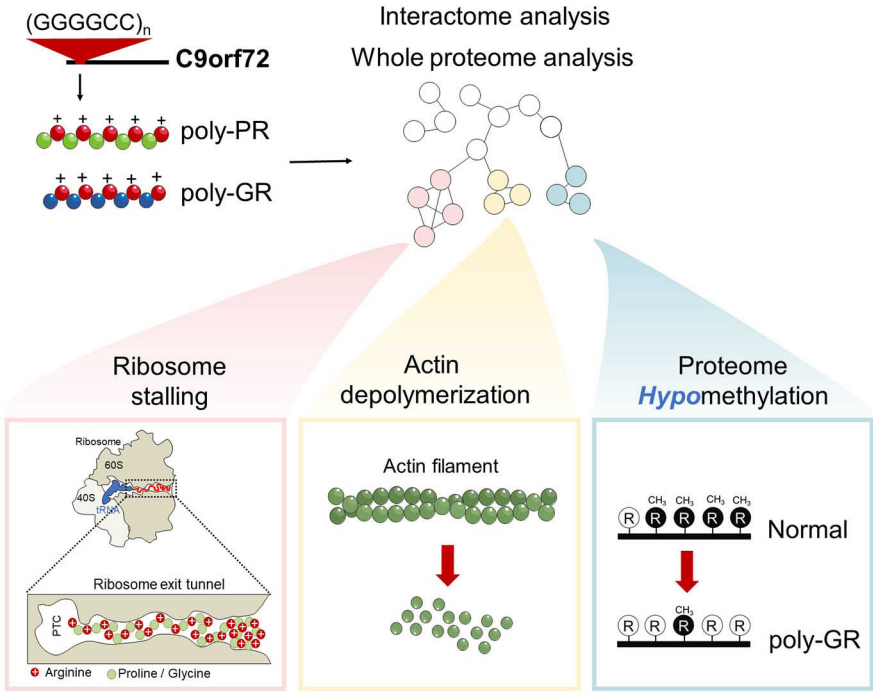
Correspondence

dhatters@unimelb.edu.au

In Brief

C9ORF72-associated Motor Neuron Disease patients feature abnormal expression of 5 dipeptide repeat (DPR) polymers. We found the most toxic DPRs, PR and GR, were particularly promiscuous binders to endogenous proteins. This included ribosomal proteins, translation initiation factors and translation elongation factors. The corresponding biological impacts were multipronged and included stalling of ribosomes during translation, hypomethylation of endogenous proteins, and the destabilization of the actin cytoskeleton. The findings point to new mechanisms of toxicity in disease caused by arg-rich DPRs.

Graphical Abstract



Highlights

- Quantitative proteome interactions with 5 different *C9ORF72* dipolypeptides (DPRs).
- The arg-rich DPRs promiscuously bound to the proteome compared with the other DPRs.
- Long repeat lengths of arg-rich DPRs, but not short lengths, stalled ribosomes.
- The arg-rich DPRs also reduced arginine methylation and actin cytoskeleton assembly.

Radwan et al., 2020, Molecular & Cellular Proteomics *19*, 640–654
April 2020
https://doi.org/10.1074/mcp.RA119.001888

ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis

Authors

Johannes Griss, Guilherme Viteri, Konstantinos Sidiropoulos, Vy Nguyen, Antonio Fabregat, and Henning Hermjakob

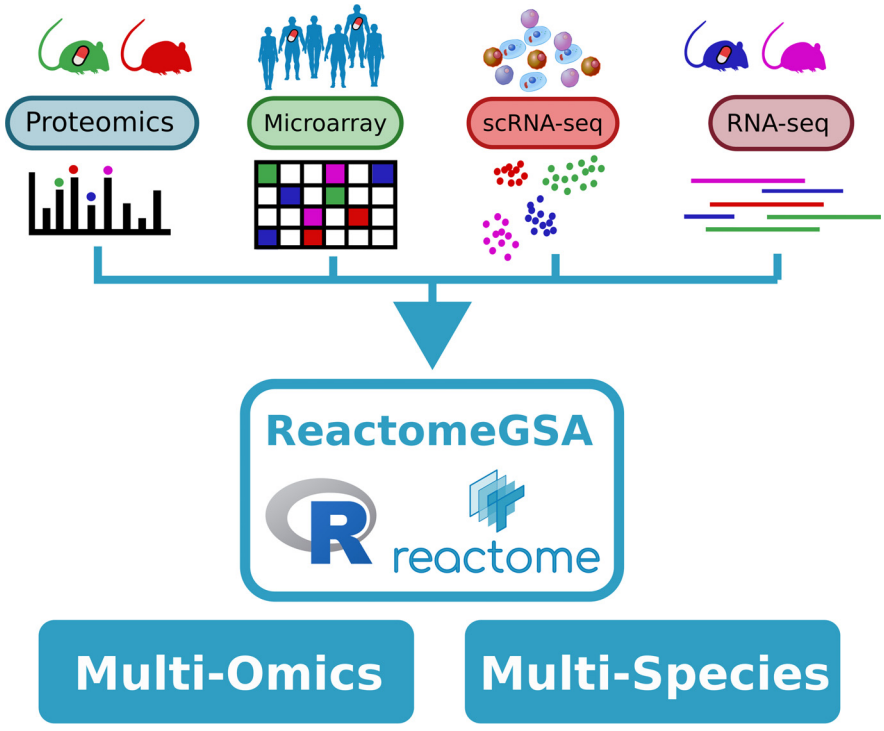
Correspondence

johannes.griss@meduniwien.ac.at; hhe@ebi.ac.uk

In Brief

We present the novel ReactomeGSA resource for comparative pathway analyses of multi-omics datasets. ReactomeGSA is accessible through Reactome's web interface and the novel ReactomeGSA R Bioconductor package with explicit support for scRNA-seq data.We showcase ReactomeGSA's functionality by characterizing the role of B cells in anti-tumour immunity. Combining multi-omics data of five TCGA studies reveals marked opposing effects of B cells in different cancers. This showcases how ReactomeGSA can quickly derive novel biomedical insights by integrating large multi-omics datasets.

Graphical Abstract



Highlights

- ReactomeGSA is a novel tool for multi-species, multi-omics pathway analysis.
- Its quantitative pathway analysis methods offer high statistical power.
- Combining data of five TCGA studies shows B cells have opposing effects in cancers.
- ReactomeGSA reveals differences in key pathways between transcript- and protein-level.

Griss et al., 2020, Mol Cell Proteomics *19(12),* 2115–2124

https://doi.org/10.1074/mcp.TIR120.002155

Fast and Accurate Bacterial Species Identification in Urine Specimens Using LC-MS/MS Mass Spectrometry and Machine Learning

Authors

Florence Roux-Dalvai, Clarisse Gotti, Mickaël Leclercq, Marie-Claude Hélie, Maurice Boissinot, Tabiwang N. Arrey, Claire Dauly, Frédéric Fournier, Isabelle Kelly, Judith Marcoux, Julie Bestman-Smith, Michel G. Bergeron, and Arnaud Droit

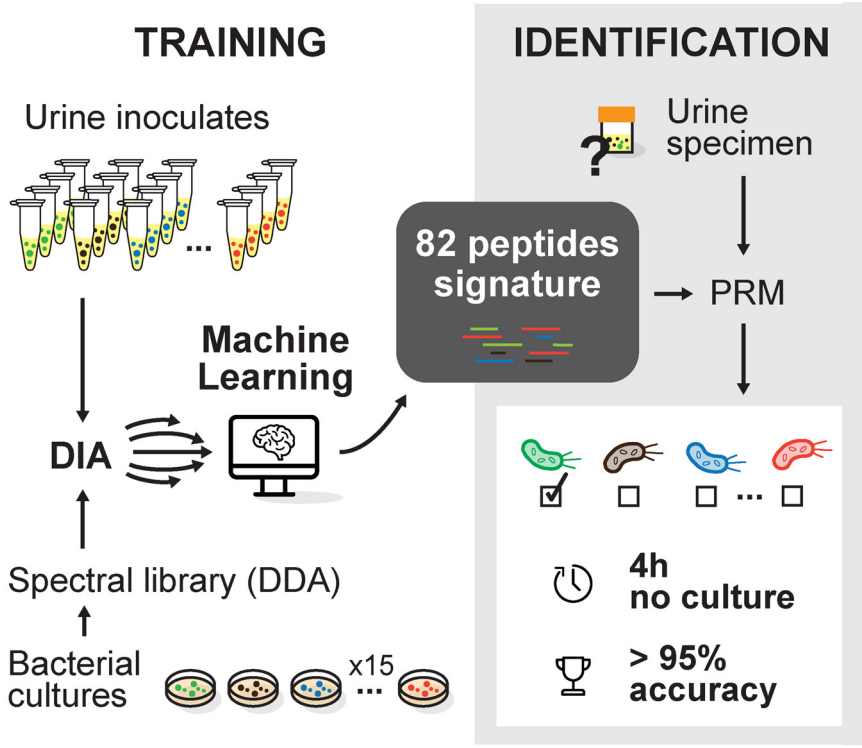
Correspondence

arnaud.droit@crchuq.ulaval.ca

In Brief

We have developed a new method for the identification of bacterial species causing Urinary Tract Infections. The first training step used DIA analysis on multiple replicates of bacterial inoculates to define a peptide signature by machine learning classifiers. In a second identification step, the signature is monitored by targeted proteomics on unknown samples. This fast, culture-free and accurate method paves the way of the development of new diagnostic approaches limiting the emergence of antimicrobial resistances.

Graphical Abstract



Highlights

- Fast and culture-free method for the identification of the 15 bacterial species causing UTIs.
- Combination of DIA analysis and machine learning algorithms to define a peptide signature.
- High accuracy, good linearity and reproducibility, sensitivity below standard threshold.
- Transferability to other laboratories and other mass spectrometers.

Roux-Dalvai et al., 2019, Molecular & Cellular Proteomics *18*, 2492–2505
December 2019
https://doi.org/10.1074/mcp.TIR119.001559

Proteomics and Metaproteomics Add Functional, Taxonomic and Biomass Dimensions to Modeling the Ecosystem at the Mucosal-luminal Interface

Authors

Leyuan Li and Daniel Figeys

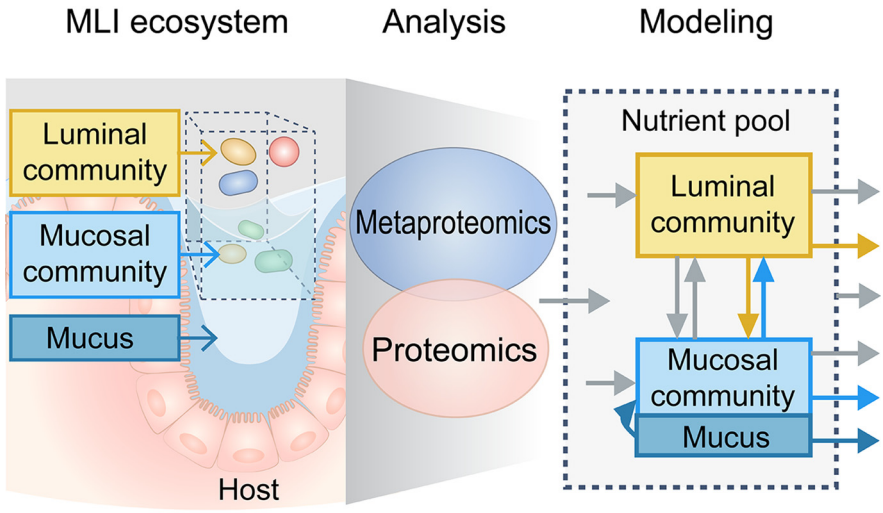
Correspondence

dfigeys@uottawa.ca

In Brief

Proteomics and metaproteomics are important tools for studying the spatiotemporal heterogeneous ecosystem in our gut. We review strategies and their applications to gut ecology studies, such as building a dynamical model of the MLI.

Graphical Abstract



Highlights

- The gut mucosal-luminal interface is a spatiotemporal heterogeneous ecosystem.
- Proteomics and metaproteomics are tools to study the host and microbiome functionality.
- Insights into functional diversity, biomass, and matter flow can be obtained.
- Such data can be complementary inputs for building ecology models of the microbiome.

Li and Figeys, 2020, Mol Cell Proteomics *19(9)*, 1409–1417

https://doi.org/10.1074/mcp.R120.002051

Proximity Dependent Biotinylation: Key Enzymes and Adaptation to Proteomics Approaches

Authors

Payman Samavarchi-Tehrani, Reuben Samson, and Anne-Claude Gingras

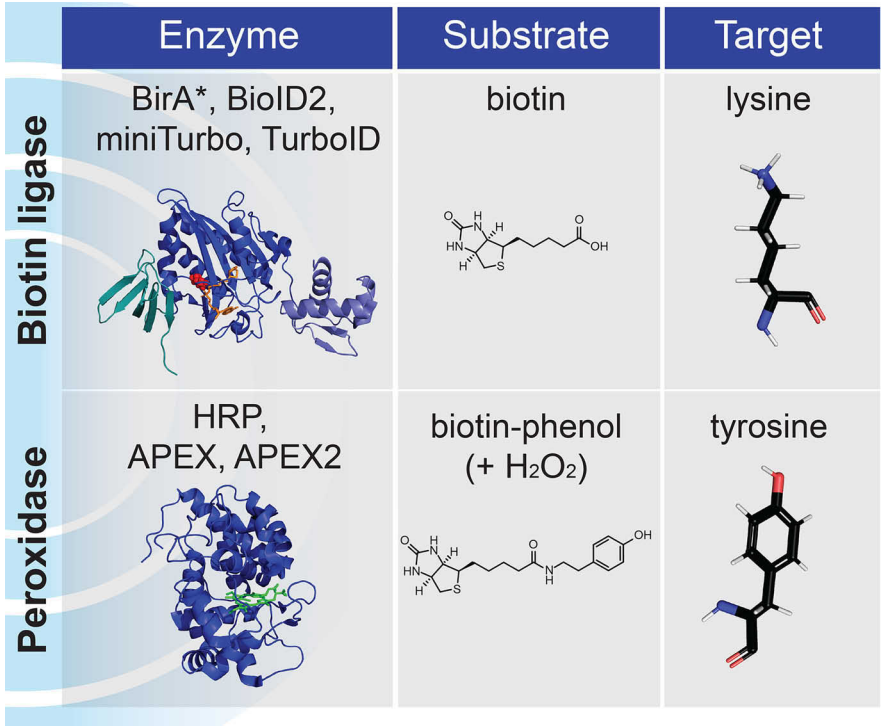
Correspondence

gingras@lunenfeld.ca

In Brief

Proximity-dependent biotinylation approaches such as BioID and APEX overcome classical limitations of biochemical purification and have gained widespread use in recent years for revealing cellular neighborhoods. Here we focus on the structural diversity and mechanisms of the two classes of enzymes, biotin protein ligases and peroxidases, and discuss current and emerging applications of these enzymes for proximity dependent biotinylation. We provide guidelines for enzyme selection and experimental design for performing and interpreting proximity-dependent biotinylation experiments.

Graphical Abstract



Highlights

- Proximity-dependent biotinylation (PDB) approaches involve fusion of a bait with an enzyme.
- BioID (biotin protein ligase) and APEX (peroxidase) are distinct enzymes used in PDB.
- Past, present and future development and applications of PDB are discussed.
- We review labeling mechanisms and kinetics to provide guidance for experimental design.
- We discuss controls and considerations for data interpretation.

Samavarchi-Tehrani et al., 2020, Molecular & Cellular Proteomics *19*, 757–773
May 2020
https://doi.org/10.1074/mcp.R120.001941