



Proteomics – Getting started

How to prepare protein samples for mass spectrometry analysis at SPARC

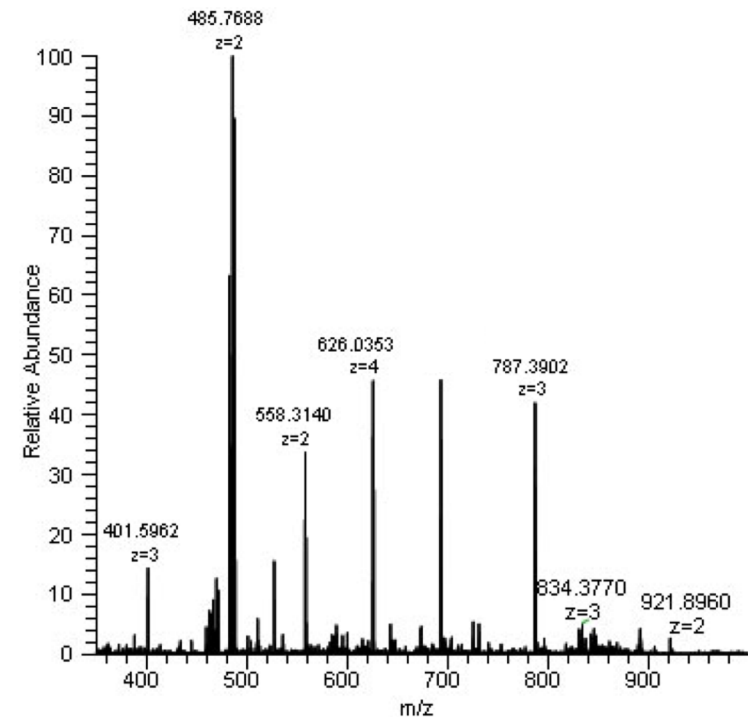
Presented by Leanne Wybenga-Groot
at SickKids Spotlight Series, Jan. 15, 2020

What is Proteomics?

- The entire complement of proteins present in a cell or tissue is known as its proteome.
- Proteomics is the study of proteomes and their functions.
- Proteome is more complex and dynamic than genome
 - 1 gene \rightarrow \geq 1 protein
 - Protein modifications
 - Δ protein abundance
 - Protein interactions

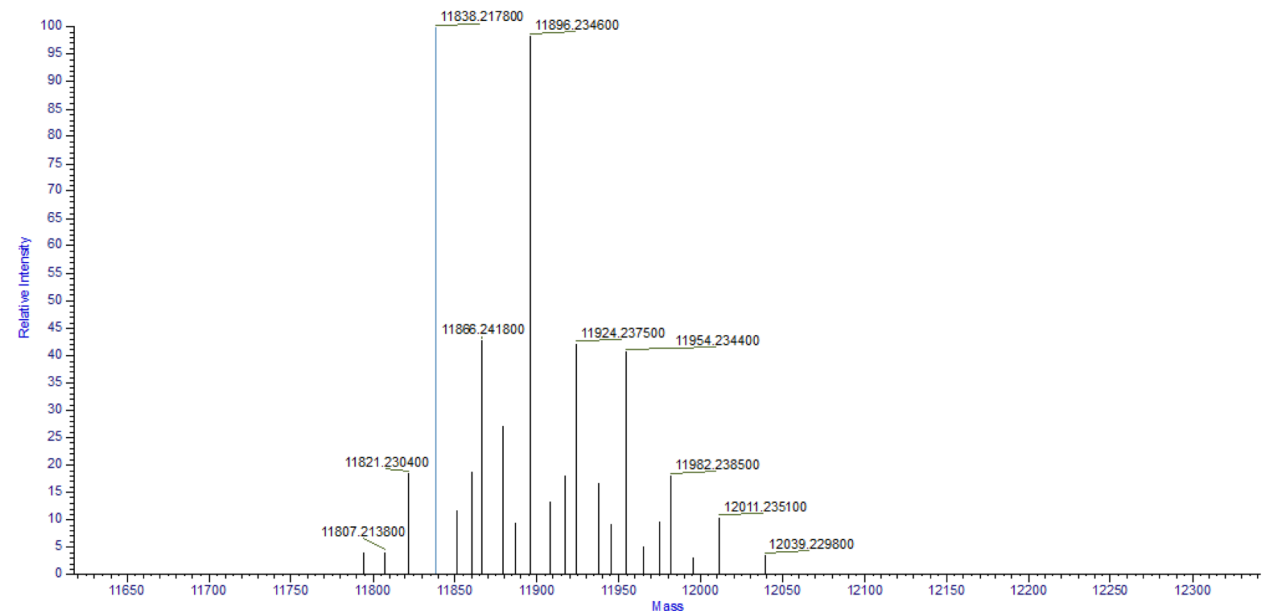
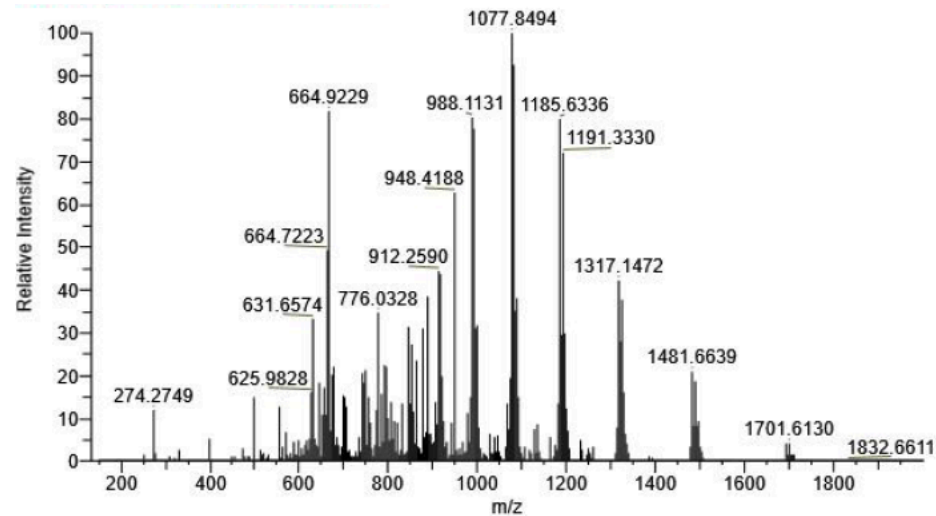
What is Mass Spectrometry?

- Analytical technique that measures the mass-to-charge ratio (m/z) of ions
- Results presented as a mass spectrum, a plot of intensity vs. m/z
- At SPARC Molecular Analysis, we perform mass spectrometry on PROTEIN samples



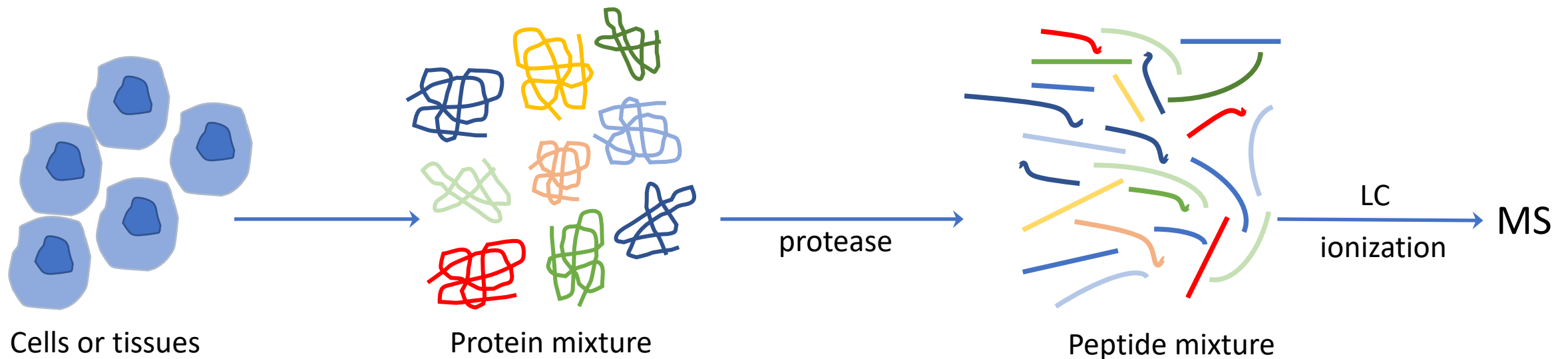
Intact Mass Analysis

- Purpose: you want to know the precise MASS of your protein
- Suitable for purified protein or peptide
- Sample is NOT digested before analysis but kept intact
- Contact SPARC staff for details of how to get started



Bottom-up MS

- Purpose: you want to identify proteins in a complex sample
- Suitable for cell & tissue lysates, BioID or IP experiments, gel bands, etc
- Proteins are digested into peptides with a protease, introduced into MS and identified by tandem MS (MS/MS)
- Liquid chromatography is used to separate the complex sample into simpler samples and introduce peptides to MS (LC MS/MS)



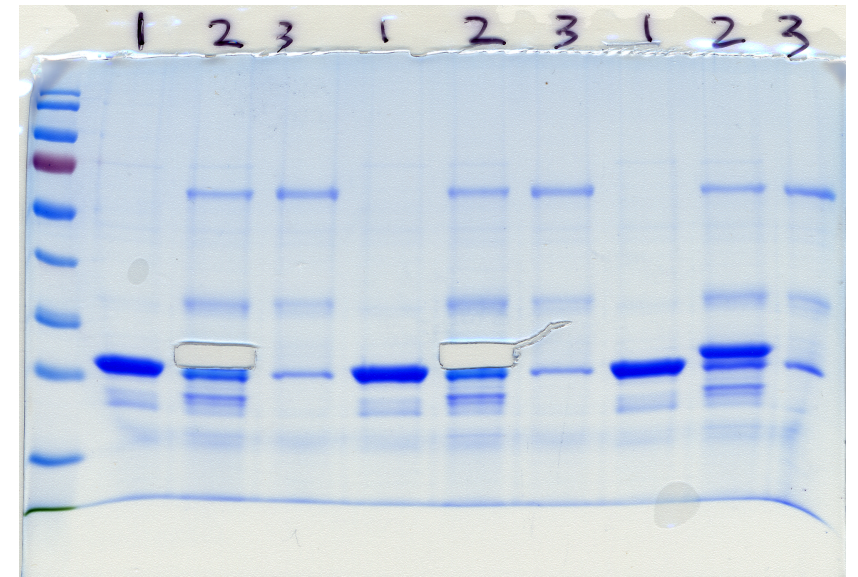
Preparing samples for MS analysis

- Minimize keratin contamination!! Wear gloves, lab coat, use clean reagents and glassware.
- We like 10-30 ug of protein sample, but can achieve good results with less depending on sample complexity (1-5 ug).
- We will need to know the biological source or species of your sample (eg. human, mouse, E. coli)
- We prefer to know the protein concentration of your sample
- We need to know what solvent or buffer your sample is in

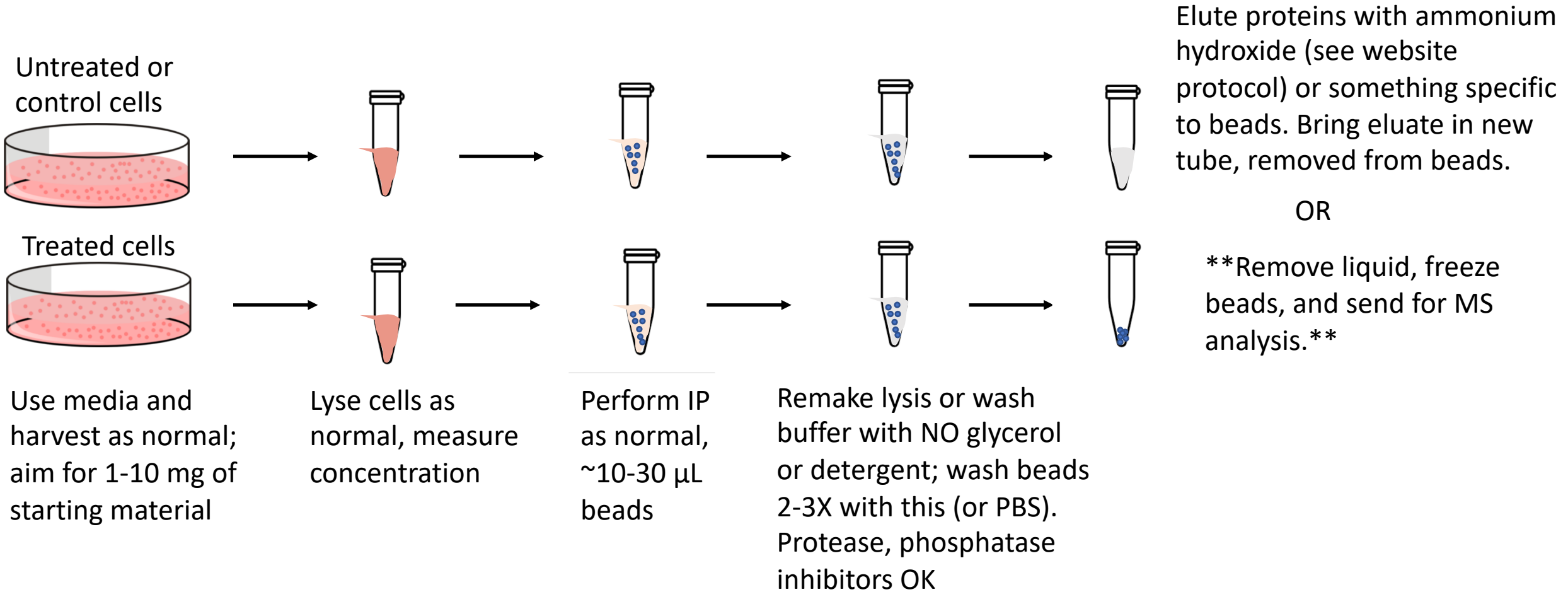


Preparing a gel band for MS analysis

- Use new glass plates for SDS-PAGE and clean, new boxes for staining.
- Cut out band in laminar flow hood using clean materials.
- Cut gel slice 2-3 mm wide only; avoid excess gel!
- Do not combine multiple gel bands in same tube.
- Store gel slices in 1% acetic acid at 4°C.



Preparing IP or BioID samples for MS



Preparing solutions for MS analysis

- Cell or tissue lysates
 - Can use detergents in lysis buffer; we will perform acetone precipitation or S-Trap to remove it, but expect to lose sample
 - Sample is more complex, thus need 3-4 hr LC MS/MS run
 - Can be labelled with TMT tags and multiplexed (run together). For this, need 50-100 μg of protein per sample.
- Secretomes
 - Collect 25-50 mL media from cell plate
 - Serum free for at least 24 hr
 - We will concentrate media and process as normal

What do you get from us?

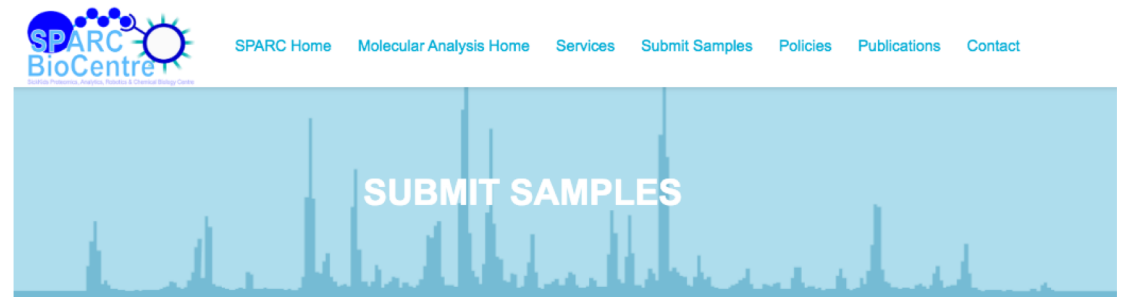
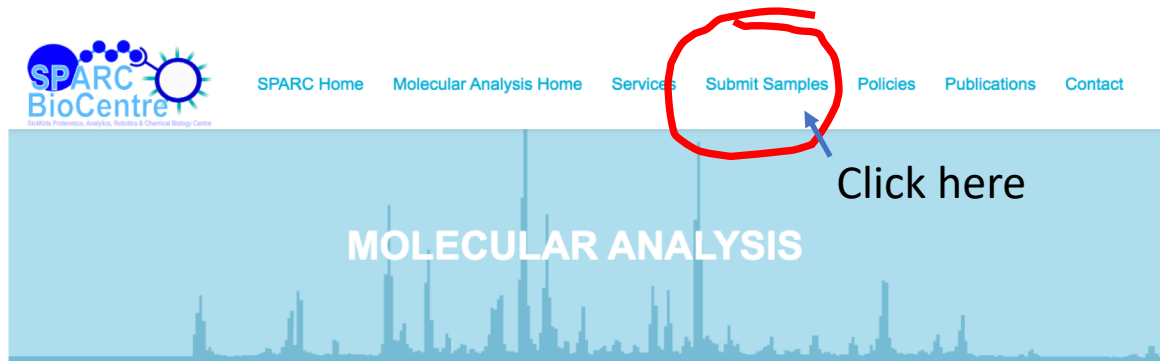


- Consultation – come talk to us in 21.9440 or send an email
- A list of proteins identified in your sample, typically in Scaffold format

#	Visible?	Starred?	Accession	Molecular Weight	Protein	Trypsin
Bio View: Identified Proteins (25)						
1	✓	✗	gi 148235701 (+3)	36 kDa	1	1
2	✓	✗	gi 116517311 (+7)	254 kDa	1	1
3	✓	✗	gi 148697878 (+7)	48 kDa	1	1
4	✓	✗	gi 116283990 (+17)	60 kDa	1	1
5	✓	✗	gi 13435867 (+2)	103 kDa	6	6
6	✓	✗	gi 111308159 (+4)	71 kDa	1	1
7	✓	✗	gi 111185567 (+4)	55 kDa	1	1
8	✓	✗	gi 149255332	23 kDa	1	1
9	✓	✗	gi 149266757 (+2)	566 kDa	1	1
10	✓	✗	gi 149272298	8 kDa	1	1
11	✓	✗	gi 123789115 (+2)	106 kDa	1	1
12	✓	✗	gi 12643781 (+10)	271 kDa	1	1
13	✓	✗	gi 123298587 (+22)	33 kDa	1	1
14	✓	✗	gi 111185907 (+8)	232 kDa	1	1
15	✓	✗	gi 113680425	49 kDa	1	1
16	✓	✗	gi 110431346 (+8)	38 kDa	1	1
17	✓	✗	gi 112983636 (+20)	57 kDa	1	1
18	✓	✗	gi 148681587 (+11)	26 kDa	1	1
19	✓	✗	gi 148664748 (+3)	121 kDa	1	1
20	✓	✗	gi 148707543	12 kDa	1	1
21	✓	✗	gi 148707629 (+3)	201 kDa	1	1
22	✓	✗	gi 124249228	28 kDa	17	17

What's next?

Go to lab.research.sickkids.ca/sparc-molecular-analysis/



Announcements

"Proteomics – Getting started; How to prepare protein samples for mass spec analysis and the cost involved."

Leanne will be speaking during the second half of next week's Spotlight Seminar, which will be held on Wednesday, January 15, 12:00 - 1:00pm. [Click here for more information.](#)

At SPARC BioCentre (Molecular Analysis), we apply state-of-the-art technologies, including mass spectrometry, amino acid analysis, and extracellular flux analysis by Seahorse, for the molecular characterization of biological systems. This includes identification and quantification of a broad range of large and small molecules including proteomes and proteins, and small molecule analytes such as peptides, metabolites, and measures of metabolism. SPARC is operated on a fee-for-service cost-recovery basis by an experienced team of scientists and technicians, with [Dr. Michael Moran](#) as our Scientific Director. We are happy to work with researchers from early consultation and planning phases, to delivery of data, data analysis, and preparation of publications and grant proposals.

The SPARC BioCentre (Molecular Analysis) is a proud member of the [Pan-Canadian Proteomics Centre](#).

Ready to submit samples?

At SPARC BioCentre (Molecular Analysis), we use iLab for our mass spectrometry, cell metabolism (Seahorse), amino acid analysis, and Edman sequencing project management. Use the link below to submit a request or create an account through iLab.

Note: if you are submitting samples of human origin, we will require your REB approval number, date of expiry, and a copy of the approval letter for our records.

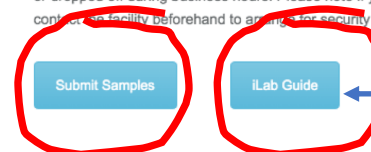
To initiate a project, please submit your request using the Project Submission button below. Please do not hesitate to [contact us](#) to discuss the design of your experiments or sample preparation aspects.

Once your project request has been submitted, your samples can be shipped to:

Leanne Wybenga-Groot
SPARC BioCentre, Room 21.9400
Peter Gilgan Centre for Research and Learning (PGCRL)
The Hospital for Sick Children
72 Elm Street
Toronto, ON M5G 1H3

or dropped off during business hours. Please note if you plan on dropping off your samples personally, you must contact the facility beforehand to arrange for security clearance and bring photo ID.

Click here



Use this guide to register an iLab account

Once you have an iLab account...

- Request a service and fill in form as best you can; provide Cost Centre # if you are internal to SickKids. Otherwise, provide billing info.
- We will price the service and contact you if we need more info
- PI (or lab designate) approves the cost of service
- Bring samples to us
- We process your sample and send data via email/Dropbox within 1-2 weeks of your samples arriving for standard projects
- Your PI will be invoiced through SickKids myFinance at the end of each month

Questions??

- Contact one of us or pop by PGCRL 21.9440



CONTACT



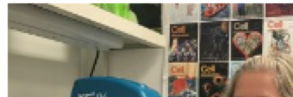
Shipping Address

Attn: SPARC, Room 21.9400
Peter Gilgan Centre for Research and Learning (PGCRL)
The Hospital for Sick Children
72 Elm Street
Toronto, ON M5G 1H3

Mailing Address

SPARC BioCentre
The Hospital for Sick Children
Peter Gilgan Centre for Research and Learning (PGCRL)
686 Bay Street, 21st Floor
Toronto, ON M5G 0A4
Office Hours: 8:30 a.m. to 5 p.m.
Monday through Friday (except for holidays).

**Please note when dropping off samples to the SPARC BioCentre, you must make arrangements with someone from SPARC to add your name to the PGCRL security list. If your name is not on the security list, you will not be allowed access to the SPARC labs.



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