

MARDI 16 SEPTEMBRE 2025

MAS, Paris 13e

10 rue des terres au curé



LA PROTÉOMIQUE
À LARGE ÉCHELLE
POUR L'ÉTUDE DU MICRO-
ENVIRONNEMENT TUMORAL

GROUPE MICROENVIRONNEMENT TUMORAL



Proteom'IC core facility

Emilie-Fleur GAUTIER





Proteom'IC core facility



Proteomics analyses using mass spectrometry + multi-omics functional analyses



Staff: 8 permanent Engineers and Engineer Assistants



Emilie-Fleur
GAUTIER, *PhD*



Cédric
BROUSSARD



Virginie
SALNOT



Marjorie
LEDUC, *PhD*



Johanna
BRUCE



Guilhem
CLARY



Morgane
LE GALL



Anne
DEGAVRE



Maryam
ABOUTIMAN
PhD Student



Laurine MUNIER
Master 2
student



Elissa KHADRA
Master 2
student

Contacts:

U1016-proteomique@inserm.fr



Scientific advisors



Pierre Sohier
Pathologist, *PhD*,
APHP, Hôpital
Cochin, Team
Aractingi



Ismaël Boussaïd
PharmD, *PhD*,
APHP, Hôpital Cochin,
Team M. Fontenay/Y.
Simoni



Frédérique Verdier
DR2, *PhD*,
Institut Cochin,
Team C. Lavazec



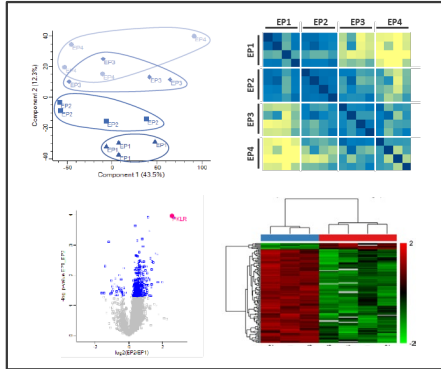
Gwladys Bertin
IR, *PhD*,
Institut de Recherche
pour le Développement
(IRD)



Services – nLC-MS/MS

Bottom up

From proteins extraction to statistical and functional analyses



Comparative quantitative analysis of global proteomes

Relative or absolute quantification in copy number per cell

Around 8000 proteins quantified in classic cell pellets or tissues



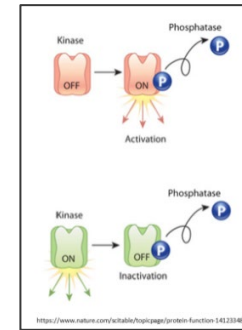
Identification and comparative quantification of protein interacting partners (for proteins/DNA/RNA)

AP-MS / Turbo and Bio-ID / Co-IP/pull down

Several hundred of proteins quantified

Starting material: eluates

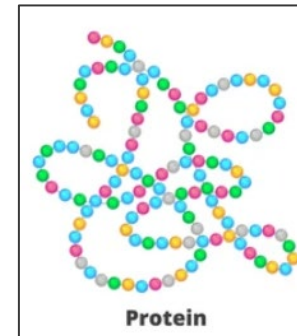
Recommendations for sample preparation on our websites



Comparative analysis of global phospho-proteomes, and other Post Translational Modifications on demand

Relative quantification

Several thousands of phosphosites quantified in classic cell pellets or a tissues, exact position of the identified phosphosites, quantifications (fold changes, statistics)



In-gel or in solution purified protein identification or characterization (modifications, cleavages)



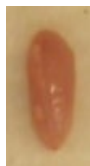
Services – very various sample types

Cell pellets

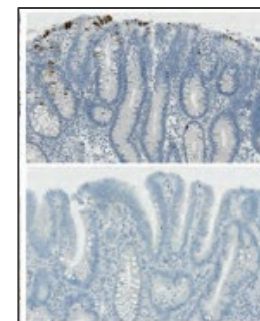


Cell pellets

Tissues

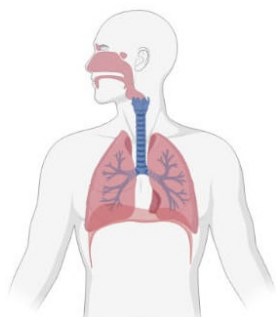


Frozen Tissue or tissue samples pulverized by nitrogen



Formalin-fixed paraffin-embedded (FFPE) samples

Biological fluids



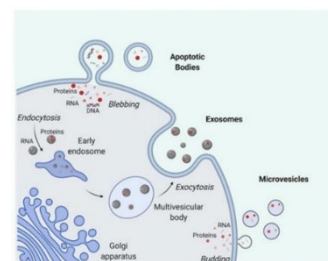
Sputum



Tears

Cerebrospinal fluid ...

Secreted proteins

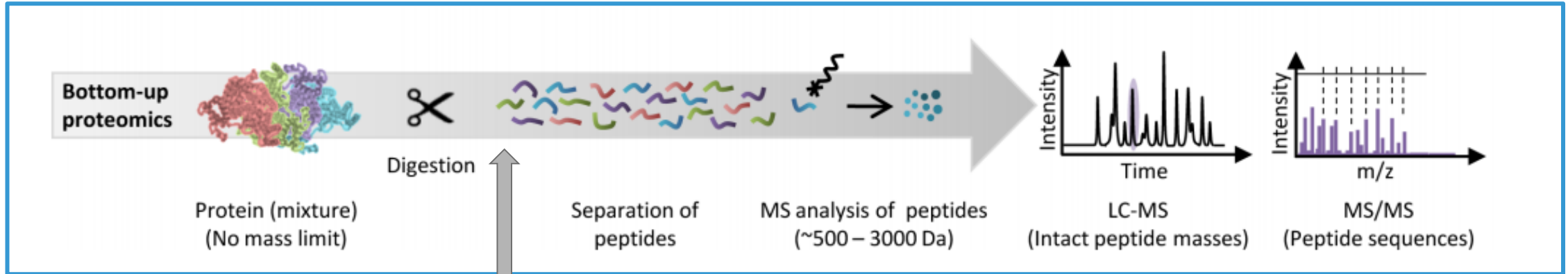


Microvesicles, exosomes



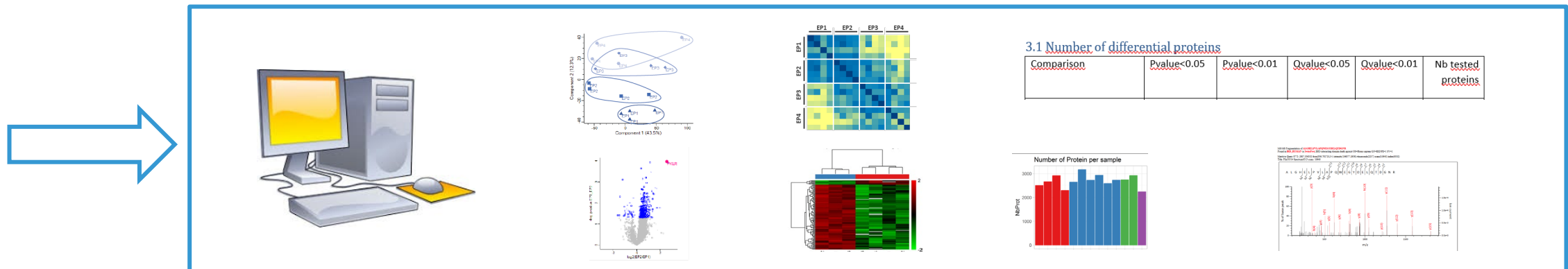
For comparative analyses, Minimum of n=4

Services – from protein extraction to statistical analysis, and...



Linda Switzer, Journal of proteome research, 2013

Optional additional steps of
peptides enrichment or
separation

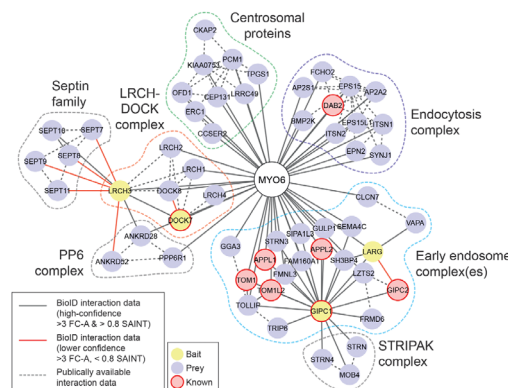




Services – functional analyses

Functional bio-analysis for the extraction of biological informations for:

- proteomics data
- transcriptomics data
- miRNomics data
- epigenomics data
- metabolomics data
- integrative analysis



Annotations and Term enrichments
 Interaction networks
 Integrative Analyses
 Tools for protein partners selection

Thomas O'Loughlin et al 2018

Equipment

1 computer :



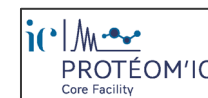
Softwares :

GSEA, Perseus, String, PANTHER

-> Global functional analysis
 -> Training
 -> Computer with softwares can be booked  openiris.io

Postcode: new bioinformatical tool developed by our platform for the analysis of post-transcriptional regulations

New



Elissa
KHADRA

M2 student



Zoila
IQBAL

M2 student



Ismaël
Boussaïd

Scientific advisor



Morgane
LE GALL

IE-CN



Proteomics analysis of FFPE samples with laser capture microdissection



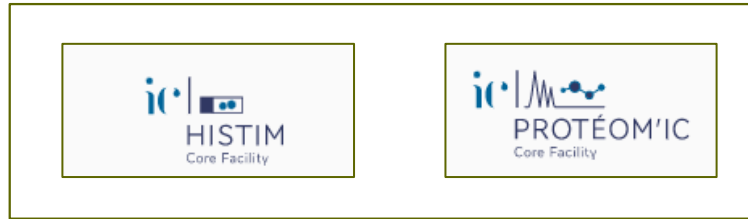
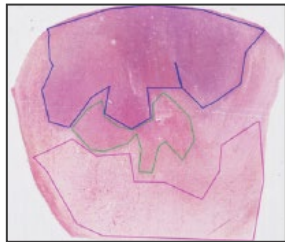
Pierre Sohier

Pathologist, PhD, APHP,
Hôpital Cochin, Team
 Aractingi, Institut Cochin
 Scientific Advisor



Eric Pasmant

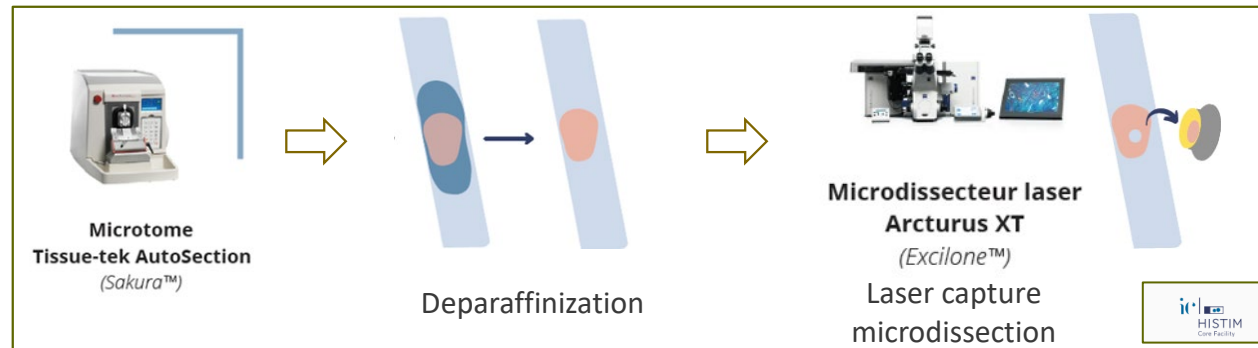
Team leader
 Institut Cochin



Maryline Favier
HISTIM



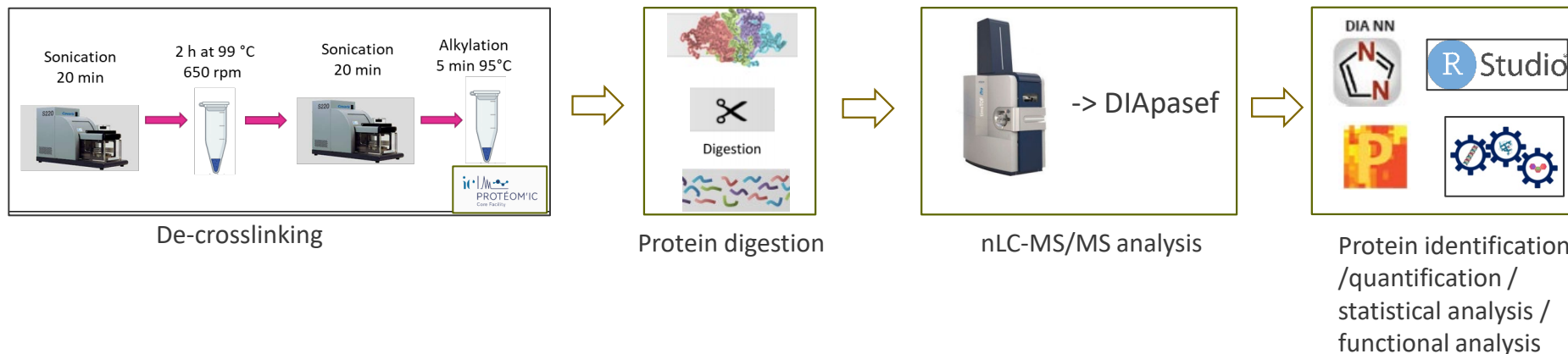
Cédric Broussard
PROTEOM'IC



Sarah Kamami,
 M2 student



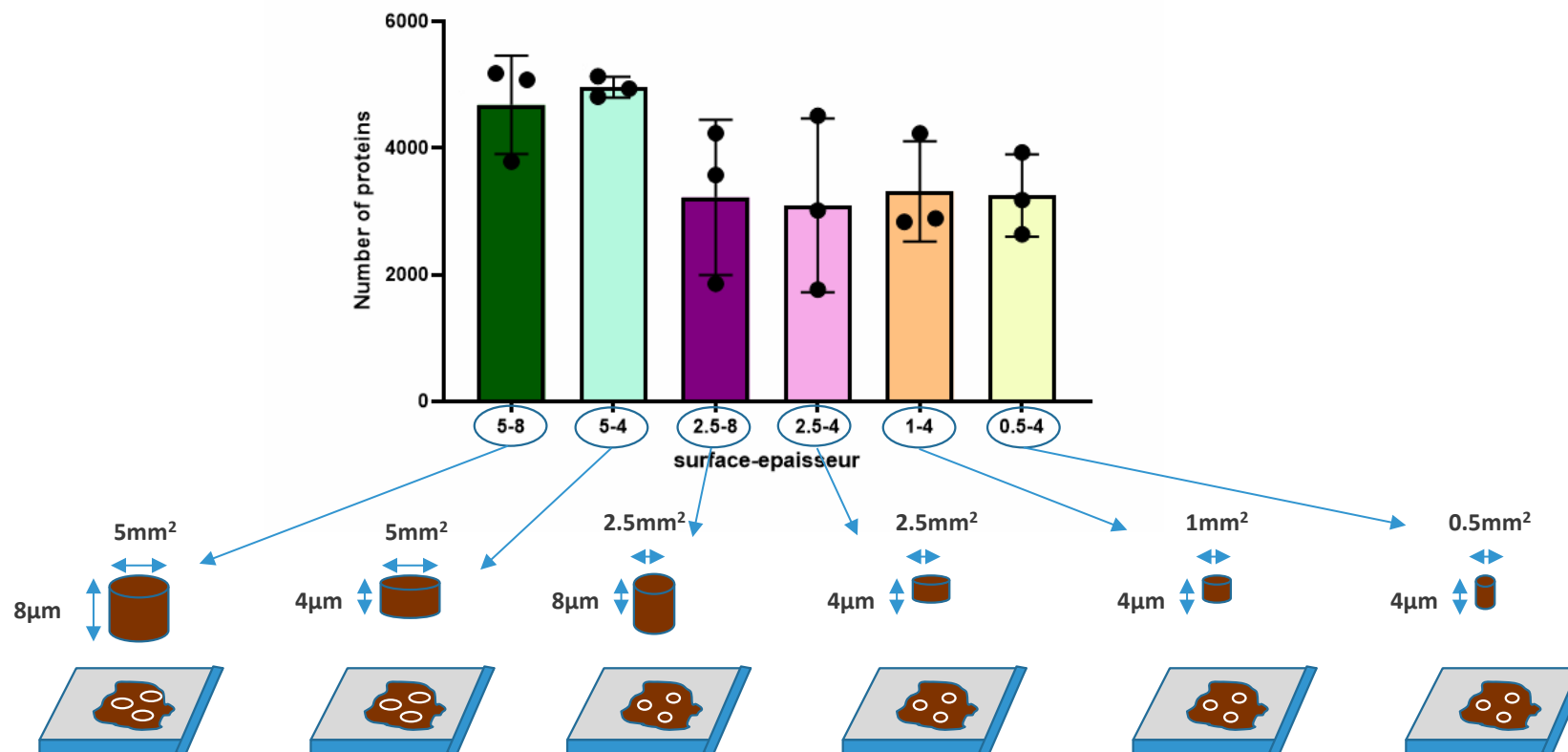
Mohamed Amin
Mathlouthi,
 M2 student





Staining for laser microdissection tissue selection

Cumulative tissue surface area



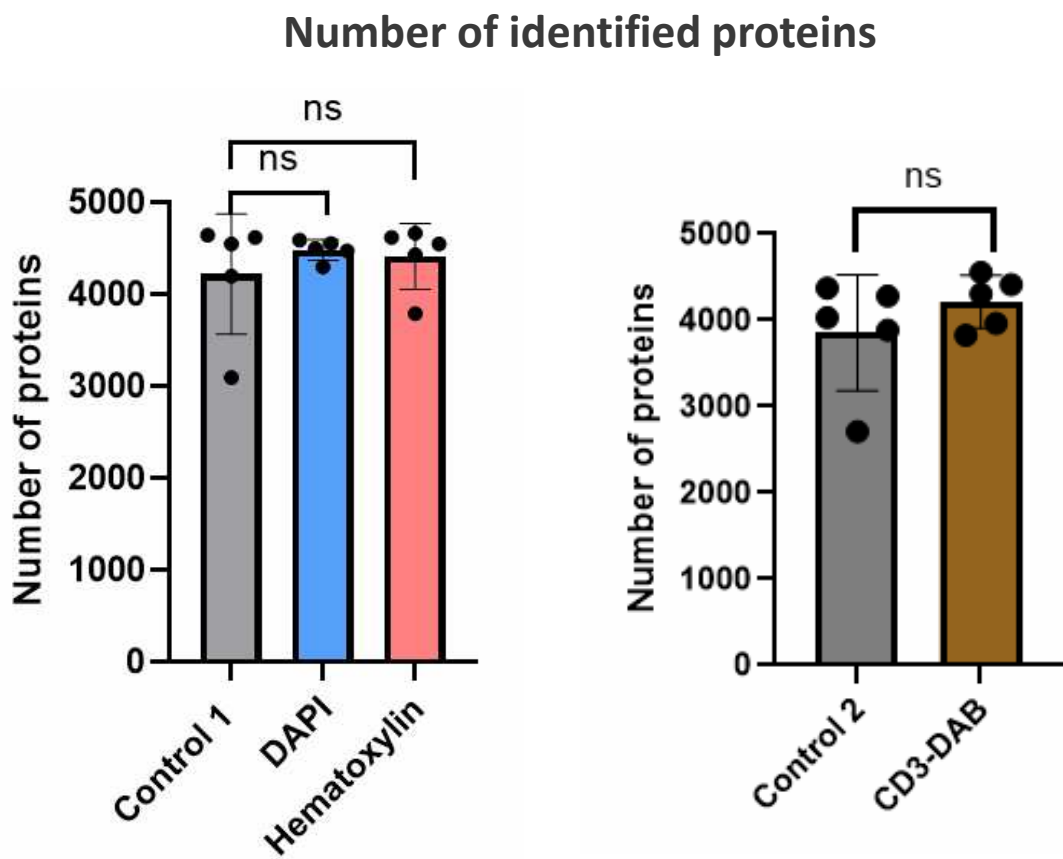

Cédric
BROUSSARD
IE-HC


Laurine
MUNIER
Master 1

Mouse
Spleen
FFPE tissue



Staining for laser microdissection tissue selection



Cédric
BROUSSARD
IE-HC



Laurine
MUNIER
Master 1

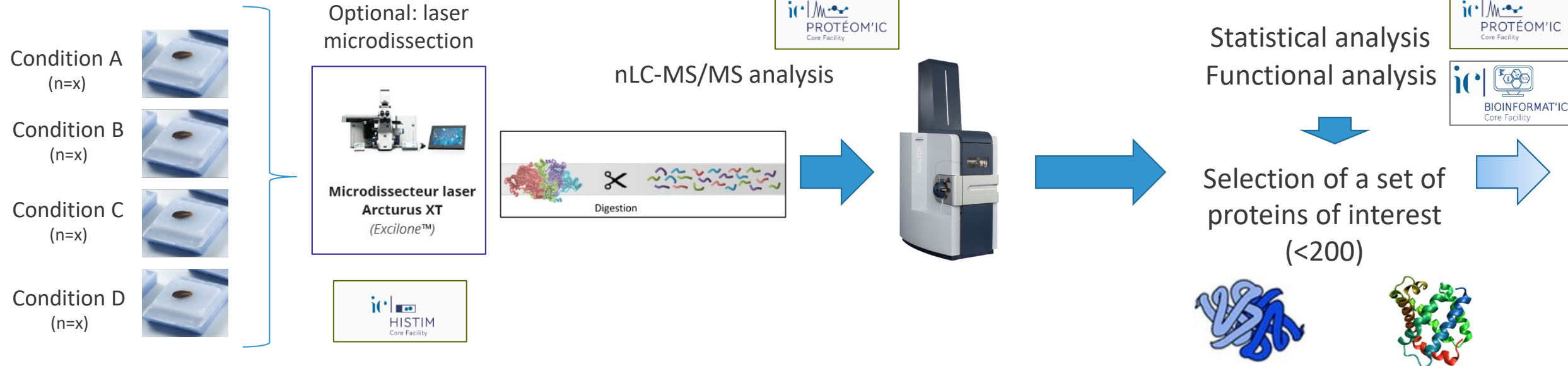
Quantifications
Pearson
correlations >0.9

C1-1	C1-2	C1-3	C1-4	C1-5	D1	D2	D3	D4	D5	H1	H2	H3	H4	H5	C: Grou	T: Nam
NaN	0,96	0,97	0,94	0,97	0,97	0,97	0,97	0,98	0,97	0,97	0,97	0,97	0,95	0,97	C1	C1-1
0,964	NaN	0,97	0,95	0,96	0,97	0,97	0,97	0,97	0,97	0,96	0,97	0,96	0,95	0,97	C1	C1-2
0,968	0,966	NaN	0,94	0,97	0,97	0,96	0,97	0,97	0,97	0,98	0,98	0,97	0,95	0,97	C1	C1-3
0,939	0,947	0,939	NaN	0,92	0,94	0,94	0,94	0,94	0,95	0,94	0,94	0,92	0,93	0,94	C1	C1-4
0,969	0,962	0,973	0,924	NaN	0,98	0,97	0,97	0,98	0,97	0,97	0,98	0,95	0,97	0,97	C1	C1-5
0,972	0,968	0,975	0,937	0,981	NaN	0,971	0,977	0,98	0,972	0,971	0,981	0,977	0,955	0,977	Dapi	D1
0,968	0,967	0,961	0,937	0,966	0,971	NaN	0,974	0,974	0,976	0,963	0,969	0,964	0,959	0,973	Dapi	D2
0,969	0,97	0,969	0,943	0,968	0,977	0,974	NaN	0,974	0,979	0,967	0,977	0,963	0,951	0,975	Dapi	D3
0,978	0,967	0,974	0,939	0,977	0,98	0,974	0,974	NaN	0,979	0,978	0,978	0,975	0,957	0,978	Dapi	D4
0,971	0,966	0,972	0,947	0,965	0,972	0,976	0,979	0,979	NaN	0,971	0,975	0,962	0,954	0,974	Dapi	D5
0,975	0,963	0,98	0,935	0,969	0,971	0,963	0,967	0,978	0,971	NaN	0,98	0,973	0,951	0,973	Hemat	H1
0,974	0,967	0,98	0,937	0,975	0,981	0,969	0,977	0,978	0,975	0,98	NaN	0,978	0,957	0,978	Hemat	H2
0,972	0,962	0,972	0,925	0,978	0,977	0,964	0,963	0,975	0,962	0,973	0,978	NaN	0,957	0,974	Hemat	H3
0,95	0,952	0,952	0,933	0,952	0,955	0,959	0,951	0,957	0,954	0,951	0,957	0,957	NaN	0,964	Hemat	H4
0,973	0,967	0,97	0,942	0,97	0,977	0,973	0,975	0,978	0,974	0,973	0,978	0,974	0,964	NaN	Hemat	H5

Cresyl violet, DAPI, Hematoxylin, antibody-DAB: no differences compared to controls



Workflow for spatial proteomics at Institut Cochin





Thank you



Contact : U1016-proteomique@inserm.fr

<https://institutcochin.fr/plateformes/proteomic>

<https://3p5.u-paris.fr/>

<https://www.ibisa.net/plateformes/proteom-ic-21.html>

