CLINICAL METAPROTEOMICS WORKFLOW TO STUDY HOST-MICROBIOME DYNAMICS

Pratik Jagtap

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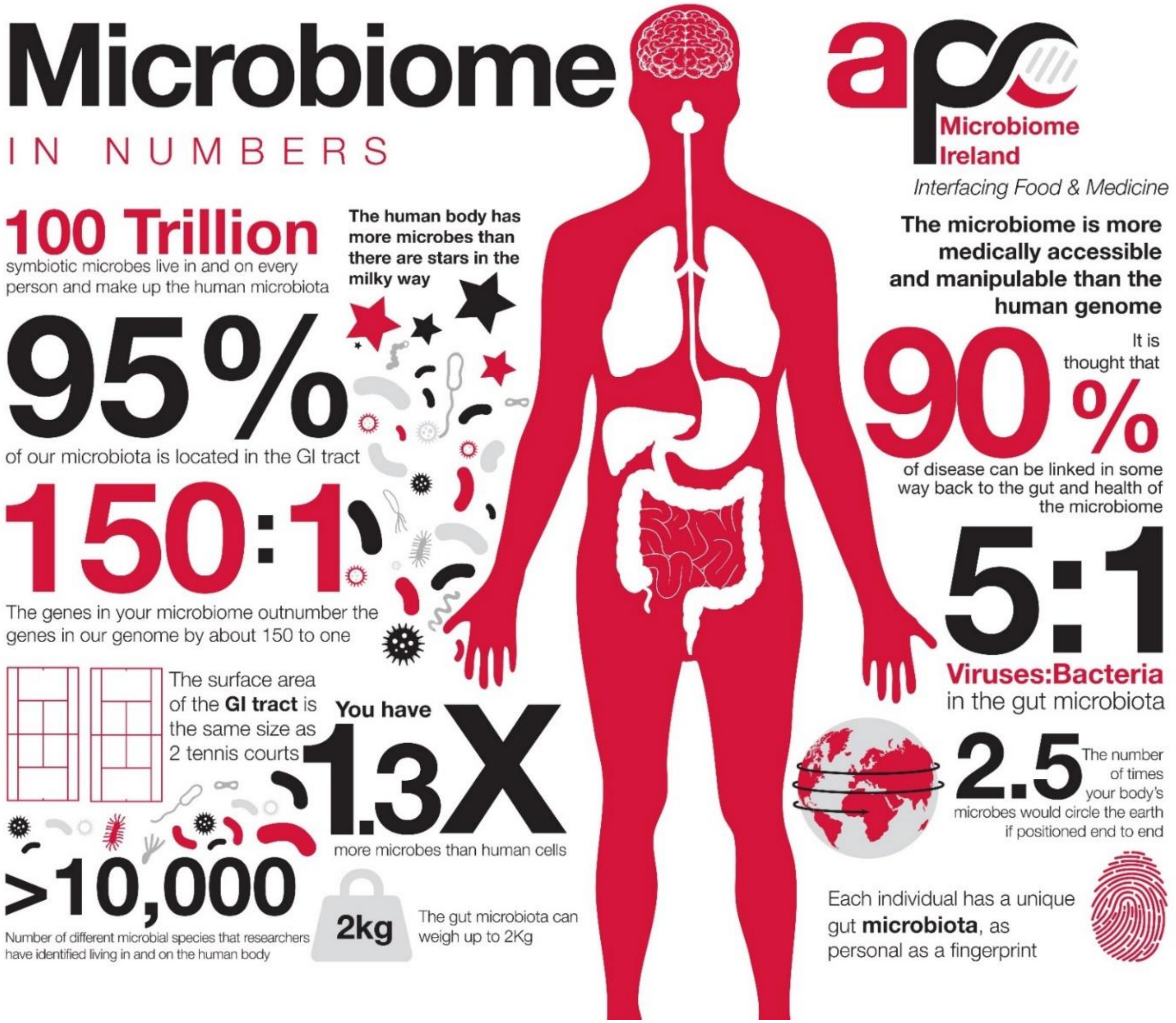
*Learn more at **galaxyp.org***

z.umn.edu/itcrgalaxyvideo

CLINICAL METAPROTEOMICS WORKFLOW TO STUDY HOST-MICROBIOME DYNAMICS

- ***MICROBIOME RESEARCH***
  - ***MASS SPECTROMETRY DATA ANAYSIS***
  - ***METAPROTEOMICS RESEARCH***
  - ***GALAXY BIOINFORMATICS PLATFORM***
- ***CLINICAL METAPROTEOMICS WORKFLOW***
  - ***CLINICAL METAPROTEOMICS:COVID-19 PANDEMIC***
  - ***CLINICAL METAPROTEOMICS:CYSTIC FIBROSIS***
  - ***CLINICAL METAPROTEOMICS: ORAL CANCER***
- ***METAPROTEOMICS EDUCATION***

MICROBIOME RESEARCH



Microbiome

IN NUMBERS

apc Microbiome Ireland

Interfacing Food & Medicine

100 Trillion symbiotic microbes live in and on every person and make up the human microbiota

The human body has more microbes than there are stars in the milky way

95% of our microbiota is located in the GI tract

150:1 The genes in your microbiome outnumber the genes in our genome by about 150 to one

The surface area of the **GI tract** is the same size as 2 tennis courts

You have 1.3X more microbes than human cells

>10,000 Number of different microbial species that researchers have identified living in and on the human body

2kg The gut microbiota can weigh up to 2Kg

The microbiome is more medically accessible and manipulable than the human genome

It is thought that **90%** of disease can be linked in some way back to the gut and health of the microbiome

5:1 **Viruses:Bacteria** in the gut microbiota

2.5 The number of times your body's microbes would circle the earth if positioned end to end

Each individual has a unique gut **microbiota**, as personal as a fingerprint

https://worldmicrobiomeday.com/resources/

https://www.nature.com/articles/d41586-020-00193-3

MICROBIOME

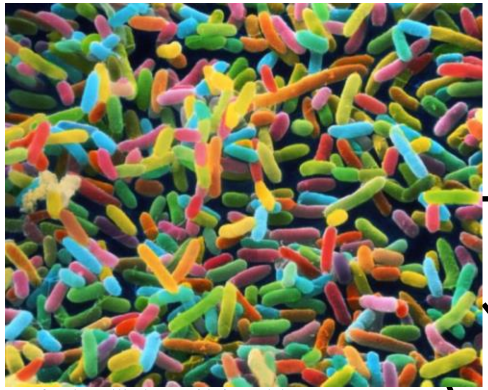
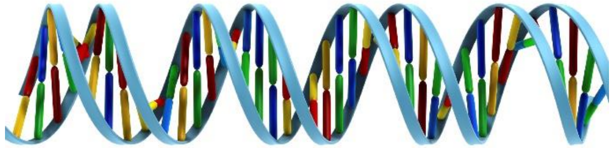


Image from https://thedoctorweighsin.com/what-everyone-should-know-about-the-infant-microbiome/

Potential to unravel the **mechanistic details of microbial interactions with host / environment** by analyzing the **functional dynamics of the microbiome.**



METAGENOMICS

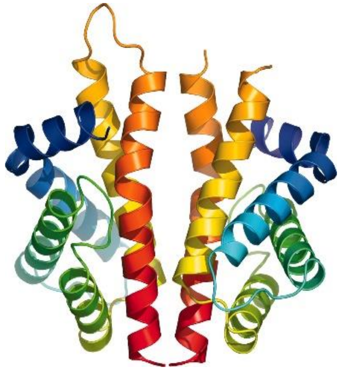
TAXONOMY

function

METATRANSCRIPTOMICS

TAXONOMY

function

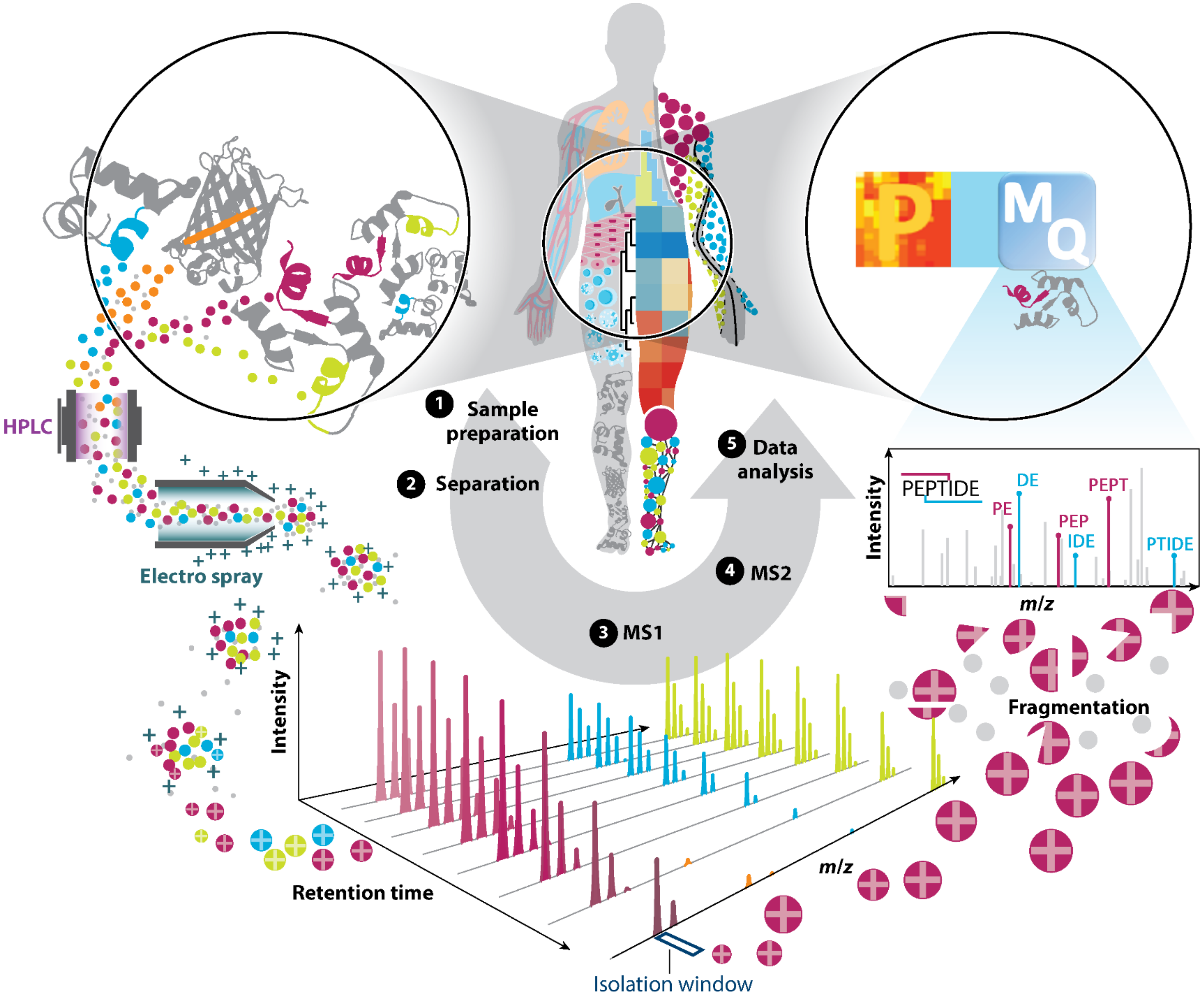


METAPROTEOMICS

TAXONOMY

FUNCTION

MASS SPECTROMETRY AND PROTEOMICS



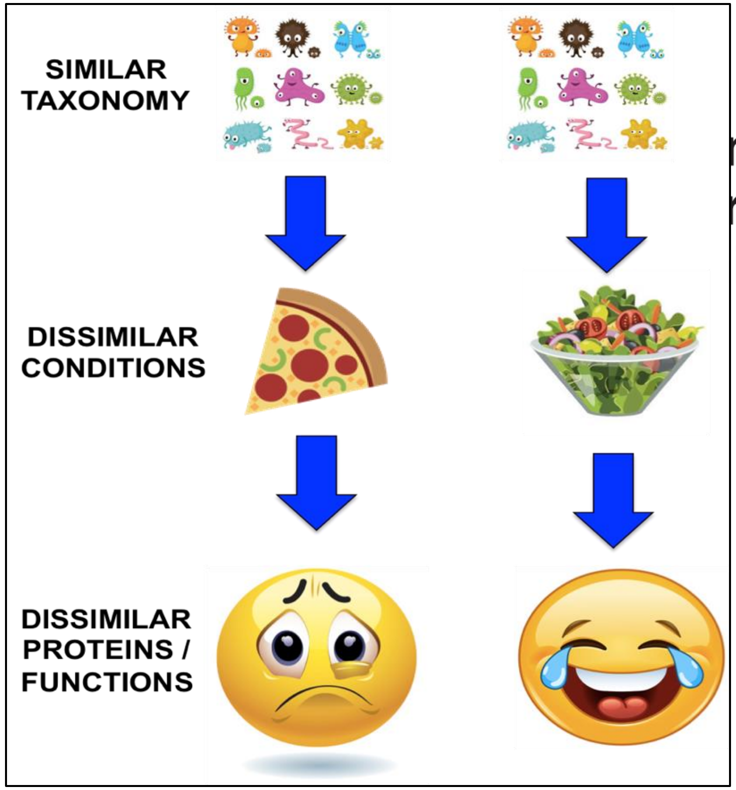
Sinitcyn P, et al. 2018.
Annu. Rev. Biomed. Data Sci. 1:207–34

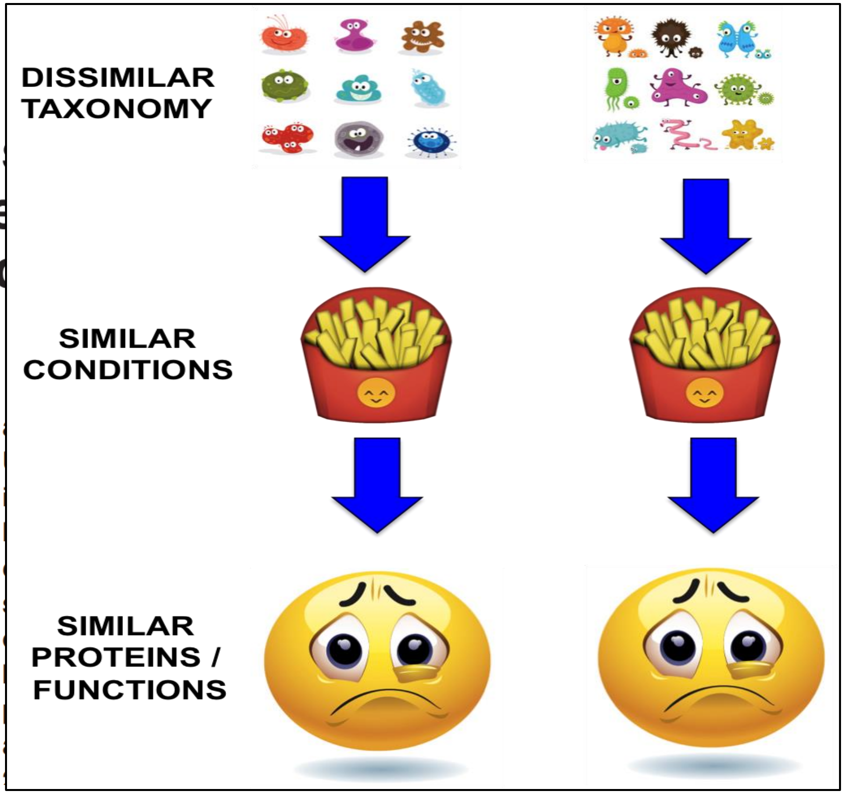
METAPROTEOMICS

Bond and Wilmes 2004

“The large-scale characterization of the entire protein complement of environmental microbiota at a given point in time”

Environ. Microbiol. 6, 911–920.





Bond and Wilmes 2015

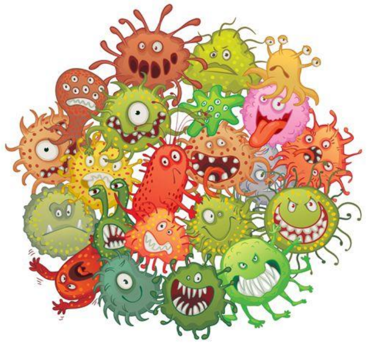
“Through the application of metaproteomics to different microbial consortia over the past decade, we have learnt much about key functional traits in the various environmental settings where they occur.”

Proteomics. doi:10.1002/pmic.201500183.

METAPROTEOMICS ANALYTICAL CHALLENGES

SINGLE-ORGANISM PROTEOMICS

METAPROTEOMICS



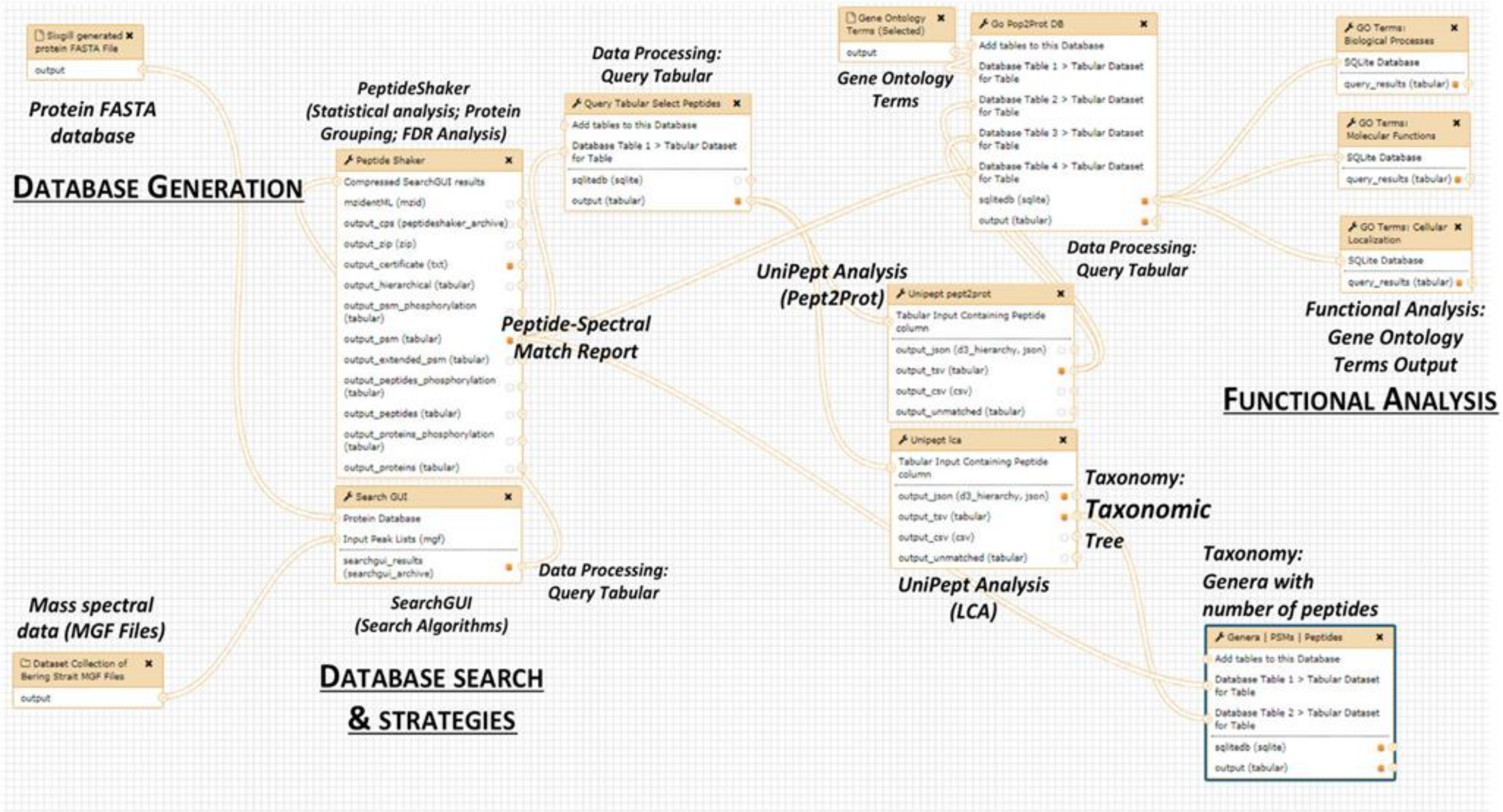
SEARCH DATABASE

	Single-organism proteomics	Metaproteomics
SIZE	SMALL TO MEDIUM SIZE (10 K TO 100K SEQUENCES)	LARGE (1 MILLION AND ABOVE)
COMPLEXITY	SINGLE + CONTAMINANTS	MULTI-ORGANISM DATABASE WITH HOMOLOGOUS PROTEINS

Disparate tools and multiple processing steps.

- SEARCH ALGORITHMS BEING DEVELOPED TO ADDRESS LARGE AND COMPLEX DATABASE SEARCHES
- PROTEIN GROUPING AT MULTI-ORGANISM LEVEL
- IDENTIFICATION STATISTICS AFFECTED BY LARGE DATABASES
- TAXONOMY BASED ON UNIQUE PEPTIDE IDENTIFICATIONS
- FUNCTIONAL ANALYSIS BASED ON PROTEINS IDENTIFIED

SOLUTION: GALAXY BIOINFORMATICS PLATFORM



Protein FASTA database

DATABASE GENERATION

PeptideShaker (Statistical analysis; Protein Grouping; FDR Analysis)

Data Processing: Query Tabular

Peptide-Spectral Match Report

Mass spectral data (MGF Files)

SearchGUI (Search Algorithms)

Data Processing: Query Tabular

DATABASE SEARCH & STRATEGIES

Gene Ontology Terms

Data Processing: Query Tabular

UniPept Analysis (Pept2Prot)

UniPept Analysis (LCA)

Taxonomy: ***Taxonomic Tree***

Taxonomy: Genera with number of peptides

Functional Analysis: Gene Ontology Terms Output

FUNCTIONAL ANALYSIS

Software tools can be used in a sequential manner to generate analytical workflows that can be reused, shared and creatively modified.

Blank *et al* Proteomes 2018, 6(1), 7; https://doi.org/10.3390/proteomes6010007

The Galaxy Interface

Main viewing window
(workflow development, results visualization etc)

Tools

History

Welcome to GalaxyP

GalaxyP is a multiple 'omics' data analysis platform with particular emphasis on mass spectrometry based proteomics. GalaxyP is developed at the University of Minnesota, deployed at the Minnesota Supercomputing Institute, and is an extension of the popular Galaxy project. The GalaxyP project is supported by a grant from NSF.

This public Galaxy instance is meant for testing with small-scale data sets, and sharing workflows and tools. Users with larger data analysis needs are encouraged to install a local instance of Galaxy and access GalaxyP tools via the Tool Shed.

GalaxyP

Updates

Febuary 13, 2015
All Galaxy Tools running nominally

Febuary 12, 2015
All Galaxy Tools running nominally

imported: Test1 Workflow for human proteogenomics : Peptides to PSME - PeptideShaker Output
18 shown, 15 hidden
4.0 MB

33: BLAST-P Filtered Peptide Report
32: BLAST-P Filtered Peptides
16: Regex Find And Replace on data 14
15: Regex Find And Replace on data 13
14: Filter sequences by length on data 12
13: Filter sequences by length on data 12
12: Tabular-to-FAST

GalaxyP
galaxyp.org

CLINICAL METAPROTEOMICS WORKFLOW TO STUDY HOST-MICROBIOME DYNAMICS

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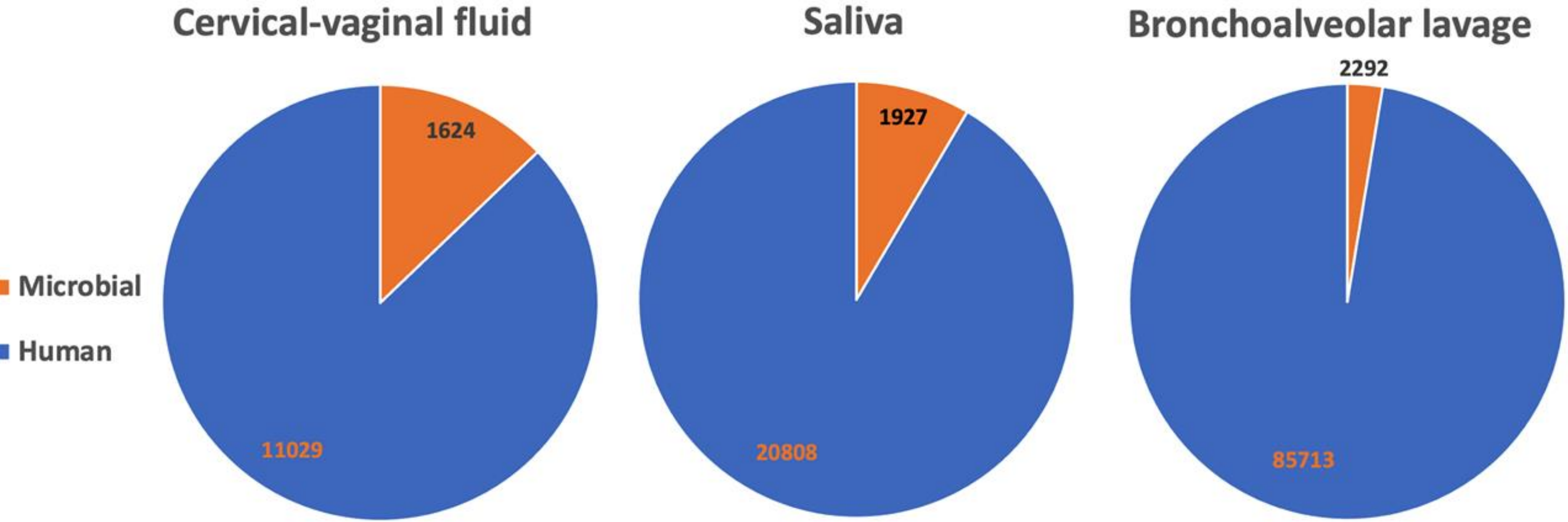
CLINICAL METAPROTEOMICS WORKFLOW TO STUDY HOST-MICROBIOME DYNAMICS

Katherine Do[1], Subina Mehta[1], Surbhi Bihani[2], Monica E. Kruk[1], Aryan Gupta[2],
Kevin Murray[1], Andrew Rajczewski[1], Reid Wagner[3], Dechen Bhuming[1], Kristin Boylan[4],
Amy Skubitz[4], Theresa Laguna[5,6], Sanjeeva Srivastava[2], **Timothy Griffin[1], Pratik Jagtap[1]**

[1] Biochemistry, Mol. Biology and Biophysics, University of Minnesota, Minneapolis, USA
[2] Indian Institute of Technology Bombay, Mumbai, India
[3] Minnesota Supercomputing Institute, University of Minnesota, Minneapolis, USA
[4] Department of Laboratory Medicine and Pathology, University of Minnesota, Minneapolis, MN, USA
[5] Department of Pediatrics, University of Washington School of Medicine, Seattle, WA, USA
[6] Department of Pediatrics, Division of Pulmonary and Sleep Medicine, Seattle Children's Hospital, Seattle, WA, USA

Do K *et al* (2024). A novel clinical metaproteomics workflow enables bioinformatic analysis of host-microbe dynamics in disease. mSphere https://doi.org/10.1128/msphere.00793-23

CLINICAL METAPROTEOMIC STUDIES DETECT LIMITED NUMBER OF MICROBIAL PEPTIDES

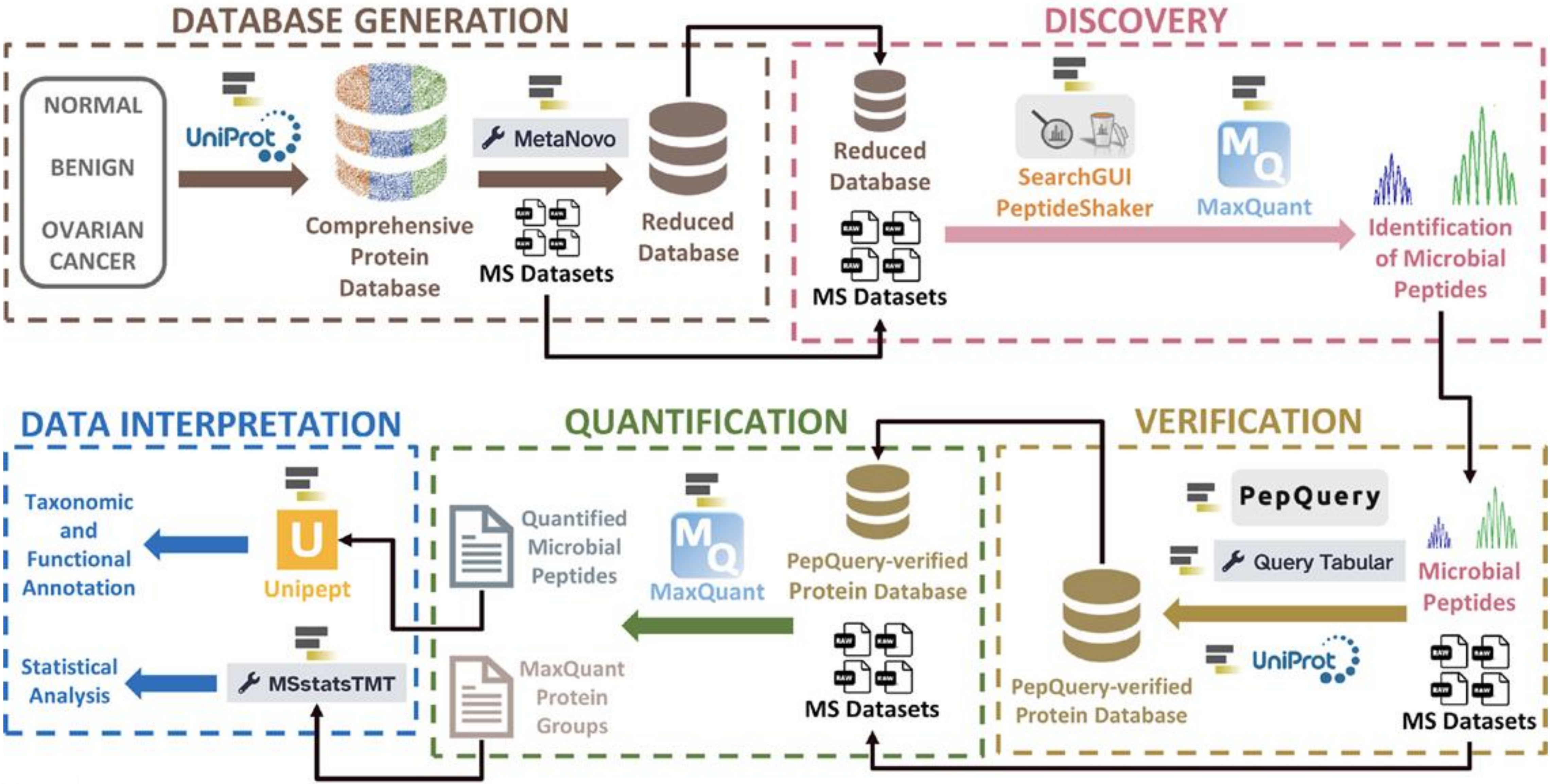


Afiuni-Zadeh *et al* (2018) Sci Rep . 8(1):10868.
doi: 10.1038/s41598-018-29092-4.

Jagtap *et al* (2012) Proteomics 12(7): 992–1001.
doi: 10.1002/pmic.201100503

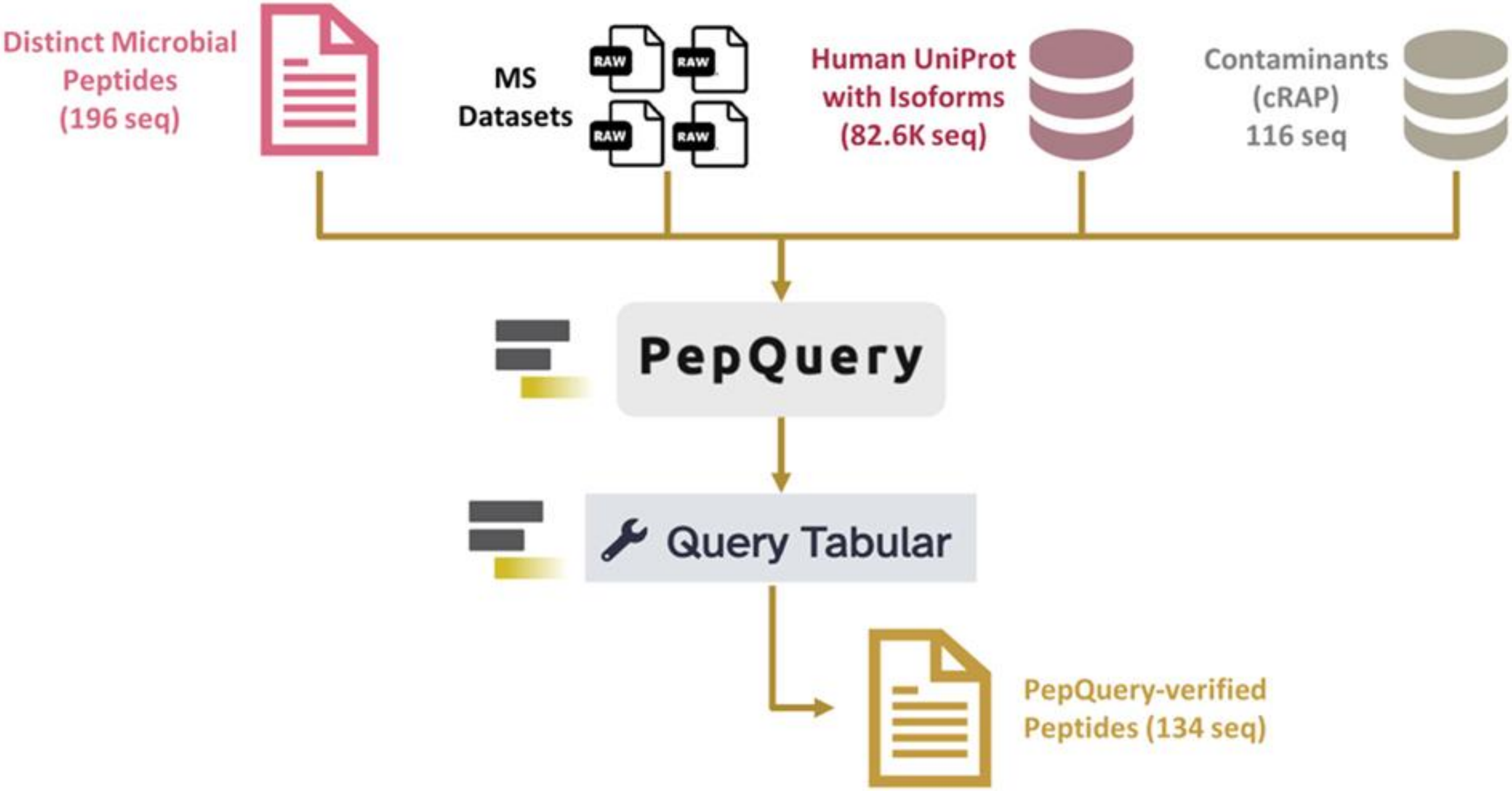
Kruk *et al* (2024) mSystems
doi: 10.1128/msystems.00929-23

OVERVIEW OF CLINICAL METAPROTEOMICS WORKFLOW



Do K *et al* (2024). mSphere https://doi.org/10.1128/msphere.00793-23

VERIFICATION AND VERIFIED DATABASE GENERATION MODULE



Do K *et al* (2024) mSphere https://doi.org/10.1128/msphere.00793-23

DATA INTERPRETATION MODULE

Quantification Module

Quantified Microbial Peptides (155 peptides)

MQ Evidence (5199 lines)

MQ Protein Groups (1313 proteins)

Unipept

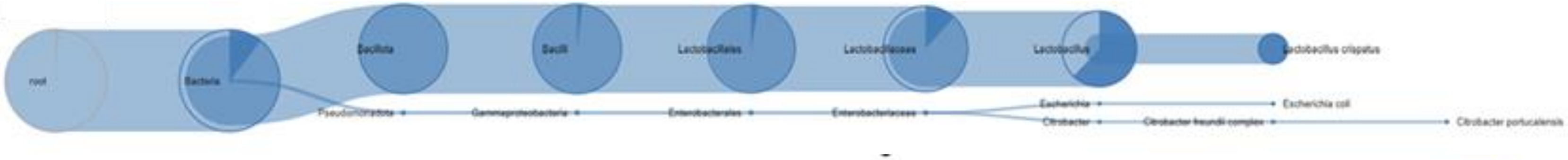
Taxonomic and Functional Annotation

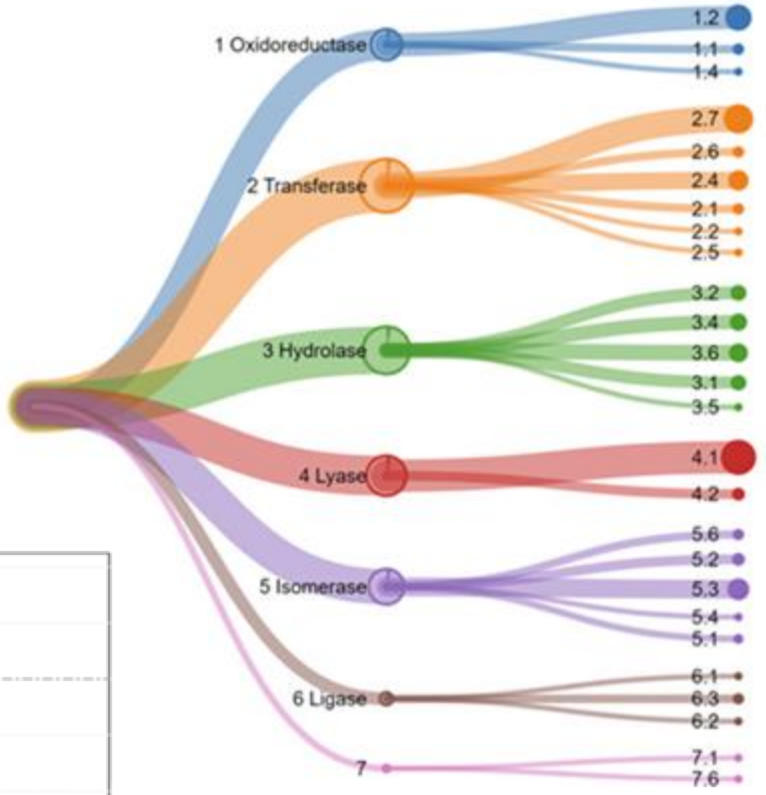
Microbial Proteins (61 proteins)

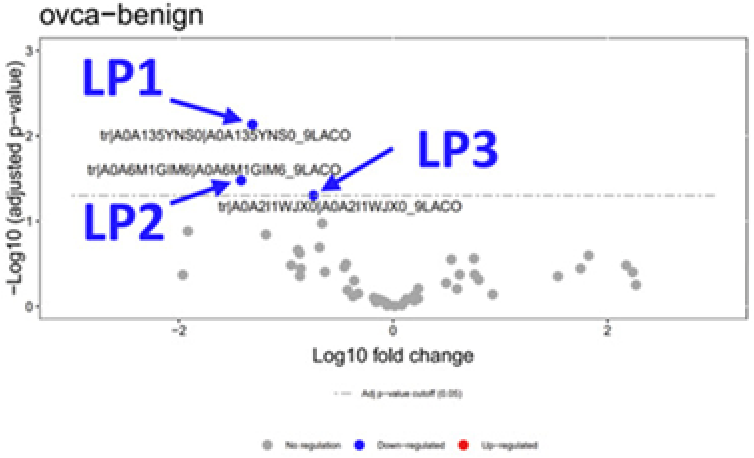
Human Proteins (1117 proteins)

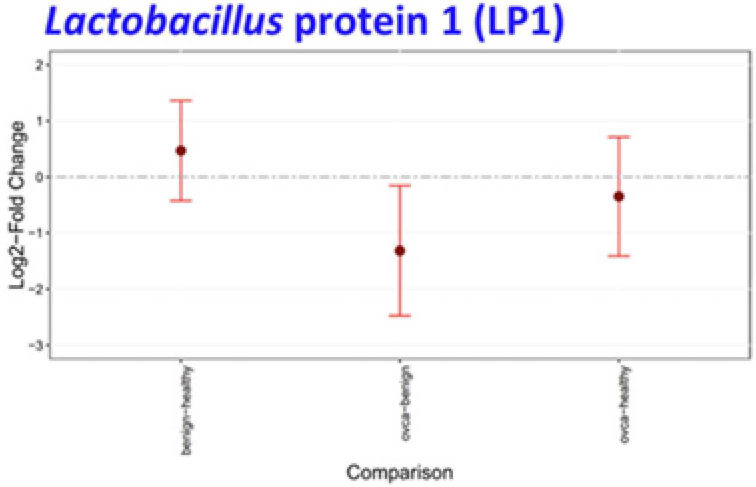
MSstatsTMT

Statistical Analysis






ovca−benign


Lactobacillus **protein 1 (LP1)**

Do K *et al* (2024) mSphere https://doi.org/10.1128/msphere.00793-23

The workflow modules, training data and documentation are available via the Galaxy Training Network.
https://training.galaxyproject.org/training-material/learning-pathways/clinical-metaproteomics.html

GALAXY TRAINING NETWORK

https://galaxyproject.org/events/gcc2021/training/

https://training.galaxyproject.org/training-material/topics/proteomics/

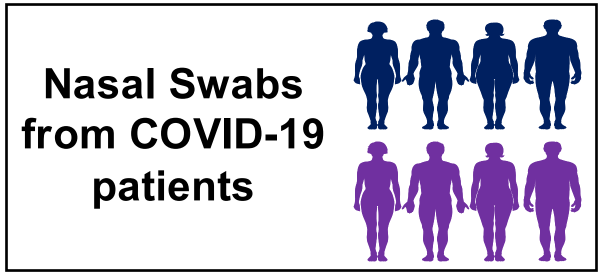
CLINICAL METAPROTEOMICS: COVID-19 PANDEMIC

ACS Publications
Most Trusted. Most Cited. Most Read.
Journal of proteome research

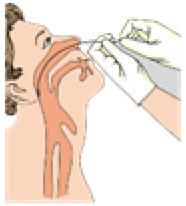
Bihani S *et al* (2023) Metaproteomic Analysis of Nasopharyngeal Swab Samples to Identify Microbial Peptides in COVID-19 Patients. J Proteome Res 22(8):2608-2619. doi: 10.1021/acs.jproteome.3c00040.

Surbhi Bihani

IIT BOMBAY

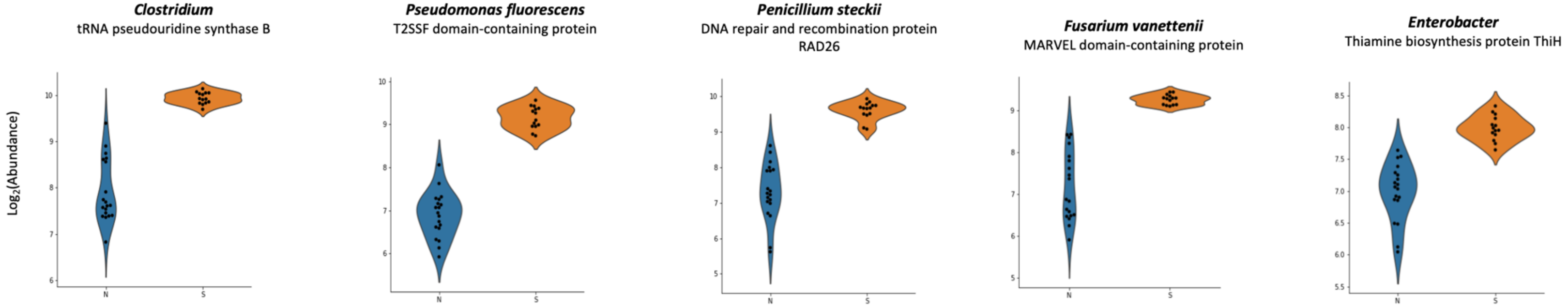


Nasal Swabs from COVID-19 patients



Sample Collection

Sample processing



Clostridium
tRNA pseudouridine synthase B

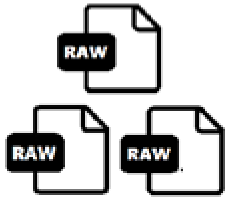
Pseudomonas fluorescens
T2SSF domain-containing protein

Penicillium steckii
DNA repair and recombination protein RAD26

Fusarium vanettenii
MARVEL domain-containing protein

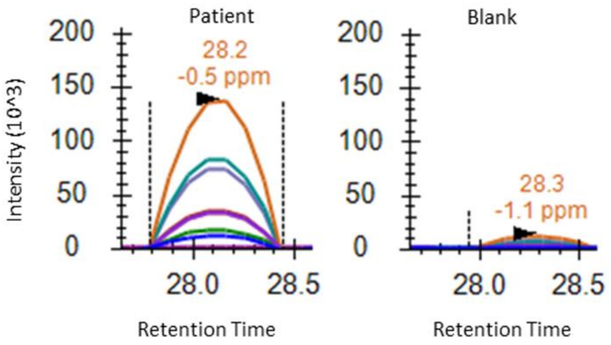
Enterobacter
Thiamine biosynthesis protein ThiH

Data Acquisition



TARGETED ANALYSIS OF POTENTIAL PATHOGENS IN COVID PATIENTS

QGIQNIPVVSQTGK (*Streptococcus parasanguinis*)

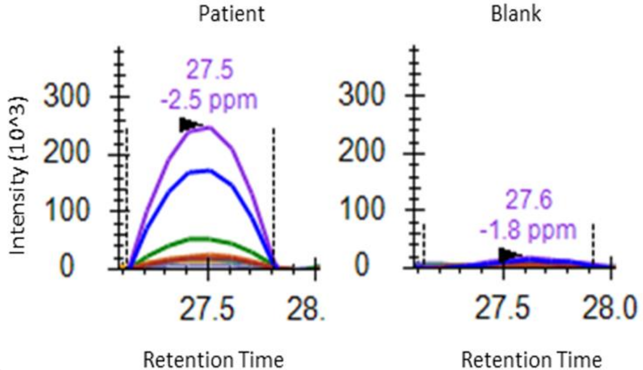


Streptococcus parasanguinis

Dominant isolate of dental plaque

Opportunistic pathogen associated with subacute endocarditis

GLFGDELCK (*Burkholderia cenocepacia*)

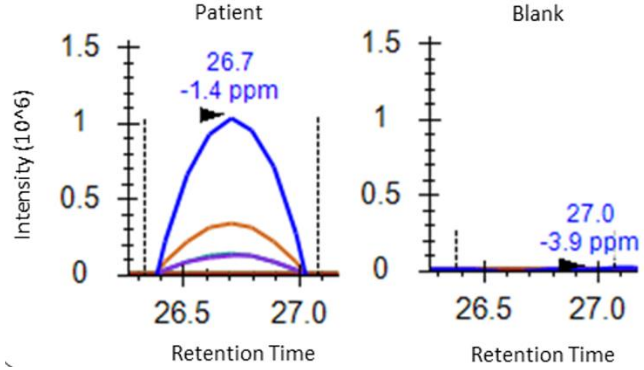


Burkholderia cenocepacia

Opportunistic pathogen

Cause systemic infections in immunocompromised individuals including cystic fibrosis patients.

IVDQEGAIVPK (*Cryptococcus floricola*)

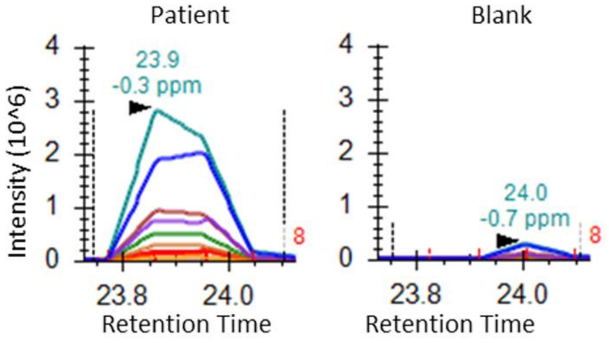


Cryptococcus floricola

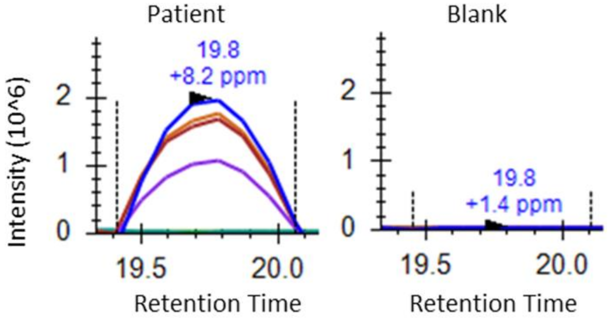
Infect immunocompromised hosts

Infection initiates in the lungs.

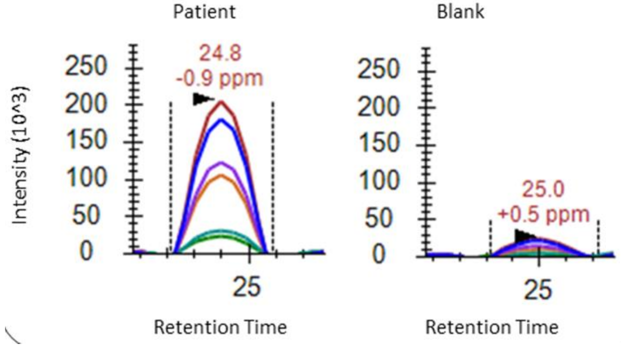
ICVLHGDK (*Clostridium sp.*)



DETDDQFEK (*Staphylococcus sp.*)



TPTLVSDLR (*Pseudomonas sp.*)



CLINICAL METAPROTEOMICS: CYSTIC FIBROSIS

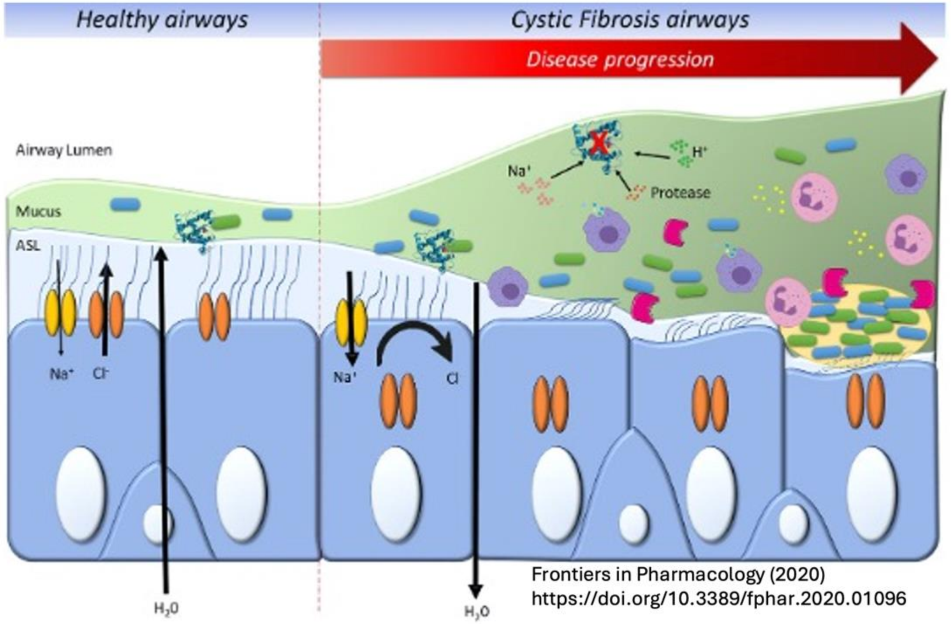
Kruk M *et al* (2024) An integrated metaproteomics workflow for studying host-microbe dynamics in bronchoalveolar lavage samples applied to cystic fibrosis disease. mSystems (https://doi.org/10.1128/msystems.00929-23).

CYSTIC FIBROSIS AND THE MICROBIOME

- **Life-shortening Mendelian disease.**
- **Mutations in the CF transmembrane conductance regulator (CFTR) gene, which encodes an epithelial anion channel.**
- **Abnormal anion transport across epithelia of secretory glands including lung.**

↓

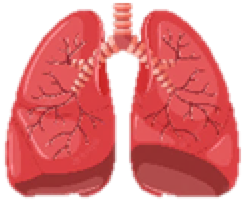
- **Thick mucus which predisposes patients to chronic bacterial infections and airway inflammation.**
- **Progressive and irreversible airway damage.**
- **Reduced quality and length of life in CF.**

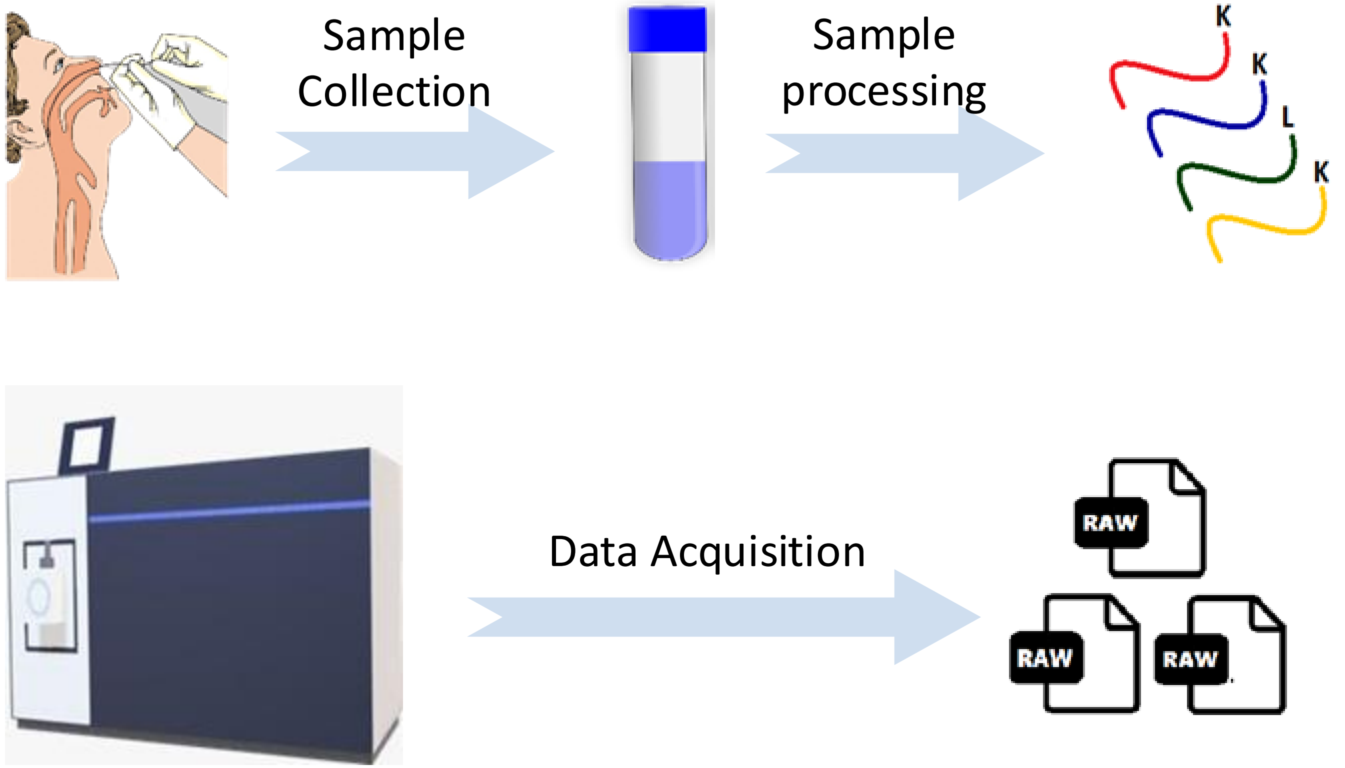


Frontiers in Pharmacology (2020)
https://doi.org/10.3389/fphar.2020.01096

CYSTIC FIBROSIS DATASETS

BALF from Cystic Fibrosis or Disease Control Samples




Sample Collection

Sample processing

Data Acquisition

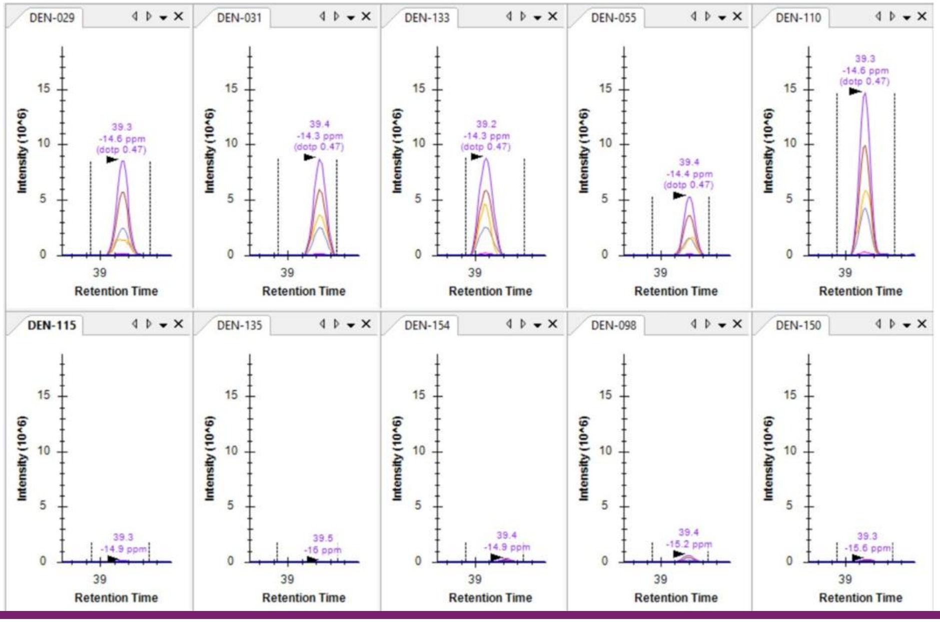
Monica E. Kruk

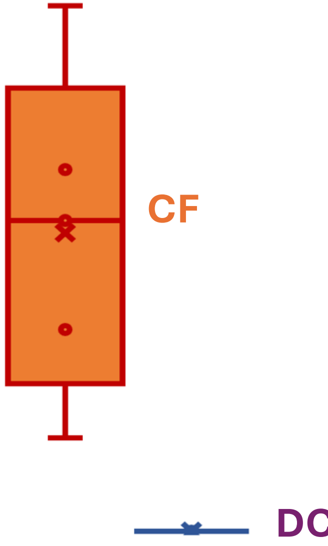
MICROBIAL PEPTIDES FROM CYSTIC FIBROSIS PATIENTS

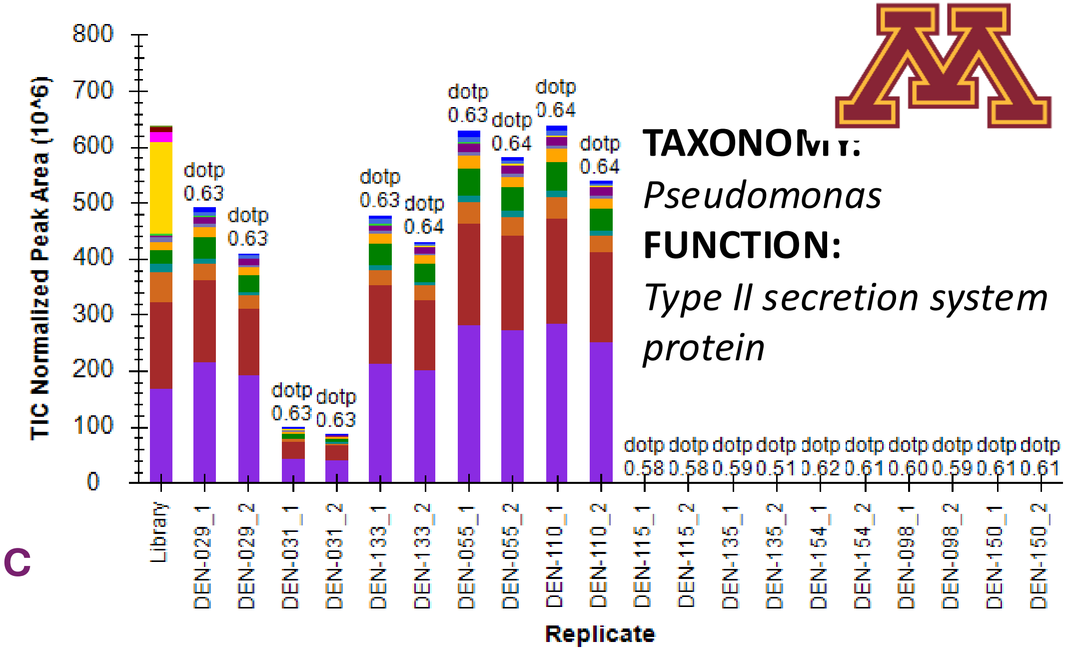
DWLDSLLQR

CF

DC

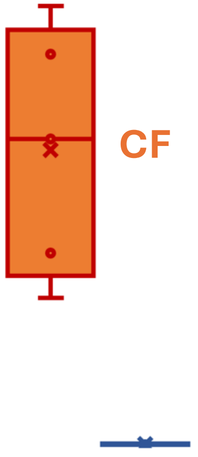






TAXONOMY:
Pseudomonas
FUNCTION:
Type II secretion system protein

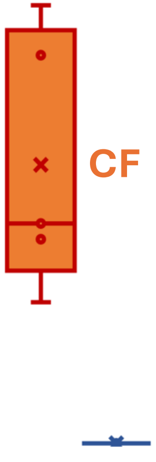
MKIGNLGGAYR



TAXONOMY:
Streptococcus agalactiae

FUNCTION:
DNA recombination enzyme

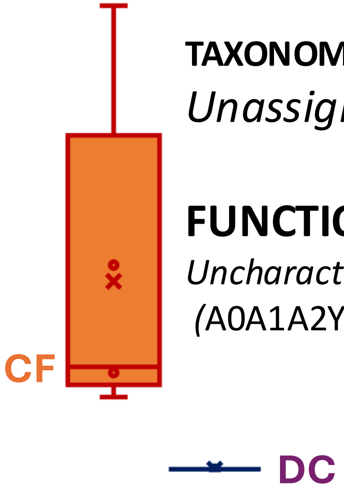
VLGARGHR



TAXONOMY:
Bacteria *(UniPept)*

FUNCTION:
Membrane kinase activity
Nucleoside triphosphate hydrolase
(A0A119BW38)

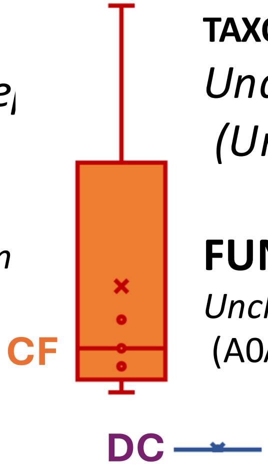
AALGAYDLR



TAXONOMY:
Unassigned (UniPe

FUNCTION:
Uncharacterized protein
(A0A1A2YS21)

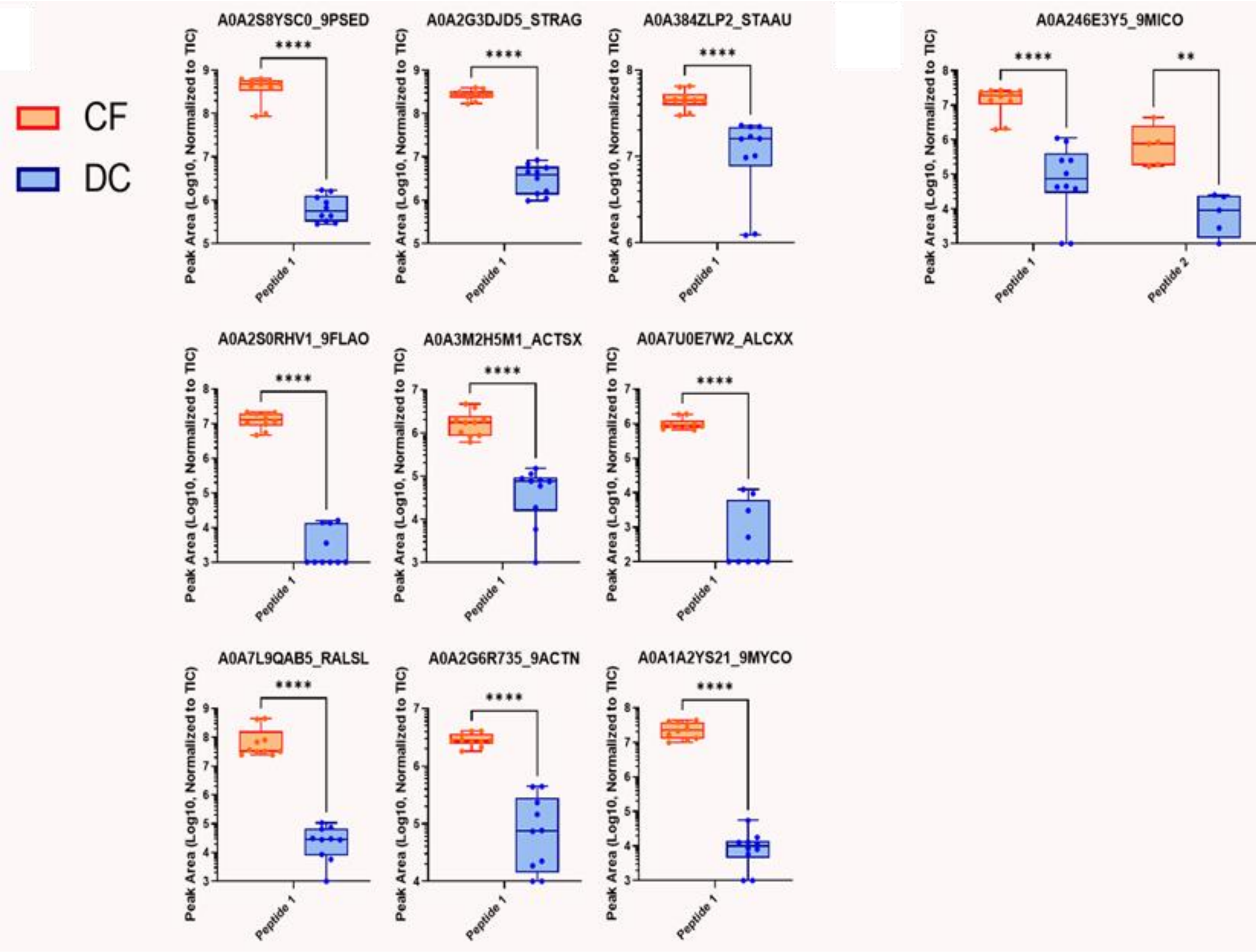
ATVEELHLEGI



TAXONOMY:
Unassigned (UniPept)

FUNCTION:
Uncharacterized
(A0A1H9MU03)

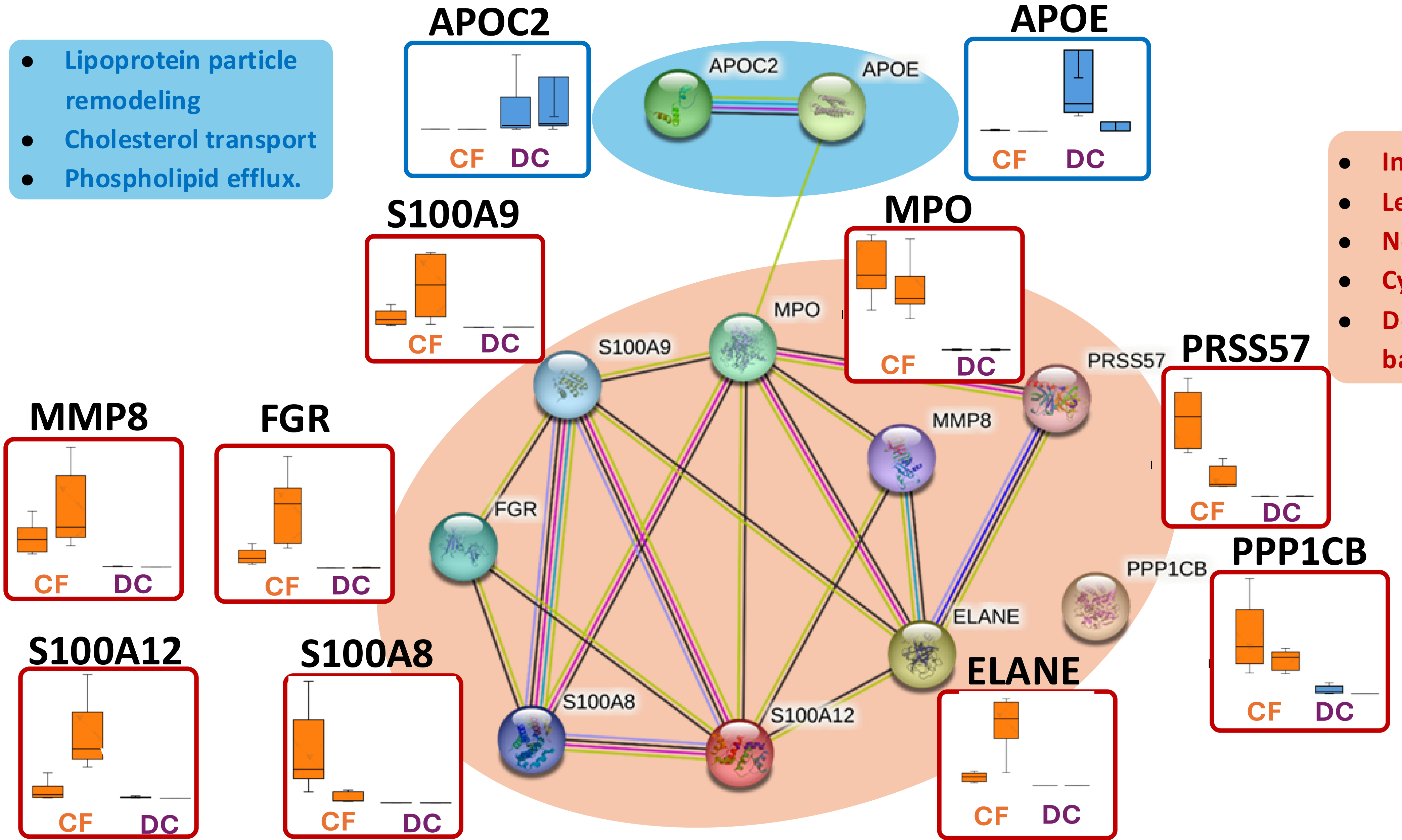
MICROBIAL PEPTIDES FROM CYSTIC FIBROSIS PATIENTS



TARGETED ASSAY FOR HOST-MICROBIAL PROTEIN DYNAMICS IN CLINICAL CF SAMPLES

- Lipoprotein particle remodeling
- Cholesterol transport
- Phospholipid efflux.

- Inflammatory response
- Leukocyte migration
- Neutrophil degranulation
- Cytokine production
- Defense response to bacteria



CLINICAL METAPROTEOMICS

- **We have developed a MS-based Galaxy-driven <u>bioinformatics workflow</u> for processing of microbial and host proteins, generating <u>verified microbial peptide candidates</u> suitable for <u>targeted analysis</u> within individual patient samples.**

- **We have utilized this workflow to detect and validate microbial peptides during a) co-infection during the COVID-19 pandemic (Bihani *et al* 2023, JPR); b) CF disease progression studies by comparing it with disease control (Kruk *et al* 2024, mSystems (In Press)) and c) Ovarian cancer studies (Mehta *et al*, work in progress).**

- **We hope that the workflow availability through Galaxy Training Network will help users detect differentially expressed host and microbial proteins in disease state.**

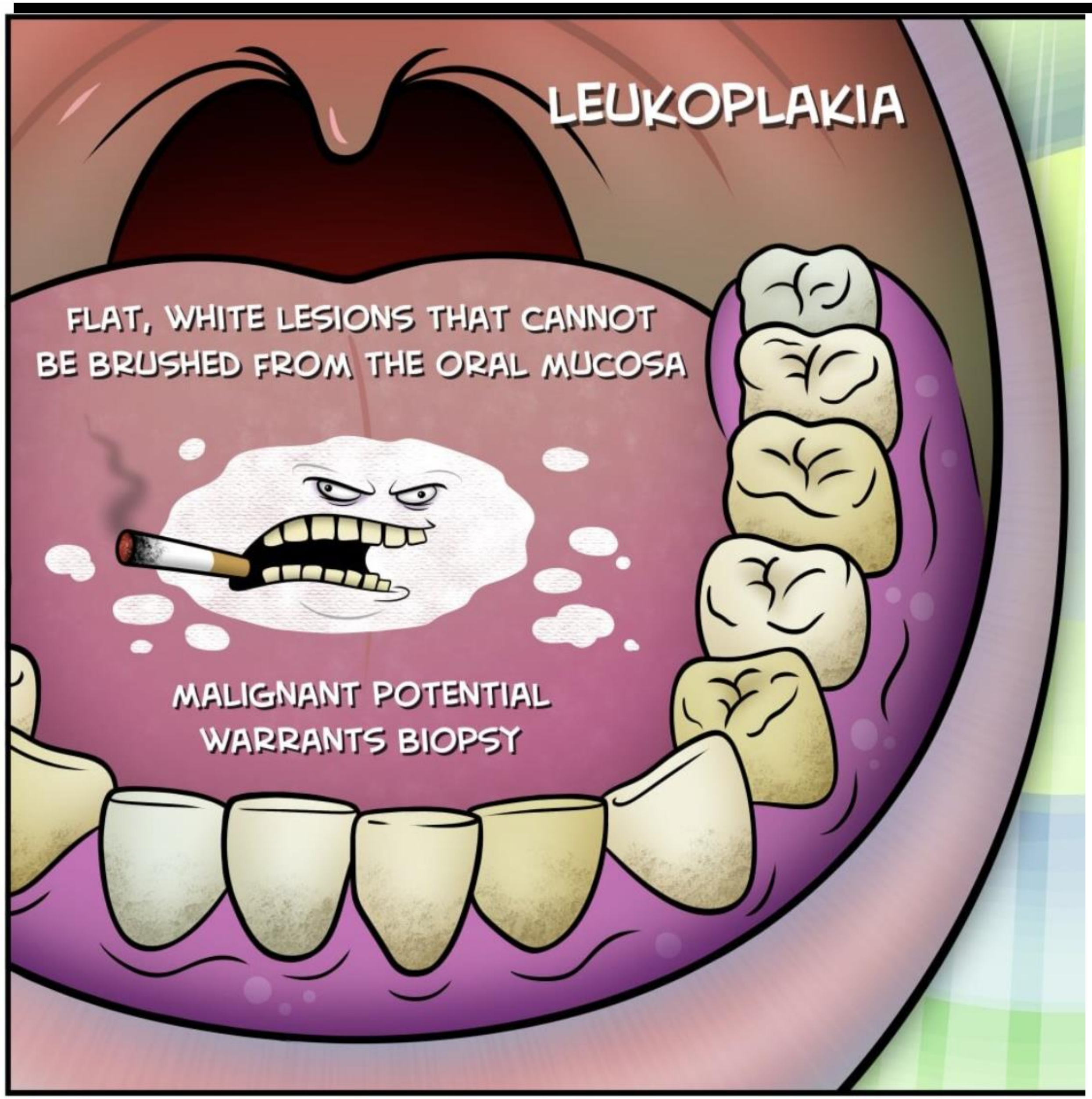
INVESTIGATING KEY HOST, MICROBIAL AND VARIANT PEPTIDES FOR DETECTION OF ORAL CANCER USING ADVANCED MULTI-OMICS METHODS.

Pratik Jagtap[1], *Ruben Shrestha*[2], *Beverly Wuertz*[3], *Monica Kruk*[4], *Subina Mehta*[1], *Alvaro Sebastian Vaca Jacome*[2], *Matthew Willetts*[4], *Frank Ondrey*[3], *Timothy Griffin*[1]

[1]*Biochemistry, Molecular Biology and Biophysics, University of Minnesota, Minneapolis, USA*
[2]*Bruker Scientific LLC, San Jose, CA;*
[3]*Otolaryngology Department, University of Minnesota, Minneapolis, Minnesota;*
[4]*Bruker Scientific, LLC, Billerica, MA*

WORK NOT PUBLISHED YET

ORAL LEUKOPLAKIA: ORAL CANCER RISK



WWW.MEDCOMIC.COM

BACKGROUND

- PAINLESS, SLOW-GROWING LESION on MUCOUS MEMBRANES of ORAL CAVITY
- POTENTIAL PRECANCEROUS CONDITION

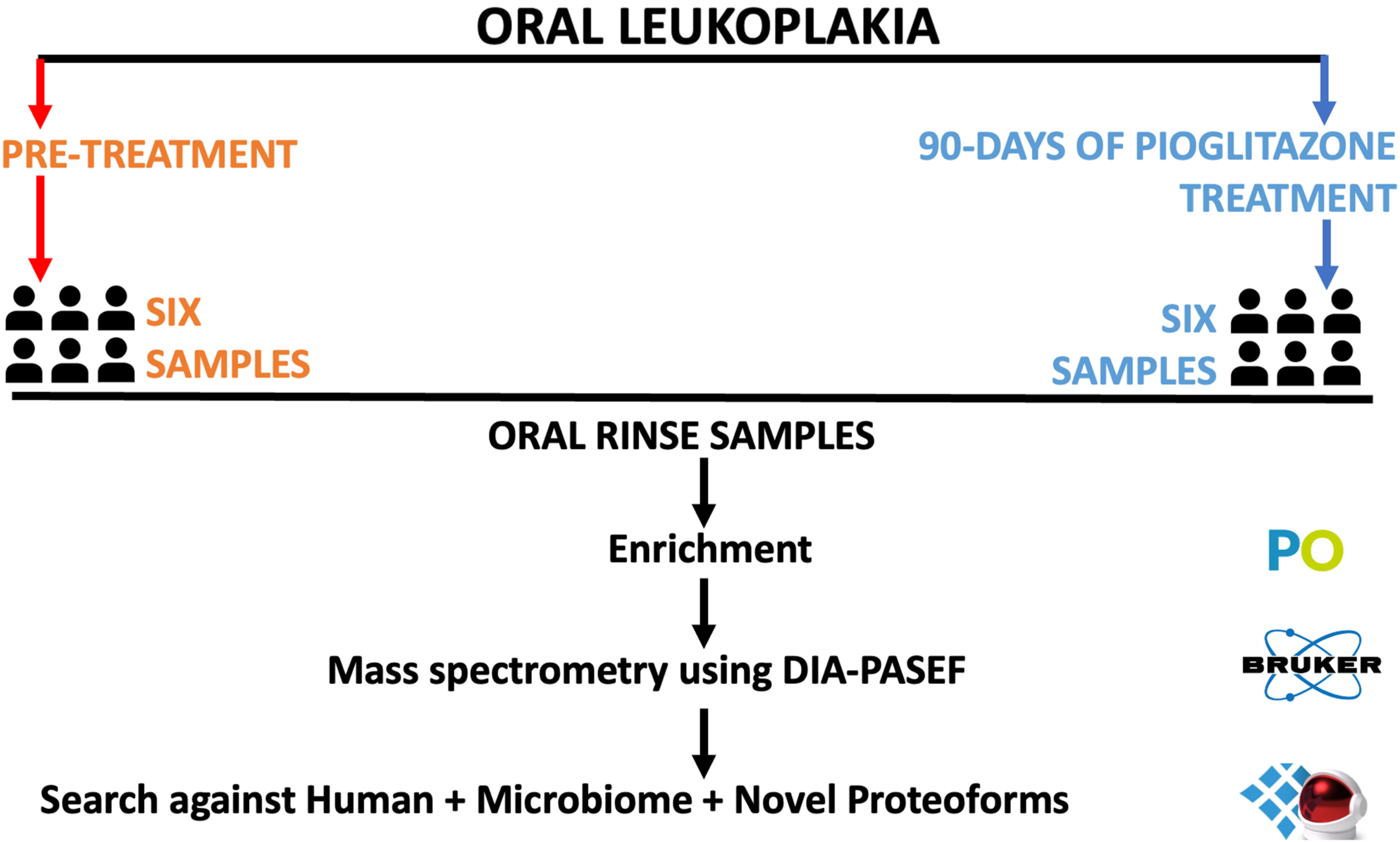
CAUSES

MOST COMMON

- HEAVY SMOKING
- CHEWING TOBACCO
- EXCESSIVE ALCOHOL USE
- POOR ORAL HEALTH
- LONG-TERM TRAUMA to ORAL CAVITY
- ADVANCED AGE
- HPV INFECTION

https://www.osmosis.org/answers/erythroplakia

EXPERIMENTAL WORKFLOW



ORAL LEUKOPLAKIA

PRE-TREATMENT

90-DAYS OF PIOGLITAZONE TREATMENT

SIX SAMPLES

SIX SAMPLES

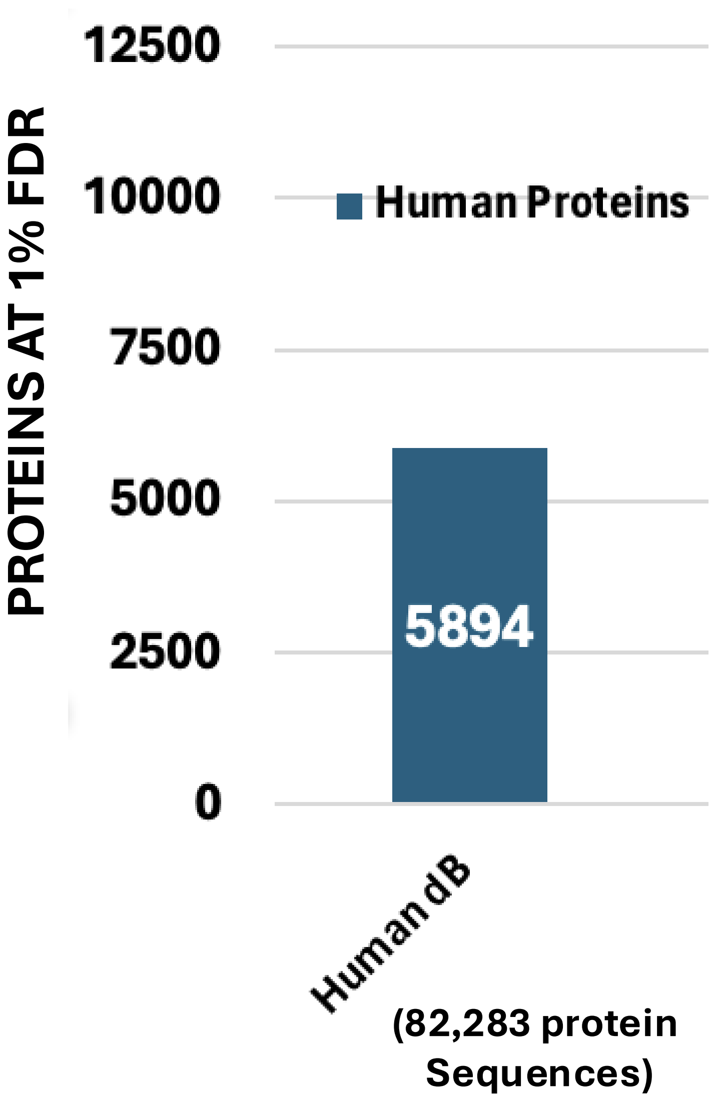
ORAL RINSE SAMPLES

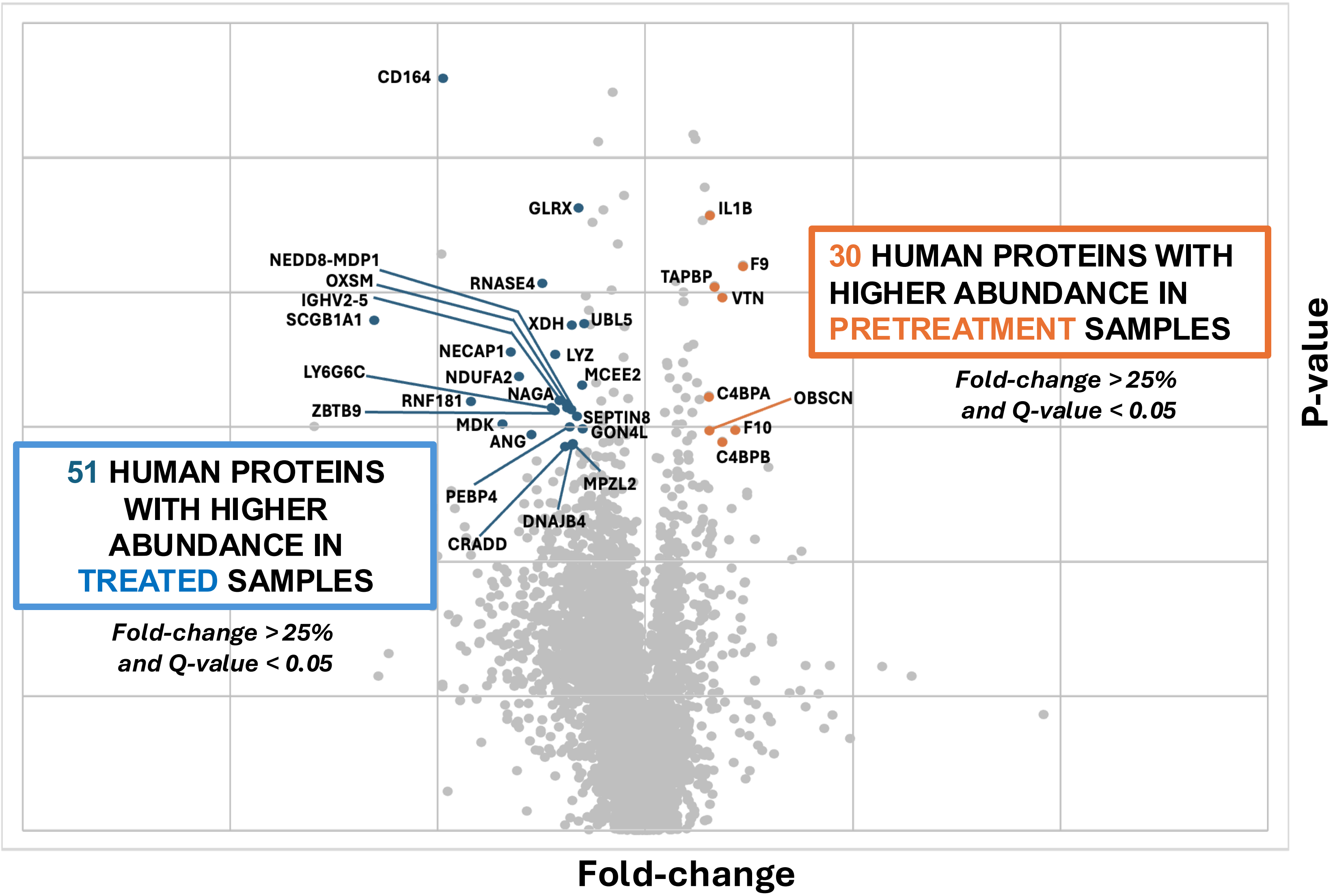
Enrichment

Mass spectrometry using DIA-PASEF

Search against Human + Microbiome + Novel Proteoforms

PROTEINS DETECTED AND DIFFERENTIALLY ABUNDANT PROTEINS





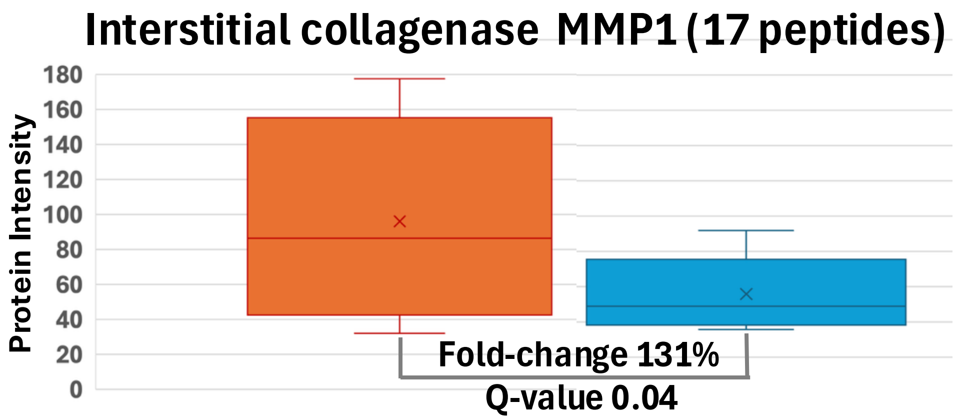
30 HUMAN PROTEINS WITH HIGHER ABUNDANCE IN PRETREATMENT SAMPLES

Fold-change > 25% and Q-value < 0.05

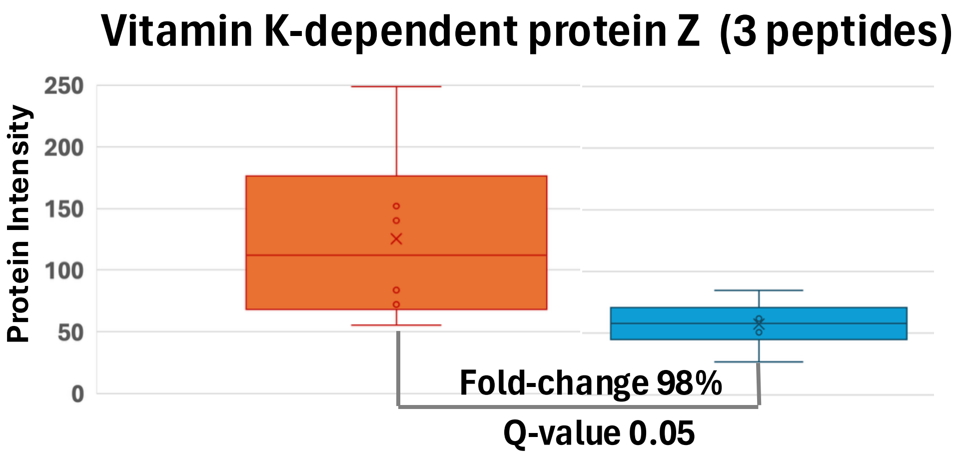
51 HUMAN PROTEINS WITH HIGHER ABUNDANCE IN TREATED SAMPLES

Fold-change > 25% and Q-value < 0.05

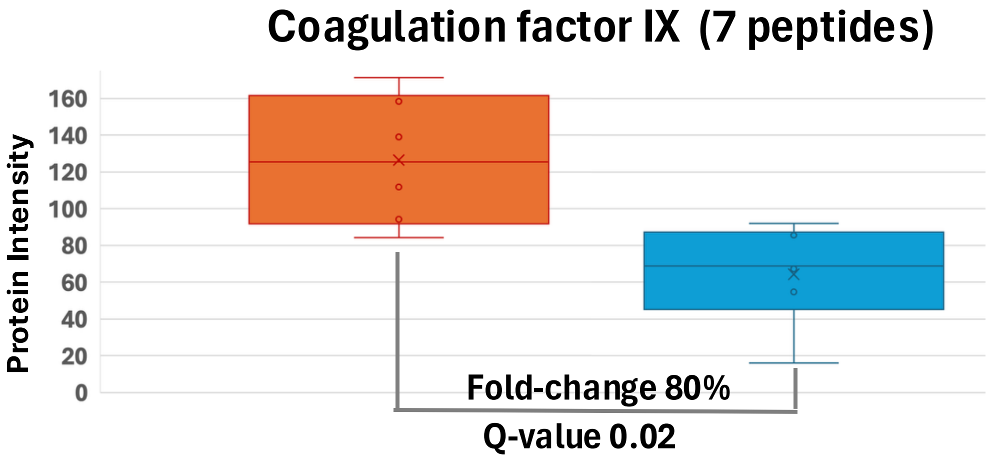
MMP1 & COAGULATION CASCADE: DOWNREGULATED AFTER TREATMENT


Interstitial collagenase MMP1 (17 peptides)

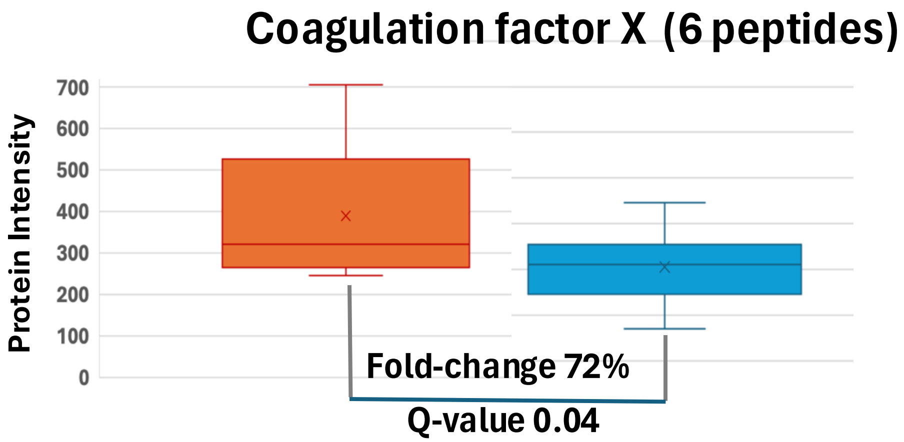
Fold-change 131%
Q-value 0.04


Vitamin K-dependent protein Z (3 peptides)

Fold-change 98%
Q-value 0.05


Coagulation factor IX (7 peptides)

Fold-change 80%
Q-value 0.02

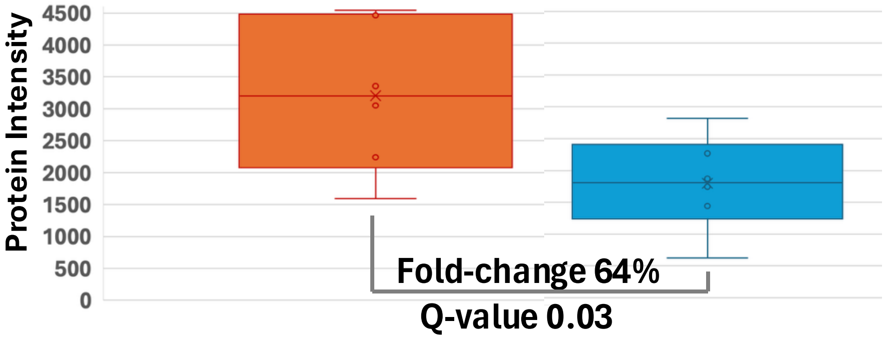

Coagulation factor X (6 peptides)

Fold-change 72%
Q-value 0.04

Coagulation Cascade

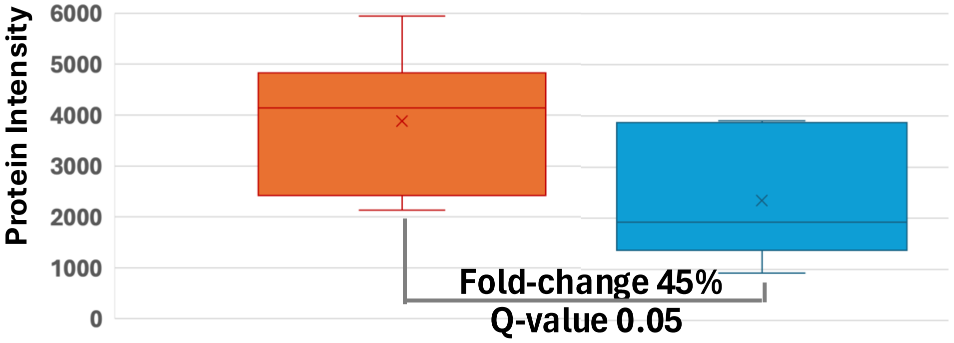
COMPLEMENT CASCADE: DOWNREGULATED AFTER TREATMENT

VITRONECTIN (12 peptides)



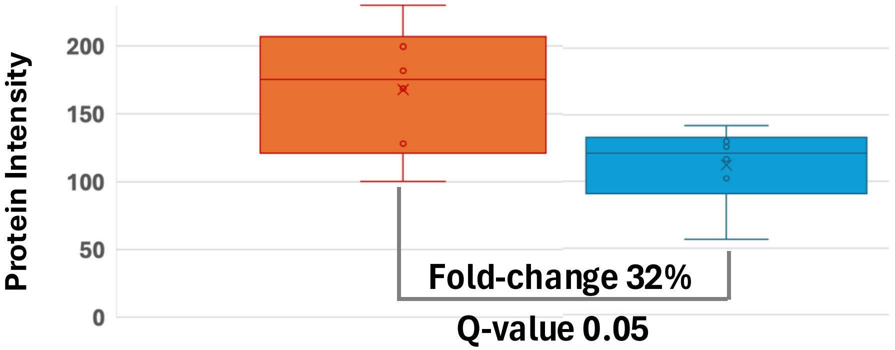
Fold-change 64%
Q-value 0.03

C4b-binding protein alpha chain (18 peptides)



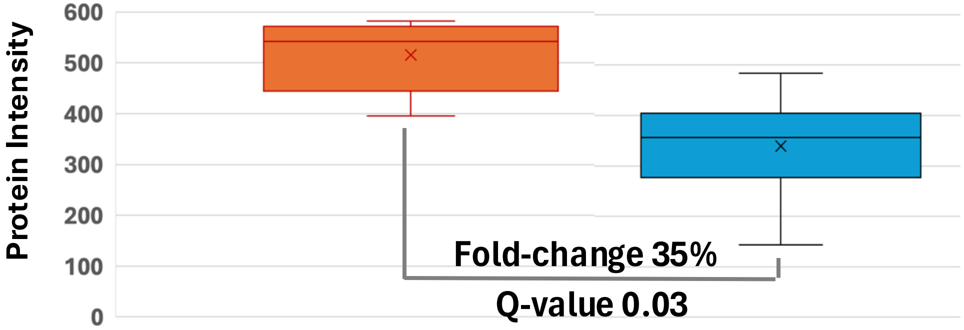
Fold-change 45%
Q-value 0.05

Carboxypeptidase B2 (9 peptides)



Fold-change 32%
Q-value 0.05

Complement component C8 beta chain (18 peptides)

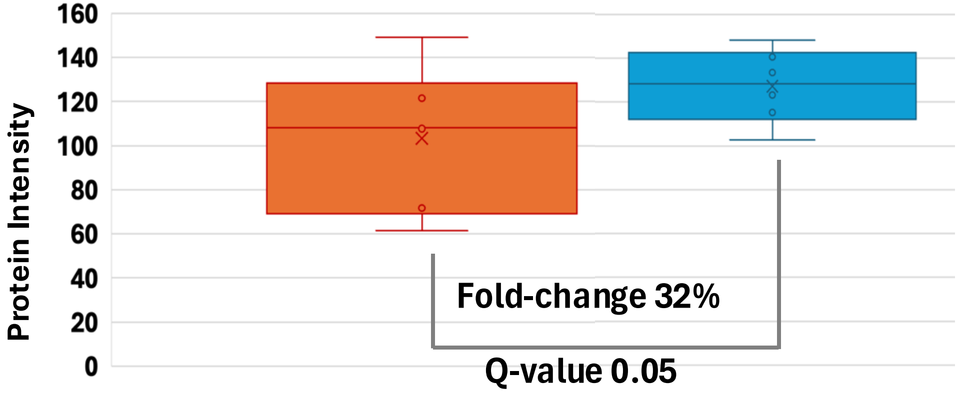


Fold-change 35%
Q-value 0.03

Regulation of Complement cascade

APOPTOSIS: UPREGULATED AFTER TREATMENT

DESMOGLEIN-2 (16 peptides)

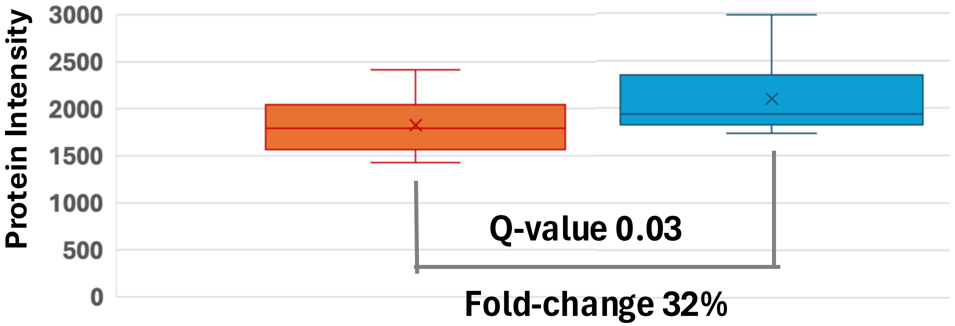


Fold-change 32%

Q-value 0.05

- Component of intercellular desmosome junctions mediating cell-cell adhesion.
- Involved in apoptotic pathway.
- Prognostic marker in renal cancer, pancreatic cancer, lung cancer, head and neck cancer, colorectal cancer and cervical cancer.

Apoptosis-associated speck-like protein containing a CARD (13 peptides)



Q-value 0.03

Fold-change 32%

- An adaptor protein that is composed of two protein-protein interaction domains
- Functions as key mediator in apoptosis and inflammation via the activation of caspases.
- Prognostic marker in renal cancer

CANCER RELEVANCE OF DIFFERENTIALLY ABUNDANT PROTEINS

	PROTEIN DESCRIPTION	RENAL	STOMACH	HEAD & NECK	PANCREATIC	ENDOMETRIAL	BREAST	UROTHELIAL	PROSTATE	LIVER	LUNG	COLORECTAL	CERVICAL	GLIOMA	THYROID	ORAL
HIGHER ABUNDANCE IN TREATED SAMPLES	Cathepsin D	🟩					▨					🟥	▨			
	Lysozyme C		▨	🟩												▨
	Golgi reassembly-stacking protein 2	🟥		🟥												
	Receptor-type tyrosine-protein phosphatase S	🟥			🟩											▨
	Sialate O-acetylesterase	🟩	▨			🟩										
	Plexin-B3						🟥									
	Glycerol-3-phosphate phosphatase	🟩						🟩								
	Cystatin-D						▨									
	Serine hydroxymethyltransferase, cytosolic	🟩								🟩						
	Di-N-acetylchitobiase															
	Desmoglein-2	🟩		🟥	🟥						🟥	🟩	🟥			
	Chitinase-3-like protein 2	🟥		🟩										🟥		▨
	Apoptosis-associated speck-like protein containing a CARD	🟥														🟥
	Xanthine dehydrogenase/oxidase							🟩								
HIGHER ABUNDANCE IN PRE-TREATMENT SAMPLES	Carboxypeptidase B2									🟩						▨
	C4b-binding protein alpha chain				▨	🟩				🟩						
	Vitronectin	🟥								🟩						▨
	Ferritin light chain	🟥														▨
	Cytochrome P450 4F3									▨						▨
	Complement component C8 beta chain									🟩						
	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	🟩														
	Mitochondrial adenyl nucleotide antiporter SLC25A24											🟩				
	Coagulation factor X	🟥			🟩					▨						
	Interstitial collagenase	🟥		▨						🟥			🟥			▨
	Coagulation factor IX									🟩						
	Signal peptidase complex catalytic subunit SEC11			🟥		🟩									🟩	

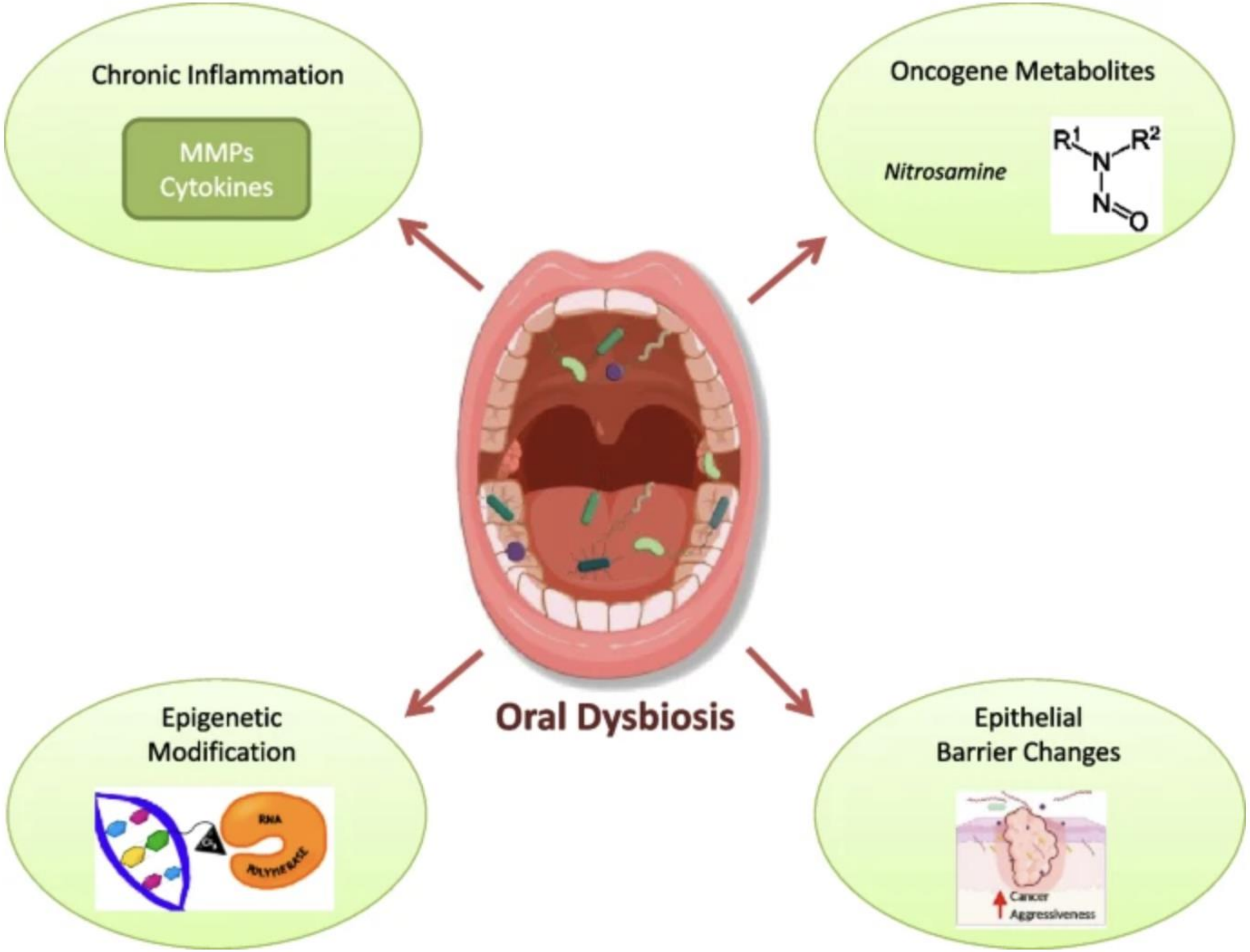
🟩 FAVORABLE PROGNOSIS VALUE

🟥 UNFAVORABLE PROGNOSIS VALUE

▨ HIGHER ABUNDANCE

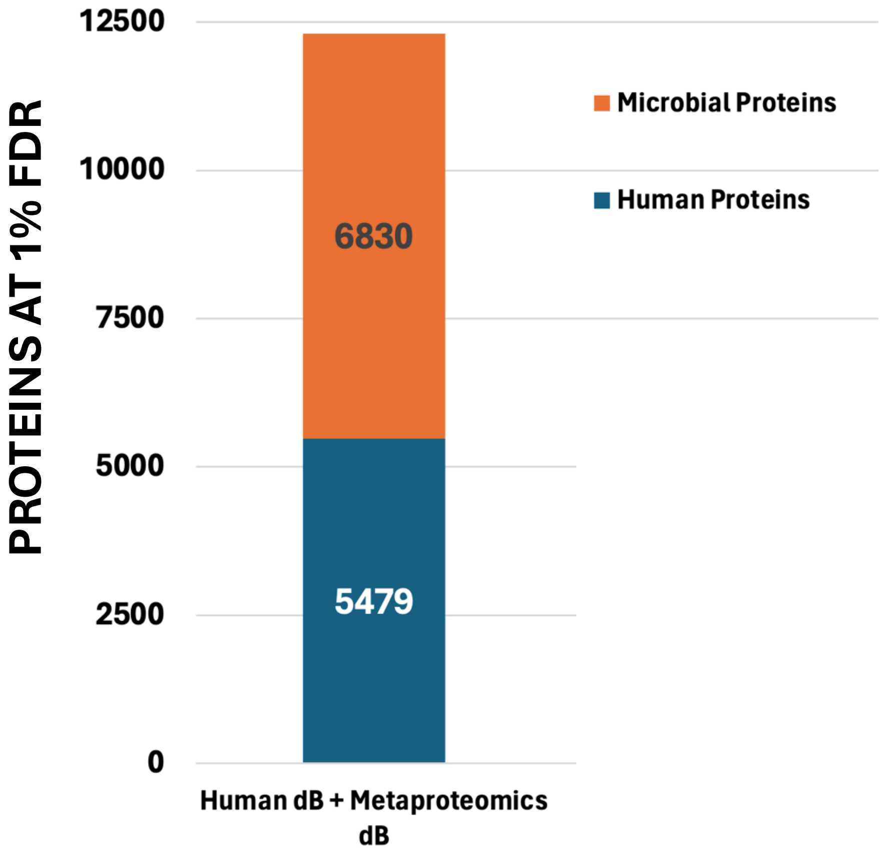
THE HUMAN PROTEIN ATLAS
https://www.proteinatlas.org/

ROLE OF BACTERIA IN ORAL CANCER DEVELOPMENT

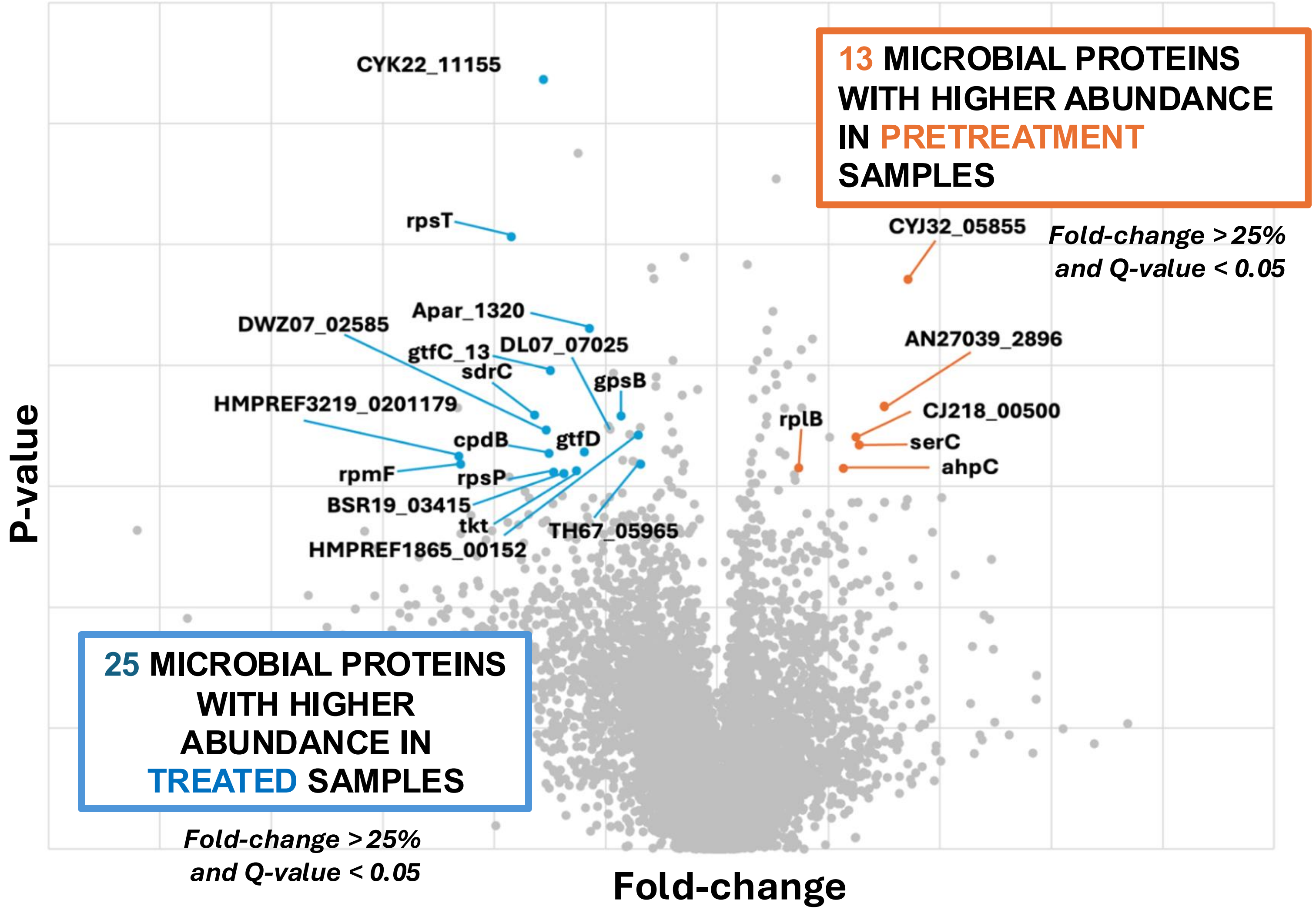


Asili, P., et al. J Gastrointest Canc (2023). https://doi.org/10.1007/s12029-022-00901-4

MICROBIAL DATABASE SEARCH RESULTS



(198,609 protein sequences)



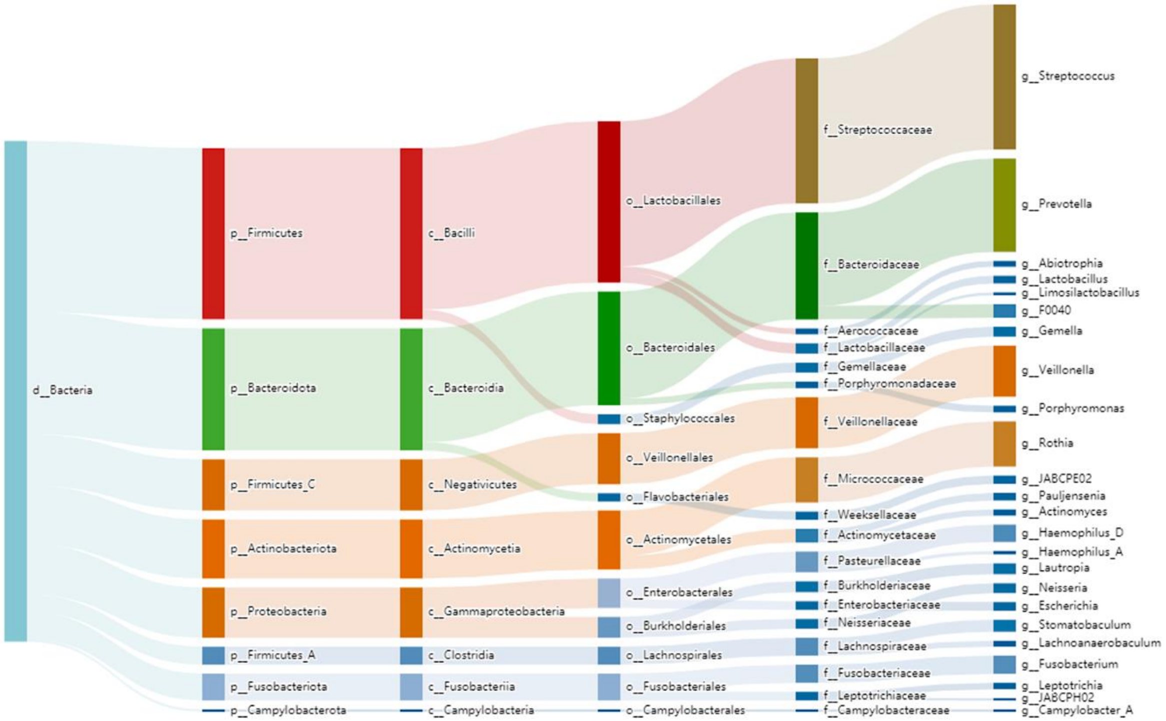
13 MICROBIAL PROTEINS WITH HIGHER ABUNDANCE IN PRETREATMENT SAMPLES

Fold-change > 25% and Q-value < 0.05

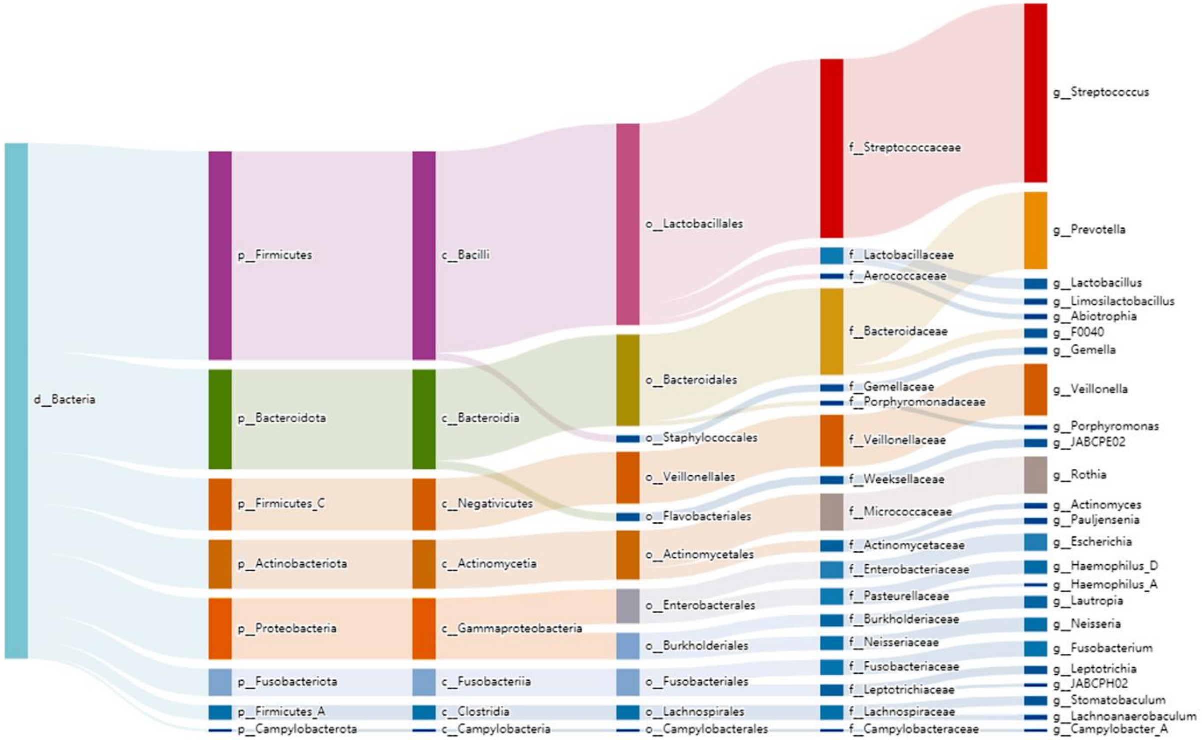
25 MICROBIAL PROTEINS WITH HIGHER ABUNDANCE IN TREATED SAMPLES

Fold-change > 25% and Q-value < 0.05

MICROBIAL TAXONOMY OUTPUTS



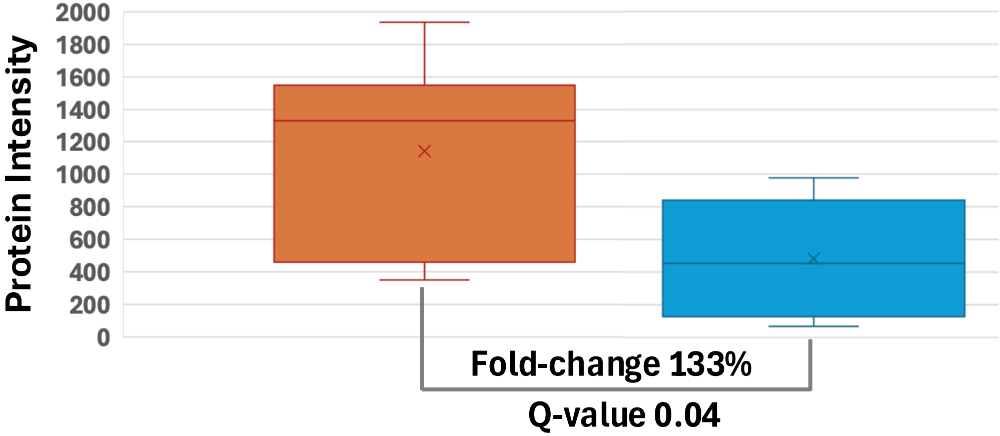
Genera detected in pretreated samples



Genera detected in treatment samples

MetaLab *and* MetaX *analysis by Kai Cheng, Qing Wu (Daniel Figeys Lab, University of Ottawa)*

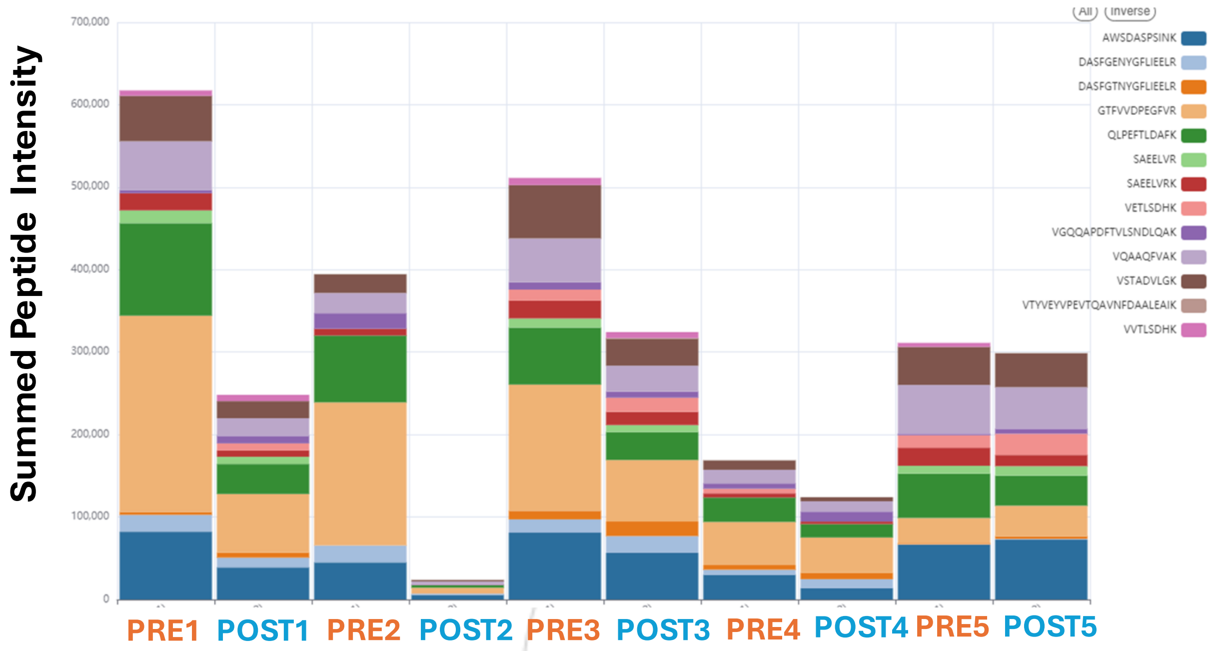
MICROBIAL PROTEINS DOWNREGULATED AFTER TREATMENT



Alkyl hydroperoxide reductase C (11 peptides)

Fold-change 133%
Q-value 0.04

- **Responsible for the detoxification of reactive oxygen species.**
- **Survival under environmental stresses or during infection.**



In this study, the protein was expressed by *Veillonella* genus.

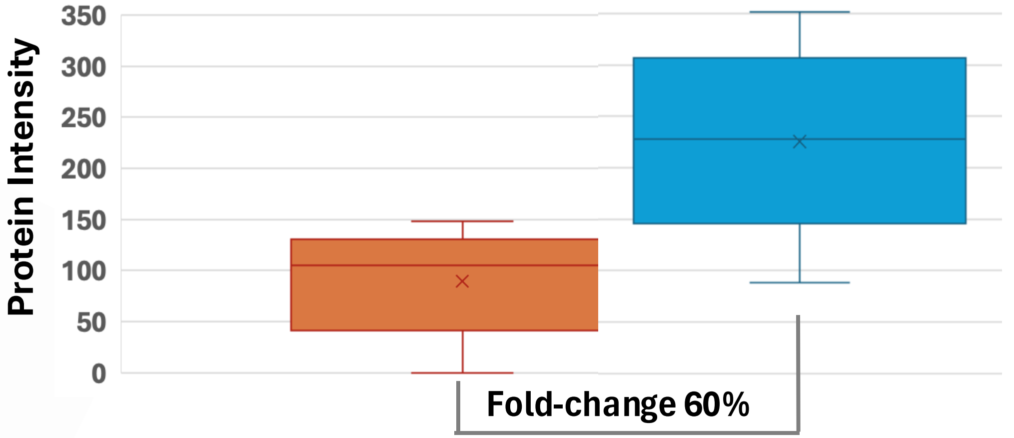
Veillonella

MetaLab *and* MetaX *analysis by Kai Cheng, Qing Wu (Daniel Figeys Lab, University of Ottawa)*

MICROBIAL PROTEINS UPREGULATED AFTER TREATMENT

- **Glucosyltransferase that catalyzes the transfer of glucosyl residues to dextran polymer.**
- **Involved in biofilm formation.**

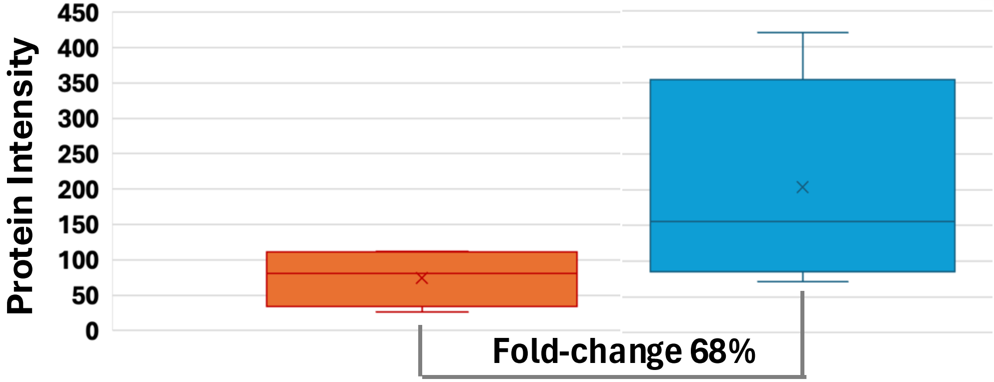
Dextransucrase (61 peptides)



Fold-change 60%

Q-value 0.02

serine-type D-Ala-D-Ala carboxypeptidase (21 peptides)



Fold-change 68%

Q-value 0.03

- **Involved in bacterial cell wall synthesis by mediating peptidoglycan cross-linking.**

DIFFERENTIALLY ABUNDANT MICROBIAL PROTEINS

PROTEIN DESCRIPTIONS	UNIPROTIDS	% CHANGE	QVALUE	# UNIQUE PEPTIDES
Alkyl hydroperoxide reductase C	E4LFM1	133.47	0.04	11
Dextransucrase	E9DP35, J7SIV6, J7TRB0	-62.27	0.02	**61**
Serine-type D-Ala-D-Ala carboxypeptidase	A0A2A5QD93	-67.91	0.03	21
Serine protease	E3H076	-44.89	0.05	4
Uncharacterized protein	A0A2S7ZRS7	-46.03	0.01	5
RND transporter, HAE1 family	E1L728	-37.59	0.03	5
Ribosomal subunit protein S16	A5VKN7;C8P927	-64.94	0.03	3
Glutamate--ammonia ligase	Q5M2N1	-58.15	0.04	7
Elongation factor Ts	A0A0X8K315	-46.57	0.03	8

ORAL CANCER DATASET: CONCLUSIONS AND FUTURE WORK

- **Several human, microbial and variant proteins were detected to be differentially abundant in pretreatment and treated samples.**

- **Pathways such as coagulation and complement cascade were downregulated and apoptotic pathways were upregulated after treatment.**

- **Microbial functions associated with glucosyltransferase activity were upregulated and oxidative stress functions were downregulated after treatment.**

- **Peptides associated with differentially abundant human and microbial will be used for targeted analysis.**

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- Frank Ondrey

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- Sebastian Vaca
- Matthew Willets
- Jon Lenz

UNIVERSITY OF MINNESOTA
Driven to Discover®
COLLEGE of BIOLOGICAL SCIENCES

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- Monica Kruk
- Subina Mehta
- Reid Wagner

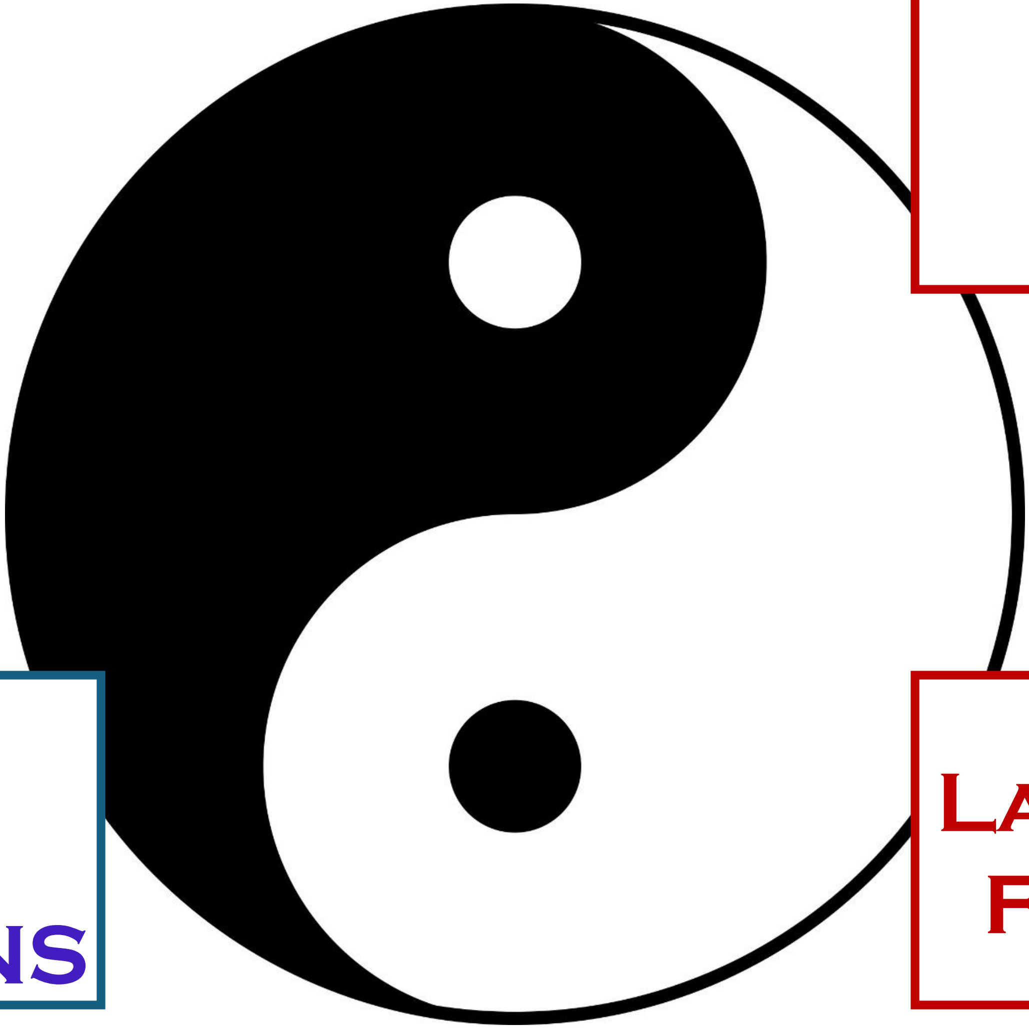
uOttawa

- Kai Cheng
- Qing Wu
- Daniel Figeys

CLINICAL METAPROTEOMICS WORKFLOW TO STUDY HOST-MICROBIOME DYNAMICS

- *MICROBIOME RESEARCH*
  - *MASS SPECTROMETRY DATA ANAYSIS*
  - *METAPROTEOMICS RESEARCH*
  - *GALAXY BIOINFORMATICS PLATFORM*
- *CLINICAL METAPROTEOMICS WORKFLOW*
  - *CLINICAL METAPROTEOMICS:COVID-19 PANDEMIC*
  - *CLINICAL METAPROTEOMICS:CYSTIC FIBROSIS*
  - *CLINICAL METAPROTEOMICS: ORAL CANCER*
- ***METAPROTEOMICS EDUCATION***

METAPROTEOMICS: STRENGTHS & CHALLENGES



FUNCTIONAL COMPOSITION

HOST-MICROBIOME INTERACTION

QUANTIFYING BIOMASS CONTRIBUTIONS

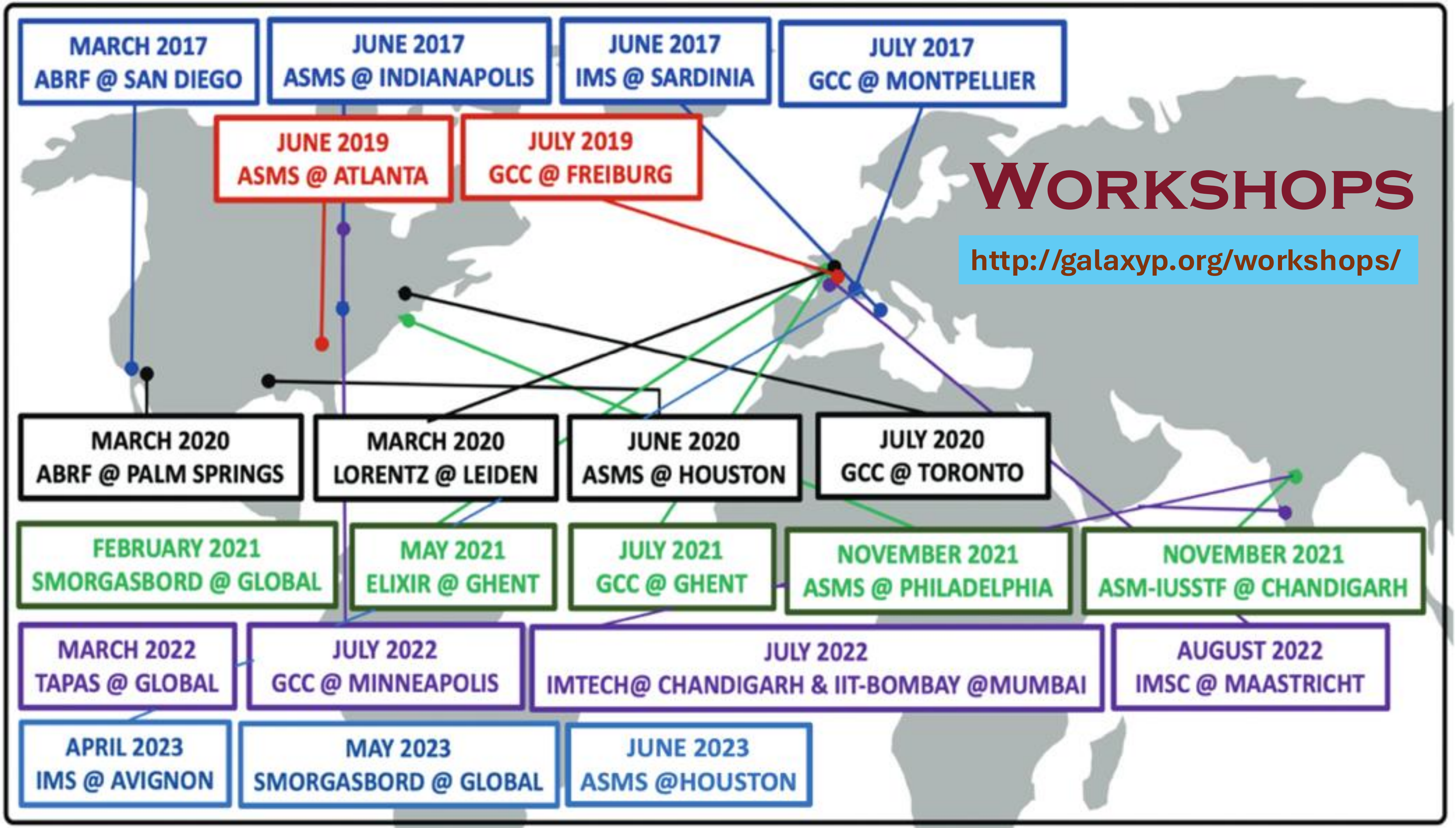
PROTEIN EXTRACTION

VARIABILITY & ABUNDANCE

Large Databases
False Positives

WORKSHOPS

http://galaxyp.org/workshops/



MARCH 2017
ABRF @ SAN DIEGO

JUNE 2017
ASMS @ INDIANAPOLIS

JUNE 2017
IMS @ SARDINIA

JULY 2017
GCC @ MONTPELLIER

JUNE 2019
ASMS @ ATLANTA

JULY 2019
GCC @ FREIBURG

MARCH 2020
ABRF @ PALM SPRINGS

MARCH 2020
LORENTZ @ LEIDEN

JUNE 2020
ASMS @ HOUSTON

JULY 2020
GCC @ TORONTO

FEBRUARY 2021
SMORGASBORD @ GLOBAL

MAY 2021
ELIXIR @ GHENT

JULY 2021
GCC @ GHENT

NOVEMBER 2021
ASMS @ PHILADELPHIA

NOVEMBER 2021
ASM-IUSSTF @ CHANDIGARH

MARCH 2022
TAPAS @ GLOBAL

JULY 2022
GCC @ MINNEAPOLIS

JULY 2022
IMTECH@ CHANDIGARH & IIT-BOMBAY @MUMBAI

AUGUST 2022
IMSC @ MAASTRICHT

APRIL 2023
IMS @ AVIGNON

MAY 2023
SMORGASBORD @ GLOBAL

JUNE 2023
ASMS @HOUSTON

EDUCATION PORTAL @ METAPROTEOMICS INITIATIVE

https://metaproteomics.org/education/

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MOCA MINNESOTA OVARIAN CANCER ALLIANCE

MASONIC CANCER CENTER UNIVERSITY OF MINNESOTA

http://galaxyp.org/contact/

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