

CLINICAL METAPROTEOMICS WORKFLOW TO STUDY HOST-MICROBIOME DYNAMICS

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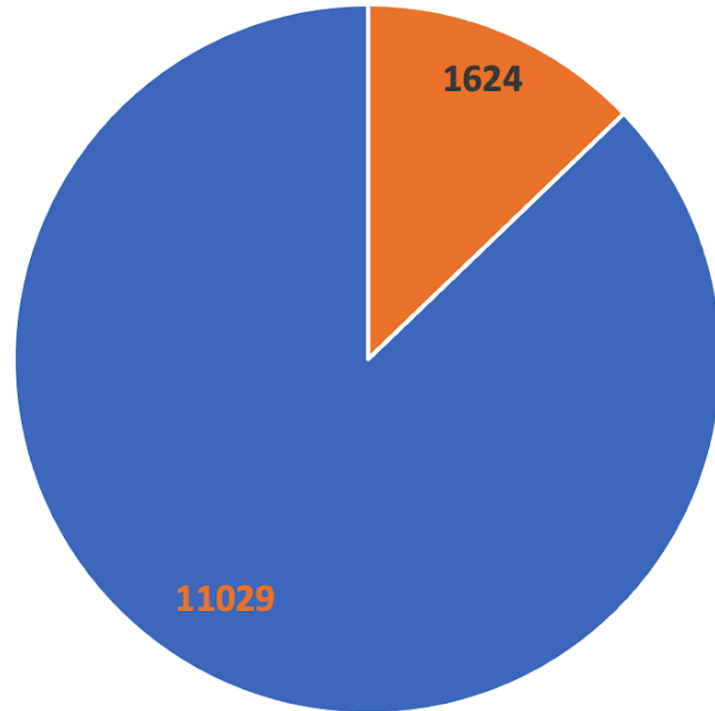
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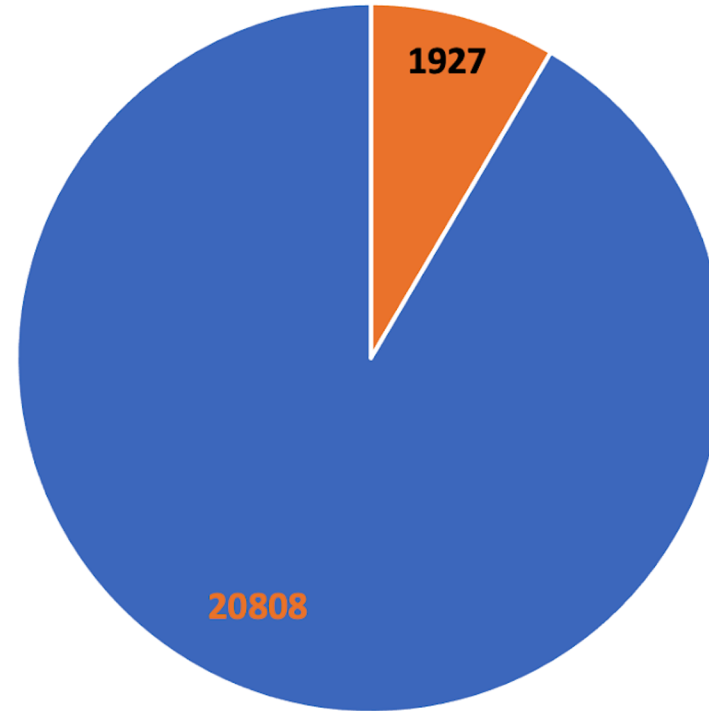
CLINICAL METAPROTEOMIC STUDIES DETECT LIMITED NUMBER OF MICROBIAL PEPTIDES

Cervical-vaginal fluid



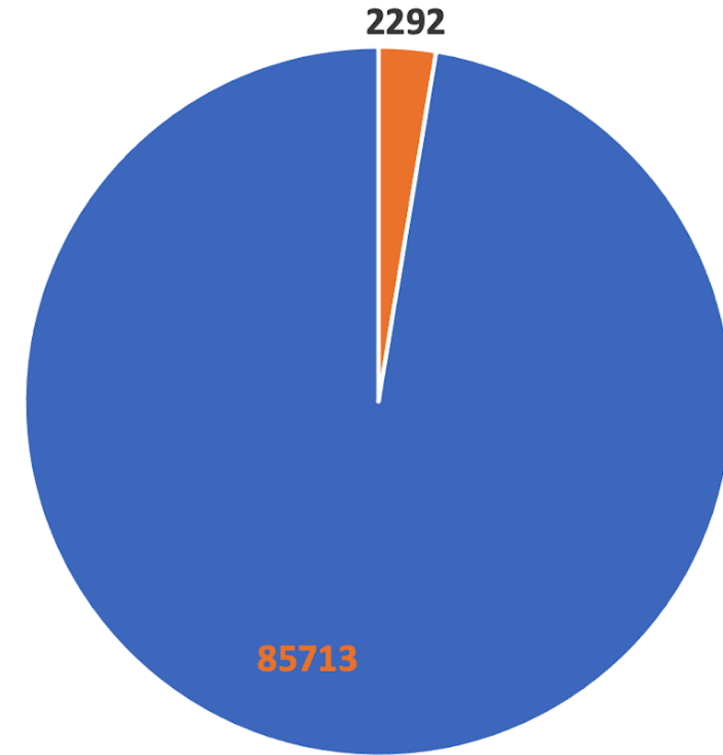
Afiuni-Zadeh *et al* (2018) *Sci Rep* . 8(1):10868.
doi: 10.1038/s41598-018-29092-4.

Saliva



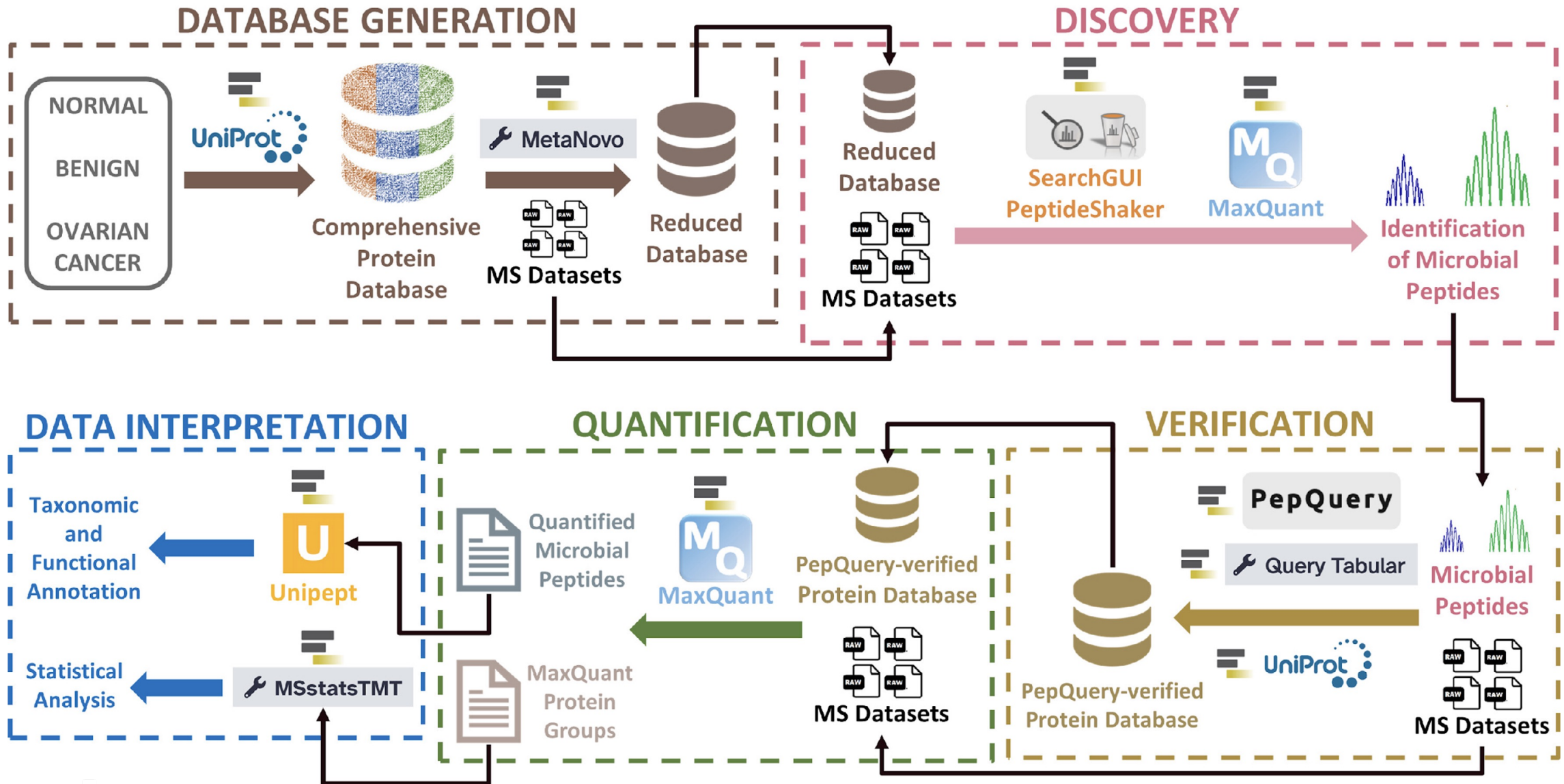
Jagtap *et al* (2012) *Proteomics* 12(7): 992–1001.
doi: 10.1002/pmic.201100503

Bronchoalveolar lavage



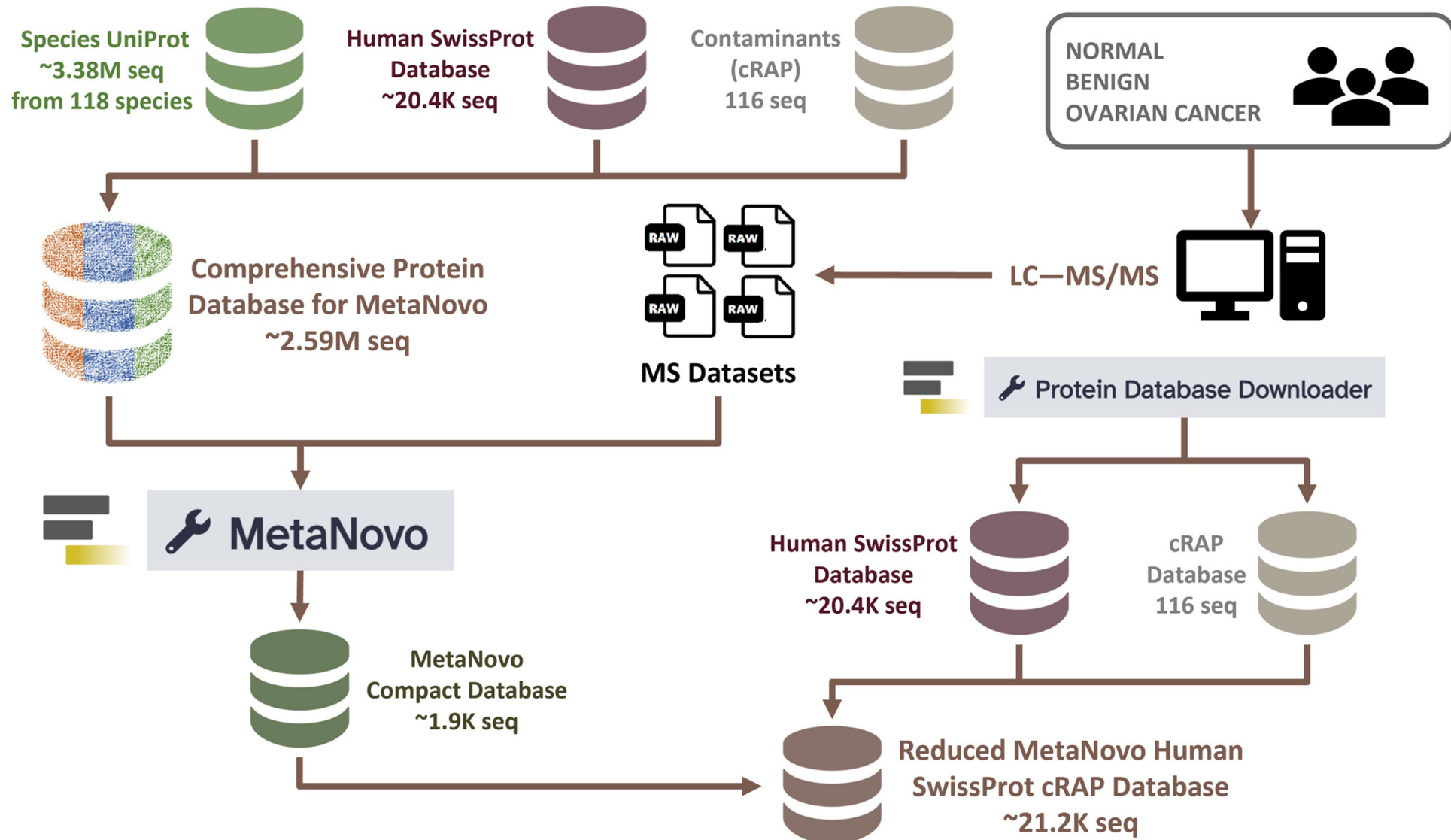
Kruk *et al* (2024) *mSystems*
In Press

OVERVIEW OF CLINICAL METAPROTEOMICS WORKFLOW



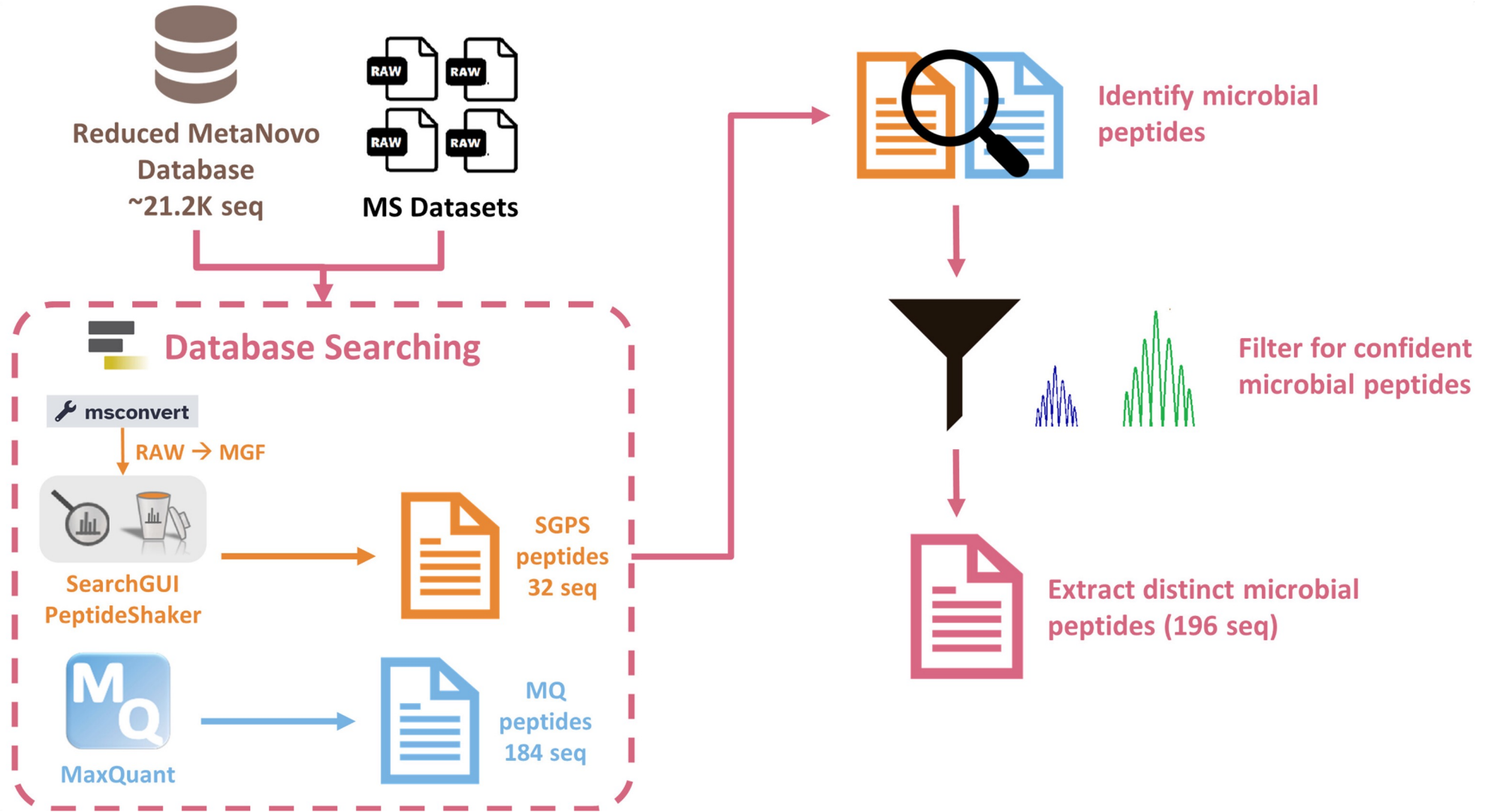
Do K, Mehta S *et al* (2024). A novel clinical metaproteomics workflow enables bioinformatic analysis of host-microbe dynamics in disease. *mSphere* <https://doi.org/10.1128/msphere.00793-23>

DATABASE GENERATION MODULE



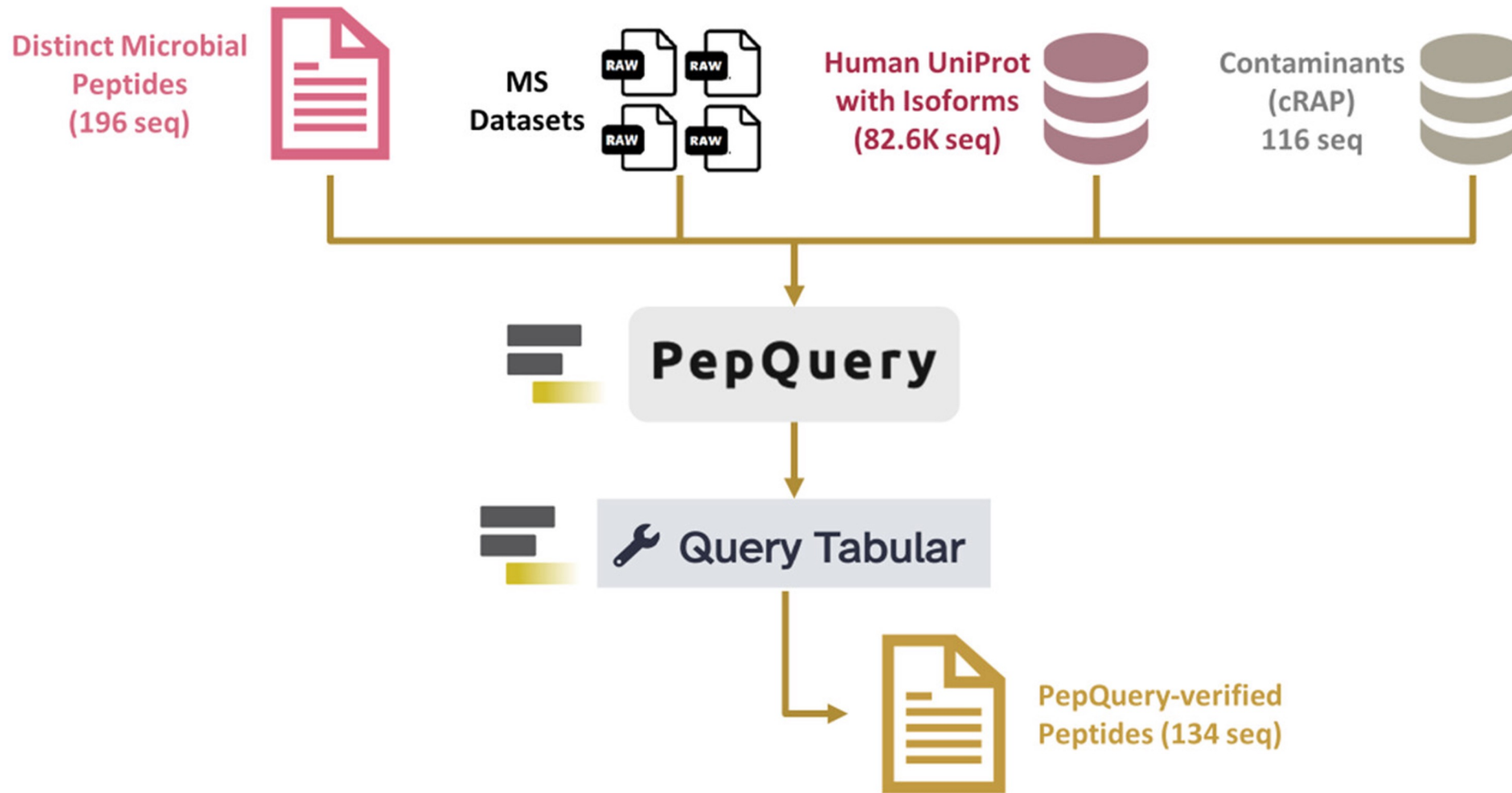
Do K, Mehta S *et al* (2024). A novel clinical metaproteomics workflow enables bioinformatic analysis of host-microbe dynamics in disease. *mSphere* <https://doi.org/10.1128/msphere.00793-23>

DISCOVERY MODULE



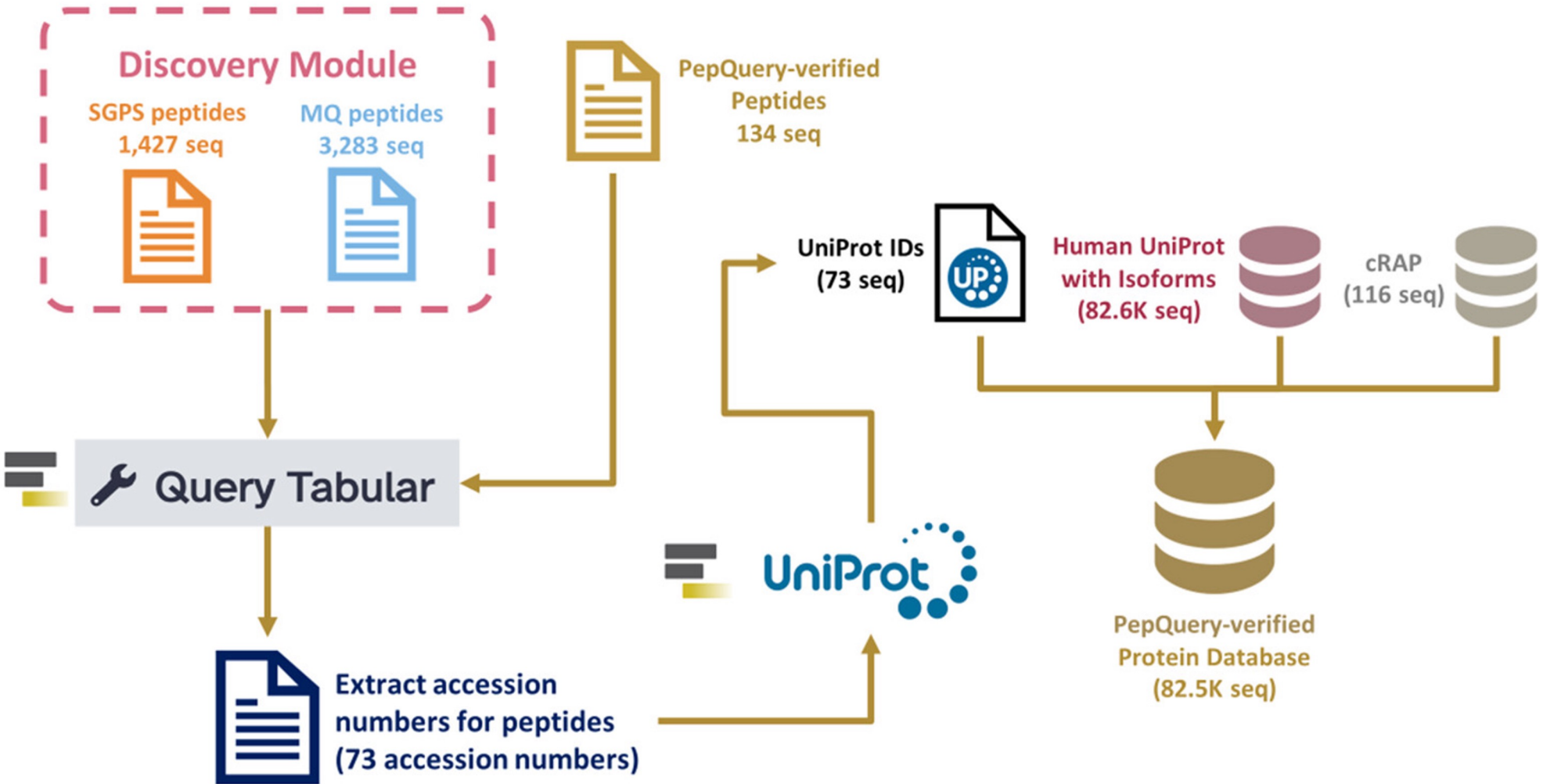
Do K, Mehta S *et al* (2024). A novel clinical metaproteomics workflow enables bioinformatic analysis of host-microbe dynamics in disease. *mSphere* <https://doi.org/10.1128/msphere.00793-23>

VERIFICATION AND VERIFIED DATABASE GENERATION MODULE



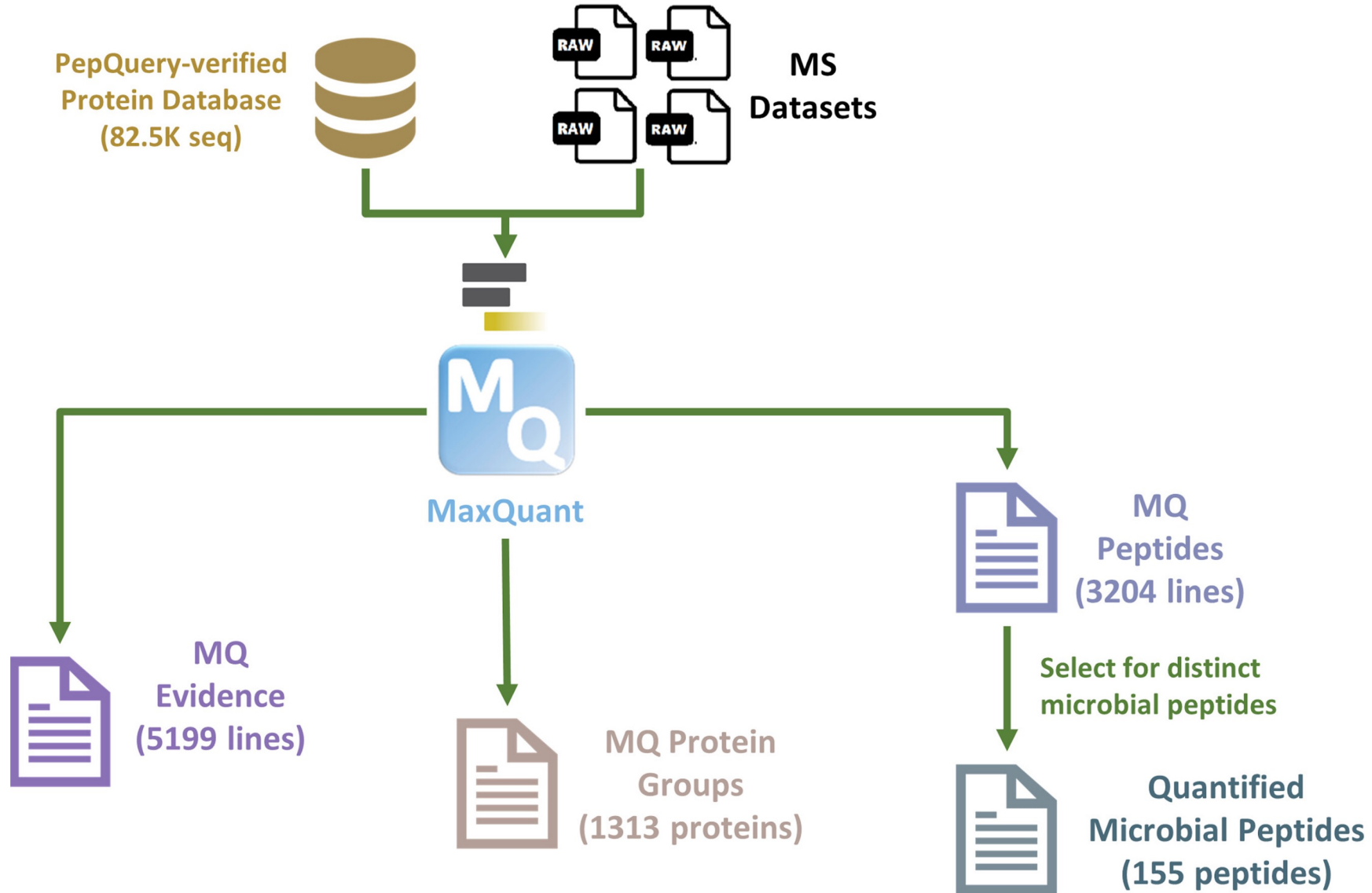
Do K, Mehta S *et al* (2024). A novel clinical metaproteomics workflow enables bioinformatic analysis of host-microbe dynamics in disease. *mSphere* <https://doi.org/10.1128/msphere.00793-23>

VERIFICATION AND VERIFIED DATABASE GENERATION MODULE

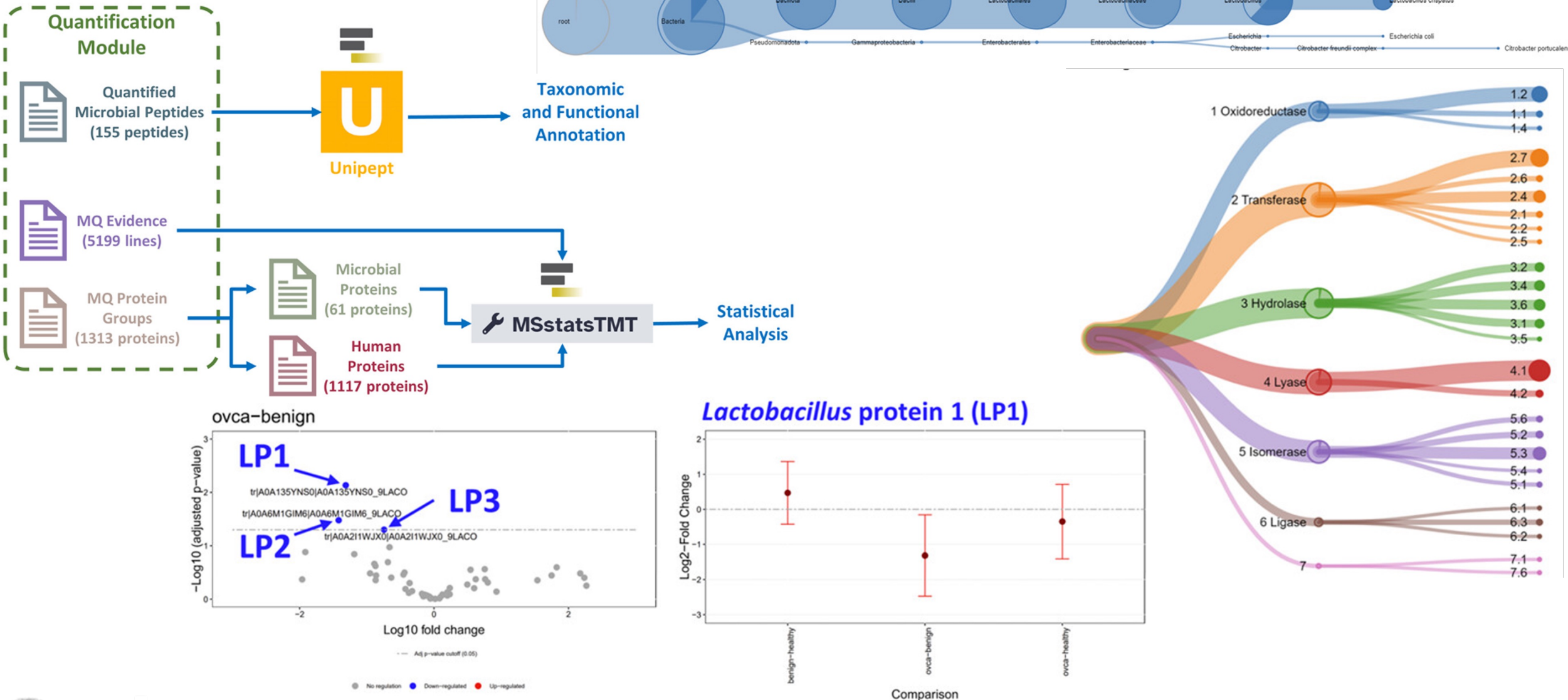


Do K, Mehta S *et al* (2024). A novel clinical metaproteomics workflow enables bioinformatic analysis of host-microbe dynamics in disease. *mSphere* <https://doi.org/10.1128/msphere.00793-23>

QUANTIFICATION MODULE



DATA INTERPRETATION MODULE



Do K, Mehta S *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 METAPROTEOMICS PUBLICATIONS

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.

mSystems

Kruk M *et al* (2024) An integrated metaproteomics workflow for studying host-microbe dynamics in bronchoalveolar lavage samples applied to cystic fibrosis disease. *mSystems* (In Press).

Mehta S *et al* (Work in Progress) A novel host and microbial biomarker panel for early detection of ovarian cancer.

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>

CLINICAL METAPROTEOMICS

- We have developed a MS-based Galaxy-driven bioinformatics workflow for processing of microbial and host proteins, generating verified microbial peptide candidates suitable for targeted analysis 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.

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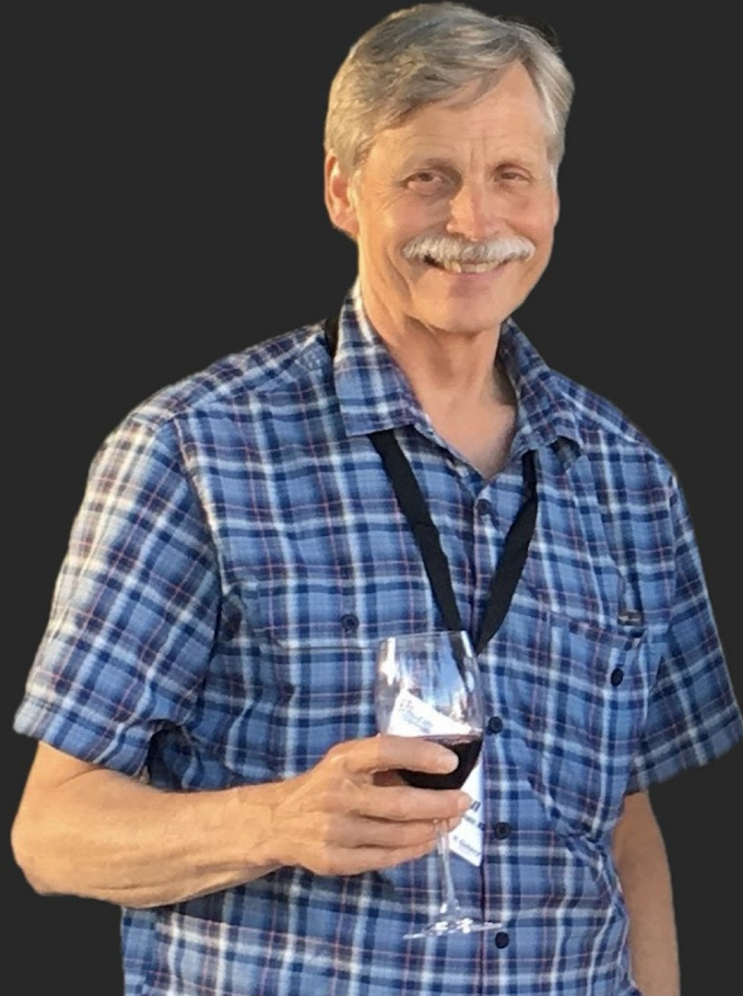
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**James Johnson
(1953-2024)**



JJ, we miss you!