

# Identification of peptides presented by major histocompatibility complex in macrophages through immunopeptidomics

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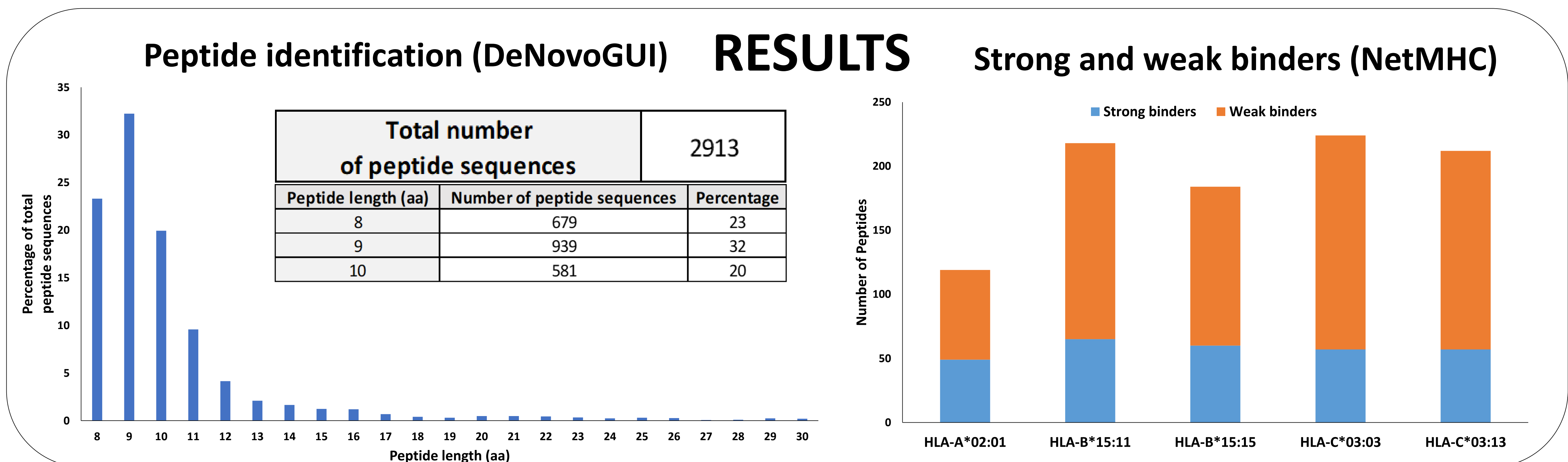
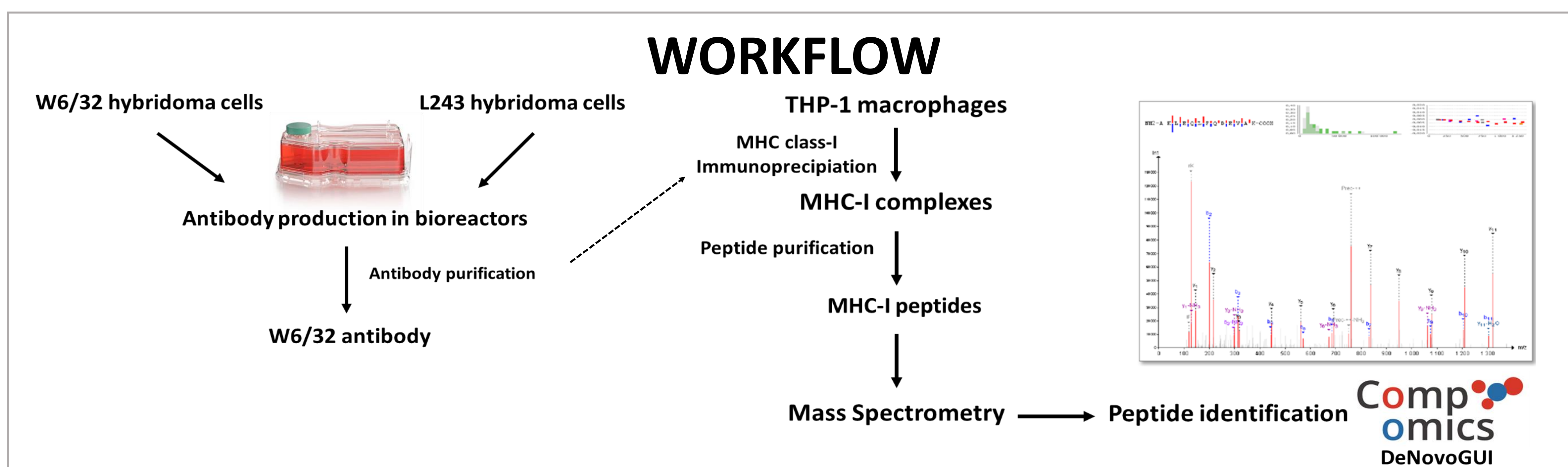
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## Tuberculosis

- Tuberculosis (TB) is a contagious and airborne infectious disease
- 1.6 million worldwide deaths in 2021, amongst these 187 000 deaths among people with HIV
- Major cause of deaths related to antimicrobial resistance

## Aim of the project

- Identification of peptides presented by MHC-I molecules in macrophages under physiological and pathological conditions using mass spectrometry instrumentation and data analysis.
- Identification of the most relevant peptides for vaccine design and development.



## Conclusions

- We have identified 2913 unique MHC-I-bound peptides under physiological conditions.
- Most peptides have the expected length for MHC-I-bound peptides.
- Peptides were ranked by affinity for several HLA isotypes.
- Peptides are predicted to bind to their HLA types.

## Work in progress

- Optimization of the peptide identification data
- Technical validation of identified peptides by spectral matching with synthetic peptides
- Mass Spectrometry analysis of THP-1 cells infected with *Mycobacterium avium*

## References

Bettencourt, P. et al. NJP Vaccines 2020

## Peptide-binding motif (Weblogo)

