



# IO17 | Large Scale Bioinformatics for Immuno-Oncology

## Neoantigens: exercise 3

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## Exercise 3: peptide-MHC binding prediction



To use TIminer, Docker must be running on your computer!

From Patient\_1's data, we have:

- Predicted the HLA types: *Patient\_1\_HLA.txt*
- Annotated the mutations: *Patient\_1\_VEP\_37\_mutations.txt*
- Predicted the sequences of the mutated proteins:  
*Patient\_1\_VEP\_37\_proteins.txt*

Predict the mutated peptides, **8-11 amino acid** long, which bind to the patient's HLAs with TIminer (function `TIminerAPI.executeNetmhcpan`), considering a **IC<sub>50</sub> cut-off of 500 nM** for the binding affinity.

**Important note:** To reduce the computational time, we will consider only the first HLA-A type, namely a tab-delimited text file with the same format of the output file of `Input/Patient_1_HLA.txt`, but with all HLA types equal: *Patient\_1\_HLA-A.txt*.

## Brainstorming: prioritization of candidate neoantigens

This computation will take a while...

While you are waiting for the results, discuss in pairs what might be the features to consider for prioritizing tumor neoantigens for experimental validation.

- *IC50 binding affinity*
- *rank of the predicted affinity*
- ...

## Questions on peptide-MHC binding prediction

Once you get the results of exercise 3, answer the questions related to this exercise at:

<https://b.socrative.com/login/student/>

# How to access the questions on Socrative (1)


1. Access Socrative with student access at: <https://b.socrative.com/login/student/>
2. Join the **IO17** room



Student Login

Room Name

JOIN

 English ▾

## How to access the questions on Socrative (2)

3. Enter your name and click „done“ to start the quiz

I017

Enter your name

Francesca Finotello

**DONE**