Frequently asked questions for MixMHC2pred

What kind of predictions can I make with MixMHC2pred

MixMHC2pred is a predictor of HLA-II ligand displayed at the cell surface. It combines predictions of affinity to HLA-II molecules including binding core offset preferences, as well as peptide N-/C-terminal motifs and peptide length preference (which are likely emerging from the peptide processing steps).

Peptides ranking high in MixMHC2pred predictions are more likely to elicit CD4+ T cell recognition.

How should I interpret the output of MixMHC2pred

- *Peptide* gives the sequence of the peptides, in the same order as provided in input.
- *BestAllele* gives the name of the best allele (based on the allele with best predicted score for the given peptide).
- *%Rank* gives the predicted score for the best allele, given as a percentile rank (i.e., the percentage of random peptides that would have a score higher than the peptide provided in input - a value of 0 is the best possible prediction and a value of 100 is the least good score).
- *%Rank_perL* is similar to *%Rank* but computed based only on peptides having the same length than the given peptide. This score thus doesn't follow the length distribution observed in naturally presented ligands.
- *BestCore* and *Best_s* indicate the best predicted core binding sequence and offset respectively, for the peptide towards the given allele.

Peptides that are too short (less than 12 amino acids) or that contain non standard amino acids have *NA* or *nan* values instead of their scores.

How can I rank my peptides based on MixMHC2pred predictions

The best way to rank your peptides is to use the global score with the best allele (*%Rank*), the best predicted peptides have the lowest scores.

Can I use MixMHC2pred for commercial purposes

If you plan to use MixMHC2pred for commercial purposes, you are required to obtain a separate license. To do so, please contact eauffarth@licr.org at the Ludwig Institute for Cancer Research Ltd.

Who should I contact in case of a technical or other issue

Julien Racle (julien.racle@unil.ch). Please provide as much details as possible and ideally send also an example input file that is causing the issue.

How should I cite MixMHC2pred

If you are using MixMHC2pred, please refer to

Racle, J., et al. Robust prediction of HLA class II epitopes by deep motif deconvolution of immunopeptidomes. *Nat. Biotechnol.* 37, 1283–1286 (2019).

It is available here.