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_...* give the predicted score for the best allele and separately for each allele asked. The score is given as a percentile rank (i.e., the percent of random peptides that would have a score higher than the peptide provided in input among peptides of sizes 12-25 amino acids; best score is about 0, worst score is 100).
- *%Rank_best_perL* is similar to *%Rank_best* 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.
- *Core_best* indicates the best predicted core binding sequence for each peptide towards its best allele.
- *CoreP1_...* give the most likely binding core position for the given peptide towards the allele (this tells the position of the first amino acid from the binding core (which has a size of 9 aa in the predictions), starting at a value of 1 (i.e. if binding core corresponds to the 9 first amino acids from the peptide, this *CoreP1 = 1*)).

Peptides that are too short (less than 12 amino acids), too long (more than 25 amino acids) or that contain non standard amino acids have *NA* 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_best*), 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.