Frequently asked questions for MixMHC2pred

What kind of predictions can I make with MixMHC2pred

MixMHC2pred is a predictor of MHC-II ligands displayed at the cell surface. It combines predictions of affinity to MHC-II molecules together with other features linked to antigen processing and presentation. It can work for any human MHC-II allele (HLA-DR/-DP/-DQ) as well as for many mouse, cattle and chicken alleles.

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

How should I interpret the output of MixMHC2pred

- *Peptide* and *Context* give the sequence of the peptides (respectively context), 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 12-21 amino acids; best score is about 0, worst score is 100).
- *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*)).
- *subSpec_...* tell in which sub-specificity the given peptide is likely bound toward the given allele. The value *1* corresponds to the main sub-specificity (the only one for multiple alleles). But for example for *DRB1*08:01* allele a 2nd sub-specificity exists and is indicated by the value *2*. For alleles accomodating reverse binding, a value of *-1* indicates that the given peptide is bound in the reverse orientation.

Peptides that are too short (less than 12 amino acids), too long (more than 21 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 nbulgin@lcr.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., Machine learning predictions of MHC-II specificities reveal alternative binding mode of class II epitopes. *bioRxiv* (2022) (available here).

and

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