

# MetaMHCIIpan: a consensus approach for pan-specific HLA-DR binding predictions

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## Abstract

**Background:** Binding of antigen peptides to Major Histocompatibility Complex Class II (MHC-II, mainly HLA-DR for human) molecules is a core step in the adaptive immune responses. Accurate identification of MHC-restricted peptides is of great importance for elucidating the underlying mechanism of immune recognition, as well as for developing effective epitope-based vaccines and promising immunotherapies for many severe diseases. Due to extreme polymorphism of MHC-II alleles and the high cost of biochemical experiments, the development of computational methods for accurate prediction of binding peptides of MHC-II molecules, particularly for the ones with few or no experimental data, has become a topic of increasing interest. Recently a few so called pan-specific methods have been developed to meet this need, including our newly proposed method, TEPITOPEpan. The performance of these methods is however not good enough.

**Methods:** MetaMHCIIpan is a consensus method which integrates by AvgTanh the outputs of multiple pan-specific methods for predicting binding peptides. Four state-of-the-art pan-specific predictors and two leading normal allele-specific predictors are involved in this study. After checking the performance of various combinations, an optimal one is selected as the default setting of MetaMHCIIpan.

**Results:** Experimental results over three benchmark datasets showed MetaMHCIIpan with the default predictor combination, which outperformed all individual predictors in prediction accuracy, being statistically significant. MetaMHCIIpan is freely available at <http://www.biokdd.fudan.edu.cn/Service/MetaMHCIIpan>.

**Keywords:** Immunoinformatics, MHC peptide binding prediction, pan-specific

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