# pHLAHub: A Web-Based Consensus Prediction Tool for Peptide-HLA Binding and Epitope Analysis

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Human leukocyte antigen (HLA) differentiates foreign peptides from host peptides and present them to cytotoxic T-cells, playing a vital role in immune defense. Computational prediction of peptide-HLA binding and its resultant epitope can facilitate neoantigen screening for personalized cancer vaccines and immunotherapies. However, overlapping training datasets and difference in model output complicates fair assessment between prediction models. Therefore, strategies to select the best model among the state-of-the-art models remain elusive. In this study, we developed pHLAHub, a freely accessible web-based platform that assembled ten models reported as state-of-the-art models for peptide-HLA binding and epitope prediction. Models include both binding probability and eluted ligand predictors. Users can type in a full protein sequence and specify peptide lengths, which process the sequence into peptide fragments by windows. Prediction results are then tabulated for comparison. In addition, pHLAHub generates a consensus prediction by integrating the results of user-selected models, providing a more generalized insights of the predicted results. The platform also presents a simple visualization tool to highlight the binding region, or possibly the linear epitope, of the input protein that exceeds the user-defined threshold. By allowing users to integrate and assess multiple different models simultaneously, pHLAHub offers a more robust and generalized prediction of the peptide-HLA binding.