T-cell responses are activated by specific peptides, called epitopes, presented on the cell surface by MHC molecules. Binding of peptides to the MHC is the most selective step in T-cell antigen presentation and therefore an essential factor in the selection of potential epitopes. Several in-vitro methods have been developed for the determination of peptide binding to MHC molecules, but these are all costly and time-consuming. In consequence, significant effort has been dedicated to the development of in-silico methods to model this event. Here, we describe two such tools, NetMHCcons and NetMHCIpan, for the prediction of peptide binding to MHC class I and class II molecules, respectively, involved in the activation pathways of CD8+ and CD4+ T cells.