

Abstract

Immunogenic epitopes in a polyepitope construct may induce immunity against multiple antigenic targets only if epitopes are correctly processed and presented. Applications that combine multiple supertypes and integrate variables that measure the quality of polyepitopes can be used to make better polyepitopes yet there are no publicly accessible tools. In this research project, the researcher developed a web-based polyepitope optimization prototype. The prototype runs on 3-tier application architecture: MYSQL was used for the database tier, PHP for the application tier that runs on Apache HTTP server and the presentation layer was implemented on a web browser. The researcher collected epitopes data and information from online databases; the Immune Epitope Database (IEDB), HIV molecular immunological database and National Center for Biotechnology Information (NCBI). The epitopes were analyzed using Microsoft Excel 2003 and uploaded onto a local database. Polyepitopes were generated, optimized and tested on an online web server NetChop 3.1 which was used to validate one of the polyepitope quality measurement variables- proteasome cleavage predictions. The results of data analysis indicate that the immune system recognize epitopes in clusters and the main clusters are 9-mers(9 amino acid long), 15mers, 20mers and 25mers. The polyepitope optimization results indicate that polyepitope optimization algorithms that integrate proteasome cleavage prediction, transporter associated with antigen processing (TAP) binding prediction and Major Histocompatibility Complex (MHC) binding predictions can be used to develop better polyepitopes which can be used to make better vaccines within a shorter time and at a lower cost.

Key words: polyepitope, epitopes, optimization, mer, TAP, proteasome, MHC, prototype.