

CHEP: A computer program to find specific protein motifs implemented for CTL epitopes.

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CHEP is a preliminary version of computer program that is competent of comparing protein sequences through pair wise sequence alignment written in the Visual Basic 6. It detects and predicts presence of specific motifs in a given protein in relative to the reference sequences. This software at present is capable of evaluating protein sequences against approximately 200 CTL epitopes identified so far, in tumor cells. Assessing the performance of the CHEP on a tumor associated protein PRAME indicated that program was capable of identifying and predicting CTL epitopes with significant precision. The result included 18 out of 19 high affinity HLA-*0201 binding-PRAME peptides which had been determined experimentally. In addition to perform a query of proteins, it is possible to explore the content of database comprises of epitope sequences, HLA types and references etc. and is also capable of accepting the new entries. Moreover this program can be easily modified for identification of conserved regions and motifs in the proteins in addition to CTL epitopes. Therefore it can be used in laboratories for customize sequence analysis of proteins for experimental purposes.

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