

ABSTRACT



The present invention relates a method for predicting a protein or polypeptide (B) that interacts with a specific protein or polypeptide (A), wherein the method is characterized by comprising:

1) decomposing the amino acid sequence of protein or polypeptide (A) into a series of oligopeptides having a pre-determined length as sequence information;

2) searching, within a database of protein or polypeptide amino acid sequences, for a protein or polypeptide (C) comprising an amino acid sequence for each member of the series or for a protein or polypeptide (D) comprising an amino acid sequence homologous to an amino acid sequence for each member of the series;

3) carrying out local amino acid sequence alignment between said protein or polypeptide (A) and the detected protein or polypeptide (C) or detected protein or polypeptide (D); and

4) predicting whether the detected protein or polypeptide (C) and/or protein or polypeptide (D) is a protein or polypeptide (B) that interacts with the protein or polypeptide (A) based on the results of the local amino acid sequence alignment and a value calculated from a frequency of amino acids and/or a frequency of said oligopeptides in said amino acid sequence database; and to

a recording medium for carrying out the above method, a device comprising the recording medium, and proteins obtained thereby.