

The MEPS server for identifying protein conformational epitopes

Castrignanò T (1), D'Onorio De Meo P (1), Carrabino D (1), Orsini M (2),
Floris M (2), Tramontano A (3,4)

- (1) CASPUR, Consorzio Interuniversitario per le Applicazioni di Supercalcolo per Università e Ricerca, Roma
(2) Center for Advanced Studies, Research and Development in Sardinia (CRS4), Bioinformatics Unit, PULA (CA)
(3) Department of Biochemical Sciences, University 'La Sapienza', Roma
(4) Istituto Pasteur-Fondazione Cenci Bolognetti, University 'La Sapienza', Roma

Motivation

One of the most interesting problems in molecular immunology is epitope mapping, that is the identification of the regions of interaction between an antigen and an antibody. The solution to this problem, even if approximate, would help in designing experiments to precisely map the residues involved in the interface and could be instrumental both in designing peptides able to mimic the interacting surface of the antigen and in understanding where important regions of an antigen are located in its three-dimensional structure.

Methods

We have developed and implemented a method that, given the structure (or a model of the structure) of an antigen or of a set of antigens identifies all peptide sequences able to mimic the surface of the antigen.

Results

The server can either provide an exhaustive list of all peptides of a given length, or search for possible sequence on the surface of the protein, given the amino acid sequence of a fragment and a maximum number of allowed mismatches. In the first case, sequences corresponding to putatively mimicking peptides are stored, together with information about their location in the protein sequence and structure, as a FASTA formatted file. This allows users to directly search the sequences with the many widely available programs for data base searching. BLAST searches are directly available via the server.

Availability: <http://www.caspur.it/meps>

Contact email: anna.tramontano@uniroma1.it