Immunome Research

Software

EpitopeViewer: a Java application for the visualization and analysis of immune epitopes in the Immune Epitope Database and Analysis Resource (IEDB)

John E Beaver[1], Philip E Bourne[1,2] and Julia V Ponomarenko*[1]

Address: [1]San Diego Supercomputer Center, University of California, San Diego, 9500 Gilman Drive, La Jolla, California 92093, USA and [2]Department of Pharmacology, University of California, San Diego, 9500 Gilman Drive, La Jolla, California 92093, USA

Email: John E Beaver - jbeaver@sdsc.edu; Philip E Bourne - bourne@sdsc.edu; Julia V Ponomarenko* - jpon@sdsc.edu

* Corresponding author

Abstract

Background: Structural information about epitopes, particularly the three-dimensional (3D) structures of antigens in complex with immune receptors, presents a valuable source of data for immunology. This information is available in the Protein Data Bank (PDB) and provided in curated form by the Immune Epitope Database and Analysis Resource (IEDB). With continued growth in these data and the importance in understanding molecular level interactions of immunological interest there is a need for new specialized molecular visualization and analysis tools.

Results: The EpitopeViewer is a platform-independent Java application for the visualization of the three-dimensional structure and sequence of epitopes and analyses of their interactions with antigen-specific receptors of the immune system (antibodies, T cell receptors and MHC molecules). The viewer renders both 3D views and two-dimensional plots of intermolecular interactions between the antigen and receptor(s) by reading curated data from the IEDB and/or calculated on-the-fly from atom coordinates from the PDB. The 3D views and associated interactions can be saved for future use and publication. The EpitopeViewer can be accessed from the IEDB Web site http://www.immuneepitope.org through the quick link 'Browse Records by 3D Structure.'

Conclusion: The EpitopeViewer is designed and been tested for use by immunologists with little or no training in molecular graphics. The EpitopeViewer can be launched from most popular Web browsers without user intervention. A Java Runtime Environment (RJE) 1.4.2 or higher is required.

Background

The Immune Epitope Database and Analysis Resource (IEDB) aims to catalog and provide tools for the analysis of immune epitopes, defined by the IEDB as molecules recognized by immune receptors (antibodies, MHC molecules and T cell receptors) [1,2]. The three-dimensional (3D) structures of epitopes and antigens in complex with immune receptors are important components of the IEDB. The basic information on these molecular structures is available from the Protein Data Bank (PDB) [3].

As of February 2007 the PDB contained more than 700 structures of complexes of immunological interest. These raw data from the PDB are curated to provide epitope entries in the IEDB. Tools are needed to aid immunologists in fully understanding the molecular interactions of interest.

Current molecular visualization tools that enable the user to visualize and render biochemical structures include popular and freely available standalone applications that