CALIFORNIA STATE SCIENCE FAIR
2013 PROJECT SUMMARY

Name(s)

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Project Number

S0506

Project Title

Novel Software Tool for Structural Analysis of MHC Interactions with Immune Epitopes

Abstract

Objectives/Goals

In the perpetual fight against disease, it is vital for immunologists and computational biologists to retrieve and process information quickly and efficiently. While the growing wealth of structural information in the PDB (Protein Data Bank) provides invaluable insights into epitope recognition by MHC proteins(cell membrane proteins exposing pieces of inner cell proteins to immune Tcells), this information can easily appear obscure and overwhelming. My project goal is to bridge the complex world of protein structural data and the sequence data immunologists typically use in their research.

Methods/Materials

I developed algorithms running in the Molsoft ICM environment and web presentations using HTML5 canvas. Biological information from the Pocketome database (processed Protein Data Bank, PDB) in used as input. Java, SQL, BioJava and PDB RESTFUL and NCBI web services were used to study existing protein databases, such as the Immuno Epitope Data Base (IEDB), and protein alignment methods.

Results

A novel software tool for 2D and 3D representation of the 4D molecular interactions observed in MHC-Peptide complexes achieves this goal. (The fourth dimension is the variation of binding peptides). My software tool accepts spatial atom positions and analyzes distances between MHC and peptide residues (amino acids) to generate a 2D bubble chart displaying chemical interactions where the X axis represents the sequence of peptide residues and Y axis represents the sequence of MHC residues; the bubbles at the XY intersections indicate the bond strength (using size and color) and type (using shape). To represent multiple complexes per graph and allow for analysis of binding site variation, I developed an alignment algorithm which finds spatial correlations between residues in different peptides binding to the same MHC. This algorithm generates a 3D view (with correlated residues uniformly colored) and an alignment table.

Conclusions/Discussion

I achieved the project goal and progressed to further develop the tool. Future work includes web publication. This tool will offer an invaluable resource for researchers working on life-saving vaccines, therapeutics and adjuvants, providing insight into MHC-Peptide complexes.

Summary Statement

This project bridges the gap between the complex world of protein structures and sequence-based data immunologists typically use for the design of vaccines through the development of novel software tools.

Help Received

My amazing mentors Dr. Julia Ponomarenko, San Diego SuperComputer Center, and Dr. Irina Kufareva, UCSD Skaggs School of Pharmacy and Pharmaceutical studies, provided an introduction to the field of immune-informatics and guidance.