Example of report on immunology

Education

Epitopes constitute parts of antigens which bind themselves specifically on lymphocytes and receptors. As a result, they induce either antibody or cell mediated immunity. Basically, there are continuous and discontinuous epitopes (Yang & Yu, 2009, p. 77). The later are characterized by linear peptide fragments, usually of 19-12 mers. Usually, these are recognized by the distinctive T cells after they have been processed and presented on to MHC molecules. The later on the other hand comprise of 15-22 structurally complicated mers. They are characterized by a distinctive folding protein. This can be recognized by both the T and b helper cells while it is in its primary innate structure. According to Yang and Yu (2009, p. 77-96), discontinuous epitodes cannot be predicted easily because of their complexity.

Just like in other fields of study, knowledge of important epitopes identities is vital in the field of Immunology and Medicine in general. This can be employed for designing vaccines, preventing diseases, diagnosing and treating diseases amongst other uses. Currently, yang and Yu (2009, p. 79) cite that a host of available databases and software can easily be used to predict epitopes quickly and cheaply. These have been developed over time in a bid to enhance effective functioning. Certainly, relative outcomes play an important role of enhancing timely implementation of important decisions in the field of immunology. To a great extent, it empowers the medics, thus enabling them to provide quality service to their clientele. In the long run, this knowledge improves performance and enhances the quality of life of the entre populace.

With respect to the prediction of T cell epitopes, this is made possible

through the initial prediction of vital MHC binding sites. Nonetheless, it is worth appreciating that there are considerable differences between the means employed for predicting MHC class 1 binding sites and MHC class II binding sites. In this respect, the groove in MHC 1 binding tends to be closed as opposed to its counterpart's MHC II, that is usually open ended, making it difficult for it to accommodate the peptides that vary in length. Thus compared to the prediction of MHC II bidning sites, prediction of MHC I's binding sites tends to be more accurate. Classic examples of common software employed in predicting MHC I's T cell include SYFPEITHI and BIMAS (Goldsby, Kindt, Osborne & Kuby (2007, p. 61).

With regard to the prediction of B cell epitodes, idyllic tools such as Tongaonkar, Kolaskar, Woods and Hopp are readily available. These have been tested and proven to be effective over time. Specifically, they are used for predicting B cell epitodes that are seemingly continuous. Notably, there are distinct similarities between the B cell prediction and the T cell prediction of cell epitopes. The prediction of T cell epitopes depends greatly on important amino acid properties. Relative properties include the characteristic hydrophilic regions as well as their relative surface exposure. The discontinuous epitopes belonging to the B cells, on the other hand, require the fundamental 3D structure that also characterizes the antibody-antigen complex. In their review, Yang and Yu (2009, p. 81) cite that the respective epitopes can effectively be predicted by certain tools including Urmila Kulkami, Disctope and Kolaskar.

Questions

Is the same peptide dominant? Is it predicted that HLA-B*08 can present this peptide?

Seemingly, CD8 epitope that is found in the ovalbumin is the most dominant in mice. This was derived from the SYFPEITHI database. Results were gotten by using H2-kb to search. In this, SIINFEKL that had a score of 25 was obtained. In humans' HLA-B*08, a different epitope ERKIKUYL that had 32 as the highest score was predicted. Nonetheless, it is worth noting that HLA-B*08 is representative of SIINFEKL peptide. However, it is not dominant because its score is an insignificant 16.

Does BIMAS http://www-bimas. cit. nih. gov/molbio/hla_bind/ also predict this as the dominant peptide?

Yes, relative prediction results indicate that SIINFEKL peptide is dominant.

Use the Hopp-Woods tool at http://www. vivo. colostate. edu/molkit/hydropathy/index. html and find out the most hydrophilic region of the protein. Why might it be important to know this?

Seemingly, the most hydrophilic regions include amino acids number 290 and 190. Relative determination of these regions has two main implications. First, it enables knowledge of the protein's regions that are exposed externally for recognition by vital immune system cells.

Secondly, Smooker (2011, p. 71) posits that such determination allows for effective designing of vaccines. In this regard, the vaccines that would be developed based on this knowledge would yield more effective results.

If you were going to design a peptide vaccine to (A) induce CTL’s, or (B) induce antibodies from the following sequence, which regions would you choose? Assume you will test in H2-Db mice.

For reasons of inducing CTL’s, one can use the LSAENLVSC dominant peptide in designing an ideal vaccine. However, amino acid 47, which is also the most hydrophilic part, can be employed for designing a vaccine that induces antibodies.

Using PAProc, http://www. paproc. de/ predict the proteolytic products from ovalbumin after processing by the human wild-type 1 proteosome.

Is the dominant H2-kb epitope in mice available for loading onto human MHC?
Notably, it is impossible to load the dominant epitope onto human MHC. This is attributable to the recognition that the relative epitope is cleaved into three distinct sequences through the human wild-type 1 proteosome.

Around what proportion of the protein would be available for presentation?

Fundamentally, the division of the amino acids entire number of cleaved sequences having 8 amino acids and more by the number of the entire amino acids found on the respective protein. Thus, the proportion is represented by

Go to http://tools. immuneepitope. org/tools/bcell/iedb_input Input the ovalbumin sequence. Use each of the algorithms to see the output. What does each predict for the ovalbumin sequence, and why is this important?

Are any of the peptides predicted by more than one method?

For predicting Beta-Turn of the protein's secondary structure, the Chou and Fasman method is employed.

For predicting the accessibility to important epitopes, emini is used

For predicting relative flexibility of epitopes under review, Karplus and Schulz are used.

For predicting inherent antiigenicity of the respective epitopes, Kolaskar and Tongaonkar tools are used

For important hydrophilicity prediction, parker is used

Lastly, for predicting the linear epitopes, bepipred is used.

Nonetheless, in instances where there is commonality between multiple methods, this enhances the reliability of the respective sequence. As a result, it becomes more reliable to design an effective vaccine against. However, it is worth noting at this point in time is the recognition that peptides like KDSTRTQ and SSVDSQ can reportedly be effectively predicted using multiple methods.

Reference List

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