**Title:** Prediction of Epitopes of Bacillus cereus Hemolysin  
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**Abstract:**  
**Introduction:** Bacillus cereus, which is best known as the cause of two distinct food poisoning syndromes, has also been implicated in a wide variety of illnesses. The virulence factor of this bacterium remain ill defined partly because a large number of proteins, like hemolysin. Hemolysins are exotoxins produced by bacteria that cause lysis of red blood cell by damaging their cell membrane. In this study, we try to design new vaccine against Bacillus cereus hemolysin enzyme for diarrhea therapeutic procedures.

**Method:** The identification and characterization of B-cell epitopes play an important role in vaccine design, immunodiagnostic test, and antibody production. Therefore, computational tools for reliably predicting linear B-cell epitopes in proteins are highly desirable. Here we use ElliPro server is a web based tool that aims to predict immunogenic regions in either a protein three-dimensional structure or a linear sequence. The ElliPro output consist of the immunogenicity and corresponding probability scores are computed by ElliPro for each surface residue.

**Results:** As it is shown in the result, the first peptide with highest score is the best option for epitope prediction and we can use this peptide for vaccine design against Bacillus cereus hemolysin enzyme.

**Conclusion:** to reduce bacterial drug resistance and faster effect of vaccine in comparison to oral drug vaccine design against this bacterium is recommended.

**Hemolysin, Bacillus cereus, ElliPro server, Epitope prediction**

**Presentation:** Poster