

عنوان مقاله:

Identification of functionally and structurally important residues of Outer Membrane Protein P1 in Haemophilus influenzae

محل انتشار:

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خلاصه مقاله:

Haemophilus influenzae (formerly called Pfeiffer's bacillus or Bacillus influenzae) is a Gram-negative, coccobacillary, facultatively anaerobic pathogenic bacterium belonging to the Pasteurellaceae family. The presence of the capsule in encapsulated type b (Hib), a serotype causing conditions such as epiglottitis, is known to be a major factor in virulence. Their capsule allows them to resist phagocytosis and complement-mediated lysis in the non-immune host. The unencapsulated strains are almost always less invasive. Haemophilus influenzae infections cause some severe and fatal, especially in children such as meningitis and epiglottitis. The property of an antigen to bind specifically complementary antibodies is known as the antigen's antigenicity; likewise, the ability of an antigen to induce an immune response is called its immunogenicity. Attempts should be made to discover peptides that could mimic protein epitopes and possess the same immunogenicity as the whole protein. Subsequently, theoretical methods for epitope prediction have been developed leading to synthesis of such peptides that are important for development of immunodiagnostic tests and vaccines. The present study was designed to in silico resolving the major obstacles in the control or in prevention of the diseases caused by Haemophilus influenzae. We exploited bioinformatic tools to better understanding and characterizing the Outer Membrane Protein P1 structure in Haemophilus influenzae and select appropriate regions as effective B cell epitops.

کلمات کلیدی:

Haemophilus influenza, Outer Membrane Protein P1, bioinformatics

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