

عنوان مقاله:

Homology modeling and topology prediction of Tbp1 in Neisseriameningitidis

محل انتشار:

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نویسندگان:

Marjan Babadi Akashe - *Departeman of biology, Science and Art University, Yazd, Iran*

Fateme Sefid - *Department of Biology, shahed University ,Tehran-Qom Express Way*

Elham Khosravi - *Departeman of biology, Science and Art University, Yazd, Iran*

Rana Sabzi - *Departeman of biology, Science and Art University, Yazd, Iran*

خلاصه مقاله:

Neisseria meningitidis, an obligate human pathogen, is the most common cause of pyogenic meningitis worldwide, and is the only bacterium capable of generating outbreaks of bacterial meningitis. It also causes overwhelming meningococcal septicaemia that can kill within hours of the appearance of the first symptoms. Production of a cross-protective vaccine capable of generating long-lasting immunity against the disease among infants and older age groups is still a high priority worldwide. An ideal meningococcal vaccine should be safe; offer long-lasting immunity to all age groups; cross-protect against all meningo- coccal serogroups, serotypes and serosubtypes; be given orally or nasally; and be easily incorporated into the WHO Expanded Program on Immunisation. These include constitutively expressed and environmentally regulated OMPs. Most investigations on bacterial pathogens, including *N. meningitidis*, are with organisms grown in vitro under conditions that do not necessarily reflect those in vivo. This is likely to give, at best, only a partial picture of bacterial characteristics associated with virulence and with immune responses important for protection. . Here we describe the topology and 3D structure of a novel antigen which was discovered by mining the bacterial genome and that is very effective in inducing bactericidal antibodies. This antigen .is a very good candidate for inclusion in universal vaccines against *N.meningitidis*

کلمات کلیدی:

N.meningitidis, iron, Topology and 3D structure, TBP

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