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## Bacterial vaccine development and virulence factor prediction using reverse vaccinology program Vaxign

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A s an emerging and revolutionary vaccine development approach, reverse vaccinology starts with the prediction of vaccine candidate proteins by informatics analysis of genome sequences. Reverse vaccinology has been widely used in development of vaccines for many different bacterial pathogens, including serogroup B *Neisseria meningitidis* (MenB), *Bacillus anthracis, Brucella spp., Mycobacterium tuberculosis, Streptococcus pneumoniae, uropathogenic E. coli*, etc. In reverse vaccinology, predicted proteins are selected based on defined desirable attributes. Vaxign, a component program of the comprehensive VIOLIN vaccine database and analysis system, is the first web-based vaccine design program based on reverse vaccinology. The Vaxign pipeline predicts a list of attributes associated with vaccine design, including protein subcellular location, transmembrane helices, adhesin probability, conservation among pathogenic strains, sequence exclusion from genomes of nonpathogenic strains, sequence similarity to host proteins, and epitope binding to MHC class I and class II alleles. Over 150 genomes for over 15 bacterial pathogens have been used for generating pre-computed results using the Vaxign algorithm. All pre-computed results are available for query with user-friendly Vaxign web interface. In addition, Vaxign allows for dynamic vaccine candidate prediction based on users' input sequences (up to 500 sequences at a time). The Vaxign pipeline can also be used to predict virulence factors and support genome annotations. In this presentation, we will demonstrate how Vaxign can be used to predict vaccine candidates and virulence factors for *Staphylococcus aureus*. New features, e.g., result ranking and ontology-based literature mining, are being developed and incorporated into the Vaxign program.

## Biography

Yongqun "Oliver" He is an associate Professor in the University of Michigan Medical School. He is experienced in both vaccinology and computer sciences. His primary interests are host-vaccine interaction mechanism analysis, vaccine development, computational vaccinology, and bioinformatics. His group has developed many vaccine informatics programs including the VIOLIN vaccine database and analysis system and Vaxign vaccine design program. He initiated and leads the development of the community-based vaccine ontology (VO). He has published over 50 peer-reviewed papers and is an editorial board member of several journals.

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