

## Guest Editorial

### Immunoinformatics: An approach for the development of vaccine Candidate

Computational immunology is a field of science that encompasses high-throughput genomic and bioinformatics approaches to immunology. The main aim of this field is to solve the immunological problems by computational approaches and then convert these results into immunologically meaningful interpretations. The accelerating use of bioinformatics tools and techniques along with the significant amount of experimental data has made a significant impact on the immunology research. This has led to a rapid growth in the field of computation immunology, and a number of immunology-focused resources and software, which help in understanding the properties of the whole immune system, have become available.

For effective vaccine development, antigen discovery and validation is a prerequisite. The compilation of information concerning pathogens, virulence factors and antigenic epitopes has resulted in many useful databases. However, most such immunological databases focus almost exclusively on antigens where epitopes are known. The data are so diverse that they can be categorized in different databases according to their use in the research. Until now there are total 31 different immunological databases noted in the Nucleic Acids Research (NAR) Database Collection ([http://www.oxfordjournals.org/our\\_journals/nar/database/cat/14](http://www.oxfordjournals.org/our_journals/nar/database/cat/14)). These online resources have made a significant impact on the immunology research. After the recent advances in sequencing and proteomics technology, there have been many fold increase in generation of molecular and immunological data.

Immunoinformatics research stresses mostly on the design and study of algorithms for mapping potential B- and T-cell epitopes, which speeds up the time and lowers the cost needed for laboratory analysis of pathogen gene products. Computational strategies are far faster than experimental approaches for identification of MHC-binding peptides.

To speed up the mapping process, immunoinformatic tools are now in access. Although, in silico tools (SYFPEITHI and BIMAS, Rankpep, IEDB and Propred1 etc. ) have been used in the past to predict specific epitope, but there is no consensus on the most of the algorithms. Controversy has centered around whether immunoinformatics can identify all of the epitopes responsible for protective immunity. Previous studies demonstrated that a consensus epitopes (predicted by different software) can elicit the desired immune response. Epitope-mapping algorithms, of which several are available, are relevant not only to vaccine design but also for characterizing and modifying immune responses in the context of autoimmunity, endocrinology, allergy, transplantation diagnostics and the engineering of therapeutic proteins.

Immunoinformatics is mainly beneficial because conventional methods need to dedicate time to pathogen cultivation and subsequent protein extraction. Although pathogens grow quickly, extraction of their proteins and then testing of those proteins on a large scale is expensive and time-consuming. Application of Immunoinformatics will be helpful for reducing time and saving resources for the development of relevant vaccines candidate.



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