

## Development of Vaccine against Immunogenic Epitopes from a Viral Genome Using the Bioinformatics Approach

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### ABSTRACT

In the field of medical biology, viral infection has always been a major global concern. The emergence of new virus variants due to the high mutability rate has exacerbated the situation in combating viral infection, as evidenced by the recent case of SARS COVID 19. Development of a new drug or vaccine to combat the viral infection is a tedious and time taking task. Bioinformatics tools can help in reducing the time and cost required for the development of novel drugs or vaccines. This workshop will demonstrate the use of bioinformatics tools to identify immunogenic epitopes from the viral genome that will be further considered for development of vaccines. The first step towards development of vaccines includes identification of immunogenic epitopes against specific human leukocyte antigen (HLAs). As the cytotoxic T lymphocytes (CTL) with the aid of T cell receptor (TCR) identifies the antigenic peptide. For this workshop the immunogenic epitopes specific to CTL will be identified from SARS-Cov2 viral genome. The first step involves downloading the complete genome and the coding sequences of the studied virus. The next step involves identification of CTL epitopes, for this an online tool NetCTLpan will be used. In the next step the above predicted epitopes will be checked for their immunogenicity against human major histocompatibility complex 1(MHC1) (Antigen presenting cell). An online tool called Immune Epitope Database (IEDB) immunogenicity tool will be used to predict the immunogenic scores. The conserved nature of the epitopes among other variants of SARS-Cov2, the proteome sequences from different variants were subjected to multiple sequence alignment using the MAFFT online server. Later the MEGA software will be used to check if the epitope motifs are conserved. Further the identified conserved immunogenic epitopes will be screened against HLAs, to predict the binding stability with HLAs. Docking studies can be complemented with simulation analysis as well.

**Keywords:** CTL, Epitopes, HLAs, TCR, MHC1, Vaccine

**Abbreviations:** HLAs: Human Leukocyte Antigen; CTL: Cytotoxic T Lymphocytes; TCR; T Cell Receptor; MHC: Major Histocompatibility Complex 1

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