

**Invitation to M.Tech. Thesis Defense of Sadhana Tripathyl: May 30, 2022 (Monday): 11:45 AM-12.30 PM IST**

In Partial Fulfilment of the Requirements for the Degree of

**M.Tech. CB**

**Sadhana Tripathy (MT20214)**

Will defend her thesis

**Title: “Manual Curation of Virus Based Vaccines and Prediction of B-Cell Epitopes using Machine Learning Techniques”**

IIIT-D Faculty and Students are invited

**Date: May 30, 2022 (Monday)  
Time:** **11.45 AM-12.30 PM IST**

**Venue: Room No: A-320 (Meeting Room), R & D Building**

**Examiner: Internal:   Jaspreet Kaur Dhanjal**

**External/~~Internal~~: Manish Kumar (University of Delhi)**

**Advisor: G P S Raghava**

**Co-Advisor NA**

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**Abstract**

Unprecedented rise of newly emerging and re-emerging cases of infectious viral diseases have threatened humanity throughout. Vaccines stand as the safest and most effective way to manage scale and spread of infectious diseases. First viral vaccine was developed in 1796 against smallpox, which successfully eradicated this deadly virus from the planet. Over the years, numerous vaccines have been developed against viral infections, which save millions of premature deaths every year. In this study, we have made an attempt to integrate the resources associated with viral vaccines which are scattered across literature and websites. The manually curated repository of viral vaccines, ViralVacDB is a web-based platform that provides coverage to different viral diseases and vaccines associated information. This repository provides information about 421 vaccines:139 approved vaccines and 282 vaccines under development. Various web-based interfaces have been configured in ViralVacDB to facilitate the scientific community to retrieve information in a user-friendly manner. The database is available at https://webs.iiitd.edu.in/raghava/viralvacdb/. B-cell is responsible for eliciting adaptive immunity responses. Recognition of B-cell epitopes plays a crucial role in designing and development of synthetic vaccines. In past, various computational methods have been developed to predict either linear or conformational B-cell epitopes. In this study, we have tried to classify linear and conformational B-cell epitopes and non-epitopes using different machine learning models based on various sets of features.