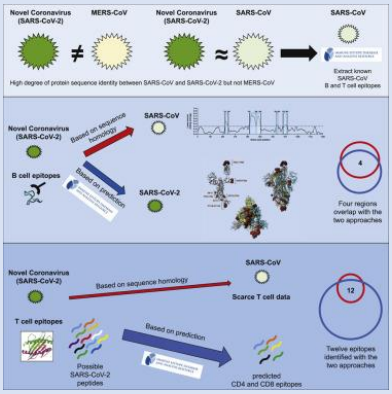
A SEQUENCE HOMOLOGY AND BIOINFORMATIC APPROACH CAN PREDICT CANDIDATE TARGETS FOR IMMUNE RESPONSES TO SARS-COV-2

Abstract:

The Immune Epitope Database and Analysis Resource (IEDB) is used to catalog available data related to other coronaviruses- SARS-CoV-, as there is limited information about (SARS-CoV-2) and the high sequence similarity between them

by identification of specific regions will facilitate effective vaccine design against this virus of high priority.



Keywords:

SARS-CoV; COVID-19; SARS-CoV-2, coronavirus; T cell epitope; B cell epitope; infectious disease; sequence conservation.

Introduction:

we used the IEDB and ViPR resources to compile known epitope sites from other coronaviruses, map corresponding regions in the SARS-CoV-2 sequences, and predict likely epitopes. We also used validated bioinformatic tools to predict B and T cell epitopes that are likely to be recognized in humans and to assess the conservation of these epitopes across different coronavirus species.

Limited information is currently available on which parts of the SARS-CoV-2 sequence are recognized by human immune responses but there is a significant body of information about epitopes for coronaviruses in general, and in particular for BETACORONAVIRUSES like SARS-CoV and MERS-CoV, which cause respiratory disease in humans.

1- Ten experimentally defined regions within SARS-CoV have high homology with SARS-CoV-2.

2-Parallel bioinformatics predicted potential B and T cell epitopes for SARS-CoV-2.

3-Independent approaches identified the same immunodominant regions.

4-The conserved immune regions have implications for vaccine design against multiple CoVs.