

## Conservation of *in-silico* Predicted Epitopes of SARS-CoV-2 and Other Native Corona Viruses from Different Geographic Regions

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The conservation between antigenic epitopes derived from homologous regions of SARS-CoV-2 proteome and other endemic CoVs could create cross reactive immunity in the endemic regions. Here we explore the immunogenicity of the SARS-CoV-2 viral proteome through *in silico* epitope prediction and analyse the cross reactivity of predicted epitopes of SARS-CoV-2 with SARS, MERS, other HCoVs, and different zoonotic CoVs found in Bats, Pangolins, Palm Civets and Minks. The epitope prediction tools available in IEDB; BepiPred 2.0, DiscoTope 2.0, NetMHCpan 4.0, and 2.22 algorithm were used to predict B cell linear, B cell discontinuous, MHC-I T cell, and MHC- II T cell epitopes respectively. To evaluate the potential for cross-reactivity, the protein sequence homology was compared between the SARS-CoV-2 and the other CoVs using 'Epitope Conservancy Analysis' module in IEDB. A total of 21, 76, 333 and 131 linear-B cell, discontinuous-B cell, MHC-I T cell, and MHC-II T cell epitopes were predicted. The conservation level of both B cell and T cell epitopes from SARS-CoV-2 was high (~75% and 90% respectively) with the majority of SARS-CoV isolates, while it was moderate to low (30%-50%) with endemic HCoVs. However, the level of epitope conservation of SARS-CoV-2 was high with CoVs of *Rhinolophus* bats (Average >90%) and Malayan pangolin (*Manis javanica*) (Average >85%). These results suggest a possibility of existing remnant immunity in individuals residing in the areas where *Rhinolophus* bats and pangolins reside due to exposure to the zoonotic CoVs in them. This is postulated based on the very high level of epitope conservation between SARS-CoV-2 and these zoonotic CoVs.

**Keywords:** *in-silico* epitope prediction, SARS-CoV-2, zoonotic CoVs, antigenicity, epitope conservation, cross-reactivity