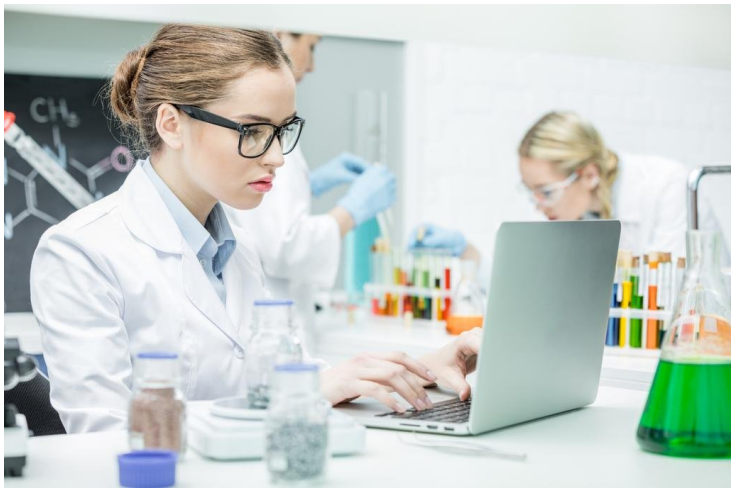
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IIT-M develops database on coronavirus antibodies

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â??Ab-CoVâ?? can be a vital resource for researchers to develop therapeutic strategies against new variants of coronaviruses



A team of researchers at the Indian Institute of Technology Madras (IIT-M) has developed an online open-source database of coronaviruses' neutralising antibodies encompassing crucial features such as binding affinity and neutralisation profiles (IC_{50} and EC_{50}) of antibodies.

The database called 'Ab-CoV' contains detailed information about all COVID-related antibodies identified so far, including the source of each antibody, and the viral protein(s) and virus strains they recognise. 'Ab-CoV' can also aid in the development of drugs against new variants of SARS-CoV-2.

Ab-CoV database includes 1,780 coronavirus-related antibodies including 211 nanobodies and contains more than 3,200 data points on half maximal inhibitory concentration (IC_{50}), half maximal effective concentration (EC_{50}) & binding affinity (K_D).

Stressing the uniqueness of Ab-CoV, Prof. M. Michael Gromiha, Faculty, Department of Biotechnology, IIT Madras, said, "Some of the data in the Ab-CoV database has already been used to understand the relationship between structural features and binding affinities of spike protein-antibody complexes as well as antibody repurposing."

Further, Prof. M. Michael Gromiha said, "Ab-CoV also has a wide range of search and display options through which users can directly search and download the processed data, based on the antibody's name, viral protein epitope, neutralised viral strain, antibody, and nanobody. It also has the option to view structures of antibodies or viral proteins in a 3D model."