

# COVIDep: a web-based platform for real-time reporting of vaccine target recommendations for SARS-CoV-2

**To the Editor** — The COVID-19 pandemic, caused by the novel coronavirus SARS-CoV-2, has brought much of the world to a virtual lockdown. As the virus continues to spread rapidly and the pandemic intensifies, the need for an effective vaccine is becoming increasingly apparent. A critical part of vaccine design is to identify targets, or epitopes, that can induce an effective immune response against SARS-CoV-2. This process is challenged by our limited understanding of this novel coronavirus and of its interplay with the human immune system.

In response to this challenge, we have developed COVIDep ([COVIDep.ust.hk](https://www.covidep.hk)), a first-of-its-kind web-based platform that pools genetic data for SARS-CoV-2 and immunological data for the 2003 SARS virus, SARS-CoV, to identify B-cell and T-cell epitopes to serve as vaccine target recommendations for SARS-CoV-2 (Fig. 1a). For T-cell epitopes, it provides estimates of population coverage, globally and for specific regions. COVIDep is flexible and user-friendly, comprising an intuitive graphical interface and interactive visualizations. In addition to producing formatted, exportable lists of the identified B-cell and T-cell epitopes and their basic characteristics, COVIDep includes displays for each of the SARS-CoV-2 proteins, showing the locations of the identified epitopes on the primary structure. Further graphical displays are provided to aid interpretation of the data, including a temporal and geographical breakdown of the analyzed sequences, and a display of the observed genetic variation (amino acid mutation frequencies) for each SARS-CoV-2 protein. The platform is updated daily, based on the latest SARS-CoV-2 sequence data in the GISAID database

([www.gisaid.org](https://www.gisaid.org)). Periodic updates are important because SARS-CoV-2 sequences are being made available at an increasing rate through international data-sharing efforts, and the identification of vaccine targets is influenced by newly observed genetic variation.

The vaccine targets recommended by COVIDep exploit the genetic similarities between SARS-CoV-2 and SARS-CoV, along with known immune targets for SARS-CoV that have been determined experimentally (available in the ViPR database; [www.viprbrc.org](https://www.viprbrc.org)). The system implements a protocol that identifies, from among the SARS epitopes that can induce a human immune response, those that are genetically similar in SARS-CoV-2. This approach, proposed and tested in our preliminary study<sup>1</sup> based on limited early data, identified known SARS-CoV epitopes that had an identical genetic match in SARS-CoV-2. These epitopes presented initial vaccine target recommendations for potentially eliciting a protective, cross-reactive immune response against SARS-CoV-2. Similar results were reported in a subsequent independent study<sup>2</sup>, in which a related approach exploiting genetic similarity between SARS-CoV and SARS-CoV-2 was used to identify potential SARS-CoV-2 vaccine targets.

The use of SARS-CoV immunological data to inform vaccine targets for SARS-CoV-2 is being supported by experimental results. There is evidence of cross-neutralization by SARS-CoV-derived antibodies binding to genetically similar regions of SARS-CoV-2's spike protein<sup>3–5</sup>. Conversely, studies have demonstrated that specific SARS-CoV-derived antibodies that bind to the spike's receptor-binding domain, which has significant genetic differences in SARS-CoV-2, have limited cross-reactivity<sup>6</sup>. T cell responses against

spike protein epitopes that are genetically similar in SARS-CoV and SARS-CoV-2 have also been reported in COVID-19-infected patients<sup>7,8</sup> and in a preclinical vaccine trial<sup>9</sup> (Fig. 1b). Epitopes recommended by COVIDep have notable overlap with the findings in these and other<sup>10,11</sup> experimental studies (see Figs. 2 and 3 in ref. <sup>12</sup>). The recommendations provided by COVIDep may be used to broadly guide vaccine designs and associated experimental studies, and may help to expedite the discovery of an effective vaccine for COVID-19. □

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Syed Faraz Ahmed <sup>1</sup>,  
Ahmed A. Quadeer <sup>1</sup>✉ and  
Matthew R. McKay <sup>1,2</sup>✉

<sup>1</sup>Department of Electronic and Computer Engineering, The Hong Kong University of Science and Technology, Hong Kong, China.

<sup>2</sup>Department of Chemical and Biological Engineering, The Hong Kong University of Science and Technology, Hong Kong, China.

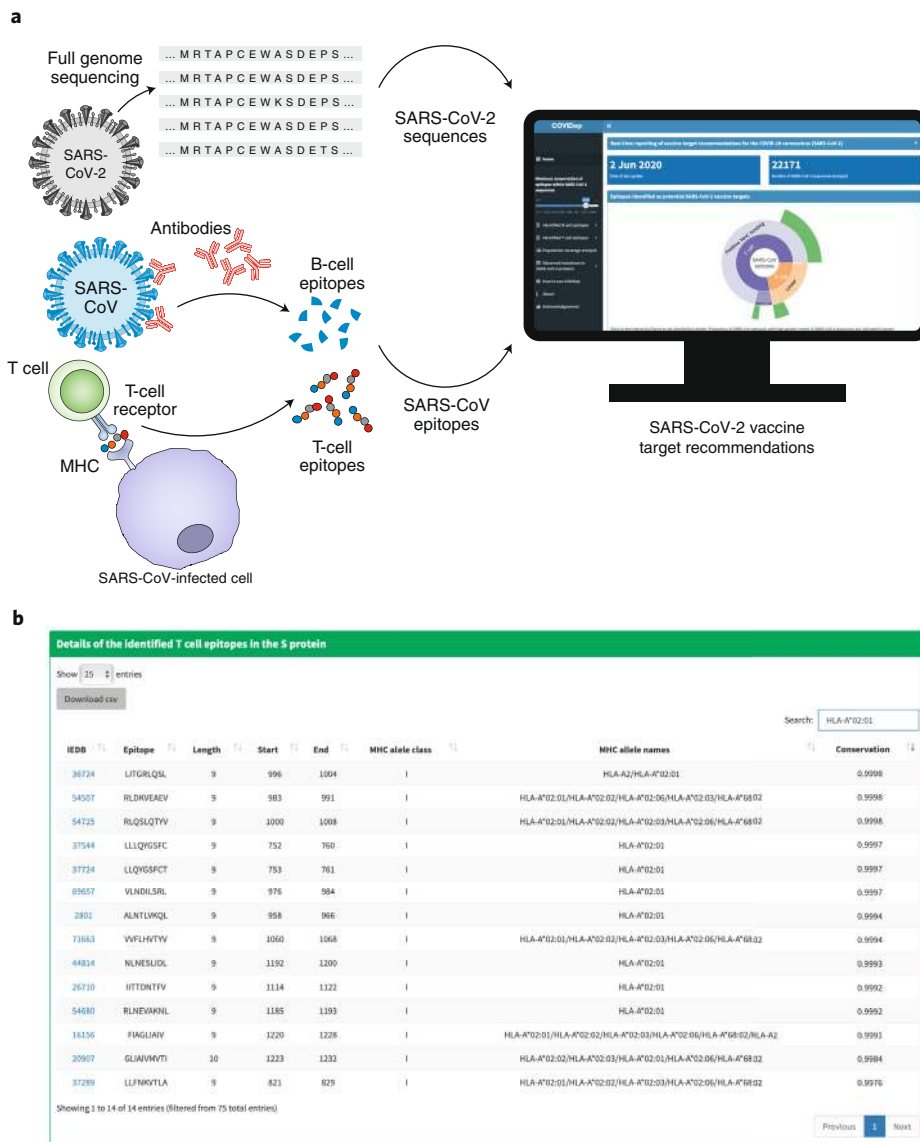
✉ e-mail: [ceaaquadeer@ust.hk](mailto:ceaaquadeer@ust.hk); [m.mckay@ust.hk](mailto:m.mckay@ust.hk)

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**Fig. 1 | COVIDep provides an up-to-date set of B-cell and T-cell epitopes that can serve as potential vaccine targets for SARS-CoV-2.** a, The identified epitopes are experimentally derived from SARS-CoV and have a close genetic match with the available SARS-CoV-2 sequences (see Supplementary Figure 1 for a detailed protocol description). b, An example of the T-cell epitopes reported by COVIDep (as of 20 May 2020) for the spike protein of SARS-CoV-2. Here, the Search box (in the top right) was used to select only the HLA-A\*02:01-restricted epitopes. (An explanation of all interactive COVIDep visualizations is incorporated in the 'How to use COVIDep' page of the platform.) Of the 14 epitopes listed in the display, 9 (IEDB IDs 36724, 54507, 54725, 69657, 71663, 2801, 54680, 16156 and 37289) overlap with epitopes against which cytotoxic CD8<sup>+</sup> T-cell responses have been observed in peripheral blood mononuclear cells isolated from COVID-19 patients<sup>7,8</sup>. T-cell responses were also recorded against protein regions overlapping with the epitope with IEDB ID 71663 in a preclinical trial of a DNA vaccine candidate<sup>9</sup>.

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### Data availability

The SARS-CoV-2 full genome sequence data used in COVIDep is periodically downloaded from the Global Initiative on Sharing Avian Influenza Database (GISAID; [www.gisaid.org](http://www.gisaid.org)). The SARS-CoV epitope

sequence data was downloaded from the Virus Pathogen Database and Analysis Resource (ViPR; [www.viprbrc.org](http://www.viprbrc.org)). The population coverage statistics of HLA alleles were obtained from the Immune Epitope Database and Analysis Resource (IEDB; [www.iedb.org](http://www.iedb.org)).

### Code availability

The source code for the developed platform is available at the COVIDep GitHub repository ([github.com/COVIDep](https://github.com/COVIDep)).

### Competing interests

The authors declare no competing interests.