




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

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Supplementary Information

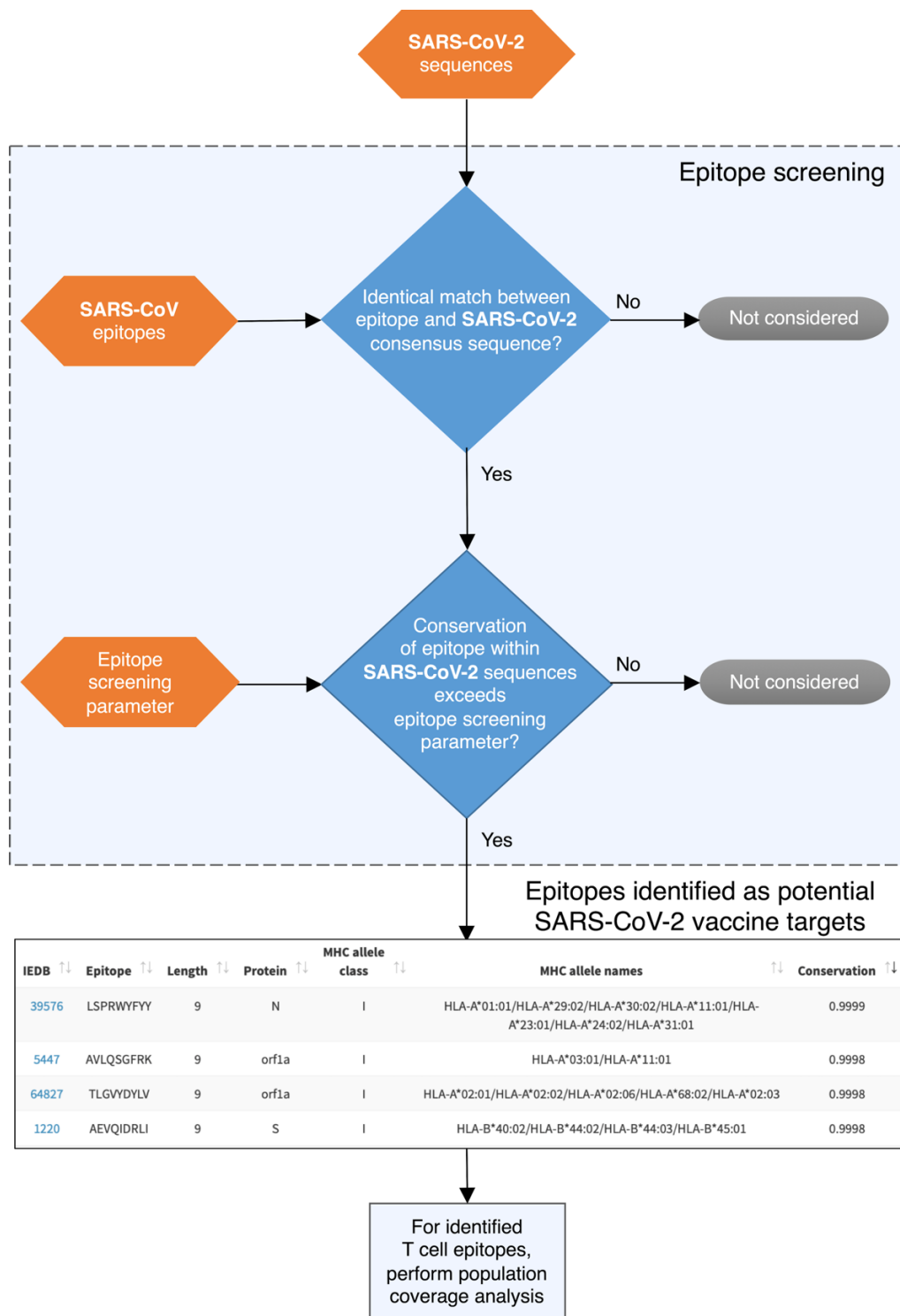
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Supplementary Figure 1. Epitope screening protocol used by COVIDep for providing vaccine target recommendations for SARS-CoV-2. COVIDep periodically pools SARS-CoV-2 sequence data from the GISAID database (gisaid.org) and compares with experimentally-determined T cell and B cell epitopes of SARS-CoV, obtained from the ViPR database (viprbrc.org). The T cell epitopes were determined based on either positive T cell assays or positive MHC binding assays for SARS-CoV. For the B cell epitopes, both linear and discontinuous epitopes were considered. The system outputs those epitopes that are genetically similar in SARS-CoV-2, based on an epitope screening parameter. This user-defined parameter allows the user to select epitopes based on their conservation in the SARS-CoV-2 sequence data, where conservation is defined as the fraction of SARS-CoV-2 sequences with the exact epitope sequence. The value of this parameter is set to 0.95 as default; however, the user may change this value to adjust the stringency of the screening criterion. For example, reducing the value of the parameter will allow for the consideration of epitopes with greater genetic variation, potentially increasing the set of recommended SARS-CoV-2 vaccine targets. For the identified T cell epitopes, the population coverage analysis tool available at IEDB (iedb.org) is used to estimate the percentage of a specified population that can elicit a response against them.