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## Using AlphaFold to understand multi-domain proteins from SARS-CoV-2

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Here, we demonstrate the use of AlphaFold on proteins from SARS-CoV-2. While the solved structures only cover a part of the viral genome we have plenty of annotated protein-coding genes, which structures can now be predicted computationally. We discuss both the benefits as well as the potential shortcomings of these predictions and show how they can be combined with information from other tools and experimentally determined structures to get new insights into the structural biology of the virus.

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