

# High Yield Method to Scale and Purify Full Length SARS-CoV-2 Membrane (M) Protein

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## BACKGROUND

The SARS-CoV-2 Membrane (M) protein is the most abundant structural protein of the SARS-CoV-2 virus. However, large scale production and purification of this protein has proven extremely challenging, due to toxic effects of protein expression on most standard expression systems (e.g., E. coli). Consequently, all currently available sources of SARS-CoV-2 protein consist of only smaller fragments of the protein that range in in size from 182 to 216 amino acids in length. Such shorter smaller protein fragments are easier to produce and purify.

## BRIEF DESCRIPTION

Prof. Thomas Kuhlman at the University of California, Riverside has developed a high yield method to scale and purify native, full-length SARS-CoV-2 Membrane (M) protein. This method may be utilized to scale the production and purification of M protein for research purposes.

## APPLICATION

- High yield method to produce full-length SARS-CoV-2 M protein for research use.

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## OTHER INFORMATION

### KEYWORDS

SARS-CoV-2, M protein, membrane protein, purification, scale-up, COVID-19

### CATEGORIZED AS

- [Research Tools](#)
- [Protein Synthesis](#)

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