Structural model of the SARS coronavirus E channel in LMPG micelles

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ABSTRACT

Coronaviruses (CoV) cause common colds in humans, but are also responsible for the recent Severe Acute, and Middle East, respiratory syndromes (SARS and MERS, respectively). A promising approach for prevention are live attenuated vaccines (LAVs), some of which target the envelope (E) protein, which is a small membrane protein that forms ion channels. Unfortunately, detailed structural information is still limited for SARS-CoV E, and non-existent for other CoV E proteins. Herein, we report a structural model of a SARS-CoV E construct in LMPG micelles with, for the first time, unequivocal intermolecular NOEs. The model corresponding to the detergent-embedded region is consistent with previously obtained orientational restraints obtained in lipid bilayers and *in vivo* escape mutants. The C-terminal domain is mostly α-helical, and extramembrane intermolecular NOEs suggest interactions that may affect the TM channel conformation.