

The Envelope protein (E protein) of SARS-CoV-2 forms a pentameric viroporin and is found in high copy number in the host cell's Endoplasmic Reticulum Golgi Intermediate Compartment (ERGIC) upon infection. Experimental evidence shows that the E protein induces ERGIC membrane curvature, participating in the budding process that allows for viral exocytosis and infection of new cells. The mechanism through which this small, integral membrane protein bends membranes remains unknown. Coarse-grained molecular dynamics simulations of a membrane-embedded E-protein yield membrane deformations that are unusually long-range. Even more surprisingly, these deformations become more pronounced as the simulation box increases. Here, we test the effects of leaflet thickness on the amplitude of E protein-induced membrane deformations. We use our simulation analysis software nougat to quantify asymmetric thickness deformations and leaflet curvature. Furthermore, we compare these deformations with predictions from continuum elastic simulations to elucidate possible mechanisms.