Supplementary information

Drug repositioning identifies salvinorin A and deacetylgedunin (DCG)-enriched plant extracts as novel SARS-CoV-2 inhibitors.

Mariana J. Shayo, Baraka Samwel, Daniel M Shadrack, Joel Cassel, Joseph M. Salvino, Luis J. Montaner, Geradius Deogratias, Ian Tietjen, Lucy Kiruri, Samsoni Hilonga, Ester Innocent

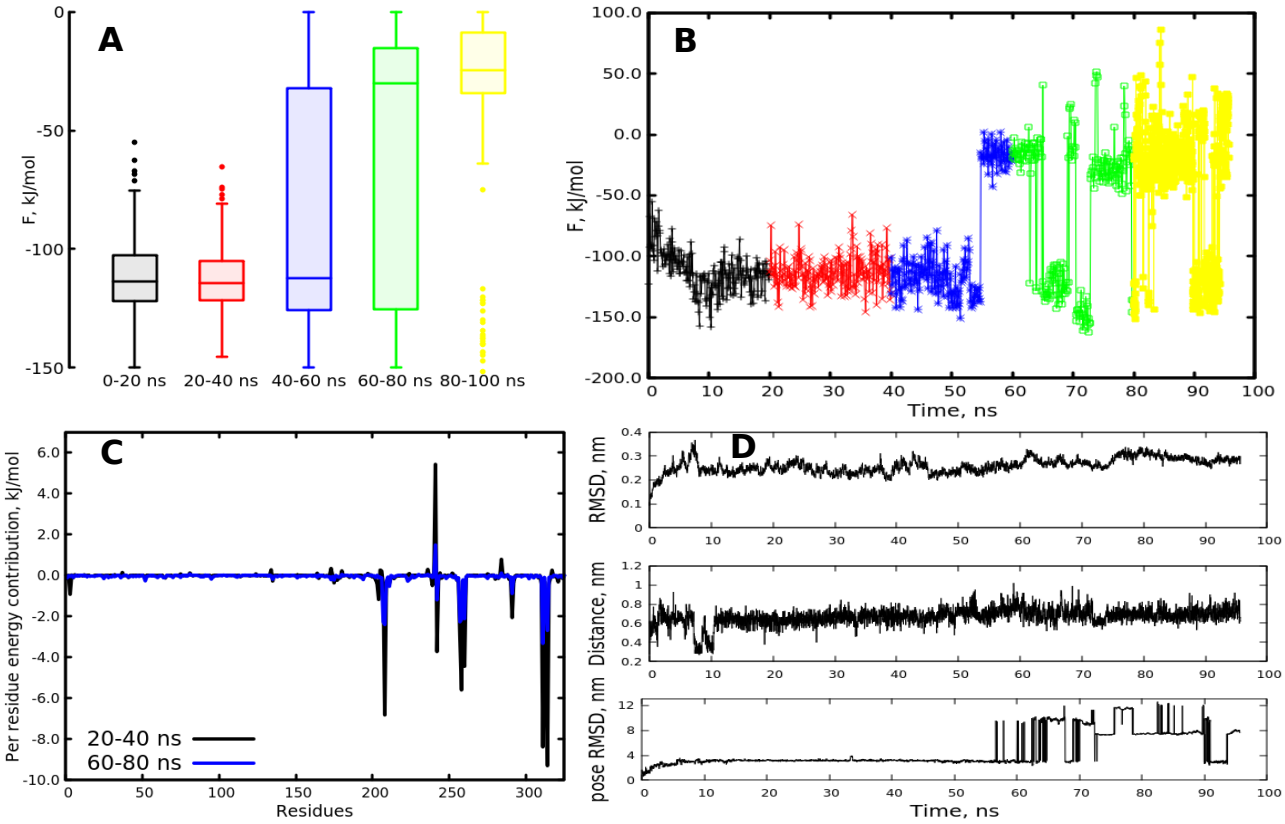

Figure S1: Illustrates the correlation of binding free energy with three prominent reaction coordinates. Panels A and B depict the fluctuations and unbinding behavior of salvinorin A from the TMPRSS2 protein, observed from 50 ns onwards. This unbinding behavior is further confirmed by the per-residue contribution shown in Panel C, indicating that the ligand returns to the protein active site upon unbinding, thereby ruling out off-target binding. Panel D mirrors these fluctuations with selected reaction coordinates, revealing that only pose RMSD exhibits behavior similar to the observed free energy fluctuations. This suggests that pose RMSD could serve as an effective reaction coordinate for correlating in vitro or in vivo activity.