Matrix Structural Analysis W Mcguire

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HDX-MS analysis provides additional insight into the state of this key structural motif. Peptides in HR1-C helix (residues 570–579 and 583–593) are more protected in hVLPs than in BG505.SOSIP (Figure 5 C), indicating increased backbone hydrogen bonding interactions in corresponding residues.

Cryo-ET of Env on intact HIV virions reveals structural ...
The spike protein is very large, often 1200-1400 amino acid residues long; it is 1273 residues in SARS-CoV-2. It is a single-pass transmembrane protein with a short C-terminal tail on the interior of the virus, a transmembrane helix, and a large N-terminal ectodomain exposed on the virus exterior.. Spike glycoprotein forms homotrimers in which three copies of the protein interact through their ...