Figures/Preliminary Results *

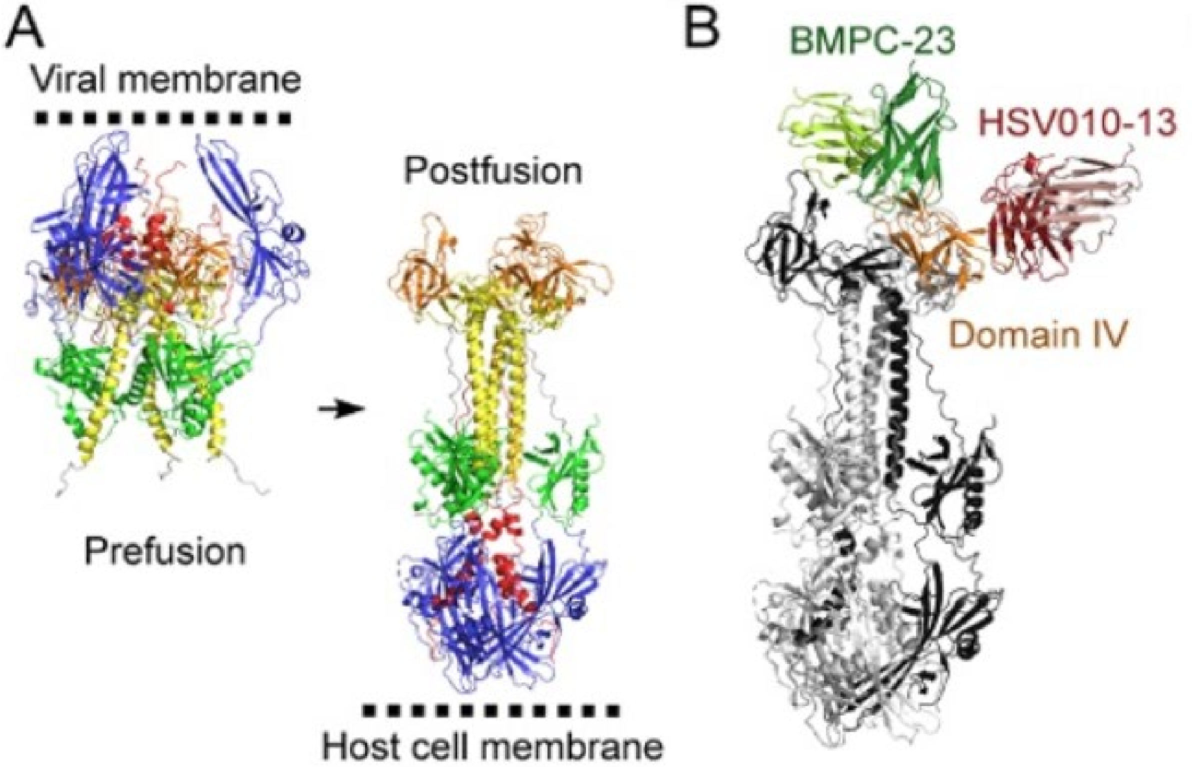

Fig. 1. Mapping of binding site for BMPC-23: (A) Structures of HSV-1 gB in the prefusion (6z9m) and postfusion (2gum) states were aligned on domain VI to illustrate the orientation of domain IV relative to the viral and host cell membranes. (B) Models built with cryo-EM densities for BMPC-23 and 10-13 were aligned and a single Fab from each structure is shown. Densities were only of sufficient quality to build models of the Fv (variable) domains.