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Composite Model of Full GP Structure of Ebola Virus Envelope Glycoprotein

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Description

Depicted is a composite model of the Ebola surface glycoprotein (GP) in its trimeric configuration (monomers comprise GP1GP2 subunits) and represents a single GP spike projecting from the surface of the Ebola Virus. This figure combines the published X-ray crystallographic (core) [1] and cryoelectron tomography (global) [2] structures, together now with *in silico* modeled sections of the mucin-like domain and separately the GP stalk [3]. The latter are missing from earlier published crystal structure determinations. The core Ebola Virus glycoprotein GP 3CSY structure (of homo-trimers of truncated GP1-GP2 monomers) was determined by x-ray crystallography at 3.4 Angstroms and is shown both at the bottom left (space filled depiction) and in the centre of the image within a composite model (white – in protein cartoon structure depiction) [1]. *In silico* modeling with Phyre was performed to obtain a structural model of the GP mucin-like domain (space filled top right monomer) [3], and also incorporated into the central composite image (yellow – top). An *in silico* model for the GP membrane proximal stalk domain was additionally composed and is represented in trimeric configuration (space filled - bottom right) and in the centre composite (yellow strands – at the bottom) [3]. These *in silico* modelled structures are mapped into the composite shown in the centre with 3 separate mucin-like domains represented in yellow at the top of the trimer model, and at the base of that structure a homotrimeric stem (also in yellow) [4,5]. Together these components: the mucin-like (*in silico* modeled), core binding and fusion (x-ray crystal defined) and GP-membrane stalk (*in situ* modeled) regions cover the whole GP (i.e. GP1+GP2) monomer sequence and represent the pre-fusion conformation. These have been mapped in 3D space as trimers, and dispayed within the GP structure framework provided by the cryo-electron tomograph of the global GP trimer configuration. The tomograph is shown in surface view in the top left of the figure and in the central composite image as a blue mesh background. Note: the structures of the central composite are enlarged relative to their peripherally displayed individual elements.
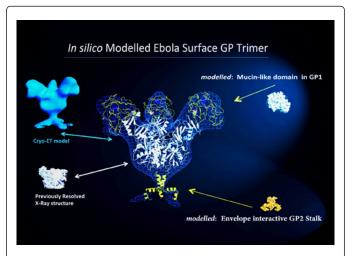

Figure 1: Compilation of a full trimeric prefusion model of the Ebola virus (EBOV) surface envelope glycoprotein GP.

References

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