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This paper reports an X-ray crystal structure and two cryoEM reconstructions. Crystallography and electron microscopy data processing and refinement statistics can be found in Supplementary File 1. Further details regarding data processing can be found in the materials and methods, sections ‘Crystallization and structure determination’, ‘Cryo-EM grid preparation, data acquisition and data processing’, and ‘Quantification of the frequency of lattice formation on VLP surface in the presence and absence of Fab P-4G2’. For the supporting functional assay, comprising the neutralization data presented in Figures 2 and 3, the details of the data analysis can be found in the legends of Figure 2 and Figure 3, and in materials and methods section ‘Hantavirus-pseudotyped VSV neutralization assay’.

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* You should include a definition of biological versus technical replication
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Replicates are not applicable to the crystallography and electron microscopy data that comprise the primary results of this paper. For the supporting functional assay, comprising the neutralization data presented in Figures 2 and 3, each neutralization assay was carried out three times in duplicate. The details of the data analysis can be found in the legends of Figure 2 and Figure 3, and in materials and methods section ‘Hantavirus-pseudotyped VSV neutralization assay’.

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Crystallography and electron microscopy data processing and refinement statistics can be found in Supplementary File 1. Further details regarding data processing and analysis can be found in the materials and methods, sections ‘Crystallization and structure determination’, ‘Cryo-EM grid preparation, data acquisition and data processing’, and ‘Quantification of the frequency of lattice formation on VLP surface in the presence and absence of Fab P-4G2’.

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Atomic coordinates and structure factors of the PUUV Gc-Fab P-4G2 complex crystal structure have been deposited in the PDB under accession code 6Z06. Cryo-EM reconstructions of the PUUV VLP surface alone and in the presence of Fab P-4G2 from areas of continuous and discontinuous lattice have been deposited in the EMDB at the EBI under accession codes **EMD-11966, EMD-11965 and EMD-11964,** respectively. Coordinates of protein structures fitted into these cryo-EM reconstructions have been deposited in the **PDB database** (accession code**7B09** for the Fab P-4G2-PUUV Gc and PUUV Gn fitted into**EMD-11964**, and accession code **7B0A** for PUUV Gc and PUUV Gn fitted into**EMD-11966**, respectively). All the deposited data will be released upon publication of the article.