SUPPLEMENTAL REFERENCES

Brunger, A.T., Adams, P.D., Clore, G.M., DeLano, W.L., Gros, P., Grosse-Kunstleve, R.W., Jiang, J.S., Kuszewski, J., Nilges, M., Pannu, N.S.*, et al.* (1998). Crystallography & NMR system: A new software suite for macromolecular structure determination. Acta Crystallogr. D Biol. Crystallogr. *54 (Pt 5)*, 905-921.

Chen, C., Vincent, O., Jin, J., Weisz, O.A., and Montelaro, R.C. (2005). Functions of early (AP-2) and late (AIP1/ALIX) endocytic proteins in equine infectious anemia virus budding. J. Biol. Chem. *280*, 40474-40480.

DeLano, W.L. (2002). The PyMOL Molecular Graphics System and Users Manual (San Carlos, CA, DeLano Scientific).

Emsley, P., and Cowtan, K. (2004). Coot: model-building tools for molecular graphics. Acta Crystallogr. D Biol. Crystallogr. *60*, 2126-2132.

Garrus, J.E., von Schwedler, U.K., Pornillos, O.W., Morham, S.G., Zavitz, K.H., Wang, H.E., Wettstein, D.A., Stray, K.M., Cote, M., Rich, R.L.*, et al.* (2001). Tsg101 and the vacuolar protein sorting pathway are essential for HIV-1 budding. Cell *107*, 55-65.

Group, C.C.P. (November 4. 1994). The CCP4 Suite:Programs for Protein Crystallography. Acta Crystallogr. D50, 760-763.

Holm, L., and Sander, C. (1998). Touring protein fold space with Dali/FSSP. Nucleic Acids Res. *26*, 316-319.

Howlin, B., Butler, S.A., Moss, D.S., Harris, G.W., and Driessen, H.P.C. (1993). TLSANL: TLS parameter analysis program for segmented anisotropic refinement of macromolecular structures. J. Appl. Crystallogr. *26*, 622-624.

Johnsson, B., Lofas, S., and Lindquist, G. (1991). Immobilization of proteins to a carboxymethyldextran-modified gold surface for biospecific interaction analysis in surface plasmon resonance sensors. Anal Biochem. *198*, 268-277.

Jones, T.A. (1992). A, yaap, asap, @#*? A set of averaging programs. In Molecular Replacement, E.J. Dodson, S. Gover, and W. Wolf, eds. (Warrington, SERC Daresbury Laboratory), pp. 91-105.

Jones, T.A., Zou, J.Y., Cowan, S.W., and Kjeldgaard (1991). Improved methods for binding protein models in electron density maps and the location of errors in these models. Acta Crystallogr. A *47 (Pt 2)*, 110-119.

Katoh, K., Shibata, H., Suzuki, H., Nara, A., Ishidoh, K., Kominami, E., Yoshimori, T., and Maki, M. (2003). The ALG-2-interacting protein ALIX associates with CHMP4b, a human homologue of yeast Snf7 that is involved in multivesicular body sorting. J. Biol. Chem.