

As shown in Figure 5, HIV-1 Δ PTAP release and infectivity were indeed stimulated very dramatically (\sim 25-fold) by ALIX overexpression (Figure 5, panels 1 and 4, compare lanes 1 and 2). Hence, raising cellular ALIX levels could restore HIV-1 Δ PTAP infectivity to within \sim 20% of the wild-type virus. Importantly, ALIX overexpression did not alter intracellular Gag expression or processing (panel 2), which demonstrates that the enhancement occurred at late stages in particle assembly or budding. Control experiments also confirmed that the p6^{Gag}₃₆YPLASL₄₁-ALIX interaction was responsible for this enhancement because ALIX overexpression did not stimulate the release of an HIV-1 Δ PTAP virus that also lacked a functional ALIX-binding site (compare lanes 2 and 4). Indeed, the secondary Δ YP mutation actually reduced HIV-1 Δ PTAP release and infectivity by an additional 5-fold (compare lanes 3 and 4 to lane 1) presumably because the mutation also inhibited the ability of *endogenous* ALIX to mediate low-level release. These experiments demonstrate that ALIX can replace TSG101 in its role of supporting the efficient release of infectious HIV-1, provided ALIX is present at sufficient levels to overcome the modest affinity of the ₃₆YPLASL₄₁-ALIX interaction.

ALIX YPX_nL-Binding Activity Is Required for Virus Release

The rescue of HIV-1 Δ PTAP release and infectivity upon ALIX overexpression provided a convenient assay for testing which ALIX activities were required for functional virus release. This assay was initially used to test whether ALIX mutations that inhibited YPX_nL binding *in vitro* also inhibited virus release through the ALIX pathway. As described previously, overexpression of wild-type ALIX enhanced the release and infectivity of HIV-1 Δ PTAP \sim 25-fold (Figure 6A, compare lanes 1 and 2). In contrast, ALIX proteins with point mutations that inhibited YPX_nL binding (Val498Asp, Phe676Asp, and Ile683Asp) failed to rescue HIV-1 Δ PTAP release or infectivity (compare lanes 2 and 3–5). These mutations did not affect ALIX expression or stability (panel 3), nor did they affect cellular Gag levels (panel 2). Similar data were obtained for a series of other mutations within the YPX_nL-binding site (Phe495Asp, Val509Asp, and Leu680Asp), whereas mutations in a second conserved hydrophobic patch located on arm1 (Leu401Asp, Ile405Asp, and Leu556Asp) did not diminish ALIX rescue significantly ($<$ 2-fold, data not shown). These data reinforce the idea that ALIX binds YPX_nL late domains within the site shown in Figure 2B and demonstrate that ALIX mutations that impair YPX_nL binding also inhibit virus release and infectivity.

ALIX Recruitment of CHMP4/ESCRT-III Is Required for HIV-1 Δ PTAP Release

In addition to binding YPX_nL late domains, ALIX also binds CHMP4/ESCRT-III proteins through the Bro1 domain, suggesting that ALIX may serve to connect retroviral Gag proteins to the ESCRT-III machinery (Katoh et al., 2003; Kim et al., 2005; Martin-Serrano et al., 2003; Odor-

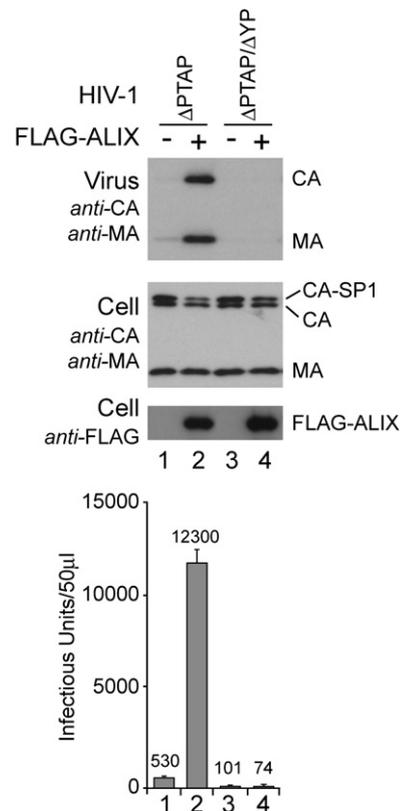


Figure 5. ALIX Overexpression Rescues HIV-1 Δ PTAP Release and Infectivity

Virus release, cellular Gag protein levels, exogenous ALIX expression, and viral infectivity are shown as analyzed by western blotting (panels 1–3) or MAGIC infectivity assays (panel 4). Lanes 1 show HIV-1 Δ PTAP cotransfected with an empty pCI-neo vector control, lanes 2 show HIV-1 Δ PTAP cotransfected with a vector expressing FLAG-ALIX, lanes 3 show HIV-1 Δ PTAP Δ YP cotransfected with an empty vector control, and lanes 4 show HIV-1 Δ PTAP Δ YP cotransfected with a vector expressing FLAG-ALIX. For reference, wild-type HIV-1 titers were typically \sim 65,000 IU/50 μ l, and overexpression raised ALIX levels \sim 50-fold over endogenous protein levels as estimated by western blotting with anti-ALIX antibodies (not shown). Error bars in infectivity assays represent standard deviations of three separate infectivity experiments.

izzi et al., 2003; Strack et al., 2003; von Schwedler et al., 2003). We therefore tested whether the interaction between ALIX and CHMP4A was required for virus budding. Previous work showed that mutations in an exposed hydrophobic patch on yeast Bro1p inhibited Snf7p (CHMP4) binding and prevented proper MVB sorting (Kim et al., 2005). We found that a mutation within the equivalent patch on human ALIX, Ile212Asp, similarly inhibited the ALIX_{Bro1}-CHMP4A interaction, as assayed in a GST pulldown experiment (Figure 6B). As expected, wild-type ALIX_{Bro1} bound to a GST-CHMP4A fusion protein but not to GST alone (compare lanes 2 and 3). In contrast, the ALIX_{Bro1,I212D} mutant did not bind GST-CHMP4A detectably (compare lanes 3 and 6).