ALIX binds a YPX₃L motif of the GPCR PAR1 and mediates ubiquitin-independent ESCRT-III/MVB sorting

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Introduction

G protein–coupled receptors (GPCRs) are the largest family of signaling receptors expressed in mammalian cells and mediate vast physiological responses. The temporal and spatial fidelity of GPCR signaling is critical for appropriate cellular responses. Moreover, dysregulated GPCR signaling has been implicated in numerous human diseases including neurodegeneration and cancer progression (Hanyaloglu and von Zastrow, 2008; Marchese et al., 2008). In addition to desensitization, GPCR trafficking is important for the precise regulation of signaling responses. This is particularly true for protease-activated receptor 1 (PAR1), a G protein–coupled receptor (GPCR) for thrombin, which is internalized after activation and sorted to lysosomes independent of ubiquitination and the ubiquitin-binding ESCRT components hepatocyte growth factor–regulated tyrosine kinase substrate and Tsg101. In this paper, we report that PAR1 sorted to ILVs of MVBs through an ESCRT-III–dependent pathway independent of ubiquitination. We further demonstrate that ALIX, a charged MVB protein 4–ESCRT-III interacting protein, bound to a YPX₃L motif of PAR1 via its central V domain to mediate lysosomal degradation. This study reveals a novel MVB/lysosomal sorting pathway for signaling receptors that bypasses the requirement for ubiquitination and ubiquitin-binding ESCRTs and may be applicable to a subset of GPCRs containing YPX₃L motifs.
ILVs and ILV formation (Wollert and Hurley, 2010). ESCRT-III polymerizes on endosomal membranes and is the main driver of ILV scission. The AAA-ATPase vacuolar protein sorting 4 (Vps4) disassembles and recycles ESCRT-III components and is essential for ESCRT function. In addition to receptor sorting at the MVB, ESCRT mediates viral budding and cytokinesis through processes that require ESCRT-I and -III and ALIX, an ESCRT-III–interacting protein, but not ESCRT-0 or -II (Strack et al., 2003; Carlton et al., 2008). Whether there are differences in ESCRT requirements for the sorting of signaling receptors at the MVB in mammalian cells remains unclear.

Most GPCRs require posttranslational modification with ubiquitin and ESCRTs for sorting from endosomes to lysosomes. The chemokine receptor CXCR4 is ubiquitinated after activation and sorted from endosomes to lysosomes through a pathway that requires HRS and Vps4 (Marchese et al., 2003). PAR2, a GPCR related to PAR1, also undergoes agonist-induced ubiquitination and is sorted to lysosomes through an HRS-dependent pathway (Hasdemir et al., 2007). However, not all GPCRs require direct ubiquitination for MVV sorting and lysosomal degradation, as exemplified by the δ-opioid receptor (DOR). A ubiquitination-deficient DOR mutant is efficiently sorted to ILVs of MVBs similar to wild-type (WT) receptor (Henry et al., 2011). However, degradation of DOR requires HRS and Vps4 but not Tsg101 (Hislop et al., 2004), indicating that receptor sorting can occur independent of ubiquitination and requires some but not all components of the ubiquitin-binding ESCRT machinery. Thus, it remains to be determined whether a signaling receptor can bypass the requirement for both ubiquitination and ubiquitin-binding components of the ESCRT machinery and sort to MVV/lysosomes.

We previously showed that activated PAR1 is efficiently sorted from endosomes to lysosomes and degraded independent of ubiquitination (Wolfe et al., 2007). In contrast to DOR, however, neither HRS nor Tsg101 is essential for lysosomal degradation of PAR1 (Gullapalli et al., 2006). Thus, it is not known whether activated PAR1 ultimately sorts to ILVs of MVBs and requires any components of the ESCRT machinery for lysosomal degradation. Here, we report that activated PAR1 sorts to ILVs of MVBs through a pathway that requires ALIX and ESCRT-III function but not receptor ubiquitination. Moreover, our findings indicate that ALIX binds to a YPX3L motif of PAR1 and recruits ESCRT-III to mediate MVV/lysosomal sorting.

Results

Activated PAR1 sorts to ILVs of MVBs independent of ubiquitination

Activated PAR1 WT is internalized, sorted efficiently to lysosomes, and rapidly degraded with a half-life of 30 min (Trejo and Coughlin, 1999). In previous work, we showed that a PAR1 lysine-less 0K mutant defective in ubiquitination is degraded comparably with WT receptor after activation (Wolfe et al., 2007), suggesting that PAR1 degradation occurs independent of ubiquitination. To investigate the mechanism of ubiquitin-independent degradation of PAR1, we first determined whether agonist promoted lysosomal sorting of the PAR1 0K mutant by examining its colocalization with the lysosomal-associated membrane protein 1 (LAMP1) in HeLa cells using immunofluorescence confocal microscopy. In the absence of agonist stimulation, PAR1 WT and 0K mutant cycle constitutively between the plasma membrane and early endosomes (Paing et al., 2006; Wolfe et al., 2007). Consistent with these studies, we found that PAR1 WT and 0K mutant localized predominantly to the cell surface and early endosomes and showed no significant colocalization with LAMP1 under control conditions (Figs. 1 A and S1 A). However, after 60 min of agonist stimulation, PAR1 WT colocalized extensively with LAMP1-positive vesicles (Fig. 1 A), as previously reported (Trejo et al., 2000). Activation of PAR1 0K mutant with agonist for 60 min also resulted in substantial receptor colocalization with LAMP1 (Fig. 1 A). The colocalization of activated PAR1 WT and 0K mutant with LAMP1 was verified by determining Pearson’s correlation coefficient for PAR1 WT and LAMP1 (r = 0.30 ± 0.05; n = 6) and 0K mutant (r = 0.30 ± 0.08; n = 6). Thus, after activation, PAR1 0K mutant is efficiently sorted to lysosomes like WT
receptor, suggesting that ubiquitination is not essential for PAR1 lysosomal sorting.

A critical step in lysosomal sorting and degradation of most proteins in mammalian cells requires incorporation into ILVs of the MVB. To determine whether PAR1 directly enters ILVs of MVBs independent of receptor ubiquitination, we performed immuno-EM on ultrathin cryosections of HeLa cells expressing PAR1 WT or ubiquitin-deficient 0K mutant. To examine endocytic sorting of the cell surface cohort of PAR1 WT and 0K mutant after agonist activation, receptors were prelabeled with anti-FLAG antibody at 4°C and then treated with agonist for 20 min. After agonist stimulation, activated PAR1 WT (12-nm gold particles) sorted to an endosomal compartment that colabeled with the late endosome/MVB marker CD63 (6-nm gold particles; Fig. 1 B), suggesting that activated PAR1 traffics to MVBs. Remarkably, the ubiquitination-deficient PAR1 0K mutant also localized to ILVs of CD63-positive MVBs after agonist activation (Fig. 1 C), indicating that PAR1 traffics to ILVs of MVBs independent of receptor ubiquitination. To ensure that antibody prelabeling did not alter the internalization and sorting of PAR1, we examined the colocalization of PAR1 WT and 0K mutant with LAMP1 by immunofluorescence confocal microscopy in parallel. As expected, PAR1 WT and 0K mutant localized to the cell surface and early endosomes and did not colocalize with LAMP1 after incubation for 20 min in the absence of agonist (Fig. S1, B and C). In contrast, however, stimulation of PAR1 WT and 0K mutant with agonist for 20 min caused significant colocalization with LAMP1 (Fig. S1, B and C), consistent with that observed in cells not prelabeled with antibody (Fig. 1 A). Together, these data demonstrate that ubiquitination of activated PAR1 is not required for entry into ILVs of MVBs and suggest that a novel pathway exists for the sorting of nonubiquitinated receptors to the lysosome.

ESCRT-III and Vps4 mediate PAR1 lysosomal degradation

To define the ubiquitin-independent lysosomal degradation pathway of PAR1, we examined the function of ESCRT-III components, which do not contain any known ubiquitin-binding domains (Hurley and Hanson, 2010). Charged MVB protein 4 (CHMP4) is the most abundant subunit of ESCRT-III, which serves as the critical mediator of ILV scission, and exists as three isoforms: CHMP4A, B, and C (Wollert and Hurley, 2010). We first determined the expression of CHMP4 isoforms in HeLa cells using RT-PCR and CHMP4 isoform–specific primers (Fig. 2 A, lanes 6–8). RT-PCR assay of HeLa cell RNA revealed the presence of all three isoforms, including CHMP4A, B, and C (Fig. 2 A, lanes 1 and 2). To assess CHMP4 function in PAR1 degradation, siRNAs that specifically target each of the three CHMP4 isoforms expressed in HeLa cells were used. HeLa cells transfected with CHMP4 isoform–specific siRNA SMARTpools exhibited a substantial decrease in CHMP4A, B, and C mRNA transcripts, as revealed by RT-PCR (Fig. 2 A, lanes 3–5). Consistent with diminished mRNA transcripts, CHMP4-specific siRNAs also caused significant depletion of endogenous CHMP4A and CHMP4B protein, as detected by immunoblotting (Fig. 2 B). Because there are no anti-CHMP4C antibodies commercially available, we were unable to examine endogenous CHMP4C protein expression in siRNA-transfected cells.

To assess the function of CHMP4 in PAR1 degradation, HeLa cells expressing FLAG-PAR1 were transfected with either nonspecific or CHMP4-specific siRNAs. Cells were then incubated with agonist for 60 min, and PAR1 degradation was assessed. In nonspecific siRNA-transfected cells, an ~50% decrease in the amount of PAR1 protein was detected after 60 min of agonist incubation compared with unstimulated control cells (Fig. 2 B, lanes 1 and 2). The extent of PAR1 degradation was similar in nonspecific and CHMP4A siRNA–transfected cells after agonist stimulation, suggesting that CHMP4A is not essential for PAR1 degradation (Fig. 2 B, lanes 1–4). In contrast, agonist-induced degradation of PAR1 was significantly inhibited in cells transfected with either CHMP4B or CHMP4C siRNA SMARTpools (Fig. 2 B, lanes 5–8), indicating that both CHMP4B and C isoforms are necessary for PAR1 degradation. Cells transfected with single siRNAs targeting CHMP4B resulted in loss of endogenous CHMP4B expression and also blocked agonist-promoted PAR1 degradation (Fig. S2). These results
suggest that CHMP4 mediates agonist-induced PAR1 lysosomal degradation.

The AAA-ATPase Vps4 catalyzes ESCRT-III disassembly and recycling and is critical for ESCRT function (Hurley and Hanson, 2010). To examine the role of Vps4 in agonist-induced PAR1 degradation, we used a catalytically inactive Vps4 E228Q variant, which functions as a dominant-negative mutant (Babst et al., 1998; Bishop and Woodman, 2000). HeLa cells coexpressing PAR1 and either Vps4 WT or E228Q mutant fused to GFP were incubated with agonist, and receptor degradation was assessed. Interestingly, agonist-promoted PAR1 degradation was significantly inhibited in cells coexpressing Vps4 E228Q mutant compared with Vps4 WT–expressing cells (Fig. 3 A), indicating that Vps4 mediates MVB sorting of PAR1. Agonist-promoted PAR2 degradation was similarly inhibited in Vps4 E228Q mutant–expressing cells compared with control cells expressing WT Vps4 (Fig. 3 B). PAR1 and PAR2 degradation induced by agonist was also inhibited in cells transfected with siRNAs targeting both Vps4A and B isoforms (Fig. S3, A and B). These results suggest that Vps4 is required for both ubiquitin- and nonubiquitin-mediated lysosomal sorting of GPCRs.

Next, we evaluated Vps4 function in MVB/lysosomal sorting of activated PAR1 and PAR2 by immunofluorescence confocal microscopy. Cells coexpressing FLAG-PAR1 or FLAG-PAR2 and either Vps4 WT or E228Q mutant fused to GFP were incubated with anti-FLAG antibody at 4°C to ensure only the cell surface receptors were labeled and then stimulated with agonist. In the absence of agonist, PAR1 and PAR2 localized predominantly to the cell surface, whereas agonist-stimulated PAR1 and PAR2 redistributed from the cell surface to endosomes (Fig. 3 C and D). As expected, coexpression of Vps4 E228Q mutant resulted in accumulation of internalized PAR2 in enlarged vesicles, defined as a class E phenotype that results from disruption of ESCRT-III recycling (Fig. 3 D; Babst et al., 1998; Bishop and Woodman, 2000). In contrast, PAR1-containing endosomes were unperturbed in Vps4 E228Q mutant–expressing cells and appeared similar to those in adjacent untransfected cells and cells expressing Vps4 WT (Fig. 3 C). aberrant localization of CD63 observed in cells coexpressing PAR1 and Vps4 E228Q mutant indicates disruption of the MVB compartment (Fig. 3 C). Thus, in contrast to ubiquitinated cargo, PAR1 fails to accumulate at the MVB when the pathway is disrupted, suggesting that MVB sorting of PAR1 is distinctly regulated.

To confirm ESCRT-III function in PAR1 lysosomal degradation, we examined whether activated PAR1 forms a complex with CHMP4. We first assessed the coassociation of endogenous CHMP4B with activated PAR1 in HeLa cells by coimmunoprecipitation. HeLa cells expressing FLAG-PAR1 WT were incubated with agonist for various times, PAR1 was immunoprecipitated, and association of CHMP4B was examined. In the absence of agonist, PAR1 and CHMP4B interaction was undetectable (Fig. 4 A). However, an interaction between PAR1 and endogenous CHMP4B was detected after 10 min of agonist stimulation, and the proteins remained associated for ~20 min (Fig. 4 A). These findings coincide with the time course for agonist-induced PAR1 localization to ILVs of MVBs and suggest that CHMP4B is a component of the ESCRT-III complex that binds to activated PAR1. Next, we examined PAR1 interaction with CHMP4C in HeLa cells transfected with an HA-tagged CHMP4C, as CHMP4C antibodies are not available. HeLa cells coexpressing FLAG-PAR1 and HA-CHMP4C were incubated with agonist for various times, PAR1 was immunoprecipitated, and CHMP4C association was assessed. In unstimulated control cells, CHMP4C failed to interact with PAR1 (Fig. 4 B). However, after activation of PAR1 for 10 min, a marked increase in CHMP4C association with PAR1 was detected (Fig. 4 B). Next, we examined whether the ubiquitin-deficient PAR1 0K mutant interacted...
with CHMP4 proteins. Similar to WT PAR1, both CHMP4B and CHMP4C coimmunoprecipitated with activated PAR1 0K mutant after 10 min of agonist stimulation (Fig. 4 C), indicating that CHMP4B and CHMP4C are components of the PAR1 ubiquitin–independent sorting complex. In contrast, FLAG-tagged β2-adrenergic receptor (β2-AR), a classical GPCR, failed to coimmunoprecipitate with HA-CHMP4B or HA-CHMP4C in PAR1-expressing cells stimulated with the PAR1-specific agonist for 10 min (Fig. 4 D). Together, these findings demonstrate that ESCRT-III binds specifically to activated PAR1 and regulates MVB/lysosomal degradation.

The ESCRT-III-associated protein ALIX is required for PAR1 degradation

To further define the PAR1 ubiquitin–independent lysosomal sorting pathway, we investigated the function of ALIX, a CHMP4-interacting protein that recruits ESCRT-III to membranes (Fisher et al., 2007). We first examined whether PAR1 interacted with endogenous ALIX in HeLa cells. Cells expressing FLAG-PAR1 were stimulated with agonist for various times, PAR1 was immunoprecipitated, and association of endogenous ALIX was assessed. In cells treated with agonist for 10 min, PAR1 association with endogenous ALIX was markedly increased compared with untreated control cells (Fig. 5 A, lanes 1 and 2), whereas PAR1 and ALIX interaction was diminished after 20 min of agonist exposure (Fig. 5 A, lanes 1–3). In contrast, PAR2 and ALIX interaction was negligible in control and agonist-treated cells (Fig. 5 A, lanes 4 and 5). PAR1 also associated with HA-ALIX in an agonist-dependent manner (Fig. S4 A), whereas HA-ALIX failed to bind to β2-AR in cells treated with PAR1-specific agonist (Fig. S4 B) or to activated PAR2 (Fig. S4 C). Next, we examined the association of endogenous ALIX with ubiquitination-deficient PAR1 in HeLa cells. In contrast to control cells, activation of the PAR1 0K mutant for 10 min resulted in endogenous ALIX association (Fig. 5 B), suggesting that ubiquitination is not required for ALIX interaction with activated PAR1.

ALIX has been shown to link certain viral proteins to the ESCRT-III complex, a process important for viral budding (Usami et al., 2007). Therefore, we examined whether ALIX was required for agonist-induced PAR1 interaction with CHMP4. HeLa cells coexpressing FLAG-PAR1 and HA-CHMP4B transfected with nonspecific or ALIX-specific siRNAs were treated with agonist, PAR1 was immunoprecipitated, and CHMP4 association was assessed. In nonspecific siRNA control cells, a 10-min incubation with agonist resulted in robust PAR1 association with CHMP4B (Fig. 5 C, lanes 1–4). In striking contrast, activated PAR1 interaction with CHMP4B was virtually ablated in ALIX-deficient cells (Fig. 5 C, lanes 5–8). These findings suggest that ALIX links PAR1 to the ESCRT-III machinery to facilitate lysosomal sorting.

Next, we assessed ALIX function in agonist-induced PAR1 lysosomal degradation. HeLa cells expressing FLAG-PAR1 were transfected with ALIX-specific siRNAs and stimulated with agonist for various times, and PAR1 degradation was examined. In ALIX-deficient cells, agonist-promoted degradation of PAR1 was significantly inhibited compared with the extent of PAR1 degradation observed after 60 min of agonist stimulation in siRNA-treated control cells (Fig. 6 A). However, internalization of activated PAR1 occurred normally in ALIX-deficient cells (Fig. S4 D), indicating that ALIX mediates PAR1 sorting to a lysosomal degradative pathway after internalization. Depletion of endogenous ALIX expression also caused a significant defect in agonist-promoted degradation of endogenous PAR1-expressed human endothelial cells (Fig. 6 B). Moreover, agonist-induced degradation of ubiquitination-deficient PAR1 0K mutant was also impaired in ALIX-deficient cells, whereas activated PAR2 degradation
ALIX binds to a highly conserved YPX₃L motif in PAR1 via its central V domain

ALIX contains an N-terminal Bro1 domain, a central V domain, and C-terminal proline-rich region. ALIX binds to YPX₃L motifs present in the late domain of viral Gag proteins via its central V domain (Fisher et al., 2007; Zhai et al., 2008) and is critical for ESCRT-III recruitment and viral budding (Usami et al., 2007). A search of the PAR1 cytoplasmic domains for such a sequence revealed a highly conserved motif within the second intracellular loop of the receptor (Fig. 7 A). The PAR1 Y²⁰⁶⁰PMQSL²¹¹ motif conforms to the ALIX-binding motif YPX₃L (with n = 3) and is not present in PAR2 cytoplasmic domains (Fig. 7 A). A search of several hundred class A GPCRs for such a motif revealed the presence of a highly conserved sequence that conforms to the YPX₃L motif residing in the second intracellular loop of seven other mammalian GPCRs (Table 1). Only one class A GPCR harbors a conserved YPX₃L motif within the cytoplasmic tail domain (Table 1). To examine the importance of the YPX₃L motif in PAR1 degradation, we mutated the critical Y206 to alanine, as analogous Y mutations in YPX₃L motifs of viral Gag proteins abrogated ALIX interaction and function (Strack et al., 2003). The PAR1 Y206A mutant expressed at the surface and internalized after activation comparable with WT PAR1 (Fig. S5, A and B), suggesting that the PAR1 Y206A mutant traffics to and from the cell surface normally.

Next, we examined whether the PAR1 YPX₃L motif was necessary for interaction with ALIX. HeLa cells coexpressing FLAG-PAR1 WT or Y206A mutant together with HA-ALIX were stimulated with agonist, and coassociation was examined (Strack et al., 2005). In contrast to PAR1 interaction with WT ALIX, the HA-ALIX F676D mutant failed to bind to WT PAR1 (Fig. S5, A and B), suggesting that the YPX₃L motif is an important determinant for ALIX interaction. We also examined whether the ALIX V domain is required for association with PAR1. The ALIX central V domain binds directly to YPX₃L sequences of viral Gag proteins, and mutation of the critical phenylalanine to aspartic acid (F676D) was shown to disrupt this interaction (Zhai et al., 2008). In contrast to PAR1 interaction with WT ALIX, the HA-ALIX F676D mutant failed to bind to PAR1 after 10 min of agonist incubation (Fig. 7 C). To confirm direct interaction between the PAR1 YPX₃L motif and the ALIX V domain, we performed in vitro binding assays using a biotinylated PAR1 ICL2 peptide containing the YPX₃L motif in pull-down experiments with purified GST-tagged ALIX. Strikingly, the ALIX V domain showed robust interaction with the PAR1 YPX₃L containing ICL2 peptide (Fig. 7 D), whereas neither the ALIX V domain harboring the F676D mutant nor the ALIX Bro1 domain bound to the PAR1 ICL2 peptide (Fig. 7 D). Together, these findings strongly suggest that ALIX can bind directly to the YPX₃L motif of PAR1 via its central V domain.

Our experiments indicate that the PAR1 YPX₃L motif is critical for binding to ALIX. Therefore, we tested whether the PAR1 YPX₃L motif was necessary for agonist-promoted PAR1 degradation. Incubation with agonist for 60 min caused an ~50% loss of PAR1 protein (Fig. 8 A). In contrast to WT remaining intact (Fig. 6 C). Together, these findings support a function for ALIX in ubiquitin-independent MVB sorting of activated PAR1.

To confirm that ALIX is required for PAR1 degradation, we performed knockdown rescue experiments in cells cotransfected with two siRNAs targeting endogenous ALIX together with FLAG-tagged PAR1 and an siRNA-resistant HA-ALIX WT variant. In cells depleted of endogenous ALIX, agonist-induced degradation of PAR1 was significantly impaired compared with siRNA-treated control cells (Fig. 6 D, lanes 1–4). However, coexpression of siRNA-resistant HA-ALIX WT restored activated PAR1 degradation in cells lacking endogenous ALIX (Fig. 6 D, lanes 5 and 6). In contrast, agonist failed to induce PAR1 degradation in cells depleted of endogenous ALIX and expressing an siRNA-resistant HA-ALIX Bro domain deletion mutant (Fig. 6 D, lanes 7 and 8). The N-terminal Bro domain of ALIX mediates interaction with CHMP4 (Kim et al., 2005). These findings suggest that ALIX-mediated MVB/lysosomal sorting of PAR1 requires interaction with CHMP4 and is a distinct pathway from that used by ubiquitinated GPCRs.

Figure 5. ALIX associates with PAR1 and mediates interaction with CHMP4. (A and B) HeLa cells expressing either FLAG-tagged PAR1 WT, 0K mutant, or PAR2 were stimulated with 100 μM SFLRRN or 100 μM SLIGKV for various times at 37°C. Equivalent amounts of cell lysates were immunoprecipitated (IP) and examined as described in Fig. 4 B. IB, immunoblotting. (C) HeLa cells expressing FLAG-PAR1 WT or Y206A mutant together with HA-CHMP4B and either 100 nM nonspecific (ns) or ALIX-specific siRNAs. Equivalent amounts of cell lysates were immunoprecipitated and analyzed as described in Fig. 4 B.
PAR1, agonist-stimulated degradation of the PAR1 Y206A mutant was significantly inhibited (Fig. 8 A). Next, we examined whether PAR1 Y206A mutant remained at the limiting membrane of MVBs or sorted to an internal compartment by evaluating its sensitivity to proteinase K digestion after activation and internalization. Proteinase K protection assays have been used previously to assess EGFR sorting to ILVs of MVBs (Malerød et al., 2007). HeLa cells expressing PAR1 WT or PAR1, agonist-stimulated degradation of the PAR1 Y206A mutant was significantly inhibited (Fig. 8 A). Next, we examined whether PAR1 Y206A mutant remained at the limiting membrane of MVBs or sorted to an internal compartment by evaluating its sensitivity to proteinase K digestion after activation and internalization. Proteinase K protection assays have been used previously to assess EGFR sorting to ILVs of MVBs (Malerød et al., 2007). 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were efficiently degraded after exposure to proteinase K in samples supplemented by Triton X-100, which allows proteinase K access to internal membranous compartments (Fig. 8 B, lanes 3, 6, 9, and 12). The early endosomal antigen protein 1 (EEA1) was also efficiently degraded in all proteinase K–treated samples, demonstrating effective plasma membrane permeabilization and proteinase K activity (Fig. 8 B). In addition, the PAR1 Y206A mutant internalized to EEA1-positive endosomes like WT receptor in cells treated with agonist for 10 min (Fig. 8 C), and both sorted from the EEA1-containing endosomes after 20 min (Fig. 8 C). The extent of colocalization with EEA1 at 10 min was quantified by determining the Pearson’s correlation coefficient for PAR1 WT ($r = 0.50 \pm 0.1; n = 6$) and Y206A ($r = 0.43 \pm 0.09$; $n = 6$).

Y206A mutant were incubated with agonist for 15 min at 37°C, washed, and gently permeabilized with digitonin. Membranes were isolated, divided into aliquots, and either left unstimulated, treated with proteinase K, or treated with proteinase K supplemented with 0.1% Triton X-100. Activation of PAR1 WT resulted in a greater accumulation of receptor in proteinase K–treated samples compared with unstimulated control samples (Fig. 8 B, lanes 2 and 5), indicating that activated PAR1 WT is sorted into protective endosomal compartments. In contrast, PAR1 Y206A mutant failed to accumulate in protective endosomal compartments compared with unstimulated control (Fig. 8 B, lanes 8 and 11), suggesting the PAR1 Y206A mutant is defective in MVB sorting. However, both PAR1 WT and Y206A mutant were efficiently degraded after exposure to proteinase K in samples supplemented by Triton X-100, which allows proteinase K access to internal membranous compartments (Fig. 8 B, lanes 3, 6, 9, and 12). The early endosomal antigen protein 1 (EEA1) was also efficiently degraded in all proteinase K–treated samples, demonstrating effective plasma membrane permeabilization and proteinase K activity (Fig. 8 B). In addition, the PAR1 Y206A mutant internalized to EEA1-positive endosomes like WT receptor in cells treated with agonist for 10 min (Fig. 8 C), and both sorted from the EEA1-containing endosomes after 20 min (Fig. 8 C). The extent of colocalization with EEA1 at 10 min was quantified by determining the Pearson’s correlation coefficient for PAR1 WT ($r = 0.50 \pm 0.1; n = 6$) and Y206A ($r = 0.43 \pm 0.09$; $n = 6$).

Table 1. Human GPCRs with conserved YPX₃L motifs

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<td>P32245</td>
<td>Cytoplasmic tail</td>
<td>318-YPLGGLCDLSSRY-stop</td>
</tr>
</tbody>
</table>

A search of 397 class A GPCR cytoplasmic sequences for YPX₃L motifs was completed by sequence alignment using the GPCR database (Vrolijk et al., 2011). Of these, several GPCRs contained sequences conforming to the YPX₃L motif in the ICL2 (bold) and were aligned starting with the DRY/F motif. The list includes the GPCR family name, International Union of Basic and Clinical Pharmacology (IUPHAR) nomenclature, and NCBI accession numbers.
In this study, we define a new ubiquitin-independent MVB/lysosomal sorting pathway for signaling receptors that requires ALIX and ESCRT-III function in mammalian cells. We demonstrate that activated PAR1 is sorted to ILVs of MVBS independently of receptor ubiquitination but requires ESCRT-III function. Our data further indicate that PAR1 degradation is regulated by ALIX, which binds directly to a YPX3L motif localized within the PAR1’s intracellular loop via its central V domain and mediates CHMP4/ESCRT-III recruitment to the receptor. Thus, PAR1 bypasses the requirement for ubiquitination and ubiquitin-binding ESCRTs but requires ALIX and ESCRT-III for sorting to ILVs of MVBS (Fig. 9).

We previously showed that lysosomal sorting of PAR1 occurs independent of ubiquitination and the ubiquitin-binding ESCRT components HRS and Tsg101 (Gullapalli et al., 2006; Wolfe et al., 2007), but whether PAR1 sorts to ILVs of MVBS remained unknown. Here, we show that a ubiquitination-deficient PAR1 mutant sorted to ILVs similar to WT receptor, indicating that ubiquitination is not essential for ILV sorting of PAR1. Our experiments further indicate that CHMP4, the major subunit of ESCRT-III and driver of ILV scission, is essential for agonist-induced PAR1 degradation. In contrast to other ESCRT complexes, ESCRT-III does not contain any known ubiquitin-binding subunits, suggesting that ubiquitin binding is not essential for ESCRT-III-mediated PAR1 degradation. Moreover, ubiquitination is not a prerequisite for cargo passage into ILVs, as ESCRT-III subunits recruit enzymes that appear to deubiquitinate cargo before ILV entry (Kyuuma et al., 2007). Thus, unlike most cargo sorted to ILVs of MVBS via the canonical ESCRT pathway, our findings indicate that PAR1 is uniquely sorted by ESCRT-III independent of ubiquitination. This pathway is also distinct from the entirely ESCRT-independent ILV sorting pathway previously described for the melanosome constituent Pmel and the proteolipid protein (Theos et al., 2006; Trajkovic et al., 2008; van Niel et al., 2011). Other cargo, such as the yeast Sna3 and mammalian DOR, are also not directly ubiquitinated, but certain ubiquitin-binding ESCRT components facilitate MVB/lysosomal sorting (Hislop et al., 2004; McNatt et al., 2007; Oestreich et al., 2007; Watson and Bonifacino, 2007).

Our findings also reveal a novel function for ALIX, a CHMP4–ESCRT-III interacting protein, in mediating MVB/lysosomal sorting of PAR1. ALIX directly binds to and recruits CHMP4–ESCRT-III to membranes via interaction with its Bro domain and is important for abscission during cytokinesis and budding of certain viruses (Strack et al., 2003; Morita et al., 2007). However, ALIX function in cargo sorting at MVBS in mammalian cells is not known. Bro1, the yeast homolog of ALIX, facilitates the sorting of ubiquitinated cargo at MVBS (Odorizzi et al., 2003). In yeast, Bro1 recruits the deubiquitinating enzyme Doa4 to the late endosome, which is essential for cargo deubiquitination and sorting at the MVB. However, in mammalian cells, ALIX does not appear to function in lysosomal sorting of ubiquitinated cargo, as depletion of ALIX by siRNA failed to affect degradation of EGFR (Cabezas et al., 2005), a receptor that requires direct ubiquitination and ESCRTs for degradation. We found that the association of ALIX with activated PAR1 coincided with PAR1 sorting to ILVs at the MVB. Moreover, degradation of endogenous and ectopically expressed PAR1 was significantly impaired in ALIX-deficient cells and was restored by expression of an siRNA-resistant ALIX WT variant, indicating that ALIX function is specific for this pathway. ALIX also mediated degradation of ubiquitin-deficient PAR1, but not the related PAR2, which requires ubiquitination for lysosomal sorting. In addition, ALIX is required for activated PAR1 recruitment of CHMP4 subunits, the critical components of ESCRT-III, and the ALIX Bro domain important for CHMP4 interaction is necessary for the rescue of agonist-promoted PAR1 degradation in cells deficient in endogenous ALIX expression. Thus, ALIX has the capacity to mediate cargo sorting at the MVB in mammalian cells through a pathway that requires ESCRT-III recruitment. ALIX-mediated MVBS sorting of PAR1 also appears to be distinctly regulated, as PAR1 does not accumulate at MVBS when ILV sorting is blocked, compared with ubiquitinated cargo that use canonical ESCRT components. The mechanistic basis for this observation is not known but may involve trafficking of PAR1 from the MVB to a different compartment and/or recycling back to the cell surface.

This study is the first to demonstrate ALIX-mediated MVBS/lysosomal sorting of a mammalian cell host protein via a YPX3L motif. The ALIX central V domain has been shown to

Discussion

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This study is the first to demonstrate ALIX-mediated MVBS/lysosomal sorting of a mammalian cell host protein via a YPX3L motif. The ALIX central V domain has been shown to
bind to YPX₃L motifs of retroviral Gag proteins (Fisher et al., 2007; Zhai et al., 2008). We found that ALIX directly interacts with a highly conserved YPX₃L motif within the PAR1’s intracellular loop via its V domain to facilitate MVB/lysosomal degradation. Previous studies showed that the HIV-1 and EIAV viruses recruit the ESCRT machinery through interaction with ALIX (Strack et al., 2003; Zhai et al., 2008) The HIV-1 structural Gag protein harbors a tetrapeptide motif that binds to Tsg101 (Garrus et al., 2001; Martin-Serrano et al., 2003) and a YPX₃L motif that interacts with the V domain of ALIX (Strack et al., 2003; Fisher et al., 2007) to mediate ESCRT-III recruitment. In contrast, EIAV Gag proteins only possess an ALIX-binding YPX₃L motif that is critical for ESCRT-III recruitment (Martin-Serrano et al., 2003) and viral budding (Tanzi et al., 2003). Similar to HIV-1 and EIAV (Strack et al., 2003), mutation of the critical tyrosine within the YPX₃L motif of PAR1 disrupted interaction with ALIX and impaired PAR1 MVB/lysosomal degradation. In vitro binding assays confirmed that the V domain of ALIX binds directly to the YPX₃L motif of PAR1. Thus, ALIX directly interacts with PAR1 and mediates MVB/lysosomal sorting via an ESCRT-III–dependent pathway.

In summary, this study provides the first molecular insight into a mechanism by which a signaling receptor can sort to ILVs of MVBs independent of ubiquitination and ubiquitin-binding ESCRTs. Unlike most ubiquitinated cargo, we show that PAR1 sorts to ILVs of MVBs through a distinct ubiquitin-independent pathway that requires ALIX and ESCRT-III function but not the canonical ubiquitin-binding ESCRT components. These findings unveil a new mechanism that enriches the diversity of MVB sorting pathways for signaling receptors. This work also suggests that ubiquitination of mammalian GPCRs is likely to have additional functions besides mediating receptor sorting at the MVB. ALIX has also been shown to bind to the cytoplasmic tail domains of the transferrin receptor (Géminard et al., 2004), the GPCR vasopressin V2R (Yi et al., 2007), and D1- and D3 dopamine GPCRs (Zhan et al., 2008) and appears to regulate various aspects of receptor trafficking. However, these cargo lack the ALIX-binding YPX₃L motif, and, thus, mechanismically how ALIX functions in these pathways is not known. Remarkably, we discovered seven other mammalian GPCRs that contained conserved YPX₃L motifs within their second intracellular loop, raising the intriguing possibility that ALIX mediates MVB/lysosomal sorting of a subset of GPCRs in mammalian cells.

Materials and methods

Antibodies and reagents
PAR1 peptide agonists (SFLRN and TFLRNPNDK) and PAR2 peptide agonist (S1GKVK) were synthesized and purified by reverse-phase high-pressure liquid chromatography at the Tufts University Core Facility. Polyclonal anti-FLAG and -HA antibodies were obtained from Rockland Immunochemicals. Anti-LAMP1 and -CD63 antibodies were obtained from the Developmental Studies Hybridoma Bank. Anti-EEA1 antibody was obtained from BD. Monoclonal anti-PAR1 WEDE antibody was purchased from Beckman Coulter. Polyclonal CHMP4A and CHMP4B antibodies as well as monoclonal anti-Alix (3A9) and anti-Vps4 antibodies were obtained from Santa Cruz Biotechnology, Inc. The monoclonal anti-HA and -GF antibodies were purchased from Covance. The M2 anti-FLAG and -actin antibodies were obtained from Sigma-Aldrich. The HA antibody conjugated to HRP was purchased from Roche. HRP-conjugated goat–anti-rabbit and goat–anti-mouse antibodies were purchased from Bio-Rad Laboratories. Alexa Fluor 488, 594, and 647 secondary antibodies were purchased from Invitrogen.

siRNA and cDNA transfections
HeLa cells or endothelial cells were transfected with 100 nM siRNA using either Lipofectamine 2000 (Invitrogen) or Oligofectamine (Invitrogen), respectively, and examined after 48 h. The CHMP4A, CHMP4B, CHMP4C, Vps4A, Vps4B, and ALIX siRNAs were purchased as SMARTpools from Thermo Fisher Scientific. The single CHMP4B siRNAs used were 1′-5′-AGAGGAGUUUGAGCAAGAG-3′ and 2′-5′-CGGAAGAGAUGUUAACGAA-3′. Nonspecific siRNA (5′-GGGCAAGGUCGCCGCAACC-3′) was used as a negative control. The AKT knockdown rescue experiment was performed by cotransfecting HEK293 cells with ALIX-specific siRNAs (5′-GUCAUCUCAGUUAUUGA-3′ and 5′-UCGAGGAGCUUCUGGAA-3′; Thermo Fisher Scientific) together with cDNAs containing HA-ALIX WT or HA-ALIX Bro domain mutant harboring silent mutations within the siRNA-targeted region using Lipofectamine 2000 reagent.

Immunoelectron microscopy
HeLa cells stably expressing full-length FLAG-PAR1 or FLAG PAR1 0K mutant were grown in 10-cm dishes (1 · 10⁵ cells/dish) for 48 h. Cells were washed and preincubated on ice for 1 h with anti-FLAG antibody to label only receptors at the cell surface. Cells were washed to remove unbound antibody and treated with agonist for 20 min at 37°C, fixed with 4% PFA in 0.1 M phosphate buffer, pH 7.4, overnight at room temperature, washed with 0.1 M glycine/phosphate buffer, and then embedded in 10% gelatin/phosphate buffer infused with 2.3 M sucrose/phosphate buffer overnight at 4°C. 1-mm³ cell blocks were mounted onto specimen holders and snap frozen in liquid nitrogen. Ultracytomicrotomy was performed at −100°C on an ultramicrotome with an EM FCS cryoattachment (Ultracut UCT; Leica) using a diamond knife (DIATOME US). 80–90-nm frozen sections were picked up with a 1:1 mixture of 2.3 M sucrose and 2% cold water fish skin gelatin. Immunolabeling was performed by placing grids on 2% gelatin at 37°C for 20 min and rinsed with 0.15 M glycine/PBS, and the sections were blocked using 1% cold water fish skin gelatin. Previously titrated primary antibodies were diluted in 1% BSA/PBS. Incubation with primary antibodies for 1 h at room temperature was followed by gold-conjugated goat anti–mouse IgG and IgM (Jackson Immunoresearch Laboratories, Inc.) or gold-conjugated goat anti–rabbit IgG, both diluted 1:25 in 1% BSA/PBS at room temperature for 30 min. Grids were viewed using a transmission electron microscope (1200EX II; JEOL) and photographed using a digital camera (Gatan) at the University of California San Diego Electron Microscopy Facility.

PAR degradation essay
HeLa cells stably expressing FLAG-PAR1, FLAG-PAR1 0K, or FLAG-PAR2 were plated in 12-well dishes (1.5 · 10⁴ cells/well) and grown overnight on June 24, 2017.
at 37°C and transfected with either siRNAs or cDNA plasmids. After 48 h, cells were washed and treated with or without 100 µM SFLRN (PAR1-specific agonist) or 100 µM SUGKV (PAR2-specific agonist) for various times at 37°C. Cells were placed on ice, washed with PBS, and lysed in Triton X-100 lysis buffer (50 mM Tris-HCl, pH 7.4, 100 mM NaCl, 5 mM EDTA, 50 mM NaF, 10 mM NaFp, and 1% Triton X-100) supplemented with protease inhibitors. Cell lysates were collected and sonicated for 10 s at 10% amplitude (model 450 sonifier; Branson). Immunoprecipitations were performed on immunoprecipitation assay lysis buffer (5 mM EDTA, 50 mM Tris-HCl, 150 mM NaCl, 0.5% [wt/vol] Na-deoxycholate, 1% [volume/volume] NP-40, and 0.1% [wt/vol] SDS) supplemented with protease inhibitors, and equivalent amounts of lysates were immunoprecipitated using the anti-PAR1 VWEDE antibody. PAR1 degradation was assessed as previously described (Russo et al., 2009).

Coimmunoprecipitation assay
Hela cells stably expressing FLAG-PAR1 were grown in six-well plates (4.0 × 10^5 cells/well), grown overnight at 37°C, washed and treated with or without 100 µM SFLRN (PAR1-specific agonist) or 100 µM SUGKV (PAR2-specific agonist) for various times at 37°C, fixed with 4% PFA, permeabilized with 100 µg/ml Proteinase K, and then incubated with one-step 2,2'-azino-bis-3-ethylbenzthiazoline-6-sulfonic acid (Thermo Fisher Scientific). Concentrations were determined using BCA assay and GST fusion proteins were eluted, and protein concentrations were determined using BCA assay and GST fusion proteins (10 µg) and then incubated with immobilized biotinylated PAR1 ICL2 peptide for 1 h at 4°C. After washing, samples were eluted in 2x sample buffer resolved by SDS-PAGE and analyzed by immunoblotting to detect GST–ALIX association. The input, 25%, was run on an SDS-PAGE gel and stained with Coomassie to visualize proteins.

Protease K protection assay
The protease K protection assay was performed as previously described (Malerad et al., 2007), with minor modifications. Hela cells were plated in six-well culture dishes (4.0 × 10^5 cells/well), grown overnight at 37°C, and treated with or without agonist. Cells were placed on ice and incubated for 5 min with PBS, harvested, and gently permeobilized using 6.5 µg/ml digitonin. Membranes were collected by centrifugation and resuspended in buffer (100 mM K2HPO4/KH2PO4, 0.5 mM MgCl2, and 250 mM sucrose). Membranes were then divided into three aliquots either left untreated, treated with 2.5 µg/ml protease K, or treated with protease K supplemented with 0.1% Triton X-100 for 10 min at room temperature. Proteins were digested for 1 h at 4°C. Protein concentrations were determined using BCA assay and GST fusion proteins (10 µg) and then incubated with immobilized biotinylated PAR1 ICL2 peptide for 1 h at 4°C. After washing, samples were eluted in 2x sample buffer resolved by SDS-PAGE and analyzed by immunoblotting to detect GST–ALIX association. The input, 25%, was run on an SDS-PAGE gel and stained with Coomassie to visualize proteins.

RT-PCR
The first-strand cDNA was generated from mRNA extracted from either Hela or using SuperScript II reverse transcription (Invitrogen) following the manufacturer’s instructions. The RT enzyme was omitted from the cDNA synthesis reaction in the control samples. The first-strand cDNA was amplified via PCR using primer pairs specific for CHMP4A (forward 5'-GGATACCAGGCGTACACACG-3' and reverse 5'-GGAGGCAAGTTCCATCTGCTC-3'), CHMP4B (forward 5'-CCCATGACACATGGACATC-3' and reverse 5'-ACCCAGAGTGCCTCATTCTG-3'), CHMP4C (forward 5'-GACCTACAGGACACATTGCA-3' and reverse 5'-AGTCTACGAGAAGGACAC-3'). The PCR amplification products were resolved by 1.8% (wt/vol) agarose gel electrophoresis and visualized by ethidium bromide staining.

Cell surface ELISA
Hela cells were plated at 5 × 10^5 cells/well in a 24-well culture dish, grown overnight, and transfected, as previously described. After 48 h, cells were either left untreated or treated with 100 µM SFLRN (PAR1-specific agonist) for varying times at 37°C, and the amount of receptor remaining at the cell surface was determined, as previously described (Soto and Trejo, 2010). In brief, cells were fixed in 4% PFA, washed, and then incubated with monoclonal anti-EEA1, -LAMP1, or -CD63 antibodies and then incubated with biotinylated goat anti-mouse secondary antibodies conjugated to Alexa Fluor and imaged by confocal microscopy. To specifically track activated PAR1 or PAR2 from the cell surface, cells were pretreated with anti-FLAG antibody for 1 h at 4°C to ensure only surface FLAG-PAR1 or PAR2-bound antibody, stimulated with agonist for various times at 37°C, and then processed for microscopy. First, fixed cells were mounted in FluorSave reagent (EMD). The fluorochromes used were Alexa Fluor 488, 594, and 647 and GFP. Images were acquired with a disk-spinning unit confocal system (Olympus) configured with a microscope (IX81; Olympus) fitted with a PlanApo 60× oil objective (1.4 NA; Olympus) and a digital camera (ORCA-ER; Hamamatsu Photonics). Fluorescent images of 0.28-µm-thick X–Y sections were acquired at room temperature using SlideBook software (version 4.2). Data were analyzed using Prism software (version 4.0; GraphPad Software). Statistical analysis was determined, as indicated, by performing either Student’s t or two-way analysis of variance. The following protein sequences were acquired from the National Center for Biotechnology Information protein database: Rattus norvegicus (available from GenBank under accession no. AAA42274.4), Xenopus laevis (GenBank accession no. AAA18491.8), Mus musculus (GenBank accession no. AAA40438.3), Papio hamadryas (GenBank accession no. AA84191.1), Crictetus longicaudatus (GenBank accession no. AAA86747.1), Bos taurus (NCBI Protein database accession no. NP_001109656.1), Equus caballus (NCBI Protein database accession no. NP_001504007.2), Taeniopygia guttata (NCBI Protein database accession no. XP_002189106.1), Danio rerio (GenBank accession no. CAM13317.1), and Homo sapiens PAR1 (GenBank accession no. AAA36743.1) and PAR2 (GenBank accession no. AA997012.1). Sequences were aligned using ClustalX 2.1 software (Larkin et al., 2007).
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Figure S1. **PAR1 WT and OK mutant are sorted from endosomes to lysosomes after agonist stimulation.** (A) HeLa cells expressing FLAG-PAR1 WT or OK mutant were pretreated with 0.2 mM leupeptin. Cells were then incubated without (Control) or with 100 µM SFLRN (SF) for 60 min at 37°C, fixed, permeabilized, and incubated with anti-FLAG and -EEA1 antibodies. Immunolabeled cells were processed and imaged by confocal microscopy. Colocalization of PAR1 and EEA1 is revealed by the yellow color in the merged image and is representative of many cells examined in three independent experiments. Bars, 10 µm. The data (mean ± SD) represent Pearson’s correlation coefficients for quantification of colocalization that were calculated from dual-channel images of whole cells (n = 6) and were significantly different, as calculated by Student’s t test (***, P < 0.001; n = 3). (B and C) HeLa cells expressing either FLAG-PAR1 WT or OK mutant were prelabeled with anti-FLAG antibody at 4°C to label the surface cohort of receptor. Cells were warmed to 37°C and incubated for 20 min with (+SF 20 min) or without (control) 100 µM SFLRN agonist, fixed, permeabilized, and coimmunostained for LAMP1. Images are representative of multiple cells from three independent experiments. Bars, 10 µm. The data (mean ± SD) represent Pearson’s correlation coefficients for quantification of colocalization that were calculated from dual-channel images of whole cells (n = 6) and were significantly different, as calculated by Student’s t test (***, P < 0.001; n = 3).
Figure S2. Depletion of CHMP4B by individual siRNAs inhibited PAR1 degradation. HeLa cells expressing FLAG-PAR1 were transfected with either nonspecific (ns) or two individual siRNAs targeting CHMP4B, designated 1 and 2. Cells were stimulated with 100 µM SFLRN for 60 min at 37°C. The amount of PAR1 remaining was determined from an equivalent amount of cell lysates by immunoblotting (IB). Membranes were stripped and probed for endogenous CHMP4B and actin. The asterisk denotes a nonspecific band in the anti-CHMP4B immunoblot. The data (mean ± SD) are expressed as a fraction of untreated control (Ctrl) from three different experiments. The amount of PAR1 remaining in CHMP4B siRNA–treated cells was significantly different compared with nonspecific siRNA-treated cells, as determined by a two-way analysis of variance (*, P < 0.01; ***, P < 0.001; n = 3).

Figure S3. Vps4 mediates PAR1 and PAR2 lysosomal degradation. (A and B) HeLa cells expressing FLAG-PAR1 or FLAG-PAR2 were transfected with 100 nM of nonspecific (ns) or Vps4A and B SMARTpool siRNAs and then stimulated with 100 µM SFLRN or 100 µM SLIGKV at 37°C, as indicated. The amount of PAR1 or PAR2 remaining was detected by immunoblotting (IB). Cell lysates were immunoblotted with anti-Vps4 and -actin antibodies. IP, immunoprecipitation. The data (mean ± SD) are expressed as the fraction of PAR1 or PAR2 remaining compared with untreated control (Ctrl) and were analyzed by a two-way analysis of variance (PAR1: **, P < 0.01, n = 3; PAR2: ***, P < 0.001, n = 3).
Figure S4. **HA-ALIX coimmunoprecipitates with PAR1, and ALIX depletion does not affect PAR1 internalization.** (A) Untransfected (UT) HeLa cells or HeLa cells coexpressing PAR1 WT and HA-ALIX were stimulated for the indicated times with 100 µM SFLLRN at 37°C. Cell lysates were immunoprecipitated (IP) with either IgG or anti-FLAG antibodies, and immunoprecipitates were analyzed by immunoblotting (IB) using anti-HA antibodies. Cell lysates were immunoblotted with anti-HA and -actin antibodies as controls. (B) PAR1-expressing HeLa cells were cotransfected with FLAG-tagged β2-adrenergic receptor (β2AR) and either HA-ALIX or pcDNA empty vector and stimulated for 10 min with 100 µM SFLLRN at 37°C. FLAG-β2AR was immunoprecipitated with anti-FLAG antibody, and immunoprecipitates were analyzed by immunoblotting using anti-HA antibodies. Cell lysates were immunoblotted with anti-HA and -actin antibodies as controls. (C) HeLa cells expressing FLAG-PAR2 were transfected with HA-ALIX, stimulated with 100 µM SLIGKV, lysed, and immunoprecipitated with anti-FLAG antibody or IgG control, and the presence of PAR2 and ALIX was assessed by immunoblotting. (D) PAR1-expressing HeLa cells were transfected with either 100 nM of nonspecific (ns) siRNA or ALIX-specific siRNA. Cells were then prelabeled at 4°C with anti-FLAG antibody before incubation with 100 µM SFLLRN for the indicated times at 37°C. Cells were fixed, and the amount of antibody remaining on the cell surface was quantitated by ELISA. The data are expressed as the fraction of surface receptor remaining as compared with control (Ctrl) untreated cells (mean ± SD) from three independent experiments.

Figure S5. **ALIX depletion and mutation of the PAR1 YPX$_3$L motif do not affect PAR1 internalization.** (A) HeLa cells stably expressing either FLAG-tagged PAR1 WT or Y206A mutant clone 1 (C1) or 2 (C2) were prelabeled with anti-FLAG antibody at 4°C. Cells were fixed, and the amount of antibody remaining at the cell surface was determined by ELISA. The data (mean ± SD) are expressed as the absorbance determined at OD at 405 nm from three separate experiments. UT, untransfected. (B) HeLa cells stably expressing either FLAG-PAR1 WT or Y206A mutant were prelabeled with anti-FLAG antibody for 1 h at 4°C and then incubated with 100 µM SFLLRN for the indicated times at 37°C. Cells were fixed, and the amount of antibody remaining at the cell surface was determined by ELISA. The data (mean ± SD) are expressed as the fraction of cell surface receptor remaining as compared with control (Ctrl) untreated cells from three independent experiments.