We present evidence for two subpopulations of coatomer protein I vesicles, both containing high amounts of Golgi resident proteins but only minor amounts of anterograde cargo. Early Golgi proteins p24\textsubscript{2}, β\textsubscript{1}, δ\textsubscript{1}, and γ\textsubscript{3} are shown to be sorted together into vesicles that are distinct from those containing mannosidase II, a glycosidase of the medial Golgi stack, and GS28, a SNARE protein of the Golgi stack. Sorting into each vesicle population is Arf-1 and GTP hydrolysis dependent and is inhibited by aluminum and beryllium fluoride. Using synthetic peptides, we find that the cytoplasmic domain of p24\textsubscript{1} can bind Arf GTPase-activating protein (GAP)1 and cause direct inhibition of ArfGAP1-mediated GTP hydrolysis on Arf-1 bound to liposomes and Golgi membranes. We propose a two-stage reaction to explain how GTP hydrolysis constitutes a prerequisite for sorting of resident proteins, yet becomes inhibited in their presence.

**Introduction**

The cell recycles most of its constituents of the secretory pathway. This is needed to offset anterograde transport of newly synthesized proteins and lipids and is achieved via two different mechanisms, one coatomer protein (COP)*I independent and the other COPI dependent (for review see Storrie et al., 2000). Whereas COPI-independent recycling is so far only poorly understood, COPI-dependent recycling has been investigated extensively, revealing sorting motifs and recycling transport intermediates (e.g., COPI vesicles) operating throughout the pathway. One such sorting motif, the K(X)KXX present in many resident proteins of the early secretory pathway (Nilsson et al., 1989; Jackson et al., 1990), was shown to interact specifically with coatomer, the cytoplasmic coat complex of the COPI coat (Cosson and Letourneur, 1994; Letourneur et al., 1994). This was demonstrated in vitro and by yeast genetics, thus firmly linking the role of COPI vesicles to recycling. In accordance, we found recently that COPI vesicles formed in vitro contain high amounts of Golgi resident glycosylation enzymes (Lanoix et al., 1999). Upon inhibition of GTP hydrolysis, the level of resident proteins in vesicles was diminished. We also found that regardless of GTP hydrolysis, the level of anterograde cargo recovered in vesicles was low comparable to that observed in the cisternal membranes. This suggests that GTP hydrolysis by Arf-1 selectively favors incorporation of resident proteins into budding COPI vesicles. These findings are in agreement with the postulates of the cisternal maturation process where anterograde cargo is transported through cisternal progression and resident proteins recycle via COPI vesicles (for review see Glick and Malhotra, 1998).

Of the many constituents thought to recycle, the p24 family has recently received considerable attention. These reside at the ER-Golgi interface and are conserved from yeast to mammals. We showed previously that four p24 members, α\textsubscript{2}, β\textsubscript{1}, δ\textsubscript{1}, and γ\textsubscript{3} exist in a heterooligomeric complex consisting roughly of equimolar amounts of each member (Füllekrug et al., 1999). **This was demonstrated in vitro and by yeast genetics, thus firmly linking the role of COPI vesicles to recycling. In accordance, we found recently that COPI vesicles formed in vitro contain high amounts of Golgi resident glycosylation enzymes (Lanoix et al., 1999). Upon inhibition of GTP hydrolysis, the level of resident proteins in vesicles was diminished.** We also found that regardless of GTP hydrolysis, the level of anterograde cargo recovered in vesicles was low comparable to that observed in the cisternal membranes. This suggests that GTP hydrolysis by Arf-1 selectively favors incorporation of resident proteins into budding COPI vesicles. These findings are in agreement with the postulates of the cisternal maturation process where anterograde cargo is transported through cisternal progression and resident proteins recycle via COPI vesicles (for review see Glick and Malhotra, 1998).

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*Abbreviations used in this paper: CGN, cis-Golgi network; COP, coatomer protein; GAP, GTPase-activating protein; GlcNAc-T1; N-ace–tylglucosaminyltransferase I; GT-1, galactosyltransferase; KDR, KDEL receptor; Mann, mannosidase; RSA, rat serum albumin; TGN, trans-Golgi network.*

**Key words:** Golgi; COPI; recycling; p24 proteins; ArfGAP1
leave the ER. This was shown in two ways. First, mutations in residues that are required for export of one member resulted in ER arrest of all four members. Second, systematic expression of one, two, three, or four of the members in different combinations provided further evidence for complex formation as a prerequisite for ER export, most likely for entry into budding COP II vesicles (Dominguez et al., 1998; Füllekrug et al., 1999). As the co-precipitating p24 complex was revealed in Golgi membranes, it is possible that complex formation is also required for entry into COPI vesicles. This notion predicts sorting of all four p24 proteins into the same COPI vesicle. Even though all eight can be deleted in yeast without loss of cell viability or protein transport (Springer et al., 2000), p24 proteins have been abscised important functions in mammalian cells. For example, p24B1 (p23) has been suggested to serve as a coat receptor needed in the formation of retrograde COPI vesicles (Malsam et al., 1999), and likewise p24B2 (p24) has been suggested to serve as a coat receptor needed for the formation of anterograde COPI vesicles (Goldberg, 2000). This was based on the observation that cytoplasmic domain of p24B1 and p24B2 can interact directly with coatomer (Fiedler et al., 1996; Sohn et al., 1996; Dominguez et al., 1998; Goldberg, 2000). However, several resident proteins with cytoplasmic K(X)KXX motifs bind coatomer equally well (e.g., E19 and p24α1) and sometimes even better (for a comparative study see Dominguez et al., 1998). If using binding as a criteria, each coat receptor binding protein would then constitute a receptor. What sets p24 proteins apart is that cytoplasmic domains of some members can induce a conformational change in coatomer, causing it to polymerize (Reinhard et al., 1999). This is important, since coatomer is able to stimulate Arf-1–mediated GTP hydrolysis 1,000-fold in an Arf GTPase-activating protein (GAP1)–dependent fashion, at least in solution (Goldberg, 1999). A tripartite complex for optimal GTP hydrolysis was suggested. In a subsequent study, Goldberg showed that a synthetic peptide corresponding to the cytoplasmic domain of p24B2 inhibits coatomer and ArfGAP1-dependent GTP hydrolysis. Inhibition of hydrolysis was thought to occur through coatomer via its interaction with the p24B2 cytoplasmic domain. Such downmodulation of GTP hydrolysis was proposed to enable formation of priming complexes (Springer et al., 1999) where coatomer remain attached to the membrane via the resident proteins and Arf-1(G177)ArfGAP1 long enough to allow for polymerization of the COPI coat, leading to vesicle formation. However, the role of coatomer in stimulating GTP hydrolysis by Arf-1 has been challenged recently in studies using full-length myristoylated Arf-1 bound to phospholipid vesicles. Under these conditions, coatomer had no effect on ArfGAP1-dependent GTP hydrolysis on Arf-1 (Safer et al., 2000). Nevertheless, the proposed ability of p24B1 (and perhaps other Golgi resident proteins) to downmodulate ArfGAP1 activity and hence Arf-1–mediated GTP hydrolysis as a prerequisite for sorting contrasts our previous findings, showing a clear requirement for GTP hydrolysis by Arf-1 for sorting of Golgi resident glycosylation enzymes into COPI vesicles (Lanoix et al., 1999).

To investigate sorting of p24 proteins and other Golgi resident proteins into COPI vesicles and possible cargo modulation of ArfGAP1 activity, we use a modified in vitro budding assay where consumption of formed vesicles is blocked, thereby overcoming previous technical limitations. We find that p24α2, β1, δ1, and γ3 are sorted together in a GTP hydrolysis– and Arf-1–dependent manner into COPI-derived vesicles and that these vesicles are distinct from those containing mannosidase (Mann) II and GS28. We also tested for the effect of the cytoplasmic domain of p24B1 on ArfGAP1 activity. We find that on liposomes and Golgi membranes, the cytoplasmic domain peptide of p24B1 binds to ArfGAP1 and strongly inhibits Arf-1–mediated GTP hydrolysis directly. Analysis with peptides bearing amino acid substitutions suggests that inhibition is mediated through the previously identified F/YXXXXF/Y motif that is present in some p24 proteins (Dominguez et al., 1998).

Results

GTP-dependent sorting of p24 proteins into COPI-derived vesicles

To ensure a reproducible build-up of COPI-derived vesicles, we had previously subjected membranes to a salt wash before the budding event (Lanoix et al., 1999). A drawback of this was that esterified membranes such as the cis-Golgi network (CGN) and trans-Golgi network (TGN) tended to be lost during the washing procedure. However, performing the budding assay using nonwashed membranes often resulted in a low recovery of Mann II signal compared with that obtained when using salt-washed membranes. A likely explanation for this is that by removing peripheral components, such as NSF and α-SNAP, formed vesicles cannot readily fuse back once uncoated. To avoid vesicle fusion, we performed the budding reaction in the presence of a dominant negative mutant of α-SNAP, L294A (α-SNAPθ), which is known to effectively block NSF-dependent fusion (Barnard et al., 1997) by locking the 20S fusion complex on the membrane (McBride et al., 1999). The effect of the α-SNAPθ mutant on salt-washed and nonwashed membranes is shown in Fig. 1 A. Using salt-washed membranes, the level of Mann II in vesicles was high (~20% of that observed in Golgi membranes), whereas the level of p24 proteins was very low in both the Golgi and the vesicle fraction, which suggests that most of the CGN had been lost due to the salt wash. In contrast, when using nonwashed membranes the level of Mann II in vesicles was reduced greatly, whereas the amount of p24 proteins was now high. Upon addition of the α-SNAPθ mutant, the level of Mann II increased significantly, whereas the level of p24 proteins remained unaffected. The idea that the salt wash had removed peripheral NSF and α-SNAP, thereby preventing vesicle consumption, was supported by the lower Mann II signal upon addition of recombinant and complexed NSF/α-SNAP (Fig. 1 B). Addition of the α-SNAPθ mutant together with NSF/α-SNAPθ blocked reduction. From a technical standpoint, addition of the α-SNAPθ mutant clearly improved the recovery of resident proteins when using nonwashed membranes, permitting us to use membranes that more accurately represent the entire Golgi apparatus including the CGN and TGN.
or using mock-depleted cytosol (Mo) gave rise to comparable levels to those observed in the control using untreated cytosol (Ctr). Thus, both p24- and Mann-containing vesicles were formed in a COPI-dependent manner. We next examined to what extent anterograde cargo had been incorporated into formed vesicles. Three different cargo proteins were examined: the polymeric immunoglobulin receptor (pIgR), apolipoprotein E (ApoE), and rat serum albumin (RSA). As can be seen in Fig. 1 D, only small amounts of anterograde cargo were detected in the vesicle fraction (Mann II, p24α2, β3, and γ3 are also shown for comparison). This suggests that in the total pool of vesicles, only minor amounts of anterograde cargo had been incorporated. Since budding was performed under conditions where vesicle consumption is blocked, it negated the possibility that putative anterograde vesicles could have been missed if these had fused back at a higher rate than those containing resident proteins. Moreover, since addition of the α-SNAPdn mutant clearly improved the Mann II signal it argues in favor of the budding assay faithfully producing transport intermediates (e.g., vesicles) that are noncontinuous with the membrane before termination of the budding reaction. This is important, since concerns have been raised suggesting that perhaps the in vitro assay mainly registered a fragmentation event caused by subsequent salt treatments, which we use to release formed vesicles from membranes before fractionation and analysis. We conclude that COPI-derived vesicles formed in this improved budding assay carry mainly resident proteins.

### Evidence for a p24 subpopulation of COPI-derived vesicles

Since p24 proteins reside in the early part of the secretory pathway and Mann II in the Golgi stack centered around the medial cisternae (Velasco et al., 1993; Rabouille et al., 1995; Sohn et al., 1996; Rojo et al., 1997; Dominguez et al., 1998; Füllekrug et al., 1999), one would predict only a small overlap between these proteins in recycling COPI vesicles. This is reflected in the budding assay by the differential response to the α-SNAPdn mutant, improving a selective recovery of Mann II but not p24 proteins (Fig. 1 A, right). To examine this more directly, we immunosolated p24-containing vesicles using magnetic beads coated with a cytoplasmic domain antibody to p24γ3 (Füllekrug et al., 1999). Affinity purified antibody attached to magnetic beads was first tested for its ability to bind Golgi membranes (Fig. 2 A, left). After incubation, membranes bound to beads were analyzed at the ultrastructural level and for protein content by SDS-PAGE followed by Western blotting. As can be seen, large membrane structures were observed on beads only when using the p24γ3 antibody (Sp) but not on beads coated with an irrelevant control antibody (Ctr). Addition of magnetic beads to the vesicle fraction (Fig. 2 A, right) revealed binding of vesicular structures with a diameter of 50–60 nm, the expected size of uncoated COPI vesicles using the p24γ3 antibody (Sp). No vesicles were seen binding to beads coated with the control antibody (Ctr). Western blots probed with antibodies to Mann II, p24α2, β3, δ1, and γ3 showed that no preferential parts of the Golgi (Gt) had been selected for (Fig. 2 B, Gt compared with Sp). No signal could be detected when using beads coated with the control antibody (Ctr).

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**Figure 1.** Accumulation of COPI vesicles in the presence of the α-SNAPdn mutant. (A) Vesicles formed using salt-washed Golgi membranes were compared with vesicles formed using nonwashed membranes in the absence or presence of the α-SNAPdn mutant. Proteins from solubilized membranes or vesicles were separated by SDS-PAGE and subjected to Western blot analysis using specific primary antibodies to Mann II, p24α2, p24α3, and p24β; followed by ECL. Note the lower amount of Mann II in the absence of the α-SNAPdn mutant. Golgi membranes are shown in increasing amounts expressed as the percentage of starting material. (B) Vesicles were formed using salt-washed Golgi membranes in the presence or absence of exogenously added NSF/α-SNAP+ and/or the α-SNAPdn mutant. (C) Coatomer was depleted (Dp) from cytosol using specific monoclonal antibodies, recognizing native coatomer or mock (Mo) depleted using an irrelevant antibody and used in budding reactions with nonwashed membranes and the α-SNAPdn mutant. Depleted cytosol was rescued (Rs) subsequently by adding back exogenously purified coatomer and compared with vesicles formed using untreated cytosol (Ctr). (D) Vesicle budding was performed using nonwashed membranes in the presence of the α-SNAPdn mutant and tested for anterograde cargo incorporation (pIgR, RSA, and ApoE). Vesicles were also generated in the presence of an ATP depletion system (ATP-) for comparison. Proteins from solubilized membranes or vesicles were separated by SDS-PAGE and subjected to Western blot analysis and revealed by the ECL method using antibodies.

Therefore, we added the α-SNAPdn mutant into subsequent budding experiments.
Figure 2. **Immunoisolation of p24-containing vesicles reveals subpopulations of COPI vesicles.**

(A–D) Magnetic beads precoated with either an irrelevant control antibody (Ctr) or specific (Sp) antibodies to the cytoplasmic domain of p24 were incubated with nonwashed Golgi membranes (A, left, and B) or with COPI vesicles formed from such membranes in the presence of the α-SNAP\textsuperscript{dn} mutant (A, right, and C and D). Isolated membranes and vesicles were pelleted, fixed, embedded, and processed for EM or solubilized and subjected to SDS-PAGE. After transfer to nitrocellulose, Mann II, p24\textsubscript{y3}, p24\textsubscript{α2}, p24\textsubscript{δ1}, and p24\textsubscript{β1} were detected using specific antibodies followed by ECL. Vesicles remaining in the supernatant (Supn) after immunoisolation were also monitored in terms of their protein content (C, left lanes). (D) Immunoisolated vesicles were probed for the anterograde cargo marker, RSA, and compared with p24\textsubscript{y3}, p24α\textsubscript{2}, p24δ\textsubscript{1}, and p24β\textsubscript{1}. Lanes containing total Golgi (Gt) and 20% of total vesicles (V\textsubscript{tot}) used for immunoisolation are included for comparison.

In immunoisolated vesicles (Fig. 2 C, beads, Sp), the four p24 proteins were detected roughly at the same relative intensities as those seen in the total vesicle population (V\textsubscript{tot}). Thus, p24\textsubscript{y3} did not appear to segregate away from p24α\textsubscript{2}, β\textsubscript{1}, or δ\textsubscript{1}, suggesting that p24α\textsubscript{2}, β\textsubscript{1}, δ\textsubscript{1}, and γ\textsubscript{3} were present in the same COPI-derived vesicle population. A small amount of Mann II was detected in p24-containing vesicles, but as can be seen the majority remained in vesicle superna-
tant left over after immunosoliation (Fig. 2 C, supn, Sp compared with Ctr). This was also the case for GS28, a vesicle SNARE protein of the Golgi stack (Fig. 2 C, supn, Sp compared with Ctr) (Nagahama et al., 1996; Subramaniam et al., 1996; Hay et al., 1998). Next, we examined to what extent anterograde cargo was present in p24-containing vesicles. Immunisolated vesicles were probed for RSA and for comparison p24α, β, δ, and γ. Only a small amount of RSA was seen in isolated vesicles (Fig. 2 D, beads, Sp) at a comparable level to that observed in the total vesicle popula-

Figure 3. Immunolocalization of p24 proteins in cells and vesicles. (A–C) Subcellular localization of p24β (b, green) as determined by indirect immunofluorescence localization. For comparison, labeling of Mann II (red) is shown in A. The extent of overlap is shown in C. (D) Thin frozen sections of NRK cells were labeled with antibodies to p24β (10 nm gold). Gold particles were found at one side of the Golgi stack, codistributing with antibodies to p24γ (5 nm gold, arrows). (E and F) Vesicles bound to grids were labeled with antibodies against two different p24s and revealed by protein A gold conjugates. The majority of the labeled vesicles contained both p24 proteins of each combination. (G) Quantification of p24 proteins in pair-wise labeling experiments. Different antibodies and protein A gold sizes (pAG) were used. Vesicles labeled with only one type of gold particle (two or more of the same gold particle) are expressed as the percentage of single labeled (SL), and vesicles containing both types of gold particle (two or more different gold particles) are expressed as double labeled (DL).
tion (compare with Fig. 1 D), making it unlikely that COP-derived p24-containing vesicles transport anterograde cargo. The immunoisolation data suggests that p24β1 is present in vesicles together with p24α2, δ1, and γ3. Whereas the steady-state localization of p24α2, δ1, and γ3 has been mapped to the cis side of the Golgi stack at the ultrastructural level (Sohn et al., 1996; Rojo et al., 1997; Dominguez et al., 1998; Füllekrug et al., 1999), Golgi localization of p24β1, has only been determined at the level of light microscopy (Gommel et al., 1999). Therefore, we determined the steady-state localization of p24β1 by immuno-EM. A rabbit peptide antibody was raised against the cytoplasmic domain antibodies. Since cytoplasmic domain antisera, we could not monitor this member. Two sets of representative double labeling experiments of COPI-derived vesicles, showing p24β1, δ1, and γ3 in different combinations, are shown in Fig. 3, E and F. A range of different antibody concentrations and gold particle sizes were tested. As summarized in Fig. 3 G, the majority of vesicles revealed double labeling. In summary, we conclude from the above data that at the level of the Golgi stack, p24 proteins enter budding COPI vesicles together, presumably in order to recycle back to the ER. Isolated vesicles were distinct from those containing Mann II and GS28, and neither contained significant amounts of anterograde cargo.

Peripheral punctate staining was also observed as seen previously when staining for p24α2, δ1, and γ3. In NRK cells at the ultrastructural level, p24β1 (10 nm) showed extensive colocalization with p24γ3 (5 nm, arrows) mapped previously to the cis side of the Golgi stack (Füllekrug et al., 1999). This completes the mapping of all four p24 proteins to the cis side of the Golgi stack.

The extent of different p24 proteins in the same COPI-derived vesicle was also examined using affinity purified cytoplasmic domain antibodies. Since cytoplasmic domain antibodies to p24α2, failed to produce significant labeling despite the obvious presence of this member in vesicles as determined by Western blotting, we could not monitor this member. Two sets of representative double labeling experiments of COPI-derived vesicles, showing p24β1, δ1, and γ3 in different combinations, are shown in Fig. 3, E and F. A range of different antibody concentrations and gold particle sizes were tested. As summarized in Fig. 3 G, the majority of vesicles revealed double labeling. In summary, we conclude from the above data that at the level of the Golgi stack, p24 proteins enter budding COPI vesicles together, presumably in order to recycle back to the ER. Isolated vesicles were distinct from those containing Mann II and GS28, and neither contained significant amounts of anterograde cargo.

A need for GTP hydrolysis and a role for GAP in protein sorting

We showed previously that Mann II and two glycosyltransferases, N-acetylglucosaminyltransferase I (GlcNAc-T1) and galactosyltransferase (GT-1), are sorted and concentrated into COPI vesicles in an Arf-1 GTP hydrolysis–dependent manner (Lanoix et al., 1999). Yet, resident proteins such as p24 proteins are proposed to inhibit GTP hydrolysis, thereby ensuring that coatamer can remain on the membrane in order to form “priming complexes” required for vesicle formation (Springer et al., 1999). To investigate this, we first tested whether the four p24 proteins require GTP hydrolysis by Arf-1 for incorporation into vesicles. As seen in Fig. 4 A, we observed a clear decrease for p24α2, β1, δ1, and γ3 upon addition of GTPyS, a nonhydrolyzable analogue of GTP or the GTP-

![Figure 4. A requirement for GTP hydrolysis by Arf-1. (A) Vesicles were formed in the presence of GTP, GTPyS, or Arf-1G71L. (B) Vesicles were formed in the presence of GTP, GTPyS, Befx, or AIfx. Proteins from solubilized membranes or vesicles were separated by SDS-PAGE and subjected to Western blot analysis using specific primary antibodies to Mann II, β-COP, p24γ3, p24α2, p24δ1, GS28, p24β1, and the KDR followed by ECL.](image-url)
restricted mutant of Arf-1, ArfQ71L. A similar inhibition, though less striking, was observed upon probing for the KDEL receptor (KDR). As expected, coatomer was most readily detected (monitored using monoclonal antibodies to β-COP) on vesicles generated under conditions where GTP hydrolysis was inhibited. However, a small amount of coatomer persisted on vesicles generated in the presence of GTP. This was observed consistently using our modified assay, suggesting that perhaps uncoating efficiency was somewhat lowered.

The requirement for GTP hydrolysis in sorting was further investigated using phosphate analogs, aluminum, or beryllium fluoride (AlFx or BeFx). Previous studies have highlighted the dramatic effects of these compounds in both the COPI and COPII systems. A recent study examining the dynamics of COPII coat assembly on liposomes (Antonny et al., 2001) demonstrated that BeFx can mimic the γ-phosphate of GTP on GDP bound to the small GTPase Sar1, resulting in the generation of a stable COPII complex. Other studies have shown that AlFx induced the assembly of the COPI coat (Donaldson et al., 1991), possibly due to inhibition of GTP hydrolysis (Finazzi et al., 1994). We thus tested if these fluoride complexes would affect sorting in a manner similar to that observed with GTPγS. As can be seen in Fig. 4 B, vesicles were still formed in the presence of AlFx or BeFx as evidenced from the β-COP signal, which was comparable.
to that seen upon addition of GTPγS. As with GTPγS, incorporation of Mann II, GS28, and the four p24 proteins was inhibited, thus providing further evidence for a GTP hydrolysis–dependent sorting event. We conclude that GTP hydrolysis by Arf-1 is a prerequisite for proper sorting of p24 proteins into COPI-derived vesicles.

Since GTP hydrolysis by Arf-1 is required, the observed inhibition by BeF₃ and AlF₃ suggests a possible role for ArfGAP1, a Golgi-localized Arf GAP, in the sorting process. How is this then reconciled with the proposed need for an inhibition of GAP activity (and hence GTP hydrolysis) to form priming complexes (Springer et al., 1999)? Since evidence exists in favor of cargo modulation of ArfGAP1 activity by the cytoplasmic domain of p24₁ (Goldberg, 2000; unpublished data), we tested for the ability of p24 cytoplasmic domain peptides to inhibit ArfGAP1 activity. In solution using Δ17Arf-1 in the presence of coatomer, we observed a strong inhibition in the presence of the p24β₁ peptide but not with the p24δ₁ peptide, essentially confirming previous observations (Goldberg, 2000; unpublished data). When using full-length myristoylated Arf-1 bound to phospholipid vesicles, coatomer stimulation of GAP activity is not observed (Szafer et al., 2000), whereas on Golgi membranes coatomer approximately doubles ArfGAP1 activity (Szafer et al., 2001). Therefore, it was of interest to examine the effect of p24 peptides under conditions that more closely resemble those prevailing in the cells. The result of an experiment where GAP activity on Arf-1 was monitored on liposomes in the presence of 0.2 mM p24₀₂, p24β₁, or p24δ₁ cytoplasmic domain peptides is shown in Fig. 5 A. As can be seen, addition of the p24₀₂ peptide had little if any effect on GAP activity, whereas both p24β₁ and p24δ₁ caused inhibition. Strongest inhibition was obtained with the p24β₁ peptide. To examine which amino acid residues in the p24β₁ peptide are important for inhibitory effect, we substituted two amino acids at the time throughout the cytoplasmic domain (Table I). The effect of each peptide except for the p24β₁ (RR) peptide, which could not be solubilized, is shown in Fig. 5 B. Strikingly, the p24β₁ (FF) peptide showed no inhibitory effect. Similarly, the p24β₁ (YL) peptide showed only a minor inhibitory effect, whereas p24β₁ (EV) revealed partial inhibition. No loss of inhibitory effect was seen with p24β₁ LK, VV, and the A peptide, which contained an additional alanine residue at the COOH terminus. A similar pattern was observed when using Golgi membranes in place of the liposomes (Fig. 5 C). In this experiment, Golgi membranes were preincubated with myristoylated Arf-1 and γ²–P–GTP to allow for the binding of the nucleotide to Arf-1. Nucleotide exchange was then stopped by the addition of BFA followed by addition of ArfGAP1. The decrease in the amount of membrane-bound GTP was monitored as a measure for GTP hydrolysis on Arf-1 (Szafer et al., 2001). A strong inhibition was obtained using the p24β₁ peptide at 0.2 mM. Under these conditions, neither p24₀₂ nor p24δ₁ revealed significant inhibition (unpublished data), suggesting that the inhibition on Golgi membranes was p24β₁ specific. We also examined selected p24β₁ substitution peptides. As seen with liposomes, substituting YL or FF to AA resulted in a loss of inhibition.
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hibitory activity (Fig. 5 D). Again, the p24β1 (LK) peptide was comparable to the p24α2 wild-type peptide and showed strong inhibition.

To test the functional consequence of the inhibition of GAP activity, we tested the effect of p24 peptides on sorting and vesicle formation in the vesicle-budding assay (Fig. 6 A). Vesicle formation was performed as above but in the presence of 0.1 or 0.01 mM p24α2, β1, or α2 peptides. As controls, vesicle formation was performed in the absence of peptides (two GTP controls are shown) or in the presence of HCl, which was added to the same extent to the residual amounts present in the peptide solutions (of 0.1 mM solubilized peptides). Addition of 0.1 mM p24β1 cytoplasmic domain peptide gave rise to a strong decrease in p24α2, β1, δ1, and γ2. Incorporation of Mann II was decreased also, suggesting that the p24β1 peptide acted on ArfGAP1 regardless of whether vesicles formed from early or medial-Golgi membranes. A similar but less complete inhibition was seen with the p24δ1, peptide, whereas no inhibition was observed upon addition of the p24α2 peptide. At 0.01 mM concentration, the p24β1 cytoplasmic domain peptide gave rise to a similar decrease in p24 proteins, and Mann II recovered in the vesicle fraction, whereas now the inhibition observed with the p24δ1 peptide was less obvious. Selected p24β1 substitution peptides were also examined for their ability to affect sorting and vesicle formation (Fig. 6 B). Again, substituting FF or YL to AA removed the inhibitory effect seen with the p24β1 wild-type peptide. Furthermore, when using the EV to AA substitution peptide, only a minor inhibitory effect could be seen mirroring the partial activity seen when used in the liposome based assay (compare with Fig. 5 B). It is interesting to note that both the p24β1 wild-type peptide and the LK to AA substitution peptide showed strong inhibitory effect in the assay. The amount of coatomer (revealed by a mAb to

Figure 7. GTP hydrolysis–driven sorting coupled with ArfGAP1 modulation. The model is divided into four steps from left to right and then from bottom to top. (I) GDP bound to Arf-1 attached to the membrane is replaced with GTP by Arf-1 guanine exchange factor. Cytosolic coatomer binds Arf-1GTP but is quickly released upon GTP hydrolysis by Arf-1. This step requires ArfGAP1 and is denoted in green as having a high activity (HA) on Arf-1. Resident cargo proteins bind coatomer directly through cytoplasmic domain motifs (e.g., K(X)X). In order for coatomer to capture resident proteins, coatomer first needs to be released from the membrane. This "sorting step" requires GTP hydrolysis by Arf-1. If resident cargo proteins are in addition induced to cluster (Weiss and Nilsson, 2000), coatomer is predicted to bind more strongly, thus favoring these over other resident proteins. (II) The activity of ArfGAP1 is downmodulated by captured resident cargo proteins. The rate of GTP hydrolysis by Arf-1 is as a consequence slowed down, enabling coatomer to remain on the membrane. The presence of resident cargo proteins promotes polymerization of the coat leading up to vesicle formation and budding (III). Though downmodulated in its activity, residual ArfGAP1 activity will permit Arf-1 to hydrolyze its GTP, and coatomer is released back into the cytosol. For simplicity, the release of coatomer, Arf-1, and ArfGAP1 from the vesicle is shown as one event.
the βCOP subunit) detected in the vesicle fraction was still comparable to that observed in the control (HCl but no peptide added), suggesting that vesicles still formed but that sorting had been affected. When adding the p24β₁ and p24α₂ wild-type peptides together, the amount of βCOP was reduced slightly, whereas sorting remained strongly inhibited. Taken together, this indicates that those p24β peptides that inhibit sorting in the vesicle budding assay and show inhibitory effects in ArfGAP1 activity assays (Fig. 5) do so by interacting with ArfGAP1 directly.

To test for a direct interaction between cytoplasmic domain peptides and ArfGAP1, we monitored ArfGAP1 binding to cytoplasmic domain peptides of six different p24 proteins and the E19 adenovirus protein and RER1, the latter two included as controls. Peptides were attached to Sepharose beads as described previously (Dominguez et al., 1998) and incubated with rat liver cytosol or with purified components. Binding was examined at two different conditions, in the presence of 230 Na mM/40 mM KCl or 115 mM KAc (Lanoix et al., 1999). Cytosolic ArfGAP1 could be seen binding strongly to the cytoplasmic domains peptide of p24β₁ and to a lesser extent to p24δ₂ (Fig. 6 C) at both high and low salt concentrations. Minor binding was also observed to two cytoplasmic domain peptides of the γ subfamily, γ₁ and γ₄. The other peptides showed little or no binding. We also monitored binding of Arf-1. No binding of Arf-1 could be revealed to either of the peptides using cytosol or purified Arf-1 (unpublished data). The p24β₁ substitution peptides were also tested using purified full-length recombinant ArfGAP1 expressed and purified from insect cells. All substitution peptides except for p24β₁FF and RR revealed ArfGAP1 binding. This included the YL, LK, and EV peptide, which showed binding but to a lower extent than that seen in the wild-type peptide. Thus, the inability of the p24β₁ FF peptide to bind ArfGAP1 corresponds well with its lack of inhibitory activity in the assays described in Fig. 5 and Fig. 6, A and B. This suggests that the two phenylalanines (FF) possibly in combination with upstream amino acids such as tyrosine (Y) and leucin (L) mediate the observed inhibitory activity of the p24β₁ cytoplasmic domain peptide. Since we could not assay for the RR peptide in the two ArfGAP1 activity assays or in the vesicle budding assay due to insolubility problems of the peptide, we cannot exclude the possibility that the two arginines might also play a role.

The need for GTP hydrolysis by Arf-1 and a downregulation of ArfGAP1 activity is best explained in a two-stage mechanism (Fig. 7, I and II). First, release of coatomer is required for rebinding to membrane patches occupied by resident proteins. Coatomer units are predicted here to detach resident proteins, ArfGAP1 activity is lowered as a consequence of cargo modulation (denoted in green and HA for high activity). Wherever coatomer units successfully capture resident proteins, ArfGAP1 activity is lowered as a consequence of cargo modulation (denoted in red and LA for low activity). We presented evidence in favor of a direct interaction between ArfGAP1 and cytoplasmic domain peptides of p24β₁ (and to a lesser extent, p24δ₁) and their ability to downmodulate ArfGAP1 activity on membranes in the absence of coatomer. However, we do not rule out an involvement of coatomer also in this process. Thus, the cytoplasmic domain of the resident protein is shown as interacting both with ArfGAP1 and with coatomer, and the two latter are also shown as interacting. A binding release cycle (Fig. 7 I) coupled with downmodulation of ArfGAP1 by resident cargo (Fig. 7 II) will lead to the enrichment of “priming complexes.” Polymerization of the COPI coat (Fig. 7 III) is then promoted by the presence of high concentration of resident proteins (Reinhard et al., 1999): at least four cytoplasmic domains of p24β₁/coatomer unit were required for optimal coat polymerization. The vesicle can then bud and although downmodulated, ArfGAP1 will stimulate GTP hydrolysis by Arf-1, resulting in coat release (Fig. 7 IV).

Discussion

Multiple populations of COPI-derived vesicles

The cisternal maturation model predicts that anterograde cargo remains in cisternal membranes and that cisternae mature in a cis-to-trans direction, whereas resident proteins move in the opposite direction via COPI vesicles. All anterograde cargo is predicted to move at the same rate, whereas resident proteins are sampled at different stages and concentrated into budding COPI vesicles. In the vesicular transport model, each cisterna instead constitutes a stable compartment, and anterograde cargo move via COPI anterograde vesicles from cisterna to cisterna in a cis-to-trans direction. In an attempt to merge the two models, Pelham and Rothman (2000) proposed recently that vesicles containing either anterograde or retrograde cargo would bud and fuse randomly with adjacent cisternae. At the same time, cisternae would progress slowly forward. The prediction of this model is that neither anterograde nor retrograde cargo should be concentrated into budding COPI vesicles. This prediction is clearly not born out by our findings where incorporation of resident proteins is favored over anterograde cargo, a notion in direct support of a cisternal maturation scenario. Selective sorting of resident proteins into more than one population of COPI vesicles is supported by our findings that Mann II/GS28 and the four p24 proteins, α₂, β₁, δ₁, and γ₃, segregate into distinct subpopulations, neither of which contain significant amounts of anterograde cargo. We monitored three different anterograde cargo markers in the vesicle population, one membrane bound (pIgR) and two soluble (RSA and ApoE), all of which distribute equally across the Golgi stack en route to the cell surface. The two soluble cargo proteins are highly abundant in rat liver, which underscores the selectivity of the observed sorting process in favor of resident proteins. Of interest to note is that GS28 is represented poorly in the vesicle subpopulation containing p24 proteins. This is consistent with the observation that upon shifting cells to 15°C to block ER to Golgi transport (Saraste and Kuismanen, 1984) GS28 does not redistribute to peripheral structures (Hay et al., 1998). Under these conditions, proteins such as p24α₂, β₁, δ₁, and γ₃, KDR and ERG153/58 of the CGN/cis cisternae do redistribute to peripheral structures, indicating that GS28 resides in later cisternae (e.g., medial and trans). It will be interesting to see if p24-containing vesicles contain SNARE proteins, such as membrin,
rsec22b, and rbet1, and whether syntaxin 5 is present in both vesicle populations. The latter has been shown to bind GS28 or membrin/rsec22b/rbet1, yielding distinct complexes (Hay et al., 1998). Using immunosolated p24-containing vesicles, it should also be possible to investigate their preferred target membranes (e.g., the ER and/or CGN) (Love et al., 1998).

Vesicle formation and concentration of resident proteins upon sorting
As in our previous study (Lanoix et al., 1999), vesicles generated in vitro using rat liver Golgi and cytosol were uncoated. However, some coatomer was detected on vesicles in this study but much less than that would have been observed if these had been formed under conditions where GTP hydrolysis was inhibited (Fig. 4). We term these COPI-derived vesicles, since they form in a COPI-dependent manner, and display the expected size of 50–60 nm but have lost most of their original coat. We rule out that isolated vesicles represent cisternal membrane fragments caused by mechanical fragmentation, since in the presence of an ATP depletion system, in the absence of coatomer, or at +4°C vesicles could not be detected (Lanoix et al., 1999). Likely, GTP hydrolysis by Arf-1 induces formation of domains enriched in resident proteins in a coatomer-dependent manner. We favor this possibility, since such sorting domains would constitute assemblies of priming complexes required for vesicle budding (Fig. 7; Springer et al., 1999). Also, since the Mann II signal increased upon addition of the α-SNAPΔα mutant (Fig. 1B) to inhibit NSF mediated fusion it argues that discontinuous transport intermediates (e.g., vesicles) indeed form. Under these conditions, we can further rule out the possibility that putative anterograde vesicles could have been missed if these had a shorter half-life than retrograde vesicles.

In the previous study, we observed that Mann II was concentrated about fourfold over cisternal membranes as judged by Western blotting (after correcting for phospholipids in vesicles and membranes) or by immuno-EM (comparing the linear density of Mann II) of vesicles formed under conditions where GTP hydrolysis was permitted or inhibited by GTPγS (Lanoix et al., 1999). A higher concentration effect (up to 10-fold) was estimated by enzymatic activity assays for GlcNAc-T1 and GT-1. Whereas Mann II is very abundant (∼1.5% of total Golgi proteins) in the Golgi, both GlcNAc-T1 and GT-1 represent ∼0.1% of Golgi resident proteins. The high degree of concentration of GlcNAc-T1 and GT-1 was questioned recently. It was argued that concentration of resident proteins into vesicles would be unlikely, since Golgi cisternae already contain high amounts of resident proteins (Pelham and Rothman, 2000). This is based on the estimate that both ER and Golgi membranes contain 30,000–40,000 protein molecules per square micron (Quinn et al., 1984). If so, a concentration factor of three to four times might seem more feasible than one order of magnitude. The idea that there is room for concentration is supported by recent findings by Luini and coworkers, revealing extensive plasticity in Golgi stacks. These can be seen shrinking or enlarging as a consequence of temperature shifts without losing their resident protein content (Luini, A., personal communication; Griffiths et al., 1989). How-
what was observed when using GTPγS. Therefore, the inhibitory effects of BeF₃ and AlF₃ suggested a direct role for ArfGAP1 (and perhaps other GAPs acting on Arf-1) in protein sorting. Experimental evidence in favor of this comes from work by Goldberg (2000) where he monitored Arf-1 activity in the presence of synthetic peptides corresponding to the cytoplasmic domains of p24 proteins. He showed in a coatomer-dependent assay that GTP hydrolysis by Arf-1 together with ArfGAP1 was downregulated in the presence of a cytoplasmic domain peptide of p24β, in solution. He interpreted this as a conformational change in coatomer caused upon binding to the cytoplasmic domain peptide, which resulted in a reduced ability of coatomer to stimulate GAP activity on Arf-1. However, a coatomer-stimulated GTP hydrolysis through ArfGAP1 was challenged recently, showing that if using full-length Arf-1, coatomer stimulation was undetected (Szafer et al., 2000). In the study presented here, we observed a clear inhibitory role of the p24β cytoplasmic domain peptide but independent of coatomer, both on liposomes and Golgi membranes. Therefore, we suggest that this cytoplasmic domain peptide can exert its ability to inhibit GTP hydrolysis through a direct interaction with ArfGAP1 rather than through coatomer. The region mediating ArfGAP1 binding and inhibitory activity corresponds well to the previously identified cytoplasmic domain motif, Y/FXXXYY/F, in p24β, for Sec23/24 binding (Dominguez et al., 1998). In that study, p24β was examined, since this peptide binds both to coatomer and Sec23/24. However, p24β was shown to bind Sec23/24 stronger than p24β, similar to what we observe with ArfGAP1. Since Sec23 is the GAP for the small GTPase Sar1 of the COPII coat (Yoshihisa et al., 1993), it is likely that both p24β and p24β have evolved to bind GAPs to ensure incorporation into COPII and COPI vesicles, allowing p24 proteins to operate at the ER-to-Golgi interface. The ability of p24β to downregulate ArfGAP1 activity raises the question if resident proteins that recycle from later compartments can also modulate ArfGAP1. Since the p24β cytoplasmic domain peptide inhibited both Mann II and the p24 proteins and the fact that the Arf-1Q71L mutant blocks sorting infers that ArfGAP1 is required for sorting into both vesicle populations. Therefore, one would predict that resident proteins other than p24β should be able to bind and modulate ArfGAP1 activity for protein sorting. If so, this would offer an attractive mechanism ensuring that vesicles could only form when cargo proteins are present. As proposed by Schekman and coworkers (Springer et al., 1999), downregulation of GAP activity slowing down GTP hydrolysis by Arf-1 (or Sar1 for the COPII coat) will allow coatomer to reside longer on the membrane (Fig. 7). Such a “priming complex” would then be able to interact laterally with other priming complexes to form a lattice, serving as a vesicle-budding site. This model also predicts that vesicle formation is coupled with the presence of cargo, a notion supported by recent findings examining sorting of vesicular stomatitis virus G protein into COPII vesicles (Aridor et al., 1999). The important addition to the scheme proposed by Springer et al. (1999) is that GTP hydrolysis is initially required for the sorting event and a subsequent downmodulation of GAP activity for the formation of the priming complex.

In conclusion, we have presented evidence in favor of two populations of COPI-derived vesicles formed from Golgi membranes. Both contain predominantly Golgi resident proteins and only minor amounts of anterograde cargo. Sorting into each vesicle population requires GTP hydrolysis by Arf-1. Subsequently, the ability of ArfGAP1 to stimulate Arf-1-mediated GTP hydrolysis is decreased by the resident proteins, thereby stabilizing coatomer on the membrane, allowing the COPI coat to polymerize.

Materials and methods

Reagents

Antipain aprotonin, apyrase benzamidine, beryllium chloride, GSH, GTP, leupeptin, pepstatin, PMFS, potassium acetate, polyvinylpyrrolidione (PVP-40T), soybean trypsin inhibitor, and Tween 20 were from Sigma-Aldrich. Aluminum chloride was from ICN Biomedicals. ATP, creatine phosphate, and creatine kinase were from Roche. 1,4-dithiothreitol and Hepes were from BioMol GmbH. PD-10 columns, sucrose, and the ECL detection kit were from Amersham Pharmacia Biotech. 30% (wt/vol) acrylamide/0.8% (wt/vol) bis-acrylamide solution was from Bio-Rad Laboratories. Sodium cacodylate was from BDH Chemicals. Glutaraldehyde, glycerol, and potassium fluoride were from Merck. Ethanol was from Kemetyl. Osmium tetroxide was from Electron Microscopy Sciences. Uranyl acetate was from Janssen. Defatted dry milk was from De-Vau-Ge Gesundkostwerk GmbH. Protran nitrocellulose membranes (0.45 μm) were from Schleicher and Schuell. X-OMat XAR5 films were from Eastman Kodak Co. Dynabeads M-500 subcellular was purchased from Dynal.

Antibodies

Polyclonal antibodies against α-, β-, and γ1 have been described previously (Dominguez et al., 1998; Fullekrug et al., 1999). Rabbit polyclonal antibodies to the cytoplasmic domain of p24β were raised against a synthetic peptide (QFYYKLKRFEVRVY) conjugated to KLH and affinity purified using the same peptide coupled to acrylamide support. Rabbit polyclonal antibodies to ArfGAP1 were raised against truncated recombinant His-tagged ArfGAP1 (1–257) (Makler et al., 1995) expressed in bacteria. Antibodies were affinity purified over ΔArfGAP1 recombinant attached to nickel beads (QIAGEN). Polyclonal antibody against Mann II was purchased from K. Moremen (University of Georgia, Athens, Greece). Polyclonal antibody against plgR and Apo E were gifts from A. Hubbard (The Johns Hopkins University, Baltimore, MD) and John Bergeron (McGill University, Montreal, Canada), respectively. Affinity purified mAb CMA10 was a gift from J. Rothman (Memorial Sloan Kettering Cancer Center, New York, NY), and GS28 was purchased from BD Transduction Laboratories. Polyclonal rabbit and mouse anti-IgC antibodies were purchased from Sigma-Aldrich. Polyclonal sheep antibodies to RSA was from Biodes International. RPR-2labeled polyclonal antibodies against rabbit, mouse, and sheep were purchased from Dianova.

Production and purification of NSF, His-tagged α-SNAPm, α-SNAPΔn mutant, and GAP

Recombinant His-tagged NSF, α-SNAPm, and α-SNAPΔn mutant were purified on Ni-NTA agarose as described (Barnard et al., 1997). Recombinant proteins were desalted using a PD-10 column preequilibrated in 20 mM Hepes, pH 7.2, 150 mM NaCl, 1 mM MgCl₂, 5% glycerol, 1 mM GSH, and 1 mM ATP. In the case of NSF, 5 mM ATP. Recombinant His-tagged α-SNAPΔn mutant was aliquoted and snap frozen directly after elution and diluted in boiling buffer at 37°C before use. NSF was complexed with α-SNAPΔn before addition as described previously (Otter-Nilsson et al., 1999). Recombinant His-tagged ΔArfGAP1 containing amino acids 1–257 was purified as described (Cukiernik et al., 1995). Purified fractions were pooled, and glycerol was added (10% final) before aliquoting, snap freezing, and storing at –80°C. Full-length His-tagged ArfGAP1 inserted into baculovirus and infected into Sf9 cells was purified essentially as described (Huber et al., 2001).

Membrane and cytosol preparation

Highly purified rat liver Golgi membranes and rat liver cytosol were prepared and treated as described (Slusarewicz et al., 1994; Lanoix et al., 1999). Typically, the purification was 100-fold over homogenate. Cytosol was subjected to centrifugation at 41,000 rpm for 60 min at 4°C using a Ti45 rotor. Supernatant was then aliquoted, snap frozen, and stored at
30°C. For the budding assay, 50 μl of frozen rat liver cytosol was thawed and diluted with 1 ml of budding buffer (25 mM Hepes, pH 7.0, 115 mM potassium acetate, 2.5 mM MgCl₂). The cytosol was then centrifuged at 60,000 rpm for 60 min at +4°C using a TLA 100.2 rotor. The supernatant was further cleared by centrifugation at 13,000 rpm for 15 min at 4°C. Immunodepletion of cytosolic cofactor was performed as described previously (Lanoix et al., 1999).

**Vesicle budding assay**

The standard assay mixture contained 40 μg of either salt-washed or non-washed Golgi membranes, 5 mg/ml of rat liver cytosol, an ATP-regenerat-
ing system (1 mM ATP, 5 mM creatine phosphate, and 10 U/ml creatine kinase), 1 mM DTT, a protease inhibitor cocktail, and 0.5 mM GTP in a final volume of 250 μl. To inhibit NSF-dependent fusion, 0.5 μM recombinant His6-tagged α-SNAP mutant was added. The mixture was incubated for 30 min at 37°C and put at +4°C. The salt concentration was then raised to 250 mM to release bound vesicles from membranes, and the mixtures were centrifuged at 13,000 rpm for 15 min at 4°C. The medium speed supernatants containing vesicles were loaded on a two-step sucrose cushion made up of 50 μl of 30% wt/wt sucrose and 5 μl of 30% wt/wt sucrose and centrifuged at 45,000 rpm for 45 min at +4°C using a TLA 45 rotor. Vesicles were found at the 30%/50% sucrose interface and were resuspended in 300 μl. Immediately after the assay was performed, vesicles were found at the 30%/50% sucrose interface and were resuspended, pooled, aliquoted, snap frozen, and stored at −80°C.

Dynamobeads were coupled to goat anti–rabbit polyclonal antibodies according to the manufacturers description. For immunosolubilization of Golgi membranes, Eppendorf tubes containing 7.5 μl Dynamobeads precoated with α-rabbit IgG were incubated with 1 μg of affinity purified α-p24gp antibody or with 1 μg of control antibody for 90 min at 4°C on a rotating wheel in 200 μl buffer A (budding buffer, 0.5 mg/ml fat-free dry milk, and 0.5 mM MgCl₂/PVP-40T). beads were then washed three times in buffer A to remove unbound antibodies and resuspended in 250 μl buffer A. Golgi membranes (9.6 μg) and protease inhibitors were then added to each tube and incubated for 4 h at 4°C. Beads were finally washed three times with 500 μl of buffer B (budding buffer, 2 mg/ml fat-free dry milk, and 1 mg/ml PVP-40T), and Golgi membranes bound to the beads were analyzed by SDS-PAGE and Western blotting or processed for EM. For immunosolubilization of vesicles, beads were prepared as above but 15 μl of beads/tube was used instead and incubated with 80 μl of vesicles and protease inhibitors in a final volume of 300 μl of buffer C (budding buffer, 0.5 mg/ml of nonfat dry milk, 0.5 mg/ml PVP-40T, and 0.5 M KCl) for 4 h at 4°C. Beads were then washed three times with 500 μl of buffer C and bound material was analyzed by SDS-PAGE and Western blotting or processed for EM as described below.

**GAP activity assays**

GTP hydrolysis by myristoylated Arf-1 in the presence of phospholipid vesicles (40% phosphatidylcholine, 30% phosphatidyleserine, and 30% phosphatidylethanolamine) was assayed as described (Huber et al., 2001) except that KCl was added to give 200 mM GTP hydrolysis by Golgi membranes bound ARF1 was assayed as described (Szafer et al., 2001). Briefly, rat liver Golgi membranes were washed with 0.75 M KCl to remove endogenous GAP; this treatment also removed cofactor that was present in the membrane preparation. The membranes were incubated at 30°C with 2 μM bovine myristoylated ARF1 in a GTP-loading mixture consisting of 4 μM [γ-32P]GTP (~200,000 cpm), 0.18 M KCl, 0.2 mM MgCl₂, 25 mM Tris, pH 7.5, 1 mM DTT, a protease inhibitor cocktail, and 1 mM ATP plus ATP-regenerating system (5 mM phosphocreatine and 50 μg/ml creatine phosphokinase) in a final volume of 50 μl. After 15 min, nucleotide exchange was stopped by the addition of 0.3 mM brefeldin A from a

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