Peroxisome Biogenesis: Involvement of ARF and Coatomer

Michael Passreiter,* Markus Anton,* Dorothee Lay,* Rainer Frank,‡ Cordula Harter,* Felix T. Wieland,* Karin Gorgas,§ and Wilhelm W. Just*

*Biochemie-Zentrum, ‡Zentrum für Molekülare Biologie Heidelberg, and §Institut für Anatomie und Zellbiologie II, Universität Heidelberg, D-69120 Heidelberg, Germany

Abstract. Peroxosomal membrane protein (Pmp)26p (RnPex11p), a major constituent of induced rat liver peroxisomal membrane, was found to contain a COOH-terminal, cytoplasmically exposed consensus dilsine motif with the potential to bind coatomer. Biochemical as well as immunocytochemical evidence is presented showing that peroxisomes incubated with preparations of bovine brain or rat liver cytosol recruit ADP-ribosylation factor (ARF) and coatomer in a strictly guanosine 5’-O-(3-thiotriphosphate)–dependent manner. Consistent with this observation, ldlF cells expressing a temperature-sensitive mutant version of the e-subunit of coatomer exhibit elongated tubular peroxisomes possibly due to impaired vesiculation at the nonpermissive temperature. Since overexpression of Pex11p in Chinese hamster ovary wild-type cells causes proliferation of peroxisomes, these data suggest that Pex11p plays an important role in peroxisome biogenesis by supporting ARF- and coatomer-dependent vesiculation of the organelles.

Regarding the biogenesis of peroxisomes various concepts have been postulated. Based on morphological data that demonstrated close spatial relationships between peroxisomes and the ER, Novikoff and Novikoff (44) favored the idea that new peroxisomes are formed by budding and fission from the ER. However, a series of biochemical studies initiated by de Duve and coworkers (36, 51) in the early 1970s, focusing on the biogenetic route of catalase as a peroxisomal marker, did not reveal an ER involvement in the import of catalase. Subsequent findings of Goldman and Blobel (19) and particularly the group of Lazarow and coworkers (52, 54) confirmed this view demonstrating that peroxisomal matrix proteins, such as catalase, urate oxidase, and enzymes of the peroxisomal β-oxidation pathway, are synthesized on free polyribosomes and thus are imported posttranslationally. Accordingly, Goldman and Blobel (19) postulated a model in which peroxisomal matrix proteins are found in nascent peroxisomes, whereas peroxisomal membrane proteins (Pmps) are sorted to the peroxisomes via the ER. However, when Fujiki et al. (16) demonstrated that Pmp22p, a major constituent of the peroxisomal membrane is synthesized on membrane-free polyribosomes, these authors no longer considered ER involvement but, instead, proposed an autonomous mechanism of peroxisome formation (37).

Very recently, this view has again been questioned by studies on Pex15p, a phosphorylated peroxisomal membrane protein (Pmp) of Saccharomyces cerevisiae and a chimeric product of Pex3p and catalase in the yeast Hansenula polymorpha (4, 14). Overexpression of both of these polypeptides was reported to cause remarkable induction of multimembrane layers reminiscent of the ER. These observations again may ascribe a distinct role to the ER in the biogenesis of peroxisomes.

As our knowledge on membrane vesiculation has increased considerably within the last few years, we have learned that, with only a few exceptions (34), protein coats are required to shape membranes into vesicles. Therefore, irrespective of whether formation of new peroxisomes occurs by an autonomous or endomembrane system-derived process, both most likely may implicate coat protein-mediated membrane vesiculation. The protein coats identified so far are the clathrin coat involved in endocytosis and vesiculation of the trans-Golgi net work (50) as well as the coat proteins (COP) I and COP II (56, 57, 60). Although still a matter of debate, COP I–coated vesicles are believed to mediate anterograde intra-Golgi transport and retrograde Golgi to ER transport, whereas COP II–coated vesicles bud from the ER and likely transport cargo to the ER-Golgi intermediate compartment (ERGIC; references 3, 9, 59). Assembly and membrane binding of clathrin is

1. Abbreviations used in this paper: ARF, ADP-ribosylation factor; COP, coat protein; GDP-βS, guanosine 5’-O-(2-thiodiphosphate); GTP-γS, guanosine 5’-O-(3-thiotriphosphate); Pmp, peroxisomal membrane protein; PTS, peroxisomal targeting signal; PVDF, polyvinylidene difluoride; RT-PCR, reverse transcriptase PCR; SLO, streptolysin O; ERGIC, ER Golgi intermediate compartment.
mediated by adaptor proteins that, like clathrin, are recruited from a soluble pool (50). Formation of COP I– and COP II–coated vesicles, on the other hand, requires binding of ADP-ribosylation factor 1 (ARF) and SAR1, respectively, small GTPases that initiate coat assembly in their GTP-bound state (5, 61).

We have investigated the structure and function of major components of rat liver peroxisomal membranes and the mechanism of their membrane integration (10, 24, 29, 32, 49). In the course of these studies we noticed by thyroïd hormone induction of a membrane protein, Pmp26p, and concomittant abundance of organelles with a diameter of <0.2 μm (24, 30). Since these observations indicated a function of Pmp26p in peroxisome biogenesis and proliferation, we cloned and sequenced the Pmp26p-cDNA from a rat liver cDNA library. Here we describe the molecular structure and membrane topology of Pmp26p. Interestingly, we found a COOH-terminal dileucine motif exposed toward the cytoplasm. Such motifs have been shown to be involved in binding coatomer and may help to generate vesicles for the retrieval of ER resident transmembrane polypeptides from the ERGIC back to the ER (8, 38).

In studies with purified rat liver peroxisomes and permeabilized hepatocytes, we show a GTP-γS-dependent recruitment of ARF and coatomer to the peroxisomal membrane as well as a change in peroxisome morphology of a cell line defective in one of the coatomer subunits. Our results suggest that ARF and coatomer are involved in peroxisome biogenesis.

Materials and Methods

Molecular Biology

Isolated peroxisomnal membranes of clofibrate-induced rat liver peroxisomes were subjected to SDS-PAGE and the polypeptides blotted onto polyvinylidene difluoride (PVDF) membranes. Pex11p was excised from the membrane and the tryptic fragments were analyzed by HPLC and microsequencing. The following peptide sequences were identified: (1) AF(I)QATEQSIQATDLVPR; (2) NLETSVSTGR; (3) SVGLTSGIN; (4) NFE(C)DILIPLN. According to the sequence of peptide 1, two decapeptides (SIQAT) not encoded by the primers. A 35-mer oligonucleotide of (4) NFE(C)DILIPLN. According to the sequence of peptide 1, two de-

Binding of Coatomer and ARF to Rat Liver Peroxisomes

Cytosol from bovine brain was isolated as described (70) except that fresh unfrozen tissue was used. The same procedure was applied for the isolation of cytosol from rat liver. These cytosol preparations usually had a protein content of ~40 mg/ml. To study binding of coatomer and ARF, the organelles (250 μg) were incubated with 20 mg bovine brain cytosol (10 mg rat liver cytosol) and 20–50 μM GTP-γS (guanosine 5'-O-[3-thiodiphosphate]) or GDP-βS (guanosine 5'-O-[2-thiodiphosphate]) in a total volume of 3 ml essentially as described (39). After incubations, peroxi-

Isolation of Subcellular Organelles and Membrane Topology of Pex11p

Male Wistar rats weighing 120–150 g were treated with clofibrate (0.5%) or trifluoroacetate (TFA, 1%), both added to the chow for 10 consecutive days. Liver peroxisomes and mitochondria were isolated by isopycnic cen-

Binding of Coatomer to Synthetic Peptides

The coupling of peptides to thiopeoproyl–Sepharose was performed via an NH2-terminal cysteine residue and followed quantitatively. Equal molar amounts of each coupled peptide were used in the coatomer binding as-

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at 4°C. After incubation, the Sepharose beads were washed twice with high salt buffer and three times with 25 mM Tris-HCl, pH 7.4, 100 mM NaCl, 1 mM EDTA, 0.5% NP-40, and finally with 25 mM Tris-HCl, pH 7.4, by low speed centrifugation. The bound material was eluted with 4% SDS, 5% mercaptoethanol, 10 mM Tris-HCl, pH 6.8, and analyzed for the presence of α- and β-COP by SDS-PAGE and immunoblotting.

**Light and Electron Microscopy**

CHO wild-type cells and mutant ldlF cells were grown as described (21, 22, 53). Immunofluorescence staining of peroxisomes was performed as described previously using anti-Pmp69 peptide antiserum (53). Tissue samples of liver induced with clofibrate or trifluoroacetate were fixed by perfusion and embedded in LR-White (41). Ultrathin sections were incubated for 24 h with the polyclonal anti-Pex11p antiserum affinity purified against a COOH-terminal Pex11p tail peptide. The first antibody was visualized by 14-nm protein A–gold on sections that were stained with uranyl acetate and lead citrate.

For preembedding immuno gold labeling, isolated peroxisomes were primed with bovine brain cytosol in the presence of GTP-γS or GDP-βS as described above. The organelles were washed and incubated with the first antibodies at 37°C for 30 min and at 10°C for 4 h and with the gold-labeled second antibodies for 2 h at 4°C. Washing was performed by pelleting the organelles at 15,000 g for 10 min onto a 55% wt/wt sucrose cushion and resuspending the pelleted organelles in 0.25 M sucrose, 25 mM glycyglycine, pH 7.4, 1 mM EDTA. The final pellets were fixed for 30 min on ice with 2.5% glutaraldehyde in 0.1 M cacodylate buffer, pH 7.6 containing 0.05% CaCl2, rinsed in buffer and embedded in agar. The agar-embedded specimens were processed by the osmium-tannic acid postfixation method as described (62).

Transmission electron microscopy after DAB-staining of catalse and Epon embedding was done as previously described (20).

**Results**

**Molecular Characterization and Membrane Topology of Pex11p**

We cloned the cDNA encoding Pex11p from a rat liver λgt10 cDNA library. The cDNA-derived polypeptide sequence contains 246 amino acid residues with a calculated molecular weight of 27,922 D (Fig. 1). Hydropathy analysis (33) as well as the use of the ProteinPredict program (55) revealed two putative transmembrane spanning sections in Pex11p (amino acid residues 85–104 and 218–238) the first exhibiting the characteristics of an amphipathic α-helix with the polar residues of Arg93, Tyr96, and Asp100 positioned to one side of the helix. The presence of transmembrane domains within Pex11p is compatible with its complete resistance to extraction by sodium carbonate (24), a frequently used criterium indicating membrane integration. Computer search revealed amino acid sequence homology to the peroxin Pex11p, represented by Pmp27p of Saccharomyces cerevisiae and Pmp30/31p of Candida boidinii (15, 58), with a similarity of 49% and an identity of 25% between Pmp26p and ScPmp27p. This weak but significant identity is spread over the entire molecule, indicating a certain degree of evolutionary conservation of the gene. Although there may be differences between Pmp26p and yeast Pex11p, such as membrane topology (40) and topogenic signals (see below), the obvious homology in amino acid sequence suggests that Pmp26p is the rat ortholog of the Pex11p family and therefore, we will name it Pex11p (RnPex11p; reference 11).

By two different approaches we studied the membrane topology of Pex11p. First, the molecule was tagged at the COOH terminus with a c-myc epitope and the tagged polypeptide, Pex11p-Cmyc, expressed in AT3 cells (results not shown). Peroxisomal localization was demonstrated by colocalizing Pex11p-Cmyc with Pmp69p, which served as a peroxisomal membrane marker. When these cells were differentially permeabilized by digitonin, a monoclonal anti-myc antibody visualized the protein tag. Since digitonin effectively permeabilizes the plasma membrane but leaves peroxisomes impermeable for the antibody (64), this result indicates that the myc epitope in Pex11p may be exposed toward the cytoplasm.

Second, intact, isolated peroxisomes were treated with low concentrations of exogenously added subtilisin, and the membrane-associated cleavage products were analyzed by SDS-PAGE and Western blotting. Using a polyclonal antiserum against Pex11p, we observed the uncleaved polypeptide as well as one major fragment of 18 kD. An antiserum directed against the COOH-terminal KXKXX dilysine motif was underlined in bold. Peroxisomal localization was demonstrated by colocalizing Pex11p-Cmyc with Pmp69p, which served as a peroxisomal membrane marker. When these cells were differentially permeabilized by digitonin, a monoclonal anti-myc antibody visualized the protein tag. Since digitonin effectively permeabilizes the plasma membrane but leaves peroxisomes impermeable for the antibody (64), this result indicates that the myc epitope in Pex11p may be exposed toward the cytoplasm.

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![Image](https://www.journalarticle.com/article/fig1.jpg)

**Figure 1.** Nucleotide and nucleotide-derived amino acid sequence of rat liver Pex11p-cDNA. Two putative transmembrane spans, as revealed by the Kyte-Doolittle algorithm (33) and the ProteinPredict program (55) are shaded. The consensus PTS2 sequence and the consensus-like sequence of a mPTS are underlined by a double and a single broken line, respectively. The COOH-terminal KKKXX dilysine motif is underlined in bold. These sequence data are available from GenBank/EMBL/DDBJ under accession number AJ224120.
was not the case, these proteolysis experiments, in agreement with the immunofluorescence data on the epitope-tagged Pex11p, suggest that Pex11p is inserted into the membrane by two transmembrane domains and that both the NH₂ and COOH termini face the cytoplasm (Fig. 2 B).

The amino acid residues of positions 16–24 contain the exact consensus sequence of peroxisomal targeting signal 2 (PTS2), originally described in rat liver peroxisomal prethiolase (46) and later on in several other peroxisomal matrix enzymes of different species (67). The presence of a PTS2 in ScPmp27p remains to be proven, because the published consensus motif does not fit with amino acid residue 8 (Y instead of H/Q) of this peptide sequence. In addition to the PTS2, Pex11p contains a sequence in a loop domain between the two transmembrane spans that is strikingly similar but not identical to a peroxisomal membrane targeting signal (mPTS) recently identified in Pmp47p of Candida boidinii (13).

Rat Liver Peroxisomes Bind Coatomer and ARF

As revealed by the sequence data, the COOH terminus of Pex11p carries a dlysine motif of the general type KKKXX. Nilsson et al. (43) first described this motif and demonstrated its function in ER retention of integral membrane proteins. The motif that consists of two lysine residues positioned COOH-terminally at −3 and at either −4 or −5 was subsequently shown to be essential for coatomer binding to Golgi membranes, facilitating the retrieval of ER resident proteins from the ER-Golgi intermediate compartment back to the ER (7, 8, 38).

The presence of this motif in a peroxisomal membrane protein at a site accessible from the cytoplasm prompted us to investigate the ability of peroxisomes to bind coatomer. To this end, we incubated highly purified peroxisomes in the presence of bovine brain cytosol and GTP-γS. Control incubations were performed without cytosol and by re-placing GTP-γS for GDP-βS. The reisolated peroxisomes were analyzed by Western blotting for binding of the various coatomer subunits. As shown in Fig. 3, specific association of coatomer subunits was only detected when both cytosol and GTP-γS were present in the incubations. All seven coatomer subunits were found to be associated with the peroxisomal membrane.

The observed GTP-γS dependence of coatomer binding to peroxisomes suggested an involvement of ARF. ARF belongs to the family of small GTPases and was shown to trigger Golgi-derived vesicle budding and uncoating (61). Therefore, we tested binding of ARF to peroxisomes by Western blotting of organelles reisolated from incubations with cytosol and GTP-γS or GDP-βS. Bound ARF, which was identified using an antiserum directed against ARF 1, was recognized on reisolated peroxisomes only in those incubations containing both cytosol and GTP-γS (Fig. 3). These peroxisomes exactly cosedimented with coatomer and ARF upon isopycnic centrifugation in a Nycodenz density gradient suggesting tight binding of coatomer and ARF to the organelles.

Most critical for the interpretation of these results is the degree of purity of the isolated peroxisomes, particularly with respect to Golgi contamination. According to a previously published protocol we isolated highly purified peroxisomes with catalase activity enriched ~50-55-fold over the crude homogenate. In these peroxisomal preparations, using a sensitive radioactive assay, galactosyltransferase activity was not detectable (25). Based on the activities of

![Figure 2. Membrane topology of Pex11p. (A) Treatment of intact isolated rat liver peroxisomes (200 μg) with subtilisin (1 μg) shortened Pex11p to a 18-kD fragment that is recognized by the anti-Pex11p antiserum raised against the entire Pex11p (anti-Pex11p) but not by an antibody directed against its COOH-terminal peptide (anti-C-term). The characteristic fragmentation of Pex11p is only obtained with intact peroxisomes and does not occur in the presence of Triton X-100 (TX-100). The antipeptide antiserum cross-reacted with an unidentified 23-kD peroxisomal polypeptide (arrowhead). (B) Proposed membrane topology of Pex11p. The polypeptide is inserted into the peroxisomal membrane by two hydrophobic transmembrane spans exposing the NH₂ and COOH termini to the cytoplasm. mPTS, peroxisomal membrane targeting signal.

![Figure 3. GTP-γS-dependent binding of coatomer and ARF to isolated rat liver peroxisomes. Peroxisomes (250 μg) were incubated with bovine brain cytosol (20 mg) in the presence of GTP-γS or GDP-βS (50 μM). Controls were run without peroxisomes and/or without cytosol. After incubation the organelles were recovered by centrifugation and 10-μg aliquots were subjected to SDS-PAGE and immunoblotting using monospecific antibodies against the seven coatomer subunits and ARF 1. The immunoreactivities of the different anti-COP antibodies against isolated bovine brain coatomer and recombinant ARF 1 are shown on the separate lane.](image-url)
membranes and peroxisomes (Pox) were separated by SDS-PAGE and visualized by immunoblotting using antiserum directed against Golgi P23 and Pmp69p, respectively. Note that the antipeptide representing the COOH-terminal tail of rat peroxisomal acyl-CoA oxidase carrying a PTS1 (CRYHLK-PLQSKL) were unable to bind coatomer (Fig. 7, lanes 3 and 5). As controls, the COOH-terminal octapeptide of ScPmp27p (CMQDMWKAT) that contains one lysine residue at position −3, and an undecapeptide representing the COOH-terminal tail of rat peroxisomal acyl-CoA oxidase carrying a PTS1 (CRYHLK-PLOSKL) were unable to bind coatomer (Fig. 7, lanes 5 and 6). In lane 1, 10% of the cytosol present in a binding assay is analyzed. These results provide evidence that the COOH-terminal tail of Pex11p is directly involved in coatomer binding.

Specific localization of Pex11p to the peroxisomal membrane was also shown by postembedding immunoelectron microscopy of rat liver sections obtained from animals treated with peroxisomal proliferators (Fig. 8, A and B). Compared with untreated liver in which peroxisomes are only scarcely labeled, the labeling density increased remarkably after induction of the peroxisomal compartment. Whereas Pex11p in most peroxisomes exhibited a

### Table 1. Activity of Glucosylceramide- and Sphingomyelin-Synthase in Purified Rat Liver Golgi and Peroxisome Fractions

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<th>Peroxisomes</th>
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<tr>
<td>GlCer-Synthase [nmol min⁻¹ mg⁻¹]</td>
<td>ND</td>
<td>765 × 10⁻³</td>
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<tr>
<td>SM-Synthase [nmol min⁻¹ mg⁻¹]</td>
<td>0.141 × 10⁻³</td>
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rather uniform membrane distribution, in some others it appeared to be concentrated in clusters (Fig. 8 B). Based on the idea of coatomer-mediated peroxisomal vesiculation, clustering of Pex11p might precede budding. We also analyzed in vitro peroxisomal coatomer binding by preembedding immunogold labeling using the mouse monoclonal antibody CM1A10 alone (Fig. 8, C–E) or in combination with an anti-Pmp69p peptide antiserum (Fig. 8 F). Whereas the peroxisomal marker, Pmp69p (decorated with 6-nm gold particles), uniformly labels the organellar membrane, coatomer (decorated with 12-nm gold particles) is detected on some peroxisomes in cap-like patches (Fig. 8 C) as well as on budding and vesiculated structures (Fig. 8, D–F). This characteristic pattern was predominately observed when peroxisomes were incubated in the presence of cytosol and GTP-γS, and not when GDP-βS replaced GTP-γS.

**Phenotypic Changes of Peroxisome Morphology by Overexpression of Pex11p or Functional Inactivation of Coatomer**

The presence of a KXXXX motif in Pex11p and the ability of the corresponding peptide to bind coatomer in vitro led us to assume an interaction of coatomer with Pex11p in vivo. Therefore, we transfected CHO cells with Pex11p-cDNA and isolated several stably transfected cell clones. Using immunological techniques, we then analyzed control cells transfected with vector containing no insert (clone LC11) and Pex11p-cDNA transfecants (clone SE5) for their content of Pex11p as well as their peroxisomal phenotype. Overexpression of Pex11p was demonstrated by immunoblotting, as shown in Fig. 9 A. However, the degree of overexpression was hardly determined with accuracy, since the amount of Pex11p in the control clone LC11 was extremely low. Comparative visualization of the peroxisomal compartment of LC11 and SE5 cells by immunofluorescence and electron microscopy showed an increase in number and a decrease in size of SE5 peroxisomes (Fig. 9, B and C). Quantitative evaluation revealed twice the number of peroxisomes in SE5 cells, demonstrating that proliferation had occurred.

If coatomer is involved in peroxisomal vesiculation, as suggested by the phenotypic change of peroxisomes upon overexpression of Pex11p, a defect in coatomer function would be expected to block vesiculation, causing an enlargement of individual peroxisomes. The temperature-sensitive ldlF CHO mutant, recently established by Guo et al. (21, 22), contains a point mutation in e-COP (Glu251 to Lys251) resulting in an instability of this coatomer subunit at the nonpermissive temperature of 39.5°C. As visualized by immunofluorescence, ldlF cells, exposed for 24 h to this temperature, exhibited a dramatic change in the morphology of the Golgi apparatus and peroxisomes. The Golgi apparatus disappeared (not shown) and dissociated into
vesicular structures (see Fig. 10 B). Peroxisomes instead of being spherical and highly dispersed were heavily clustered (Fig. 9, D and E) and appeared as strikingly elongated tubules consistent with impaired peroxisomal vesiculation. The peroxisomal morphology of wild-type CHO cells kept at the nonpermissive temperature for the same time span was indistinguishable from normal controls (not shown).

Fine structural analysis largely confirmed the data obtained by immunofluorescence and in addition provided insight into details of the peroxisomal compartment in this mutant cell line. At permissive temperature, peroxisomes appear as small round or rod-shaped particles (~150 nm in mean diameter) that are scattered throughout the cytoplasm, though a few are always present near the Golgi apparatus (Fig. 10 A, arrowhead). At nonpermissive temperature, peroxisomes are tubular and tortuous, frequently exceeding 1 μm in length (Fig. 10, B–E). They occur isolated or in clusters (Fig. 10, B and C), the majority intimately associated to smooth ER cisternae. Occasionally, they are arranged in parallel forming rows or stacks (Fig. 10, C–F) that are located at the periphery of lipid vacuoles (Fig. 10 D) or near the nucleus (Fig. 10, E and F). Continuities between the perinuclear cisternae and ER (Fig. 10 F) are frequently found developing into characteristic ER–peroxisome clusters that are also easily identified at the light microscopic level (Fig. 9 D).

Discussion

Membrane Topology and Intracellular Localization of Pex11p

We have characterized RnPex11p, an integral peroxisomal membrane protein with an NH₂-terminal PTS2 and a COOH-terminal d lysine motif both oriented to the cytoplasm, and a putative luminal mPTS sequence. At present it is not clear which signal is responsible for correct peroxisomal targeting of Pex11p. The PTS2 exactly matches the consensus sequence (67) and is located 15 amino acids distant from the NH₂-terminal methionine, quite similar as in rat thiolase B (46). Its presence in a peroxisomal membrane protein is highly unusual and thus, its functional significance has to be proved. Our data on membrane integration and intracellular location of Pex11p indicate that it is directly inserted into the peroxisomal membrane because (a) sequence comparison with typical ER targeting signal peptides did not reveal an ER signal sequence in the Pex11p cDNA-derived structure (69), (b) the in vitro translation product of Pex11p on SDS gels has the same molecular mass as mature Pex11p, and (c) is not inserted into ER membranes neither co- nor posttranslationally (results not shown), but is inserted posttranslationally into peroxisomal membranes.

Specificity of Coatomer Binding to Peroxisomes

The following observations demonstrate specificity of coatomer recruitment to peroxisomes.

First, coatomer binding is strictly dependent on GTP-γS and does not occur with GDP-βS that is assumed to render ARF in its inactive state. This not only holds for isolated peroxisomes but also for peroxisomes in a permeabilized cell system. After binding, both coatomer and ARF co沉淀d in a Nycodenz gradient with peroxisomes, suggesting their close physical association. In mammalian tissues at least six distinct ARFs have been identified so far that are highly conserved and function at distinct intracellular locations (27, 42, 45). Our observation that peroxisomes recruit more coatomer from liver cytosol than from brain cytosol might indicate at least one peroxisome-specific cytosolic factor, because liver contains far more per...
oxisomes than brain. Moreover, cytosol prepared from livers of rats treated with peroxisome proliferators that strongly increase the number of hepatic peroxisomes, is about twice as active in delivering coatomer to peroxisomes as normal rat liver cytosol (result not shown). The cytosolic factor might be a peroxisome-specific subtype of ARF that cross-reacts with the polyclonal antibody against ARF1 used in this study. This ARF subtype remains to be identified. However, at present we cannot exclude the possibility that additional GTP-binding proteins are involved that might be activated by GTP-γS.

Second, protease-pretreated peroxisomes have completely lost their coatomer binding capacity suggesting that binding is mediated by at least one peroxisomal membrane factor (Fig. 7A), most likely the cytosolic COOH-terminal domain of Pex11p that in vitro binds coatomer efficiently (Fig. 7B).

Third, mitochondria and ER-derived microsomal vesicles are unable to bind coatomer or bind it with much lower efficiency than peroxisomes, respectively (Fig. 5, A and B). Since the microsomal preparations used for these assays still contained Golgi membranes, the observed residual microsomal coatomer binding activity might well be due to the presence of this contamination.

Based on protein content Golgi membranes are about five times more efficient in recruiting coatomer from the
cytosol than peroxisomes. This may be explained by different amounts of organelles used: whereas the protein to phospholipid ratio of highly purified Golgi fractions on a mg scale was analyzed to be 1.4, that of peroxisomes was 9 (Brügger, B., personal communication). If the amount of peroxisomes and Golgi used for the assays is based on phospholipid rather than protein content (which may reflect more accurately comparable amounts of membranes) then one equivalent of peroxisomal membrane binds approximately the same amount of coatomer as one equivalent of Golgi membrane.

Peroxisomal binding of coatomer does not seem to involve subspecies of the coat complex other than those that mediate biogenesis of Golgi-derived COP I–coated vesicles. The complete set of COPs is recruited to the peroxisomes, different from the binding of subcomplexes as Aniento et al. (1) have suggested on endosomal vesicles.

### Peroxisome Biogenesis

There is general agreement that biological membranes cannot be synthesized de novo (47), but are derived from existing membranes. As mentioned, cells are equipped with various protein coats that mediate membrane budding and vesiculation (50, 56, 57, 60). The way peroxisomes are formed is being a matter of continuous discussion during the last 20 years. A variety of models have been forwarded, and most recently, the ER has again been invoked as a peroxisomal precursor organelle (4, 14). Our finding of an inducible membrane protein in peroxisomes that binds to coatomer, together with a GTP-γS–dependent recruitment to the peroxisomal membrane of ARF and the coatomer complex strongly indicates that coatomer is involved in peroxisomal biogenesis. Coatomer may either function in the formation of vesicles that would retrieve ER resident membrane proteins escaped from the ER (provided that the ER is a donor organelle, indeed), and/or in fission of peroxisomes to generate nucleating centers for the growth of new organelles. Consistent with this view are (a) the phenotypic changes of the peroxisomal compartment after overexpression of Pex11p or functional inactivation of coatomer, as described here, and (b) previous observations of a peroxisome population of lower equilibrium density but with protein import competence strikingly exceeding that of mature peroxisomes (26, 28, 31).

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