Solitary and Repetitive Binding Motifs for the AP2 Complex $\alpha$-Appendage in Amphiphysin and Other Accessory Proteins$^{*,3}$

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Adaptor protein (AP) complexes bind to transmembrane proteins destined for internalization and to membrane lipids, so linking cargo to the accessory internalization machinery. This machinery interacts with the appendage domains of APs, which have platform and β-sandwich subdomains, forming the binding surfaces for interacting proteins. Proteins that interact with the subdomains do so via short motifs, usually found in regions of low structural complexity of the interacting proteins. So far, up to four motifs have been identified that bind to and partially compete for at least two sites on each of the appendage domains of the AP2 complex. Motifs in individual accessory proteins, their sequential arrangement into motif domains, and partial competition for binding sites on the appendage domains coordinate the formation of endocytic complexes in a temporal and spatial manner. In this work, we examine the dominant interaction sequence in amphiphysin, a synapse-enriched accessory protein, which generates membrane curvature and recruits the scission protein dynamin to the necks of coated pits, for the platform subdomain of the α-appendage. The motif domain of amphiphysin1 contains one copy of each of a DX(F/W) and FXDXF motif. We find that the FXDXF motif is the main determinant for the high affinity interaction with the α-adaptin appendage. We describe the optimal sequence of the FXDXF motif using thermodynamic and structural data and show how sequence variation controls the affinities of these motifs for the α-appendage.

Clathrin-mediated endocytosis is the process whereby proteins and lipids destined for internalization from the plasma membrane are packaged into vesicles with the aid of a clathrin coat. Purified coated vesicles from brain contain three major components as follows: clathrin, AP180, and AP2 complexes (1–3). Clathrin triskelia oligomerize to provide the scaffold around the forming vesicle (and can form similar cages in solution (4)). With its terminal domain, clathrin interacts with other endocytic proteins, including the AP2 complex, AP180, epsin, disabled-2 (Dab2), and amphiphysin. These interactions are mediated via short motifs; for example, clathrin binds to amphiphysin through motifs such as LLDLD or PWXXW (5, 6). Because oligomeric clathrin presents an array of binding sites for these motifs, it serves as a network hub, organizing binding partners within the lattice. The AP complexes, as well as many accessory proteins and alternative cargo adaptors such as AP180, Dab2, epsin, and amphiphysin, recruit clathrin to PtdIns(4,5)P$_2$-rich areas in the membrane and promote its polymerization into a lattice. Because of its significant number of interaction partners, another key hub in the endocytic interactome is the AP2 complex (7–9). It consists of four subunits (α, β2, μ2, and ε2) and forms a stable heterotetramer in solution (10). Using electron microscopy it was shown that the AP2 complex can be subdivided into the following: (i) a trunk domain, which interacts with cargo proteins and PtdIns(4,5)P$_2$, and (ii) two appendage domains made from the C termini of the α- and β-subunits, which interact with a large number of accessory proteins by binding to short motifs in these proteins. For example, the α-adaptin appendage binds to DX(F/W), FXDXF, WX(W/F/W), and FXFXFXL motifs (7, 11–16). These can be highly clustered in motif domains of the accessory proteins.
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where they are also frequently found close to clathrin-binding motifs. The appendage domains are connected to the trunk domain by flexible linkers, which lack a defined secondary structure in solution.

Although the AP2 appendages are only 16% identical in terms of their sequences, they are structurally very similar (12, 17). We and others have previously proposed that both the α- and β2-appendage domains bind to DX(F/W) motifs in accessory proteins (7, 8, 12, 18). The DX(F/W) motifs on accessory proteins are often found in proline-rich regions. For example, rat epsin1 has nine DPW motifs, and the majority of these are found in a proline-rich stretch of 105 amino acids, a region that by CD spectroscopy has no obvious structure (19). Human Eps15 contains 15 DPF and two other DXF motifs in a stretch of 230 amino acids. These motifs may allow clustering of the AP2 complexes at the endocytic assembly zones and enhance the binding to PtdIns(4,5)P2-containing membranes (8, 20). DX(F/W) motifs bind to sites on the platform subdomains of the appendages, centered around a hydrophobic pocket (Trp-840 in α; Trp-841 in β2) (12, 17) in a tight turn conformation (18). In the study by Brett et al. (18), the authors also found a secondary binding site for DPW motifs on the β-sandwich subdomain of the α-appendage. More importantly, they found that an FEDNF peptide from amphiphysin binds to the top of the α-appendage using the site around Trp-840 but in a different conformation by inserting the first Phe residue into the hydrophobic pocket. It was therefore proposed that FXDXF is a general high affinity binding motif for the α-adaptin appendage.

Recently, a fourth binding motif for the α-adaptin appendage has been identified in the proteins NCEP, stonin, synaptopasin, connedenn, and others (15, 21–23). The binding motif consensus WX(F/W) resembles the second clathrin-binding motif PWXXW, but the proline residue seems to mediate the discrimination between the binding partners.

Recently, we showed how multiple adaptin-binding motifs provide an avidity effect where the overall apparent affinities for AP2 complexes will depend on the type, number, and spacing of binding motifs as well as the clustering of available appendage domains (7, 8). The unclustered cytoplasmic AP2 complex has single α- and β2-appendage domains, whereas in the coated pit there will be many such domains from clustered AP2 complexes. However, when AP2 complexes are bound to polymerized clathrin, the β2-adaptin appendage domain is predicted to be largely occupied by clathrin, and steric hindrance is thought to exclude most accessory proteins. AP2 complexes at the edge of coated pits, where there is a lower concentration of clathrin, are predicted to still be free to bind the full complement of accessory proteins. The complement of accessory proteins bound to AP2 complexes in the cytosol is again proposed to be different (8). Thus, Eps15 has been shown to be restricted to the edges of a nascent coated pit as its interaction with AP2 adaptors is displaced by clathrin (24, 25). A similar scenario applies for amphiphysin1, which contains an FXDXF, a DPF, and a DLW motif, the latter two of which overlap with two clathrin-binding motifs (Fig. 1A). As a result, amphiphysin would also be primarily localized to the edges of the invaginating pit, ending up at the neck of the nascent vesicle. This would be a convenient way for amphiphysin to ensure that its C-termi-
GST-Amph1AB was not cleaved to prevent degradation of the protein. Myc-tagged proteins (pCMV-myc) were used for expression in COS-7 fibroblasts. The appendage domain of human β2-adaptin (residues 701–937) was expressed in BL21 cells as an N-terminal His6 fusion protein (in pET-15b) and purified by passage over nickel-nitrilotriacetic acid, followed by Q-Sepharose and gel filtration chromatography. Mutations were generated by PCR using overlapping primers incorporating the base pair changes.

**Transfections, Antibodies, and Cell Extracts**—COS-7 cells were transfected using GeneJuice (Novagen) according to the manufacturer’s protocol. Overexpressed Amph1AB was detected using a polyclonal anti-Myc antibody (Cell Signaling, green in merged images). The endogenous AP2 complex was detected using a Sigma monoclonal antibody (Cell Signaling). Cells were imaged using a Bio-Rad Radiance confocal system. For extracts, two 70-mm dishes of COS cells were scraped in 1 ml of phosphate-buffered saline + 0.1% Triton X-100, or one rat brain was homogenized in 10 ml of phosphate-buffered saline + 0.1% Triton X-100 and cleared by centrifugation.

**Pull Downs from COS-7 Cell or Rat Brain Extracts with GST Appendages**—For interaction experiments, the extracts described above were incubated with 30–50 μg of GST fusion protein on glutathione-Sepharose beads for 1 h at 4 °C, and then the bead-bound proteins were washed four times with 150 mM NaCl, 20 mM HEPES, pH 7.4, 2 mM DTT, protease inhibitors, and 0.1% Triton X-100. Interaction partners were analyzed by SDS-PAGE and Western blotting. All experiments were repeated three to five times. The α- and δ-adaptin and amphiphysin1 were detected using monoclonal antibodies from BD Biosciences, and β1,2- and γ-adaptin were detected with monoclonal antibodies from Sigma.

**Isothermal Titration Calorimetry**—Binding of peptides and proteins to α- and β2-adaptin appendage domains was investigated by isothermal titration calorimetry (30) using a VP-ITC (MicroCal Inc.). All experiments were performed in 100 mM HEPES, pH 7.4, 50 mM NaCl, 2 mM DTT at 10 °C unless otherwise stated. The peptides or proteins were injected from a syringe in 40–50 steps up to a 3–4-fold molar excess. The cell contained 1.36 ml of protein solution, and typically the ligand was added in steps of 4–8 μl every 3.5 min. Concentrations were chosen so that the binding partners in the cell were at least 5-fold higher than the estimated dissociation constant, if possible. The ligands in the syringe were again at least 10-fold more concentrated. Titration curves were fitted to the data using ORIGIN (supplied by the manufacturer) yielding the stoichiometry N, the binary equilibrium constant Ks (= K1−1), and the enthalpy of binding ΔH. The entropy of binding ΔS was calculated from the relationship ∆G = −RTlnKs and the Gibbs-Helmholtz equation. The values were averaged from two to three titrations. Protein concentrations were determined by measuring the A280. Peptides were purchased at >95% purity from the Institute of Biomolecular Sciences, University of Southampton, UK, and weighed on an analytical balance. Where possible, peptide concentrations were verified by measuring A280 or A230. The resulting errors on the concentrations are estimated to be <10% for the proteins and the peptides.

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Unless otherwise stated, the values for the stoichiometry N were within this error region around N = 1.

**Co-crystallography and Structure Determination**—Co-crystals of α-adaptin appendage and the synaptojanin WVXF peptide were grown by hanging-drop vapor diffusion against a reservoir containing conditions centered around 1.2 M ammonium sulfate, 3% isopropyl alcohol, and 0.05 M sodium citrate. Hinge drops were 2 μl and contained 22 μM α-adaptin appendage and 277.5 μM synaptojanin WVXF peptide (sequence NPKG-WVTFEFEE). Crystals were obtained after incubation for ~1 week at 18 °C. To obtain crystals containing peptides bound to the top side, α-adaptin appendage-WVXF co-crystals were soaked in a solution of mother liquor containing amphiphysin1 FEDNFVP peptide. Crystals were cryo-protected by transfer to Paretone-N (Hampton Research) and were flash-cooled in liquid nitrogen. Data to 1.6 Å were collected at 100 K at Station 9.6 SRS Daresbury, UK. Crystals were monoclinic and belonged to space group C2 (a = 146.6 Å, b = 67.3 Å, c = 39.7 Å, β = 94.53°). Data collection statistics are shown in supplemental Table 1. Reflections were integrated using MOSFLM (31) and were scaled using the CCP4 suite of crystallographic software (32). A difference Fourier, calculated using our model of the α-appendage bound to the WVXF peptide, revealed beautiful density for the amphiphysin peptide. The model was completed using COOT (33) and O (34) and was refined using REFMAC5 (35). The validated coordinates and structure factors for the crystal structure containing the synaptojanin WVXF and the amphiphysin1 FEDNFVP have been deposited in the Protein Data Bank (36) (PDB code 2vj0). Figures were generated using Aesop and the peptide interaction map was generated using the output from LIGPLOT (37) as a starting point.

**RESULTS**

The region in amphiphysin1 necessary for binding to the AP2 complex has been mapped to residues 322–340, and binding is enhanced if the region is extended to 322–363 (38). This includes the FEDNF328 and the DPF359 motifs (Fig. 1A). A further extension to include the PWXXW had no additional effect on binding. Using isothermal titration calorimetry, we found that a construct from residues 1–378, which forms a dimer because of its N-terminal BAR domain (26), binds to the α-adaptin appendage with an affinity of 1.6 μM but does not interact with the β2-adaptin appendage (Fig. 1B). This affinity is very similar to the one measured for the 12-mer DNF-peptide INFFEDNFVPPEI (7). In addition, the stoichiometry of the interaction between the α-adaptin appendage and the amphiphysin protein, as well as the DNF 12-mer, is 1:1. A longer construct, residues 1–390, comprising the FXDXF, DPF, and the PWXXW motifs, had a similar affinity, although a contribution of a second very weak binding site becomes visible (data not shown). Thus, the FEDNF in amphiphysin1 is the major determinant for the binding to the α-adaptin appendage.

**Adaptor Binding by Amphiphysin via FXDNF and DPF Motifs**—We extended these observations by mutagenesis of both motifs sequentially and simultaneously and show that AP2

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* M. G. J. Ford and G. J. K. Praefcke, unpublished data.
* M. Noble, personal communication.
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![Diagram](https://example.com/diagram.png)

**FIGURE 1. Interaction of amphiphysin with appendage domains.** A, schematic representation of the domain architecture of mammalian amphiphysin. The motif domain is located between the N-terminal BAR and the C-terminal SH3 domain. The blow-up shows the sequence conservation between rat amphiphysin1 and -2. Red blocks represent the DXF motifs that were used as peptides to determine the specificity of the interaction, and yellow blocks represent clathrin-binding motifs. B, profiles of typical calorimetric titrations of the α-adaptin and β2-adaptin appendage domain into a solution of GST-amphiphysin1 (residues 1–378), at 10 °C (upper panel), and the integrated data normalized to the concentration of the appendage domain (lower panel). The fit yields a dissociation constant of 1.6 μM, ΔH of −16 kcal/mol, and ΔS of −30 cal/mol-K.

binding to the DNF motif at residue 326 is stronger than binding to the DPF at residue 357 (Fig. 2A). Mutations of both DNF and DPF motifs to SGA are even more effective than the single mutants in disrupting binding. In pulldown experiments from brain and COS-7 cell extracts, α- and β-adaptins follow the same pattern, because they are part of the same complex (AP2). We already know from Fig. 1 that amphiphysin is specific for α-adaptin. There is also no interaction of γ- and δ-adaptins with amphiphysin, showing that AP1 and AP3 complexes in COS-7 extracts do not bind to amphiphysin (Fig. 2A). From this it is clear that both motifs contribute to AP2 binding, but there is a clear difference in affinity for the α-adaptin appendage. In Amph2 the FEDAF motif is the major binding sequence for AP2 adaptors (Fig. 2C).

Given the strong effect of mutagenesis of the FXDXF motifs in amphiphysin1 and -2, we tested how well other residues might substitute (Fig. 2, B and C). The initial surprise was that FXDPF does not substitute for FXDNF but that FXDPW does. The structural basis for this is not clear, but different peptides can bind in different conformations. The FXEDNF peptide from amphiphysin and the FKDSF from synaptoplin bind in an extended conformation where the first F in this binds into the pocket formed by Phe-836, Phe-837, and Trp-840 (7, 18). This cannot be the case for most DXF(F/W) peptides that do not have an equivalent Phe residue, and the proline residue in the DP(F/W) motifs forces the peptide into a loop structure. Binding is also possible when the Asn residue in the FEDDNF motif of amphiphysin1 is replaced by Ser, Ala, Asp, or Ile, whereas Gly and Leu abolish the interaction. For amphiphysin2, we looked at a more limited set of substitutions (Fig. 2C), but again the change of FXDAF to FXDPF weakens the interaction. The FXDXF is the major binding motif of amphiphysins; however, we should be very cautious in extending this observation to other proteins that have other nonconserved residues (see below). An interesting observation was that the presence of the hinge domain of the α-adaptin appendage increased the binding of amphiphysin1 to the top binding site (Fig. 2D). This is reminiscent of the interaction of the hinge region of β-adaptin with the clathrin terminal domain. Addition of a peptide derived from the proline-rich region of dynamin did not abolish this effect so that an interaction between a proline-rich stretch in the α-hinge with the SH3 domain of amphiphysin can be ruled out (data not shown).

**Use of DXF in Vivo**—We and others have shown that overexpression of DXF domains can inhibit endocytosis (33, 39–41). In the case of amphiphysin, overexpression of the full-length protein in COS-7 cells inhibits endocytosis of transferrin (27, 38), and this can be rescued by co-expression of dynamin. Thus, part of the inhibitory phenotype is because of sequestration of dynamin. This effect can be mimicked by overexpression of the SH3 domain (42). Given that amphiphysin has a very low affinity for dynamin in solution (100–200 μM) but binds to dynamin very tightly when bound to beads implies that the clustering of amphiphysins results in a strong avidity for dynamin. Thus, if we can prevent the clustering of amphiphysin by blocking the recruitment to sites of endocytosis by mutagenesis of the DXF motifs, we should prevent the inhibitory potential of the overexpressed protein. Fig. 3A shows that overexpression of WT amphiphysin1 inhibits transferrin uptake and results in a redistribution of AP2 adaptors when compared with nontransfected control cells at the same plane of focus. Point mutants of the DNF and the DPF motifs partially rescue the transferrin uptake inhibition phenotype as well as the adaptor redistribution. The rescue is most efficient with the FXDNF+DPF double mutant (Fig. 3B). For the single mutants the FEDNF → FESGA protein shows a weaker inhibition of endocytosis than the DPF → SGA version. We conclude that both motifs of amphiphysin are indeed involved in binding AP2 adaptors in vivo. Also, as argued above, this experiment underlines that dynamin is recruited to sites of endocytosis by amphiphysin if it is clustered at active zones.

**Affinities of FXDXF Motifs**—We have shown that DPF peptides have an affinity for the α-adaptin appendage in the range of 100 μM (12). Recently, we found that the FXDXF peptides from amphiphysin1 and the 170- kDa isoform of synaptoplin have a higher affinity, in the range of 2–20 μM (7). The
the interaction of the first Phe from FXDXF motifs was tested by swapping the residues Phe and Glu before the FXDNF, and this led to a drop of the affinity to about 180 μM. Exchanging the FXDNF to FXDF or FXDSF (corresponding to the residues of human synaptotagmin1 p170) keeps the affinity below 10 μM, and exchanging to FXDAF or FXDF (corresponding to the residues of amphiphysin2 and HIP1, respectively) results in a medium affinity of about 20–30 μM. The FXDF peptide from amphiphysin2 has a similar affinity as the FXDNF to DAF exchange in amphiphysin1.

Taken together, the changes of the affinities perfectly match the order we obtained from the pulldown experiments with amphiphysin mutants (Fig. 2, B and C). All the peptides tested have a stoichiometry of 1:1 except Amph1-DPF 12-mer where two peptides bind to each appendage domain. This peptide contains an overlapping clathrin box (LLLDLD) and also contains a version of an FXXF motif that can also interact weakly with α-adaptin (7, 11).

Given the different affinities of amphiphysin peptides that all follow the FXDXF consensus motif, we looked at possible high affinity interaction motifs in other endocytic proteins by sequence comparison. A 12-mer peptide of the FXDXF in Dab2 had a very low affinity. Previously, we found weak affinities for an FXDPW peptide from epsin1, and the same applies to an FXDPF peptide from Eps15, an FXDAF peptide from AP180, and an FXDF peptide from the phospholipase A2-activating proteins (PLAA). A medium affinity was found for an FXDF peptide from mouse Eps15. However, we know that this is not dependent on the FXDXF but the overlapping presence of an FXXF, XL motif (7). Another medium affinity interaction was found for an FXDF from Huntingtin interacting protein 1 (HIP1). Recently, a variation of the FXDXF α-adaptin-binding motif has been described in the AP180 homolog clathrin assembly lymphoid myeloid leukemia protein (CALM), where the aspartic acid is replaced by a serine (43). We could not detect binding of a corresponding 12-mer peptide to the α-adaptin appendage, but changing the FXDNF in the amphiphysin1 12-mer to FESNF had only a very mild effect leading to a 3-fold decrease in affinity.

Affinities of DX(F/W) Motifs—Many accessory proteins contain multiple copies of DX(F/W) and not necessarily a high affinity FXDXF or WXXΦ motif, and some of them are still able
to interact significantly with the α-adaptin appendage. To check whether the affinity of the DPF motif of amphiphysin1 is typical also for other DX(F/W) motifs, we measured the binding of several peptides derived from Eps15, epsin1, PLAA, and Dab2 (Fig. 4, A and B). None of these peptides containing a single DX(F/W) motif bound tighter than 200 μM, and the affinities were only slightly greater in the case of double DPF peptides from Eps15 and Dab2. It is worth noting that these peptides bound with a 1:1 stoichiometry to the α-adaptin appendage implying the need for a certain distance between DX(F/W) motifs to bind simultaneously to two α-adaptin appendages.

High Resolution Structure—To better understand the interaction between the FXDX motif from amphiphysin and the α-adaptin appendage domain, we solved the structure of the core Amph1 FXDNF 7-mer peptide bound to the α-adaptin appendage at 1.6 Å resolution. The structure was obtained by soaking the FEDNFVP peptide into a crystal of the α-adaptin appendage in complex with a WVXF peptide from synaptojanin (sequence NPKGWVTFE)E to the side of the sandwich domain. An amphiphysin peptide has previously been crystallized with the α-appendage (7, 8, 12, 18), but our higher resolution allows us to analyze the interaction of the α-adaptin appendage with the peptides in greater detail (Fig. 5). The core of the sandwich subdomain-binding WVXF peptide interacts as in the previously published structure (PDB code 1W80 (7)). All residues of the amphiphysin peptide, with the exception of the side chain of Glu, are well resolved in the structure, and all except the Glu and the Pro are involved in the interaction with the α-adaptin appendage. The two bulky side chains of the Phe residues interact with the hydrophobic sites around Trp-840 and Tyr-915, as described previously. The side chain of the Glu corresponding to the first X of the FXDXF is flexible and not visible. This Glu may bond, via a water, to Arg-920 of the α-adaptin appendage, although clearly the side chain is highly flexible. An important interaction for the motif is the salt bridge between the conserved Asp and Arg-916 from the α-adaptin appendage, whereas the interaction with Arg-905 of the α-adaptin appendage determines the specificity for the X2 position.

Predictions of Trafficking Proteins That Bind Appendage Domains—Many of the endocytic proteins that bind to adaptors contain multiple copies of DX(F/W) motifs clustered in so-called motif domains. Using a specially written computer
program (Sequence Motif Search Program),\textsuperscript{10} we find that 
$\text{D}(F/W)$ motifs occur more often than expected in human, 
worm, fly, slime mold, and yeast protein nonredundant data 
bases. We found that the easiest way to filter the results with 
confidence was to search for the co-occurrence with other endo-
cytic motifs. A number of other motifs appear in endocytic pro-
teins like the $\alpha$-adaptn domain-binding motifs $\text{WVXF}$ or 
$\text{FXXFXX}$. In the clathrin terminal domain-binding motifs 
$\text{LLLDL}$ or $\text{PWXXW}$, or the Eps15-homology domain-binding 
sequence $\text{NPF}$. The program allows the user to search any subset 
(or even all) of the results for the coincidence of any motifs. For 
example, a search for a degenerate consensus motif $(F/E/D)(D/$ 
$S)(N/S/D/A/I)$, to look only for high affinity $\text{DP}$ motifs. For 
sequence $\text{NPF}$. The program allows the user to search any subset 
and the co-occurrence of a $\text{DPF}$ motif, leads 
to about 10 hits in the human data base. As well as the expected 
appearance of amphiphysin and HIP1, a MAPKKK, a tyrosine 
kinase, and a Kelch-BTB homolog were also identified. This 
program\textsuperscript{10} will facilitate the search for any novel motif-containing 
proteins across a wide range of sequenced genomes. This may be 
of interest to any investigators working in fields where short motifs 
are important binding determinants.

**DISCUSSION**

Amphiphysin fulfills a critical function in clathrin-mediated 
endocytosis by inducing curvature at the neck of a coated pit, 
while at the same time recruiting the scission molecule 
dynamin to this position (44). Amphiphysin itself is recruited to 
sites of endocytosis via its interactions with phospholipids in 
the plasma membrane (26, 28, 45), with the $\alpha$-adaptn append-
dage domain of the AP2 complex (12, 46) and the N-terminal 
domain of clathrin (5, 47). It contains only two binding motifs for 
the $\alpha$-adaptn appendage domain and interacts only weakly with 
the $\beta$-adaptn appendage domain. This is in contrast to many 
other endocytic proteins like human Eps15 with 15 DPW, epsin1 
with 9 DPW, or AP180 with 4 DPW motifs. Nevertheless, 
amphiphysin is a major AP2-binding protein (7, 27). Therefore we 
set out to investigate the molecular basis for the high affinity that 
the motifs in amphiphysin must have to achieve efficient binding.

In recent crystallization experiments, the platform subdo-
main of the $\alpha$-adaptn appendage has been proposed to bind 
ligands in two different modes. The $\text{DF}(F/W)$ motif binds with 
the Phe or Trp in a large hydrophobic pocket centered around 
Trp-840. In the second binding mode, FDXF motifs bind 
with the first Phe in the Trp-840 pocket (7, 18). In the first 
mode the proline will allow the necessary kink in the back-
bone to allow the Asp to form a hydrogen bond with the 
backbone of the peptide and also to interact with Arg-905 via 
a water. A first proposal of this mode of binding would be 
that the surrounding residues will have very little influence 
on the binding affinity.

We found that in amphiphysin1 the FDXF motif is the 
major determinant for the interaction with the $\alpha$-adaptn 
appendage domain in vitro and in vivo. This is underscored by 
the similar affinities of the DNPF 12-mer peptide and the con-
struct comprising the N-terminal BAR domain and the motif 
domain. It also confirms our previous observation that the 
FEDNF 12-mer peptide but not a FEDPF version blocks clath-
rin-mediated endocytosis in isolated nerve terminals of bipolar 
cells (48). The DPF motif is also able to interact with the 
$\alpha$-adaptn appendage domain although with an affinity that is 
at least an order of magnitude weaker than the FDXF motif.

The FDXF motif was proposed to be responsible for the 
interactions of other endocytic proteins containing this 
sequence (7, 13, 18). We showed that this is a strong binding 
motif for the $\alpha$-adaptn appendage in amphiphysin1 and the 
170-kDa isoform of synaptojanin (7); however, the generali-

\textsuperscript{10}H. T. McMahon, personal communication.
zation does not hold true for many other proteins such as Dab2, Eps15, AP180, and epsin1. In fact, by mutating this motif in the motif domain of amphiphysin1 and by titrations of peptides with different variants of this motif, we found that the fourth residue in the FXDXF motif is critical for a high affinity interaction. The interaction of this residue with the α-adaptin appendage is strong with residues like Asn, Ser, and Asp. These residues are found in motifs from amphiphysin1 and the 170-kDa isoform of synaptojanin, which have a high affinity because they can interact with the side chain of Arg-905 of the α-adaptin appendage. Small residues like Ala and Ile are also tolerated and give rise to a medium affinity, such as that observed in amphiphysin2 and HIP1. Other residues like Val or Leu weaken the interaction.

### TABLE 1

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<th>$T\Delta S$ (kcal mol$^{-1}$)</th>
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<tr>
<td>Amph1-DNF to DIF 12 mer</td>
<td>INPFEDIFVPEI</td>
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<td>-2.8</td>
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<td>Amph1-DNF to SNF 12mer</td>
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<td>Amph1-FKDNF 12mer</td>
<td>INFKDNPVPEI</td>
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<tr>
<td>Amph2-DAF 12mer</td>
<td>LSLPPDDAFVPEI</td>
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<td>-3.0</td>
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<tr>
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<td>Syjn-FKDSF*</td>
<td>LGDKDSFDLGQ</td>
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<td>LGDFEDNLQS</td>
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<tr>
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<td>DMPFCDPFTSTT</td>
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<tr>
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<td>TVDPFDQFLLPS</td>
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<tr>
<td>GAK-DLF</td>
<td>KPDLFGEFLNSD</td>
<td>&gt;300</td>
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Dissociation constants for the interactions of peptides and the α-adaptin appendage as determined by ITC at 10 °C. Note that the dissociation constant $K_d$ is the inverse of the association constant $K_a$ obtained from the binding experiments. The values for $\Delta H$ and $T\Delta S$ are given for the association reaction. The experiments marked with an asterisk have been determined previously (7).
such that the affinity is similar to a standard DP(F/W) motif. The results were confirmed in titration experiments using FXDXF peptides from different proteins (Table 1). The weak FXDXF motifs have affinities in the same range as isolated DP(F/W) motifs and may well contribute to binding when they are clustered together like in AP180, CALM, or Dab2 (12, 43, 49) or combined with a β-sandwich–binding motif like in connexin (21).

In our and other’s structural work the X2 residues function as acceptors for a hydrogen bond from Arg-905 (7, 18). The interaction with an FXDFD could even increase the contribution from this position by ionic attraction. It is not clear, however, why Ile is tolerated at this position but Val and Leu are not.

The first X in the FXDXF is very flexible in our structure, indicating looser requirements here. It may be possible that the Glu of FEDNF motifs bonds via a water to Arg-920 of the α-adaptin appendage, which is not possible for the FKDSF from human synaptojanin which was used in our previous structure.

The Asp at the third position of the FXDXF motif is highly conserved. However, recent data by Meyerholz et al. (43), as well as our Amph1 FXXSNF peptide, show that a hydrogen bonding partner like Ser is sufficient for binding to Arg-916 from the α-adaptin appendage in certain contexts.

In the case of the FXDPW motifs of epsin1, PLAA, and the FEDPW version of the amphiphysin peptide, the precise binding mode has not been conclusively resolved by our study, and further structural data are needed to clarify whether they adopt the extended FXDXF or the DP(F/W) loop conformation. Certainly, we conclude from this that there are different modes of binding centered at the large hydrophobic pocket on the α-adaptin appendage involving Phe-836, Phe-837, and Trp-840 with the surrounding charged and hydrophobic residues influencing the strength of the interactions.

We conclude that FXDXF is not a general high affinity binding motif for α-adaptin but that certain residues at the fourth position are favorable for binding (Asn, Ser, Ala, Ile, and Asp) and that additional determinants in the surrounding residues...
Classification of AP2 α-Appendage-binding Motifs

Contribute as well. Therefore, the core consensus sequence for a medium to high affinity binding motif for the α-adaptin appendage is F(E/D)(D/S)(N/S/D/AA)/F.

The affinity of the DNF 12-mer from amphiphysin I explains how this protein can be a major ligand for the AP2 complex, although it contains only two binding motifs, especially when amphiphysin dimers bind to clustered AP2 in assembly zones. Therefore, by predicting endocytic proteins only on the basis of having multiple DX(F/W) motifs, we would have missed such proteins. If DX(F/W) motifs are simply a means of ensuring recruitment to an adaptor complex, then one high affinity motif will substitute for multiple low affinity motifs, which will work rather like Velcro (8, 9, 44). Together with the WVXF motif binding to the side of the β-sandwich subdomain and the still unidentified binding site for the FXFXYL motif, the α-adaptin appendage domain is able to interact with up to four different types of motifs.

Recently, it has been reported that the N-terminal region of NECAP also interacts with FXDXF motifs with a similar affinity to the α-adaptin appendage (50). The structure of this domain revealed that it belongs to the pleckstrin homology domain superfamily, but the lipid-binding residues are not conserved. The relative affinities for FXDXF motifs from several endocytic proteins showed that the NECAP PHear binding consensus sequence differs from that of α-adaptin appendage domain. Because NECAP also interacts strongly with the side site of the α-adaptin appendage domain via its C-terminal WVXF motif, they may indeed serve as a third appendage domain of the AP2 complex.

Short sequence motifs occurring in repeats also play a role in other trafficking pathways. Well studied examples are the FG superfamily, but the lipid-binding residues are not conserved. The relative affinities for FXDXF motifs from several endocytic proteins showed that the NECAP PHear binding consensus sequence differs from that of α-adaptin appendage domain. Because NECAP also interacts strongly with the side site of the α-adaptin appendage domain via its C-terminal WVXF motif, they may indeed serve as a third appendage domain of the AP2 complex.

The relative affinities for F(E/D)(D/S)(N/S/D/AA)/F motifs with a similar affinity for clathrin (24). We and others have shown that the same mechanism is also used in AP1 and GGA-dependent trafficking from the Golgi, where FXX(F/W) motifs interact with the γ- and GGA-appendage domains (11, 14, 16, 57–59).

A further level of complexity is added by the fact that several α- or γ-appendage-binding proteins also interact with the β1- and β2-adaptin appendage domains, which are also present in the AP1 and AP2 complexes (7, 8, 11, 17, 24, 60, 61). Because the binding sites on the appendage domains and the binding motifs are at least partially overlapping, the affinity, copy number, and the relative position of the motifs determine the specific recruitment of an accessory protein to a clathrin-coated pit. Amphiphysin is the major recruiter of dynamin to the neck of a clathrin-coated pit at the plasma membrane and is specific for the α-adaptin appendage only. There should be other proteins taking over this function at the Golgi. Good candidates are sorting nexin 9 and the pacsins, which, like amphiphysin, contain BAR domains for membrane interactions and SH3 domains for dynamin recruitment.

Acknowledgments—We thank our laboratory members for fruitful discussions.

REFERENCES

Classification of AP2 α-Appendage-binding Motifs