



Cooperative regulation of extracellular signal-regulated kinase activation and cell shape change by filamin A and beta-arrestins.

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Mark G.H. Scott, Vincenzo Pierotti, Hélène Storez, Erika Lindberg, Alain Thuret, et al.. Cooperative regulation of extracellular signal-regulated kinase activation and cell shape change by filamin A and beta-arrestins.: FLNA AND β arr COOPERATE TO REGULATE ERK AND CELL SHAPE. Molecular and Cellular Biology, 2006, 26, pp.3432-45. 10.1128/MCB.26.9.3432-3445.2006 . inserm-00069767

HAL Id: inserm-00069767

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Submitted on 13 Dec 2006

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gions that give the molecule flexibility. Dimerization occurs via the carboxy-terminal repeat 24 of FLNA. Both the actin-binding and dimerization domains are required for the branching of actin filaments. FLNA interacts with a number of proteins with roles in signaling and cytoskeletal reorganization and is regulated by phosphorylation. Of particular note is the fact that FLNA binds to several members of the GPCR family, including dopamine D2/D3 (30, 31), calcium-sensing receptor (5, 20), and μ -opioid receptor (39), as well as other classes of receptors, such as the insulin receptor (19). FLNA also interacts with the Rho family GTPases Rho, Rac, Cdc42, and GTP-bound RalA (38). The p21-activated kinase 1, a downstream effector of Rac1 and Cdc42, binds and phosphorylates FLNA and is reciprocally activated by FLNA in a two-way regulatory interaction (47). Finally, like β arr, FLNA has also been implicated in MAPK signaling induced by a variety of extracellular stimuli. Indeed, FLNA can interact with the MAPK kinases MEK1 and MKK4 (34) and is phosphorylated by ribosomal S6 kinase (49), an ERK target.

Using a cytoplasmic yeast two-hybrid system (Sos recruitment system) we identified FLNA as a β arr-binding partner and have assessed here its role in GPCR-induced β arr-mediated ERK activation and cytoskeletal rearrangement. Our data indicate that FLNA and β arr cooperate to orchestrate cell shape change via a signaling pathway that involves ERK activation.

MATERIALS AND METHODS

Abbreviations. The following abbreviations are used in this paper: AT1AR, angiotensin II type 1a receptor; β arr, β -arrestin(s); CaR, calcium-sensing receptor; FLN, filamin; FLNA, filamin A; GPCR, G protein-coupled receptor; Gal4AD, Gal4 activation domain; LexABD, LexA DNA binding domain; M1MR, muscarinic M1 receptor; Sos, Son of sevenless; SRS, Sos recruitment system; GEF, guanine nucleotide exchange factors; JNK, Jun N-terminal kinase; ERK, extracellular signal-regulated kinase; MAPK, mitogen-activated protein kinase(s); MAP2K, MAPK kinase(s); mGAP, mammalian GTPase-activating protein; HA, hemagglutinin; Ura, uracil; GST, glutathione S-transferase; GFP, green fluorescent protein; YFP, yellow fluorescent protein; IgG, immunoglobulin G; ACh, acetylcholine; siRNA, small interfering RNA; RNAi, RNA interference; PBS, phosphate-buffered saline; P-ERK1/2, phospho-ERK1/2; SDS-PAGE, sodium dodecyl sulfate-polyacrylamide gel electrophoresis; and SEM, standard error of the mean.

cDNA expression constructs. (i) **Yeast two-hybrid expression vectors.** The plasmid pSosGly was generated by inserting an adaptor coding for five glycine residues in frame with and 3' to the carboxy terminus of the hSos cDNA sequence, using the NcoI and AatII sites contained in pSos (Stratagene), to reduce structural interference between the two proteins in the chimera upon expression. Subsequently, full-length β arr2 (amino acids 1 to 410) was amplified by PCR and introduced downstream of and in frame with the SosGly fusion by use of BssHII and SalI sites to create pSosGly β arr2. A series of pSosGly β arr2 C-terminal truncations was created by introducing stop codons at various places in the β arr2 cDNA within pSosGly β arr2 by use of a QuikChange mutagenesis kit (Stratagene). By use of this methodology, pSosGly β arr2 Δ C4 (coding for amino acids 1 to 392 of β arr2), pSosGly β arr2 Δ C3 (amino acids 1 to 380), pSosGly β arr2 Δ C2 (amino acids 1 to 359), pSosGly β arr2 Δ C1 (amino acids 1 to 337), and pSosGly β arr2 Δ C (amino acids 1 to 316) were generated.

Plasmids for expression of FLNA(22-24), containing amino acids 2363 to 2647 of FLNA, fused to the Gal4AD or LexABD were constructed by excising FLNA(22-24) from pMyr-FLNA(22-24) obtained in the SRS screen (see below) by use of EcoRI and XhoI sites and insertion into EcoRI/XhoI sites of pGAD-GE or EcoRI/SalI sites of pLex10, respectively. To generate β arr1 and β arr2 fused to the Gal4AD, full-length β arr were amplified by PCR and cloned into pGAD-GE using XhoI/XbaI sites. Similarly, β arr2 was amplified by PCR and inserted into the SalI site of pLex10 to create a LexABD- β arr2 hybrid. pLex-Ras and pGAD-Raf have been described previously (42) and were kindly provided by S. Benichou (Institut Cochin, Paris, France).

(ii) **Bacterial expression vectors.** To allow the production of a bacterial FLNA fusion protein for use in pulldown experiments, pHis₆-TAT-HA-FLNA(22-24) was generated by cloning the EcoRI/XhoI fragment of FLNA(22-24) into pTAT-HA (a kind gift from S. Dowdy, HHMI, Washington University School of Medicine) between KpnI and XhoI restriction sites. β arr cDNAs were amplified by PCR and cloned into pGEX-5X-1 (Amersham) by use of PspAI/XhoI (for β arr1) or SalI/NotI (for β arr2) sites to allow the production of GST- β arr fusion proteins.

(iii) **Mammalian expression vectors.** pMyc-FLNA(22-24) and pFLAG-FLNA(22-24) were generated by excising FLNA(22-24) cDNA from pMyr-FLNA(22-24) by use of EcoRI and XhoI sites and inserting it in frame to and downstream of Myc and FLAG tags in pCMVTag3B and pCMVTag2B (Stratagene), respectively, by use of the same sites. cDNAs corresponding to amino acids 2363 to 2554, 2363 to 2522, 2386 to 2647, and 2427 to 2647 of FLNA were amplified by PCR and cloned between EcoRI and XhoI sites in pCMVTag3B to create pMyc-FLNA(2363-2554), pMyc-FLNA(2363-2522), pMyc-FLNA(2386-2647), and pMycFLNA(2427-2647), respectively. pMyc-FLNA(22-24) alanine-scanning mutants 1 to 9 (see Fig. 4) were generated using a QuikChange mutagenesis kit.

Full-length β arr1 (amino acids 1 to 418) and full-length β arr2 were amplified by PCR; β arr1 was cloned into pCMVTag2A and β arr2 to pCMVTag3A by use of EcoRV and SalI sites to generate pFLAG- β arr1 and pMyc- β arr2, respectively. The N-terminal domain of β arr2 (amino acids 1 to 185) and the C-terminal domain of β arr2 (amino acids 186 to 410) were amplified by PCR and cloned either between the EcoRI and XhoI sites (for the N-terminal domain) or between the BamHI and SalI sites (for the C-terminal domain) of pCMVTag3B to create pMyc- β arr2N(1-185) and pMyc- β arr2C(186-410), respectively. The integrity of all constructs was verified by nucleotide sequencing (MWG or Institut Cochin sequencing facility). Sequences of all primers used are available on request.

pcDNA3.1-HA-M1MR was obtained from the Guthrie cDNA Resource Center and pEYFP-tubulin from Clontech. The plasmids for pcDNA3.1-HA-AT1AR, pCMV5- β arr1, pcDNA1-AT1AR-DRY/AAV, and full-length pCMV-FLNA expression plasmid were gifts of M. G. Caron, R. J. Lefkowitz (HHMI, Duke University Medical Center), L. Hunyady (Semmelweis University, Budapest, Hungary), and C. J. Loy (National University of Singapore, Singapore), respectively. R. Seger (The Weizmann Institute of Science, Israel) provided the pMEKK97A and pGFP-ERK2 constructs. p β arr2-FLAG has been described previously (41).

SRS library screening. Library screening was performed sequentially. First, cdc25H yeast cells (Stratagene) were cotransformed with pSosGly β arr2 Δ C1 bait plasmid (containing amino acids 1 to 337 of β arr2) and a plasmid (pYes2-GAP, a kind gift of A. Aronheim, Rappaport Faculty of Medicine, Haifa, Israel) containing mGAP to reduce Ras GTPase false positives obtained in the screen (3). Subsequently, pSosGly β arr2 Δ C1/mGAP-containing cdc25H yeast cells were transformed with a human thymus cDNA library fused to a myristylation signal (Stratagene) under the control of the galactose-induced pGal1 promoter. Following library transformation, yeast cells were plated onto Leu⁻/Ura⁻/Trp⁻ agar plates containing 2% galactose (to induce library expression) and 1% raffinose and placed at 25°C for 40 h before being shifted to 37°C (nonpermissive temperature). Clones that grew at 37°C after 5 to 7 days were scored as potential β arr interactors, and plasmid DNA was subsequently extracted and sequenced. By use of this approach, approximately 1.5×10^6 clones were screened. To determine the specificity of the interactions, prey plasmids were retransformed into pSosGly β arr2 Δ C1/mGAP cdc25H yeast. Three days after transformation, yeast cells growing at 25°C on Leu⁻/Ura⁻/Trp⁻ plates containing 2% glucose were subsequently patched onto Leu⁻/Ura⁻/Trp⁻ plates containing either 2% glucose or 2% galactose-1% raffinose and assessed for growth at 37°C 3 to 5 days later. Clones that grew at 37°C in the presence of galactose (prey induced) but not glucose (prey repressed) were considered bona fide interactors.

Classical yeast two-hybrid assay. The L40 yeast reporter strain containing a LexA-inducible gene, HIS3, was cotransformed with pLexABD and pGal4AD hybrid expression vectors and plated on selective medium. Transformants were subsequently assayed for histidine auxotrophy as previously described (42).

Cell culture. COS and Hep2 cells were maintained in Dulbecco's modified Eagle medium supplemented with 10% fetal calf serum (GIBCO), penicillin, and streptomycin (100 IU of penicillin and 100 μ g of streptomycin/ml; Sigma) at 37°C in a humidified 5% CO₂ atmosphere. Human A7 and M2 melanoma cells were a generous gift of T. P. Stosel and Y. Ohta (Brigham and Women's Hospital, Harvard Medical School). The M2 melanoma cells are FLNA deficient. The A7 cell line was derived from M2 melanoma cells through the stable expression of a plasmid encoding full-length FLNA (11). M2 and A7 cells were maintained in minimal essential medium with Earle's salt supplemented with 8% newborn calf

serum, 2% fetal calf serum, penicillin, and streptomycin at 37°C in a humidified 5% CO₂ atmosphere. In addition, A7 cells were subcultured in the presence of 0.5 mg/ml G418 (GIBCO) to maintain the presence of the FLNA-containing plasmid.

Immunoprecipitation and immunoblotting. Approximately 3×10^6 COS cells growing in 100-mm dishes were transiently cotransfected with 1 μ g FLAG epitope-tagged β arr or FLNA expression constructs using GENEJuice (Novagen) and 1 μ g of plasmids encoding Myc fusion or wild-type proteins, as indicated in the figure legends. Forty-eight hours posttransfection, cells were lysed in 1 ml of cold glycerol lysis buffer (50 mM Tris [pH 8.0], 150 mM NaCl, 2 mM EDTA, 1% Triton X-100, 10% glycerol, 100 μ M Na₃VO₄, 1 mM NaF, supplemented with protease inhibitors) and clarified by centrifugation at $13,000 \times g$ for 20 min at 4°C. Immunoprecipitations were performed on 500 μ g of cell lysates by use of 20 μ l of a 50% slurry of monoclonal M2 anti-FLAG-affinity agarose, with constant agitation overnight at 4°C. Following incubation, immune complexes were washed four times with lysis buffer, and immunoprecipitated proteins were detected by Western blot analysis. Additionally, cell lysates (25 μ g) were subjected to Western blot analysis to confirm expression of transfected constructs. Coimmunoprecipitation experiments with full-length FLNA or endogenous proteins were performed as described above with the following modifications. Cells were lysed in 1 ml of lysis buffer 1 (50 mM Tris [pH 7.5], 150 mM NaCl, 1% NP-40, 0.5% sodium deoxycholate, 100 μ M Na₃VO₄, 1 mM NaF, supplemented with protease inhibitors) and clarified by centrifugation at $13,000 \times g$ for 20 min at 4°C. Following immunoprecipitation, immune complexes were washed twice with lysis buffer 1, twice in lysis buffer 2 (50 mM Tris [pH 7.5], 500 mM NaCl, 0.1% NP-40, 0.05% sodium deoxycholate), and twice in lysis buffer 3 (50 mM Tris [pH 7.5], 0.1% NP-40, 0.05% sodium deoxycholate). Coimmunoprecipitation experiments with FLAG- β arr1, GFP-ERK2, and FLNA(22-24) were performed as previously described (45).

Western blotting for FLAG fusion proteins was performed using rabbit polyclonal anti-FLAG antibody (Sigma) at a 1:1,000 dilution. Coprecipitated Myc fusion, β arr1, and full-length FLNA proteins were detected by use of rabbit polyclonal anti-Myc (Santa Cruz) at a 1:1,000 dilution, anti- β arr1 (a kind gift of J. Benovic, University of Philadelphia) at a 1:1,000 dilution, and monoclonal FLNA (Chemicon) antibodies at a 1:1,000 dilution, respectively. Horseradish peroxidase-conjugated polyclonal donkey anti-rabbit or anti-mouse IgG was used as a secondary antibody.

ERK activation experiments were performed essentially as previously described (46). COS cells growing in six-well plates (approximately 3.5×10^5 cells/well) were transfected with plasmids encoding HA-M1MR, HA-AT1AR, or AT1AR-DRY/AYY (250 ng/well) and GFP-ERK2 (125 ng/well) with or without FLAG- β arr1 or -2 (375 ng/well) and with or without Myc-FLNA(22-24) (125 ng/well). Following overnight serum starvation, cells were stimulated with either 100 μ M acetylcholine or 1 μ M angiotensin II for 5 min and subsequently lysed in 300 μ l cold glycerol lysis buffer/well. To determine expression of transfected proteins and phospho-ERK, aliquots of clarified whole-cell lysates (25 μ g) were subjected to SDS-PAGE, transferred to nitrocellulose, and immunoblotted with anti-ERK1/2 (Upstate) at a 1:20,000 dilution, anti-phospho-ERK1/2 (Cell Signaling) at a 1:2,000 dilution, or anti-Myc and anti-FLAG rabbit polyclonal antibodies as described above. Horseradish peroxidase-conjugated polyclonal donkey anti-rabbit IgG was used as a secondary antibody.

A7 and M2 cell lysates (30 μ g) were subjected to SDS-PAGE, transferred to nitrocellulose, and probed with anti-FLNA mouse monoclonal antibody and anti- β arr (A2CT, a kind gift from Robert J. Lefkowitz, HHMI, Duke University Medical Center) at a 1:5,000 dilution, anti-MEK1 (Cell Signaling) at a 1:1,000 dilution, and anti-ERK1/2 rabbit polyclonal antibodies. Horseradish peroxidase-conjugated polyclonal donkey anti-rabbit or anti-mouse IgG was used as a secondary antibody. Blots were developed using either an ECL kit (Amersham) or Supersignal chemiluminescence reagent (Pierce).

Immunofluorescence. A7 and M2 cells were seeded onto coverslips in six-well plates and used for immunofluorescence 2 days later. Cells were fixed and processed for fluorescence microscopy as previously described (40).

Hep2 cells were transfected and processed for immunofluorescence essentially as previously detailed (25) with some modifications. Briefly, cells were grown to 60 to 70% confluence in 100-mm dishes (approximately 7×10^6 cells) prior to transfection by electroporation in HEBS buffer (20 mM HEPES, 137 mM NaCl, 5 mM KCl, 0.7 mM Na₂HPO₄, 6 mM D-glucose) using two 450-V, 125- μ F pulses (Gene Electropulser II; Bio-Rad) and 0.5 μ g of relevant cDNAs in the presence or absence of 20 μ g of relevant siRNA. Forty-eight or 72 (for siRNA transfections) hours posttransfection, cells were treated as described in the figure legends. Following treatment, cells were fixed in 4% paraformaldehyde-PBS for 20 min at 4°C and quenched for 10 min in 0.27% NH₄Cl-0.37% glycine in PBS at room temperature. A 1% bovine serum albumin-0.2% saponin-PBS mixture was

subsequently used to block and permeabilize fixed cells. Primary antibody incubations with rat anti-HA (3F10; Roche) or rabbit anti- β arr (A2CT) at a 1:100 dilution, anti-MEK1 (Santa Cruz) at 1:250 dilution, or a mouse anti-FLNA at a 1:200 dilution were performed for 1 h at room temperature. Cells were subsequently washed with 1% bovine serum albumin-0.2% saponin-PBS and incubated with Alexa Fluor donkey anti-rat (647), anti-rabbit (594), or anti-mouse (488) immunoglobulin (Molecular Probes) at a 1:800 dilution for 45 min at room temperature. After being washed, coverslips were mounted on slides in 90% glycerol (Sigma)-3% N-propyl-galate (Sigma)-PBS. Where indicated, coverslips were stained with Alexa Fluor 594 phalloidin (Molecular Probes) according to the manufacturer's instructions before mounting. Essentially the same protocol was used for the detection of P-ERK1/2 in Hep2 cells with the following exception. A mouse anti-P-ERK antibody (Sigma) was used at a 1:100 dilution, and the fluorescently labeled secondary antibodies described above were replaced with a tyramide signal amplification kit (Molecular Probes), which was used according to the manufacturer's instructions. To quantify the extent of agonist-induced ruffling in M1MR- and AT1AR-transfected Hep2 cells, 100 appropriately transfected cells were counted and scored as ruffling or nonruffling. Cells on two coverslips were counted per transfection, and the scoring was repeated on at least three separate transfections.

Confocal images were taken at room temperature with a Bio-Rad MRC 1024 laser scanning confocal system with a Nikon Plan Apo 60 $\times$ oil immersion lens and an Optiphot 2 microscope equipped with Bio-Rad Lasersharp 2000 software to acquire the images. Images were optimized for contrast in Adobe Photoshop, but no further manipulations were made.

siRNA transfection. M2 and A7 cells (approximately 4×10^6 cells/dish) and Hep2 cells (approximately 7×10^6 cells/dish) were transfected with siRNAs directed against β arr, FLNA, or control siRNA (20 μ g per 100-mm dish) by use of Genesilencer as previously described (1) or by electroporation (for Hep2 cells). The siRNAs targeting β arr or control siRNA have been described previously (1), and the siRNA sequence targeting FLNA is 5'-GGGCTGACAACA GTGTGGTGC-3', corresponding to base pairs 3074 to 3094 relative to the start codon as previously described for use in an shRNA vector (36). All assays were performed 72 h after siRNA transfection.

Purification of TAT-HA-FLNA(22-24) peptide. An overnight culture of BL21(DE3)pLysS (Novagen) transformed with His₆-TAT-HA-FLNA(22-24) plasmid was diluted 1/20 and grown for 5 h at 37°C. Bacteria were resuspended and lysed by sonication in 8 M urea, 20 mM HEPES, 100 mM NaCl, pH 8.0 (lysis buffer). Insoluble material was eliminated by centrifugation at $17,000 \times g$ for 20 min, and the filtered supernatant was applied to a HiTrap chelating high-performance column (Amersham Biosciences) loaded with 100 mM NiSO₄. The column was washed with lysis buffer, and bound protein was eluted with a 10 to 250 mM imidazole gradient in lysis buffer. Elution was monitored at a wavelength of 254 nm. Fractions containing protein were collected, diluted with 2 volumes of 25% glycerol in PBS, and applied to a Sephadex G-25 column preequilibrated with PBS-20% glycerol. The excluded fraction was characterized by SDS-PAGE and Coomassie staining.

Preparation of GST- β arr and in vitro binding assays. GST- β arr1 or - β arr2 fusion proteins were expressed in BL21(DE3)pLysS (Novagen) and purified on a GSTrap fast-flow column (Amersham Biosciences) according to the manufacturer's instructions. Products eluted with 10 mM glutathione were desalted on a HiTrap desalting column (Amersham Biosciences) in PBS and characterized by SDS-PAGE and Coomassie staining.

For in vitro binding assays, 25- μ g portions of GST fusion proteins were immobilized on 20 μ l glutathione-Sepharose beads for 1 h at 4°C in PBS. Beads were washed twice in 1 ml PBS and twice in binding buffer (50 mM Tris-HCl [pH 7.5], 150 mM NaCl, 1% NP-40, 0.5% sodium deoxycholate, supplemented with protease inhibitors). Fifty μ g of TAT-HA-FLNA(22-24) was then added in a final volume of 500 μ l of binding buffer. After 1 h at 4°C, beads were washed four times with 1 ml of binding buffer. Complexes were applied on 10% SDS-PAGE gels, and proteins were revealed by Ponceau red staining and Western blotting with anti-HA 3F10 monoclonal antibody and anti-GST polyclonal antibody (generous gift of N. Varin, Institut Cochin, Paris, France).

RESULTS

Identification of FLNA as a β arr-interacting protein. To identify proteins interacting with β arr, we made use of a cytoplasmic yeast two-hybrid system based on the membrane translocation of Sos called the SRS (4). The SRS uses cdc25H, a strain of yeast which grows normally at 25°C but which harbors

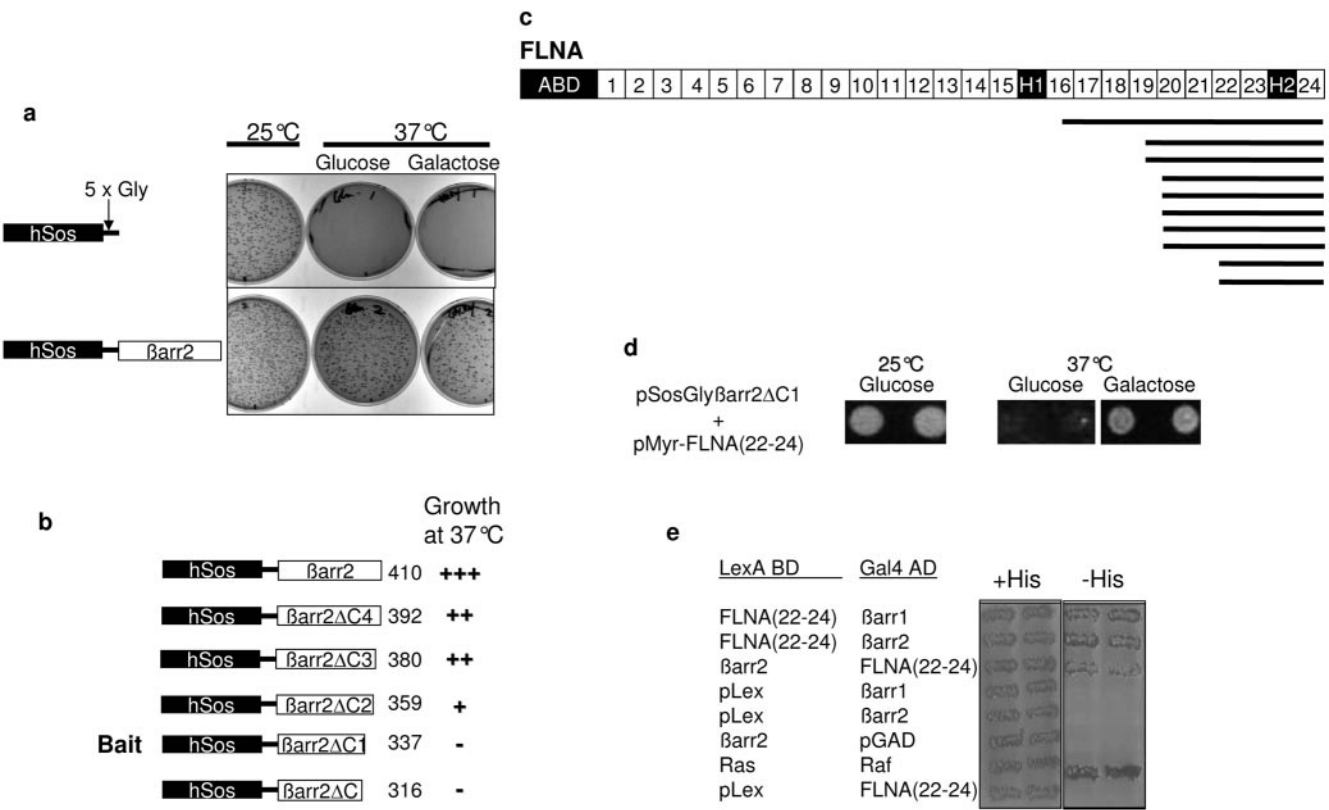


FIG. 1. Identification of FLNA as a *βarr*-binding protein. (a) An adaptor coding for five glycine residues was inserted between the cDNAs for hSos and full-length *βarr2* to reduce potential structural interference between the two proteins upon expression. When the pSosGly*βarr2* chimera (containing amino acids 1 to 410 of *βarr2*) was introduced into *cdc25H* yeast in the absence of prey proteins, it promoted growth at 37°C, while a control plasmid containing the SosGly fusion alone did not. This indicates that full-length *βarr2* on its own is capable of targeting Sos to the membrane and is therefore not suitable as a bait. (b) To identify potential viable baits, a series of *βarr2* C-terminal truncations (containing amino acids 1 to 316, 1 to 337, 1 to 359, 1 to 380, or 1 to 392) was cloned in frame to and downstream of the hSosGly coding sequence. *Cdc25H* yeast cells were transformed with the truncations, incubated for 3 days, and subsequently replica plated and assessed for growth at 37°C. Growth at 37°C of the truncations is indicated. *βarr2*ΔC1, a bait containing amino acids 1 to 337 and giving no background in yeast, was subsequently used to screen the library. (c) Schematic representation of FLNA indicating the actin-binding domain (ABD), 24 repeat regions, and two hinge domains (H1 and H2). The 10 partial FLNA clones identified in the SRS screen of a human thymus cDNA library are depicted as black bars. (d) Retransformation of the smallest prey plasmid, pMyr-FLNA(22-24), containing amino acids 2363 to 2647 of FLNA, into pSosGly*βarr2*ΔC1-containing *cdc25H* yeast. Colonies that grew at 25°C following transformation were patched onto both galactose (prey expression-induced) and control glucose (prey expression-repressed) Trp⁻/Leu⁻/Ura⁻ dropout plates. Growth at 37°C was assessed 2 or 3 days later. Yeast patches grew on galactose-containing plates only at 37°C, confirming the interaction between *βarr2* and FLNA. (e) The L40 yeast reporter strain containing the indicated plasmids was analyzed for histidine auxotrophy. Transformants were patched on selective medium with histidine (+His) and then replica plated onto medium lacking histidine (-His) and incubated for 2 or 3 days. Growth in the absence of histidine indicates interaction between full-length *βarr1* and *βarr2* with FLNA(22-24). The Ras-Raf interaction was used as a positive control.

a thermosensitive mutation in the yeast Ras GEF *Cdc25*, abolishing growth at 37°C. Membrane localization of hSos bypasses the requirement for a functional yeast Ras GEF, *Cdc25*, permitting growth at the restrictive temperature. Interaction between two-hybrid proteins can result in hSos membrane localization. For this method, the bait is fused to hSos, whereas the cDNA-derived prey proteins are fused to a myristylation signal targeting them to the membrane. Protein-protein interaction results in the membrane translocation of hSos, allowing the yeast to grow at 37°C in the presence of galactose.

As full-length *βarr2* self-activated the SRS (Fig. 1a) we used a C-terminally truncated form of *βarr2* (pSosGly*βarr2*ΔC1) containing amino acid residues 1 to 337 to screen a human thymus cDNA library (Fig. 1b). Approximately 1.5×10^6 library colonies were screened, and 10 of the 135 positive clones identified were found to encode the actin-binding protein

FLNA (Fig. 1c). The smallest partial clone obtained in the SRS screen [pMyr-FLNA(22-24)] contained amino acids 2363 to 2647 of FLNA, corresponding to the majority of repeat 22 through to its carboxy terminus (Fig. 1c). The specificity of the interaction was confirmed by growth on Leu⁻/Ura⁻/Trp⁻ plates containing galactose at 37°C following retransformation of pMyr-FLNA(22-24) into pSosGly*βarr2*ΔC1-expressing *cdc25H* yeast (Fig. 1d).

To ascertain if FLNA could interact with full-length *βarr*, we used a classical two-hybrid system in L40 reporter yeast. Cotransfection of FLNA(22-24) with *βarr1* or *βarr2* constructs conferred the ability of yeast to grow on Leu⁻/Trp⁻/His⁻ plates, whereas cotransfection of FLNA(22-24) or *βarr* with control vectors did not (Fig. 1e), indicating that both full-length *βarr1* and *βarr2* are able to interact with FLNA. Confirming the findings obtained by the yeast two-hybrid system,

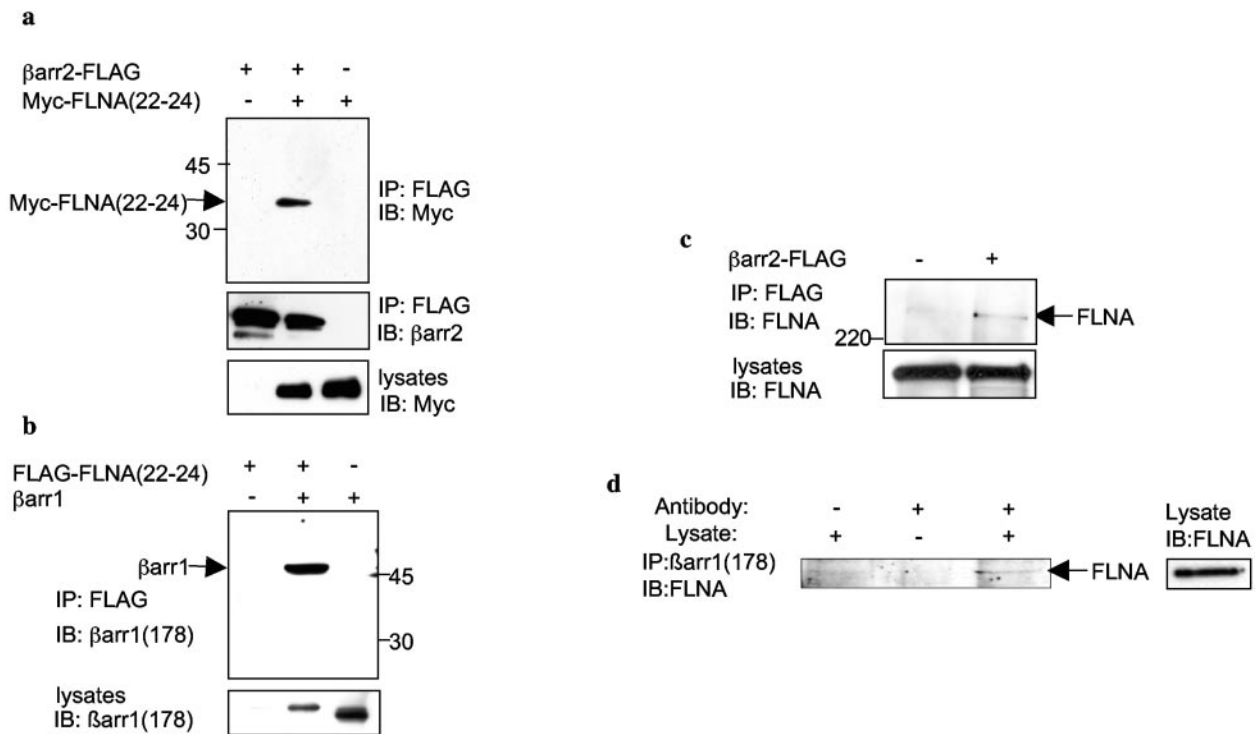


FIG. 2. β arr and FLNA associate in mammalian cells. (a) COS cells growing in 100-mm dishes were transfected with 1 μ g of C-terminally FLAG-tagged β arr2 (β arr2-FLAG) or empty control vector with 1 μ g Myc-FLNA(22-24) containing amino acids 2363 to 2647 of FLNA or empty control vector. Immunoprecipitations (IP) were performed as described in Materials and Methods. Immunoprecipitates were analyzed by SDS-PAGE and probed with polyclonal anti-Myc antibody at a 1:1,000 dilution. Lysates of Myc-FLNA(22-24) represent 10% of the input used in the coimmunoprecipitation experiment. IB, Western blotting. (b) COS cells were transfected with 1 μ g of FLAG-tagged FLNA(22-24) or empty control vector with or without 1 μ g of β arr1 cDNA in pCMV5. Immunoprecipitates were analyzed by SDS-PAGE and probed with anti- β arr1-specific antiserum at a 1:1,000 dilution. Lysates of β arr1 represent 5% of the input used in the coimmunoprecipitation experiment. (c) COS cells were transfected with 2 μ g of β arr2-FLAG or empty control vector. Immunoprecipitates were analyzed by SDS-PAGE and probed with an anti-FLNA antibody at a 1:1,000 dilution to detect endogenous full-length FLNA. Lysates of FLNA represent 5% of the input used in the coimmunoprecipitation experiment. (d) Endogenous FLNA from Hep2 cell lysates was coimmunoprecipitated with endogenous β arr1 using anti- β arr1 antibodies [β arr1(178)]. Immunoprecipitates were analyzed as described above.

β arr2 containing a FLAG epitope tag coimmunoprecipitated with Myc-tagged FLNA(22-24) from COS (Fig. 2a) and HeLa cells (data not shown). Similarly, FLAG-epitope-tagged FLNA(22-24) coimmunoprecipitated with β arr1 (Fig. 2b) and β arr2 (data not shown) from COS cells. Endogenous full-length FLNA also coimmunoprecipitated with FLAG-epitope-tagged β arr2 (Fig. 2c), and, finally, endogenous FLNA could be coimmunoprecipitated with endogenous β arr1 from Hep2 cells (Fig. 2d).

As coimmunoprecipitation experiments cannot rule out the possibility that the interaction between FLNA and β arr occurs indirectly via other proteins, we performed pulldown experiments using purified recombinant proteins. GST fusion proteins of β arr1 and β arr2 were incubated with purified His₆-TAT-HA-FLNA(22-24). Complexes were isolated with glutathione-Sepharose, subjected to SDS-PAGE, and transferred to nitrocellulose. Ponceau red staining revealed that purified FLNA(22-24) can interact directly with both β arr1 and β arr2 (Fig. 3). Binding was specific, as no FLNA(22-24) was detected in the presence of GST alone. Taken together, these data indicate that FLNA is a β arr-binding protein and that the interaction takes place via amino acids 2363 to 2647 of FLNA, corresponding to the distal two-thirds of repeat 22 through to its carboxy terminus.

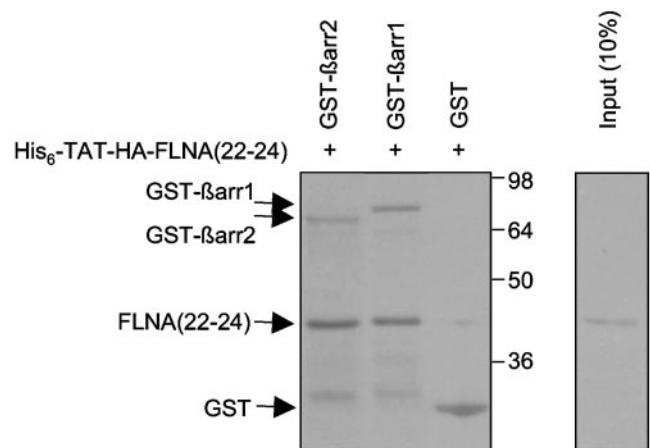


FIG. 3. Direct binding of β arr to FLNA(22-24) in vitro. GST alone, GST- β arr1, or GST- β arr2 bound to glutathione-Sepharose was incubated with purified His₆-TAT-HA-FLNA(22-24). Complexes were isolated and washed as described in Materials and Methods. Ten percent of the His₆-TAT-HA-FLNA(22-24) peptide used in the pulldown experiments was loaded as a control. After samples were resolved by SDS-PAGE, the gel was transferred to nitrocellulose membrane and stained with Ponceau red solution. Positions of purified proteins are depicted. The identities of these proteins were confirmed by immunoblot experiments using anti-HA and anti-GST antibodies (not shown). GST- β arr1 retained 21% $\pm$ 5% of the input, and GST- β arr2 retained 17% $\pm$ 2% ($n = 4$).

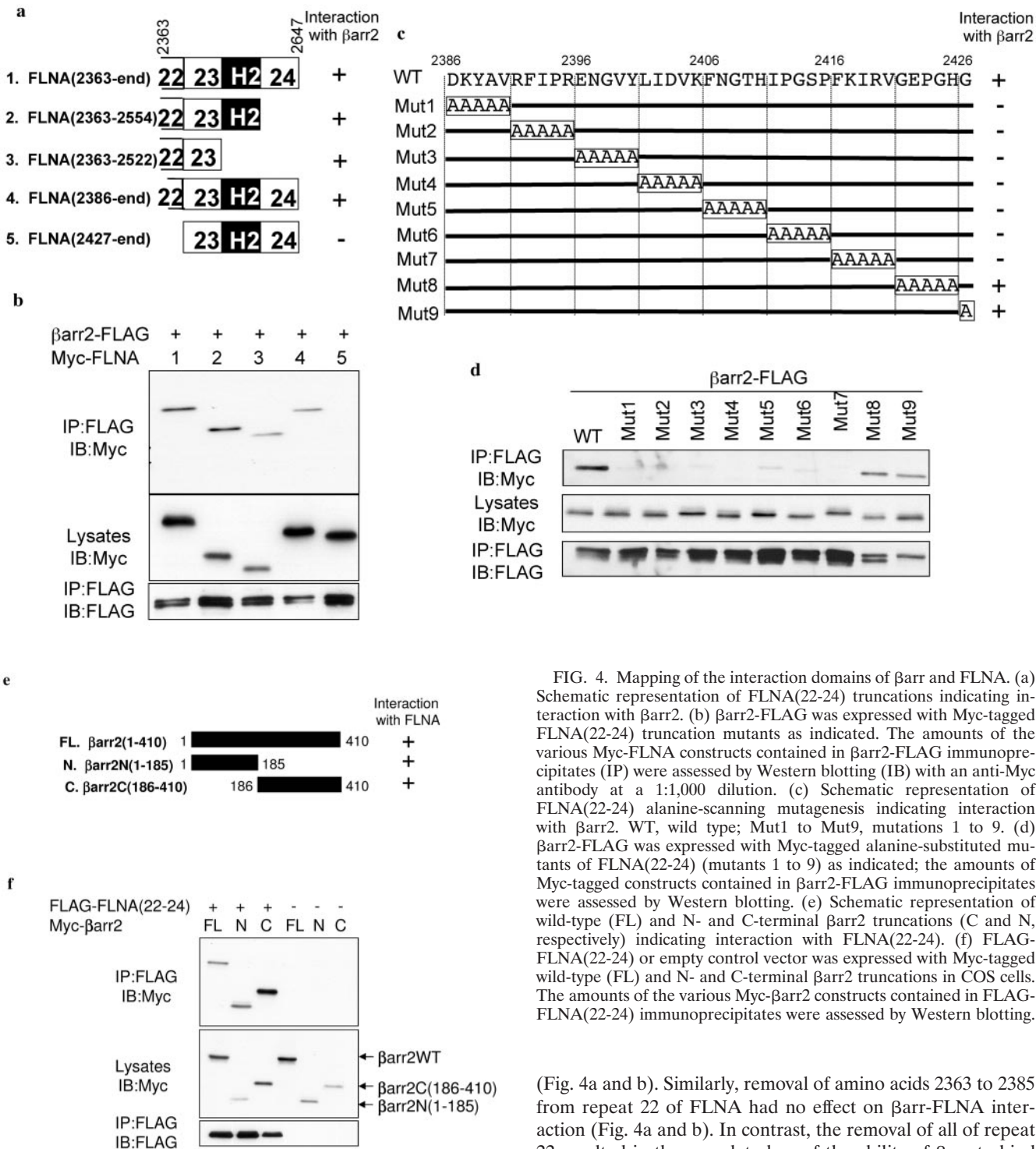


FIG. 4. Mapping of the interaction domains of β arr and FLNA. (a) Schematic representation of FLNA(22-24) truncations indicating interaction with β arr2. (b) β arr2-FLAG was expressed with Myc-tagged FLNA(22-24) truncation mutants as indicated. The amounts of the various Myc-FLNA constructs contained in β arr2-FLAG immunoprecipitates (IP) were assessed by Western blotting (IB) with an anti-Myc antibody at a 1:1,000 dilution. (c) Schematic representation of FLNA(22-24) alanine-scanning mutagenesis indicating interaction with β arr2. WT, wild type; Mut1 to Mut9, mutations 1 to 9. (d) β arr2-FLAG was expressed with Myc-tagged alanine-substituted mutants of FLNA(22-24) (mutants 1 to 9) as indicated; the amounts of Myc-tagged constructs contained in β arr2-FLAG immunoprecipitates were assessed by Western blotting. (e) Schematic representation of wild-type (FL) and N- and C-terminal β arr2 truncations (C and N, respectively) indicating interaction with FLNA(22-24). (f) FLAG-FLNA(22-24) or empty control vector was expressed with Myc-tagged wild-type (FL) and N- and C-terminal β arr2 truncations in COS cells. The amounts of the various Myc- β arr2 constructs contained in FLAG-FLNA(22-24) immunoprecipitates were assessed by Western blotting.

Mapping the binding domains of FLNA and β arr. To further refine the β arr-binding region of FLNA within repeat regions 22 to 24, we created a series of FLNA(22-24) truncations. Deletion either of repeat 24 or of repeat 24 and the second hinge domain (H2) together had no effect on the binding of β arr to FLNA in coimmunoprecipitation experiments

(Fig. 4a and b). Similarly, removal of amino acids 2363 to 2385 from repeat 22 of FLNA had no effect on β arr-FLNA interaction (Fig. 4a and b). In contrast, the removal of all of repeat 22 resulted in the complete loss of the ability of β arr to bind FLNA (Fig. 4a and b). This indicates that amino acids 2386 to 2427 contained within repeat 22 of FLNA are essential for β arr binding. Similar results were obtained in yeast two-hybrid experiments (data not shown). This region is located near the regions of FLNA which interact with most FLNA-binding GPCRs, encompassing repeat domains 14 to 21 or repeat 24 (5, 13, 20, 31, 39). Of particular interest with regard to MAPK signaling is the fact that this region (residues 2386 to 2427 of FLNA) is contained within previously identified binding sites

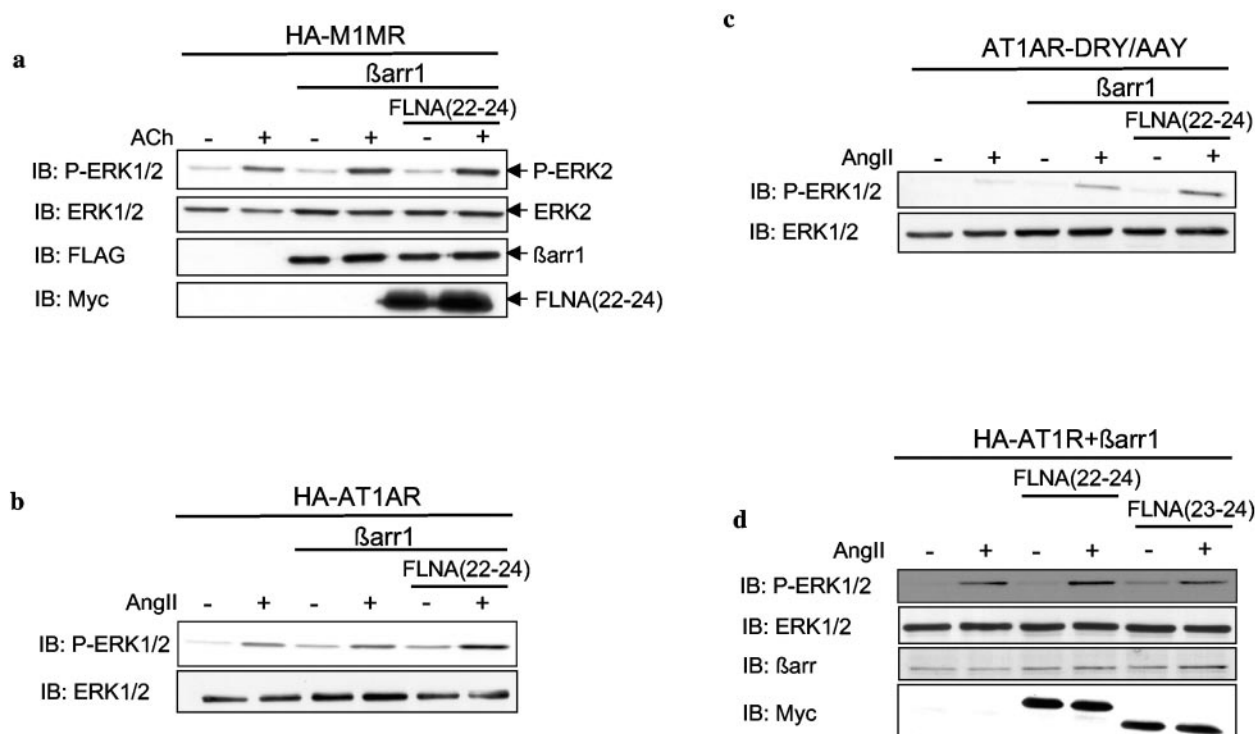


FIG. 5. GPCR-induced β arr-mediated activation of ERK is enhanced by FLNA(22-24). (a) Serum-starved COS cells transfected with plasmids encoding HA-M1MR, GFP-ERK2, FLAG- β arr1, or empty control vector and Myc-FLNA(22-24) or empty control vector were left untreated or were stimulated with 100 μ M ACh for 5 min at 37°C. Cell lysates were resolved by SDS-PAGE, and phosphorylation of ERK2 was assessed by immunoblotting (IB) using an anti-phospho-ERK1/2 antibody at a 1:1,000 dilution. Total GFP-ERK2, FLAG- β arr1, and Myc-FLNA(22-24) expression levels were confirmed by probing the immunoblots with anti-ERK1/2 (1:20,000 dilution), anti-FLAG (1:1,000 dilution), and anti-Myc (1:1,000 dilution) antibodies, respectively. Gels were scanned, and phospho-ERK2 and total ERK2 levels were determined using NIH ImageJ. The phospho-ERK2:total ERK2 ratio was calculated for receptor-stimulated cells expressing M1MR, β arr1, and ERK2 (lane 4), and this value was normalized to 100% ERK activation. The phospho-ERK2:total ERK2 ratio was subsequently calculated for ACh-stimulated cells expressing M1MR, β arr1, ERK2, and FLNA(22-24) (lane 6), which, when compared to cells expressing M1MR, β arr1, and ERK2 (100%), gave a result of $148\% \pm 13\%$. The data represent the mean $\pm$ SEM of four independent experiments ($P < 0.05$). (b and c) Serum-starved COS cells transfected with plasmids encoding HA-AT1AR (b) or AT1AR-DRY/AAAY (c), GFP-ERK2, FLAG- β arr1, or empty control vector and Myc-FLNA(22-24) or empty control vector were left untreated or were stimulated with 1 μ M AngII for 5 min at 37°C. Cell lysates were resolved by SDS-PAGE, and phospho-ERK2 and total ERK2 levels were assessed by immunoblotting as described for panel a. Expressions of FLAG- β arr1 and Myc-FLNA(22-24) were confirmed by immunoblotting as described for panel a (not shown). (d) Serum-starved COS cells transfected with plasmids encoding HA-AT1AR, GFP-ERK2, FLAG- β arr1, and either Myc-FLNA(22-24), Myc-FLNA(23-24), or empty control vector were left untreated or were stimulated with 1 μ M AngII for 5 min at 37°C. Cell lysates were resolved by SDS-PAGE, and expressions of phospho-ERK2, total ERK2, FLAG- β arr1, Myc-FLNA(22-24), and Myc-FLNA(23-24) were assessed by immunoblotting as described for panel a.

for the two FLNA-interacting MAP2K proteins, MEK1 (amino acids 2282 to 2647) and MKK4 (amino acids 2282 to 2454) (34). In an attempt to identify the specific residues contained within amino acids 2386 to 2427 of FLNA that are responsible for the binding of β arr, a series of quintuple alanine-scanning substitutions in this region were created in FLNA(22-24) and tested for their abilities to bind β arr in coimmunoprecipitation experiments (Fig. 4c and d). The data demonstrate that several successive substitutions severely impair or abolish the ability of β arr to interact with FLNA(22-24). These results therefore indicate that multiple amino acid residues contained within the 2386 to 2420 FLNA region likely participate in β arr binding.

To determine which region of β arr is important for FLNA(22-24) binding, coimmunoprecipitation experiments were carried out using either the N-terminal part (amino acids 1 to 185, corresponding to the short N-terminal extremity and to the amino-terminal globular domain) or the C-terminal part (186 to 410, corresponding to the carboxy-terminal globular domain and C-terminal tail) of β arr2 (Fig. 4e and f). FLNA(22-24) was actually

found to bind both domains of β arr2, indicating the existence of a complex interaction which involves the presence of multiple binding sites on β arr for FLNA. Similar data were obtained in yeast two-hybrid experiments (data not shown).

FLNA(22-24) enhances GPCR-induced β arr-mediated activation of ERK in COS cells. β arr have recently been shown to play an important role in MAPK signaling, functioning as scaffolds for GPCR-stimulated MAPK activation by binding component kinases of the cascades, such as Raf-1 and ERK2. Interestingly, FLNA has also been implicated in the regulation of MAPK signaling with regard to the GPCR CaR (5, 20, 34) and, as mentioned above, interacts with the MAP2Ks MKK4 and MEK1. The MEK1-binding site on FLNA overlaps the β arr-binding site identified here. Since the β arr-MEK1 complex may occur, at least in part, through indirect interaction (33), we investigated whether the interaction between β arr and FLNA contributes to agonist-evoked GPCR activation of ERK, looking at the effect of FLNA(22-24) overexpression on β arr-mediated ERK activation in COS cells. Overexpression of

β arr1 (Fig. 5a and b) or β arr2 (data not shown) moderately enhanced M1MR- and AT1AR-induced GFP-ERK2 phosphorylation, as assessed by immunoblotting of COS cell lysates with anti-phospho-ERK antibodies, in agreement with previous findings (46). GFP-ERK2, which has been shown to behave like wild-type ERK1/2 (46), was used in these experiments to control for ERK phosphorylation in the transfected pool of cells. When β arr1 was overexpressed in combination with FLNA(22-24), M1MR-induced ERK activation was significantly potentiated (enhancement of $48\% \pm 13\%$; $P < 0.05$ [$n = 4$]) compared to stimulated control cells overexpressing β arr1 alone (Fig. 5a), indicating a role for FLNA in GPCR-induced ERK activation. A similar potentiation was seen with the AT1AR when β arr1 was overexpressed with FLNA(22-24) (Fig. 5b). As activation of ERK can occur via both G protein-dependent and G protein-independent (i.e., β arr-dependent) mechanisms, we made use of a mutant AT1AR, which is mutated in its DRY motif (DRY/AAY) and thereby rendered severely impaired in $G\alpha_q/11$ coupling in COS cells (24), to determine if the observed potentiation of ERK activation by FLNA(22-24) mentioned above does indeed involve a β arr-dependent pathway. A number of recent studies indicate that activation of ERK via this mutant receptor is completely independent of G proteins and is exclusively mediated by β arr (48, 2). AngII-induced activation of ERK via the DRY/AAY receptor was increased fourfold by β arr1 and further enhanced approximately twofold when β arr1 and FLNA(22-24) were both overexpressed (Fig. 5c). This finding confirms that the increase in active ERK observed when FLNA(22-24) and β arr1 are both overexpressed is via a β arr-dependent pathway and not via a $G\alpha_q/11$ -dependent pathway. Since FLNA(23-24) did not coimmunoprecipitate with β arr (Fig. 4), we anticipated that this fragment would not potentiate β arr-mediated activation of ERK as observed with FLNA(22-24). As expected, AngII-induced activation of ERK via the AT1AR was potentiated when β arr1 was overexpressed with FLNA(22-24) but not with FLNA(23-24) (Fig. 5d). This finding is consistent with the hypothesis that the β arr-binding site contained within FLNA(22-24) contributes to the increased activation of ERK when both proteins are overexpressed.

Taken together, the above results indicate that the interaction of β arr with FLNA may control the extent of GPCR-induced β arr-mediated ERK activation. As the carboxy terminus of FLNA has been implicated in binding to MAPK cascade components (see above), we tested whether FLNA(22-24) expression could increase the previously reported interaction between β arr and ERK2. The amount of GFP-ERK2 detected in FLAG coimmunoprecipitates was markedly increased upon coexpression of FLAG- β arr1 with FLNA(22-24) (Fig. 6), which is consistent with the idea that FLNA can facilitate the formation of β arr-ERK complexes.

FLNA is essential for full β arr-mediated ERK activation following M1MR activation. Since FLNA(22-24) potentiates GPCR-mediated β arr-dependent ERK activation, we investigated whether this functional activity could be recapitulated by the full-length protein. The specific effect of FLNA expression on β arr-mediated ERK activation was investigated by use of FLNA-deficient M2 cells and their FLNA-replete counterpart, A7 cells (Fig. 7), as a model. Both cell types contained equivalent amounts of the MAPK signaling proteins β arr, MEK1,

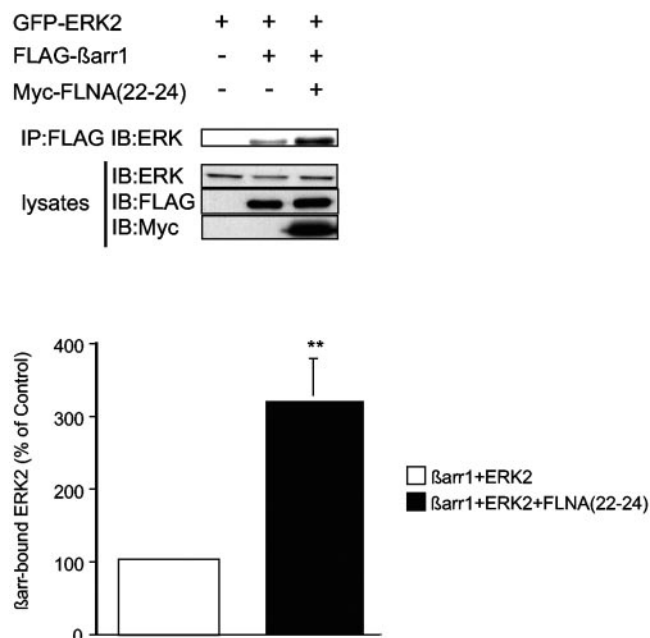


FIG. 6. FLNA(22-24) enhances β arr-ERK2 association. COS cells were transiently transfected with plasmids encoding GFP-ERK2, FLAG- β arr1, and Myc-FLNA(22-24) as indicated. FLAG immunoprecipitates were probed for coprecipitated ERK2. Equivalent expression of constructs was confirmed by immunoblotting of cell lysates. The histogram shows the amount of GFP-ERK2 detected in FLAG- β arr1 immunoprecipitates. Data are normalized to 100% for cells expressing β arr and GFP-ERK2 and represent the mean $\pm$ SEM of five independent experiments (**, $P < 0.02$).

and ERK (Fig. 7a, left panels), and the distributions of β arr in both cell types were similar (Fig. 7a, right panels). This model was used to confirm that maximal ERK activation requires cooperation between β arr and full-length FLNA. siRNA against β arr, recently employed to investigate the role of β arr in GPCR-induced ERK activation (1, 2, 48), was used to inhibit β arr expression in both M2 and A7 cells. The siRNA directed against β arr led to an approximately 50% decrease in endogenous β arr levels in both M2 and A7 cells, as assessed by Western blotting (Fig. 7b). In A7 cells transfected with the M1MR and control siRNA oligonucleotides, a robust activation of ERK was observed following receptor activation (Fig. 7c, lanes 1 and 2). The siRNA-mediated reduction of β arr in A7 cells impaired M1MR-induced ERK activation by approximately 30% (Fig. 7c, lanes 3 and 4). M2 cells transfected with M1MR and control siRNA oligonucleotides demonstrated reduced receptor-activated levels of active ERK compared to A7 cells (Fig. 7c, lanes 6 and 2, respectively). In M2 cells with reduced levels of β arr following transfection with specific siRNA, the induction of ERK was similar to that of cells transfected with control oligonucleotides (Fig. 7c, lanes 8 and 6, respectively). Similar results were obtained using the AT1AR (data not shown).

Finally, to confirm that the different levels of ERK activation achieved in M1MR-transfected M2 and A7 cells were correlated with the presence or absence of FLNA, full-length FLNA cDNA was transiently transfected in M2 cells; this enhanced ERK activation following M1MR stimulation (Fig. 7d). Taken

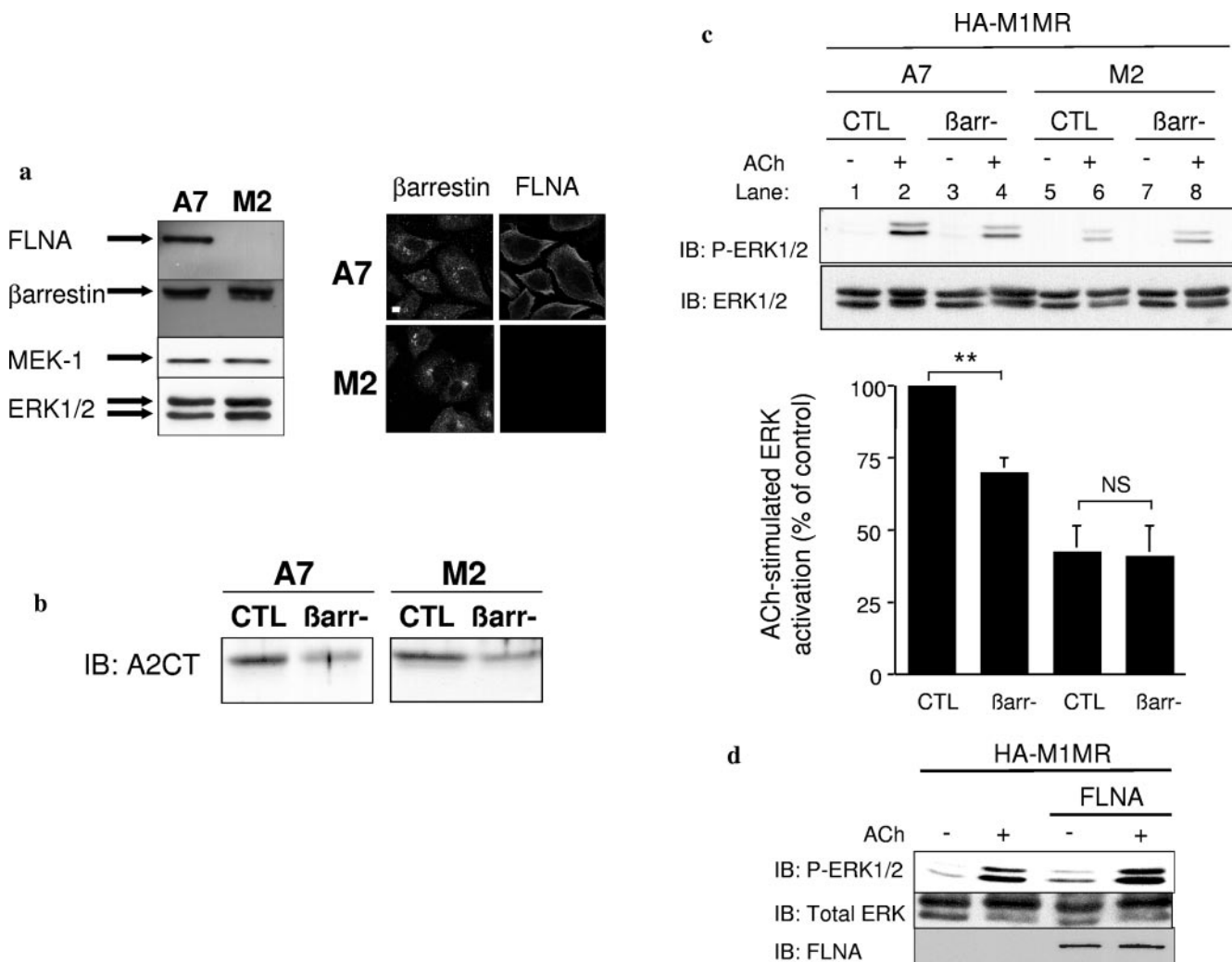


FIG. 7. Requirement of FLNA for M1MR-induced β arr-mediated ERK activation. (a) M2 and A7 cells were lysed, and equivalent amounts of proteins were subjected to SDS-PAGE and immunoblotted with the indicated antibodies (left panel) as described in Materials and Methods. M2 and A7 cells were grown and fixed on coverslips as described in Materials and Methods. Cells were then processed for fluorescence microscopy using A2CT directed against β arr and an anti-FLNA antibody and revealed by Alexa Fluor 594- or 647-conjugated antibodies (right panel). Scale bar, 5 μ m. (b) Serum-starved M2 and A7 cells transfected with control (CTL) or β arr siRNA oligonucleotides were lysed 72 h posttransfection, and equivalent amounts of protein were subjected to SDS-PAGE and immunoblotted (IB) with the anti- β arr antibody A2CT at a 1:5,000 dilution. (c) Serum-starved M2 and A7 cells transfected with a plasmid encoding HA-M1MR and either control or β arr1/2 siRNA oligonucleotides were left untreated or were stimulated with 100 μ M ACh for 5 min at 37°C. Flow cytometry was performed with anti-HA antibodies on M2/A7 cells transfected with the HA-M1MR to determine receptor density at the cell surface. Mean fluorescence intensity in A7 cells ($n = 3$) was 3.76 ± 0.35 times higher than that in M2 cells. A7 cells are considerably larger than M2 cells, and the number of surface receptors/milligram protein was finally found to be equivalent between the cell types. Equal receptor amounts of cell lysates (corresponding to equivalent protein levels) were resolved by SDS-PAGE, and phosphorylation of ERK1/2 was assessed by immunoblotting using an anti-phospho-ERK1/2 antibody (1:1,000 dilution). Total ERK1/2 levels were controlled using an anti-ERK1/2 antibody (1:20,000 dilution). Data shown represent the mean $\pm$ SEM calculated from three independent experiments. The results in each experiment were normalized to the level of ERK phosphorylation in stimulated A7 cells transfected with control siRNA. Significance was evaluated using a t test. **, $P < 0.02$. NS, not significant. (d) Serum-starved M2 cells transfected with a plasmid encoding HA-M1MR and either pCMV-FLNA encoding full-length FLNA (32) or a control plasmid were left untreated or were stimulated with 100 μ M for 5 min at 37°C. P-ERK1/2 and total ERK1/2 levels were assessed by immunoblotting as described for panel c. FLNA was detected using an anti-FLNA antibody (1:1,000 dilution).

together, these data indicate that to achieve full activation of ERK via the M1MR in this model system, the simultaneous expression of both FLNA and β arr is essential.

Colocalization of β arr, FLNA, and active ERK in membrane ruffles in Hep2 cells following M1MR activation. FLNA is an actin cross-linker that is appreciated as an important player in actin remodeling. It is enriched in membrane ruffle structures, which contain bundles of actin filaments that are more densely

packed than those of the underlying cell lamellae. β arr have recently been shown to be involved in GPCR-induced actin cytoskeletal changes, which require β arr-dependent MAPK activation (16, 17, 23). If β arr, FLNA, and active ERK do cooperate to orchestrate receptor-mediated cell shape changes, they would be expected to colocalize in areas of active cytoskeletal remodeling following receptor activation. We therefore extended our studies to Hep2 cells, which undergo

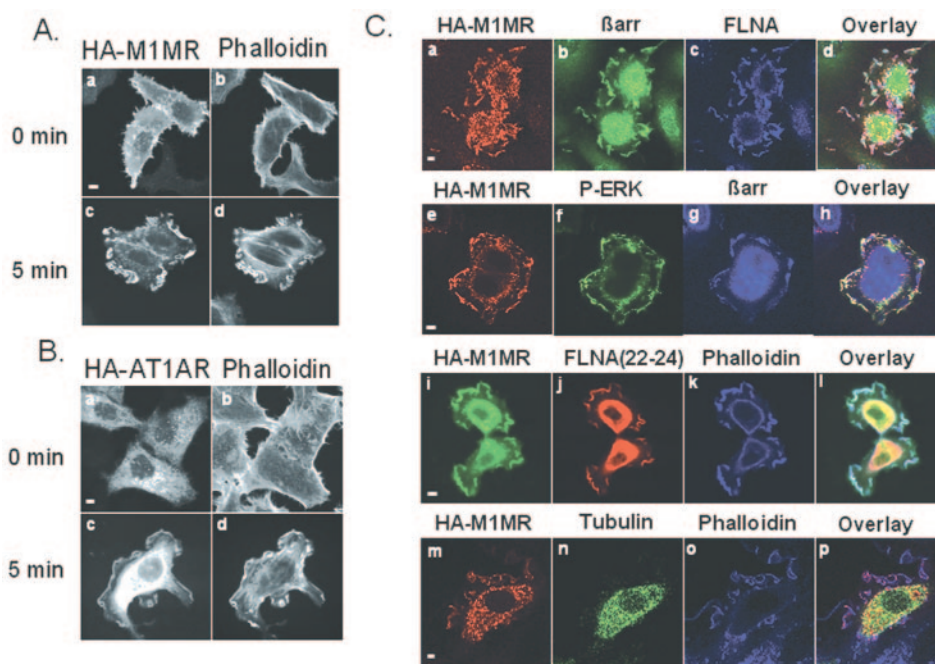


FIG. 8. M1MR, β arr, FLNA, and active ERK colocalize in membrane ruffles in Hep2 cells following agonist stimulation. (A) Hep2 cells transfected with HA-M1MR were left untreated or were stimulated with 100 μ M ACh for 5 min, fixed, processed for immunofluorescence with an anti-HA (3F10) antibody, and revealed using an Alexa Fluor 488 antibody (a and c). Alexa Fluor 594 phalloidin was used to stain for actin (b and d). (B) Hep2 cells transfected with HA-AT1AR were left untreated or were stimulated with 1 μ M AngII for 5 min, fixed, and processed for immunofluorescence as described for panel A. (C) Hep2 cells transfected with HA-M1MR were stimulated with 100 μ M ACh for 5 min, fixed, and processed for immunofluorescence using anti-HA (panels a and e), anti- β arr (panels b and g), anti-FLNA (panel c), and anti-P-ERK1/2 (panel f) antibodies. Hep2 cells cotransfected with HA-M1MR and Myc-FLNA(22-24) (panels i through l) or HA-M1MR and YFP-tubulin (panels m through p) were stimulated with 100 μ M ACh for 5 min, fixed, and processed for immunofluorescence as described for panel A. Panel n shows fluorescence emitted by YFP-tubulin. Scale bars, 5 μ m.

substantial membrane ruffling in response to various stimuli (10). In Hep2 cells expressing M1MR, agonist treatment (acetylcholine) for 5 min resulted in extensive cell shape change with the rapid formation of membrane ruffles, a marker of cytoskeletal reorganization (Fig. 8A, compare panels a [unstimulated control cells] and c). Actin was localized to these membrane structures following receptor stimulation, as assessed by phalloidin staining (Fig. 8A, compare panels b and d). Under these conditions, $70\% \pm 0.8\%$ ($n = 3$) of the M1MR-transfected cells formed ruffles (Fig. 9D). Similar results were obtained with the AT1AR (Fig. 8B, compare panels a and b [unstimulated control cells] with c and d), with $68\% \pm 3.6\%$ ($n = 3$) of transfected cells demonstrating ruffling following angiotensin II stimulation (Fig. 9E). Interestingly, receptor, endogenous β arr, and FLNA were colocalized in these membrane ruffles following agonist stimulation, as shown in Fig. 8C, panels a through d. As anticipated, active phosphorylated ERK was also found in ruffles following receptor activation (Fig. 8C, panels e through h). As FLNA(22-24), which lacks the actin-binding domain, was found to potentiate ERK activation (Fig. 5) like full-length FLNA, one would expect to observe a colocalization of FLNA(22-24) with phosphorylated ERK in membrane ruffles following receptor stimulation. As shown in Fig. 8C, panels i through l, FLNA(22-24) was indeed colocalized with activated receptor in the membrane ruffles of Hep2 cells. To rule out potential artifactual colocalization of proteins due to variations of cell thickness in the ruffling cells,

Hep2 cells were cotransfected with M1MR and YFP-tubulin as a negative control. Activated M1MR, but not tubulin, was concentrated in actin-rich ruffles (Fig. 8C, panels m through p). This suggests that the observed enrichment of M1MR, β arr, and FLNA immunofluorescence in the membrane ruffles of agonist-treated cells does indeed reflect true colocalization. In conclusion, the GPCR-stimulated colocalization of β arr, FLNA, and P-ERK at membrane ruffles is consistent with a cooperative role for β arr- and FLNA-mediated ERK activation in this GPCR-dependent process.

Essential requirement for β arr, FLNA, and active ERK for M1MR- and AT1AR-induced membrane ruffling in Hep2 cells.

To investigate the requirement for β arr and FLNA in M1MR- and AT1AR-induced ruffling in Hep2 cells, we employed siRNAs to reduce the expression of endogenous levels of these proteins. M1MR-transfected Hep2 cells showed a significant reduction in endogenous β arr levels following siRNA cotransfection (Fig. 9A, panel a) and exhibited a severely impaired ruffling response. Only $18\% \pm 3.8\%$ ($n = 3$) of the M1MR- and β arr RNAi-cotransfected cells ruffled compared to cells cotransfected with M1MR and control siRNA (Fig. 9A, compare panels b and c with d and e and Fig. 9D). Similar results were obtained by use of Hep2 cells cotransfected with the AT1AR and β arr RNAi, where, compared to their control RNAi-transfected counterparts, only $20\% \pm 1.59\%$ ($n = 3$) of the ruffling response was observed (Fig. 9E and data not shown). Similarly, a reduction in FLNA levels by RNAi (Fig.

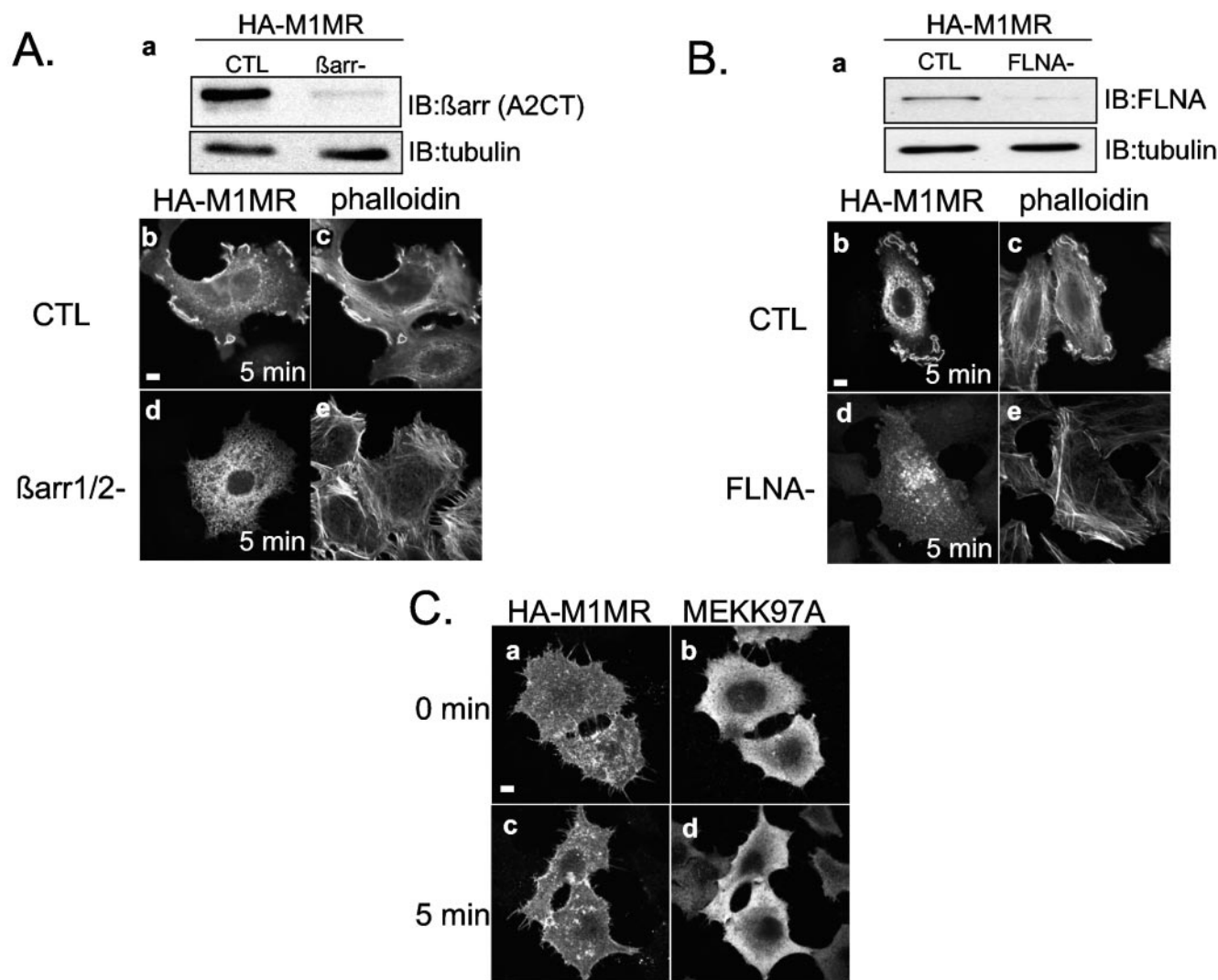


FIG. 9. β arr, FLNA and active ERK are all required to achieve full M1MR- and AT1AR-induced ruffle formation in Hep2 cells. (A) (a) Representative blot showing Hep2 cells transfected with either control (CTL) or β arr RNAi oligonucleotides. IB, immunoblotting. (b through e) Hep2 cells transfected with HA-M1MR and either control or β arr siRNA oligonucleotides were stimulated with 100 μ M ACh for 5 min, fixed, and processed for immunofluorescence using an anti-HA (3F10) antibody (b and d) and Alexa Fluor 594 phalloidin to stain for actin (c and e). (B) (a) Representative blot showing Hep2 cells transfected with either control or FLNA RNAi oligonucleotides. (b through e) Hep2 cells transfected with HA-M1MR and either control or FLNA siRNA oligonucleotides were stimulated with 100 μ M ACh for 5 min, fixed, and processed for immunofluorescence as described for panel A. (C) Hep2 cells cotransfected with HA-M1MR and MEK(K97A) were left untreated or were stimulated with 100 μ M ACh for 5 min, fixed, and processed for immunofluorescence using anti-HA (3F10) and anti-MEK antibodies. (D) Histogram showing the quantification from three independent experiments of ACh-induced membrane ruffling in Hep2 cells transfected with the HA-M1MR and either control, β arr1/2, or FLNA RNAi oligonucleotides or MEK(K97A) expression vector. Phalloidin staining was routinely used for quantification, and approximately 100 appropriately transfected cells were scored as ruffling or nonruffling per experiment. The results shown represent the means $\pm$ standard errors of the means from three independent transfections. ***, $P < 0.001$. Significance was evaluated using a t test. (E) Histogram showing the quantification from three independent experiments of AngII-induced membrane ruffling in Hep2 cells transfected with the HA-AT1AR and either CTL, β arr1/2, or FLNA RNAi oligonucleotides or MEK(K97A) expression vector. Approximately 100 appropriately transfected cells were scored as ruffling or nonruffling per experiment. The results shown represent the mean $\pm$ standard error of the mean from three independent transfections. **, $P < 0.02$; ***, $P < 0.001$. Significance was evaluated using a t test. (F) Representative blot showing Hep2 cells transfected with either control or FLNA RNAi oligonucleotides. Immunoblotting was performed with anti-FLNA or anti-FLNB isoform-specific antibodies (1:1,000 dilution; Chemicon). The blot demonstrates that the knockdown is specific for FLNA and does not affect FLNB. Scale bars, 5 μ m.

9B, panel a) inhibited M1MR-induced membrane ruffling compared to that of control RNAi-transfected cells (Fig. 9B, compare panels d and e with b and c and Fig. 9D); the reduction was comparable to that observed in β arr-depleted cells. Essentially identical results were obtained using the AT1AR

receptor (Fig. 9E and data not shown). To further substantiate the functional connection between the cooperative effect of β arr and FLNA on cytoskeletal rearrangement, on one hand, and ERK activation, on the other hand, the direct involvement of active ERK in ruffle formation was investigated in the same

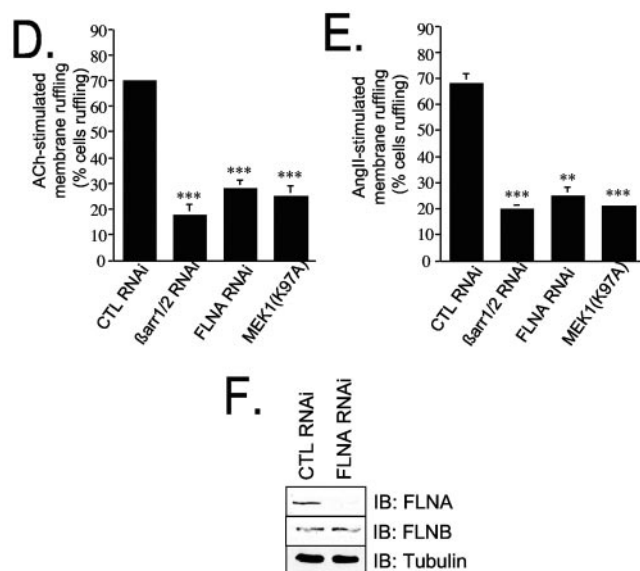


FIG. 9—Continued.

model system. Transfection of Hep2 cells with a plasmid encoding MEK1(K97A), a dominant negative mutant of MEK1 which interacts with ERK and inhibits its activation, reduced M1MR-stimulated membrane ruffling to levels similar to those observed for cells transfected with β arr1/2 and FLNA siRNAs. This finding indicates that active ERK is also required for ruffle formation in these cells (Fig. 9C, panels c and d, and D). Similar results were obtained with Hep2 cells cotransfected with the AT1AR and MEK1(K97A) (Fig. 9E and data not shown). Taken together, these results indicate an essential requirement for β arr, FLNA, and active ERK in M1MR- and AT1AR-mediated cell shape change in our system, with the selective inhibition of each component being sufficient to cause a profound (60% or more) impairment of ruffle formation.

DISCUSSION

The studies described here indicate that the scaffolding and actin-binding protein FLNA interacts with β arr and support a model where these two molecules cooperate to achieve full GPCR- and β arr-dependent activation of ERK. We also present evidence to suggest that the extent and the subcellular localization of the ERK activation, which is achieved through this double scaffold, is capable of controlling cytoskeletal rearrangements such as the formation of membrane ruffles in Hep2 cells.

The involvement of FLNA in ERK activation downstream of an activated GPCR was documented for the CaR (5, 20), and it was proposed that the functions of FLNA in this process would be to stabilize the receptor at the plasma membrane and to target signaling proteins to the receptor (50). Our data indicate that β arr, which interact with both FLNA- and ligand-activated GPCRs, likely represent a third critical component of the GPCR-FLNA signaling complex. In particular, genetic or siRNA-mediated reduction of either β arr or FLNA was found to significantly impair M1MR-induced ERK activation. FLNA has also been shown to have effects on ERK signaling for

receptors of other families, such as the insulin receptor (19). In FLNA-deficient M2 cells, activation of ERK via the insulin receptor is enhanced compared to that seen for FLNA-replete A7 cells, and FLNA has thus been proposed to play a negative role in ERK signaling via this receptor (19). Our findings on M1MR-induced ERK activation in M2 and A7 cells are in clear contrast to this result, with the divergent effects observed upon FLNA depletion likely explicable by different mechanisms used to activate ERK by GPCRs and the insulin receptor in this cell model.

FLNA binds the MAP2Ks MEK1 (weak interaction) and MKK4 (strong interaction) (34), which are upstream activators of ERK and JNK, respectively. The minimal β arr-binding site on FLNA identified by deletion mapping and alanine-scanning mutagenesis appears to be located between amino acids 2386 and 2420, contained within tandem repeat 22 of FLNA. Interestingly, the β arr-binding site is contained within the previously identified binding sites for MEK1 (amino acids 2282 to 2647; repeats 21 to 24) and MKK4 (amino acids 2282 to 2454; repeats 22 to 23) (34). It is therefore tempting to speculate that FLNA plays a positive role in β arr-mediated ERK activation by acting as a platform for the efficient recruitment of signaling molecules involved in this signaling pathway in an example of macromolecular cooperation. Indeed, the formation of signaling complexes between MEK1, ERK, and β arr appears to depend, at least in part, on indirect interaction, as the overexpression of c-Raf1 increases the binding of both kinases to β arr (33). Accordingly, FLNA could perform a role similar to that of c-Raf1 by promoting the formation of a stabler or more-efficient β arr-MAPK scaffold. Evidence in favor of this model is provided by coimmunoprecipitation experiments that demonstrate an increase in β arr-associated ERK2 in the presence of FLNA(22-24) and by the observation that full-length FLNA or FLNA(22-24) can potentiate β arr-mediated activation of ERK. In addition, as full-length FLNA binds to cytoskeletal elements at the periphery of the cytoplasm, including subcortical actin, it would serve to localize and amplify the β arr-MAPK cascade within this cell compartment. Of interest is the fact that β arr2 can also bind to the MAP3K ASK1, to JNK3, and indirectly, via JNK3, to the FLNA-binding MAP2K MKK4 to assemble an efficient JNK3 cascade (35). The role of FLNA in the signaling of this β arr2-MAPK scaffold therefore certainly merits further investigation. Finally, the functional significance of the interaction between FLNA and β arr is not restricted to MAPK signaling only. During the preparation of this work, it was reported that the dopamine D3 receptor, FLNA, and β arr form a basal ternary signaling complex (26). Increases in GPCR kinase activity decreased the stability of the complex, resulting in a reduction of D3R G protein-signaling potential.

FLNA is enriched in membrane ruffles, which are subcellular compartments characterized by inhibited actin filament turnover, a high level of other actin cross-linkers, such as ezrin, and a high level of Rac activity (9). Membrane ruffles are thought to arise following inefficient lamellipodium adhesion and retraction towards the cell body. In Hep2 cells overexpressing the M1MR or AT1AR, short-term agonist stimulation causes rapid membrane ruffling. Activated receptor, FLNA, β arr, and active ERK are localized to these ruffles. In this study, we have demonstrated that knockdown of endogenous

FLNA or β arr levels inhibits M1MR- and AT1AR-induced ruffling. Transfection of a dominant negative MEK [MEK1(K97A)], which cannot activate ERK, also inhibits M1MR- and AT1AR-induced ruffling. Taken together, these findings indicate that β arr, FLNA, and active ERK are functionally important in the formation of membrane ruffles in Hep2 cells following M1MR and AT1AR stimulation.

Among the other FLN isoforms, FLNC has been reported to be expressed predominantly in muscle, whereas FLNB was found to be broadly distributed (43). FLNA knockdown with specific siRNA did not change the level of FLNB expression in Hep2 cells, as indicated by immunoblot studies with specific antibodies (Fig. 9F). This observation is consistent with the fact that the cooperation between β arr and FLN is mostly restricted to the FLNA isoform. Alternatively, the existence of a marked difference in FLNA and FLNB concentrations in Hep2 cells might explain why the specific reduction of FLNA levels caused submaximal inhibition of membrane ruffling in these cells.

Other GPCRs, such as protease-activated receptor-2 (16) and fMLPR (8), induce membrane ruffling upon agonist activation. In the case of protease-activated receptor-2, the ruffling response has been shown to be β arr and ERK dependent (16) whereas for the fMLPR, β arr regulates ruffling via a Ral GDP dissociation stimulator-RalA effector pathway (8). Lymphocytes derived from β arr2-deficient mice have altered chemotactic responses (14), and CXCR4- and AT1AR-mediated chemotaxis in HEK cells occurs via β arr2- and p38-dependent signaling pathways (23, 44). These data together with our results indicate that following GPCR stimulation, β arr play an important role in regulating the actin cytoskeleton and subsequent cell shape change in processes such as cell motility. Our results also suggest that FLNA could serve to localize β arr-mediated MAPK activation to specific cell compartments, providing a link between β arr-mediated signaling events and cytoskeletal reorganization.

In addition to binding MAPK cascade components, repeat regions 22 to 24 of FLNA are important in recruiting Rho family GTPases and some regulatory cofactors implicated in cytoskeletal regulation. The small GTPases Rho, Rac, and Cdc42 bind FLNA repeats 22 to 24 constitutively, and RalA binds repeat 24 in a GTP-dependent manner. Trio, a guanine nucleotide exchange factor for Rho GTPases, binds FLNA via repeats 23 and 24 (7), suggesting that switching Rho GTPases bound to FLNA on and off may serve to regulate the spatial positioning of actin assembly within the cell. This is of particular interest with regard to β arr, as it was recently shown that β arr1 is involved in the activation of the small GTPase RhoA, promoting stress fiber formation following AT1AR stimulation (6).

To conclude, we have identified the actin binding and scaffolding molecule FLNA as a β arr-binding partner, in agreement with recently published data (26). β arr and FLNA act cooperatively to activate the MAPK ERK following GPCR stimulation. In addition, β arr, FLNA and active ERK play obligate roles in cell shape change in Hep2 cells following GPCR stimulation. We propose that FLNA integrates β arr-mediated signaling events and actin cytoskeleton regulation.

ACKNOWLEDGMENTS

We thank A. Aronheim, S. Benichou, J. L. Benovic, M. G. Caron, S. Dowdy, R. J. Lefkowitz, C. J. Loy, H. Lunsady, Y. Ohta, R. Seger, and T. Stossel for providing cDNAs and reagents as detailed in the text; L. Achour for her contribution to fluorescence-activated cell sorter experiments; J. Liotard for technical assistance; and A. Benmerah, H. Enslen, F. Porteu, and S. Shenoy for helpful discussion.

This work was funded by grants from the Wellcome Trust, the Agence Nationale pour la Recherche, Ligue Contre le Cancer (Comité de l'Oise), CNRS, and INSERM. During the performance of this work, M.G.H.S. was supported by postdoctoral fellowships from the Wellcome Trust, Fondation pour la Recherche Médicale, and SIDACTION.

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