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Cloning and Characterization of A-kinase Anchor Protein 100 (AKAP100)

A PROTEIN THAT TARGETS A-KINASE TO THE SARCOPLASMIC RETICULUM*

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Differential localization of the type II cAMP-dependent protein kinase (PKA) is achieved by interaction of the regulatory subunit (RII) with A-kinase anchor proteins (AKAPs). Anchoring is a likely means to adapt PKA for regulation of cAMP-responsive events through colocalization of the kinase with preferred substrates. Using an interaction cloning strategy with an RIIa protein probe, we have identified a 655-amino acid protein (named AKAP100). Recombinant AKAP100, expressed in Escherichia coli, binds RII α in a solid-phase overlay assay. The cellular and subcellular distribution of AKAP100 was analyzed by various methods. Northern blot analysis with the AKAP100 cDNA as a probe detected an 8-kilobase message in some human tissues including various brain regions; however, the message was predominately expressed in cardiac and skeletal muscle. Anti-AKAP100 antibodies confirmed expression in the rat cardiac and skeletal muscle cell lines, H9c2 and L6P, whereas immunohistochemical analysis revealed that AKAP100 was localized to the sarcoplasmic reticulum of both cell types. RII was also detected in these regions. AKAP100 was detected in preparations of RII purified from L6P cell extracts by cAMP-agarose affinity chromatography. Collectively, these results suggest that AKAP100 functions to maintain the type II PKA at the sarcoplasmic reticulum.

Considerable research has focused on determining the role of cAMP in signal transduction since it was discovered as an intracellular second messenger of hormone action (1-2). Cyclic AMP is released from distinct locations at the cell membrane by hormonal activation of adenylate cyclase and diffuses or is transported to its site of action. The predominant effect of cAMP is to activate a cAMP-dependent protein kinase (PKA).¹ Four molecules of cAMP bind each dormant PKA holoenzyme, activating the kinase by releasing the catalytic (C) subunits from the regulatory (R) subunit-cAMP complex (2). Active PKA potentiates the hormonal response by phosphorylating key enzymes and structural proteins, thus modifying their function.

Although the mechanics of PKA activation are well understood, it is still unclear how individual hormones that utilize this ubiquitous cAMP signaling pathway are able to exert localized and specific effects (3-5). To accommodate these pleotrophic properties, PKA must be localized in a microenvironment with the adenylate cyclase complex or in a cellular microcompartment that preferentially concentrates cAMP. Therefore, selective activation of compartmentalized PKA is a plausible mechanism to ensure the selectivity of a hormonal response, and, accordingly, the cellular location of the kinase must be highly regulated (3, 6).

The cellular location of PKA is dictated by the regulatory (R) subunit (7). Two classes of R subunit exist, RI and RII, which form the type I and type II PKA holoenzymes, respectively (8, 9). The RI isoforms (RI α and RI β) are thought to be primarily cytoplasmic, although RI is membrane bound in erythrocytes (10) and may associate with the T-cell receptor in activated lymphocytes (11). In contrast, a significant proportion of the RII isoforms (RII α and RII β) are particulate, and up to 75% of the cellular RII pool associates with the plasma membrane, cytoskeletal components, endoplasmic reticulum, secretory granules, or nuclei (9, 12-16). The subcellular localization of RII is maintained through high affinity interaction with a family of adapter proteins called A-kinase anchor proteins (AKAPs) (12, 17-19). RII dimerization is required for AKAP binding (20-21). More recently, the first 5 amino acids of each RII protomer have been shown to be critical for AKAP interaction, specifically isoleucines at position 3 and 5 (22). The acceptor site on the AKAPs for PKA is more defined; anchoring proteins contain a conserved amphipathic helix of 14-18 amino acids, which must be maintained in the correct conformation to permit binding to the kinase (19, 23, 24). Synthetic peptides patterned after the amphipathic helix bind RII and the type II PKA holoenzyme with nanomolar affinity and can block interaction with AKAPs (24). These "anchoring inhibitor peptides" have been used to disrupt the RII-AKAP interaction in neurons and uncouple the regulation of AMPA-kainate receptors by PKA (25). In accordance with the targeting subunit hypothesis (26), each AKAP must contain additional binding sites responsible for targeting to cellular structures and/or interaction with other proteins. In an effort to identify AKAP binding proteins, complementary DNAs that encode proteins that associate with AKAP79, a neuronal anchor protein (24), were isolated using the yeast two-hybrid system (27, 28). A cDNA for the phosphatase 2B, calcineurin, was isolated and is consistent with earlier observations that PKA and calcineurin copurify through a number of chromatography steps (29). Biochemical and immunological studies have confirmed that both PKA and calcineurin are targeted to subcellular sites by association with AKAP79, possibly to regulate the phosphorylation state of key neuronal substrates (28).

In this report, we describe the cloning and characterization

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The nucleotide sequence(s) reported in this paper has been submitted to the GenBank $^{\text{TM}}$ / EMBL Data Bank with accession number(s) U17195. ‡ To whom correspondence should be addressed: Vollum Institute

The abbreviations used are: PKA, cAMP-dependent protein kinase; AKAP, A-kinase anchor protein; bp, base pair(s); PBS, phosphate-buffered saline; BSA, bovine serum albumin; PAGE, polyacrylamide gel electrophoresis.

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of a novel AKAP, AKAP100, which is selectively expressed in the brain, cardiac, and skeletal muscle. Biochemical and immunochemical analyses suggest that AKAP100 and RII associate *in vivo* at the sarcoplasmic reticulum.

EXPERIMENTAL PROCEDURES

Cloning Strategy—Human cDNA expression libraries were screened by direct overlay with 32 P-labeled RII α as a probe with modifications to the method of Lohmann et al. (17) as described in Ref. 18. Plaques were lifted onto nitrocellulose filters as described (30). Phosphorylation of RII α by the C subunit of PKA was performed with [γ - 32 P]ATP as described (31). All sequencing reactions were performed by the dideoxy chain termination method of Sanger et al. (32).

RNA Analysis—Filters containing immobilized samples of mRNAs of selected human tissues (Clontech) and of human brain regions (provided by Dr. Jeff Arriza, Vollum Institute, Portland, OR) were probed with a ³²P-radiolabeled 1400-base pair fragment encompassing the 3'-coding region of the AKAP100 cDNA. Radiolabeling of the AKAP100 cDNA probe was achieved by the random priming method described in Ref. 33 using $[\alpha^{-32}P]dCTP$. Nitrocellulose filters were prehybridized in 400 mm sodium phosphate, pH 6.6, 1 mm EDTA, 5% SDS, 1 mg/ml BSA, 50% formamide for 2 h at 42 °C. The radiolabeled cDNA probe was denatured by heating at 100 °C for 10 min and then added directly to the nitrocellulose filters. Hybridization was performed in the same buffer at 42 °C overnight with gentle agitation. Non-hybridized probe was removed by washing (three times) in excess $0.1 \times SSC$, 0.1% SDS, and 1 mm EDTA at 53 °C for a total of 2 h. ³²P-Radiolabeled β-actin cDNA was used to probe both of these blots under similar conditions. Hybridizing mRNA species were detected by autoradiography.

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Expression of Recombinant AKAP100—Construction of the AKAP100 expression vector pET11d AKAP100kfc was performed by simultaneous ligation of two DNA fragments into the bacterial expression vector pET11dkfc (34). Initially, a 1398-bp EcoRI-BamHI fragment was excised from the original cDNA clone. Second, an 821-base pair fragment encompassing the 5'-end of the AKAP100 coding region was amplified by polymerase chain reaction. Primers were designed to create an NcoI site at the 5'-end (5'-TCCCAAACCATGGCCTTTACTGGCAG-3') and the T3 site at the 3'-end (5'-ATTAACCCTCACTAAAG-3'). Digestion of the polymerase chain reaction product with NcoI and EcoRI removed a 597-bp fragment. The expression plasmid pET11d AKAP100kfc was constructed by ligating the 1398-bp EcoRI-BamHI and 597-bp NcoI-EcoRI fragments into an NcoI-BamHI cut vector. The fidelity of the AKAP100 coding region was confirmed by nucleotide sequencing. Expression of AKAP100kfc protein was achieved in Escherichia coli pLysS cells as described (35). Soluble Kfc protein was purified by affinity chromatography on calmodulin-agarose as described (34). Protein was concentrated by ultrafiltration (Amicon).

RII Overlays—Overlay assays were performed by the method of Lohmann et al. (18), and quantitative overlays were performed as described (22). Binding was detected by autoradiography and was measured by densitometry after scanning into a computer and analyzed by the National Institutes of Health Image 1.55 program. In control experiments, ³²P-labeled RII probe was pre-incubated with Ht31-(493–515) anchoring inhibitor peptide (0.5 mm) as described (36).

Western Blot Analysis—Proteins were separated by SDS-PAGE as described (37, 38) and electrotransferred to polyvinylidene difluoride membrane (Immobilon, Millipore). Rabbit polyclonal antibodies to AKAP100 (produced by Bethyl Laboratories, Inc., Montgomery, TX) were affinity purified using AKAP100 protein coupled to Affi-Gel 15 (Bio-Rad) and used at 1:250 dilution. Anti-RII antibodies, raised in rabbits (36), were affinity purified and used at 1:5000 dilution.

Preparation of H9c2 and L6P Cell Extracts-Rat cardiac muscle and skeletal muscle cell lines H9c2 and L6P were grown in 75-cm2 tissue culture flasks (NUNC) in Dulbecco's modified Eagle's medium containing 10% fetal calf serum until confluent. The cells were washed three times with phosphate-buffered saline (PBS), pH 7.4, and scraped from the tissue culture flasks. The cell pellet was concentrated by centrifugation at 3000 \times g for 5 min at 4 °C, resuspended in buffer A (50 mm Tris-HCl, pH 7.5, 0.1% Triton X-100 0.05 mm dithiothreitol, 0.5 mm $MgCl_2$, 0.125 mm EDTA, 0.1 μ M leupeptin, 0.1 μ M pepstatin, 0.1 mm benzamidine, 0.1 mm phenylmethylsulfonyl fluoride), and sonicated for 30 s (three bursts of 10 s) on ice. After sonication, the cell suspension was centrifuged at 14,000 × g for 20 min at 4 °C, and the pellet was resuspended in buffer A. Protein concentrations of the supernatant and pellet fractions were measured by Bradford assay (Pierce). Equal concentrations of protein (100 µg), unless otherwise stated, were loaded onto SDS-PAGE gels for subsequent analyses.

Immunocytochemistry—Immunofluorescence studies were formed on rat cardiac muscle H9c2 cells grown in Dulbecco's modified Eagle's medium containing 10% fetal calf serum on glass coverslips in 6-well tissue culture (NUNC) plates for 72 h at 37 °C. Cells were fixed in 3.7% formalin in PBS, pH 7.4, extracted in absolute acetone at -20 °C, and rehydrated in PBS + 0.1% BSA before incubation with affinity-purified primary antibodies (1:100 dilution anti-goat RII and 1:250 dilution AKAP100) for 1 h at room temperature. Control experiments with antibody to signal sequence receptor (1:50 dilution, kindly provided by Dr. T. A. Rapoport, Max-Delbruck center for Molecular Medicine, Germany) and preimmune sera were performed under identical conditions. Cells were washed with excess PBS + 0.1% BSA (3 times) before incubation with secondary antibodies (1:100) for 1 h at room temperature. RII was detected with fluorescein isothiocyanateconjugated donkey anti-goat IgG, and AKAP100 was detected with Texas Red donkey anti-rabbit IgG. Unbound secondary antibodies were removed by washing with excess PBS + 0.1% BSA (three times). Coverslips were mounted with VectashieldTM mounting medium. Staining patterns were observed on a Leitz Fluovert FU confocal photomicroscope under oil immersion using a 63/1.4 OEL PL APO lens.

Purification of the RII-AKAP100 Complex by cAMP-Agarose—RII-AKAP complexes were isolated from rat skeletal muscle cell extracts as previously described (36). Unbound protein was removed from the cAMP-agarose by washing with hypotonic buffer plus 1 M NaCl and four additional washes with hypotonic buffer. Finally, specifically bound proteins were eluted from the affinity resin by incubation at room temperature with hypotonic buffer containing 75 mm cAMP.

Other Methods—Antibodies against AKAP100 peptide and recombinant AKAP100 were produced by Bethyl Laboratories, Inc. (Montgomery, TX). Oligonucleotide sequencing primers were purchased from the Center for Gene Research and Biotechnology, Oregon Science University (Corvallis, OR).

RESULTS

Cloning of AKAP100—Clones encoding AKAPs were isolated from a human hippocampal cDNA expression library by the RII overlay method using $RII\alpha$ as a probe. One positive clone was isolated from ~250,000 recombinants. This clone was called hhBD-1 (1888 bp) and contained a partial open reading frame of 599 amino acids (Fig. 1A). When Northern blots were screened with a hhBD-1 probe, the only mRNA species detected in human tissues was 8 kilobases, confirming that hhBD-1 was a partial fragment of the full-length cDNA. The human hippocampal cDNA library was rescreened with a 1400-bp HindIII-BamHI fragment excised from the 5'-end of hhBD-1, but this did not yield clones with any additional information. However, a random and oligo(dT)-primed human fetal brain cDNA library (provided by Dr. W. Michael Gallatin, ICOS Corp., Seattle, WA) was screened with the same probe, and 12 positive clones were identified from ~500,000 recombinants. DNA from seven of the positive clones was sequenced and indicated that one clone, called hFB 7-1 (1314 bp), overlapped with hhBD-1 and yielded 822 bp of additional 5'-sequence. A composite sequence of 2595 is presented in Fig. 1A and contains an open reading frame encoding a 655-amino acid protein with a predicted M_r 78,172. However, the protein migrates on SDS-polyacrylamide gels with an apparent molecular mass of 100 kDa (see below); thus, in accordance with the nomenclature proposed for RII anchoring proteins by Hirsch and colleagues (39), we have named the protein AKAP100.

Comparison of the AKAP100 sequence to the DNA and protein data base did not identify any overall similarity to other known proteins. Computer-aided analysis of the AKAP100 sequence identified a putative amphipathic α -helix located between residues 392 and 408 (Fig. 1B). This region is compared with the RII-binding regions of other AKAPs (Fig. 1C). Both of these findings are consistent with the notion that residues 392–408 of AKAP100 form the RII-binding domain.

The Tissue Distribution of AKAP100 mRNA—To establish the tissue expression pattern of AKAP100, filters of immobilized poly(A)⁺ RNA from several human tissues were screened

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532 GTG GCT GAT GAR AGC GAT GTC ART GTC AGC ATG ATT GTT AAT GTC TCT TGC ACC TCT GCT Val Ala sap Glu Ser Asp Val Am Val Ser Het Ile Val Am Val Ser Cye Thr Ser Ala TOC ACT GAT GAT GAR GAT GAC AGG GAC CTG CTC TCC AGG TCT ACC CTT ACC CYe Thr Asp Asp Glu Asp Asp Ser Asp Leu Leu Ser Ser Ser Thr Leu Thr 832 101 952 141 1021 1012 161 1131 1072 181 TOA TOT CAT ACC CAT GAG TTA GOG ACA AAG COT GAA AAT AAG AAA ACT ATT TTC AAA GTT Ser ser hie Thr his Glu Leu Gly Thr Lys Arg Glu Aen Lys Lys Thr Ile Phe Lys Val 1132 201 1191 ART ARE GET COR THE GTG GCT GRC ATG GRE RAT GCC ART ATT GRE GGT ATT COR GRE AGG Amm Lym Amb Pro Tyr Val Ala Amp Net Glu Amm Gly Amm Ile Glu Gly Ile Pro Glu Ary 1252 CAA ANG GGC AAA CCG AAT GTG ACT TCA ANG GTA TCA GAA AAT CTT GGT TCA CAT GGG Gln Lys Gly Lys Pro Asn Val Thr Ser Lys Val Ser Glu Asn Leu Gly Ser His Gly 1371 AAT ACT GCT GGC AAG GAA TIT GTT TCC CAA GAT GTT AGA CAT CTT CCA AAG AAA TGT Aan Thr Ala Gly Lys Glu Phe Val Ser Gln Asp Val Arg His Leu Pro Lys Lys Cys 1431 1432 301 1491 320 AAT CAC CAC CAT TIT GAA AAT CAA AGC ACT GCC TCT ACT CCC ACT GAG AAG TCT TTC Amn His His His Phe Glu Amn Gln Ser Thr Ala Ser Thr Pro thr Glu Lys Ser Phe GRA CTG OCT TTA GRA ACC AGG TTT RAC ARC AGA CAR GRC TCT GAT GCG CTG ARA TCA TCT Glu Lou Ala Lou Glu Thr Arg Pho Asn Asn Arg Gln Asp Ser Asp Ala Lou Lys Ser Ser GAT GAT GCA CCG AGT ATG GCT GGA AAA TCT GCT GGT TGT TGC CTA GCA CTT GAA CAA AAC Aap Aap Ala Pro Ser Met Ala Gly Lys Ser Ala Gly Cys Cys Leu Ala Leu Glu Gln Aan GOA ACA GAG GAA ANT GCT TCT ATC AGC GAC ATT TCC TGT TGC AAC TGT GAG CCA GAT GTT Gly The glu Glu Asn Ala See lie See Aep lie See Cye Cye Asn Cye Glu Pro Aep Val TTC CAT CAA AAA GAT GCC GAA GAT TGT TCA GTA CAC AAC TTT GTT AAG GAA ATC ATT GAC Phe His Gin Lys Asp als Glu Asp Cys Ser Val His Asn Phe Val Lys Glu Ile Ile Asp 1672 1791 420 ATG OCT TOG ACA OCC CTA ARA AGT ARA TOT CAR CCT GAR ARC GAG GTG GCT GCT CCT ACT Not als set Thr als Lou Lys Ser Lys Ser gin Pro Glu Asn Glu Val Als Als Pro Thr 1732 1851 TCA TTA ACT CAN ATC ANG GRG AAN GTG TTG GAG CAT TCT Ser Lou Thr Gln 11e Lys Glu Lys Val Lou Glu His Ser 1852 1911 1912 1972 A GAG GAG CCT TOT TTC TCT AGT GCT CCT CCA AAT GAA TCT GCA GTT CCC AGC GAA GCT y Glu Glu Pro Cye Phe Ser Ser Ala Pro Pro Amn Glu Ser Ala Val Pro Ser Glu Ala GAT GAT GCA GAT ACA GTG GCT CTT TCA AGT CCT TCC TCT CAG GAA AGA GCT GAG GTT GGA Amp Amp Ala Amp Thr val Ala Leu Ser Ser Pro Ser Ser Gln Glu Arg Ala Glu Val Gly CCT TCA ANG CTT GAC AGT GAA AAG GAA AGT TCC GGA AAA CCA GGT GAA TCT GGA ATG CCA Pro Ser Lys Leu Asp ser Glu Lys Glu Ser Ser Gly Lys Pro Gly Glu Ser Gly Het Pro 2272 2332 601 2391 620 GAA GAA CAT AAT GCT GCT TCA GCC AAA TCT AAA GTT CAA GAC CTC TCC Clu Glu His Asn Ala Ala Ser Ala Lys Ser Lys Val Gln Asp Leu Ser 2392 ACA GAC AAG GCC GCA TTG GAT CCC AGC CCC AAA ACT TTA ACC TOT GAA GAA AAT Thr Asp Lys Ala Ala Leu His Pro Ser Pro Lys Thr Leu Thr Cys Glu Glu Asn



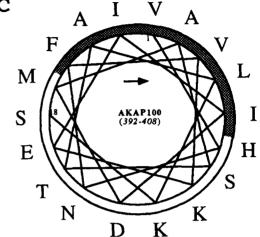


Fig. 1. Sequence of AKAP100. A, the nucleotide sequence (upper line) and deduced amino acid sequence (lower line) of a cDNA encoding the protein kinase A anchor protein AKAP100. The boxed region indicates the putative RII-binding region, and a sequence used to raise peptide antisera is underlined. B, sequence homology between AKAP100 (residues 396–411) and the RII-binding regions of three other AKAPs, MAP2, AKAP150, and Ht31. Boxed regions show amino acid identity, and conservative changes (*) are indicated. C, helical wheel representation of AKAP100 (residues 392–408) drawn as a α -helix of 3.6 amino acids/turn. The shaded area indicates hydrophobic residues, and the open area indicates hydrophilic residues. Amino acids are indicated in the one-letter code. The arrow indicates the direction of the helix.

with a radiolabeled 1400-bp *HindIII-BamHI* fragment excised from hhBD-1. A single mRNA species of 8 kilobases was detected in certain human tissues and a variety of brain regions

(Fig. 2, A and C). The AKAP100 mRNA was most highly expressed in the heart and skeletal muscle (Fig. 2A). When the filters were probed with a β -actin probe, equal levels of mes-

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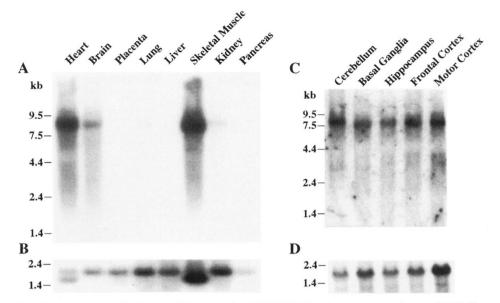


Fig. 2. The tissue distribution of the AKAP100 mRNA. 2 µg of poly(A)+ RNA from human tissues (human MTN, Clontech) (A) and selected brain regions (5 μ g) (C) on nitrocellulose were probed with a ³²P-radiolabeled 1400-bp HindIII-BamHI fragment excised from the 5'-end of hhBD-1 as described under "Experimental Procedures." Human tissues (human MTN, Clontech) (B) and selected brain regions (D) were probed with 32 P-radiolabeled β -actin. Hybridizing mRNA species were detected by autoradiography. The tissue source of each RNA is indicated above each lane.

sage were detected in each lane (Fig. 2, B and D).

Expression and Characterization of AKAP100—To confirm that AKAP100 was an RII binding protein, the full-length cDNA was expressed in E. coli using the kfc fusion system (34) as described under "Experimental Procedures." A 115-kDa protein was detected by SDS-PAGE in bacterial extracts of induced cells and was purified to homogeneity by affinity chromatography on calmodulin-Sepharose (Fig. 3A). The expression of the recombinant fusion protein was monitored by Western blot (Fig. 3A) using anti-peptide antisera raised against residues 188-203 of AKAP100 (Val-Lys-Arg-Val-Ser-Glu-Asn-Asn-Gly-Asn-Gly-Lys-Asn-Ser-Ser-His). The recombinant protein bound ³²P-RII as assessed by a direct overlay (Fig. 3C). Solid-phase RII binding was blocked when overlay blots were incubated with the anchoring inhibitor Ht31-(493-515) peptide (Fig. 3D). This peptide has been previously shown to block RII-AKAP interaction (24, 36). Nonspecific binding to a band of 80 kDa was detected upon prolonged exposure of the control blot (Fig. 3D).

The binding affinity of AKAP100 was assessed by quantitative overlays using RII α protein at a specific activity of 2.1–1.5 × 10⁵ cpm/pmol. The binding to immobilized AKAP100 and Ht31 over a range of 0.01-10 nmol/100 µl was detected by autoradiography and was measured by densitometry. Both proteins bound RII with high affinity, with half-maximal binding values calculated at 10 μ M for AKAP100 and 2.5 μ M for Ht31 (Fig. 4). Collectively, these data are consistent with the notion that the AKAP100 cDNA encodes a high affinity RII binding protein.

The Subcellular Location of AKAP100—The tissue distribution of AKAP100 mRNA suggested that the protein may be predominately expressed in cardiac and skeletal muscle tissues. To test this hypothesis, affinity-purified polyclonal AKAP100 antisera, raised against purified recombinant AKAP100, was used to probe protein extracts from a variety of muscle cell lines including the rat cardiac muscle (H9c2) and rat skeletal muscle (L6P) cell lines. A single immunoreactive protein of 100 kDa was detected by Western blot for both H9c2 (Fig. 5, lane 2) and L6P (see below) cells. There was no immunoreactivity when identical blots were probed with preimmune serum (Fig. 5, lane 3). Numerous RII binding proteins ranging

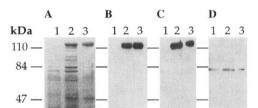


Fig. 3. Recombinant AKAP100 binds RIIα. The entire coding region of AKAP100 was expressed using the pET11dkfc plasmid. Expression of recombinant protein was induced by the addition of 0.4 mm isopropyl-1-thio-β-D-galactopyranoside to growing bacterial cultures. Bacterial extracts (100 μ g) or purified protein were separated by electrophoresis on 10% (w/v) SDS-polyacrylamide gels and electrotransferred to polyvinylidene difluoride membranes. Blots were stained with Coomassie Blue (A) and analyzed by autoradiography (B-D). B, AKAP100 was detected by Western blot with anti-peptide antibodies. RII binding proteins were detected by a solid-phase binding assay (17) using 32 P-radiolabeled RII α as a probe in absence (C) or presence (D) of 1 μM anchoring inhibitor Ht31-(493-515) peptide. Sample sources, indicated above each lane, are uninduced bacterial lysate (lane 1), isopropyl-1-thio-β-D-galactopyranoside-induced bacterial lysate (lane 2), and affinity-purified protein (lane 3). Molecular mass markers are indicated on each panel.

in size from 250 to 40 kDa were detected in both cell lines by direct overlay (data not shown).

The subcellular location of AKAP100 was examined using indirect immunofluorescence techniques (Fig. 6). In quiescent H9c2 cells (Fig. 6A), AKAP100 staining was restricted to the perinuclear regions (Fig. 6C) and exhibited a similar staining pattern to the sarcoplasmic reticulum marker protein, signal sequence receptor (Fig. 6B). Conversely, the staining pattern of the Golgi marker protein, mannosidase II, was distinct from AKAP100 (data not shown). Double immunofluorescence staining for AKAP100 (Fig. 6C) and RII (Fig. 6D) suggested that both proteins had overlapping cellular distributions and were concentrated in the same cellular compartment. This observation was confirmed by confocal microscopy showing that AKAP100 and RII have overlapping staining patterns in 0.1micron-thick focal sections of H9c2 cells (Fig. 6, C and \bar{D}). Control experiments confirmed that no staining was observed with preimmune serum (Fig. 6, E and F) or secondary antibody alone (data not shown). These experiments are consistent with



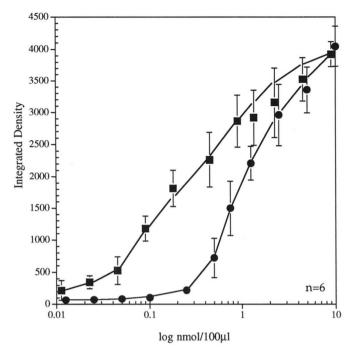


Fig. 4. Quantitation of AKAP binding to RII α . The binding of $^{32}\text{P-radiolabeled}$ RII α to AKAP100 and a fragment of the human thyroid anchoring protein Ht31 was measured by a quantitative overlay procedure. Aliquots of purified anchoring proteins, ranging from 0.01 to 10 nmol/100 μ l were immobilized onto nitrocellulose filters. Individual filters were probed with excess $^{32}\text{P-radiolabeled}$ RII α (specific activity ranging from 2.1 to 1.5 \times 10⁵ cpm/nmol). Unbound $^{32}\text{P-radiolabeled}$ RII α was washed off with Tris-buffered saline (pH 7.4). Detection of binding was by autoradiography. Quantitation of binding over the range of AKAP concentrations was measured by densitometry of the autoradiographs. Signals were normalized for the specific activities of each RII α probe. Binding curves for AKAP100 (O) and Ht31 (\blacksquare) are presented from six experiments, and the standard deviation is indicated.

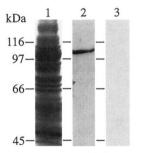


Fig. 5. **AKAP100** is present in an H9c2 cell lysate. A solubilized extract $(250 \ \mu g)$ of H9c2 cells was stained with Coomassie Blue ($lane\ 1$) or probed for AKAP100 ($lane\ 2$) using purified antibodies. Detection was by enhanced chemiluminescence. Preimmune sera is shown in $lane\ 3$. Molecular mass markers are indicated.

the localization of AKAP100 and a significant proportion of RII to the sarcoplasmic reticulum of H9c2 cells. An indistinguishable staining pattern for AKAP100, RII, and marker proteins was obtained when these experiments were repeated in L6P cells (data not shown).

Purification of the RII-AKAP100 Complex—To examine whether AKAP100 was associated with RII in cell lysates, we attempted to purify the RII-AKAP100 complex using affinity chromatography on cAMP-agarose. L6P cells were used for these experiments because they grow more rapidly and, thereby, provide more starting material. Western blot analysis of solubilized L6P cell lysates indicated that the lysates contained RII that was purified by affinity chromatography on cAMP-agarose (Fig. 7A). Identical blots probed with anti-

AKAP100 antibodies indicated that a proportion of the AKAP100 present in the lysate copurified with RII (Fig. 7*B*). These results provide evidence that RII-AKAP100 complexes exist and can be purified from cell lysates.

DISCUSSION

In this report, we describe the cloning and characterization of a novel A-kinase anchor protein, AKAP100, which is specifically localized to the sarcoplasmic reticulum. AKAP100 is selectively expressed in certain tissues, and high levels of the 8-kilobase message are detected in various brain regions and cardiac and skeletal muscle. This finding is supported by cloning studies that isolated the original cDNA fragment from a human hippocampal library. The calculated molecular weight of AKAP100 is 78,172, although the protein migrates with a mobility of M_r 100,000 on SDS-polyacrylamide gels. Apparently, anomalous migration on SDS-PAGE gels is a characteristic of several AKAPs. For example, the bovine neural-specific anchoring protein, AKAP75, has a calculated molecular weight of 47,085 but migrates with an apparent mobility of 75 kDa on SDS-PAGE gels (24). This has led Hircsh and colleagues (39) to suggest that the abundance of acidic residues in the aminoterminal portion of the protein alters its migration pattern. Consistent with this hypothesis, AKAP100 also contains stretches of acidic side chains between residues 80 and 110 of the protein.

A growing body of evidence suggests that AKAPs contain a conserved RII-binding site responsible for interaction with PKA. Recently, we have shown that RII binding proceeds through sites in the extreme amino terminus of RII, and isoleucines 3 and 5 on each RII protomer are required for interaction with an amphipathic helix on the surface of the AKAP (22). Site-directed mutagenesis studies have demonstrated that an intact α-helical structure is required for RII-AKAP interaction (23), and synthetic peptides encompassing the amphipathic helix regions of three AKAPs (Ht31, AKAP79, and AKAP95) block RII-AKAP interaction in vitro (19, 24, 36). On the basis of these observations, it seems likely that residues 392-408 may form the RII-binding site on AKAP100. This region exhibits a high probability of amphipathic α-helix formation and shares 30-40% sequence identity with the RIIbinding regions of other AKAPs (Fig. 1B); deletion constructs lacking residues 392-410 are unable to bind RII by the overlay assay.² Moreover, the anchoring inhibitor peptide, Ht31-(393-415), effectively competes with AKAP100 for RII binding in direct overlays.

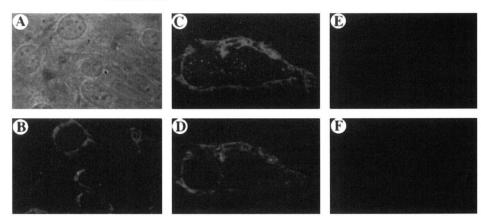
It would also appear that AKAP100 binds RIIα with high affinity, as half-maximal binding to the immobilized anchoring protein was measured in the micromolar range. Although it is technically infeasible to measure precise binding constants due to aggregation of AKAP100, it would appear that the intracellular levels of AKAP100 and RII (assessed by Western blotting) are within a concentration range sufficient to permit complex formation in vivo. This notion is supported by our evidence that AKAP100 is copurified with RII from L6P cell lysates by affinity chromatography on cAMP-agarose. Since recombinant AKAP100 does not display any intrinsic cAMP binding affinity, it is therefore likely that the anchoring protein was purified as complex with RII. In addition, both RII and AKAP100 were detected in the flow-through from the cAMP-agarose (Fig. 7). There are two potential explanations for this observation: the amount of RII in the cell lysate was in excess of the capacity of the cAMP-agarose preventing retention of all RII complexed with AKAP and an undetermined proportion of AKAP100 was not associated with RII. This observation is consistent with

² B. M. Little and J. D. Scott, unpublished observation.

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Fig. 6. Immunocytochemical analysis of rat cardiac muscle cell line (H9c2). H9c2 cells were formalin-fixed (A) and incubated with anti-sequencespecific receptor antibodies (B), anti-AKAP100 antibodies (C), anti-RII antibodies (D), or preimmune serum for AKAP100 (E) and for RII (F) under the conditions described under "Experimental Procedures." Fluorescein isothiocyanate-conjugated anti-rabbit secondary antiserum was used in panels B, C, and E). Texas red conjugated anti-goat secondary antiserum was used in panels D and F.

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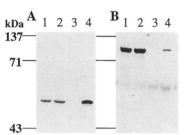


Fig. 7. AKAP100 copurifies with RII on cAMP-agarose. Detection of proteins on Western blots is shown for fractions isolated from cAMP-agarose affinity chromatography. Separate filters were probed for either RIIa (A) or AKAP100 (B) using purified antibodies and enhanced chemiluminescence detection. A solubilized extract of L6P cells (lane 1) was incubated with cAMP-agarose. Unbound protein (lane 2) was separated from the affinity matrix by centrifugation, and the pellet containing protein bound to cAMP-agarose was washed extensively in washing buffer. After a final wash (lane 3), proteins remaining bound to the affinity matrix were eluted in 75 mm cAMP (lane 4) and boiled in sample buffer. Fractions (100 µg, lanes 1 and 2; 10 µg, lane 4) were separated on 7.5% SDS-polyacrylamide gels and electrotransferred to polyvinylidene difluoride membranes. Molecular mass markers are indicated.

similar findings for AKAP79 and AKAP95 (24, 36), which indicate that a proportion of the RII-binding sites on anchoring proteins are unoccupied. Furthermore, our findings show that only a fraction of RII purified is associated with AKAP100 (Fig. 7B, lane 4). This is because the cAMP-agarose purification protocol isolates the total R subunit pool, which includes soluble RI, soluble RII, and RII associated with other AKAPs present in the L6P cell extract.

Previous studies have proposed that the type II PKA is associated with native sarcoplasmic reticulum vesicles (40). This finding is supported by our immunocytochemical data showing that AKAP100 and a significant proportion of the cellular RII pool appear to be localized at the sarcoplasmic reticulum. In light of both observations, we suggest that AKAP100 functions to adapt PKA for a role in the phosphorylation of proteins in or surrounding the sarcoplasmic reticulum. Although the precise identity of these target substrates remains to be determined, anchoring of kinases close to ion channels is an attractive hypothesis. Levitan and others (13, 40-44) have proposed that targeting of kinases and phosphatases could permit the precise regulation of ion channel phosphorylation status. This view is supported by evidence suggesting that anchoring of PKA by AKAPs is required for modulation of glutamate receptor ion channels. Intracellular perfusion of cultured hippocampal neurons with anchoring inhibitor peptides derived from the conserved kinase-binding domain of AKAP79 or Ht31 prevented PKA-mediated regulation of the AMPAkainate currents (25). Therefore, the AKAP100-PKA complex might interact directly with ion channels or may be targeted to structural proteins within the sarcoplasmic reticulum. For example, the ryanodine receptor, which forms the intracellular Ca²⁺ release channel of the sarcoplasmic and endoplasmic reticulum, is activated by PKA (45), influencing Ca2+ mobilization within the cell (46, 47). Other reports have suggested PKA activity is closely associated with a reconstituted calciumactivated potassium channel (41) and a sarcoplasmic reticulum-associated chloride channel (40). Moreover, recent studies suggest that voltage-dependent potentiation of the L-type Ca2+-gated channels in skeletal muscle requires anchored PKA. Catterall and colleagues (48) have shown that perfusion of the Ht31 anchoring inhibitor peptide prevents cAMP-responsive potentiation of the channel. In addition, AKAP100 may function to target other enzymes involved in signal transduction to the sarcoplasmic reticulum, as we have recently demonstrated that AKAP79 forms a ternary complex with PKA and the phosphatase 2B, calcineurin (28). These results suggest that both kinase and phosphatase are targeted to subcellular sites by association with a common anchor protein to regulate the phosphorylation state of key substrates.

In conclusion, these studies suggest that AKAP100 is a novel protein that binds $RII\alpha$ with high affinity. The anchoring protein is selectively expressed in certain human tissues and has been localized to the sarcoplasmic reticulum in rat cardiac H9c2 cells. Current studies are focusing on identifying other proteins that interact with AKAP100 to establish those molecules responsible for targeting the entire complex to the sarcoplasmic reticulum.

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