An Endoplasmic Reticulum Retention Signal Located in the Extracellular Amino-terminal Domain of the NR2A Subunit of N-Methyl-d-aspartate Receptors*\(^5\)

Received for publication, April 8, 2009. Published, JBC Papers in Press, June 1, 2009, DOI 10.1074/jbc.M109.004960

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\(^*\) This work was supported by National Natural Science Foundation of China Grants 30730038 and 30800308 and National Basic Research Program of China Grant G2002CB713808 (to J. H. L.). This work was also supported by the National Institutes of Health Grant REY016754A and American Heart Association Grant 0655201Y (to J. Z.). The on-line version of this article (available at http://www.jbc.org) contains Supplemental Figs. 1–4.

N-Methyl-d-aspartate (NMDA) receptors play critical roles in complex brain functions as well as in the pathogenesis of neurodegenerative diseases. There are many NMDA isoforms and subunit types that, together with subtype-specific assembly, give rise to significant functional heterogeneity of NMDA receptors. Conventional NMDA receptors are obligatory heterotetramers composed of two glycine-binding NR1 subunits and two glutamate-binding NR2 subunits. When individually expressed in heterogeneous cells, most of the NR1 splice variants and the NR2 subunits remain in the endoplasmic reticulum (ER) and do not form homomeric channels. The mechanisms underlying NMDA receptor trafficking and functional expression remain uncertain. Using truncated and chimeric NMDA receptor subunits expressed in heterogeneous cells and hippocampal neurons, together with immunostaining, biochemical, and functional analyses, we found that the NR2A amino-terminal domain (ATD) contains an ER retention signal, which can be specifically masked by the NR2A ATD in the surface expression of NMDA receptors. Interestingly, no such signal was found in the ATD of the NR2B subunit. We further identified the A2 segment of the NR2A ATD to be the primary determinant of ER retention. These findings indicate that NR2A-containing NMDA receptors may undergo a different ER quality control process from NR2B-containing NMDA receptors.

Ionotropic glutamate receptors (iGluRs)\(^2\) mediate most of the excitatory neurotransmission in the central nervous system. They play key roles in complex brain functions as well as in the pathogenesis of neurodegenerative diseases. Based on pharmacological properties and sequence similarities, iGluRs can be grouped into three major subtypes: GluR1 to -4 subunits form \(\alpha\)-amino-3-hydroxy-5-methyl-4-isoxazolepropionate (AMPA) receptors, GluR5 to -7 and KA1 and -2 subunits make up kainate receptors, and NR1 together with NR2A to -D subunits comprise the NMDA receptors (1). All iGluR subunits share a unique membrane topology with a large extracellular NH\(_2\)-terminal domain, three transmembrane segments (TM1 (transmembrane domain 1), TM3, and TM4), a P-loop region, and a cytoplasmic COOH terminus (2, 3). Based on the sequence homology to bacterial periplasmic binding proteins, the NH\(_2\)-terminal domain of iGluRs can be divided into two domains in tandem: the amino-terminal domain (ATD), which includes the first 400 or so amino acids (4), and the following S1 domain preceding TM1, which forms the ligand-binding domain together with the extracellular loop between TM3 and TM4 (S2 domain) (5, 6).

Among iGluRs, NMDA receptors are special in that conventional NMDA receptors are obligatory tetrameric membrane proteins composed of two glycine-binding NR1 and two glutamate-binding NR2 subunits. The NR1 subunit is essential for the formation of functional NMDA receptor channel, whereas the NR2 subunit modifies channel properties, such as current kinetics and channel conductance (1). The major NR1 splice variant and the NR2 subunits are retained in the ER when expressed alone in heterogeneous cells. Only when expressed together do they form functional receptors on the cell surface (7–9). In the last decade, enormous progress has been made in understanding the phenomenology and mechanisms of functional plasticity of NMDA receptors. However, much less is known about the mechanisms underlying the ER retention of NMDA receptor subunits. Previous studies focused on the COOH terminus have shown that the NR1a subunit contains an ER retention signal, RRR, in the C1 cassette, whereas a motif, HLFY, found in the NR2B subunit immediately following the TM4 (10) or, at least, the presence of any two amino acid residues after NR2 TM4 (11) is required for the export of NR1-NR2 complexes from the ER. Recently, novel ER retention signals were identified in the TM3 of both NR1 and NR2B subunits. In addition, TM3 of both NR1 and NR2B and TM4 of NR1 are necessary for masking ER retention signals found in TM3 (12).

In the present study, we focused on the functional role of the ATD in the surface expression of NMDA receptors. Interest-
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Initially, we found an ER retention signal located in the ATD of the NR2A subunit but not in the corresponding domain of the NR2B. It is suggested that NR2A-containing NMDA receptors may undergo an ER quality control process different from that of NR2B-containing NMDA receptors.

EXPERIMENTAL PROCEDURES

Plasmid Construction—The expression vectors for XFP-NR1a, XFP-NR2A, XFP-NR2B, and GABA_A, α1-YFP have been described previously, in which XFP indicates CFP, YFP, or GFP (13, 14). The ATD-deleted, XFP-tagged NR1a, NR2A, or NR2B subunits used in this study were constructed from XFP-NR1a, XFP-NR2A, and XFP-NR2B, respectively, using conventional DNA mutagenesis techniques. In this report, NR1a ΔATD means that the first 390 amino acid residues of the NR1a subunit were deleted, NR2A ΔATD means that the first 391 amino acid residues of the NR2A subunit were deleted, and NR2B ΔATD means that the first 392 amino acid residues of the NR2B subunit were deleted (Fig. 1A). NR2A ATD-2B and NR2B ATD-2A represent chimeras in which the ATD of the first subunit was substituted with the ATD of the second subunit (Fig. 4A). For example, NR2A ATD-2B means that the ATD of the NR2A subunit was substituted with that of the NR2B subunit. NR2A ΔATD-A1, NR2A ΔATD-A2, or NR2A ΔATD-A3 were constructed by inserting an NR2A A1, A2, or A3 segment into the SacII site of NR2A ΔATD whereas NR2A ΔATD-A2-2B was constructed by inserting the NR2B A2 segment into the SacII site of NR2A ΔATD, as illustrated in Fig. 8A. pDisplay-GFP was constructed by fusing GFP with the pDisplay vector between the XmaI and SacII sites by PCR amplification. The chimeras between the ATD of the NR1a, NR2A, or NR2B subunit and pDisplay-GFP were made by fusing the ATD of these subunits into the pDisplay-GFP at the SalI site and were named GFP-ATD-A1, GFP-ATD-A2, or GFP-ATD-A3, respectively (Fig. 5A). GFP-ATD-a, GFP-ATD-b, or GFP-ATD-c was constructed by fusing the ATD of the NR1a subunit or the GluR2 subunit into the pDisplay-GFP at the Sal or SacII site (see Fig. 5A and supplemental Fig. 4A). GFP-A2a or GFP-A2b was constructed by inserting the A2 segment of the NR2A or NR2B subunit into the pDisplay-GFP at the SacII site, respectively (Fig. 8C). NR2A A2-2A means the A2 segment of the full-length NR2B subunit was substituted with that of the NR2A subunit (Fig. 8A), and GFP-ATD-b,2A-2A means the A2 segment of the GFP-ATD2b was substituted with that of the NR2A subunit (Fig. 8C), which was subcloned by using an In-Fusion™ 2.0 Dry-Down PCR cloning kit (Clontech). According to the results from amino acid sequence alignment of the A2 segment of the NR2A and NR2B subunits, we selected 10 residues in the NR2A A2 segment with highly diverse side chain chemical natures (Fig. 8E). Each of them was replaced with the corresponding residue in the NR2B A2 segment. For example, I176Y means the isoleucine at position 176 of the NR2A subunit was replaced with a tyrosine (corresponding to Tyr179 in the NR2B A2 segment). All site-directed mutagenesis manipulation was done using the QuikChange mutagenesis kit (Stratagene, La Jolla, CA). GFP-A2a,2a-a, GFP-A2a,2a-b, and GFP-A2a,2a-c were constructed by fusing part of a (Ile151–Asp156), b (Asn193–Leu238), or c (Ile239–Asp282) of the NR2A A2 segment into the pDisplay-GFP at the SacII site, respectively (Fig. 8F). For each construct, the amino acid number (relative to the first methionine in the open reading frame) at the appropriate junction is indicated in Figs. 1A, 4A, and 8, A and F. All constructs were verified with DNA sequencing.

Cell Culture and Transfection—HEK 293 cells and COS-7 cells were grown in Dulbecco’s modified Eagle’s medium, supplemented with 10% fetal bovine serum and antibiotics (all from Invitrogen), and transfected with appropriate plasmids (3–4 µg/35-mm dish, 6–8 µg/60-mm dish) using Lipofectamine 2000 (Invitrogen) according to the manufacturer’s protocol. The transfection mixture was replaced 3–5 h after transfection with fresh culture medium. Ketamine (0.5 mM; Sigma) and kynurenic acid (1 mM; Sigma) were added to the media to protect the cells from NMDA receptor-mediated toxicity. Cells were examined within 2 days after transfection in an extracellular solution composed of 145 mM NaCl, 5 mM KCl, 2 mM CaCl2, 5 mM glucose, 0.01 mM glycine, and 5 mM HEPES at pH 7.4 with NaOH. Hippocampal neuronal cultures were prepared according to the protocol described previously (13). At 5 days in vitro, appropriate plasmids (3–4 µg/35-mm dish) were added with 4 µl of Lipofectamine 2000. After a 3-h incubation at 37 °C, cells were washed twice with serum-free medium, and the serum-containing culture medium was added. Expression of exogenous DNA was typically detected in 7 days in vitro neurons.

Surface Immunostaining and Quantitative Analysis—The methods used for surface immunostaining and quantitative analysis have been described previously (11, 13). Briefly, the transfected HEK 293 cells or hippocampal neurons were incubated with rabbit anti-GFP antibody (Chemicon) for 7 min, rinsed three times in extracellular solution, and then incubated with Cy3-conjugated goat anti-rabbit secondary antibody (Jackson ImmunoResearch Laboratories) for another 7 min. After another brief wash in extracellular solution, cells were immediately fixed and examined through a 60×, 1.4 numerical aperture oil immersion objective on a TE 2000 inverted microscope (Nikon, Tokyo, Japan) equipped with Metamorph version 5.0 software (Universal Imaging, West Chester, PA). All procedures were performed at room temperature. Surface expression of XFP-tagged NMDA receptor (NR) subunits in HEK 293 cells or hippocampal neurons was measured as the percentage of surface-stained cells (red) in the population of total cells transfected with XFP fusion proteins (green). For each sample, more than 200 XFP-positive HEK 293 cells or 50 XFP-positive hippocampal neurons were counted, and the means were obtained from three different cultures. The average intensities of surface (Cy3) and total fluorescence (GFP) were determined for regions outlined around the transfected HEK 293 cells or for regions outlined around the cell body of transfected hippocampal neurons. The optical signal level from non-transfected HEK 293 cells or for regions outlined around the cell body of transfected hippocampal neurons was considered as background. Intensity measurements are expressed in arbitrary units per unit area. For each sample, more than 60 XFP-positive HEK 293 cells or 30 XFP-positive neurons were counted, and the means were obtained from three different cultures. All data are presented as the mean ± S.E. Differences were tested using Student’s t test or a one-way ANOVA test followed by the Newman–Keuls multiple comparison test.
**Electrophysiology**—The electrophysiological methods have been described previously (11). The extracellular recording solution contained 145 mM NaCl, 3 mM KCl, 10 mM HEPES, 3 mM CaCl₂, 8 mM glucose, 2 mM MgCl₂ (310 mosmol, pH adjusted to 7.30 with NaOH). Patch pipettes were filled with an intracellular solution containing 136.5 mM potassium gluconate, 17.5 mM KCl, 1 mM MgCl₂, 10 mM HEPES, 0.2 mM EGTA (310 mosmol, pH adjusted to 7.20 with KOH). Recordings were made at −60 mV during the application of 100 μM glutamate and 10 μM glycine or 50 μM D-AP5, an antagonist of NMDA receptors.

**Immunocytochemistry**—Cultured COS-7 cells were fixed in 4% paraformaldehyde in PBS for 10 min and permeabilized in PBS containing 0.4% Triton X-100 and 5% bovine serum albumin for 30 min at room temperature. Cells were then incubated in primary mouse monoclonal PDI antibody (a marker for ER; Abcam), 58K antibody (a marker for Golgi; Abcam), 19 S S5A antibody (a marker for proteosomes; Abcam), EEA1 antibody (a marker for early endosome; BD Biosciences), LAMP2 antibody (a marker for lysosome; Abcam), or NR1a (BD Biosciences) antibody, with or without primary rabbit polyclonal GFP antibody, in PBS containing 5% bovine serum albumin for 1 h. After washing three times with PBS, cells were observed on a Fluoview FV1000 confocal microscope (Olympus). The primary antibody was used at 1:200 for PDI, 58K, LAMP2, EEA1, and PDI antibody, with or without primary rabbit polyclonal GFP antibody, in PBS containing 5% bovine serum albumin for another 1 h. After washing three times with PBS, cells were observed on a Fluoview FV1000 confocal microscope (Olympus). The primary antibody was used at 1:200 for PDI, 58K, LAMP2, EEA1, and GFP antibody and 1:100 for NR1a and 19 S S5A antibody, whereas the secondary antibody was used at 1:2000.

**Detection of FRET Using Three-cube FRET Measurement**—The fluorescence imaging workstation for FRET and the FRET quantification method have been described previously (14). Briefly, the fluorescence imaging workstation consisted of a TE2000 inverted microscope (Nikon, Tokyo, Japan) equipped with a halogen lamp light source (100 watts), Dual-View™ (Optical Insights, LLC, Santa Fe, NM), and a SNAP-HQ cooled CCD camera (Roper Scientific, Trenton, NJ). MetaMorph version 5.0 software (Universal Imaging, West Chester, PA) was used to control the CCD camera and for analysis of the cell image data. Three-cube FRET filter cubes were as follows (excitation: dichroic; emission; company): YFP (S500/20 nm; Chroma); FRET (S430/25 nm; 455dclp; S470/30 nm; Chroma); and CFP (S430/25 nm; 455dclp; S470/30 nm; Chroma). Binning 2 × 2 modes and a 200-ms integration time were used. Average background signal was determined as the mean fluorescence intensity from a blank area and was subtracted from the raw images before carrying out FRET calculations. The FRET ratio (FR) was calculated with Equation 1 (14–16).

\[
FR = \frac{S_{\text{FRET}}(DA) - R_{\text{D1}}S_{\text{CFP}}(DA)}{R_{\text{A1}}S_{\text{YFP}}(DA)} \quad (\text{Eq. 1})
\]

\(S_{\text{CFP}}(\text{SPECIMEN})\) denotes an intensity measurement, where CUBE indicates the filter cube (CFP, YFP, or FRET), and SPECIMEN indicates whether the cell is expressing donor (D; CFP), acceptor (A; YFP), or both (DA). \(R_{\text{D1}} = S_{\text{FRET}}(D)/S_{\text{CFP}}(D)\), and \(R_{\text{A1}} = S_{\text{FRET}}(A)/S_{\text{YFP}}(A)\).

**Crude Membrane Preparation and Deglycosylation Analysis**—To prepare a crude membrane suspension, the transfected HEK 293 cells were suspended and homogenized in lysis buffer (phosphate buffer, pH 7.4, containing 20 mM EDTA, 1 mM AEBSF, 50 μg/mI leupeptin, and 10 μg/ml aprotinin). Samples were then centrifuged (30,000 × g for 30 min at 4 °C), and cell membranes were resuspended in 50 μl of lysis buffer plus 1% SDS and 5% β-mercaptoethanol and boiled for 5 min before adding 1% Nonidet P-40 plus protease inhibitors as above. Samples were then partitioned into thirds; samples were treated with 0.4 units of N-glycosidase F (Roche Applied Science), 0.006 units of endoglycosidase H (Roche Applied Science), or control saline and incubated overnight. Reactions were terminated with 4 × SDS-PAGE sample buffer and boiling for 5 min. Membrane proteins were resolved on a 6% SDS-polyacrylamide gel and visualized using immunoblot analysis with anti-GFP antibody.

**RESULTS**

Neither the NR1a ATD nor the NR2B ATD Is Required for the Formation and Surface Expression of NR1a/NR2B Receptors—In order to determine the role of the ATD in the trafficking of NMDA receptors, we generated a series of ATD deletions in fluorescent protein-tagged NR1a, NR2B, and NR2A subunits (Fig. 1A). We first used surface immunostaining to determine whether ATD deletion affected the trafficking of NR1a/NR2B-containing NMDA receptors to the cell membrane. Because the fluorescent protein was tagged to the extracellular side of each subunit, the expression of NR1a or NR2B in the plasma membrane could be detected in live cells by immunostaining of the fluorescent proteins. We used a polyclonal anti-GFP antibody followed by a Cy3-conjugated secondary antibody to label the receptors; expression in the plasma membrane was indicated by the presence of red puncta scattered on the cell surface. When we co-expressed CFP-NR1aATD and YFP-NR2B, CFP-NR1a and YFP-NR2BATD, or CFP-NR1aATD and YFP-NR2BATD, we detected clearly positive surface staining (Fig. 1B). To further quantitatively analyze the ability of NMDA receptors containing ATD-deleted NR subunits to traffic to the plasma membrane, we measured the percentage of cells with positive immunolabeling over the number of transfected cells indicated by the presence of YFP fluorescence. The results showed that when NR1a was co-expressed with YFP-NR2B, 77.6 ± 1.8% of cells had positive surface labeling. Similarly, when HEK 293 cells were co-transfected with NR1aATD and YFP-NR2B, NR1a and YFP-NR2BATD, or NR1aATD and YFP-NR2BATD, the percentage of cells with positive surface labeling decreased compared with NR1a/YFP-NR2B but was still high (57.8 ± 5.5, 51.6 ± 5.0, and 55.8 ± 6.9%, respectively) (Fig. 1C). Subsequent intensity analysis revealed no significant differences in the fluorescence intensities of the surface labeling or total YFP among NR1a/YFP-NR2B, NR1aATD/YFP-NR2B, NR1a/YFP-NR2BATD, and NR1aATD/YFP-NR2BATD (Fig. 1D). These data indicate that the ATD of NR1a or NR2B subunits was not required for the successful delivery of NR1a/NR2B receptors to...
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A

XFP-NR1aΔATD

1

XFP

390

S1

XFP-NR2BΔATD

1

XFP

392

S1

XFP-NR2AΔATD

1

XFP

391

S1

B

CFP

YFP

Cy3

NR1a

NR2B

Anti-GFP

NR1aΔATD

NR2B

Anti-GFP

NR1a

NR2BΔATD

Anti-GFP

NR1aΔATD

NR2BΔATD

Anti-GFP

C

Surface staining cells (% in the co-transfected cells)

**

D

Surface

YFP

Intensity per unit area

F

Peak Current (pA)

NR1a

NR2B

NR2BΔATD

NR1a ΔATD

NR1a + NR2B

NR2B ΔATD

NR1a ΔATD + NR2B ΔATD

NR1a + NR2B ΔATD

NR2B ΔATD

NR1a ΔATD + NR2B ΔATD

NR1a + NR2B ΔATD

NR2B ΔATD

NR1a ΔATD + NR2B ΔATD

NR1a + NR2B ΔATD

NR2B ΔATD

NR1a ΔATD + NR2B ΔATD

NR1a + NR2B ΔATD

NR2B ΔATD

NR1a ΔATD + NR2B ΔATD

NR1a + NR2B ΔATD

NR2B ΔATD

NR1a ΔATD + NR2B ΔATD

NR1a + NR2B ΔATD

NR2B ΔATD
the cell surface, although the ability of these receptors to be trafficked to the cell membrane was reduced to some degree. We further investigated the expression and trafficking of NR1a or NR2B subunits with the ATD deleted in cultured hippocampal neurons (supplemental Fig. 1). These experiments showed that YFP-NR1a_ATD or YFP-NR2B_ATD expressed alone in hippocampal neurons was able to express in the cell membrane, probably by co-assembly with endogenous NR2 or NR1 subunits.

To determine whether the surface-expressed complexes were functional, we recorded NMDA receptor currents in response to local application of saturating doses of glutamate (100 μM) and glycine (10 μM) in HEK 293 cells. Representative current traces through these deletion mutants evoked by a 500-ms glutamate application are shown in Fig. 1E, and the mean peak current amplitudes are shown in Fig. 1F. In close agreement with the live cell surface immunostaining results, currents were obtained from cells transfected with NR1a/YFP-NR2B, NR1a_ATD/YFP-NR2B, NR1a/YFP-NR2B_ATD, and NR1a_ATD/YFP-NR2B_ATD, the average amplitudes of the glutamate-evoked currents in picoamperes were 326.86 ± 69.20 (n = 6), 149.36 ± 19.24 (n = 7), 114.54 ± 15.55 (n = 7), and 172.84 ± 22.34 (n = 7), respectively. These data strongly suggested that deletion of the whole ATD did not eliminate the formation of functional channels between NR1a and NR2B subunits.

Surface Expression of NMDA Receptors Composed of ATD-deleted NR1a and Full-length NR2A Was Abolished—When HEK 293 cells co-expressing CFP-NR1a_ATD and the full-length YFP-NR2A subunit were analyzed for cell surface expression by immunostaining, no positive staining was detectable (Fig. 2A). This was true even for cells exhibiting clear intracellular CFP or YFP fluorescence signals, indicating strong expression of NR subunit proteins. This result is consistent with previous findings that the mutant NR1a subunit missing ATD cannot form receptors with the NR2A subunit in the plasma membrane (17). However, when CFP-NR1a subunits were co-expressed with YFP-NR2A_ATD subunits or when CFP-NR1a_ATD subunits were co-expressed with YFP-NR2A_ATD subunits, we found positive surface staining (Fig. 2A). In addition, significant surface staining was also observed when YFP-NR2A_ATD was expressed in hippocampal neurons (supplemental Fig. 1), which indicated that ATD-deleted NR2A subunits were able to co-assemble with endogenous NR1 subunits and express in the surface membrane. We also measured the percentage of transfected cells with positive surface staining. When HEK 293 cells were co-transfected with NR1a/YFP-NR2A, 66.0 ± 3.6% of cells had positive surface labeling. When NR1a/YFP-NR2A_ATD or NR1a_ATD/YFP-NR2A_ATD was co-transfected, the corresponding percentages were 46.0 ± 4.2 and 60.1 ± 1.2%, respectively (Fig. 2B). However, when NR1a_ATD/YFP-NR2A was co-transfected, the corresponding percentage was 2.4 ± 0.7%, which was significantly lower than that for NR1a/YFP-NR2A (Fig. 2B) and was not statistically different from the percentage when YFP-NR2A was expressed alone (2.9 ± 1.4%). The total intensity of YFP fluorescence showed no significant difference among NR2A or ATD-deleted NR2A, whereas the fluorescence intensity of the surface staining of NR1a_ATD/YFP-NR2A was significantly different from that of NR1a/YFP-NR2A (Fig. 2C). These results thus showed that NR1a_ATD/YFP-NR2A co-expression did not yield any surface protein, whereas the other combinations did. In agreement with the live cell surface immunostaining, no current response was detected from cells transfected with NR1a_ATD/YFP-NR2A (Fig. 2, D and E).

The Heteromers between the ATD-deleted NR1a and the Full-length NR2A Were Formed but Retained in the ER—We further compared the surface expression of full-length NR1a or ATD-deleted NR1a subunits co-expressed with GFP-tagged NR2A or NR2B subunits in HEK 293 cells using FACS analysis. We found that co-expression of NR1a/GFP-NR2A or NR1a/GFP-NR2B led to robust surface expression, with the percentage of GFP-positive cells showing surface expression being 68.0 or 71.7% (supplemental Fig. 2A), respectively. In addition, when ATD-deleted NR1a and GFP-NR2B were co-expressed, the percentage was decreased but still relatively high (50.3%). However, the percentage of GFP-positive cells showing surface expression of NR1a_ATD/GFP-NR2A was quite low (4.1%) and was similar to that of the HEK 293 cells expressing GFP-NR2A alone (3.8%) (supplemental Fig. 2A). Taken together, results from FACS measurements were quantitatively consistent with the previous immunostaining and functional data, revealing that NR1a_ATD/NR2B were able to express in the surface membrane but not NR1a_ATD/NR2A.

One possible reason for NR1a_ATD/GFP-NR2A unable to express in the cell membrane was that ATD-deleted NR1a subunit deletion constructs. NR1A represents the first 400 amino acids, and XFP (dotted box) represents the fluorescent protein CFP or YFP. The hatched box corresponds to the signal peptide, the dotted line corresponds to the deleted ATD region, and the black boxes correspond to TM. The number above each NR subunit deletion construct indicates the residues deleted. B. HEK 293 cells expressing the indicated cDNAs were surface-stained with anti-GFP antibodies. CFP was tagged to the NR1a or ATD-deleted NR1a subunit, whereas YFP was tagged to the NR2B or ATD-deleted NR2B subunit (two left columns). The right column was from surface staining using anti-GFP antibody and Cy3-conjugated secondary antibody. Scale bar, 10 μm. C. The percentages of cells with detectable surface labeling were determined for >200 YFP-expressing cells for each combination of cDNAs in three experiments. The gray boxes represent YFP. The bar graphs represent mean ± S.E., *p < 0.01, ANOVA. D, data represent mean ± S.E. of fluorescence intensities per unit area obtained for surface (black) or total YFP (white) expression. More than 60 YFP-expressing cells for each combination of cDNAs were analyzed in three experiments. E, representative glutamate-evoked currents recorded from HEK 293 cells. Glutamate (100 μM) and glycine (10 μM) were added to evoke currents. F, summary data showing the average peak amplitudes of the whole-cell currents when co-expressing NR1a or ATD-deleted NR1a and NR2B or ATD-deleted NR2B. The numbers above the histogram bars indicate the number of cells responding of the total number of recorded cells (i.e. 6/6 represents six responsive cells of six).
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A

CFP

YFP

Cy3

NR1a

NR2A

Anti-GFP

NR1a

NR2A

Anti-GFP

NR1a

NR2A

Anti-GFP

B

Surface staining cells (% in the co-transfected cells)

**

NR1a + NR2A

NR1aΔATD + NR2A

NR1aΔATD + NR2AΔATD

NR1a + NR2AΔATD

NR1aΔATD + NR2AΔATD

C

Intensity per unit area

**

Surface

YFP

NR1a + NR2A

NR1aΔATD + NR2A

NR1aΔATD + NR2AΔATD

E

Peak Current (pA)

4/5

150

0/6

4/7

6/7

VR1a + NR2A

VR1aΔATD + NR2A

VR1aΔATD + NR2AΔATD
units were not able to co-assemble with NR2A subunits. In previous studies, we analyzed the assembly of native NMDA receptor subunits using a three-cube FRET measurement (14). With the same approach, we found that FRET signals were produced when CFP-NR1aATD and YFP-NR1aATD or CFP-NR1aATD and YFP-NR2A were co-transfected into HEK 293 cells, with FRET ratios (FR) of 1.43 ± 0.04 (n = 35) or 1.47 ± 0.09 (n = 30), respectively (Fig. 3A). These values were significantly different from the FR value (1.01 ± 0.02, n = 32; p < 0.01) obtained from the co-expression of CFP-NR1a and GABA_α1-YFP (14). In addition, when CFP-NR1aATD and GABA_α1-YFP were co-transfected, the FR value was 1.09 ± 0.09 (n = 38) and showed no significant difference from that obtained from the co-expression of CFP-NR1a and GABA_α1-YFP (14). The results confirmed that the deletion of ATD did not affect the assembly of NR1a and NR2A subunits.

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Another potential reason for NR1aATD/GFP-NR2A unable to express in the cell membrane was that the ATD-deleted NR1a subunits were assembled with NR2A subunits, but they were retained in the ER. To test this possibility, we examined the subcellular localization of the NR1aATD/NR2A receptors using confocal microscopy (Fig. 3, C and D). After NR1aATD and GFP-NR2A were co-transfected into COS-7 cells, NR2A colocalized extensively with NR1a and the ER marker (PDI) but not with the Golgi marker (58K) (Fig. 3C). In contrast, when GFP-NR2A was co-expressed with NR1a in COS-7 cells, NR2A colocalized with the Golgi marker (58K) (Fig. 3D). We further tested the colocalization of GFP-NR2A when co-expressed with NR1aATD with the proteosome, endosome, and lysosome markers. The data showed that NR2A under such conditions was not colocalized with these markers (supplemental Fig. 3). To confirm the ER retention of NR1aATD/NR2A, we examined its glycosylation state. Immunoblots with GFP antibody showed that GFP-NR2A, when co-expressed with the wild-type NR1a subunit, was not completely sensitive to Endo H, indicating that under such conditions, GFP-NR2A entered Golgi (Fig. 3B). In contrast, when co-expressed with the ATD-deleted NR1a subunit, GFP-NR2A was completely sensitive to Endo H, indicating that under such conditions, GFP-NR2A was retained in the ER.

NR2A ATD But Not NR2B ATD Possesses an ER Retention Signal—The results described above suggest that the NR2A ATD may play a role in controlling the trafficking of NMDA receptors that is different from the NR2B ATD. To further test this possibility, we exchanged the ATDs between NR2A and NR2B and tested whether these chimeras could form functional...
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To further test the role of the ATD of NR subunits in membrane trafficking, we constructed a series of chimeras in which the ATD of the NR subunit was fused to the transmembrane domain of an unrelated membrane protein: pDisplay-GFP (Fig. 5A). The pDisplay vector contained an NH₂-terminal murine Igκ-chain leader sequence, which directs the biosensor protein to the secretory pathway, and a COOH-terminal transmembrane domain of platelet-derived growth factor receptor, which targets the biosensor protein to the plasma membrane. This plasmid has been used in the study of the role of the GluR2 ATD in spine growth (18). As expected, the expression of GFP-ATD₁₄ or GFP-ATD₂₅ in HEK 293 cells resulted in robust surface labeling in nearly all GFP-expressing cells (Fig. 5, B and C). However, the majority of HEK 293 cells expressing GFP-ATD₂₅ alone were not surface-labeled (Fig. 5B), and the positive surface labeling was 2.6 ± 0.5% (Fig. 5C). We further measured the surface expression of these chimeras of pDisplay-GFP and ATD from different NR subunits using fluorescence-activated cell sorting analysis (supplemental Fig. 2B) and found that expression of GFP-ATD₁₄ or GFP-ATD₂₅ led to robust surface expression with the percentage of GFP-positive cells showing surface expression being 83.1 or 81.8%, respectively. However, the percentage of GFP-positive cells containing surface expression of GFP-ATD₂₅ was quite low (3.3%).

The current amplitudes were recorded from YFP-NR1a/NR2BATD, YFP-NR2AATD, or YFP-NR1a/NR2ATD, and the mean current amplitudes in picoamperes were 4.3 and 64.3, respectively (Fig. 4, D). These results again indicated that it is the NR2A ATD that caused the NR1aΔATD/NR2A receptors to fail to express on the cell surface.

channels in the cell membrane (Fig. 4A) with wild type or ATD-deleted NR1a subunits. The results showed that when the YFP-NR1a subunit was co-transfected with NR2A_ATD or NR2BATD, significant positive surface labeling was detected: 63.0 ± 4.3 and 64.3 ± 2.3%, respectively (Fig. 4, B and C). However, when YFP-NR1aΔATD was co-expressed with NR2BATD, no surface expression was observed: 0.7 ± 0.7% (Fig. 4, B and C). In contrast, when YFP-NR1a_ATD was co-expressed with NR2ATD, positive surface labeling was again detected: 39.3 ± 6.4% (Fig. 4, B and C). Furthermore, glutamate-evoked currents were recorded from YFP-NR1a/NR2BATD, YFP-NR1a/NR2ATD, or YFP-NR1a/NR2ATD/NR2ATD, and the mean current amplitudes in picoamperes were 107.63 ± 21.50 (n = 4), 113.50 ± 33.61 (n = 4), and 148.45 ± 59.25 (n = 4), respectively (Fig. 4D). These results again indicated that it is the NR2A ATD that caused the NR1aΔATD/NR2A receptors to fail to express on the cell surface.
were analyzed in three experiments. **,

ATD is able to negate this ER retention signal. In addition, the assembly of NR2A ATD with NR1a subunit or with the ATD-deleted NR1a subunit. We found that when NR2A ATD possesses an ER retention signal, and NR1a ATD is necessary for overcoming this signal. A diagram of chimeric constructs between ATD and pDisplay-GFP. Dotted box, fluorescent protein GFP.

The ER Retention Signal Is Located in the A2 Segment of the NR2A ATD

We next compared the intracellular distribution of GFP-ATD A2 with GFP-ATD B in COS-7 cells. The immunostaining results showed that GFP-ATD A2, exclusively co-localized with the ER marker (PDI) but not with the Golgi marker (58K) (Fig. 7). Together with previous data, our results indicate that the NR2A ATD but not the NR2B ATD contains an ER retention signal. In addition, the assembly of NR2A ATD with NR1a ATD is able to negate this ER retention signal.

The ER Retention Signal Is Located in the A2 Segment of the NR2A ATD—To further clarify the location of this ER retention signal in the NR2A ATD, we divided NR2A ATD into four segments, termed A1–A4, according to homology with the signal in the NR2A ATD, we divided NR2A ATD into four segments, termed A1–A4, according to homology with the NR2A ATD but not the NR2B ATD contains an ER retention signal. **, signal peptide; black box, transmembrane domains of platelet-derived growth factor receptor.

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We further inserted the A2 segment of the NR2B with that of the NR2A subunit into NR2A A2-2B, and named the products NR2A A2-2A, NR2A A2-2A, or NR2A A2-2A, respectively. We co-expressed these chimeras with the YFP-tagged NR1a subunit or with the YFP-tagged, ATD-deleted NR1a subunit. We found that when NR2A A2-2B, whereas virtually no surface staining was observed when they expressed GFP-ATD A2 (Fig. 6, A–C).

We next compared the intracellular distribution of GFP-ATD A2 with GFP-ATD B in COS-7 cells. The immunostaining results showed that GFP-ATD A2, exclusively co-localized with the ER marker (PDI) but not with the Golgi marker (58K) (Fig. 7). Together with previous data, our results indicate that the NR2A ATD but not the NR2B ATD contains an ER retention signal. In addition, the assembly of NR2A ATD with NR1a ATD is able to negate this ER retention signal.

We further inserted the A2 segment of the NR2B subunit (Fig. 8A) into NR2A A2-2B, and named the products NR2A A2-2B, NR2A A2-2B, or NR2A A2-2B, respectively. We co-expressed these chimeras with the YFP-tagged NR1a subunit or with the YFP-tagged, ATD-deleted NR1a subunit. We found that when NR2A A2-2B was co-expressed with YFP-NR1a or YFP-NR1a A2, significant positive surface labeling was detected in 51.0 ± 3.5 and 48.3 ± 6.1% of the YFP-positive cells, respectively. However, when NR2A A2-2B was co-expressed with YFP-NR1a or YFP-NR1a A2, significant positive surface labeling was detected in 42.3 ± 1.1 and 46.0 ± 7.9%, respectively. When NR2A A2-2B was co-expressed with YFP-NR1a, the percentage significantly increased to 7.4 ± 0.3%, indicating that the surface expression of the YFP-NR1a A2/NR2A A2-2B complex was almost completely abolished. When NR2A A2-2B was co-expressed with YFP-NR1a, the percentage significantly increased to 23.3 ± 1.6% (Fig. 8B). We further inserted the A2 segment of the NR2B subunit (Fig. 8A) into NR2A A2-2B, and named the products NR2A A2-2B, NR2A A2-2B, or NR2A A2-2B, respectively. We co-expressed these chimeras with the YFP-tagged NR1a subunit or with the ATD-deleted NR1a subunit. We found that when NR2A A2-2B was co-expressed with YFP-NR1a or YFP-NR1a A2, significant positive surface labeling was detected in 51.0 ± 3.5 and 48.3 ± 6.1% of the YFP-positive cells, respectively. However, when NR2A A2-2B was co-expressed with YFP-NR1a or YFP-NR1a A2, significant positive surface labeling was detected in 42.3 ± 1.1 and 46.0 ± 7.9%, respectively. When NR2A A2-2B was co-expressed with YFP-NR1a, the percentage significantly increased to 7.4 ± 0.3%, indicating that the surface expression of the YFP-NR1a A2/NR2A A2-2B complex was almost completely abolished. When NR2A A2-2B was co-expressed with YFP-NR1a, the percentage significantly increased to 23.3 ± 1.6% (Fig. 8B). We further inserted the A2 segment of the NR2B subunit (Fig. 8A) into NR2A A2-2B, and named the products NR2A A2-2B, NR2A A2-2B, or NR2A A2-2B, respectively. We co-expressed these chimeras with the YFP-tagged NR1a subunit or with the ATD-deleted NR1a subunit. We found that when NR2A A2-2B was co-expressed with YFP-NR1a or YFP-NR1a A2, significant positive surface labeling was detected in 51.0 ± 3.5 and 48.3 ± 6.1% of the YFP-positive cells, respectively. However, when NR2A A2-2B was co-expressed with YFP-NR1a or YFP-NR1a A2, significant positive surface labeling was detected in 42.3 ± 1.1 and 46.0 ± 7.9%, respectively. When NR2A A2-2B was co-expressed with YFP-NR1a, the percentage significantly increased to 23.3 ± 1.6% (Fig. 8B).
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A

GFP-ATD_{1\alpha} Anti-GFP
GFP-ATD_{2\alpha} Anti-GFP
GFP-ATD_{2\alpha} Anti-GFP
ATD_{1\alpha} + GFP-ATD_{2\alpha} Anti-GFP

B

Surface staining cells (% in the co-transfected cells)

C

Intensity per unit area

D

GFP-A{2}_{2\alpha} Anti-GFP
GFP-A{2}_{2\beta} Anti-GFP
GFP-ATD_{2\alpha}-A{2}_{2\alpha} Anti-GFP
ATD_{1\alpha} + GFP-ATD_{2\alpha}-A{2}_{2\alpha} Anti-GFP

E

Surface staining cells (% in the co-transfected cells)

F

Intensity per unit area
was expressed in hippocampal neurons, no surface staining was detected. However, when GFP-A22B or ATD1a/GFP-
ATD2B-A2-2A was expressed in hippocampal neurons, clear surface staining was detected. This result was in close agreement
with the previous results and confirmed that the A2 segment of the NR2A subunit but not the A2 segment of the NR2B subunit contained an ER retention signal.

The A2 segment of NR2A or NR2B has ~130 amino acid residues. To further screen for any possible retention motif in
this segment, we generated a series of point mutations in GFP-
ATD2A (Fig. 8E). Ten amino acids that are different between
the NR2A A2 segment and the NR2B A2 segment according to
sequence alignment were chosen for mutagenesis (Fig. 8E).
Mutants were screened by surface staining using anti-GFP anti-
body in HEK 293 cells. Unfortunately, no mutation resulted in a
significant increase in the surface labeling of GFP-ATD2A. The
percentages of surface labeling for I176Y, F186K, M200L,
A213S, S225P, D234E, L238Y, E242V, F253Y, and K270S were
1.7 ± 1.7, 1.7 ± 1.7, 0.8 ± 0.4, 0.5 ± 0.5, 1.3 ± 1.3, 0.7 ± 0.6,
1.9 ± 1.1, 3.2 ± 0.6, 1.3 ± 1.3, and 2.8 ± 1.6%, respectively.
These results suggest that either these residues are not involved
in the ER retention of NR2A ATD or each of them alone is not
sufficient for this retention.

In order to locate the ER retention signal, we split the A2
segment into three parts, named A22A-a (Ile151–Asp192),
A22A-b (Asn193–Leu238), and A22A-c (Ile239–Asp282), and fused
these parts individually into pDisplay-GFP (Fig. 8F). Unexpected-
dly, surface staining showed that all three of these chimeras
were expressed on the surface membrane, and the percentages
of surface labeling were 79.5 ± 1.5% for A22A-a, 75.6 ± 4.9% for
A22A-b, and 77.3 ± 1.6% for A22A-c (Fig. 8G). Fluorescence
intensity analysis of surface labeling or total GFP expression
showed no significant difference among these three chimeras
(Fig. 8H). Together with the point mutation results, these find-
ings suggest that it is likely that the overall structure or confor-
mation of the A2 segment, instead of an isolated sequence, may
be involved in the ER retention of the NR2A ATD.

DISCUSSION

NMDA receptors play important roles in both normal brain
function and neurological and psychiatric disorders. The num-
ber and composition of heteromeric NMDA receptors on the
cell surface determine its activity in response to particular stim-
uli. Therefore, understanding the assembly and trafficking of
the NMDA receptor is pivotal for understanding the mecha-
isms of its diverse functions. In this study, we found that the
NR2A ATD contains an ER retention signal, and the NR1a ATD
is necessary for overcoming this retention signal. In contrast,
the NR2B ATD has no such retention signal. Our findings indi-
cate that NR2A-containing NMDA receptors have an ER qual-
ity control mechanism different from that of NR2B-containing
NMDA receptors.
An ER Retention Signal in the NR2A ATD

A

NR2A

151 282 360

A1 A2 A3 A4 S1

NR2B

150 283

A1 A2 A3 A4 S1

NR2A_ATD-A1

NR2A_ATD-A2

NR2A_ATD-A3

NR2A_ATD-A2-2B

NR2B_ATD-A2-2A

B

Surface staining cells (% in the co-transfected cells)

E

NR2A

NR2B

NR2A

NR2B

NR2A

NR2B

151 IQQAGTVMLK IMQDYDHVHLFSLTTFPGYRDF ISF KTTMVNS

150 IEOQASVMILN IMEEDYWY IFIS YTTYFPGYQDFWTVIINSTEN

194 FVGDMDQIVT LDOGTVQQLK IHSVWLLYCSKDE

194 FVGEWELLEVL LLDSLDDGSK IONQLK KLQSPI ILLYCCTKEEA

236 VRLLRAS QGTVDFWVVSQGNTIELPKFEGPSLISVSDY

237 TVYEVEVNLGTVDFWVISLQGNTIELPKFEGPSLISVSDY

282

283

F

GFP-A2_2A_a

GFP

GFP

GFP

GFP-A2_2A_b

GFP

GFP

GFP

GFP-A2_2A_c

GFP

GFP

H

Intensity per unit area

Surface

GFP
NR2A ATD Contains an ER Retention Signal—ER retention is a common feature of the quality control mechanism for complex proteins, ensuring that unassembled or otherwise defective proteins are not released from the ER (19, 20). The NMDA receptor is a heteromeric complex. Most NR1 splice variants and NR2 subunits are retained in the ER when expressed alone. When expressed together, they assemble efficiently and form functional receptors in the cell membrane. This indicates that more restrictive mechanisms are required for the ER quality control of NMDA receptors. In the present study, we found that the ATD of the NR2A subunit contains an ER retention signal (Fig. 2). We narrowed down this ER retention signal to the A2 segment of the NR2A ATD, which contains about 100 amino acids (Figs. 8). ER retention effects were abolished when the A2 segment was further divided into three parts. In addition, mutagenesis of selected amino acids in the A2 segment of NR2A ATD failed to revert the ER retention. Together, these findings suggest that the A2 segment contains a multiple site-dependent or a conformation-dependent ER retention motif. It is unlikely that a specific motif within the A2 segment is responsible for retention. ATD of the NMDA receptor is facing the extracellular or ER luminal side. There are precedents of ER retention associated with extracellular domains. For example, the extracellular domains of T cell antigen receptor α or β chains are involved in ER retention (21, 22). Kv1α subunits also contain a dominant ER retention signal in their extracellular pore region (23); an ER protein with a domain structurally resembling that of snake dendrotoxins may be involved in ER retention.

Previous studies have shown that the NR1a subunit contains two ER retention motifs, RRR and KKK, in its C1 cassette (24, 25) and potential ER retention signals in its TM3, and the NR2B subunit possesses ER retention signals in its TM3 as well as its COOH terminus (10, 12, 26). The COOH terminus of the NR2A subunit also has been shown to play a role in ER retention (10). We found that indeed the ATD-deleted NR2A subunits, when expressed alone in heterogeneous cells, were retained in the ER (data not shown), indicating an ER retention signal located in the other part of the NR2A subunit. Taken together, these studies are consistent with the idea that multiple ER retention signals are present in the NR subunits.

The ER Retention Signal in NR2A ATD Is Masked by NR1a ATD—Recently, increasing evidence indicates that the ATD is not essential for assembly or gating of NMDA receptors but rather plays a modulatory role (27–31). Here, using truncated NR subunits combined with FRET measurements, we found that deletion of the ATD did not eliminate the homo- or hetero-oligomerization of NR subunits in living HEK 293 cells (Fig. 3A). These results further indicate that the ATD is not a crucial element for subunit assembly. In addition, our results suggested a novel mechanism for the modulatory role of ATD. We showed that the ER retention signal in NR2A ATD was masked by the NR1a ATD but not the GluR2 ATD (Fig. 5 and supplemental Fig. 4), suggesting that the NR1a ATD can interact specifically with the NR2A ATD and negate the ER retention signals in the NR2A ATD.

The mechanism underlying the masking of the NR2A ATD by the NR1a ATD is still unclear. Also, the specific region of NR1a ATD involved in this process remains to be identified. The ER retention mechanism observed in Kv1α channels (23) suggests that it is possible that certain ER protein may bind to the NR2A ATD, in particular the A2 segment, and lead to its retention in the ER. The assembly of the NR1a ATD with the NR2A ATD may cause conformational changes of the NR2A ATD that result in its release from ER retention. It is also possible that the assembly of the NR1a ATD with the NR2A ATD may increase the overall structural stability of the NR2A subunit (32). A recent study (31) using a shorter NR1a deletion (350 amino acids instead of 390 amino acids in our study and 380 amino acids in the studies of Meddows and co-workers (17)) revealed different results that the ATD-deleted NR1a subunit can assemble with the NR2A subunit into functional receptors in Xenopus oocytes. We attribute this discrepancy to the different lengths of deletion our two groups used. In addition, these results suggest that the region of the NR1a ATD after 350 amino acids is important in masking the ER retention signal of the NR2A ATD.

NR2A ATD Contains an ER Retention Signal; NR2B ATD Does Not—NMDA receptors containing different NR2 subunits exhibit different channel properties, such as current kinetics and conductance (33–35). However, the structure-function relationships of NMDA receptors are still uncertain. In the present study, we identified an ER retention signal that occurs in the NR2A ATD but not in the NR2B ATD. The finding provides evidence that the ER quality control mechanism of NR2A subunits is different from that of NR2B subunits. How this difference affects the functional heterogeneity of NMDA receptor subtypes remains to be determined. Nonetheless, these results suggest that the NR2A subunit may have more restrictive “structural checkpoints” than the NR2B subunit does in the ER quality control pathway. One potential consequence of this difference is to ensure the proper folding of NR2A subunits and proper assembly of the NR1a/NR2A receptor subtype. Alternatively, it is possible that the difference provides a potential mechanism to regulate the ratio of the expression of NR2A-containing NMDA receptors and NR2B-containing NMDA receptors through modulation of the preference of assembly of different NR2 subunits with NR1 subunits.

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FIGURE 8. A2 segment of NR2A ATD contains an ER retention signal. A, schematic diagram of the NR2AATD-A1,A2,A3, NR2A ATD-A2,2b, and NR2B A2,A3. Gray bar, NR2A subunit; white bar, NR2B subunit; hatched box, signal peptide. The numbers above the NR2A or NR2B subunits indicate the residues deleted. B, the percentages of cells with detectable surface labeling were determined for >200 GFP-expressing cells for each combination of indicated cDNAs in three experiments. The bar graphs represent mean ± S.E. **, p < 0.01, unpaired t test. C, schematic diagram of chimeras between A2 segments of NR2A or NR2B subunits and pDisplay-GFP. Dotted box, GFP. D, the percentages of cells with detectable surface labeling were determined for >200 GFP-expressing cells for each indicated cDNA in three experiments. The bar graphs represent mean ± S.E. H, surface (black) and total GFP (white) expressions. More than 60 GFP-expressing cells for each indicated cDNA were analyzed in three experiments.
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Recently, several studies have indicated that under special conditions, such as inflammatory or degenerative diseases of the central nervous system, matrix metalloproteinases cleave the NR1a subunit at the extracellular NH$_2$-terminal domain and modify NMDA receptor function (36, 37). Tissue-type plasminogen activator is also known to bind to and then cleave the ATD of the NR1 subunit at arginine 260, which serves as a necessary step to enhance NMDA receptor signaling in neurons (38, 39). Based on these observations, it is possible that a similar mechanism may also exist in the ER lumen, where various extracellular and intracellular stimuli can regulate the interaction of the NR1a ATD with the NR2A ATD and control the trafficking of the NR1a/NR2A receptor subtype.

Acknowledgment—We thank Prof. Iain C. Bruce for critical reading of the manuscript.

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