



Inhibitory Synapse Formation at the Axon Initial Segment

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The axon initial segment (AIS) is the site of action potential (AP) initiation in most neurons and is thus a critical site in the regulation of neuronal excitability. Normal function within the discrete AIS compartment requires intricate molecular machinery to ensure the proper concentration and organization of voltage-gated and ligand-gated ion channels; in humans, dysfunction at the AIS due to channel mutations is commonly associated with epileptic disorders. In this review, we will examine the molecular mechanisms underlying the formation of the only synapses found at the AIS: synapses containing γ -aminobutyric type A receptors (GABA_ARs). GABA_ARs are heteropentamers assembled from 19 possible subunits and are the primary mediators of fast synaptic inhibition in the brain. Although the total GABA_AR population is incredibly heterogeneous, only one specific GABA_AR subtype—the α 2-containing receptor—is enriched at the AIS. These AIS synapses are innervated by GABAergic chandelier cells, and this inhibitory signaling is thought to contribute to the tight control of AP firing. Here, we will summarize the progress made in understanding the regulation of GABA_AR synapse formation, concentrating on post-translational modifications of subunits and on interactions with intracellular proteins. We will then discuss subtype-specific synapse formation, with a focus on synapses found at the AIS, and how these synapses influence neuronal excitation.

Keywords: GABA_A receptor, axon initial segment, collybistin, gephyrin, inhibition, synapse formation

INTRODUCTION

The firing of glutamatergic pyramidal cells is tightly controlled by inhibitory interneurons (INs). By precisely directing pyramidal cell activity, INs are able to regulate network activity, generate oscillations, and even terminate pathological hyperexcitability (Fritschy, 2008; Roux and Buzsáki, 2015). On a molecular level, INs regulate pyramidal cell firing through GABAergic neurotransmission: releasing the neurotransmitter γ -aminobutyric acid (GABA) onto inhibitory postsynaptic specializations containing GABA type A receptors (GABA_ARs) on pyramidal neuron dendrites, soma, and axon initial segments (AISs). Thus, the construction and maintenance of GABAergic synapses are essential for normal inhibitory neurotransmission and brain function. However, relatively little is known about inhibitory synaptogenesis compared to glutamatergic synapses. To complicate the picture, there are many GABA_AR subtypes composed of different subunits, which confer distinct physiological properties on the receptors. In addition, different GABA_AR subtypes are selectively stabilized at different types of synapses; the AIS, for example,

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contains primarily one kind of GABA_AR. Thus, the type of receptor present at a given synapse determines the type of inhibition that takes place. Again, little is known about how neurons direct different types of GABA_ARs to different synapses. The following review will briefly summarize what is known about the formation and trafficking of GABA_AR subtypes and the construction of inhibitory synapses overall and specifically at the AIS.

GABA_A RECEPTOR STRUCTURE AND FUNCTION

In the adult mammalian central nervous system, most fast, synaptic inhibitory neurotransmission is mediated by GABA_ARs, a group of heteropentameric, ligand-gated anion channels (Connolly and Wafford, 2004). When the neurotransmitter GABA binds to the receptor, the intrinsic ion pore opens and allows permeable ions to pass through (Bormann et al., 1987). GABA_ARs are primarily permeable to chloride (Cl⁻) anions (Fatima-Shad and Barry, 1993), and in the mature brain—where the Cl⁻ reversal potential is more negative than the resting membrane potential—the opening of the GABA_AR channel allows Cl⁻ ions to flow down their electrochemical gradient into the neuron, lowering the neuron's membrane potential and producing a hyperpolarizing response that reduces the probability of action potential (AP) firing (Busch and Sakmann, 1990; Blaesse et al., 2009).

Structurally, GABA_ARs are diverse. The receptors are assembled from 19 different known subunits: α (1–6), β (1–3), γ (1–3), δ , ϵ , θ , π , and ρ (1–3; Olsen and Sieghart, 2008), putting the number of possible subunit combinations in the thousands; however, only certain subtypes are expressed in the brain. For synaptic GABA_ARs, which this review will focus on, the typical stoichiometric ratio is as follows: 2 α :2 β :1 γ (Wisden et al., 1992; Baumann et al., 2003). GABA_AR subunits possess a similar amino acid sequence and protein structure, with each subunit composed of an extracellular N-terminal domain, four transmembrane domains (TM1–4), an intracellular loop domain (ICD) between TM3 and TM4, and an extracellular C-terminal domain (Schofield et al., 1987; Miller and Aricescu, 2014). The ICD is important for regulating GABA_AR activity, as it is the site of phosphorylation and protein-protein interactions that alter receptor trafficking and plasma membrane (PM) expression (Moss et al., 1992; Nymann-Andersen et al., 2002; O'Toole and Jenkins, 2011). In addition, the ICD is the site of greatest sequence variability between subunits, making it an attractive candidate for a locus of subtype-specific GABA_AR regulation (Arancibia-Cárcamo and Kittler, 2009). It seems likely that such differential regulation occurs, as different types of synaptic GABA_ARs are restricted to certain synapses. For instance, within pyramidal neurons in the cortex and hippocampus, GABA_ARs that contain the α 1 subunit tend to be found at synapses in the soma and dendrites, while α 2-containing GABA_ARs are enriched at synapses on the AIS (Nusser et al., 1996).

The subunit composition of a given GABA_AR not only influences receptor localization, but also determines the physiological properties of that receptor (see **Table 1** for

TABLE 1 | The distribution and synaptic roles of γ -aminobutyric acid type A receptor (GABA_AR) α subunits.

Subunit	Brain distribution	Subcellular localization	Synaptic role
α 1	60% of all GABA _A Rs Widely expressed	Synaptic in somatodendritic compartments	Phasic inhibition
α 2	15–20% of GABA _A Rs Cerebral cortex (layers 1–4), hippocampus, striatum	Primarily synaptic; enriched in perisomatic regions and at the AIS of cortical and hippocampal pyramidal neurons	Phasic inhibition
α 3	10%–15% of GABA _A Rs Cerebral cortex (layers 5–6), amygdala, thalamus	Primarily synaptic; found in some AIS	Phasic inhibition
α 4	<5% of GABA _A R Dentate gyrus, thalamus	Extrasynaptic	Tonic inhibition
α 5	<5% of GABA _A Rs Hippocampus	Extrasynaptic	Tonic inhibition
α 6	<5% of GABA _A Rs Cerebellum	Primarily extrasynaptic	Tonic inhibition

summary). In addition, the specific α subunit composition of GABA_ARs determines receptor kinetics. α 1-GABA_ARs mediate an inhibitory current with a longer decay time than α 2-GABA_ARs (Goldstein et al., 2002). Thus, GABA_AR subtypes mediate specific kinds of inhibition; restricting GABA_AR subtypes to different spatial domains allows INs to control pyramidal neuron firing in a precise but dynamic manner.

GABA_A RECEPTOR OLIGOMERIZATION AND TRAFFICKING

GABA_AR subunits are assembled into receptors in the endoplasmic reticulum (ER; Kittler et al., 2002). Oligomerization is controlled by the subunits' N-terminal domains, with assistance from resident ER chaperone proteins to ensure appropriate protein assembly and folding (Connolly et al., 1996; Moss and Smart, 2001). Only those receptors that are conformationally mature are permitted to exit the ER and continue along the GABA_AR lifecycle; receptors that are found to be incomplete or composed of inappropriate subunit combinations are retained in the ER and degraded (Gorrie et al., 1997; Saliba et al., 2007).

Conformationally mature GABA_ARs travel from the ER to the Golgi apparatus, where receptors are segregated into vesicles and transported to the PM (Vithlani et al., 2011). This forward trafficking delivers GABA_ARs to and insert them into the PM, primarily in extrasynaptic areas (Bogdanov et al., 2006). GABA_AR surface expression is also regulated by receptor internalization *via* clathrin-mediated endocytosis (Lorenz-Guertin and Jacob, 2018). The clathrin adaptor protein (AP)-2 binds GABA_AR subunits—the ICD of the GABA_AR β 1–3 and γ 2 subunits both contain AP2 binding motifs—and clathrin, anchoring receptors in endocytotic pits.

INHIBITORY SYNAPSE CONSTRUCTION

GABA_ARs are inserted into the PM at extrasynaptic locations (Bogdanov et al., 2006). At the surface, GABA_ARs are highly dynamic and diffuse laterally within the PM, where they continually move between the synaptic and extrasynaptic space (Thomas et al., 2005). Recent single-particle trafficking experiments show that both synaptic (α 1–3-containing) and extrasynaptic (α 4–6-containing) receptors can access the inhibitory synapse; however, when within the synaptic domain, the diffusion rate of synaptic GABA_ARs was reduced relative to extrasynaptic receptors, suggesting that GABA_ARs with “synaptic” subunit compositions are selectively stabilized at synapses (Hannan et al., 2019).

How are these receptors stabilized in the inhibitory synapse? Research to date suggests that protein-protein interactions play an essential role in this process: structural proteins present at the inhibitory synapse bind to GABA_ARs, reducing their lateral diffusion rate and effectively anchoring them at the synapse (Hannan et al., 2019). Though the composition of the multimolecular protein complexes present at the inhibitory synapse remains relatively unknown, a number of proteins that reside at the inhibitory synapse and appear to regulate GABA_AR clustering have been identified.

GEPHYRIN

One of the first inhibitory synaptic proteins described was gephyrin (GPN), which is still considered to be an integral structural component of the inhibitory postsynaptic domain (Tyagarajan and Fritschy, 2014). The most common splice variant of GPN is composed of three domains: an N-terminal G domain, a linker C domain, and a C-terminal E domain (Feng et al., 1998; Schwarz et al., 2001). The E and G domains of GPN self-aggregate, leading to the hypothesized formation of hexameric macromolecular GPN complexes that could serve as a lattice to stabilize receptors at the synapse (Saiyed et al., 2007). GPN was first identified as a binding partner of glycine receptors, which mediate inhibition in the spine (Prior et al., 1992). Constitutive knock-out of GPN in the mouse leads to a complete loss of glycine receptor clusters in the periphery, resulting in early postnatal death (Feng et al., 1998). However, it was also found that GPN knock-out mice show a dramatic reduction in the presence of GABA_ARs at brain synapses, providing the first evidence that GPN is also crucial for inhibitory synapse formation in the central nervous system (Kneussel et al., 1999; Fischer et al., 2000).

More recent experiments have shown that GPN co-localizes with GABA_ARs containing α 1–3 subunits at synapses (Sassoè-Pognetto et al., 2000). Isothermal titration calorimetry experiments performed with the GPN E domain and the ICDs of GABA_AR α 1–3 subunits have demonstrated that GPN interacts directly with the ICD of GABA_AR α subunits at an amino acid stretch between ICD residues 360–375 (Hines et al., 2018). The amino acid sequence in this region is not well conserved between α subunit subtypes, thus it follows that GPN binds α 1–3 with differing affinities: the

α 1 and α 3 ICDs formed tight complexes with the GPN E domain, while the α 2 ICD formed a comparatively weaker complex (Hines et al., 2018). These data suggest a GABA_AR subtype-specific affinity for GPN, dependent on the amino acid composition of the 360–375 ICD motif of the α subunit and raise the possibility that GPN, or other proteins that bind the 360–375 motif, can selectively stabilize GABA_AR subtypes at certain synapses.

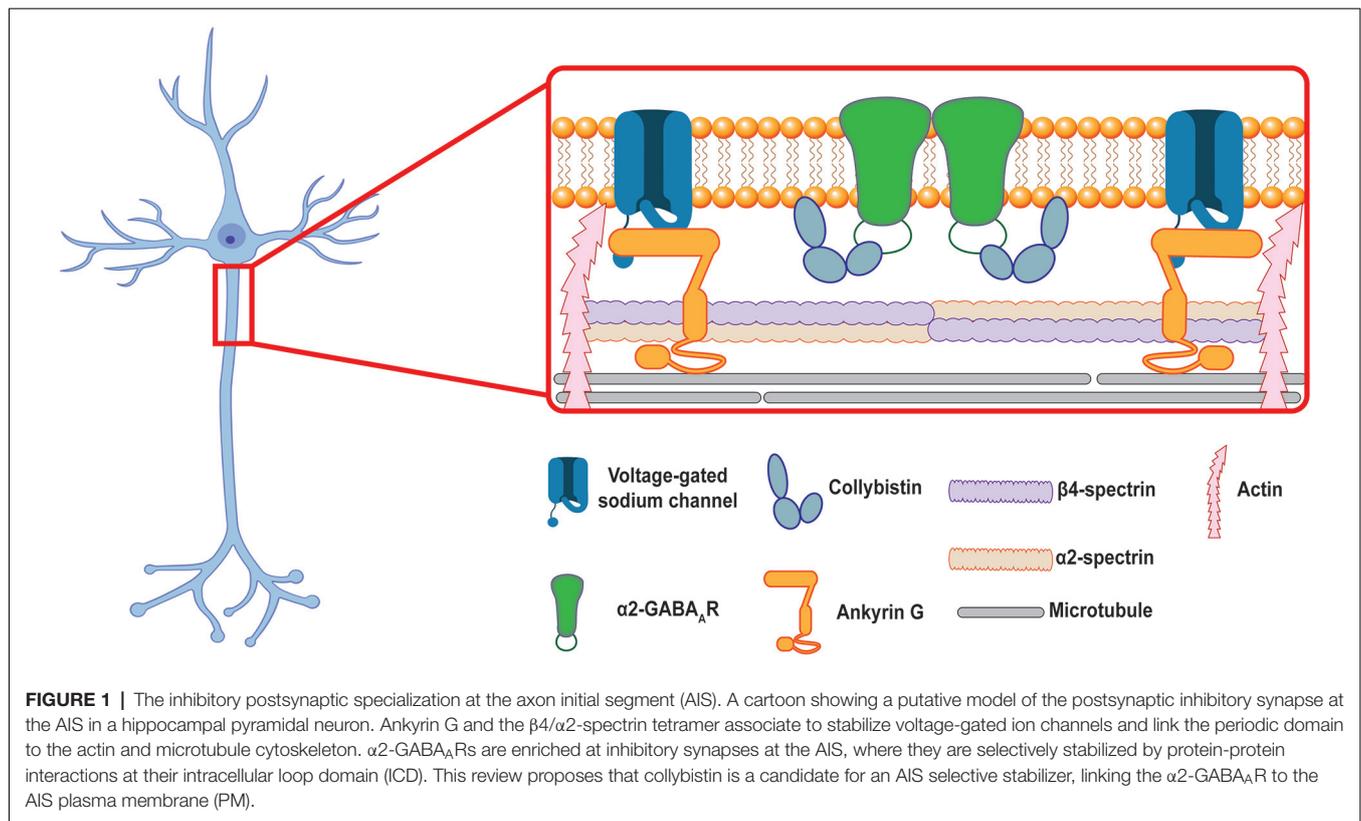
COLLYBISTIN

A more recently identified inhibitory synapse protein is collybistin (CB), a guanine nucleotide exchange factor (Reid et al., 1999). Most functional CB isoforms are composed of three domains: a catalytic double homology domain, a PM-binding pleckstrin homology domain, and an N-terminal Src homology (SH)-3 domain (Harvey et al., 2004). CB was first identified as a GPN interacting protein (Kins et al., 2000). Indeed, the GPN E domain directly binds CB's double homology domain, and co-expression of CB with GPN in heterologous cells causes the translocation of GPN clusters to the PM (Kins et al., 2000; Grosskreutz et al., 2001). CB knock-out mice show a loss of GPN clustering at inhibitory synapses in certain brain regions, such as the hippocampus, suggesting that CB plays a role in postsynaptic GPN clustering at a subset of inhibitory synapses (Papadopoulos et al., 2007, 2008).

Recent evidence showed that CB also directly interacts with certain GABA_AR subtypes. Yeast tri-hybrid screens revealed that the GABA_AR α 2 subunit interacts with the CB SH3 domain, and in fact the GPN/CB interaction is strengthened by the addition of α 2, suggesting that these three proteins can act synergistically (Saiepour et al., 2010). *In vitro* isothermal titration calorimetry showed that the CB SH3 domain preferentially binds the α 2 ICD, over either the α 1 or α 3 ICD, at residues 360–375, suggesting that this ICD motif is integral to GABA_AR subtype-specific protein-protein interactions (Hines et al., 2018). Supporting this hypothesis, knocking the α 2 360–375 motif into the α 1 subunit in mice leads to increased immunoprecipitation of endogenous CB with the chimeric α 1 subunit (Nathanson et al., 2019). This same study also showed an increase in the pull-down of GPN with mutant α 1, demonstrating a possible synergistic interaction between CB/GPN/ α 2 ICD that is overall strengthened when the interaction between two partner proteins is enhanced (Nathanson et al., 2019). The overarching question becomes: does this α 2 ICD motif and its preferential protein interactions play a role in subtype-specific synapse formation in the brain, particularly in the construction of α 2-enriched synapses at the AIS?

THE AXON INITIAL SEGMENT

At the interface between the somatodendritic and axonal compartments lies the AIS. This discrete region is composed of unique molecular machinery and maintains a barrier between the somatodendritic and axonal environments, sustaining the neuronal anatomical asymmetry necessary for the unidirectional propagation of information (Letierrier, 2018). Morphologically,



the AIS displays an electron-dense submembranous granular layer composed of a high density of voltage-gated ion channels and the highly organized, periodic protein scaffold that supports them (Xu et al., 2013). A number of electrophysiological studies established that the AIS is not only a barrier but is also the site of AP generation, as belied by its high resident concentrations of voltage-gated sodium and potassium channels, which are essential for the propagation of APs (Araki and Otani, 1955; Coombs et al., 1957; Fuortes et al., 1957).

Giant Ankyrin G is the key scaffolding protein and master organizer at the AIS; it recruits other essential AIS components, such as β IV-spectrin and voltage-gated ion channels, through either direct or indirect interactions (Zhou et al., 1998; Jenkins and Bennett, 2001; Han et al., 2017). Ankyrin G also interacts with microtubules, anchoring the entire complex in place (Leterrier et al., 2011). The AIS protein scaffold is dense and super-stable, maintaining axonal integrity and serving as a barrier to the entry of inappropriate somatodendritic proteins: the expression and/or stabilization of proteins at the AIS is tightly controlled (Albrecht et al., 2016; Huang and Rasband, 2016).

INHIBITION AT THE AXON INITIAL SEGMENT

To current knowledge, the only ligand-gated ion channels mediating neurotransmission at the AIS are GABA_ARs (Leterrier, 2018). The AIS of certain cell types—pyramidal

cells of the forebrain, for instance—contain inhibitory synapses that are exclusively innervated by one type of IN: the chandelier cell (Somogyi et al., 1983; Wang et al., 2016). Given that the AIS is the site of AP firing, any inhibitory signaling in this domain has an outside effect on neuronal excitability (Zhu et al., 2004; Glickfeld et al., 2009). As previously discussed, $\alpha 2$ -GABA_ARs are specifically enriched at the AIS (Nusser et al., 1996; Nyíri et al., 2001); since different GABA_AR subtypes have their own kinetics and mediate distinct types of inhibition, it follows that the enrichment of a particular GABA_AR subtype in a restricted domain like the AIS would have functional relevance.

To investigate the above hypothesis, mice in which residues 360–375 of the GABA_AR $\alpha 1$ subunit have been knocked-in to the $\alpha 2$ subunit (*Gabra2-1* mice) were generated. This mutation abolished $\alpha 2$'s preferential interaction with CB and led to loss of $\alpha 2+$ synapses at the AIS. Strikingly, *Gabra2-1* animals display postnatal spontaneous seizures; these seizures are often lethal, causing death around postnatal day 20 (Hines et al., 2018). These data demonstrate that the localization of $\alpha 2$ -GABA_ARs to the AIS is essential to inhibitory control of pathological excitation.

INHIBITORY SYNAPSE FORMATION AT THE AXON INITIAL SEGMENT

Clearly then, inhibition at the AIS is integral to maintaining the dynamic balance between inhibition and excitation.

However, the manner in which GABA_AR subtype-specific axo-axonic synapses are constructed and maintained remains unclear. Although α 2-GABA_ARs are enriched at the AIS, live imaging of α 1- and α 2-GABA_ARs coupled to quantum dots showed that both subtypes can enter the AIS: the AIS diffusion barrier does not seem to select for α 2-GABA_ARs (Muir and Kittler, 2014). However, these same studies demonstrated that α 2-GABA_ARs were less mobile at the AIS than α 1-GABA_ARs, indicating that while both subtypes can access the AIS compartment, α 2-GABA_ARs are somehow preferentially anchored at there. Given that inhibitory synapse formation in other neuronal compartments has been shown to depend on protein-protein interactions, it stands to reason that synapse formation at the AIS would follow the same principles.

Indeed, GPN is expressed at the AIS, forming co-clusters with α 2-GABA_ARs (Panzanelli et al., 2011), although GPN's association with GABA_ARs at the AIS is relatively weaker than its association with GABA_ARs at the soma and dendrites (Gao and Heldt, 2016), suggesting that another protein present in the AIS multimolecular scaffold could play a more important role. CB is also present at AIS inhibitory synapses in cortical and hippocampal neurons (Panzanelli et al., 2011), and its specific interactions with α 2-GABA_ARs provide a putative model for inhibitory synapse formation at the AIS: removing the 360–375 motif from the α 2 subunit ICD prevents the accumulation of α 2-GABA_ARs at axo-axonic synapses, suggesting that this motif, and the preferential protein interactions it mediates—such as that with CB—is *necessary* for GABA_AR stabilization at the AIS (Hines et al., 2018). Experiments performed in another mutant mouse, in which residues 360–375 of the α 2 subunit are knocked-in to the α 1 subunit (the *Gabra1–2* mouse), increases the affinity of the α 1 subunit for CB and leads to an increase in α 1-GABA_ARs expression at axo-axonic synapses. These data show that residues 360–375 of the α 2 subunit are *sufficient* for GABA_AR stabilization at the AIS (Nathanson et al., 2019). Given that CB has a relatively stronger association with the α 2 360–375 motif and is present at the AIS, it stands to reason that CB interactions selectively stabilize α 2-GABA_ARs at inhibitory AIS synapses.

Together, these data provide a potential model for axo-axonic synapse formation: after GABA_ARs are inserted into the extrasynaptic PM at the AIS those receptors that contain the α 2 ICD motif are able to bind intracellular scaffolding proteins, such as CB, to form stable complexes that anchor the receptor at axo-axonic synapses. Receptors that do not contain the α 2 ICD motif are not stabilized at synapses and diffuse back into the extrasynaptic space (see **Figure 1**). Other proteins

in the AIS scaffold, especially Ankyrin G, might also play a role in the selective stabilization of GABA_ARs at the AIS. Future experiments utilizing the *Gabra1–2* and *Gabra2–1* mice could provide more information about the importance of these proteins in GABA_AR stabilization. In addition, the above model only describes the *postsynaptic* side of inhibitory synapse formation. Additional mechanisms regulate the formation of presynaptic chandelier cell boutons apposing the AIS. Most recently, a transsynaptic mechanism was described: the cell adhesion molecule LICAM, localized to the AIS of neocortical pyramidal neurons, was found to be necessary for the targeting of chandelier cell boutons to the AIS (Tai et al., 2019). Although the presynaptic interactor of LICAM remains unidentified, such transsynaptic interactions provide an intriguing path for future research into synapse formation at the AIS.

CONCLUSIONS

Despite the progress made in understanding the formation of inhibitory synapses, little is known about how neurons direct GABA_AR subtype-specific synapse formation. This subtype specificity is important for the maintenance of neuronal excitability. α 2-GABA_AR-enriched synapse formation at the AIS is an especially intriguing case, as AIS inhibition is essential for normal brain function. Better understanding axo-axonic synapse formation will not only shed light on the molecular mechanisms of subtype-specific inhibitory synapse formation but may also provide new avenues of research into treatment for neurological disorders like epilepsy, which result from pathological hyperexcitability. It appears that protein-protein interactions between the ICD of GABA_AR subunits and intracellular scaffolding proteins at inhibitory synapses play an important role in this process. The make-up of the inhibitory synaptic scaffold is variable depending on cell type and subcellular domain, making such interactions good candidates for synapse-specific GABA_AR subtype enrichment. Further research will need to be done to fully explore the “interactome” of each GABA_AR subtype and the importance of each interaction at the many different types of synapses present in even one neuron.

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AN wrote the manuscript, with input from PD and SM.

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Conflict of Interest: SM serves as a consultant for AstraZeneca, Bain Capital, and Sage Therapeutics, relationships that are regulated by Tufts University. SM is also a shareholder of SAGE Therapeutics.

The remaining authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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