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Presynaptic Regulation by Liprins

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Introduction

p0005 The synapse is the fundamental structure that allows neuronal networks and circuits to form and function. Presynaptic neurotransmission requires the formation and maintenance of a pool of synaptic vesicles through axonal transport, formation of specialized vesicular release sites, and local recycling of synaptic vesicle proteins. Postsynaptically, neuronal transmission involves the targeting and the clustering of synaptic receptors followed by receptor activation through neurotransmitters. The process of organization and localization of pre- and postsynaptic proteins is thought to depend on a variety of scaffolding proteins.

p0010 Scaffolding proteins are thought to organize the constituents of the active zone and to provide physical links between the active zone and synaptic vesicle proteins. Several proteins have been identified that may function as synaptic scaffolds: RIMs (Rab3-interacting molecules), which regulate synaptic vesicle exocytosis; Unc13 and Munc13, which are thought to be involved in priming; and three classes of proteins that are speculated to organize the structure of the active zone – the large presynaptic proteins bassoon and piccolo/aczonin, found in higher organisms, the well-conserved CAST/CAZ/ERC/Brp family of proteins, and the well-conserved liprin-α family.

p0015 Liprin-α (synonyms: LAR-interacting protein 1, LIP.1, SYD-2, Dliprin-α (CG11199), and *out of step* (oos)) is a 130-kDa protein that is important for efficient neurotransmission and for shaping the structure of neuromuscular junctions (NMJs), synaptic boutons, and active zones. It contains an N-terminal coiled-coil domain that mediates homo- and heteromultimerization and a C-terminal region that contains three sterile alpha motif (SAM) domains that mediate binding to an array of partner proteins (**Figure 1(a)**). At the sequence level, liprin-α is highly conserved, from vertebrates to *Caenorhabditis elegans* and *Drosophila*. Liprin-α interacts with itself and with proteins of at least eight other classes: liprin-βs 1 and 2, leukocyte antigen-related protein (LAR), protein tyrosine phoshatases (PTPσ, PTPδ), the anaphase-promoting complex/cyclosome (APC/C), RIM, ERC, kinesin-1 and-3, G-protein-coupled receptor kinase-interacting protein (GIT), CASK, and glutamate receptor-interacting protein (GRIP) (**Figure 1(b)**), all of which appear to be involved in normal synaptic function.

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Liprin Expression, Localization, and Diversity

p0020 In addition to its localization in neurons, liprin-α is widely expressed. In mammals, the mRNAs for liprin-α 1 and -β 1–2 have been found in all tissues that have been examined (heart, brain, placenta, lung, liver (very low levels of β 1 in liver), muscle, kidney, and pancreas). In contrast, liprin-αs 2–4 may play more specialized roles because their expression is restricted. The mRNA for liprin-α 4 is found only in heart, brain, and muscle, and the mRNAs for liprin-αs 2 and 3 are solely expressed in brain tissue. In all cell types, liprin-α has been implicated in the formation of cell–cell contacts.

p0025 In nonneuronal cells, liprin-α is enriched at focal adhesions and co-localizes with the receptor protein tyrosine phosphatase (RPTP) LAR, phosphotyrosine, talin, vinculin, paxillin, and $pp125^{FAK}$. It has been suggested that liprin-α is involved in the disassembly of focal adhesions. Analysis of liprin-α may give insights into parallels between synaptic and focal adhesion assembly. In neurons, liprin-α is found both pre- and postsynaptically and at both excitatory and inhibitory types of synapses. In *Drosophila*, liprin-α localizes to synapses, with a broad distribution. However, synapse-defective *C. elegans* liprin-α (SYD-2) has been shown to cluster at the active zone.

p0030 While there are four isotypes of liprin-α in mammals, there is only a single version of liprin-α in *C. elegans* and in *Drosophila*; furthermore, little work has been done on liprin−αs 2–4. In addition, there are different splice forms of liprin-α 1 in mammals, with isoform 1B being the longest (version 1A lacks the last 30 amino acids which contain the GRIP-binding domain and accordingly does not bind to GRIP). Thus, unless otherwise specified, when we use the term liprin-α it will refer to the splice form liprin-α 1B in mammals and the single versions that are the most similar to liprin-α 1B in flies and worms.

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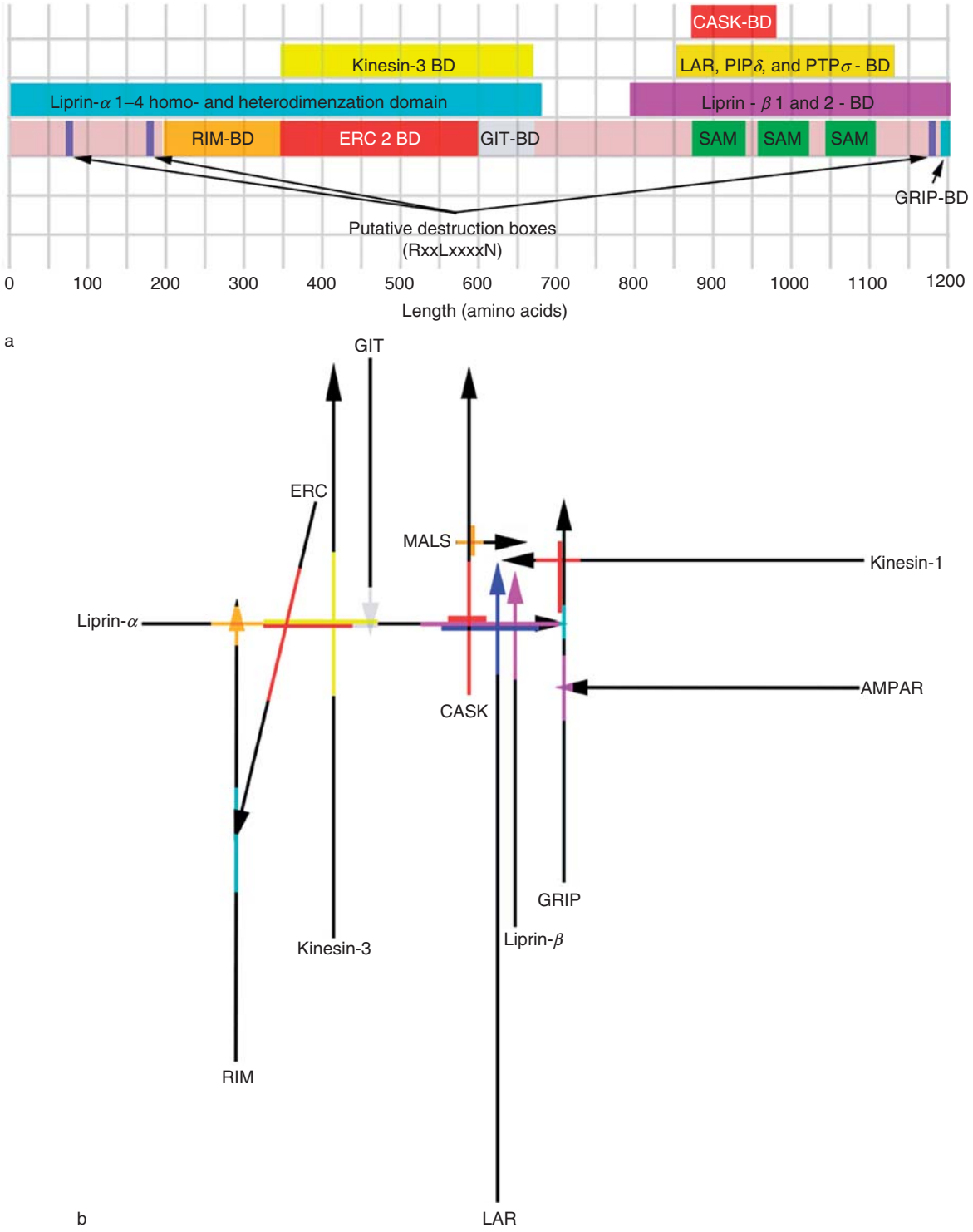
Function of Liprin-α at the Synapse

p0035 Although liprins were first characterized in nonneuronal cells, the majority of functional data on liprin-α and its binding partners has been obtained from the nervous systems of worms and flies. Liprin-α function at the synapse was first appreciated in *C. elegans*,



f0005 **Figure 1** (a) Overview of protein-binding sites of liprin-α. (b) Interaction map of liprin interactions. All proteins are drawn to scale based on the number of amino acids. Arrowheads are the C-terminus of the protein. Mapped sites of protein–protein interaction are in matching color.

where SYD-2 was identified in a screen for altered distribution of a synaptic vesicle marker at neuromuscular synapses. Although, like its vertebrate counterpart, the *C. elegans* NMJ is cholinergic, it is formed by muscle projections that reach into the neuropil to find motor axons, thus requiring morphogenetic expansion of presynaptic varicosities along the axon shaft. Behavioral assays, pharmacology, and

ultrastructural characterization showed that neuromuscular synapses function poorly and contain larger presynaptic active zones in mutants lacking liprin-α. Behaviorally, *C. elegans* mutants lacking liprin-α are sluggish in movement and retain twice as many eggs. These defects are fully rescued when liprin-α is selectively expressed in neurons, but not muscles. Since egg laying can be induced by treatment with serotonin (but not imipramine) and SYD-2 worms are resistant to aldicarb (an inhibitor of cholinesterase, which causes wild-type worms to hypercontract and die), these defects are both genetically and pharmologically consistent with a primary defect in presynaptic transmission.

p0040 In *Drosophila*, where NMJs are glutamatergic, liprin-α was identified as a binding partner of the RPTP LAR. In this context, liprin-α was shown to localize to the NMJ and was shown to be required for the overall morphological growth of the nerve terminal. In the fly, like in vertebrates, NMJs are branched expanses at the ends of axons where motor neurons make connections with muscles. Synaptic boutons, which are 0.5–2 μm in diameter, lie along NMJs and resemble beads on a string. Each bouton contains multiple active zones, typically between 50–100 nm in length. As observed in *C. elegans*, *Drosophila* NMJs lacking liprin-α display larger active zones (~2.5-fold higher mean area), suggesting that the role of liprins in the presynaptic cytomatrix is well conserved.

p0045 When liprin-α is disrupted, synaptic transmission is reduced in both flies and worms. Yet, there is an apparently paradoxical increase in the average size of active zones and a proportional increase in the number of presynaptic vesicles. Reassuringly, at the electron microsopic (EM) level, active zones appear less electron dense, and at the light microcopic level the intensities of staining for synaptobrevin, synaptotagmin, syntaxin, and rab3 are decreased. As disruption of liprin-α has the functional consequence of disrupting synaptic transmission, it is possible that active zone size is increased in a futile attempt to compensate for decreases in evoked release. If so, the observed decreases in protein density at active zones could occur because a fixed amount of material is spread over a larger area. Alternatively, the absence of a key synaptic scaffold may simply reduce the crosslinking within the cytomatrix and result in a loose network of active zone proteins. A failure to recruit all the necessary presynaptic components or a decreased concentration of the remaining proteins could reduce the efficiency of neurotransmitter release.

p0050 One great advantage of *Drosophila* as a genetic model organism for studies of synapse biology is the accessibility of the NMJ to electrophysiological characterization. Disruption of *Drosophila* liprin-α (Dlar) results in a ~30% decrease in evoked postsynaptic potentials and a ~60% decrease in quantal content (excitatory/mini-excitatory junction potentials, EJP/mEJP). The amplitude and frequency of mini-excitatory junction potentials in these mutants are comparable to those in wild type, inferring that synaptic vesicles are present at the active zones, but there is a defect in evoked release. Similar defects in evoked release are also seen when Dlar, CAST, RIM, and APC/C are disrupted in different organisms. In combination with work on these proteins, this implies that liprin-α directly or indirectly determines the size of the releasable pool. Based on these results, liprin-α may be important in some aspect of docking or priming of presynaptic vesicles. Consistent with this hypothesis, liprin-α mutants display defects in vesicle trafficking.

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p0055 Disruption of liprin-α results in ectopic accumulation of synaptic vesicle markers along the motor axon shaft (often called 'clogs') and a 50% reduction in both the number of synaptic boutons and the NMJ branches. One hypothesis to explain the effects seen in liprin-α mutants is that they result from an impairment of axonal transport. Indeed, a quantitative analysis of axon transport in living animals reveals that liprin-α positively regulates anterograde transport and negatively regulates retrograde transport. In *Drosophila* cells, liprin-α can associate with a complex including the heavy chain of kinesin-1 (Khc), consistent with the fact that *khc* mutants display similar axon clogs. Thus, liprin-α plays an interesting role in the delivery of synaptic material. Whether the regulation of axon transport is liprin's primary role or whether this is one of many functions remains to be elucidated.

Partners of Liprin-α

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APC/C and Liprin-α

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p0060 The APC/C is an E3 ubiquitin ligase that regulates the concentration of liprin-α and modulates NMJ morphology in *Drosophila*. It controls the abundance of proteins by regulating their targeting to the ubiquitin-proteasome degradation system. While it has been established that APC/C is a critical mediator of cell-cycle transitions, recent work has demonstrated that it also functions in postmitotic cells. In *Drosophila* muscles, APC/C regulates synaptic transmission by controlling the concentration of a postsynaptic glutamate receptor. While the change in postsynaptic response may be due to an alteration in liprin-α-dependent clustering of glutamate receptors, the observation that mutations in liprin-α do not affect

quantal size at the *Drosophila* NMJ suggests that APC/C may be regulating the degradation of other postsynaptic proteins. In neurons, APC/C regulates synaptic growth and synaptic transmission by controlling the concentration of the downstream effector liprin-α. When APC/C is disrupted, liprin-α intensity is increased presynaptically and the number of synaptic boutons is also increased. These changes are consistent with previous work which demonstrated that disruption of liprin-α leads to a decrease in the number of boutons in this system. Together, these findings suggest that the morphology of the NMJ is regulated through the control of liprin-α concentration downstream of APC/C.

s0030 **MALS/CASK and Liprin-*α***

p0065 Liprin-α has now been shown to be a component of the MALS/Veli–CASK–Mint-1 complex of PDZ proteins. MALS has been implicated in presynaptic vesicle cycling. When all three isoforms of MALS proteins are disrupted in mice, the mice die soon after birth; they have difficulty breathing and show impaired excitatory synaptic transmission. Of particular interest, the MALS complex seems to be important for determining the size of the releasable pool of synaptic vesicles and may be important for replenishing this pool from the reserve pool. The lack of GRIP or α-amino-3-hydroxy-5-methylisoxazole-4-propionic acid (AMPA) receptors in the MALS complex suggests no role for liprin-α in the MALS complex postsynaptically. The lack of liprin-*β* suggests that this protein is not critical for the MALS/Veli–CASK–Mint-1/liprin-α complex. The Veli–CASK–Mint-1 complex, a homologous counterpart of the LIN-2–LIN-7–LIN-10 complex of *C. elegans*, has also been implicated in several other synaptic protein interactions, such as with voltage-gated N-type calcium channels (**Table 1**). This work is consistent with a model where a MALS/Veli–CASK–Mint-1/liprin-α complex couples extracellular synaptic interactions to the intercellular organization of the presynaptic secretory machinery.

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s0035 **Liprin-*α* and CASK**

p0070 CASK (CAKI or CAMGUK in flies) is a membrane-associated guanylate kinase-associated (MAGUK) protein that has a catalytically inactive N-terminal CaM-kinase domain that interacts with Veli and Mint-1, an SH3 domain that binds N-type Ca^{2+} channels, and a central PDZ domain that interacts with other membrane proteins such as glycophorins, neurexins, and syndecan. The observation of an interaction between CASK and syndecan is particularly interesting in light of the recent demonstration that another liprin-α-interacting protein, LAR, also binds to syndecan. In addition, LAR and CASK both bind liprin-α in the same region (see **Figure 1**). We raise the possibility that the interaction between these three proteins may be relevant for their function, but determining how these proteins interact will take further investigation.

Table 1 Protein–protein interactions relevant to Liprin-α function t0005

Protein	*Protein*
CASK	MALs
CASK	Syndecan
ERC2	RIM1
GIT	Piccolo–Bassoon
GRIP	AMPA Receptor
GRIP	Kinesin-1
LAR	*β*-catenin
LAR	Syndecan
Liprin-α	APC/C Complex
Liprin-α	CASK
Liprin-α	ERC2
Liprin-α	GITs
Liprin-α	GRIP1
Liprin-α	LAR
Liprin-α	Liprin-α
Liprin-α	Liprin-*β*
Liprin-α	Kinesin-1
Liprin-α	Kinesin-3
Liprin-α	RIM1
RIM	Piccolo–Bassoon

p0075 Disruption of *caki* results in an increase in spontaneous neurotransmitter release and an impairment in the response of the giant fiber pathway to continuous stimulation. These defects appear to involve the loss of presynaptic control of exocytosis, which is similar to the defect seen in liprin-α mutants. The defect in neurotransmission seen in *caki* mutants is one of many possibilities to explain how disruption of liprin-α leads to defects in neurotransmission.

Liprin-*α* and LAR s0040

p0080 LAR family receptor protein tyrosine phosphatases (LAR, PTP*δ*, and PTP*σ*) bind liprin-α. Disruption of *Drosophila* LAR results in axonal pathfinding defects and defects in synaptic morphology and neurotransmission that are similar to those seen in liprin-α mutants. The extracellular regions of LAR-RPTP contain three N-terminal immunoglobulin-like domains and a variable number of fibronectin type III-like domains that are well conserved, from insects to humans. This suggests that these phosphatases may function as receptors for cell surface or extracellular matrix proteins. The heparan sulfate proteoglycans (HSPGs) syndecan and dallylike have recently been shown to bind to the extracellular domains of LAR

and to regulate synaptic growth and active zone form and function, respectively. The intracellular region of LAR contains two tandem phosphatase domains: the membrane proximal domain (D1), which has phosphatase activity, and the distal phosphatase domain (D2), which is devoid of catalytic activity but may regulate the substrate specificity of LAR. LAR has been shown to dephosphorylate β-catenin *in vitro*, but not liprin-α, although recent data suggest that liprin-α is tyrosine phosphorylated in some contexts. Liprin-α binds the D2 domain of LAR and co-localizes with it at focal adhesions and at NMJs. Although the functional relationship between liprin-α and LAR is not completely clear, is possible that LAR and liprin-α simply anchor each other at the active zone. In support of this hypothesis, expression of liprin-α 2 by transfection alters the distribution of LAR in cultured cells. Disruption of LAR in *Drosophila* reveals that it is not required for localization of liprin-α to the synapse; however, the reverse may be true. These results suggest that proteins other than Dlar can maintain synaptic liprin-α localization. Work in mammalian neurons suggests that the LAR–liprin-α interaction may contribute to synapse morphogenesis by regulating the synaptic delivery of a protein complex that includes AMPA receptors, GRIP, liprin-α, LAR, cadherin, and β-catenin. How the interaction between LAR and liprin-α relates to cadherin/β-catenin, syndecan, and dallylike function is an important future direction of research. In other contexts, such as epithelial cell polarity and axon guidance, LAR and its signaling partners regulate the structure of actin cytoskeleton, further raising the possibility that synaptic LAR and liprin-α play some role in cytoskeletal remodeling to control presynaptic structure.

s0045 **Liprin-α, GRIP, and GluR2**

p0085 GRIP is a multi-PDZ domain-containing protein that binds liprin-α, as well as both ephrin receptors and ligands and the kinesin-3 motor protein family member KIF1A. GRIPs have been suggested to mediate the transport of glutamate receptors, the stabilization of receptors within postsynaptic densities, and the sorting of internalized receptors. GRIP1 is found in synaptic preparations and intracellular compartments. This includes putative transport vesicles for glutamate receptors. Genetic analysis in mice shows that GRIP1 is required early during development, because a GRIP1 knockout is embryonic lethal at day 12 and the embryos suffer from defects in junction formation between dermis and epidermis.

p0090 Liprin-α isotypes 1, 3, and 4 interact with GRIP through the last seven amino acids of liprin-α, and liprin-α 1 immunoprecipitation pulls down GRIP and GluR2/3. This interaction is selective because the postsynaptic density 95-kDa protein (PSD-95) and *N*-methyl-D-aspartate (NMDA) do not associate with liprin-α 1. Of note, LAR interaction in this system is weak, as LAR does not immunoprecipate with liprin-α 1 unless it is cross-linked with dithiobis-succinimidylpropinate. In young neurons, GRIP and liprin-α are both present in the axons of cultured mouse hippocampal neurons, but in mature presynaptic regions these proteins do not co-localize, suggesting that the GRIP–liprin interaction may be more important for the assembly of synapses than for their maintenance. Although liprin-α seems to perform both pre- and postsynaptic functions, the interaction with GRIP seems to be most important postsynaptically, since *Drosophila* GRIP is only expressed in muscles and mouse liprin-α and GRIP interactions primarily involve postsynaptic proteins. Transfection with liprin-α 1A that lacks the C-terminus (TYSC) in hippocampal neurons reduces the number of AMPA receptors that cluster along dendrites. In addition, an interaction between GRIP, GIT1, and liprin-α is important for AMPA receptor targeting. This suggests that liprin-α is involved in the localization of AMPA receptors through its interactions with these proteins at postsynaptic sites.

p0095 Given the strong evidence that (1) liprin-α interacts with GRIP, (2) DGRIP is found in muscles, and (3) interaction between liprin-α and GRIP has been implicated in the clustering of glutamate receptors, it is surprising that disruption of liprin-α does not result in a decrease in postsynaptic sensitivity (i.e., the amplitude of mini-excitatory junction potentials). Nonetheless, as full rescue of synaptic function can be done by the selective expression of liprin-α (SYD-2) in neurons, it is possible that liprin-α may play a minor role in postsynaptic functioning in invertebrates, and a more important role in vertebrate synapses.

Liprin-α and GIT s0050

p0100 GIT1 was originally isolated as a protein interacting with G protein-coupled receptor kinases. The GIT family of proteins contains two known members, GIT1/Cat-1/p95-APP1 and GIT2/Cat-2/PKL/p95-APP2/KIAA0148. GIT proteins contain a GTPase-activating protein (GAP) domain for ADP-ribosylation factors (ARFs), small GTP-binding proteins implicated in the regulation of membrane traffic, and the actin cytoskeleton. In addition, GIT proteins contain various domains for protein interactions: ankyrin repeats, the Spa2 homology domain (SHD), and the G protein-coupled receptor kinase-binding domain (GRKBD). GIT proteins regulate endocytosis of various membrane

proteins and regulate the assembly of focal adhesion complexes by interacting with the Rho-type guanine nucleotide exchange factor (GEF) PIX, focal adhesion kinase (FAK), the focal adhesion adaptor protein paxillin, and liprin-α When GIT is disrupted, dendritic synapse number and AMPA receptor targeting are decreased. Piccolo has been proposed to play a role in GIT localization at active zones, but given the number of proteins that interact with GIT it seems likely that multiple proteins are influencing its distribution. As liprin-α and GIT are both found at focal adhesions and synapses, interact, and share a role in intracellular trafficking of AMPA receptors (AMPARs), it is tempting to speculate that the same machinery is used for 'trans-Golgi' trafficking, axonal transport, dendritic trafficking, and synaptic vesicle trafficking, but in a context-specific manner.

s0055 **Liprin-α and ERCs**

p0105 The ERC family of 'cytomatrix at the active zone' (CAZ) proteins contains two known members and both interact with liprin-α: ERC1/ELKS/Rab6IP2/CAST2 and ERC2/CAST1. Recent analysis of mutations in a *Drosophila* CAST ortholog, bruchpilot (NC82), reveals a requirement for CAST in synaptic development and active zone morphogenesis, consistent with the highly specific localization of this protein to the active zone. In addition, ERC interacts with other CAZ proteins, including RIM, piccolo, bassoon, and syntenin. ERC2 has been implicated in modulating liprin-α levels at the synapse: co-expressing ERC2 leads to increased levels of liprin-α. Functionally, the interaction of ERC2 with RIM1 and bassoon/piccolo has been shown to regulate neurotransmitter release. As liprin-α binds both ERC2 and RIM, the defect in synaptic evoked release that occurs when liprin-α is disrupted may occur through the disruption of these interactors. Since ERC2 and GIT interact with Rab6 and ARF, it has been suggested that liprin-α might mediate the integration of the Rab6 and ARF signaling pathways for the regulation of membrane traffic.

s0060 **Liprin-α and RIM**

p0110 RIM1 is an active zone protein that was initially identified as a putative effector for the synaptic vesicle protein Rab3A. RIM interacts with several active zone molecules, including Munc13–1 and liprin-α, to form a protein scaffold in the presynaptic nerve terminal. RIMs also bind to RIM-BPs through a C-terminal sequence, to cAMP-GEFII through an unknown site, and to Ca^{2+} channels and synaptotagmin 1 through both C2 domains. Abolishing the expression of RIM1 in mice shows that RIM1 is essential for maintaining normal probability of neurotransmitter release and for regulating release during short-term synaptic plasticity. This presumably occurs through a disruption of either vesicle priming or fusion, or both. Based on these observations, it seems likely that the presynaptic defect in evoked release seen when liprin-α is disrupted in *Drosophila* is caused in part through a disruption of RIM localization and/or function; however, mutations in *Drosophila* RIM have not been described.

Kinesins, Liprin, and Presynaptic Vesicle Precursor Transport

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There are two major subdivisions of axonal transport: fast and slow. Soluble cytoskeletal proteins such as tau, kinesin, dynein, myosin, and tubulin are transported at a rate of approximately $1\,mm\,day^{-1}$ by slow axonal transport. Membrane-bound proteins, associated with organelles such as presynaptic precursor vesicles, are transported at a rate of approximately $1\,\mu m\,s^{-1}$ by fast axonal transport. The kinesin family of molecular motors moves soluble proteins and organelles away from the cell body, and dynein moves these materials toward the cell body. When kinesin-1 is disrupted, axonal clogs that contain synaptic components occur along axons and synaptic transmission is disrupted.

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p0120 While substantial evidence suggests that liprin-α plays a direct role in determining the form and function of synapses, recent data also reveal that liprin-α is involved in the fast axonal transport of presynaptic vesicle precursors (PVPs). PVPs contain the raw materials for the assembly of synapses, and while they are thought to be transported primarily by kinesin-3 (Unc-104, Kif1a), kinesin-1 (conventional kinesin) family members may also play a role in their transport. Since axonal accumulations of endogenous synaptotagmin similar to those found in kinesin heavy chain (Khc) alleles are also observed in mutants lacking *Drosophila* liprin-α, we speculate that liprin-α is involved in the transport of a subset of synaptic components and that this subset may be transported by more than one family of kinesin.

p0125 At one time is was thought that there were molecules whose sole purpose was to link kinesins to cargos, but it now appears that most adaptors are scaffolding proteins that interact with multiple proteins and do not serve as simple linkers. Liprin-α binds to kinesin-1 and kinesin-3. Yet, the balance of the evidence is against liprin-α acting as a simple linker between PVPs and kinesins. When it is disrupted, the transport of PVPs is not halted. Instead, it shifts the probability of transport from anterograde (kinesin-mediated) to retrograde (dynein-mediated) transport. Thus, liprin-α is not required for the movement of PVPs *per se*. Instead of a simple linker, liprin-α appears as a modulator of axonal transport.

p0130 One of the most basic questions in neurobiology is how some types of neuronal components are trafficked to dendrites, and others are selectively transported into axons. Liprin-α is part of a complex that targets postsynaptic components to dendrites and involves GRIP, AMPARs, and kinesin-1. Of note, there are splice variants of liprin-α that lack the GRIP-binding domain. It is tempting to speculate that this differential targeting between axons and dendrites may involve variations in splicing. Yet further work will be required to determine if and how liprin-α could help to selectively guide components into either axonal or dendritic compartments. While several lines of evidence suggest that liprin-α regulates transport, a great deal of work remains to provide a satisfying molecular answer as to how this occurs.

s0070 ## Overview

p0135 Throughout this article we have outlined liprin-α function at the synapse and we find three reoccurring themes: (1) liprin-α binds multiple proteins that are required for efficient neurotransmitter release; (2) liprin-α regulates intercellular transport; (3) liprin-α is involved in the postsynaptic clustering and targeting of AMPARs. A great deal of effort has been devoted to identifying which proteins bind to liprin-α; now the problem is understanding the mechanism of normal functioning.

See also: Development of presynatpic functional and morphological organization (01772); Axonal and dendritic transport by dyneins and kinesins in neurons (00708); Assembly of postsynaptic specialization (01788); Glutamate receptor organization: ultrastructural insights (01790); Endocytosis and presynaptic scaffolds (01782); Postsynaptic Development, neuronal (molecular scaffolds) (00360); Active zone (01394); RIMs (01353); ERCs, Liprins, and RIM-BPs (01369); unc13/Munc13 molecules (01366); Piccolo and Bassoon (01360); Comparative biology of invertebrate neuromuscular junctions (01263); Ultrastructural Analysis of Spine Plasticity (01771); C. elegans (00798); Endocytosis and presynaptic scaffolds (01782); Synaptotagmins (01358); Rab3 (01367); Presynaptic events in Neuromuscular transmission (01276); The ubiquitin-proteasome system & plasticity (00827); Calcium channels (01370); Neurexins (01365); Neuroligins and Neurexins (01784); Drosophila (00799); AMPA receptor cell biology/trafficking (01222); Synaptic vesicles (01392); Myosin transport and neuronal function (00709).

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