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### The dynamic architecture of photoreceptor ribbon synapses: Cytoskeletal, extracellular matrix, and intramembrane proteins

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#### Abstract

Rod and cone photoreceptors possess ribbon synapses that assist in the transmission of graded light responses to second-order bipolar and horizontal cells of the vertebrate retina. Proper functioning of the synapse requires the juxtaposition of presynaptic release sites immediately adjacent to postsynaptic receptors. In this review, we focus on the synaptic, cytoskeletal, and extracellular matrix proteins that help to organize photoreceptor ribbon synapses in the outer plexiform layer. We examine the proteins that foster the clustering of release proteins, calcium channels, and synaptic vesicles in the presynaptic terminals of photoreceptors adjacent to their postsynaptic contacts. Although many proteins interact with one another in the presynaptic terminal and synaptic cleft, these protein–protein interactions do not create a static and immutable structure. Instead, photoreceptor ribbon synapses are remarkably dynamic, exhibiting structural changes on both rapid and slow time scales.

#### Keywords

Cone; Rod; Outer retina; Neurotransmission; Cytoskeleton

#### Introduction

Synapses are highly specialized contacts between neurons that have evolved to transmit signals effficiently and reliably throughout the nervous system. At chemical synapses, changes in the electrical potential of a cell are converted into a chemical signal. The classical mechanism involves a depolarization-induced Ca<sup>2+</sup> influx causing SNARE proteins to intertwine and pull vesicles to the plasma membrane (Pang & Südhof, 2010). The subsequent fusion event results in vesicles emptying their neurotransmitter contents into the synaptic cleft to signal through receptors on postsynaptic neurons. Synapses require a highly organized placement of pre-synaptic exocytotic proteins, endocytotic proteins, calcium channels, postsynaptic receptors, and other associated proteins. In photoreceptor terminals, synapses are organized around a large electron-dense structure known as the ribbon. In this review, we examine the molecular architecture of ribbon synapses in photore-ceptor terminals with a focus on interactions with the cytoskeleton and extracellular matrix (ECM). We also summarize studies showing that photoreceptor ribbon synapses are not static structures but can be altered dynamically on both fast and slow time scales.

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#### Cav channels cluster at the active zone

Physiological experiments have established that the voltage-gated calcium (Ca<sub>V</sub>) channels in rod and cone photoreceptors are high voltage-activated L-type channels (Bader et al., 1982; Corey et al., 1984; Barnes & Hille, 1989; Lasater & Witkovsky, 1991; Wilkinson & Barnes, 1996). There is no evidence for non-L-type  $Ca_V$  channels in photoreceptors. Freeze-fracture electron micrographs of photoreceptor terminals show a random array of hexagonal-shaped particles at the apex of the synaptic ridge that are thought to be Ca<sub>V</sub> channels (Raviola & Gilula, 1975; Schaeffer et al., 1982). Terminals of rods and cones in the outer plexiform layer (OPL) label with antibodies to poreforming Ca<sub>V</sub>1.2 ( $a_{1C}$ ), Ca<sub>V</sub>1.3 ( $a_{1D}$ ), and Ca<sub>V</sub>1.4 (*a*<sub>1F</sub>) subunit isoforms (Nachman-Clewner et al., 1999; Firth et al., 2001; Henderson et al., 2001; Morgans, 2001; Morgans et al., 2001, 2005; Wu et al., 2003; Mansergh et al., 2005; tom Dieck et al., 2005; Xiao et al., 2007; Specht et al., 2009; Kersten et al., 2010; Mercer et al., 2011a,b). High levels of Ca<sub>V</sub>1.3 and Ca<sub>V</sub>1.4 messenger RNA (mRNA) are present in retina (Bech-Hansen et al., 1998; Strom et al., 1998; Xiao et al., 2007) but only low levels of Cav1.2 mRNA (Kamphuis & Hendriksen, 1998), suggesting that the labeling of photoreceptors by  $Ca_V 1.2$  antibodies may be nonspecific. Mutations in  $Ca_V 1.4$  greatly diminish the electroretinogram (ERG) b-wave in knockout mice, produce malformed ribbons, and cause congenital stationary night blindness (CSNB) in humans. Combined with immunohistochemical evidence, these findings suggest that  $Ca_V 1.4$  is the principle  $Ca_V$ channel subtype in rods (Bech-Hansen et al., 1998; Strom et al., 1998; Mansergh et al., 2005; Chang et al., 2006; Striessnig et al., 2010).

The contribution of  $Ca_V 1.3$  at photoreceptor synapses is less clear. Immunoelectron micrographs show labeling for antibodies to  $Ca_V 1.3$  at the base of ribbons in mouse retina (Kersten et al., 2010). However, Ca<sub>V</sub>1.3 mutations in mouse retina do not significantly diminish the b-wave (Wu et al., 2007), and b-waves of Ca<sub>V</sub>1.3/Ca<sub>V</sub>1.4 double mutants do not appear to differ from those of  $Ca_V 1.4$  single mutants (McCall & Gregg, 2008). It may be that  $Ca_V 1.3$  channels are present only in a subpopulation of cones. For example,  $Ca_V 1.3$ antibodies label M cones but not S cones in the tree shrew retina (Morgans, 1999). Subtype differences among cones also occur in salamander retina where protein kinase A (PKA) inhibits Ca<sup>2+</sup> currents in rods and short wavelength-sensitive small single cones but enhances Ca<sup>2+</sup> currents of long wavelength-sensitive large single cones (Stella & Thoreson, 2000). PKA activation also enhances currents from heterologously expressed  $Ca_V 1.3$ channels (Qu et al., 2005; Liang & Tavalin, 2007). The pharmacological properties of Ca<sup>2+</sup> currents, including partial block by omega-conotoxin, are consistent with the presence of  $Ca_V 1.3$  channels in salamander cones (Wilkinson & Barnes, 1996). Antibodies to  $a_2 \delta_4$ subunits label photoreceptor terminals (Mercer et al., 2011*a*), and mutations in  $\beta_2$  or  $a_2\delta_4$ subunits cause diminished ERG b-waves and CSNB, suggesting that these are the principle Cay channel accessory subunits in photoreceptors (Ball et al., 2002; Wycisk et al., 2006a,b).

Excision of the synaptic terminal diminishes rod calcium currents by 95%, indicating that most of the Ca<sub>V</sub> channels are located in the terminal (Xu & Slaughter, 2005). As illustrated in Fig. 1, sites of intraterminal Ca<sup>2+</sup> influx also colocalize with synaptic ribbons in rod photoreceptor terminals. In this example, changes in intracellular Ca<sup>2+</sup> levels were visualized in a salamander rod using the Ca<sup>2+</sup>-sensitive dye, Oregon Green BAPTA-6F, (Invitrogen, Carlsbad, CA) ( $K_D = 3 \mu M \text{ Ca}^{2+}$ ), and the ribbon was labeled with a rhodamine-conjugated consensus peptide that binds selectively to the ribbon protein, ribeye (Zenisek et al., 2004). Both dyes were introduced into the rod through a patch-clamp pipette. Sites of Ca<sup>2+</sup> influx and ribbons are also colocalized in cones (Choi et al., 2008). Consistent with close proximity between Ca<sub>V</sub> channels and the ribbon, immunohistochemical studies provide evidence for clusters of Ca<sub>V</sub> channels at the base of the ribbon (Nachman-Clewner et al., 1999; Morgans, 2001; Morgans et al., 2005; Specht et al., 2009; Mercer et al., 2011*b*).

Furthermore, individual Ca<sub>V</sub> channels labeled with quantum dots conjugated to  $a_2\delta_4$  antibodies colocalize with fluorescently labeled ribeye consensus peptides (Mercer et al., 2011*a*), and immunoelectron micrographs show Ca<sub>V</sub> channels along the synaptic ridge at the base of the ribbon (tom Dieck et al., 2005; Kersten et al., 2010).

## Ca<sup>2+</sup>-dependent vesicle release and replenishment at photoreceptor synapses

At most synapses, Ca<sup>2+</sup> needs to attain high micromolar levels to stimulate release, and therefore, exocytosis is typically restricted to release sites within nanodomains of high Ca<sup>2+</sup> very close to  $Ca_V$  channels. A  $Ca^{2+}$  nanodomain is defined as the 10–100 nm range in the immediate vicinity of a Ca<sup>2+</sup> channel where Ca<sup>2+</sup> is not in equilibrium with fast buffers (Naraghi & Neher, 1997). Examples of synapses where release involves  $Ca^{2+}$  nanodomains include the squid giant synapse (Adler et al., 1991), mammalian rod bipolar cell (Jarsky et al., 2010), GABAergic basket cells in the hippocampus (Bucurenciu et al., 2008), and mature calyx of Held (Fedchyshyn & Wang, 2005; Weber et al., 2010). The release mechanism in rods and cones is much more sensitive to Ca<sup>2+</sup> than at other synapses, and exocytosis can thus be triggered by submicromolar  $Ca^{2+}$  levels (Rieke & Schwartz, 1996; Thoreson et al., 2004; Sheng et al., 2007; Duncan et al., 2010). The high Ca<sup>2+</sup> afffinity of the release mechanism at photoreceptor synapses suggests that release might involve spatially averaged Ca<sup>2+</sup> levels in the terminal and not the high Ca<sup>2+</sup> levels found in nanodomains. However, experiments comparing effects of the diffusible synthetic Ca<sup>2+</sup> chelators ethylene glycol tetraacetic acid (EGTA) and 1,2-bis (o-aminophenoxy) ethane, N,N,N',N'-tetraacetic acid (BAPTA) on release indicate that release sites are within 50-100 nm of  $Ca^{2+}$  channels in amphibian cones (Mercer et al., 2011*b*). This was shown by the finding that when 0.5 mM EGTA, 5 mM EGTA, or 5 mM BAPTA were introduced into cones, only 5 mM BAPTA reduced the amplitude of glutamatergic post-synaptic currents in second-order neurons (Mercer et al., 2011b). Comparisons of the calcium current to the size of the readily releasable pool of synaptic vesicles suggest that only a few Ca<sup>2+</sup> channel openings accompany fusion of each vesicle during the first few milliseconds of release from cones (Bartoletti et al., 2010). Thus, when cones are depolarized by a light decrement, the release of vesicles is triggered by the emergence of nanodomains of [Ca<sup>2+</sup>]; beneath open Ca<sub>V</sub> channels close to ribbon release sites, providing a tight coupling between channel opening and vesicle fusion (Mercer et al., 2011b).

In darkness, cones appear to switch from a tight coupling between  $Ca_V$  channel opening and vesicle fusion to a mode of release whereby the rate of sustained release is governed by the rate of replenishment. At the dark potential, cones are depolarized to a membrane potential of approximately –40 mV, allowing the continued influx of Ca<sup>2+</sup>, which in turn causes a depletion of the readily releasable pool of vesicles at the base of the ribbon (Jackman et al., 2009; Bartoletti et al., 2010). Under these conditions, the rate of synaptic release is limited not by the rate of individual channel openings but by the rate at which release-ready vesicles can be replenished (Jackman et al., 2009). The replenishment process is  $Ca^{2+}$  dependent (Babai et al., 2010) and so, even when the releasable pool is depleted in darkness, release is nonetheless regulated by Ca<sup>2+</sup> influx through Ca<sub>V</sub> channels. However, the Ca<sup>2+</sup>-dependent sites involved in replenishment are >200 nm from Ca<sub>V</sub> channels, further than the distance between release sites and channels (Babai et al., 2010). Because these  $Ca^{2+}$ -dependent sites of replenishment are not located within Ca<sup>2+</sup> nanodomains beneath individual channels, replenishment is regulated by the spatially averaged levels of Ca<sup>2+</sup> entering through multiple channels. In bright light, random channel openings are rare, and individual channel openings are closely synchronized with decrements in light intensity. Under these conditions, close coupling between channel openings and release events can provide an accurate read out of stimulus-dependent changes in membrane potential. When cones are depolarized in

Evidence that the  $Ca^{2+}$ -dependent replenishment mechanism involves sites >200 nm from  $Ca_V$  channel suggests that proteins along the ribbon may participate in this process. At the calyx of Held, calmodulin plays a key role in the  $Ca^{2+}$ -dependent acceleration of replenishment (Sakaba & Neher, 2001). One target of calmodulin is the GTP-binding protein, Rab3a (Park et al., 2002), and Rab3a has been shown to play a role in replenishment (Leenders et al., 2001). Rab3a interacts with RIM2 proteins along the ribbon and has been proposed to tether vesicles to the ribbon (Fukuda, 2003; Dulubova et al., 2005; tom Dieck et al., 2005; Deguchi-Tawarada et al., 2006; Uthaiah & Hudspeth, 2010). Along with calmodulin, Rab3a is an appealing candidate for regulating replenishment at the cone ribbon.

#### Synaptic Ca<sup>2+</sup> buffering and extrusion

 $Ca^{2+}$  influx can induce vesicle release and regulate replenishment, but rising  $[Ca^{2+}]_i$  levels are balanced by Ca<sup>2+</sup> extrusion and buffering mechanisms. One of the first studies of synaptic  $Ca^{2+}$  extrusion in photoreceptors was performed by Morgans et al. (1998) to determine whether the Na<sup>+</sup>/Ca<sup>2+</sup> exchanger or the plasma membrane Ca<sup>2+</sup> ATPase (PMCA) tempered increases in  $[Ca^{2+}]_i$  following a depolarizing stimulus. PMCA is considered critical for Ca<sup>2+</sup> handling at other synapses (Juhaszova et al., 2000; Wanaver-becq et al., 2003; Gover et al., 2007), but the  $Na^+/Ca^{2+}$  exchanger regulates  $Ca^{2+}$  levels in the outer segments of rod photoreceptors (Thoreson et al., 1997; Lagnado et al., 1998; Krizaj & Copenhagen, 2002). Morgans et al. (1998) demonstrated that the PMCA handled Ca<sup>2+</sup> extrusion in terminals of cone photoreceptors from the tree shrew, and that photoreceptors in the tree shrew, mouse, goldfish, and rat express a PMCA protein using a pan-PMCA channel antibody. Labeling with PMCA antibodies is found just above antibodies to Cav1.3 channels, colocalized with presynaptic post-synaptic density-95 (PSD-95) complexes and the Crumbs complex protein membrane palmitoylated protein 4 (MPP4) (Yang et al., 2007; Aartsen et al., 2009). Therefore, it seems reasonable to suggest that PMCA transporters lie some distance from synaptic release sites to avoid quenching brief  $Ca^{2+}$  signals in the active zone during dim light conditions but capable of limiting global increases in  $[Ca^{2+}]_i$ throughout the terminal. Similar PMCA expression patterns are found in the retinas of mice (Krizaj et al., 2002; Cia et al., 2005; Johnson et al., 2007), tiger salamanders (Krizaj et al., 2003, 2004), and chickens (Tolosa de Talamoni et al., 2002). However, using a C57Bl/6J mouse model, Johnson et al. (2007) found that PMCA is critical for  $Ca^{2+}$  extrusion in rod terminals, whereas the Na<sup>+</sup>/Ca<sup>2+</sup> exchanger is more important for maintaining Ca<sup>2+</sup> homeostasis in cone terminals. This corroborates the finding that PMCA2 knockout mice exhibit deflcits only in rod-mediated ERG responses (Duncan et al., 2006) and calls into question the idea that PMCAs are solely responsible for Ca<sup>2+</sup> homeostasis in the synaptic terminals of all photoreceptor cells.

Although  $Ca^{2+}$  extrusion can modulate  $Ca^{2+}$  homeostasis at photororeceptor synapses, endogenous buffering systems are also important (Thoreson, 2007). Extrusion of  $Ca^{2+}$ through PMCA or the Na<sup>+</sup>/Ca<sup>2+</sup> exchanger is slow compared to the kinetics of  $Ca^{2+}$ buffering (Klingauf & Neher, 1997; Thoreson et al., 1997; Krizaj et al., 2004; Mercer et al., 2011*b*). Local calcium buffering shapes diffusion of  $Ca^{2+}$  influx at the active zone (Klingauf & Neher, 1997) and thereby shapes the kinetics of neurotransmission. Endogenous neuronal buffers include calbindin, calretinin, and parvalbumin (Bennis et al., 2005; Rusakov, 2006). Although there is significant species-to-species variability, cone photoreceptors in most

species contain calbindin, a fast low mobility buffer, while calretinin and parvalbumin are only observed in the photoreceptors of a handful of species.

The calcium-binding proteins CaBP4 (Haeseleer et al., 2004; Lee et al., 2007) and calmodulin (Miller, 1991; Griessmeier et al., 2009) are also present at photoreceptor synapses and can buffer relatively high (>1  $\mu$ M) increases in [Ca<sup>2+</sup>]<sub>i</sub>. CaBP4 shifts the voltage activation range of Ca<sub>V</sub>1.4 towards more negative potentials, allowing channels to be effectively activated by physiological voltage levels below -40 mV (Haeseleer et al., 2004). CaBP4 weakly inhibits calcium-dependent inactivation of Ca<sub>V</sub>1.3 (Cui et al., 2007) and is a phosphorylation target of intracellular kinase pathways (Lee et al., 2007).

#### The synaptic ribbon

A striking feature of many sensory synapses is the presence of a large electron-dense structure known as the ribbon. Although its function in vesicle release is not yet fully understood, it is believed that the ribbon assists sensory neurons in maintaining graded tonic neurotransmission. Ribbons were initially proposed to function as conveyor belts that help transport vesicles to the active zone for exocytosis (Bunt, 1971). However, cytosolic ATP is not needed to release vesicles that have already been primed and attached to the ribbon, indicating that vesicle movement along the ribbon does not involve a molecular motor requiring ATP hydrolysis (Heidelberger, 1998). In fact, rather than accelerating vesicle replenishment at the base of the ribbon, the observation that vesicles are depleted from the base of the ribbon in darkness suggests that ribbons actually slow vesicle delivery (Jackman et al., 2009). Other proposed functions include the possibility that ribbons may prime vesicles for release, act like a flytrap to capture and deliver vesicles to the active zone, assist with endocytosis of previously released vesicles, or coordinate multivesicular release (Prescott & Zenisek, 2005).

Ribbons are found in bipolar and photoreceptor cells of the retina, pineal photoreceptors, hair cells, and electroreceptors. Ultrastructural studies show differences in the shapes of ribbons in different cell types. For example, ribbons of rod and cone photoreceptors and bipolar cells are typically more plate-like, whereas ribbons in hair cells are often spherical in shape (tom Dieck & Brandstätter, 2006). Synaptic ribbons in vertebrate photoreceptors are first expressed as similar precursor spheres (Regus-Leidig et al., 2009). Spherical ribbons are also found in photoreceptors from the hagfish retina suggesting that this may represent the primordial shape of the ribbon (Holmberg & Ohman, 1976). The main protein in the ribbon, ribeye, does not appear to be present in invertebrates, but photoreceptors from *Drosophila melanogaster* have T-bar structures that are sometimes compared to ribbons (Fouquet et al., 2009; Hamanaka & Meinertzhagen, 2010). Conventional vertebrate synapses also sometimes exhibit structures that resemble ribbons, such as spherical structures at the frog neuromuscular junction and punctate electron-dense projections at synapses between human hippocampal neurons (Zhai & Bellen, 2004).

Ribbons at synapses of vertebrate rod and cone photoreceptors are typically 30–40 nm wide and project 200–400 nm vertically into the cytoplasm (reviewed by Heidelberger et al., 2005; Sterling & Matthews, 2005; Schmitz, 2009). Cone ribbons have a base extending 200–700 nm along the membrane, whereas rod ribbons are 800–1500 nm long. Bipolar cell ribbons are normally smaller than photoreceptor ribbons (Sterling & Matthews, 2005). Terminals of mammalian rods typically contain one ribbon, whereas amphibian rods have multiple ribbons (Carter-Dawson & LaVail, 1979; Townes-Anderson et al., 1985; Migdale et al., 2003; Zampighi et al., 2011), but both mammalian and nonmammalian cones have larger terminals with a dozen or more ribbons. Vesicles tethered along the bottom one or two rows of the ribbon contact the plasma membrane and appear to form a readily releasable pool of vesicles that can fuse rapidly following an increase in  $[Ca^{2+}]_i$  (Sterling & Matthews, 2005; Bartoletti et al., 2010). A single ribbon at a rod synapse tethers ~25 vesicles to the plasma membrane at the base of the ribbon with a total tethered pool of ~700 vesicles (Thoreson et al., 2004; Heidelberger et al., 2005), whereas cone ribbons have a readily releasable pool of ~20 vesicles and a total tethered pool of ~110 vesicles (Innocenti & Heidelberger, 2008; Bartoletti et al., 2010).

#### Ribeye

Technological advances over the past 20 years have allowed scientists to characterize many of the key structural and functional domains of photoreceptor ribbons. The primary protein constituent of the ribbon is ribeye, which was first identified, characterized, and cloned by Schmitz et al. (2000). Ribeye is composed of a novel proline-rich A domain and a carboxyterminal B domain that is almost identical in sequence to the nuclear repressor, CtBP2. Both protein products are encoded by a single gene, but ribeye is expressed only at ribbon synapses (Wan et al., 2005; Magupalli et al., 2008). Synaptic ribbons have been visualized by fluorescent and electron microscopy using antibodies to ribeye (Schmitz et al., 2000), antibodies to CtBP2 (tom Dieck et al., 2005; Uthaiah & Hudspeth, 2010), and fluorescently labeled ribeye consensus peptides (Zenisek et al., 2004; Choi et al., 2008; LoGiudice et al., 2008).

The A domain of ribeye constitutes most of the internal scaffold of the ribbon structure, while the B domain faces into the cytoplasm where it can interact with other ribbon-related proteins (Schmitz et al., 2000; Alpadi et al., 2008; Magupalli et al., 2008). The scaffold of the ribbon is constructed from homotypic and heterotypic interactions between A and B domains of adjacent ribeye molecules. Heterotypic interactions between A and B domains are inhibited by nicotinamide adenine dinucleotide [NAD(H)] (Magupalli et al., 2008).

#### **Ribbon-associated proteins**

Although the backbone of a ribbon is constructed from interlinking ribeye peptides, a number of accessory cytomatrix proteins at the synapse appear to help organize vesicle trafficking near the ribbon (Zanazzi & Matthews, 2009). Directly beneath the ribbon in photoreceptor cells, but not most other ribbon synapses, is a trough-like electron-dense structure called the arciform density (Dowling & Boycott, 1966; Gray & Pease, 1971; Lasansky, 1973; Raviola & Gilula, 1975; Raviola & Raviola, 1982). The arciform density may help to anchor the ribbon to the plasma membrane and perhaps shape the diffusion of  $Ca^{2+}$  entering through  $Ca^{2+}$  channels beneath it, but the molecular constituents of the arciform density have not been identified.

The protein bassoon has received a great deal of attention as a ribbon coorganizer (Dick et al., 2003; tom Dieck et al., 2005; Frank et al., 2010; Regus-Leidig et al., 2010), although it is not localized exclusively to ribbon synapses (tom Dieck et al., 1998; Richter et al., 1999; Altrock et al., 2003; Hallermann et al., 2010). Bassoon is a large 420 KD protein that comigrates with ribeye in precursor spheres during development (Regus-Leidig et al., 2009) and has been localized to the base of the synaptic ribbon (Brand-stätter et al., 1999; tom Dieck et al., 2005). Bassoon may function as a ribbon-anchoring protein, but it is not clear if it is directly associated with the arciform density (Zanazzi & Matthews, 2009). Bassoon knockout animals have detached ribbons, deformed Ca<sup>2+</sup> channel clusters, and impaired vesicle attachment to the membrane in both the retina (Dick et al., 2003; tom Dieck et al., 2005) and auditory hair cells (Khimich et al., 2005; Frank et al., 2010). In the retina, bassoon knockout mice exhibit diminished ERG b-waves. In hair cells of bassoon knockout mice, fast synchronous release is inhibited more strongly than slower sustained release (Khimich et al., 2005), suggesting a role for nonribbon sites in maintaining tonic

neurotransmission in these cells. At ribbon and nonribbon synapses, bassoon mutants also show defects in vesicle replenishment, particularly for fast refilling (Frank et al., 2010; Hallermann et al., 2010). Bassoon and ribeye often colocalize with the protein piccolo (Cases-Langhoff et al., 1996), in both initial precursor spheres (Dresbach et al., 2006; Regus-Leidig et al., 2010) and fully functional ribbon-associated active zones (Dick et al., 2001; tom Dieck et al., 2005). Bassoon and piccolo share a similar structure and may share similar functions (Takao-Rikitsu et al., 2004; Mukherjee et al., 2010).

Cytomatrix at the active zone-associated structural protein (CAST) helps to organize the active zone at many synapses by interacting with bassoon, piccolo, RIM1, and RIM2, as well as indirectly with Munc13 (Hida & Ohtsuka, 2010). CAST is concentrated at the base of the ribbon along with RIM2, piccolo, and bassoon (Takao-Rikitsu et al., 2004; Deguchi-Tawarada et al., 2006). RIM proteins interact with many of the key proteins in release including synaptotagmin 1, SNAP-25, Rab3A, Munc13, and Ca<sub>V</sub> channels (Matteoli et al., 1991; Geppert et al., 1997; Wang et al., 1997; von Kriegstein et al., 1999; Coppola et al., 2001; Schoch et al., 2002; Deguchi-Tawarada et al., 2006; Gracheva et al., 2008; Kaeser et al., 2011).

RIM1 and RIM2 are differentially located with RIM1 found along the face of the ribbon and RIM2 clustered at the base of the ribbon (tom Dieck et al., 2005). ELKS has a high degree of homology to CAST and shares similar binding partners including bassoon and RIM1 (Inoue et al., 2006), but it is not concentrated as tightly at the ribbon base (Deguchi-Tawarada et al., 2006). This suggests that RIM2 may interact with CAST near the base of the ribbon, whereas interactions between RIM1 and ELKS may predominate further away from the base. CAST, ELKS, bassoon, piccolo, and RIM all appear to interact with an N-terminal region of Munc13. Interactions among these proteins may form an important node for organizing the synaptic active zone (Wang et al., 2009; Hida & Ohtsuka, 2010).

Interactions between RIM proteins and the C-terminal region of  $Ca_V$  channel  $\beta$  subunits promote the clustering  $Ca_V$  channels close to synaptic vesicles (Coppola et al., 2001; Kiyonaka et al., 2007; Gebhart et al., 2010; Han et al., 2011; Kaeser et al., 2011). Interactions between  $Ca_V$  channels and RIM proteins can also be promoted by intermediary RIM-binding proteins (Hibino et al., 2002).

 $Ca_V \beta$  subunits possess SH3-HOOK-GK domains that can potentially mediate multiple binding interactions with cytoskeletal elements, classifying them as membrane-associated guanylate kinase (MAGUK) proteins (Chen et al., 2004; Takahashi et al., 2004; Buraei & Yang, 2010). Although Ca<sub>V</sub> channel  $\beta$  subunits are MAGUKs with homology to other scaffolding proteins like PSD-95, their interactions with other cytoskeletal proteins are limited because the guanylate kinase domain is normally shielded by interactions with the  $a_1$  pore-forming subunit and the SH3 domain is shielded by other domains of the  $\beta$  subunit (Buraei & Yang, 2010).

In addition to potential cytoskeletal interactions with  $Ca_V \beta$  subunits, the pore-forming  $a_1$  subunit of  $Ca_V 1.3$  channels has a carboxyterminal sequence that recognizes class I PDZ domains (Zhang et al., 2005).  $Ca_V 1.3$  channels in photoreceptors can interact through this sequence with PDZ domains on the Usher proteins whirlin (Kersten et al., 2010) and harmonin (Gregory et al., 2011). This recognition sequence may also facilitate interactions between  $Ca^{2+}$  channels and other PDZ domain proteins (Nourry et al., 2003; Feng & Zhang, 2009).

Unc119 is located near the base of the ribbon where it plays a role in endocytosis (Karim et al., 2010) and interacts with both ribeye and the calcium-binding protein CaBP4 (Higashide et al., 1998; Alpadi et al., 2008; Haeseleer, 2008). CaBP4 can in turn interact with Ca<sub>V</sub>1.4 or

 $Ca_V 1.3$  channels (Haeseleer et al., 2004; Maeda et al., 2005; Yang et al., 2006), and these interactions may further help to localize  $Ca_V$  channels near the base of the ribbon.

Endocytic proteins like dynamin, amphiphysin, and clathrin are also expressed at ribbon synapses (Ullrich & Südhof, 1994: Sherry & Heidelberger, 2005). An amphiphysin splice variant has been identified in retinal ribbon synapses (Hosoya et al., 2004). Synaptojanin is a polyphosphoinositide phosphatase that plays a role in clathrin-mediated endocytosis (Song & Zinsmaier, 2003; Chang-Ileto et al., 2011). Synaptojanin antibodies label cone terminals more prominently than rod terminals (Holzhausen et al., 2009), and loss of synaptojanin produces floating ribbons in cone terminals (Van Epps et al., 2004). Unlike cone synapses, rod synapses develop normally without synaptojanin suggesting different roles for this protein and thus perhaps different endocytic pathways in the two cell types (Holzhausen et al., 2009).

#### **Exocytotic proteins**

There is evidence that release from ribbon synapses of inner hair cells does not involve neuronal SNARE proteins (Nouvian et al., 2011). However, photoreceptor ribbon synapses, like those of most other neurons, appear to employ SNARE proteins during vesicle fusion: synaptobrevin (VAMP1 and 2), SNAP-25, and syntaxin (Ullrich & Südhof, 1994; Brandstätter et al., 1996a, b; Greenlee et al., 1996, 2001; von Kriegstein et al., 1999; Bergmann et al., 2000; Morgans, 2000; Sherry et al., 2001, 2006; Heidelberger et al., 2003). The v-SNARE, synaptobrevin, is located exclusively on synaptic vesicles. Immunoelectron micrographs suggest that the t-SNARE, SNAP-25, may be present not only on the plasma membrane but also on vesicles along the ribbon (Brändstatter et al., 1996b; Morgans et al., 1996; Morgans & Brändstatter, 2000). It is possible that vesicular SNAP-25 may promote vesicle priming or compound fusion prior to synaptic release. Ribbon synapses also possess Munc18 proteins, which assist in assembling the SNARE complex and priming vesicles (Ullrich & Südhof, 1994). One difference between photoreceptors and most other neurons is the reliance on syntaxin 3 rather than the syntaxin 1 isoform used at many synapses (Morgans et al., 1996; Curtis et al., 2008). Additionally, retinal ribbon synapses use complexins 3 and 4 rather than complexins 1 and 2 used at most other terminals (Reim et al., 2005; Zanazzi & Matthews, 2010). In complexin 3/4 knockout mice, ~25% of the synaptic terminals exhibit free floating spherical ribbons perhaps as a result of altered synaptic activity (Reim et al., 2005).

The identity of the calcium sensor molecules that regulate exocytosis from photoreceptors is unclear. Experiments on non-mammalian rods and cones show that the sensor exhibits an unusually high affinity for Ca<sup>2+</sup> with a threshold of 400 nM and low cooperativity of approximately two Ca<sup>2+</sup> ions (Rieke & Schwartz, 1996; Thoreson et al., 2004; Sheng et al., 2007; Duncan et al., 2010). This is quite different from release at synapses employing synaptotagmin 1, which show a cooperativity of five Ca<sup>2+</sup> ions and a requirement for much higher Ca<sup>2+</sup> levels (Heidelberger et al., 1994; Bollmann et al., 2000; Schneggenburger & Neher, 2000; Beutner et al., 2001). Kreft et al. (2003) found that salamander rod terminals could be labeled with an antibody to synaptotagmin 1, but other synaptotagmin 1 antibodies do not label terminals of photoreceptors in salamander or goldfish (Berntson & Morgans, 2003; Heidelberger et al., 2003; Fox & Sanes, 2007). By contrast with these results in lower vertebrates, antibodies to synaptotagmin 1 consistently label photoreceptor ribbon synapses in the OPL of mammalian and chick retina (Greenlee et al., 1996; Bergmann et al., 2000; Berntson & Morgans, 2003; Heidelberger et al., 2003; von Kriegstein & Schmitz, 2003; Lazzell et al., 2004; Fox & Sanes, 2007; Wahlin et al., 2008). Antibodies for synaptotagmin 2 do not label photoreceptor terminals in chick, mouse, salamander, or goldfish, although there is evidence for labeling of terminals in ray retina (Fox & Sanes, 2007). In hair cells, it

has been proposed that otoferlin or synaptotagmin 4 might be the calcium sensor (Roux et al., 2006; Johnson et al., 2010). Otoferlin is absent from photoreceptor ribbon synapses (Uthaiah & Hudspeth, 2010); the distribution of synaptotagmin 4 in the retina has not been examined.

#### Cytoskeletal components

Ribeye and ribbon-associated proteins interact extensively with the intracellular cytoskeleton. Much of the early work elucidating cytoskeletal networks in photoreceptors was performed using species whose rods and cones show photosensitive contractile motion (Burnside, 1986; Nagle et al., 1986) or regenerative properties that require cytoskeletal-dependent trafficking (Mandell et al., 1993; Vecino & Avila, 2001; Hasegawa et al., 2007). These studies focused more on changes in cellular morphology than on specific molecular interactions, but they offered insight into the subcellular organization of the cytoskeleton and generally agreed that there are moderate levels of actin within the synaptic terminals of both rod and cone photoreceptors (Nagle et al., 1986; Schmitz & Drenckhahn, 1993; Schmitz et al., 1993; Katsumata et al., 2009). Actin and microtubule networks in photoreceptors help to stabilize active zone components and to aid in cargo trafficking to and from the synapse (Schmitz & Drenckhahn, 1997; Zanazzi & Matthews, 2009).

Interactions between actin and various binding partners help to sculpt pre- and postsynaptic structure (Doussau & Augustine, 2000; Hotulainen & Hoogenraad, 2010). For example, actin interacts with dystrophin and closely related spectrin proteins, all of which are found in photoreceptor terminals (Lazarides et al., 1984; Isayama et al., 1991; Spencer et al., 1991; Schmitz et al., 1993; Ueda et al., 1995, 1998; Drenckhahn et al., 1996; Blank et al., 1997, 1999; Morgans, 2000; Jastrow et al., 2006; Uthaiah and Hudspeth, 2010). One of the more common binding partners for actin in most presynaptic terminals is synapsin, but synapsin is absent from photoreceptor terminals (Mandell et al., 1990; Koontz & Hendrickson, 1993). Its absence at ribbon synapses is thought to explain the high mobility of synaptic vesicles at ribbon synapses (Holt et al., 2004; Rea et al., 2004). The network of actin fibers can exhibit tremendous plasticity as shown in hair cells where the entire actin cytoskeleton turns over every 48 h (Schneider et al., 2002). The regulation of actin varies among different retinal cell types but often involves Ca2+-dependent and CaV-associated processes (Fukuda et al., 1981; Johnson & Byerly, 1993; Job & Lagnado, 1998; Schubert & Akopian, 2004, 2006; Oertner & Matus, 2005; Cristofanilli et al., 2007; Mizuno et al., 2010). At photoreceptor synapses, single particle tracking studies show that individual Ca<sub>V</sub> channels diffuse more freely after the disruption of actin with cytochalasin, raising the possibility that an actin network helps to maintain the spatial position of photoreceptor synaptic proteins (Mercer et al., 2011*a*).

In addition to actin, the other two primary cytoskeletal proteins, intermediate filaments and microtubules, are present in photoreceptors (Gray, 1976; Nagle et al., 1986). Intermediate filaments are present in the axon and perinuclear region, whereas microtubules are found throughout the cell (Nagle et al., 1986). At many synapses, microtubules play an important role in vesicle delivery (Elluru et al., 1995; Lin-Jones et al., 2003; Gonzalez-Bellido et al., 2009) and, consistent with such a possibility, they can sometimes be observed close to the ribbon and ribbon-associated vesicles (Gray, 1976; Nagle et al., 1986; Zanazzi & Matthews, 2009).

Deficits in cytoskeletal and cytomatrix proteins can cause neurological defects including Usher syndrome (Williams, 2008), which is the most common form of deaf-blindness. Clinically, there are three subtypes of Usher syndrome, caused by at least 12 identified gene loci (Kremer et al., 2006; Maerker et al., 2008; Friedman et al., 2011; Richardson et al.,

2011). Seven USH1 loci have been identified to date and are responsible for the most severe form of deaf-blindness syndrome (Ahmed et al., 2003; Yan & Liu, 2010). These gene regions encode for various cytomatrix molecules including the scaffold proteins harmonin (USH1C) and "scaffold protein containing ankyrin repeats/SAM domain" (USH1G), the motor protein myosin VIIa (USH1B), and the cell-cell adhesion molecules cadherin 23 (USH1D) and protocadherin 15 (USH1F) (Reiners et al., 2003, 2005a, 2006; Adato et al., 2005; El-Amraoui & Petit, 2005). Three USH2 loci encode for the scaffold proteins usherin (USH2A) and whirlin (USH2D) as well as very large G-protein-coupled receptor 1b (USH2C) (Reiners et al., 2005b; Yang et al., 2010). The downstream product of the lone USH3 gene is the synaptic protein clarin-1 (Adato et al., 2002; Isosomppi et al., 2009). Many of the Usher proteins interact with one another, as well as with the actin cytoskeleton (Boëda et al., 2002; Inoue et al., 2006; Rzadzinska et al., 2004) and cell-cell adhesion molecules (Küssel-Andermann et al., 2000; Reiners et al., 2006). In hair cell stereocilia and the connecting cilium in photoreceptors, these protein networks appear to be important for intracellular protein trafficking and structural organization. In addition to being found in cilia, whirlin, myosin VIIa, harmonin, cadherin 23, protocadherin 15, and clarin-1 are also present in photoreceptor terminals where they likely help organize the structure of the ribbon synapse (El-Amraoui et al., 1996; Reiners et al., 2003, 2005*a*; Williams et al., 2009; Zallocchi et al., 2009).

#### Lipid rafts

Along with cytoskeletal interactions, the distribution of lipids within the plasma membrane is a major mechanism for segregating and compartmentalizing membrane proteins (Lenne et al., 2006). Using electron microscopy and a cholesterol-binding antibiotic, filipin, Cooper and McLaughlin (1984) found that photoreceptors display a high concentration of cholesterol in lipid rafts at margins of the ribbon-style active zone. Consistent with the presence of lipid rafts in photoreceptor terminals, Mercer et al. (2011a) found that labeling of lipid raft ganglioside GM1 glycoproteins with fluorescein isothiocyanate-conjugated toxin B stained the OPL. Cholesterol-containing lipid rafts were absent from nonribbon locations in presynaptic terminals and were not observed in the post-synaptic dendrites of horizontal and bipolar cells (Cooper & McLaughlin, 1984). P-/Q-type Ca<sub>V</sub> channels and  $a_2\delta$ Cav channel accessory subunits have been shown to localize preferentially to lipid rafts (Taverna et al., 2004; Davies et al., 2006), suggesting that membrane cholesterol may assist in clustering ion channels close to vesicle release machinery (Lang et al., 2001; Gil et al., 2004; Salaün et al., 2005; Taverna et al., 2007; Linetti et al., 2010). Consistent with such a possibility at photoreceptor synapses, depleting membrane cholesterol from photoreceptors expanded the synaptic confinement area for Ca<sub>V</sub> channels (Mercer et al., 2011a). These results also support the hypothesis that lipid rafts act as diffusion barriers to limit the lateral mobility of membrane proteins (Renner et al., 2009).

#### Summary of protein interactions within the photoreceptor ribbon synapse

Fig. 2 illustrates the coassembly of proteins at the photoreceptor ribbon synapse. Interactions among ribeye A domains form the backbone of the ribbon (Schmitz et al., 2000; Magupalli et al., 2008), whereas ribeye B domains on the outer face of the ribbon appear to link it to scaffold proteins at the base such as bassoon, piccolo, and Unc119 (Alpadi et al., 2008). Bassoon and piccolo also interact with CAST and the homologous protein ELKS (Takao-Rikitsu et al., 2004; Tokoro et al., 2007). The protein "hub" formed by CAST, bassoon, piccolo, RIM, and Munc13 proteins helps to cluster a number of proteins near the ribbon (Ohara-Imaizumi et al., 2005; Inoue et al., 2006; Wang et al., 2009; Hida & Ohtsuka, 2010). Contacts between SNARE proteins and Munc13 may help to localize SNARE complexes beneath the ribbon (Betz et al., 1997; Guan et al., 2008; Deng et al., 2011), while

interactions between RIM and Munc13 with Raba may link this ribbon complex directly to vesicles (Dulubova et al., 2005).  $Ca_V$  channels can associate with the ribbon by virtue of interactions with RIM proteins, CaBP4, and Unc119 (Hibino et al., 2002; Kiyonaka et al., 2007; Han et al., 2011; Kaeser et al., 2011). Many other proteins are found at photoreceptor ribbon synapses (Uthaiah and Hudspeth, 2010), and thus, interactions with other synaptic, scaffolding, and motor proteins (Muresan et al., 1999; tom Dieck et al., 2005; Katsumata et al., 2009) are also likely to help organize  $Ca_V$  channels, synaptic vesicles, and fusion machinery at the ribbon synapse.

#### The ECM

In addition to interactions with intracellular proteins and intra-membrane proteins, active zone-associated proteins can interact with the ECM in the synaptic cleft. A number of different synaptic cleft proteins are important for positioning presynaptic release sites across from postsynaptic receptors (Specht & Triller, 2008; Feng & Zhang, 2009; Lajoie et al., 2009). We review ECM proteins, both retina specific (e.g., pikachurin, retinoschisin, and nyctalopin) and otherwise, that have been shown to help organize photoreceptor synapses and their postsynaptic contacts in the OPL.

Alterations in the proteins dystrophin and dystroglycan cause muscular dystrophy and can produce visual deficits (Straub & Campbell, 1997; Waite et al., 2009). Both dystrophin and dystroglycan are expressed at the synapses of rod and cone photoreceptors (Schmitz et al., 1993; Ueda et al., 1995; Drenckhahn et al., 1996; Blank et al., 1997, 1999; Ueda et al., 1998; Morgans, 2000; Jastrow et al., 2006). Futhermore, mutations in dystrophin and dystroglycan can cause reductions in the ERG b-wave (Cibis et al., 1993; Fitzgerald et al., 1994; Pillers et al., 1999). A retina-specific form of dystrophin, Dp260, is localized to photoreceptor synapses (D'Souza et al., 1995), and reductions in this protein cause a selective loss of dystroglycan from the OPL (Kameya et al., 1997). Dystroglycan precursor proteins are cleaved into two subunits:  $\beta$ -dystroglycan and  $\alpha$ -dystroglycan.  $\alpha$ -dystroglycan is a heavily glycosylated extracellular protein that interacts with multiple ECM partners including  $\beta$ dystroglycan, pikachurin, fibulin, and laminin (Ibraghimov-Beskrovnaya et al., 1992; Talts et al., 1999; Sato et al., 2008). In addition to binding to a-dystroglycan outside the cell,  $\beta$ dystroglycan spans the plasma membrane and binds to dystrophin inside the cell. Dystrophin in turn interacts with the actin cytoskeleton. Disruption of  $\beta$ -dystroglycan causes changes in K<sup>+</sup> channel clustering in Müller cells but does not appear to alter dystrophin localization in the outer retina or cause changes in retinal lamination patterns (Satz et al., 2009). By contrast, as discussed below, impaired interactions between *a*-dystroglycan and pikachurin produce significant outer retinal defects.

The ECM protein pikachurin interacts with glycosylated *a*-dystroglycan at photoreceptor terminals (Sato et al., 2008; Kanagawa et al., 2010; Hu et al., 2011). The presence of pikachurin is critical for establishing contacts between rods and bipolar cells (Sato et al., 2008). Pikachurin knockout mice yield viable offspring but show morphological defects in OPL organization (Kanagawa et al., 2010) and blunted ERG responses (Sato et al., 2008). Hypoglycosylation of *a*-dystroglycan can impede dystroglycan–pikachurin interactions, causing defects in the OPL similar to those observed in pikachurin knockout mice (Kanagawa et al., 2011). Although a postsynaptic protein partner for pikachurin has not been identified, these data suggest that pikachurin provides an intermediary tether between the terminal of a photoreceptor and dendrite of a bipolar cell.

Laminin isoforms have been implicated in the functional organization of the OPL and photoreceptor outer segment layer (Libby et al., 1999; Biehlmaier et al., 2007). Laminin interacts with multiple ECM proteins including *a*-dystroglycan and retinoschisin

(Claudepierre et al., 2005; Steiner-Champliaud et al., 2006). Seven laminin subtypes have been described in the retina (Libby et al., 2000), and mutations of at least two laminin subtypes result in floating ribbons (Biehlmaier et al., 2007).

Retinoschisin is a secreted retina-specific OPL matrix protein, and mutations cause the retinopathy X-linked retinoschisis (Grayson et al., 2000; Tantri et al., 2004; Vijayasarathy et al., 2008). This protein is a large disulfide-linked ECM organizing protein, with a critical adhesion site called the discoidin domain. Defects in the discoidin domain of retinoschisin disrupt trafficking and secretion (Wu & Molday, 2003) and are thought to contribute to developmentally dependent changes in retina morphology and subsequent retinal dysfunction (Weber et al., 2002; Takada et al., 2004, 2008). The discoidin domain of retinoschisin can interact with a number of binding partners: anionic phospholipids (Vijayasarathy et al., 2007; Kotova et al., 2010), galactose (Dyka et al., 2008), Na<sup>+</sup>/K<sup>+</sup>-ATPase (Molday et al., 2007; Shi et al., 2009; Friedrich et al., 2011), photoreceptor Ca<sub>V</sub> channels (Shi et al., 2009), laminin, alpha crystallin, and the binding partner for peanut agglutinin (Steiner-Champliaud et al., 2006). Like pikachurin, a postsynaptic binding partner for retinoschisin has not been identified, but retinoschisin is nevertheless essential for proper development and function of the retina (Park et al., 2009; Sergeev et al., 2010).

The retina-specific ECM protein nyctalopin, derived from the NYX gene, has been implicated in a form of CSNB (Bech-Hansen et al., 2000; Pusch et al., 2000) and the mouse "no b-wave" (NYXnob) mutant (Gregg et al., 2003, 2007). Analysis of ERGs in CSNB patients and NYX<sup>nob</sup> mutant mice indicates a failure of transmission from photoreceptors to ON bipolar cells (Khan et al., 2005; Bahadori et al., 2006; Leroy et al., 2009). This is similar to effects of postsynaptic mutations in the glutamate receptor, mGluR6, or the transduction channel, TRPM1, at the ON bipolar synapse (McCall & Gregg, 2008; Shen et al., 2009; van Genderen et al., 2009; Koike et al., 2010; Morgans et al., 2010). Nyctalopin appears to target TRPM1 to the tips of ON bipolar cell dendrites, which may explain the similarity in ERG phenotypes when nyctalopin or TRPM1 are mutated (Cao et al., 2011; Pearring et al., 2011). Like mGluR6 and TRPM1 knockout animals, nyctalopin knockout animals show normal morphology in the OPL (Ball et al., 2003). This contrasts with mutations of presynaptic proteins (e.g., Ca<sub>V</sub> channels, bassoon, or ribeye) that lead to disorganization of the OPL, including the sprouting of ectopic synapses (McCall & Gregg, 2008). The relatively normal OPL structure of NYX mutants is consistent with the hypothesis that nyctalopin is more important for maintaining the dendritic organization of ON bipolar cells, whereas the disorganization of the OPL that accompanies mutations in pikachurin or retinoschisin suggests that these proteins are more important for presynaptic organization.

Crumbs (Crb), a transmembrane ECM protein, acts as a scaffold and is a critical element in the apical–basal development of photoreceptors (reviewed in Gosens et al., 2008). Three CRB proteins have been identified in humans and mice. Deletion or missense mutations of *Crumbs* genes can lead to Leber's congenital amaurosis and retinitis pigmentosa type 12 (den Hollander et al., 1999; Lotery et al., 2001; Meuleman et al., 2004; van den Hurk et al., 2005) indicating a pivotal role in the normal assembly and function of the retina. Gain-of-function mutations also suggest that proper expression of CRB during development is required to produce the normal laminar structure of the outer retina (Fan et al., 2003). The CRB protein assembly links photoreceptors to surrounding Müller glia at the outer limiting membrane, just beyond the outer nuclear layer (Mehalow et al., 2003; Van de Pavert et al., 2004). CRB1, CRB2, and CRB3 bind directly to protein 4.1 (EBP41)-L5 and MPP5 family to maintain neural–glial connectivity at adherens junctions in the outer limiting membrane (Knust & Bossinger, 2002; Meuleman et al., 2004; van de Pavert et al., 2004). At photoreceptor synapses, there is evidence for CRB2, CRB3, MPP4, MPP5, and Veli3 expression but not CRB1 expression (van de Pavert et al., 2004; Kantardzhieva et al., 2005,

2006; Stöhr et al., 2005; Aartsen et al., 2006). Among other functions, these proteins are thought to regulate the synaptic localization of PMCA proteins in rods (Yang et al., 2007).

Despite its name, PSD-95 is not limited to postsynaptic locations but can also be found presynaptically in terminals of photoreceptors (Koulen et al., 1998). PSD-95 contains PDZ domains that can interact with interact with a number of proteins (Nourry et al., 2003; Feng and Zhang, 2009). In photoreceptor terminals, PSD-95 has been shown to interact with Crumbs-related proteins (Aartsen et al., 2006), PMCA (Aartsen et al., 2009), and the putative calcium-activated chloride channel, TMEM16B (Stöhr et al., 2009). PMCA and calcium-activated chloride channels are not clustered tightly near the synaptic ribbon but distributed more diffusely throughout photoreceptor terminals (Morgans et al., 1998; Mercer et al., 2011*b*). PSD-95 may thus be more important for organizing proteins in surrounding parts of the synaptic terminal, whereas other proteins discussed earlier (e.g., RIM and Munc13) may be more important for organizing proteins near the ribbon.

Yamagata and Sanes (2010) showed evidence for a transsynaptic scaffold in photoreceptors involving MAGI proteins. Like PSD-95, MAGI proteins contain multiple PDZ domains (Nourry et al., 2003). MAGI proteins in the presynaptic terminals of photoreceptors appear to be linked across the synaptic cleft by extracellular Sidekick-2 proteins and cadherins to MAGI proteins in postsynaptic dendrites (Yamagata et al., 2002; Yamagata & Sanes, 2010). Sidekick-2 may be retina specific since homologous transsynaptic scaffold proteins have not yet been described at other synapses.

# Summary of protein interactions with the ECM at the photoreceptor ribbon synapse

Fig. 3 summarizes various extracellular protein–protein interactions across the OPL. As described above, PSD-95 in photoreceptor terminals can link to PMCA (Aartsen et al., 2009), TMEM16B calcium-activated chloride channels (Stöhr et al., 2009), and the Crumbs complex (Yang et al., 2007). Whereas RIM and Munc13 proteins appear to be particularly important for organizing active zone proteins close to the ribbon (Fig. 2), PSD-95 may be more important for organizing proteins in neighboring nonribbon regions of the terminal. By virtue of its interactions with laminin, Ca<sub>V</sub> channels, and Na<sup>+</sup>/K<sup>+</sup> ATPases, retinoschisin may be an important node for organizing ECM proteins (Molday et al., 2007; Shi et al., 2009; Friedrich et al., 2011). Laminin and pikachurin can also interact with the dystroglycan/dystrophin complex (Claudepierre et al., 2005; Kanagawa et al., 2010). Other links among ECM proteins remain to be discovered, such as binding partners for nyctalopin and Crumbs complex proteins.

#### Dynamic changes in ribbon proteins

The need to maintain efficient and reliable neuron-to-neuron communication would appear to dictate a relatively fixed arrangement of calcium channels, vesicle release sites, and postsynaptic receptors at many synapses, including photoreceptor synapses. The many interactions among cytoskeletal, intramembrane, ribbon-associated, and ECM proteins described above also suggest a static and heavily reinforced structure. However, despite these expectations, there is evidence for a surprising degree of structural plasticity at photoreceptor ribbon synapses, some of which operates on a very rapid time scale.

As mentioned above, mutations in a number of different presynaptic proteins can cause neurodegenerative changes that are accompanied by changes in ribbon structure. For example, mutations in  $Ca_V 1.4$ , bassoon, complexin, synaptojanin, and laminin can produce floating ribbons (Dick et al., 2003; Reim et al., 2005; tom Dieck et al., 2005; Chang et al.,

2006; Biehlmaier et al., 2007). Mutations in tubby-like protein 1 (TULP1), which underlies a form of autosomal recessive retinitis pigmentosa, also causes changes in the structure of photoreceptor ribbons (Grossman et al., 2009). TULP1 appears to play a role in intracellular membrane trafficking but its role in synaptic function is unclear. Additionally, mutations in cysteine string protein alpha, a chaperone protein that prevents SNAP-25 degradation and SNARE complex formation (Sharma et al., 2011), cause photoreceptor degeneration accompanied by floating ribbons and the appearance of electron-dense aggregates (Schmitz et al., 2006). In addition to changes in ribbon structure, mutations in presynaptic Ca<sub>V</sub> channel subunits ( $\alpha_{1F}$ ,  $\beta_2 \alpha$ ,  $\alpha_2 \delta_4$ ), and the calcium channel-associated protein CaBP4 can also promote the extension of dendritic processes from bipolar and horizontal cells into the outer nuclear layer and formation of ectopic synapses (Haeseleer et al., 2004; McCall & Gregg, 2008).

More surprising than the ability of mutations and neurodegenerative changes to induce longterm structural changes, ribbons in rods and cones can alter their structure reversibly on a diurnal basis (Abe & Yamamoto, 1984; Vollrath & Spiwoks-Becker, 1996; Adly et al., 1999; Balkema et al., 2001; Spiwoks-Becker et al., 2004). At night, rod ribbons form platelike structures, but in daytime, ribbons become much shorter and are associated with adjacent electron-dense spherical bodies. In the transition between these two forms during crepuscular conditions, the ribbons often assume a club-like appearance (Abe & Yamamoto, 1984; Vollrath & Spiwoks-Becker, 1996; Adly et al., 1999). It has recently been reported that these differences are much more pronounced in C57Bl/6J mice than Balb/cJ mice (Fuchs et al., 2011). Diurnal changes in ribbon shape appear to be driven by light, not circadian rhythms (Spiwoks-Becker et al., 2004). Diurnal structural changes have also been observed in ribbons from pineal photoreceptors (Kurumado & Mori, 1977; Kikuchi et al., 2000) and retinal bipolar cells (Hull et al., 2006). The finding that heterotypic interactions between A and B domains of ribeye are inhibited by NAD(H) has led to the proposal that metabolically driven changes in NAD(H) levels might regulate diurnal changes in ribbon structure (Magupalli et al., 2008).

Ribbons are also capable of dynamic movements on very short time scales. Bipolar cell ribbons labeled with fluorescently conjugated ribeye-binding peptide can exhibit both small (Zenisek et al., 2004; Mercer et al., 2011*a*) and occasional large rapid excursions through the cell (Zenisek et al., 2004).

Diurnal changes in postsynaptic processes have been described. However, these appear to occur only in fish retina where exposure to light stimulates the tips of horizontal cell dendrites (known as spinules) to extend into the cone pedicle and darkness causes them to retract (reviewed by Wagner & Djamgoz, 1993).

The possibility of rapid changes in the arrangement of pre-synaptic proteins has been investigated by visualizing the movements of individual Ca<sub>V</sub> channels labeled with brightly fluorescent quantum dots (Mercer et al., 2011*a*). Streptavidin-coated quantum dots, bound through a biotinylated secondary antibody, were attached to the extracellular domain of the  $a_2\delta_4$  accessory subunit of L-type Ca<sub>V</sub> channels in photoreceptors. Even though Ca<sub>V</sub> channels interact with multiple proteins, single particle tracking experiments show that individual Ca<sub>V</sub> channels are continuously in motion within the plasma membrane of photoreceptors (Mercer et al., 2011*a*). Movements of Ca<sub>V</sub> channels are confined to a small region near the ribbon that roughly matches the size of the active zone, consistent with evidence that Ca<sub>V</sub> channels cluster beneath the ribbon in photoreceptors and hair cells (Raviola & Gilula, 1975; tom Dieck et al., 2005; Frank et al., 2010). Some of the Ca<sub>V</sub> channel movement may reflect movement of the overlying ribbon but ribbon movements are much smaller than Ca<sub>V</sub> channel movements (Mercer et al., 2011*a*).

Depolarization-evoked fusion of vesicles at the base of the ribbon can abruptly increase  $Ca_V$  channel movements, propelling them away from the center of the confinement domain (Mercer et al., 2011*a*). The lipid constituents of vesicle membranes do not appear to differ from plasma membrane lipids (Takamori et al., 2006), suggesting that this increased channel movement is probably not due to changes in local lipid composition but more likely due to a brief expansion of the active zone membrane. Channels rebound towards the center of the confinement domain soon after the termination of exocytosis with a time course similar to that of endocytotic membrane retrieval. Thus, changes in the rate of vesicle fusion may cause the synaptic membrane to inflate and deflate like a balloon. These results are consistent with the suggestion that the fusion of synaptic vesicles may disorganize the arrangement of nearby exocytotic proteins and thereby contribute to postsynaptic depression (Neher & Sakaba, 2008; Hosoi et al., 2009; Kim & von Gersdorff, 2009). Disorganization of the synapse by altered membrane fusion and retrieval may also explain the presence of malformed ribbons produced by mutations of proteins involved in exocytosis and endocytosis.

Disruption of the actin cytoskeleton or depletion of cholesterol from cholesterol-rich lipid rafts at the base of the ribbon expand the size of the Ca<sub>V</sub> channel confinement domain, allowing channels to move further away from the ribbon (Mercer et al., 2011a). Ca<sup>2+</sup> channels are normally confined to a region within 50-100 nm of release sites (Mercer et al., 2011b). Increasing that distance would be expected to reduce the probability that an individual channel opening could induce vesicle fusion and thereby diminish the coupling efficiency between channel opening and vesicle fusion. Changes in postsynaptic receptor mobility can produce changes in synaptic strength (Heine et al., 2008; Petrini et al., 2009; Rust et al., 2010). For example, increasing the lateral mobility of AMPA receptors in the hippocampus promotes recovery from desensitization by speeding the return of undesensitized receptors to the synapse (Heine et al., 2008). Turnover of actin promoted by n-cofilin enhances AMPA receptor mobility and impairs both long-term potentiation and long-term depression (Rust et al., 2010). By analogy, we hypothesize that changes in  $Ca_V$ channel mobility caused by changes in endocytotic activity, actin, cholesterol-rich lipid rafts, or other partner proteins might also be a mechanism for regulating release presynaptically.

#### Conclusion

This review summarizes many of the different cytoskeletal, cytosolic, membrane, and ECM proteins that participate in assembling the synapse during development and maintaining the position of proteins in locations needed for efficient and reliable transmission. Photoreceptors share many intracellular and ECM proteins with other central nervous system synapses, but there are also a number of unique architectural elements (e.g., synaptic ribbon). A handful of proteins appear to form particularly important nodes for organizing proteins both in and around the active zone (e.g., RIM, Munc13, and PSD-95). Despite the many interactions among many different proteins, the synaptic terminals of photoreceptors are surprisingly dynamic. For example, ribbons can reversibly assemble and disassemble on a diurnal basis. On shorter time scales,  $Ca_V$  channels move continuously within the membrane and the ability of vesicle fusion to perturb these movements suggests that fusion can alter the arrangements of these and perhaps other presynaptic proteins.

In recent years, investigators have made great progress in identifying many of the key synaptic, cytoskeletal, and ECM proteins that regulate the anatomy and physiology of conventional and ribbon synapses. The more difficult task of understanding the complex functional and structural interrelationships linking these many proteins has only begun, and future studies are likely to reveal an even more complex and dynamic web of interactions.

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#### Fig. 1.

Colocalization of  $Ca^{2+}$  channels to ribbon release sites. A voltage-clamped rod from a salamander retinal slice preparation was loaded with Oregon Green BAPTA-6F (OGB-6F) (200  $\mu$ M) to visualize intracellular Ca<sup>2+</sup> changes and a rhodamine-conjugated ribeyebinding peptide (50  $\mu$ M; Zenisek et al., 2004) to visualize the ribbon. Both were introduced into the rod through a patch pipette. To activate L-type Ca<sup>2+</sup> channels, the voltage-clamped rod was depolarized from -70 to -10 mV for 100 ms. Panel (**A**) shows a single confocal section (55 ms exposure) illustrating OGB-6F fluorescence in the rod prior to the test step. Panel (**B**) shows OGB-6F fluorescence in the same confocal section during the depolarizing test step. The difference image (test step minus control) in panel (**C**) shows localized hot spots of Ca<sup>2+</sup> increase at the base of the synaptic terminal (arrows). Panel (**D**) shows

synaptic ribbons labeled with rhodamine-conjugated ribeye-binding peptide in the same rod. Note that locations of the ribbons match the sites of  $Ca^{2+}$  influx in the two terminals of the rod. OGB-6F was imaged with 488 nm excitation and 525 nm emission filters, and rhodamine was visualized using 568 nm excitation and 607 nm emission filters. Scale bar = 10  $\mu$ m.



#### Fig. 2.

Protein–protein interactions at the photoreceptor ribbon synapse. The synaptic ribbon anchors to bassoon and piccolo at the terminals of rods and cones. The vertical ribbon is complexed at the base through CAST to a hub including RIM2, Rab3a, and Munc13. This synaptic node may help to position primed vesicles close to  $Ca_V$  channels and the fusion machinery (e.g., syntaxin, SNAP-25).  $Ca_V$  channels also appear to interact with the actin cytoskeleton and, by virtue of interactions with CaBP4, RIM, and Unc119, may couple directly to the ribbon itself. Kif3a and a complex of ELKS and RIM1 appear to be located at more distant sites up the vertical face of the ribbon. In Figs. 2 and 3, solid lines show direct interactions have not yet been definitively established.



#### Fig. 3.

Structural organization and protein interactions across the OPL. There appear to be at least two major nodes of protein–protein interactions in the ECM within the OPL. The Sidekick-2 transsynaptic scaffold attaches MAGI proteins in apposed cells, with putative lateral presynaptic interactions to PSD-95. PSD-95 also appears to anchor the Cl(Ca) channel TMEM16B and PMCA extrusion pump at nonribbon sites in the terminal. The second hub of scaffolding interactions occurs between a transmembrane dystroglycan complex and the retina-specific ECM proteins pikachurin and retinoschisin. These complexes are linked through synaptic laminin and cytoplasmic actin, while also attaching to the extracellular face of transmembrane Ca<sub>V</sub> channels and the Na<sup>+</sup>/K<sup>+</sup>-ATPase.