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## Intracellular calcium channels: inositol-1,4,5-trisphosphate receptors

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### Abstract

The inositol-1,4,5-trisphosphate receptors (InsP<sub>3</sub>Rs) are the major intracellular Ca<sup>2+</sup>-release channels in cells. Activity of InsP<sub>3</sub>Rs is essential for elementary and global Ca<sup>2+</sup> events in the cell. There are three InsP<sub>3</sub>Rs isoforms that are present in mammalian cells. In this review we will focus primarily on InsP<sub>3</sub>R type 1. The InsP<sub>3</sub>R1 is a predominant isoform in neurons and it is most extensively studied isoform. Combination of biophysical and structural methods revealed key mechanisms of InsP<sub>3</sub>R function and modulation. Cell biological and biochemical studies lead to identification of a large number of InsP<sub>3</sub>R-binding proteins. InsP<sub>3</sub>Rs are involved in the regulation of numerous physiological processes, including learning and memory, proliferation, differentiation, development and cell death. Malfunction of InsP<sub>3</sub>R1 play a role in a number of neurodegenerative disorders and other disease states. InsP<sub>3</sub>Rs represent a potentially valuable drug target for treatment of these disorders and for modulating activity of neurons and other cells. Future studies will provide better understanding of physiological functions of InsP<sub>3</sub>Rs in health and disease.

### Keywords

Inositol 1,4,5-trisphosphate receptors; cell nucleus; Ca<sup>2+</sup> signalling; neurodegeneration

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## 1. Introduction

The inositol-1,4,5-trisphosphate receptors (InsP<sub>3</sub>Rs) are the major intracellular Ca<sup>2+</sup>-release channels in cells. The investigation of mechanisms of inositol-1,4,5-trisphosphate (InsP<sub>3</sub>)-induced Ca<sup>2+</sup>-release started in 1980s and InsP<sub>3</sub>R was first solubilized and purified from the rat cerebellum in 1988 by Snyder's group (Supattapone et al., 1988). Reconstitution of the purified receptor into lipid vesicles showed that InsP<sub>3</sub> and other inositol phosphates stimulate calcium flux (Ferris et al., 1989). Then cDNA of InsP<sub>3</sub>R was cloned (Furuichi et al., 1989; Mignery et al., 1990) that helps to initiate structure-function studies (Mignery and Sudhof, 1990; Miyawaki et al., 1991). Reconstitution of InsP<sub>3</sub>R into planar bilayer membranes revealed its single channel permeability, its modulation by Ca<sup>2+</sup> and by ATP (Bezprozvanny and Ehrlich, 1993, 1994; Bezprozvanny et al., 1991). Since these initial publications the functional properties of native and recombinant InsP<sub>3</sub>R have been extensively characterized by Ca<sup>2+</sup> flux measurements, planar lipid bilayer or nuclear envelope patch-clamp recordings (Bezprozvanny, 2005; Foskett et al., 2007; Mikoshiba, 2007; Wagner and Yule, 2012). Although some of these studies initially resulted in conflicting data, an agreement has been reached by the field regarding key InsP<sub>3</sub>R functional properties.

The variety of InsP<sub>3</sub>-activated Ca<sup>2+</sup> channels, including three mammalian InsP<sub>3</sub>R isoforms (InsP<sub>3</sub>R type 1 (InsP<sub>3</sub>R1), InsP<sub>3</sub>R type 2 (InsP<sub>3</sub>R2), InsP<sub>3</sub>R type 3 (InsP<sub>3</sub>R3), different slicing variants of IP<sub>3</sub>R1, *Drosophila melanogaster* InsP<sub>3</sub>R and *Caenorhabditis elegans* InsP<sub>3</sub>R have been discovered and characterised (reviewed in (Bezprozvanny, 2005; Foskett et al., 2007; Mikoshiba, 2007)). The three mammalian InsP<sub>3</sub>R isoforms are 60–70% identical in sequence (Furuichi et al., 1994) and share a common domain structure (Mignery and Sudhof, 1990; Miyawaki et al., 1991) that consists of an amino-terminal InsP<sub>3</sub>-binding domain, a carboxyl-terminal Ca<sup>2+</sup> channel domain, and a middle coupling domain containing most of the putative regulatory sites and is the most divergent (Fig. 1). InsP<sub>3</sub>R1 is predominant in the central nervous system, but most other tissues express at least two and often all three InsP<sub>3</sub>R isoforms at different ratios (Taylor et al., 1999).

The InsP<sub>3</sub>R are subjected to multiple levels of regulation (Bezprozvanny, 2005; Foskett et al., 2007; Mikoshiba, 2007; Wagner and Yule, 2012). InsP<sub>3</sub>Rs are the targets of a number of allosteric regulators, including protein kinases, adenine nucleotides, pH and divalent cations, all of which may play a part in InsP<sub>3</sub>-induced Ca<sup>2+</sup> signaling. Significant effect of phosphorylation on InsP<sub>3</sub>R is also well documented (Bezprozvanny, 2005; Foskett et al., 2007; Mikoshiba, 2007). Many protein binding with InsP<sub>3</sub>R have been described, and physiological relevance of these interactions is under intense investigation.

At this moment one can find thousands of papers from different research groups dedicated to various aspects of InsP<sub>3</sub>R structure, regulation or functional role, but there are still many questions remain to be answered. In this review we focus on InsP<sub>3</sub>R type 1, which are predominant isoform expressed in mammalian neurons. Here we will briefly review the structure and basic properties of these channels, their role in the cell functions and in several neurodegenerative disorders, such as Huntington's disease, spinocerebellar ataxias and Alzheimer's disease.

## 2. InsP<sub>3</sub>Rs in cell functions

A rise in intracellular calcium in neurons in response to InsP<sub>3</sub>Rs activation is implicated in the control of a numerous cellular functions, including neurotransmission and synaptic plasticity, proliferation, differentiation, development, gene expression, and cell death (Berridge et al., 1998). Evidence at both cellular and behavioral levels implicates InsP<sub>3</sub>Rs in memory formation, in particular they are required during long-term memory (Baker et al., 2013). It was demonstrated that InsP<sub>3</sub>R1 is extremely important in embryonic development. InsP<sub>3</sub>R1 knock-out mice have severe ataxia and tonic or tonic-clonic seizures and die by the weaning period (Matsumoto et al., 1996). Besides, InsP<sub>3</sub>R1 is a critical regulator of synaptic circuit maintenance in the mature cerebellum; this mechanism may underlie motor coordination and learning in adults (Sugawara et al., 2013). Thus, InsP<sub>3</sub>R1 are essential for proper brain development and function.

InsP<sub>3</sub>R1 are highly concentrated in the Purkinje cells of the cerebellum, with lower levels being found in other regions of the brain (Sharp et al., 1993a; Sharp et al., 1993b; Taylor et al., 1999) and in a variety of peripheral tissues (Taylor et al., 1999). Immunohistochemical studies in Purkinje cells, *Xenopus* oocytes and pancreatic epithelial cells have revealed that at a subcellular level InsP<sub>3</sub>Rs are localized in the rough and smooth endoplasmic reticulum (ER), Golgi complex and nuclear envelope, but not mitochondria or plasma membranes (Lam and Galione, 2013; Ross et al., 1989; Solovyova and Verkhratsky, 2003). Though, it has been indicated that the plasma membrane in some cell types may also contain InsP<sub>3</sub>R (Barrera et al., 2004; Dellis et al., 2006; Tanimura et al., 2000), but the role of such localization is rather contradictory.

InsP<sub>3</sub> is not the only regulator of InsP<sub>3</sub>Rs function; Ca<sup>2+</sup> plays a critical role in shaping the InsP<sub>3</sub>R-evoked Ca<sup>2+</sup> signals. Low Ca<sup>2+</sup> concentrations (<300 nM) activate the channel and increase its open probability, whereas high Ca<sup>2+</sup> concentrations inhibit channel opening (Bezprozvanny et al., 1991; Finch et al., 1991; Iino, 1990). These positive and negative feedback cycles are well suited for generating Ca<sup>2+</sup> oscillations or waves. It appears that InsP<sub>3</sub>Rs are activated by simultaneous binding of the two agonists, InsP<sub>3</sub> and Ca<sup>2+</sup>, to the cytoplasmic domain of the molecule that leads to the conformational change in the receptor complex and an increase in the frequency of its Ca<sup>2+</sup> channel opening, resulting in Ca<sup>2+</sup> release from the intracellular stores. Both InsP<sub>3</sub> and Ca<sup>2+</sup> are the two main intracellular messengers with their own regulatory pathways (Berridge, 2009, 2012; Decrock et al., 2013). So InsP<sub>3</sub>R acts as a skilled “analyst” which coordinates two complex streams of signals and forms an integrated response.

Because of complex Ca<sup>2+</sup>-mediated feedback on InsP<sub>3</sub>R activity, Ca<sup>2+</sup> signals evoked by the receptor activation are complex, restricted in space and time, and this spatiotemporal organization determines physiological effect of the signal (Berridge, 1997; Bootman et al., 2001; Konieczny et al., 2012). Intracellular InsP<sub>3</sub>-activated Ca<sup>2+</sup> signals are organized at three levels, each of them provides different signaling functions and serves as a building block for Ca<sup>2+</sup> signals at the next level (Berridge, 1996, 1997; Bootman et al., 2001). At the first, so called “fundamental”, level signals result from openings of a single InsP<sub>3</sub>R channel. At the resting conditions the cytosolic concentration of Ca<sup>2+</sup> is low and InsP<sub>3</sub>Rs are in a

conformation with low affinity for  $\text{InsP}_3$ , but the activating stimuli trigger the rise in the intracellular  $\text{Ca}^{2+}$  concentration and the production of  $\text{InsP}_3$  from the plasma membrane. These low concentrations of the two agonists activate one  $\text{InsP}_3\text{R}$  leading to a rapid localized  $\text{Ca}^{2+}$  flux called “blip” (Parker and Yao, 1996). At the next, “elementary”, level  $\text{Ca}^{2+}$  signals, so called “puffs”, arise from the concerted opening of multiple  $\text{InsP}_3\text{R}$  channels. It has been demonstrated that  $\text{InsP}_3\text{Rs}$  are initially randomly distributed in the membranes, but low concentrations of  $\text{InsP}_3$  cause them to aggregate rapidly and reversibly into clusters (Yao et al., 1995). There is no agreement about the number of  $\text{InsP}_3\text{Rs}$  in a cluster, it was proposed that from four (Rahman, 2012; Rahman and Taylor, 2009) to 25 or 35  $\text{InsP}_3\text{Rs}$  can open simultaneously during puffs (Shuai et al., 2006; Shuai and Jung, 2003; Solovey and Dawson, 2010). At resting cytosolic  $\text{Ca}^{2+}$  concentrations clustered  $\text{InsP}_3\text{Rs}$  open independently, but at increasing of  $\text{Ca}^{2+}$  they are more likely to open and close together (Dickinson et al., 2012; Taylor et al., 2009; Yamasaki-Mann et al., 2013).  $\text{Ca}^{2+}$  release from one channel acts as an activating ligand to stimulate nearby channels through  $\text{Ca}^{2+}$ -induced  $\text{Ca}^{2+}$  release (CICR). So, the spatial organization of  $\text{InsP}_3\text{R}$  channels within clusters and the distribution of clusters, together with the positive regulation by  $\text{InsP}_3$  and  $\text{Ca}^{2+}$ , enable local and long-range  $\text{Ca}^{2+}$  signals to be constructed from the activities of single  $\text{InsP}_3\text{R}$ . At intermediate  $\text{InsP}_3$  concentrations activate groups of  $\text{InsP}_3\text{Rs}$  which release  $\text{Ca}^{2+}$  to form puffs, but at high concentrations of  $\text{InsP}_3$  all the receptors are excitable and puffs then act as initiation sites to spawn a regenerative wave that spreads through the cell by CICR (Berridge, 2009). It is the third level of the intracellular  $\text{Ca}^{2+}$  hierarchy, which is associated with stronger extra-cellular agonist stimulation.  $\text{Ca}^{2+}$  released at one cluster can trigger  $\text{Ca}^{2+}$  release at adjacent clusters by CICR, leading to the generation of  $\text{Ca}^{2+}$  waves that propagate in a saltatory manner in the whole cell.

The nuclear envelope is the  $\text{Ca}^{2+}$  store with  $\text{InsP}_3\text{Rs}$  in its inner membrane (Fedorenko OA, 2008; Marchenko et al., 2005). It was indicated that the cell nucleus contains the whole set of enzymes required for the  $\text{InsR}_3$  synthesis from diphosphoinositolphosphate of the nuclear membrane, so the regulation of nuclear  $\text{InsP}_3\text{Rs}$  cannot depend on cytoplasmic processes (Gomes et al., 2006; Klein and Malviya, 2008; Rodrigues et al., 2009). Of course, in small cells  $\text{InsR}_3$  can freely penetrate into the nucleus by diffusion through the nuclear pores, but in large cells the distance from the plasma membrane to the nucleus is large enough so it is unlikely that  $\text{InsP}_3\text{Rs}$  in the nuclear membrane are activated by cytosolic  $\text{InsP}_3\text{R}$ . This point is proved by the fact that that numerous  $\text{InsP}_3$ -activated channels were recorded from the inner nuclear membrane of Purkinje and CA1 pyramidal neurons, which are the largest cells in the brain. No  $\text{InsP}_3\text{Rs}$  were found in the nuclear membrane of granule neurons of the cerebellum (Marchenko et al., 2005) and dentate gyrus (Fedorenko OA, 2007). Therefore the mechanism of regulation of nuclear  $\text{Ca}^{2+}$  may vary in different cells. There is a growing body of evidence that nuclear  $\text{Ca}^{2+}$  can affect gene transcription (Bading, 2000; Bengtson and Bading, 2012; Greer and Greenberg, 2008; Parekh and Muallem, 2011; Wiegert and Bading, 2011) through activation of nuclear  $\text{Ca}^{2+}$ -sensitive kinases and phosphatases, or through direct interaction with  $\text{Ca}^{2+}$ -dependent transcription factors, such as CREB and DREAM. However, many issues needed to be clarified, in particular the regulation of  $\text{Ca}^{2+}$  signals between the cytoplasm and the nucleus and the mechanisms of the intranuclear  $\text{Ca}^{2+}$  signaling.

### 3. Biophysical properties of InsP<sub>3</sub>R1

Biophysical properties of InsP<sub>3</sub>R1 have been studied following their isolation and reconstitution into artificial lipid planar bilayer membranes (Bezprozvanny and Ehrlich, 1993, 1994; Bezprozvanny et al., 1991; Tu et al., 2005b) and using patch-clamp recordings from nuclei isolated from a variety of cells, including mammalian neurons (Fedorenko OA, 2008; Mak and Foskett, 1997; Marchenko et al., 2005; Wagner and Yule, 2012).

The InsP<sub>3</sub>R channel is a Ca<sup>2+</sup>-selective channel, which is also permeable to other cations such as K<sup>+</sup> and Ba<sup>2+</sup> with permeability ratios  $P_{Ba}/P_K = 5-6$  and  $P_{Ca}/P_K = 4-5$  in symmetrical 140–150 mM K<sup>+</sup> solutions, with relatively little selectivity among different divalent cations (Bezprozvanny and Ehrlich, 1994; Boehning et al., 2001; Marchenko et al., 2005). The InsP<sub>3</sub>R are channels with a large single-channel monovalent ion conductance. InsP<sub>3</sub>Rs recorded in the inner nuclear membrane of rat cerebellar Purkinje cell have a slope conductance of 355 pS (Marchenko et al., 2005) in symmetric solutions with 150 mM K<sup>+</sup> and the absence of Mg<sup>2+</sup>. Similar conductance in the same conditions was recorded for expressed recombinant rat InsP<sub>3</sub>R1 present in COS-7 cell nuclei (Boehning et al., 2001). Single-channel conductance of InsP<sub>3</sub>Rs with Ba<sup>2+</sup> as the current carrier is 121 pS based on nuclear patch measurements (Marchenko et al., 2005). Conductance and selectivity of InsP<sub>3</sub>Rs from the nuclear membranes are similar to cerebellar InsP<sub>3</sub>Rs and recombinant InsP<sub>3</sub>R1 incorporated into artificial lipid bilayers (Bezprozvanny and Ehrlich, 1994; Tu et al., 2005b)

At a membrane potential 60 mV in symmetrical 150 mM KCl solution open probability ( $P_o$ ) for InsP<sub>3</sub>R recorded from the nuclear membranes of Purkinje neurons is about 0.036; with Ba<sup>2+</sup> as a current carrier under the same conditions  $P_o$  increases to 0.32 (Marchenko et al., 2005). The presence of Ca<sup>2+</sup> in solutions in concentrations 10 mM strongly decreased the  $P_o$  to 0.0023 and that apparently results from the inhibitory effect of high Ca<sup>2+</sup> concentrations in the vicinity of the receptor produced by Ca<sup>2+</sup> current through the channel rather than an effect of the presence of Ca<sup>2+</sup> at the luminal surface of the membrane, because the  $P_o$  of single inward K<sup>+</sup> currents remained practically unchanged (Bezprozvanny and Ehrlich, 1994).

InsP<sub>3</sub>Rs in the inner nuclear membrane of CA1 pyramidal neurons are activated by IP<sub>3</sub> in concentrations 50 nM and saturated ( $P_o$  95% of  $P_o$  at 10 μM IP<sub>3</sub>) in concentrations of 2 μM in the presence of 250 nM free Ca<sup>2+</sup> (Fig. 2A, 2B) (Marchenko et al., 2005). InsP<sub>3</sub>, and other ligands such as ATP, regulate channel activity mainly by modifying the sensitivity of the channels to Ca<sup>2+</sup> regulation, though in the absence of InsP<sub>3</sub>, Ca<sup>2+</sup> alone (20 nM–50 μM) is unable to activate the channels. The regulation of the receptors by Ca<sup>2+</sup> evokes much controversy (Mak et al., 1998). It has been reported that at steady-state conditions and saturating concentration of InsP<sub>3</sub> cerebellar InsP<sub>3</sub>Rs incorporated into artificial lipid bilayers were activated by Ca<sup>2+</sup> at low concentrations and inhibited by higher Ca<sup>2+</sup> concentration with the peak of activation ranged from 200 to 400 nM (Bezprozvanny et al., 1991). In nuclear patch-clamp recordings Ca<sup>2+</sup> inhibited InsP<sub>3</sub>Rs with the same efficiency both at low (0.3 μM) and saturated (10 μM) InsP<sub>3</sub> concentrations (Fig. 2C, 2D). Therefore the inhibitory effect of Ca<sup>2+</sup> on InsP<sub>3</sub>Rs does not depend on the InsP<sub>3</sub> concentration (Marchenko et al.,

2005). Experiments with flash photolysis of caged  $\text{InsP}_3$  in Purkinje neurons support these data. It has been shown that  $\text{Ca}^{2+}$  entry through plasmalemmal  $\text{Ca}^{2+}$  channels strongly suppressed  $\text{Ca}^{2+}$  release from stores induced by high (25  $\mu\text{M}$ )  $\text{InsP}_3$  concentrations (Khodakhah and Ogden, 1995). Recombinant  $\text{InsP}_3\text{R}1$  expressed in insect cells also demonstrated a bell-shaped  $\text{Ca}^{2+}$  dependence at saturated  $\text{InsP}_3$  concentrations (Tu et al., 2005a). Thus, most recent results support “narrow”  $\text{Ca}^{2+}$  dependence of  $\text{InsP}_3\text{R}1$  within physiological range of  $\text{Ca}^{2+}$  concentrations. Besides being activated by  $\text{InsP}_3$  and suitable concentrations of  $\text{Ca}^{2+}$ ,  $\text{InsP}_3\text{R}$  channel activity is also allosterically potentiated by ATP, (Bezprozvanny and Ehrlich, 1993; Mak et al., 1999; Wagner and Yule, 2012). It has been reported that other nucleotides, such ADP (Iino, 1991), AMP (Ferris et al., 1990), and GTP (Bezprozvanny and Ehrlich, 1993; Mak et al., 1999) can also potentiate  $\text{InsP}_3\text{R}1$  channel activity.

$\text{InsP}_3\text{Rs}$  have several phosphorylation sites (Bezprozvanny, 2005).  $\text{InsP}_3\text{Rs}$  are regulated by numerous kinases, including cAMP-dependent protein kinase (PKA) (DeSouza et al., 2002; Tang et al., 2003b; Vanderheyden et al., 2009; Wagner et al., 2004; Wagner et al., 2003), protein kinase C (Ferris et al., 1991), cGMP-dependent protein kinase (Haug et al., 1999; Komalavilas and Lincoln, 1994) and others. It has been reported, for example, that phosphorylation by PKA of recombinant type 1  $\text{InsP}_3\text{Rs}$  expressed in insect cells increased the  $P_o$  of the channels incorporated into artificial lipid bilayers more than 10-fold (from <2–3% to 30–40%) and increased their sensitivity to  $\text{InsP}_3$  about 4-fold (Tang et al., 2003b).

There are about 40 proteins or even more that can bind  $\text{InsP}_3\text{R}$  (Fig. 1), among them as calmodulin (Kasri et al., 2004a; Michikawa et al., 1999; Yamada et al., 1995), RACK1 (Woodard et al., 2010), protein 4.1N (Maximov et al., 2003), IRBIT (Mikoshiha, 2012), Bcl-2 (Chen et al., 2004), AKAP9 (Tu et al., 2004) and many others. Therefore,  $\text{InsP}_3\text{Rs}$  in cells act as a critical “signaling hub” that mediate cross-talk between  $\text{Ca}^{2+}$  signaling, kinases, phosphatases and protein-protein interaction mechanisms. Not surprisingly, abnormality in modulation or activity of  $\text{InsP}_3\text{R}1$  is connected with variety of neurological disorders (see below).

#### 4. Structural studies of $\text{InsP}_3\text{Rs}$

In the past decade, significant advancements have been made in determining atomic-resolution structures of  $\text{InsP}_3\text{Rs}$ . We now have a good understanding of the molecular mechanism underlying receptor recognition of the  $\text{InsP}_3$  molecule and how this binding is transformed into a protein conformational change at the  $\text{NH}_2$ -terminus, essential for the initial step of channel activation. The first high-resolution structure determined by X-ray crystallography was the  $\text{NH}_2$ -terminal  $\text{InsP}_3$ -binding core (IBC) of  $\text{InsP}_3\text{R}1$  (residues 224–604) in complex with  $\text{InsP}_3$  (Bosanac et al., 2002). The structure of the IBC contains two structurally distinct domains: the  $\beta$ -domain (IBC- $\beta$ ) and  $\alpha$ -domain (IBC- $\alpha$ ). The IBC- $\beta$  (residues 224 – 436) adopts a  $\beta$ -trefoil fold comprising 12  $\beta$ -strands and two single turn helices, whereas the IBC- $\alpha$  (residues 437– 604) adopts an armadillo repeat fold consisting of 8  $\alpha$ -helices (Fig. 3A). The IBC forms an L-shaped structure with the two domains oriented approximately perpendicular to each other; several basic amino acids cluster in a cleft formed by both domains, comprising the  $\text{InsP}_3$  binding site (Bosanac et al., 2002). The

crystal structures of the NH<sub>2</sub>-terminal suppressor domain (SD) have been determined for InsP<sub>3</sub>R1 (residues 1–223) (Bosanac et al., 2005) and InsP<sub>3</sub>R3 (residues 1–224) (Chan et al., 2010); moreover, the two structures are nearly identical showing a backbone root mean square deviation (rmsd) of ~1.3 Å (Fig. 3B). The SD folds into a hammer-like structure with a 12 β-stranded “head” domain and a helix-turn-helix “arm” domain. Furthermore, the head domain of the SD adopts a similar β-trefoil fold as found in the IBC. The InsP<sub>3</sub> binding affinity of the entire NH<sub>2</sub>-terminal region (NT; residues 1–604 of InsP<sub>3</sub>R1) is reduced by more than one order of magnitude compared with that of the IBC alone, implying that the SD inhibits or “suppresses” InsP<sub>3</sub> binding (Yoshikawa et al., 1996). Evidence suggests that not only is the SD required for suppression of InsP<sub>3</sub> binding, but it is also needed for InsP<sub>3</sub>-induced allosteric channel gating. For example, InsP<sub>3</sub>R1 lacking the SD shows no measurable InsP<sub>3</sub>-evoked Ca<sup>2+</sup> release (Uchida et al., 2003), and remarkably, a single Tyr167Ala mutation in the SD completely abolishes InsP<sub>3</sub>-evoked Ca<sup>2+</sup> release (Yamazaki et al., 2010).

Recently, four atomic-resolution NT structures of InsP<sub>3</sub>R1 have been determined. Lin et al., solved two NT structures of rat InsP<sub>3</sub>R1 at 3.8 Å resolution; moreover, they derived one structure in an InsP<sub>3</sub>-free state (*i.e.*, apo) and a second structure in an InsP<sub>3</sub>-bound state (*i.e.*, holo) from a single crystal grown in the presence of InsP<sub>3</sub> (Lin et al., 2011). Subsequently, apo and holo NT structures of rat InsP<sub>3</sub>R1 at higher resolution were separately determined from crystals grown in the absence (3.0 Å) and presence (3.6 Å) of InsP<sub>3</sub>, respectively (Seo et al., 2012) (Fig. 3C). The individual structures of the three domains comprising NT of InsP<sub>3</sub>R1 (*i.e.*, SD, IBC-β, and IBC-α) are highly similar to the separately determined SD (Bosanac et al., 2005) and IBC (Bosanac et al., 2002). Nonetheless, these NT structures represent a significant advancement in the understanding of InsP<sub>3</sub>R function by revealing the arrangement of the SD and IBC domains with respect to one another and providing important clues on the bases for tetrameric channel formation. The three domains in NT form a triangular architecture, and the SD is located on the opposite face of the InsP<sub>3</sub>-binding site, suggesting that the SD suppresses InsP<sub>3</sub> binding by an allosteric mechanism. The SD interacts with both the IBC-β and IBC-α, forming two interfaces (*i.e.*, β-interface and α-interface, respectively) (Fig. 3D). The functional importance of residues associated with the α-interface is demonstrated by the Val33Lys mutation, which almost completely abrogates the effects of the SD on InsP<sub>3</sub> binding and attenuates the maximal open probability of the full-length channel (Bosanac et al., 2005; Rossi et al., 2009). The most marked conformational change caused by InsP<sub>3</sub> binding is the significant decrease in the domain orientation angle between IBC-β and IBC-α (Fig.3C). This ligand binding-induced structural change in IBC occurs with the hinge region between IBC-β and IBC-α set as the pivot point, resulting in a narrowing of the InsP<sub>3</sub>-binding cleft and a clam-like closure. Consequently, the SD rotates (~9°) towards the IBC, accompanied by a swing that is approximately perpendicular to the IBC ‘clam closure’ (Fig. 3C).

Recently, Ludtke et al. determined the cryo-EM structure of InsP<sub>3</sub>R isolated from the rat cerebellum at 9.5 Å resolution (Ludtke et al., 2011; Murray et al., 2013), dramatically improving our view of the tetrameric full-length InsP<sub>3</sub>R channel compared to earlier studies (da Fonseca et al., 2003; Hamada et al., 2002; Jiang et al., 2002; Sato et al., 2004; Serysheva

et al., 2003). The tetrameric structure of InsP<sub>3</sub>R1 revealed a mushroom-shaped overall architecture with a fourfold symmetry axis along a central plug (Fig. 3D). The cytoplasmic region is located apical to the transmembrane domain with several large openings or “windows” between the two regions (Fig. 3E) and consists of a relatively rigid exterior surface with a more structurally variable and probably flexible interior (*i.e.* exhibiting higher statistical variability in the calculated density map), possibly due to multiple conformations of InsP<sub>3</sub>R1 in the closed state. Docking the high resolution crystal structures of InsP<sub>3</sub>R1-NT into this full-length cryo-EM structure shows that InsP<sub>3</sub>R1-NT forms a tetrameric ring around the fourfold symmetry axis, with the hot spot loop (HS-loop; so-called due to the high structural homology with a loop where a cluster of disease-associated mutations in ryanodine receptor domain A have been mapped) of InsP<sub>3</sub>R1 (residues 165–180) involved in intersubunit interactions (Fig. 3E). Importantly, Li et al. produced covalently linked tetrameric InsP<sub>3</sub>R1-NT through site-specific cysteine insertions in the intersubunit interface that was modeled in the docking studies and demonstrated that InsP<sub>3</sub> inhibits cross-linked tetrameric InsP<sub>3</sub>R1-NT in a concentration-dependent manner, suggesting that InsP<sub>3</sub> binding closes the clam-like IBC, disrupting these intersubunit interactions and allowing the channel to open (Fig. 4C) (Li et al., 2013). Taken together, these observations indicate that the InsP<sub>3</sub>R1-NT plays a critical role in the allosteric modulation of ion channel conductance through a modification of quaternary arrangement.

Very recently, the structure of InsP<sub>3</sub>R1-NT in complex with calcium binding protein 1 (CaBP1) was determined using nuclear magnetic resonance (NMR) spectroscopy-based chemical shift perturbation mapping and paramagnetic relaxation enhancement (PRE) data (Fig. 4A) (Li et al., 2013). The structure showed that exposed hydrophobic residues in Ca<sup>2+</sup>-bound CaBP1 (*i.e.* Val101, Leu104, and Val162) interact with clustered hydrophobic residues (*i.e.* Leu302, Ile364, and Leu393) in the IBC-β domain of InsP<sub>3</sub>R1 (Fig. 4A). Superimposing the structure of the InsP<sub>3</sub>R1-NT/CaBP1 complex with the tetrameric InsP<sub>3</sub>R1-NT shown in Fig. 4B revealed that the four molecules of CaBP1 form a ring-like structure around the central cytosolic vestibule. Further, chemical cross-linking experiments showed that CaBP1 enhances the production of cross-linked tetrameric InsP<sub>3</sub>R1-NT (Li et al., 2013). In aggregate with data demonstrating that Ca<sup>2+</sup>-CaBP1 inhibits InsP<sub>3</sub>-evoked Ca<sup>2+</sup> release (Haynes et al., 2004; Kasri et al., 2004b; Li et al., 2013) a novel regulatory molecular mechanism has been proposed where CaBP1 clamps the intersubunit interactions and thereby inhibits channel opening (Fig. 4C) (Li et al., 2013).

## 5. The role of InsP<sub>3</sub>Rs in neurodegenerative diseases

The role of InsP<sub>3</sub>R1 has been shown for several neurodegenerative diseases such as Huntington’s disease, spinocerebellar ataxias (SCAs) and Alzheimer disease (AD) (Bezprozvanny, 2009, 2011; Bezprozvanny and Mattson, 2008; Kasumu and Bezprozvanny, 2012).

HD is an autosomal-dominant neurodegenerative disorder and it is caused by polyglutamine (polyQ) expansion in the amino-terminal region of a protein huntingtin (Htt). Huntington disease (HD) is an autosomal-dominant neurodegenerative disorder with the age of onset between 35 and 50 years and inexorable progression to death 15–20 years after onset. The

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symptoms include motor abnormalities including chorea and psychiatric disturbance with gradual dementia (Vonsattel and DiFiglia, 1998). Neuropathological analysis reveals selective and progressive neuronal loss in the striatum (caudate nucleus, putamen and globus pallidus) (Vonsattel and DiFiglia, 1998; Vonsattel et al., 1985). GABAergic medium spiny striatal neurons (MSN) are the most sensitive to neuronal degeneration in HD (Vonsattel and DiFiglia, 1998; Vonsattel et al., 1985). It is widely accepted that mutant Htt (mHtt) protein acquires a “toxic gain of function” (Tobin and Signer, 2000). A number of potential “toxic functions” of mutant Htt have been suggested. Our laboratory is focused on connection between mutant Htt and deregulated neuronal  $Ca^{2+}$  signaling. We first discovered that mHtt binds directly and specifically to the C-terminal region of the type 1  $IP_3$  receptor ( $IP_3R1$ ) (Tang et al., 2003a). Recently, unbiased high-throughput screening assays confirmed mHtt binding to  $IP_3R1$  (Kaltenbach et al., 2007). Interestingly the affinity of mHtt to  $IP_3R1$  increases when mHtt is associated with HAP1A (Tang et al., 2003a). Moreover, mHtt, but not normal Htt, augmented  $IP_3R1$  activity in planar lipid bilayers (Tang et al., 2003a). Similarly, application of subthreshold concentrations of DHPG, an mGluR1/5 agonist, sensitized  $Ca^{2+}$  release in YAC128 primary MSN cultures (Tang et al., 2003a). This is consistent with the fact that glutamate-induced apoptosis of MSNs from YAC128 mice is mediated by mGluR1/5 and NR2B receptors (Tang et al., 2005). In fact, specific blockade of  $IP_3R1$  with 2-APB and Enoxaparin is neuroprotective in the same model (Tang et al., 2005). In more recent experiments, we demonstrated that viral delivery of a peptide that disrupts mHtt association with  $IP_3R1$  protected YAC128 MSNs *in vitro* and *in vivo* (Tang et al., 2009). We also reported that  $Ca^{2+}$  stabilizing agent dantrolene exerts beneficial effects in mouse model of HD (Chen et al., 2011). We also demonstrated that continuous overactivation of  $InsP_3R1$  pathway causes compensatory upregulation of neuronal store-operated  $Ca^{2+}$  entry in HD neurons, which contributes to  $Ca^{2+}$  overload and pathology (Wu et al., 2011). The alterations in ER enzymes that have been observed in HD postmortem brains (Kerner et al., 1997; Mao and Wang, 2001, 2002; Tallaksen-Greene et al., 1998; Testa et al., 1995) are consistent with malfunction of ER  $Ca^{2+}$  handling in HD MSN neurons. In recent studies it was discovered that  $InsP_3R1$  association of ER stress chaperone protein GRP78 is impaired in HD R6/2 model mice, resulting in misregulation of  $InsP_3R1$  gating (Higo et al., 2010). These results provide additional support for the role of  $InsP_3R1$  in HD pathology.

Many SCAs are caused by polyQ-expansion in ataxin proteins and typically affect cerebellar Purkinje cells. SCAs are generally characterized by cerebellar atrophy and a progressive incoordination of movement known as ataxia (Filla et al., 1999; Lastres-Becker et al., 2008; Schols et al., 2004). Although there is a phenotypic overlap with cerebellar atrophy and ataxia in all SCA patients, other brain regions may be affected in different type of disease. The pathogenesis of SCAs is not fully understood, however, several different pathogenic mechanisms have been studied in SCAs such as dysregulation of transcription and gene expression, alterations in calcium homeostasis and synaptic neurotransmission, mitochondrial stress and apoptosis (reviewed in (Bezprozvanny and Klockgether, 2010; Carlson et al., 2009; Kasumu and Bezprozvanny, 2012; Matilla-Duenas et al., 2009)).

Studies in our laboratory primarily focused on the role of InsP<sub>3</sub>Rs in pathogenesis of SCA type 2 (SCA2). The SCA2 is caused by an expansion and translation of unstable glutamine (Q) repeats in the gene encoding ataxin-2 from the normal 22 to more than 31 extra glutamine repeats (Imbert et al., 1996; Pulst et al., 1996; Sanpei et al., 1996). PolyQ-expanded ataxin-2 (ATXN2<sup>exp</sup>) protein, similar to wildtype ataxin-2 (ATXN<sup>wt</sup>), is widely expressed in the body tissues. Similar to wildtype ataxin-2, polyglutamine-expanded ataxin-2 protein is ubiquitously expressed in cells without severe aggregation and formation of inclusion bodies (Huynh et al., 2000). Cerebellar PCs in SCA2 patients are mostly affected with a loss of over 75% (Schols et al., 2004). The role of calcium signaling in the pathogenesis of SCA2 is supported by the genetic association between polymorphisms in the CACNA1A gene and the age of disease onset in patients diagnosed with SCA2 (Pulst et al., 2005). The role of aberrant neuronal calcium signaling in SCA2 pathogenesis was strengthened further by a finding in our lab that ATX2<sup>exp</sup> but not wildtype ATX2 (ATX2<sup>wt</sup>) specifically binds InsP<sub>3</sub>R1 (Liu et al., 2009). In a lipid bilayer reconstitution experiment, we found the presence of ATX2<sup>exp</sup> substantially sensitized IP<sub>3</sub>R 1 to activation by InsP<sub>3</sub> (Liu et al., 2009). Consistent with involvement of excitotoxic mechanism, we discovered that PC cells in SCA2 mouse undergo dark cell degeneration (DCD) mode of cell death (Kasumu and Bezprozvanny, 2012). Long-term feeding of SCA2-58Q mice with a calcium stabilizer dantrolene alleviated the age-dependent motor coordination deficits and PC cell loss in these mice (Liu et al., 2009). More recently we performed partial suppression of InsP<sub>3</sub>-induced Ca<sup>2+</sup> release in PC cells of SCA2-58Q mice by using inositol 5-phosphatase viral construct (Kasumu et al., 2012). We discovered that this approach prevented the onset of PC dysfunction, alleviated motor incoordination, and reduced age-dependent PC degeneration in SCA2-58Q mice (Kasumu et al., 2012). These results indicate that partial suppression of InsP<sub>3</sub>-induced Ca<sup>2+</sup> release is a viable therapeutic strategy for treatment of SCA2 and possibly other SCAs (Kasumu et al., 2012). Remarkably, insufficient InsP<sub>3</sub>R-mediated Ca<sup>2+</sup> signaling also leads to the ataxic phenotype and PC degeneration, such as observed in SCA15/16 patients haploinsufficient for the InsP<sub>3</sub>R1 gene (Hara et al., 2008; Iwaki et al., 2008; van de Leemput et al., 2007). An ataxic phenotype is also observed in *opt* mice with reduced levels of InsP<sub>3</sub>R1 protein (Street et al., 1997) and a severe ataxia is observed in InsP<sub>3</sub>R1 knockout mice (Matsumoto et al., 1996). These findings indicate that the reduced Ca<sup>2+</sup> release via InsP<sub>3</sub>R1 also leads to PC dysfunction and ataxic phenotype and that there is a relatively narrow range of optimal InsP<sub>3</sub>-mediated Ca<sup>2+</sup> signaling that is compatible with proper function and long-term survival of PCs. Deviation from this optimal range in either direction of InsP<sub>3</sub>-mediated Ca<sup>2+</sup> signaling results in PC dysfunction and an ataxic phenotype (Kasumu et al., 2012).

Alzheimer disease (AD) is another neurodegenerative disease in whose pathogenesis abnormal InsP<sub>3</sub>R signaling is likely to be involved. AD progresses slowly and affects neurons mainly in the cortex and hippocampus. The exact mechanism of AD pathogenesis is not known. One to two percent of AD cases constitute early onset familial Alzheimer disease cases. FAD is caused by mutations in genes coding presenilin 1 (PS1), presenilin 2 (PS2) or amyloid precursor proteins (APP). The first observation of exaggerated InsP<sub>3</sub>R-mediated Ca<sup>2+</sup> release from ER has been detected in fibroblasts from AD patients (Ito et al., 1994). Later similar results have been obtained in AD mouse models as well as in *Xenopus*

oocytes expressing human PS1 and PS2 mutant constructs (Bezprozvanny and Mattson, 2008; Stutzmann, 2007). The mechanism of abnormal InsP<sub>3</sub>R signaling in AD is not fully understood. Our laboratory discovered that presenilins function as ER Ca<sup>2+</sup> leak channels, and FAD mutations in presenilins result in elevated ER Ca<sup>2+</sup> levels (Nelson et al., 2007; Tu et al., 2006; Zhang et al., 2010). Increased ER Ca<sup>2+</sup> levels are in turn result in enhanced InsP<sub>3</sub>R1-mediated Ca<sup>2+</sup> release. The role of presenilins as ER Ca<sup>2+</sup> leak channels was recently confirmed in unbiased screen for modulators of calcium homeostasis (Bandara et al., 2013). An alternative hypothesis is that mutant presenilins enhance InsP<sub>3</sub>R1 gating via direct protein-protein interaction (Cheung et al., 2010; Cheung et al., 2008). Future studies will be need to understand the mechanism of InsP<sub>3</sub>R1 dysregulation in AD and its importance for pathology.

## 6. Conclusions

A remarkable progress has been made since original discovery of InsP<sub>3</sub>R family 25 years ago. Using electrophysiological and molecular methods we dissected major functional properties of all 3 mammalian InsP<sub>3</sub>R isoforms. Thanks to application of structural biology methods we start to understand function of InsP<sub>3</sub>R as a “molecular machine” in atomic details. Identification of a large number of InsP<sub>3</sub>R-binding partners highlighted a role of InsP<sub>3</sub>R as a key “signaling hub” in cells. We discovered that dysfunction of InsP<sub>3</sub>R is linked to a variety of neurodegenerative disorders, and demonstrated that InsP<sub>3</sub>R is a potential target for therapeutic interference in these and other disorders. There is no doubt that further research of InsP<sub>3</sub>R family in healthy and disease states will continue to provide additional valuable insights into basic biology and medicine.

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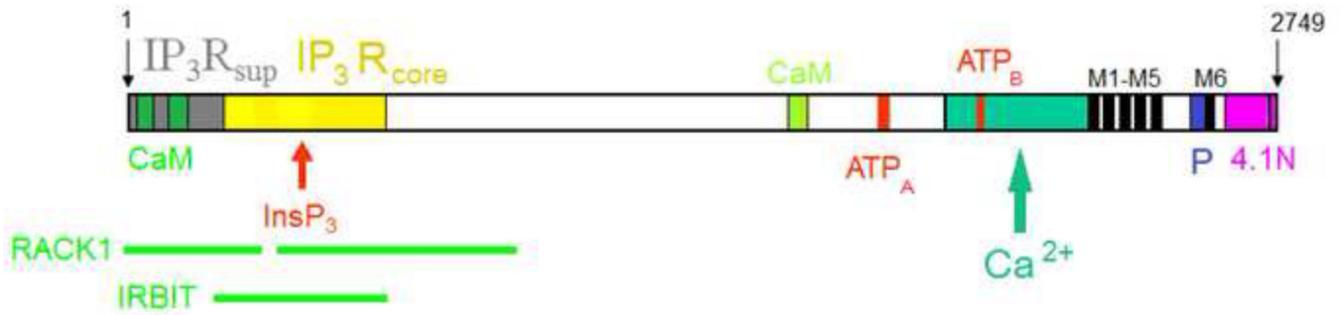
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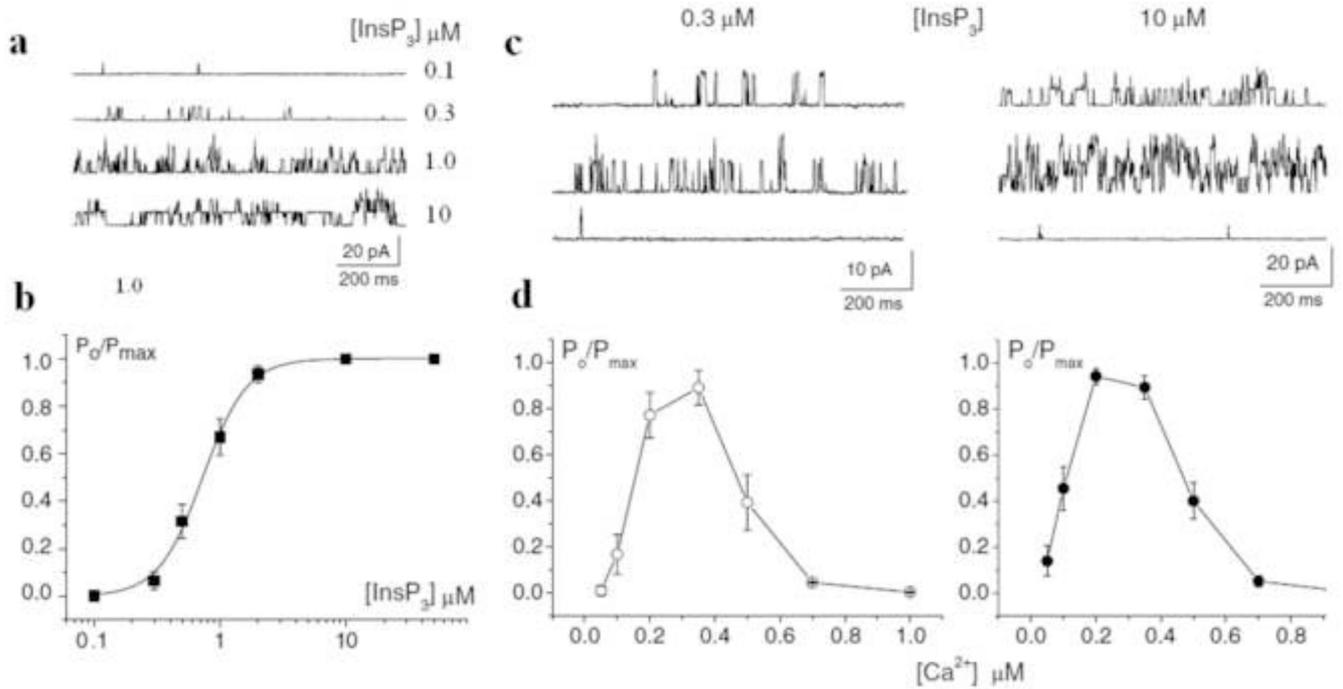
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**Figure 1. Domain structure of InsP<sub>3</sub>R1**

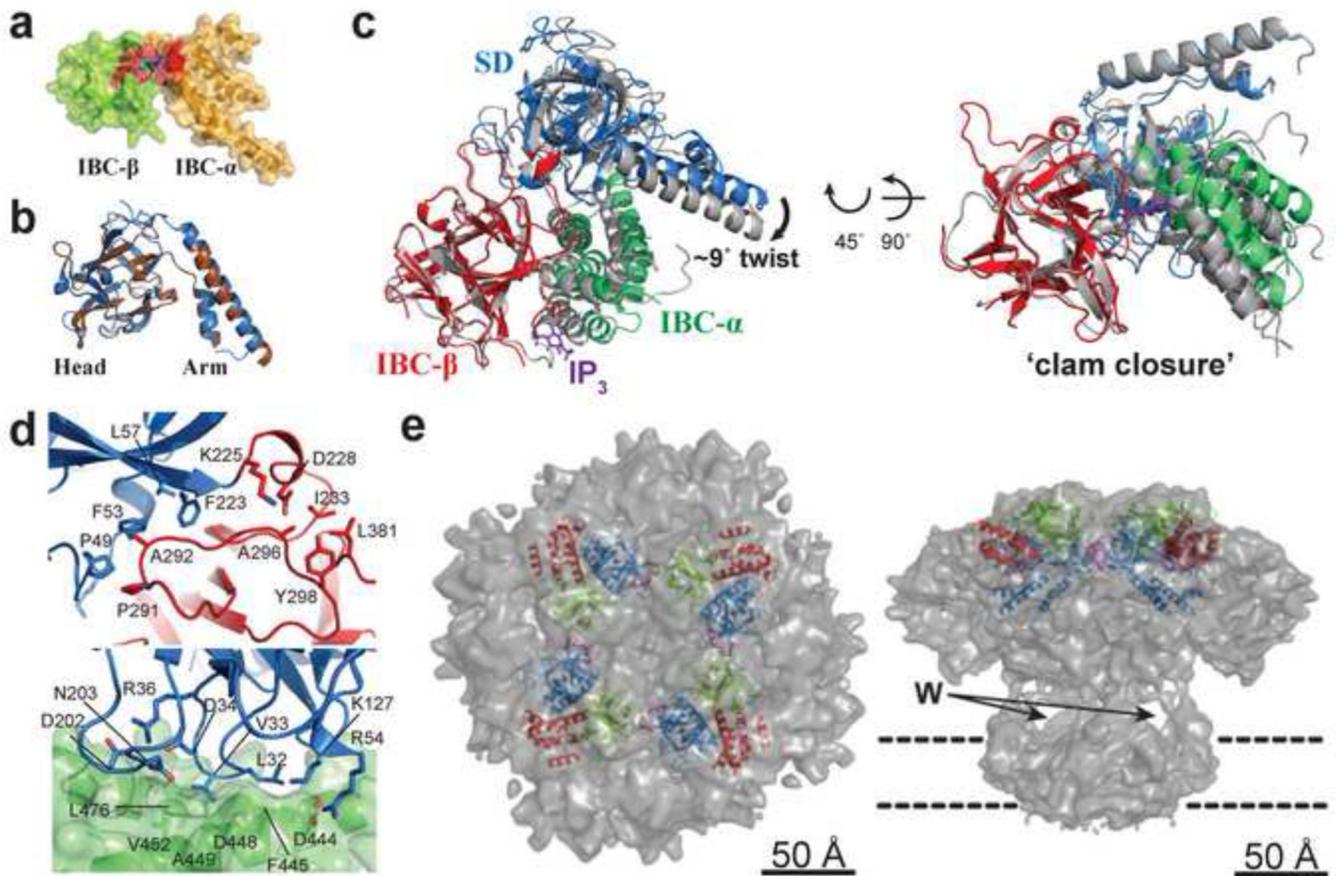
InsP<sub>3</sub>R<sub>sup</sub> and InsP<sub>3</sub>R<sub>core</sub> domains, CaM, RACK1, IRBIT and 4.1N binding sites, two ATP (A and B) binding sites, the Ca<sup>2+</sup> sensor region, the M1–M6 transmembrane domains and the pore-forming region (P) are shown.



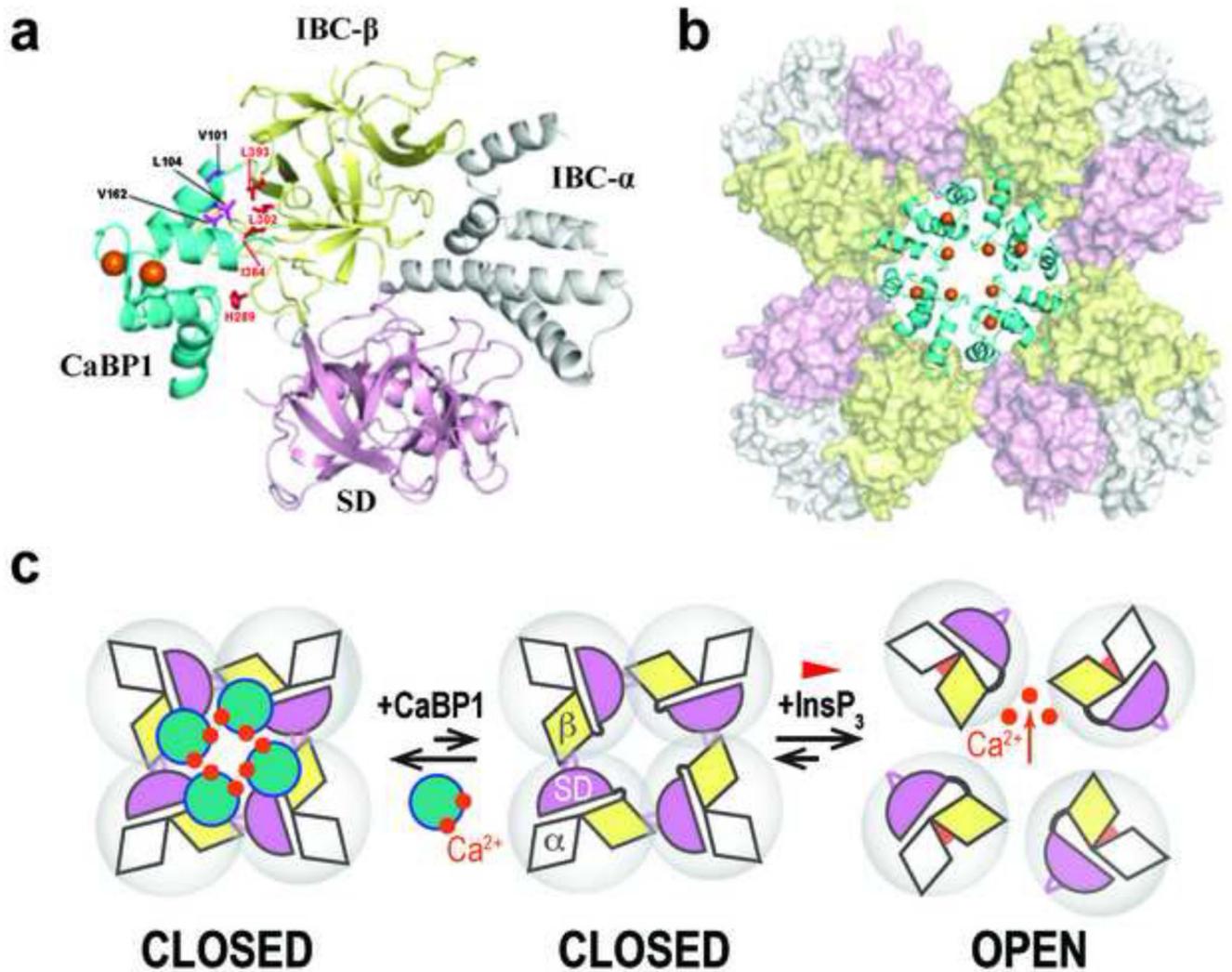
### Figure 2. Modulation of InsP<sub>3</sub>R1 by Ca<sup>2+</sup> and InsP<sub>3</sub>

InsP<sub>3</sub>R1 activity was recorded by patching cerebellar Purkinje cell nuclear membrane (Marchenko et al., 2005)

**a**, InsP<sub>3</sub>R channel activity at different InsP<sub>3</sub> concentrations. **b**, dependence of the normalised open probability of InsP<sub>3</sub>R channels on InsP<sub>3</sub> concentration. Data points represent mean ±SEM of five experiments. The solid curve is the Hill equation fit with EC<sub>50</sub>=0.68 μM and Hill coefficient =2.5. The channel activity (**c**) and normalised open probability of InsP<sub>3</sub>R channels (**d**) at different Ca<sup>2+</sup> concentrations in the presence of low (0.3 μM, left; n=5) and saturated (10 μM, right; n=7) InsP<sub>3</sub> concentrations. At both InsP<sub>3</sub> concentrations 1 μM of Ca<sup>2+</sup> almost completely inhibited the channel activity. Patch pipettes were filled with BaCl<sub>2</sub> solution, bath contained standard KCl solution with [Ca<sup>2+</sup>]<sub>i</sub> =250 nM. Holding potential was 40 mV.



**Figure 3. Structure of InsP<sub>3</sub>R1-NT relative to the full-length tetrameric receptor**  
**a**, Crystal structure of the InsP<sub>3</sub>R1-IBC in complex with InsP<sub>3</sub> at 2.2 Å resolution. Ribbon and surface representations of the IBC-β (light green) and IBC-α (orange) are shown. InsP<sub>3</sub>-coordinating regions are colored red. **b**, Superimposed structures of the InsP<sub>3</sub>R1-SD (blue) and InsP<sub>3</sub>R3-SD (brown). **c**, Superimposed apo (SD, blue; IBC-β, red; IBC-α, green) and InsP<sub>3</sub>-bound (*i.e.* holo) InsP<sub>3</sub>R1-NT (grey) structures. The structures were aligned by overlaying the IBC-β. **d**, The two interfaces between the SD and IBC (colored as in **c**). The short β-interface (top) consists predominantly of hydrophobic interactions between Pro49, Phe53, and Phe223 from the SD, and Pro291 and Ala292 from the IBC-β, and is supported by a salt bridge between Lys225 and Asp228. The longer α-interface (bottom) is stabilized by hydrophobic interactions between Val33 in the SD and a pocket formed by Val452, Phe445, Ala449, and Leu476 within IBC-α. Electrostatic interactions between Arg54 and Lys127 from the SD and Asp444 from IBC-α are also involved in forming the α-interface. **e**, Cryo-EM structures of full-length InsP<sub>3</sub>R1 in the closed state are shown from top (left) and side (right) views. The docked crystal structure of InsP<sub>3</sub>R1-NT is shown as a ribbon representation with SD in blue, IBC-β in red and IBC-α in green. The HS-loop is colored magenta. The windows (W) of InsP<sub>3</sub>R1 are indicated with arrows. The membrane bilayer boundaries are depicted with broken lines. The figures in **a** and **b** are reproduced from (Stathopoulos et al., 2012) and in **c–e** from (Seo et al., 2012).



**Figure 4. Structure of the InsP<sub>3</sub>R1-NT/CaBP1 complex and opposing effects of InsP<sub>3</sub> and CaBP1 on intersubunit interactions**

**a.** Structure of the C-lobe of CaBP1 (CaBP1-C) bound to InsP<sub>3</sub>R1-NT in a 1:1 complex. NMR structural restraints were used to define contacts between InsP<sub>3</sub>R1-NT (SD, pink; IBC-β, yellow; IBC-α, grey) and the CaBP1-C (cyan, with Ca<sup>2+</sup> atoms colored orange). Key residues at the binding interface are highlighted in magenta (CaBP1) and red (InsP<sub>3</sub>R1). **b.** Model for the tetrameric InsP<sub>3</sub>R1-NT/CaBP1-C complex (colored as in **f**) generated by superimposing the InsP<sub>3</sub>R1-NT crystal structure (Seo et al., 2012) onto the cryo-EM electron density map of InsP<sub>3</sub>R1 (Ludtke et al., 2011). **c.** Interactions between adjacent InsP<sub>3</sub>R1-NTs that are mediated by IBC-β (yellow) and the HS-loop of the SD (magenta) hold the tetrameric InsP<sub>3</sub>R1 in a closed state. InsP<sub>3</sub> binding closes the clam-like IBC, disrupting these intersubunit interactions, and allowing the channel to open. CaBP1 clamps the intersubunit interactions associated with the closed-state, thereby inhibiting channel opening. The figures are reproduced from (Li et al., 2013).