

REVIEW

Regulation of TLR7/9 signaling in plasmacytoid dendritic cells

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ABSTRACT

Plasmacytoid dendritic cells (pDCs), also known as type I interferon (IFN)-producing cells, are specialized immune cells characterized by their extraordinary capabilities of mounting rapid and massive type I IFN response to nucleic acids derived from virus, bacteria or dead cells. pDCs selectively express endosomal Toll-like receptor (TLR) 7 and TLR9, which sense viral RNA and DNA respectively. Following type I IFN and cytokine responses, pDCs differentiate into antigen presenting cells and acquire the ability to regulate T cell-mediated adaptive immunity. The functions of pDCs have been implicated not only in antiviral innate immunity but also in immune tolerance, inflammation and tumor microenvironments. In this review, we will focus on TLR7/9 signaling and their regulation by pDC-specific receptors.

KEYWORDS plasmacytoid dendritic cells, Toll-like receptors, immunoreceptor tyrosine-based activation motif, immunoreceptor tyrosine-based inhibitory motif, immunoglobulin-like transcript, BDCA2, phospholipid scramblase 1, protein kinase C and casein kinase substrate in neurons 1

INTRODUCTION

The innate immune system senses microbial infection or tissue damage by pattern recognition receptors (PRRs), which include Toll-like receptors (TLRs), RIG-I-like receptors / helicases, NOD-like receptors, and C-type lectin receptors. PRRs recognize structures conserved among microbial species, known as pathogen-associated molecular patterns. PRRs are also responsible for recognizing endogenous molecules released from damaged cells, damage-associated molecular patterns (Takeuchi and Akira, 2010). In contrast to myeloid dendritic cells that express TLR1, TLR2 and TLR3, pDCs selectively express TLR7 and TLR9 within the en-

dosomal compartments, where they engage with their RNA or DNA agonists and activate downstream signaling pathways (Kadowaki et al., 2001). Upon ligands engagement, TLR7/9 recruit the key adaptor molecule MyD88 through their Toll/IL1 receptor (TIR) domains. MyD88 recruits IL-1 receptor-associated kinase (IRAK) to TLRs through interaction of the death domains of both molecules. IRAKs are activated by phosphorylation, associate with the TNF receptor-associated factor (TRAF) domain of TRAF6 and dissociates from the receptor. Then, IRAKs/TRAF6 complex associates with transforming growth factor- β -activated protein kinase 1 (TAK1) and leads to the activation of NF- κ B and mitogen-activated protein kinases (MAPKs). In addition, IRAKs/TRAF6 complex also leads to the activation of interferon regulatory factor 7 (IRF7), the master regulator of type I IFN production. The activation of IRF7 requires multiprotein complex including IRAK4, IRAK1, TRAF6, TRAF3, I κ B kinase α (IKK α) (Akira and Takeda, 2004; Gilliet et al., 2008). In pDCs, engagement of TLR9 by type A CpG DNA in the early endosomes preferentially triggers the IRF7 signal cascade, leading to type I IFN responses; whereas engagement of TLR9 by type B CpG DNA in the late endosomes preferentially triggers the NF- κ B/ MAPKs signal cascade, leading to the production of proinflammatory cytokines TNF α and IL6 (Honda et al., 2005a; Guiducci et al., 2006). pDCs express several surface receptors, such as blood dendritic cell antigen 2 (BDCA2) and immunoglobulin-like transcript 7 (ILT7) in human pDCs and Siglec-H and Ly49Q in mouse pDCs that can modulate TLR7/9 signaling pathways. In addition, many other proteins, including microbial-derived molecules have also been shown to regulate TLR7/9 signaling.

ITAM-ASSOCIATED SURFACE RECEPTORS

Immunoreceptor tyrosine-based activation motifs (ITAMs), which contain the consensus sequence YxxL/I-(X)₆₋₈-YxxL/I (x denotes any amino acid), are used by multiple receptors to

activate immune cells. ITAM-containing transmembrane signaling adaptors include the TCR-associated CD3 γ , CD3 δ , CD3 ϵ , and CD3 ζ chains; BCR-associated Ig α and Ig β chains; the Fc ϵ RI β chain; the Fc ϵ RI-, the Fc γ RI-, and the Fc γ RIII-associated γ chain; and DNAX activation protein 12 (DAP12). Classically, ITAMs induce activation signals that involve phosphorylation of the tyrosines within the ITAMs and recruitment of Syk family tyrosine kinases. However, recent studies have shown that ITAMs also transduce inhibitory signals that negatively regulate production of proinflammatory cytokines by myeloid cells (Pasquier et al., 2005; Hamerman and Lanier, 2006; Ivashkiv, 2011).

PDC-RECEPTOR ILT7

Among the ITAM-containing adaptor molecules, Fc ϵ RI γ and DAP12 are expressed on pDCs. Several human pDC surface receptors were found to form complexes with Fc ϵ RI γ . ILT7, also known as leukocyte Ig-like receptor A4 (LILRA4), is a member of LILR family and associates with Fc ϵ RI γ to transduce the ITAM signaling (Cao et al., 2006). LILR family members contain two to four C2-type Ig like domains and can be further divided into two groups. The LILRA group has six members (LILRA1 to LILRA6) that have charged residue in the transmembrane domain and a short cytoplasmic domain (except for LILRA3, that lacks the transmembrane domain). The charged residue in the transmembrane domains of LILRA members allow them to associate with ITAM-containing adaptor molecules to activate downstream signaling after ligand engagement or antibody crosslinking (Brown et al., 2004). The LILRB group has five members (LILRB1 to LILRB5) that contain immunoreceptor tyrosine-based inhibitory motifs (ITIMs) in their cytoplasmic domain. ILT7 is a member of the LILRA subfamily that is selectively expressed on human pDCs within the immune system. Crosslinking of ILT7 by immobilized anti-ILT7 monoclonal antibody induces ITAM-mediated signaling cascade similar to B cell receptor signaling cascade, which negatively regulates the TLR7/9-induced type I IFN and cytokine responses (Cao et al., 2006). Bone marrow stromal cell antigen 2 has been identified as the physiological ligand for ILT7 that inhibits TLR-induced cytokine responses by pDCs (Cao et al., 2006; Cao et al., 2009). In addition, pDCs also express Fc ϵ RI α , the high-affinity receptor for the Fc region of IgE. Engagement of Fc ϵ RI α by IgE leads to the inhibition of CpG DNA-induced type I IFN production by pDCs via Fc ϵ RI γ (Schroeder et al., 2005). Consistent with these observations, knockdown of Fc ϵ RI γ and Syk in a pDC cell line, Gen2.2 cells, enhances TLR9-mediated type I IFN production and reverses ITAM-triggered inhibition (Bao et al., 2012) (Fig. 1). How ITAM signaling intersects and negatively regulates TLR7/9-mediated responses in pDCs remains elusive. Other LILRA family members like ILT1 (also known as LILRA2) and ILT11 (also known as LILRA5) can also associate with Fc ϵ RI γ and function as activating receptors in human monocytes and

macrophages (Nakajima et al., 1999; Mitchell et al., 2008). Their functions in pDCs remain unknown.

PDC-RECEPTOR BDCA2

BDCA2, a type II C-type lectin uniquely expressed on human pDCs, is another pDC-specific surface receptor that forms complex with Fc ϵ RI γ (Cao et al., 2007). Crosslinking of BDCA2 triggers the ITAM signaling pathway through Fc ϵ RI γ and inhibits TLR7/9 induced responses (Cao et al., 2007; Rock et al., 2007). HIV-1 encoded envelope glycoprotein gp120 is shown to be a potential ligand for BDCA2 that inhibits TLR9-mediated activation and IFN α secretion (Martinelli et al., 2007; Lo et al., 2012).

Recently, we have shown that CD2 associated adaptor protein (CD2AP) that is highly expressed in pDCs positively regulates the BDCA2-induced ITAM signaling pathway. CD2AP belongs to the CIN85/CD2AP family that includes CIN85 and CD2AP, characterized by containing three SH3 domains in the NH2 terminus, a proline-rich domain in the center region and coil-coiled domain in the C-terminus. CIN85/CD2AP have been shown to regulate T-cell activation, kidney glomeruli function, apoptosis in neuronal cells and the degradation of receptor tyrosine kinases (Dikic, 2002). CD2AP forms a complex with SH2-containing inositol phosphatase-1 (SHIP1) via its first SH3 domain. The CD2AP/SHIP1 complex enhances BDCA2/Fc ϵ RI γ signaling by inhibiting the E3 ubiquitin ligase activity of Cbl to maintain the expression level of Syk and Fc ϵ RI γ that are key adaptors for the ITAM signaling pathway (Bao et al., 2012). This suggests that, compared to other immune cells, the ITAM signaling pathway may be regulated in a special way in human pDCs.

DAP12-ASSOCIATED RECEPTORS

In addition to Fc ϵ RI γ , several surface receptors associate with the ITAM containing adaptor molecule DAP12 to transduce inhibitory signaling in pDCs. NKp44, an Ig superfamily member in human that is highly expressed on NK cells, is also present on pDCs in tonsils and on blood pDCs after culture with interleukin 3 (IL3). NKp44 associates with DAP12 and crosslinking of NKp44 inhibits type I IFN production by pDCs in response to CpG DNA. NKp44 recognizes the hemagglutinin of influenza virus and also the proliferating cell nuclear antigen that is overexpressed in cancer cells, suggesting virus and cancer cells may inhibit pDC function through ITAM-containing receptors (Arnon et al., 2001; Fuchs et al., 2005; Rosental et al., 2011). Leukocyte-associated Ig-like receptor-1, an ITIM-motif containing receptor that is highly expressed on pDCs, may have synergistic inhibitory effects with NKp44 (Bonaccorsi et al., 2010). Siglec-H, a sialic acid-binding Ig-like lectin molecule selectively expressed on mouse pDCs, associates and signals through the adapter DAP12. Ligation of Siglec-H using immobilized antibodies attenuates TLR9-induced type I IFN secretion. In ad-

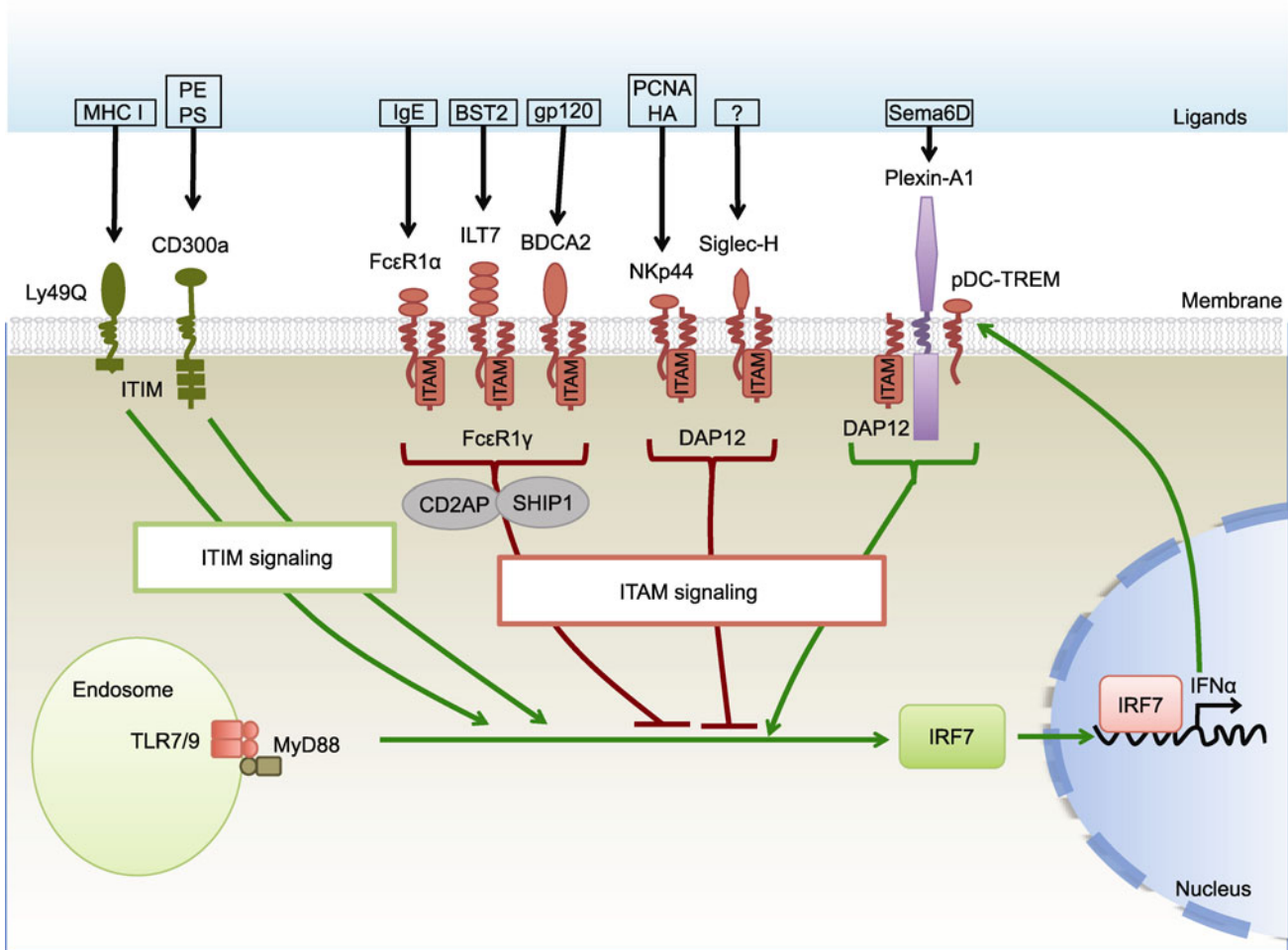


Figure 1. Regulation of TLR7/9 signaling by pDC surface receptors. pDCs express ITAM-associating or ITIM-containing receptors that play an important role in the TLR7/9-induced responses. Upon ligands engagement, TLR7/9 are activated and lead to IFN α secretion. Activation of the ITAM-associating receptors including Fc ϵ R1 α , ILT7, BDCA2, NKp44 and Siglec-H negatively regulates TLR7/9 signaling pathway, except pDC-TREM that is induced by IFN α and enhances TLR7/9 signaling. CD2AP and SHIP1 are essential components and are required for ITAM signaling pathways. In contrast, activation of ITIM-containing receptors like Ly49Q and CD300a positively regulate TLR7/9 signaling pathway.

dition, pDCs from DAP12-deficient mice lack surface Siglec-H expression and secrete more IFN in response to CpG DNA than do wild-type pDCs. Many Siglecs specifically recognize sialic acid-containing ligands. Nonetheless, although possessing all of the conserved structural features that contribute to sialic acid recognition, Siglec-H cannot bind sialic acid and the ligand for Siglec-H remains unknown (Blasius et al., 2006; Pillai et al., 2012).

In summary, pDC-receptors that associate with ITAM-containing adaptors negatively regulate TLR7/9-induced response. However, PDC-TREM, a member of the triggering receptor expressed on myeloid cells family, is preferentially expressed on TLR-stimulated pDCs and directly associates with Plexin-A1 and DAP12. Sema6D, a ligand for Plexin-A1, directly binds to Plexin-A1 and induces robust production of type I IFN, which suggests that PDC-TREM/Plexin-

A1/DAP12 complex mediates positive signaling for type I IFN production by pDCs (Watarai et al., 2008) (Fig. 1). The molecular mechanisms for the contradictory effects mediated by DAP12 in pDCs need further investigation.

VIRAL ITAM-CONTAINING PROTEINS

Many virus-encoded proteins contain ITAMs, such as the K1 protein of human herpesvirus 8; the R1 protein in rhesus monkey rhadinovirus; latent membrane protein 2A (LMP2A) in Epstein-Barr virus; gp30 in bovine leukemia virus; and the envelope protein gp52 in murine mammary tumor virus (Lanier, 2006). The LMP2A has been shown to inhibit the IFN signaling pathway by targeting IFN receptor for degradation (Shah et al., 2009). However, whether the inhibition effects depend on the ITAMs in LMP2A needs further investigation. Since pDCs are the professional type I IFN producing cells, it

will be of great value to study the functions of these viral ITAM-containing proteins in pDCs during viral infection.

For many ITAM-associated receptors, low-avidity interactions result in inhibitory consequences, whereas high-avidity interactions result in cell activation. A recent study shows that low avidity ligation of the ITAM-associated Fc α RI results in the translocation of Fc α RI and SH2 domain containing tyrosine phosphatase 1 (SHP1) to membrane lipid rafts. Subsequent ligation of activating receptors results in their colocalization with Fc α RI and SHP1 and trafficking to an inhibitory intracellular compartment where signaling molecules are deactivated by SHP1 (Pfirsch-Maisonnas et al., 2011). Nevertheless, in pDCs, high-avidity interactions of ITAM-containing receptors lead to the attenuation of TLR-induced type I IFN production. So, how ITAM signaling is uniquely regulated in pDCs remains unknown.

ITIMs-CONTAINING SURFACE RECEPTORS

Classical ITIM is defined as a consensus of a six amino acid sequence, I/V/L/S-x-Y-xx-L/V, where x denotes any amino acid. ITIMs present in the cytoplasmic domain of surface receptors with inhibitory properties which, when phosphorylated, recruit SHP1 and SHP2, or SHIP1. ITIMs have been found in a large number of inhibitory molecules from Ig superfamily and C-type lectin family (Daeron et al., 2008).

CD300 GLYCOPROTEIN FAMILY

The CD300 glycoprotein family members are type I transmembrane receptors with a single IgV-like extracellular domain. The transmembrane domains of CD300b, CD300c, CD300d, and CD300e contain a charged amino acid residue, which enables the association with the ITAM-containing adaptor DAP12, whereas the cytoplasmic domains of CD300a and CD300f contain ITIMs (Clark et al., 2009). In human pDCs, crosslinking of CD300a and CD300c with CMRF-35 antibody, which recognizes both molecules, inhibits HLA-DR expression and reduces TNF α and IL6 production while greatly enhances IRF7 expression and IFN α secretion by pDCs (Ju et al., 2008). Since CD300a contains ITIMs while CD300c associates with the ITAM-containing adaptor - DAP12, the function of CD300a and CD300c in human pDCs needs further clarification. However, human pDCs highly express CD300a and but only have low-level expression of CD300c (unpublished observation). Crosslinking of both CD300a and CD300c may preferentially trigger the ITIM signaling pathway. Recent studies show that CD300a binds to phosphatidylethanolamine and phosphatidylserine, two phospholipids that are exposed on the outer leaflet of the plasma membrane of dead cells (Nakahashi-Oda et al., 2012; Simhadri et al., 2012). The functions of these two phospholipids and their receptor CD300a in pDCs need to be further identified.

Ly49Q

Ly49Q is an ITIM-containing surface receptor and has been shown to be involved in the regulation of the TLR7/9 signaling pathway. Ly49Q belongs to the C-type lectin natural killer receptor family and is expressed on mouse pDCs. Ly49Q interactions with class I MHC are necessary for IFN α secretion by pDCs. Crosslinking of Ly49Q on mouse pDCs enhances TLR9-induced IFN α production (Fig. 1). Consistent with this, pDCs from Ly49Q knockout mice show severe defect in TLR9-dependent antiviral responses (Tai et al., 2008). Further study shows that Ly49Q colocalizes with CpG DNA in endolysosomal compartments and is necessary for the proper spatiotemporal regulation of intracellular trafficking of TLR9 (Yoshizaki et al., 2009).

Activation of ITIM will recruit SHP-1 or SHP-2 that play essential roles in TLR signaling pathways. Studies from knockout mice show that SHP-1 inhibits the production of proinflammatory cytokines but promotes the production of type I IFN in TLR3- and TLR4-mediated immune responses, whereas SHP-2 negatively regulates the TIR-domain-containing adapter-inducing IFN β (TRIF) adaptor protein-dependent type I IFN and proinflammatory cytokine production (An et al., 2006, 2008). Interestingly, the bacteria translocated intimin receptor from enteropathogenic *Escherichia coli* also contains two ITIM-like regions that recruit host cell SHP-1 and inhibit the ubiquitination of TRAF6, which results in the suppression of the enteropathogenic *Escherichia coli*-stimulated expression of proinflammatory cytokines (Yan et al., 2012). However, the molecular mechanism of the ITIM signaling pathway and the roles of SHP-1 and SHP-2 in pDCs remain elusive.

MOLECULES INVOLVED IN TLR7/9 PROCESSING AND TRAFFICKING

TLR7/9 contain an extracellular leucine-rich repeat domain that is responsible for the recognition of ligands, a transmembrane domain and a cytoplasmic TIR domains that is required for initiating intracellular signaling. TLR7/9 reside in the endoplasmic reticulum (ER) in association with polytopic membrane protein UNC93B1 and heat shock protein gp96 (Yang et al., 2007; Kim et al., 2008). The UNC93B1 delivers TLR7/9 from the ER to endolysosomes, where the ectodomains of TLR7/9 are cleaved by cathepsins and asparagine endopeptidase to generate the functional receptors for ligand recognition (Ewald et al., 2008; Ewald et al., 2011). Heat shock protein gp96 regulates intracellular trafficking of TLR9 possibly through the proteolytic processing and conformational stability of TLR9 (Brooks et al., 2012).

In pDCs (Fig. 2), depending on the cellular location of the endosome, TLR7/9 activation leads to different responses, which suggests that a unique membrane trafficking pathway is required for endosomal TLR signaling in pDCs (Honda et al., 2005a; Guiducci et al., 2006). By using a genetic screen-

ing method, adapter-related protein complex-3, biogenesis of lysosome-related organelle complexes (BLOC)-1, BLOC-2 and BLOC-3 and the solute carrier protein superfamily member Slc15a4 have been demonstrated to be required for pDCs to respond to nucleic acids through TLR7/9 (Blasius et al., 2010; Sasai et al., 2010). Recently, our group shows that phospholipid scramblase 1 (PLSCR1), an IFN-inducible protein that binds to the leucine-rich repeat domain of TLR9, is indispensable for type I IFN responses by regulating TLR9 trafficking to the endosomal compartment in pDCs (Talukder et al., 2012). Another pDC-specific adaptor molecule, protein

kinase C and casein kinase substrate in neurons 1 (PACSIN1), which has been shown to link membrane trafficking with the cytoskeleton and regulate the vesicle trafficking, plays a specific role in the type I IFN signaling cascade, which suggests that PACSIN1 may be also involved in TLR9 trafficking (Esashi et al., 2012).

THE KEY ADAPTOR MOLECULE IN PDCS, MyD88

MyD88 is an adaptor molecule contains an N-terminal death domain, a C-terminal TIR domain and linked by a short in-

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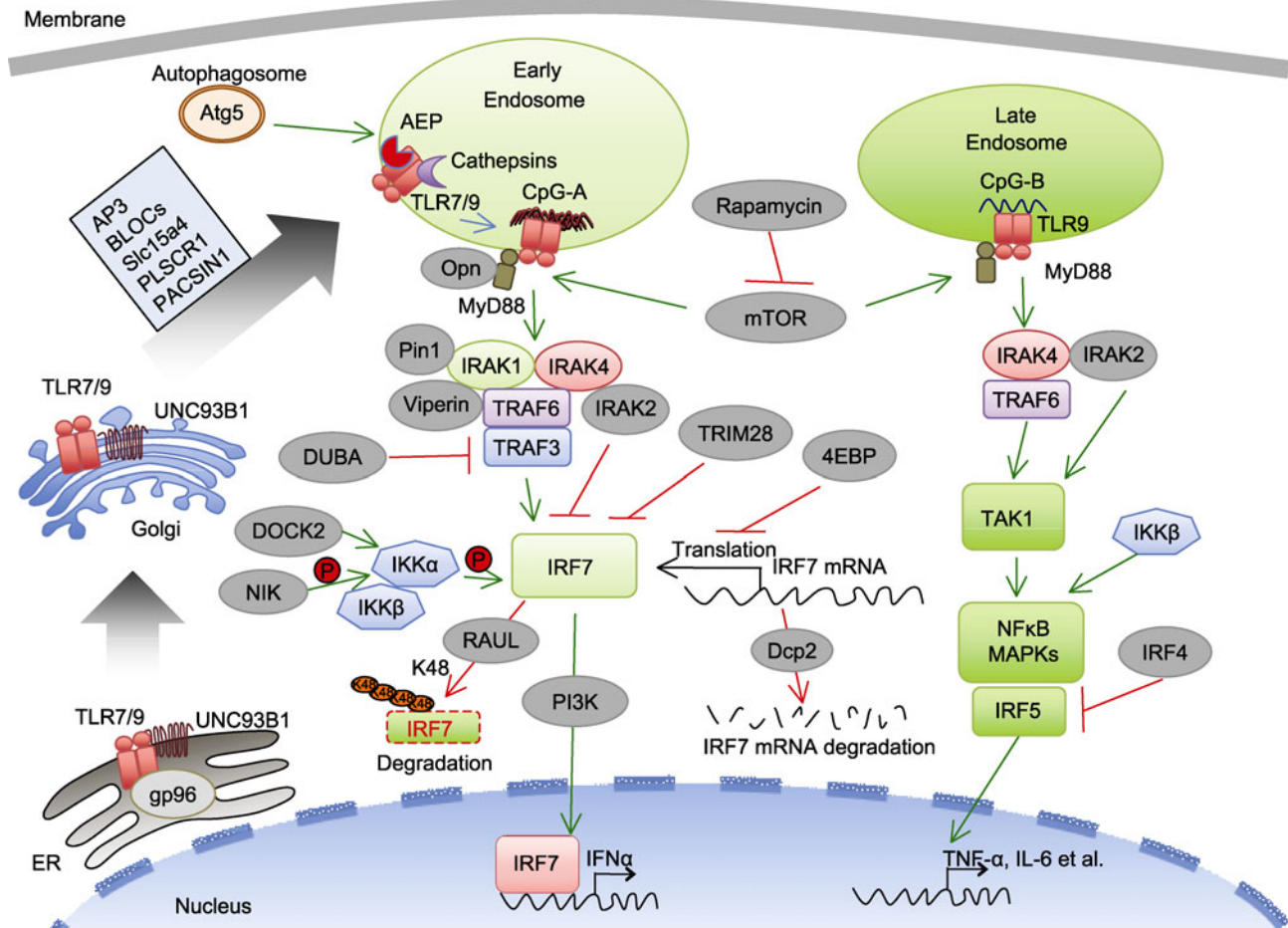


Figure 2. Regulation of the TLR7/9 signaling pathway in pDCs. In pDCs, TLR7 and TLR9 are synthesized in the endoplasmic reticulum (ER) and translocate from the ER to the endolysosome via UNC93B1. In the endolysosome, the ectodomains of TLR7/9 are cleaved by cathepsins and asparagine endopeptidase (AEP) to generate the functional receptors for ligand recognition. Following exposure to virus or nucleic acids, TLR7 and TLR9 in the endolysosome engage with their RNA or DNA agonists and induce different responses depend on the cellular localization. Molecules including Atg5, adapter-related protein complex-3 (AP3), BLOCs, Slc15a4, PLSCR1 and PACSIN1 are involved in the trafficking, splicing and modification of TLR7/9. In the early endosomes, a signalosome including IRAK4-IRAK1- TRAF6- TRAF3 is formed, which leads to IRF7 activation and type I IFN production. Pin1, Viperin, osteopontin (Opn), DOCK2, PI3K/mammalian target of rapamycin (mTOR) complex, NF-κB inducing kinase (NIK) and IKKα/β positively regulate IRF7 activation by modifying the early endosome signalosome molecules. In contrast, deubiquitinating enzyme A (DUBA) negatively regulates type I IFN response through deubiquitination of TRAF3. While IRAK2, tripartite motif-containing 28 (TRIM28), 4EBPs, RAUL and Dcp2 play negatively roles by directly modifying IRF7. In the late endosomes, a signalosome including IRAK4- TRAF6- TAK1- NF-κB/MAPKs/IRF5 is formed and leads to proinflammatory cytokine production. MTOR complex and IKKβ are necessary for the proinflammatory cytokine induction. IRF4 negatively regulates proinflammatory cytokine production through IRF5. IRAK2 negatively regulates IFN production but positively regulates proinflammatory cytokine production in pDCs.

intermediate sequence. Previous studies have shown that MyD88 knockout mice do not respond to TLR7 and TLR9 ligands (Hacker et al., 2000; Schnare et al., 2000; Hemmi et al., 2002). These findings demonstrate that MyD88 is the key adaptor molecule in TLR7/9 signaling. Upon TLR7/9 activation, MyD88 is recruited to TLR7/9 through its TIR domain and functions as a bridging protein to recruit IL-1 receptor-associated kinase 4 (IRAK4) via its death domain, enabling IRAK4-induced downstream signaling (Kawai et al., 2004). Phosphatidylinositol-3 kinase / the mammalian target of rapamycin and the p70 ribosomal S6 protein kinase can regulate TLR9 signaling possibly through stabilizing the interaction of TLR9 with the adaptor MyD88 (Cao et al., 2008). Osteopontin, a molecule that is induced in pDCs after stimulation with CpG DNA, interacts with MyD88 and selectively enhances type I IFN response (Shinohara et al., 2006). Since MyD88 is the key adaptor for both NF- κ B and IRF7 signaling pathway, it is still unclear how osteopontin specifically influences IRF7 signaling pathway but spares the NF- κ B-dependent proinflammatory cytokines.

Several other molecules have been shown to regulate MyD88. Nrdp1, an E3 ubiquitin ligase, binds to MyD88 and TANK-binding kinase 1 and induces their lysine 48 (K48)-linked polyubiquitination, leading to reduced production of proinflammatory cytokines but increased IFN-production in TLR-activated macrophages (Wang et al., 2009). Sequestosome 1 and histone deacetylase 6 suppress the formation of the MyD88-TRAF6 complex through regulation of cylindromatosis 1 recruitment and limit activation of TLR-induced activation of p38 and JNK (Into et al., 2010). Flightless I homolog can interact with MyD88 and negatively regulate TLR4 signaling pathway; while its associated protein- LRRFIP2 (LRR Fli-I-interacting protein 2) and Flap-1 (Fli-I LRR-associated protein 1, or LRRFIP1) bind to MyD88 and positively regulate TLR-induced NF- κ B activation (Dai et al., 2009). Since these studies are performed on non-pDC cells, the functions of these molecules in pDCs need further investigation.

IRAK FAMILY MEMBERS

IRAK family proteins include four members: IRAK1, IRAK2, IRAK4 and IRAK-M. IRAKs contain an N-terminal death domain and a central serine/threonine-kinase domain. Among these members, IRAK1 and IRAK4 have kinase activity, while IRAK2 and IRAK-M have no kinase activity. Upon TLR7/9 activation, IRAK4 is recruited to MyD88 through its death domain and activated. The activated IRAK4 interacts with and phosphorylates IRAK1, then IRAK4/IRAK1 complex dissociates from MyD88 and associates with TRAF6 to trigger downstream signaling pathway (Li et al., 2002; Lin et al., 2010). Studies from the knockout mice have revealed the importance of IRAK family in TLR signaling pathway. pDCs from IRAK4 knockout mice and IRAK4 kinase-inactive knock-in mice show impaired responses to TLR7/9 (Suzuki et

al., 2002; Kawagoe et al., 2007; Kim et al., 2007). In IRAK1 deficiency pDCs, TLR7/9-induced type I IFN production is greatly impaired, whereas the proinflammatory cytokines production is normal (Uematsu et al., 2005). Study from IRAK2 knockout mice shows that IRAK2 is critical for sustaining the expression of proinflammatory cytokines in response to TLR stimulation, which indicates that IRAK2 is critical in late-phase TLR responses (Kawagoe et al., 2008). Recently, IRAK2 has been indicated to play a negative role in type I IFN response while play a positive role in proinflammatory cytokine production in pDCs (Wan et al., 2011). In contrast to IRAK1 and IRAK4 that are positive regulators of TLR7/9 signaling pathway, IRAK-M is induced upon TLR stimulation and negatively regulates TLR signaling by preventing the dissociation of IRAK1 and IRAK4 from MyD88 and the formation of IRAK1-TRAF6 complexes (Kobayashi et al., 2002).

One recent study shows that Viperin, a type I IFN inducible gene residing in the cytoplasmic lipid-enriched compartments in pDCs, interacts with IRAK1 and TRAF6 and facilitates the K63-linked ubiquitination of IRAK1, which finally leads to the nuclear translocation of IRF7 (Saitoh et al., 2011). The prolyl isomerase Pin1 accelerates the cis and trans conformations of phosphorylated Ser-Pro motifs, which controls the function of many key regulators in various cellular processes. Pin1 can be activated by TLR7 and TLR9, then binds to and acts on the phosphorylated Ser-Pro motifs in IRAK1. This resulted in activation of IRAK1 and facilitated its release from the MyD88 signaling complex to activate the transcription factor IRF7 and induce type I IFN (Tun-Kyi et al., 2011).

The E3 ubiquitin ligase family of Pellino proteins has been shown to catalyze K63-linked polyubiquitination of IRAKs. Pellino family consists of three members: Pellino1, Pellino2 and Pellino3. Pellino3 is expressed in two spliced forms (Moynagh, 2009). The Pellino family member contains an N-terminal forkhead-associated domain that mediates association with IRAKs, and a C-terminal RING-like domain that confers E3 ubiquitin ligase activity and an ability to catalyze K63-linked polyubiquitination of IRAKs. Pellino members have been shown to be important mediators in TLR signaling pathway that leads to the activation of NF- κ B and MAPKs as well as IFN production (Enesa et al., 2012). The physiological roles of Pellino members in pDCs remain to be defined.

TRAF FAMILY MEMBERS

TRAF family contains 7 members. Except TRAF7, all TRAFs contain a TRAF domain on their C-terminal, and an N-terminal RING finger domain and zinc finger domains (with the exception of TRAF1 that lacks zinc finger domains). TRAF family members are intracellular signaling molecules with crucial functions in the signal transduction pathways initiated by TLR7/9 (Hacker et al., 2011). TRAF6 is essential for the activation of TLR7/9 signaling pathways, including NF- κ B/MAPKs and IRF7 pathways. TRAF6 functions to-

gether with the E2 enzyme complex Ubc13/Uev1A to catalyze the K63-linked polyubiquitin of IRF7, which leads to type I IFN production. TRAF6 also activates TAK1 in an ubiquitin-dependent manner. TAK1 is a member of the MAP kinase kinase kinase family. Once activated by TRAF6, TAK1 leads to the activation of NF- κ B and MAPKs (Ninomiya-Tsuji et al., 1999; Deng et al., 2000). By contrast, TRAF3 has been demonstrated to play a key role in type I IFN production and the anti-inflammatory cytokine IL-10, but is dispensable for the induction of proinflammatory cytokines (Hacker et al., 2006; Oganessian et al., 2006). TRAF4 has been shown to associate with p47^{phox}, a subunit of the cytosolic NADPH oxidase complex, and plays a negative role in TLR-induced responses through interaction with TRAF6 and TRIF (Takeshita et al., 2005). TRAF1 associates with TRIF and negatively regulates TLR3-induced signaling (Su et al., 2006). The exact roles of TRAF1 and TRAF4 in pDCs need further investigation.

Deubiquitinating enzyme A, an ovarian tumor domain-containing deubiquitinating enzyme, negative regulates of type I IFN responses by selectively cleaving the K63-linked polyubiquitin chains on TRAF3, resulting in its dissociation from the downstream signaling complex (Kayagaki et al., 2007). During virus infection with vesicular stomatitis virus or Sendai virus, the ubiquitin ligase TRIAD3A (also known as RNF216 isoform 1) removes the K63-linked ubiquitin chains from TRAF3 and enhances the K48-linked ubiquitylation, which leads to the proteasomal degradation of TRAF3 and, ultimately, results in the termination of the type I IFN response (Nakhaei et al., 2009).

IRF FAMILY MEMBERS

IRFs constitute a family of transcription factors that commonly possess a novel helix-turn-helix DNA-binding motif. So far, 9 family members have been identified, IRF1 to IRF9. IRF3 and IRF7 are closely related in terms of their primary structures (Taniguchi et al., 2001). However, studies from knockout mice have revealed that IRF7 but not IRF3 is master regulator of type I IFN in pDCs. In response to TLR9 ligand, pDCs from IRF7 knockout mice do not produce type I IFN, while produce normal level of proinflammatory cytokines (Honda et al., 2005b). In contrary, pDCs from IRF5 knockout mice produce normal level of type I IFN, but do not produce proinflammatory cytokines in response to TLR9 ligand. This study suggests that IRF5 plays key roles in the activation of genes for proinflammatory cytokines (Takaoka et al., 2005). pDCs from IFN α receptor (IFNAR) knockout mice showed greatly reduced type I IFN production, which suggests pDCs are entirely dependent on IFNAR feedback for type I IFN production. IRF8 plays a significant role in magnifying the second phase of IFN transcription by prolonging binding of basic transcription machinery to the IFN promoters and also contributes to pDC development (Tsujiyama et al., 2003; Tamura et al., 2005; Taylor et al., 2007). IRF9 associates with

activated STAT1 and STAT2 to form the multimeric transcription factor - interferon-stimulated gene factor 3 that initiates the transcription of the IFN-stimulated genes including IRF7; in consistent with this, pDCs from IRF9 knockout mice do not produce type I IFN (Horvath et al., 1996; Sato et al., 1998). In contrast to the positive roles of IRF3, IRF5, IRF7, IRF8 and IRF9, IRF2 and IRF4 play negative roles in TLR7/9 signaling. IRF2 functions as a negative regulator by antagonizing the type I IFN induced interferon-stimulated gene factor 3 (Hida et al., 2000). IRF4 selectively inhibits IRF5-dependent proinflammatory genes through competing with IRF5 for MyD88 interaction in a cell type specific manner (Negishi et al., 2005).

MOLECULES INVOLVED IN IRF7 MODIFICATION, ACTIVATION AND DEGRADATION

pDCs constitutively express high levels of IRF7, which is the master regulator of type I IFN production (Honda et al., 2005b). It has been shown that constitutive activation of NF- κ B p65/p50 and p38 contribute to the high expression level of IRF7 in pDCs (Osawa et al., 2006). In response to TLR9 ligand, IRF7 is activated and translocated from the cytosol to the nuclear to induce type I IFN production. IRF7 has been shown to be a substrate of TRAF6, which catalyzes K63-linked polyubiquitination of IRF7 in its C-terminal lysine sites that is necessary for IRF7 activation (Ning et al., 2008). The translational repressors 4EBP1 and 4EBP2 can negative regulate type I IFN production via translational repression of IRF7 mRNA, while the mammalian Dcp2 mRNA-decapping protein promotes IRF7 mRNA degradation (Colina et al., 2008; Li et al., 2012). The tripartite motif-containing protein 28 binds to IRF7 and increases its SUMOylation specifically, which results in transcriptional repression and subsequent impaired type I IFN production (Liang et al., 2011). The ubiquitin E3 ligase RAUL also negatively regulates type I IFN through directly catalyzing K48-linked polyubiquitination of IRF7 followed by IRF7 proteasome-dependent degradation (Yu and Hayward, 2010). IRF7 binds to its own promoter to auto-regulate IRF7 gene expression. The transcription factor FOXO3 forms a complex with nuclear co-repressor 2 and histone deacetylase 3, binds to the IRF7 promoter and negatively regulates of IRF7 gene expression. Upon type I IFN stimulation, the transcription of IRF7 is induced and the PI3K/Akt pathway is also activated, which in turn induces FOXO3 degradation. This leads to the high level of IRF7 that is essential for the maximal antiviral response (Litvak et al., 2012).

Several other molecules have also been reported to modify IRF7 activity. TRIF can associate with and activate IRF7 through TANK binding kinase 1 and its downstream kinases (Han et al., 2004). PIASy, a member of the PIAS SUMO-ligase family, inhibits IRF7 activity (Zhang et al., 2004). TRIM21 (also known as Ro52), an IFN-inducible E3 ubiquitin ligase, interacts with and ubiquitinates IRF7, which results in

results in the degradation of IRF7 (Higgs et al., 2010). One recent study shows that the E3 ubiquitin ligase Pellino3 is induced by TLR3, interacts with and ubiquitinates TRAF6, which negatively regulates the ubiquitination of IRF7, resulting in down-regulation of type I IFN expression (Siednienko et al., 2012). Their roles in TLR7/9-induced responses in pDCs need further studies.

IKK FAMILY MEMBERS

The IKK complex is the central regulator of the NF- κ B signaling. IKK complex contains two kinases (IKK α and IKK β) and a regulatory subunit, IKK γ / NEMO. IKK α and IKK β show a similar structure, which include an amino-terminal kinase domain, a helix-loop-helix domain that functions in modulating IKK kinase activity, and a leucine zipper domain that allows homo- or heterodimerization of the kinases (Israel, 2010). It has been shown that pDCs from IKK α knockout mice show selectively defects in TLR7/9-induced IFN α induction, which suggests that IKK α is a key regulator in pDCs. IKK α associates with and phosphorylates IRF7 to induce type I IFN response (Hoshino et al., 2006). NF- κ B inducing kinase acts as an upstream kinase of IKK α in activation of IRF3/7 and may play important role in TLR7/9-mediated type I IFN production (Wang et al., 2008). Inhibiting IKK β activity by using IKK β -specific inhibitors or by siRNA knockdown of IKK β also result in reduced TLR7/9-induced IFN and proinflammatory cytokine production (Pauls et al., 2012). These studies show that IKK family members play essential roles in TLR7/9-mediated signaling pathways.

DOCK2, an atypical Rac activator, controls IKK α activation and specifically regulate TLR7/9-induced type I IFN induction (Gotoh et al., 2010). Regnase-1 (Zc3h12a), an RNase that is essential for controlling immune responses by destabilizing mRNA including IL6, IL12 and the calcitonin receptor gene, has been shown to be the target of IKK complex. In response to TLR, regnase-1 is phosphorylated by IKK complex and IRAK1. The phosphorylated regnase-1 undergoes ubiquitination and degradation, which results in enhance IL6 and IL12 mRNA expression (Matsushita et al., 2009; Iwasaki et al., 2011).

E2-2, THE KEY TRANSCRIPTIONAL REGULATOR OF PDCS

E proteins comprise a family of basic helix-loop-helix transcription factors. E proteins include E12 and E47, HEB and E2-2, which form homodimers or heterodimers with other family members. E2-2 (also known as TCF4) is a member of E proteins that is preferentially expressed in pDCs. E2-2 directly activates multiple pDC-enriched genes, including transcription factors involved in pDC development (SpiB, IRF8) and function (IRF7). Deletion of murine E2-2 specifically blocks the development of pDCs and abolishes IFN response to CpG DNA. In addition, deletion of transcription

factor E2-2 from mature peripheral pDCs caused their spontaneous differentiation into cells with classical dendritic cells properties, including morphological changes, enhanced T cell priming capacity and upregulated classical dendritic cell-enriched genes. These studies suggest that E2-2 is the key specific transcriptional regulator of pDC development and of the pDC-mediated IFN response (Cisse et al., 2008; Nagasawa et al., 2008; Ghosh et al., 2010).

AUTOPHAGY-RELATED PROTEINS

Autophagy plays critical roles in maintaining cellular energy homeostasis and the cell adaptation to environmental stresses during starvation, stress and infection. Recent studies have shown that autophagy plays important roles in antiviral immune responses (Saitoh and Akira, 2010). The autophagy-related gene (Atg) 5-Atg12 conjugate, a key regulator of the autophagic process, associates with retinoic acid-inducible gene I and IFN β promoter stimulator 1 and negatively regulates type I IFN production in mouse embryonic fibroblasts in response to vesicular stomatitis virus infection (Jounai et al., 2007). Also, loss of Atg16L1, an essential component of the autophagic machinery that forms a complex with Atg5-Atg12, results in enhanced production of proinflammatory cytokines in response to TLR4, TLR7 and TLR9 ligands in mouse macrophages (Jounai et al., 2007). In addition, Atg5 and Atg7 that is required for the conjugation of Atg12 with Atg5 have been demonstrated to negatively regulate type I IFN production in mouse embryonic fibroblasts and macrophages (Jounai et al., 2007; Tal et al., 2009).

In contrast to the inhibitory effects of autophagy in other cell types, pDCs from Atg5 knockout mice show impaired type I IFN and IL12 p40 production in response to RNA virus infection, which indicates autophagy plays a positive role in pDCs (Lee et al., 2007). PDCs constitutively contain autophagosomes that are necessary for the TLR7-dependent induction of innate immune responses. However, in response to TLR9 ligands, CpG DNA and herpes simplex virus 1, pDCs from Atg5 knockout mice show impaired type I IFN but normal level of IL12 p40 (Lee et al., 2007). This study indicates that, although TLR7 and TLR9 share the signaling pathway that induces type I IFN, TLR7 and TLR9 may be different regulated to induce inflammatory cytokine production in response to their ligands.

FUTURE PERSPECTIVES

Despite the extensive studies during the past decade, the components of TLR7/9 signaling network remain elusive, especially in pDCs. The following questions are outstanding, including: (1) How do ITAM and ITIM signaling intersect with TLR7/9 signaling? (2) What are the natural ligands for pDC receptors, such as BDCA2 and Siglec-H? (3) What are the molecular mechanisms underlying the specialization of TLR9-mediated early endosomal IFN responses versus late

endosomal proinflammatory cytokine responses?

Because of the rareness of pDCs, it has been very difficult to study the signaling network in pDCs. Many new approaches have been used to study the signaling complex: (1) The pDC yeast-two hybrid library, by which we have identified PLSCR1 as a TLR9 binding molecules, will help us to identify the pDC-specific TLR7/9 signaling molecules. (2) The integrative strategy combining transcriptomics, genetic and chemical perturbations, and unbiased phosphoproteomics will facilitate the deciphering of the pDC-specific signaling network. By using this method, Polo-like kinases 2 and 4 have been identified to be essential components of antiviral signaling in pDCs (Chevrier et al., 2011). (3) The global proteomic analysis will help us to map a dynamic protein interactome network (Li et al., 2011). (4) The forward genetic approach to identify genes like AP-3, Slc15a4 and BLOC that are essential for pDC functions (Blasius et al., 2010).

PDCs are professional type I IFN producing cells and play key roles in innate and adaptive immune responses. Deciphering the unique signaling networks in pDCs that contribute to the rapid and massive amount of type I IFN production in response to viral infection will be of great help in better manipulating immune responses associated with viral infection, autoimmune diseases, cancers and vaccines.

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ABBREVIATIONS

Atg, autophagy-related gene; BDCA2, blood dendritic cell antigen 2; BLOC, biogenesis of lysosome-related organelle complex; CD2AP, CD2 associated adaptor protein; DAP12, DNAX activation protein 12; IFN, interferon; IKK, I κ B kinase; IL, interleukin; ILT, immunoglobulin-like transcript; IRAK, IL-1 receptor-associated kinases; IRF, interferon regulatory factor; ITAM, immunoreceptor tyrosine-based activation motif; ITIM, immunoreceptor tyrosine-based inhibitory motif; LILR, leukocyte Ig-like receptor; MAPKs, mitogen-activated protein kinases; PACSIN1, protein kinase C and casein kinase substrate in neurons 1; pDCs, plasmacytoid dendritic cells; PLSCR1, phospholipid scramblase 1; PRRs, pattern recognition receptors; SHIP1, SH2-containing inositol phosphatase-1; SHP-1, SH2 domain containing tyrosine phosphatase 1; TAK1, transforming growth factor- β -activated protein kinase 1; TIR, Toll/IL1 receptor; TLR, Toll-like receptor; TRAF, TNF receptor-associated factor; TRIF, TIR-domain-containing adapter-inducing IFN β

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