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Mammalian phospholipase D: Function, and therapeutics

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Abstract

Despite being discovered over 60 years ago, the precise role of phospholipase D (PLD) is still being elucidated. PLD enzymes catalyze the hydrolysis of the phosphodiester bond of glycerophospholipids producing phosphatidic acid and the free headgroup. PLD family members are found in organisms ranging from viruses, and bacteria to plants, and mammals. They display a range of substrate specificities, are regulated by a diverse range of molecules, and have been implicated in a broad range of cellular processes including receptor signaling, cytoskeletal regulation and membrane trafficking. Recent technological advances including: the development of PLD knockout mice, isoform-specific antibodies, and specific inhibitors are finally permitting a thorough analysis of the *in vivo* role of mammalian PLDs. These studies are facilitating increased recognition of PLD's role in disease states including cancers and Alzheimer's disease, offering potential as a target for therapeutic intervention.

Keywords

Phospholipase D; Phosphatidic acid; Lipid signaling; Membrane transport

1. Introduction

Hanahan and Chaikoff discovered phospholipase D (PLD) in 1947 as a factor in carrot extracts capable of causing lipid and membrane degradation. They characterized it as a phospholipid-specific phosphodiesterase, able to release free choline from phosphatidylcholine (PtdCho), using water as a nucleophilic acceptor, to produce phosphatidic acid (PtdOH or PA) [1–3]. PLDs have since been described in organisms as diverse as viruses, bacteria, plants and mammals, and the enzymes have been broadly divided into members of a 'superfamily' containing the canonical catalytic motif HxKxxxxD (HKD), and non-HKD enzymes with a broader range of substrate specificities. However,

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bacterial cardiolipin synthases (CLSs), phosphatidylserine synthases (PSSs) and endonucleases are now also known to contain HKD motifs. As such, perhaps a better definition for PLD enzymes is that of proteins possessing the ability to hydrolyze glycerophospholipids, pre-dominantly PtdCho, at the headgroup phosphodiester bond to produce the free headgroup and PtdOH.

PLD activity and PtdOH regulate a remarkable range of cellular processes including: vesicle trafficking, endocytosis, exocytosis, secretion [4–13], cytoskeletal rearrangement [14], phagocytosis [15,16], neuronal- and cardiac stimulation [17–23], matrix metalloproteinase (MMP) production [24], the oxidative respiratory burst in neutrophils [25], plant stress responses ([26,27], pathogen resistance [28], the pathogenic actions of bacteria, and spider venom [29–32], pluripotency, stem cell reprogramming, and apoptosis [33]. PLD is also implicated in a number of diseases including: inflammation, diabetes [34] oncogenesis [35], Alzheimer's disease (AD) [36–41], thrombotic disease [42,43], hypertension [44], multiple sclerosis [45], and viral infection [46].

2. Early biochemical studies of mammalian PLD

The first PLD activities were identified in plants and bacteria, however given the mammalian PLD focus of this review, and since this early history has been covered elsewhere, the reader is referred to the following articles [1,47–50]. Importantly though, the early plant studies demonstrated PLD catalyzes transphosphatidylations reactions in the presence of glycerol or short chain primary aliphatic -alcohols (such as butan-1-ol). Being stronger nucleophilic acceptors than water, the natural acceptor, they are used preferentially by the enzyme with a preference of over 1000-fold [17,51]. The resultant phosphatidylalcohol products of these reactions are metabolically stable, and unlike PtdOH are poor substrates for lipid phosphate phosphatases (LPPs [previously called phosphatidate phosphohydrolases or PAPs]) [52,53]. Their stability, presumed functional inactivity, and ability to block PtdOH production resulted in widespread use of phosphatidylalcohol formation both as a marker of PLD activity, and as a way of blocking PLD mediated PtdOH production through alternate production of phosphatidyl-alcohols.

Initially considered absent from animal tissue, interest in PLD grew following demonstration that rat-brain solubilized enzyme preparations released choline, and ethanolamine from PtdCho, and phosphatidylethanolamine (PtdEth) respectively [54,55]. Later studies confirmed PtdOH increases were direct results of PLD activity, and not of the phospholipase C (PLC)/ Diacylglycerol (DAG) kinase pathway, or *de novo* synthesis [56,57]. Attempts to purify PLD from mammalian tissues resulted in identification of multiple isoforms with differing: pH optima, and responses to: Ca^{2+} and Mg^{2+} , oleate, phosphatidylinositol 4,5-bisphosphate ($\text{PtdIns}(4,5)\text{P}_2$), and guanosine 5'-(gamma-thio) triphosphate ($\text{GTP}\gamma\text{S}$) [58–65]. PLD partially purified from HL60 membranes was potently activated by $\text{GTP}\gamma\text{S}$, could be stimulated by the small GTPase ADP-ribosylation factor (Arf), and had an absolute requirement for $\text{PtdIns}(4,5)\text{P}_2$ [66,67]. Similar activities were subsequently discovered in rat brain [68], alongside a second oleate-dependent activity [69]. Further studies revealed that the GTP-stimulated activation of PLD in neutrophils was dependent on Rho, another small GTPase [70], and a pig brain membrane PLD was identified that could be stimulated by both

small GTPases [71]. PLD activities were subsequently described in most mammalian cell types [72], and in many sub-cellular organelles including plasma membrane, nucleus, Golgi, and endoplasmic reticulum (ER) [73–77]. These activities could be stimulated by a wide variety of agonists including: serum, growth factors, phorbol esters, N-formyl-methionyl-leucyl-phenylalanine (FMLP), adenosine triphosphate (ATP), epinephrine, vasopressin and GTP γ S [56,57,78–81].

3. Cloning of the first PLD-encoding genes

Lack of DNA or protein sequences hindered initial PLD studies but this problem was surmounted following purification of PLD from cabbage (*Brassica oleracea*), and castor bean (*Ricinus communis*) [50,82,83]. The N-terminal amino acid sequence of the later enabling cDNA clone isolation, from an endosperm cDNA library, encoding a 92-kDa protein [50]. Expression of the cloned enzyme in *E.coli*, facilitated demonstration that hydrolysis and transphosphatidylation were performed by the same enzyme [50]. Identification of plant PLD sequences paved the way for identification of PLD-encoding genes in other organisms, initially in the yeast *Saccharomyces cerevisiae* [84,85]. Sequencing of the yeast *SPO14* PLD facilitated identification of homologous mammalian expressed sequence tag (EST) clones and subsequently full-length mammalian PLD1 isoforms were identified from a human HeLa cell cDNA library [34], mouse [86] and rat [87]. PLD1 encoded a predominantly membrane associated, PtdCho-specific, 1072 amino acid (aa), trans-phosphatidylation-competent protein which could be stimulated by PtdIns(4,5)P₂, and GTP γ S-loaded Arf1 [88]. Shortly after PLD1's identification, recognition of similar but distinct sequences in EST databases revealed a second mammalian PLD isoform: PLD2. Isolation of PLD2 cDNA from a mouse embryo cDNA library revealed a 932aa protein with 51% homology to PLD1 including particular homology within the central catalytic core [89–91]. PLD1 and PLD2 have a similar substrate preference, preferring mono- or di-unsaturated PtdCho, and generate structurally identical PtdOH species [92]. They both possessing four highly conserved catalytic domains I-IV with catalytic HKD motifs in domains II and IV. They also both contain N-terminal PX- and PH-domains and a polybasic PtdIns(4,5)P₂-binding region. The isoforms vary considerably between conserved domain-II, and -III, with human PLD1 (but not PLD2) possessing a variable thermolabile loop region that appears to be inhibitory, since its deletion increases basal activity threefold [93]. The region is cleaved by caspases during apoptosis conferring, heightened GTPase sensitivity and elevated activity [94–96]. PLD1 has multiple splice variants, with the isoform that was initially discovered being designated PLD1a. The PLD1b splice variant lacks 38aa/43aa in the loop region between the catalytic domains but possesses a similar regulatory and catalytic profile [34,88]. PLD1a, and 1b variants lacking the C-terminal 113aa, designated PLD1a2 and -b2, were also identified, possessing dramatically reduced (8–12% of wild-type) activity [97]. PLD1c contains an mutation close to the N-terminus generating an inactive, truncated product of unknown function, which is expressed in a number of tissues including brain, and postulated to be an inhibitor of endogenous PLD activity [91]. PLD2 also has multiple splice variants, the first variant to be identified being designated PLD2a. PLD2b possesses an 11aa C-terminal deletion, and PLD2c contains a 56 bp insertion resulting in a truncated protein of unknown biological significance, since it

lacks the catalytic HKD motifs, and is catalytically inactive [91]. A comparison of PLD1 and PLD2 structure is illustrated in Fig. 1.

4. Mammalian PLD structure

4.1 The PLD catalytic domain and potential catalytic mechanisms

Sequencing of PLD proteins identified four conserved domains (I-IV) [98], domains II, and IV containing the charged catalytic motif HxK (x)₄D (HKD) [48,99]. Substitution mutations within the HKD motifs inactivate mammalian PLD1, PLD2, and yeast Spo14 [93,97,100,101]. Two catalytic models of PLD activity have been proposed: 1) each catalytic motif functions independently; 2) each forms half of the active site [98]. Evidence supports the latter, since: a) mutation of single HKD motifs ablates activity [100], and b) individually expressed N-, and C-terminal PLD1 fragments [102,103] are catalytically inactive, but activity is reconstituted upon co-expression. In addition, several crystal structures of 'PLD superfamily' members reveal a conserved fold agreeing with this model, including that of the *Salmonella typhimurium* endonuclease Nuc, which contains a single HKD motif, and dimerizes to form an active site [104]. Other structural studies using *S. typhimurium* (strain PMF) PLD [105,106], and the human tyrosyl-DNA phosphodiesterase (Tdp1) family member also validate this model. Currently no resolved mammalian PLD structures exist however, a PLD2 3D-model has been proposed, combining homology, and *ab initio* 3D structural modeling methods, and docking conformations [107]. While theoretical, this model superimposed on bacterial PLD crystal structures, broadly agrees with biochemical studies showing that the N-, and C-terminal HKD motifs form a catalytic pocket, accommodating the PtdCho headgroup [107].

Radiolabel exchange experiments using a plant PLD, suggested a two-step "ping pong" catalysis reaction, involving a covalent phosphatidyl-enzyme intermediate, followed by hydrolysis/transphosphatidylation [48,108]. Later, a combination of labeling [109], and crystallization studies [104] using the bacterial Nuc enzyme, revealed a histidine from one HKD motif forms the catalytic nucleophile attacking the phosphate of the phosphodiester bond. This forms a phosphor-enzyme intermediate which is then hydrolyzed by water in the second half of the reaction, the other HKD motif acting as an acid, protonating the leaving group [104]. Radiolabeling studies using Nuc and another family member: the *Yersinia, pestis* murine toxin, validated this model [110], while subsequent crystallization of *S. typhimurium* PLD, and Tdp1 indicated the N-terminal motif likely provides the nucleophilic histidine [105,106,111,112]. Recent mammalian PLD2 molecular threading data also supports this model with the N-, and C-terminal histidines (H442/H756) of the HKD motifs forming a catalytic pocket, accommodating the PtdCho head group (but not that of PtdEth or PtdSer), facilitating nucleophilic attacks by H442, and water, aided by H756 [107]. The motifs lysine and aspartic acid residues are also implicated in catalysis [100,113,114], with postulated roles including intra-molecular interactions outside the active site [105,106], or interaction with-, and charge neutralization of-, the substrate [104]. Six amino acids downstream of the second HKD motif, within domain IV of mammalian PLD1 and PLD2 is the IGSANIN motif. This is essential for mammalian PLD1 catalysis, and palmitoylation, with mutation ablating activity, and causing abnormal, diffuse localization [115]. Variants in

the catalytic sequences exist in a number of family members, but they generally adhere to the consensus motif HxKx(4)Dx(6)GGxD/N for domain II, and HxKx(4)Dx(6)GS/TxN for domain IV [116].

4.2 Lipid binding domains of mammalian PLDs

Mammalian PLD1, and PLD2 possess N-terminal phox homology (PX)- and pleckstrin homology (PH) domains and an additional poly-basic PtdIns(4,5)P₂ binding site [17,117]. The interplay of lipid-binding sites likely confers localization and function, and is implicated in sub-cellular cycling [118] (see Fig. 2).

PH-domains are best known as high-affinity, high-specificity phosphoinositide (PIP) binding domains, although it is now apparent that less than 10% of them perform this function (as low as 3% in yeast) [119], such binding requiring phosphorylation at two adjacent sites on the PIP *e.g.* PtdIns(4,5)P₂, PtdIns(3,4)P₂ and PtdIns(3,4,5)P₃ [120]. Membrane targeting roles once thought to be characteristic of these domains now appear restricted to this high-affinity binding subset [121], although at least one PH-domain is reported displaying PIP-binding independent membrane localization [119]. Other PH-domain subsets exist, including PIP-binders with weaker affinities, and specificities [122,123], and those postulated to be involved in coincidence detection [120,124,125]. Surface plasmon resonance (SPR) studies indicate PLD1 binds PtdIns(4,5)P₂, PtdIns(3,4)P₂, and PtdIns3P, with the isolated PH-domain having significantly higher affinity for PtdIns(4,5)P₂ [126]. However, since PtdIns(4,5)P₂ levels are higher than agonist stimulated PtdIns(3,4)P₂ levels and PLD activity can be measured in the absence of PI3-kinase activity, the relevance of PtdIns (3,4)P₂, and PtdIns3P interactions *in vivo* are unclear [126,127]. Immuno-affinity chromatography using large-unilamellar vesicles and the purified PLD2 PH-domain indicate a 10-fold PtdIns(4,5)P₂ binding preference over PtdIns4P, PtdOH, or PtdSer though it bound these lipids to a lesser degree [128].

PLD PH-domain point mutations or deletions have variously reported effects on *in vitro* activity ranging from complete inhibition to no affect, under conditions of PtdIns(4,5)P₂ excess. A number of reports suggest PH-domain point mutation, or deletion in PLD1 [93,101], or PLD2 [93,101,128,129] does not affect *in vitro* activity. However, conflicting data exists for PLD1 [47,126], and the PH -domain is required for *in vivo* PLD2 activity [128]. PH-domain mutations in PLD1 and PLD2 result in aberrant localizations, indicating a membrane-targeting role [126,128]. The isolated PLD1 PH-domain localized weakly to perinuclear vesicles, translocating weakly to the plasma membrane upon PMA-stimulation, indicating a potential function in exocytosis [118]. The PLD1 PH-domain is palmitoylated at cysteines 240, and 241, loss of palmitoylation resulting in translocation from peri-nuclear vesicles to plasma membrane [118,130]. The PLD1 PH-domain is additionally required for efficient return from the cell surface to endosomes, and for lipid raft entry, a palmitoylation-dependent process, which appears critical for internalization [118]. The PLD PH-domains are now also recognized as protein binding domains. The PLD1 PH-domain interacts with the μ 2 subunit of adaptor protein 2 (AP2), facilitating AP2 membrane recruitment, and subsequent endocytosis of epidermal growth factor receptor (EGFR) [131]. The PLD2 PH-

domain binds aldolase [132], the kinase domain of c-Src [133], and appears to play an important role in interaction with the small GTPase Rac2 [103].

Several studies demonstrated PH-domain mutation, or removal of the PLD1 or PLD2 N-termini (including the PH-domain) didn't impair *in vitro* activity, or affect concentration dependent PtdIns(4,5)P₂ activation, indicating the presence of another PtdIns(4,5)P₂ binding site [93,101,128,129]. A conserved aromatic amino acid sequence: the "polybasic motif", between domains III, and IV of mammalian PLD1, PLD2 and the yeast Spo14 PLD, is absent in bacterial and plant PLDs not regulated by PtdIns(4,5)P₂. Substitution of these residues in mammalian PLD2 dramatically impaired PtdIns(4,5)P₂ binding and stimulation of *in vitro* catalytic activity [129]. Furthermore, a peptide corresponding to the polybasic motif bound PtdIns(4,5)P₂ with high affinity [128], and while PLD2, and Spo1 4 mutated within the polybasic motif display normal localization, they are non-functional *in vivo* [128,129]. In contrast, in PLD1, the polybasic motif acts in concert with other PLD domains to mediate localization. In COS-7 cells over-expressing tagged PLD1, the PtdIns(4,5)P₂-interaction site was sufficient for mediating PMA-stimulated translocation to the plasma membrane, however the PH-, and PX-domains were required for endosomal return [118].

PX-domains are found in the N-termini of human, yeast, and nematode PLD [98,134]. These domains frequently display binding preferences for PtdIns3P, and its derivatives, which, are enriched at the early endosome [135,136]. PLD1 is activated by PtdIns(3,4,5)P₃ *in vitro* [88,126,137,138], which specifically interacts with arginine 179 of the PLD1 (but not PLD2) PX-domain. Mutation of this residue inhibits platelet-derived growth factor (PDGF)-stimulated PLD1 membrane recruitment [137,139]. At the plasma-membrane, the PX-domain is required for further compartmentalization, with threonine 147 of PLD1 being one of three residues required for maximum PMA-stimulation, and which is reversibly phosphorylated by PKC at this location, driving PLD1 into caveolin-enriched microdomains, [140,141]. The PLD1 PX- domain is also required for efficient return from the cell surface, binding PtdInsSP to target it to endocytic vesicles [118]. Sequence alignment of the PLD1- and PLD2 PX-domains with the NADPH oxidase p47-phox, suggest they contain a 'second ion-binding pocket'. In p47- phox the conserved region enables it to bind anionic phospholipids such as PtdSer and PtdOH while it's other pocket binds PtdIns(3,4)P₂ [142]. Consistent with this, the PLD1 PX-domain can bind both lipids, raising the possibility that PLD activity could be regulated by its own product. Simultaneous occupation of both pockets resulted in a synergistic increase in membrane binding with electrostatic potential calculations suggesting occupation of the second pocket by PtdOH, PtdSer, or other ionic lipids may initiate binding to the membrane, followed by interaction with the other pocket with PtdIns(3,4,5)P₃ [139].

Non-lipid binding PLD PX-domain roles also exist including the guanine nucleotide exchange activity (GEF) activity of the PLD2 PX-domain, with specificity for the small GTPases Rac2 and Ras [143–146]. Additionally, the PLD1 and PLD2 PX-domains bind several proteins in a lipase independent manner. These include dynamin, for which they act as GTPase activating proteins (GAPs) stimulating GTPase activity, and accelerating EGFR endocytosis [131,147]). The PLD2 PX-domain additionally binds: 1) the PKC ζ kinase domain, stimulating *in vitro* kinase activity [148]; 2) the PLC γ 1 Src homology 3 (SH3)

domain, an EGF-stimulated interaction, that potentiates PLC γ activity [149]; 3) Munc-18–1 which inhibits PLD activity in an EGF-reversible manner [150]; 4) Syk kinase, promoting its activation, and downstream mast cell activation [151]; 5) Collapsin Response Mediator Protein (CRMP), an interaction that additionally requires the PLD2 C-terminus, and that acts to inhibit neuronal PLD2 [152].

4.3. The mammalian PLD N- and C-termini

The poorly conserved mammalian PLD N-termini are modification tolerant, and deletion in PLD1 or PLD2 does not majorly impact catalytic activity [93,101,102,153]. The PLD1 N-terminus however, is required for PKC-stimulation [93,102,153,154], and appears to contain negative regulatory elements since deletion of the N-terminal 325 amino acids enhances Arf-, and Rac1-dependent activities [93]. Similarly, removal of the PLD2 N-terminus dramatically increases Arf-stimulation [101]. The PLD C-termini display greater conservation, and are less modification tolerant [93,101,155]. Deletion of the PLD1 C-terminus [93], or single amino acid mutations in this region abolish activity [155]. The PLD1a2, and –1b2 splice-variants lack the C-terminal 113aa, instead possessing distinct 10aa sequences conferring partial activity (8–12% of PLD1a/1b). They display altered localization, being absent from the endosome, indicating a C-terminal sub-cellular targeting role [97]. The C-termini also contain Rho family interaction sites, with additional postulated roles in stabilizing active site conformation [155].

4.4. Other mammalian PLD structural motifs

Motif III consists of the highly conserved IYIENQFF motif [117,156]. Its exact function remains unclear, but mutations in this sequence reduce PLD activity [100]. IYIENQFF is postulated to interact with PtdCho *via* the choline headgroup's methyl group [117,156] and it is also suggested to increase the catalytic rate, or bind caveolin [117]. The amino acid residues leucine 405 and glycine 412 of the mammalian PLD1 domain I also have important functions for activity. Confusingly however, their mutation, but not deletion, seriously impacts activity [93]. Mammalian PLD1 and the *C. elegans* PLD isoform contain a loop region between domains II, and III. While the role in *C. elegans* is unclear, in human PLD1 it appears to be the region least well conserved between human and rodent isoforms, the site of alternate splicing [88], an autoinhibitory region [93], and a site of proteolytic cleavage [95].

4.5. The tissue and cellular distribution of mammalian PLD1, and PLD2

Early biochemical studies revealed PLD activities in a wide range of mammalian tissues and cell lines. Following the cloning of PLD1 and PLD2 isoform-specific expression data emerged, most of which reported mRNA levels until the advent of high-affinity antibodies [48,72]. PLD1b [91,157,158] and PLD2a are the most abundantly expressed splice variants [91,158,159] and most studies agree that PLD1 and PLD2 are ubiquitously expressed and present in almost all tissues and cell lines with the potential exception of peripheral leukocytes, lymphocytes [160,161], and renal tissue which reportedly lack PLD1 [162]. Isoform-specific tissue expression patterns exist: PLD1 is enriched in human heart, brain, pancreas, uterus, and intestine, and PLD2 is enriched in brain, placenta, lung, thymus, prostate, and uterine tissue [90,163]. Highly sensitive PLD2 brain expression analysis, using Locked Nucleotide Amplification (LNA), indicates that expression in this organ is not

ubiquitous [164]. Most functional regions of the brain expressed PLD2 with levels being detectable in the pyramidal cells of the *cornu ammonis* (CA) regions of the hippocampus, the Purkinje cells in the cerebellum and the mitral cells of the olfactory bulb [164]. However, in contrast to previous studies using antibody staining [165], PLD2 was absent from glia rich regions such as the fimbria, *arbor vitae* of the cerebellum, the internal capsule running through the *caudoputamen*, or the *corpus callosum* [164].

Early sub-cellular localization studies were limited to subcellular fractionation and activity measurements [166]. Later, studies addressing individual isoform localization were mainly limited to overexpression of tagged proteins in transformed cell lines, due to lack of specific antibodies. These yielded confusing data, arguing for, and against localization to practically every known cellular location [48,134]. Thankfully trends emerged, and more recent reports using specific antibodies are helping to clarify the situation. Continuing discrepancies as to the precise nature of their localizations are likely a reflection of the different imaging strategies, cell lines and tissues used [167,168].

The majority of localization studies have used overexpressed, tagged-proteins, and overexpressed PLD1 is frequently described as cytoplasmic [169], perinuclear [89,118,169], and vesicular [118,170–173], with co-localization studies placing it at early- and late endosomes [7,89,97,118,168–170,174], lysosome [7,170,174], autophagosomes [170], ER [89], secretory granules [7,175], Golgi [89,118,168] and actin cytoskeleton [176]. Overexpressed PLD1 has also been observed at the plasma membrane [7,169,175,177], including caveolin-rich microdomains [140], lamellipodia and ruffles [178] and to move to the plasma membrane following cell-stimulation with some [7,118,175,178], but not all agonists [89,175]. Over-expressed PLD1 has also observed in some studies within the nucleus [170,173] and overexpression studies have proved critical in determining how the proteins localization at this site is determined. PLD1 possesses a nuclear localization sequence (NLS), mutation of which abolishes nuclear import [173]. Following apoptosis-induced caspase cleavage the NLS lies within a C-terminal fragment (*CF-PLD1*) which moves exclusively to the nucleus. The NLS of wild-type PLD1 and *CF-PLD1* interact with importin- β which mediates nuclear import [95,170,173]. Four hydrophobic residues (L647, V648, 1649, 1670) within the PLD1 N-terminal HKD motif, determine PLD1 nuclear localization, their mutation causing translocation from vesicles, and an increase in PLD1-importin- β interaction with subsequent nuclear-translocation [170]. Staining with specific antibodies localizes endogenous PLD1 to many of the same localizations as the overexpressed protein including the cytoplasm/ cytoplasmic puncta [12,179], Golgi [9,12], TGN [179], nucleus [12,95,179], a perinuclear region [179], a vesicular localization [170], and plasma membrane [177]. Notably however, these studies do not detect endogenous PLD1 in the lysosomes, endosomes or secretory granules. Careful studies employing combined cell fractionation, immunofluorescence and immuno-EM have confirmed the endogenous localization of PLD1 in multiple cell lines as being within the Golgi and nucleus, and that overexpression of PLD1 forces the protein from the Golgi causing it to mislocalize [12]. This report is consistent with some overexpression studies reporting PLDs absence from the Golgi [7,174]. This study also noted much lower levels of plasma membrane PLD1 staining (if any in some cell types) than many studies employing overexpression [12]. Other studies looking at the endogenous protein have also called into

question the extent of PLD1 at the plasma membrane and have suggested that in contrast to the overexpressed protein it is absent from caveolin-rich microdomains [180].

Many PLD2 localization studies have also employed overexpressed tagged-protein, and have reported it in cytosol [181], vesicles [171], and in particular the plasma membrane [89,168,171,172,181], including in caveolin-rich micro domains [180], and membrane ruffles [171] in unstimulated cells. PLD2 has also been observed to translocate to plasma membrane ruffles [484], filopodia, and sub-PM vesicles [89] following stimulation. The endogenous protein has also been observed at the plasma membrane in multiple cell lines [11,168,179,182], although some studies suggest this is much less extensive than with overexpression and limited to discrete areas such as ruffles or regions of active recycling [11]. Endogenous PLD2 may also localize to caveolae since it co-localizes with caveolin-1 [11] and is present in caveolin rich fractions [180,182,183]. Endogenous PLD2 is also observed in cytoplasmic puncta [11,179,182], within the perinuclear area [11,179], at the TGN [179] and at the rims of the Golgi, an area distinct from that of endogenous PLD1 suggesting a potential different function within this organelle [11]. Endogenous PLD2 has also been observed to translocate to the nucleus following treatment with the Arf inhibitor brefeldin A, suggesting a potential nuclear signaling role under certain circumstances [11].

4.6. The PLD1, and PLD2 knockout mice

Given the range of cellular processes in which PLD1 or PLD2 have been implicated, the observation that mice lacking either (or both) isoforms are viable and appear overtly normal [42,184] surprised many in the field, but offered the hope that PLD inhibitors may be valuable therapeutic agents without major health risks. Absence of either isoform fails to elicit compensatory elevation of expression of the other [42,184], and both PLD1^{-/-}, and PLD2^{-/-} -knockout mice are viable, born at expected mendelian ratios, develop normally, appear healthy, are fertile, and display overtly normal behavior. However, mouse phenotypes associated with PLD1/ PLD2 absence do exist. While red-and white blood cell, and platelet counts appear normal in PLD1^{-/-} mice, platelet volume was increased slightly resulting in increased surface abundance of platelet surface receptors, including GPV, CD9 and β 1 and β 3 integrins [42]. PLD1^{-/-} mice also exhibit reduced α _{IIb} β ₃-dependent platelet activation, rendering them resistant to major pathological hemostasis events such as strokes and pulmonary embolisms [42]. Furthermore PLD1^{-/-} mice, display macroautophagy defects [185], which could potentially affect cancer cell-intrinsic metabolic pathways [186], and display decreased tumor formation and angiogenesis [43]. PLD-deficient mice (single or double PLD1/PLD2 knockout) display impaired brain development, having reduced brain growth at 14–27 days post partum [187]. They also display impaired cognitive function in social (PLD1 KO and PLD2 KO), and object recognition (PLD2 KO, and double KO). Brain microdialysis revealed severely reduced hippocampal acetylcholine (ACh) release following behavioral stimulation in PLD1^{-/-} and PLD2^{-/-} single knockout animals [187]. Since choline is a precursor for ACh production, this may be a consequence of decreased choline production due to reduced PLD activity. These observations may have relevance for cognitive dysfunction observed in fetal alcohol syndrome and Alzheimer's disease (AD) [187]. Consistent with a role in this disease, PLD2^{-/-} mice displayed protection against the synaptotoxic, and memory-impairing actions of β -amyloid in a transgenic AD model

[39,188]. PLD1 and PLD2 have also been implicated in suppression of appetite, and appear to protect against overweight [189]. In addition, PLD1 and PLD2 knockout mice consume more food than controls, and also display reduced energy expenditure, elevated body weight, and increased adipose tissue [189]. PLD1 and PLD2 knockout mice both displayed elevated free-fatty acids and are insulin and glucose intolerant [189]. Complicating interpretation of the knockout mouse phenotypes, PLDs may possess non-phospholipase roles, including scaffolding [190,191] and their absence therefore could potentially disrupt multi-protein complexes. Knockdown could also induce compensatory mechanisms including those increasing PtdOH [190].

4.7. The discovery of additional mammalian PLD isoforms

While the vast majority of mammalian PLD research has focused on PLD1 and PLD2, other potential mammalian isoforms have been reported in the literature [190]. These proteins namely PLD3 (also called Sam-9 or HUK4); PLD4; PLD5 and PLD6 (also called Mitochondrial PLD, MitoPLD, Zucchini, or Zuc), contain HKD domains or variants thereof, but have been termed non-classical PLDs, lacking the PX- and PH-domains, and -classical PLD activity required to convert PtdCho to PtdOH [192–194]. As such, these proteins remain largely outside the scope of this current article and will only be mentioned briefly. It is now clear that PLD3 and PLD4 are single-stranded nucleic acid exonucleases regulating endosomal nucleic-acid sensing, rather than PtdCho-hydrolyzing PLDs [195], PLD5 is likely catalytically inactive due to poor conservation of the catalytic domains, lacking the histidine and lysine of the first catalytic motif and the histidine of the second [116,196]. PLD5 KO mice exhibit no significant abnormalities [197], however in humans PLD5 is linked to a profibrotic uterine phenotype that occurs during childbearing years. PLD5 polymorphisms may also be associated with an increased risk of tumor progression in multiple cutaneous and uterine leiomyomatosis syndrome [198], PLD6 encodes a single HKD-motif containing protein, which binds mitochondrial outer surfaces *via* an N-terminal trans-membrane tail [199]. Initial reports studying the mouse isoform stated that PLD6 hydrolyzes cardiolipin to PtdOH and displayed no *in vitro* nuclease activity towards RNA or DNA [199–201]. Recent studies however, clearly demonstrate that PLD6 is not a lipase/phosphodiesterase, but rather a single strand specific RNase, essential for primary biogenesis of piRNAs (piwi-interacting RNAs), and suppression of transposon expression, with an important role in maintaining genomic integrity of germline cells [202–205].

4.8. Redundancy of mammalian PLD isoforms

The existence of multiple PLD isoforms within individual organisms raises the possibility of functional redundancy. Redundancy in plants is well documented [28], however the situation in other organisms is less clear [190]. The differing localizations of mammalian PLD1 and PLD2 in some cell types suggest non-redundant functions, as does the fact there is no compensatory expression increase observed in knockout mice lacking a single PLD isoform [42,184]. Furthermore, while inactivation of either isoform decreased macrophage phagocytosis, no further decrease occurred upon dual disruption [206]. Nor is PLD1's regulation of reactive oxygen species (ROS) levels in neutrophils affected by absence of PLD2 [184]. In addition, while stable expression of PLD1 or PLD2 in HEK293 cells, resulted in elevation of tissue plasminogen activator (tPA)-stimulated p38 MAPK

phosphorylation, only those expressing PLD1 demonstrated increased cyclooxygenase-2 (Cox-2), and interleukin-8 (IL-8) expression [207]. Other studies, however argue for full-, or partial redundancy of PLD1 and PLD2. These include those demonstrating dual occupation of the same sub-cellular localizations, and the fact that inhibition of mouse embryonic fibroblast (MEF) dorsal membrane-ruffling by the dual PLD1/2 inhibitor FIPI, requires inhibition or deletion of both isoforms [208]. Evidence of partial redundancy also exists, from studies in which lack of PLD1 (but not PLD2) reduced platelet activation [42], and lack of both isoforms elicited a stronger phenotype [209].

4.9. The identification of isoform-specific mammalian PLD inhibitors

Until the advent of specific PLD inhibitors, primary alcohols (primarily butan-1-ol) were the only method to inhibit the production of PLD derived PtdOH, with secondary and tertiary alcohols used as controls [51,79,184,210]. Problems associated with the technique became evident when it was revealed that the alcohol concentrations required to substantially block PtdOH production were toxic, and that routinely used concentrations gave incomplete inhibition [184,211–215]. Concerns of off-target effects also grew, and with the advent of RMAi, and small molecular inhibitors, it became evident, that many biological effects associated with primary alcohols could not be attributed to PLD inhibition [190,210,212,215,216]. In particular, the PLD-specific inhibitor: 5-Fluoro-2-indolyl des-chlorohalopemide (FIPI) didn't have any effect on a number of biological processes which were inhibited by butan-1-ol, and that had previously been attributed to PLD [212,215]. Similarly, a number of ethan-1-ol sensitive events, failed to be replicated with more reliable techniques, such as a genetic deletion of PLD [210]. The impact of these revelations was enormous. After over 100 publications demonstrating an essential PLD role in fMLP peptide signaling-activated superoxide production [216] Sato, and colleagues demonstrated that the dual PLD1/ PLD2 inhibitor 5-fluoro-2-indoyl des-chlorohalopemide (FIPI) had no effect on this process, or on PtdOH production. PtdOH increases stimulated by fMLP were instead being produced by DAG kinase mediated phosphorylation of PLC-produced DAG. Clearly, alcohol was inhibiting superoxide production through an unknown PLD-independent mechanism. To emphasize just how big an impact this finding had on the field, over 4800 PLD articles had been published prior to this finding, many of which employed primary alcohols [190]. Furthermore, later studies indicated that primary alcohols aren't equally effective 'inhibitors' for all family members, for example they poorly inhibit *Pseudomonas aeruginosa* PLD (PldA)-catalyzed PtdOH production [217]. It has also been demonstrated that some organisms such as fungi can also use the secondary alcohols, traditionally employed as controls in these experiments, for transphosphatidylation [218,219]. In addition, primary, and secondary alcohols are also reported to actually stimulate plant PLD activity [220] and the effects of primary alcohols have been mimicked by higher concentrations of secondary alcohols in algae [221,222]. Despite these caveats, inhibition of PtdOH production by primary alcohols continues to be employed within the PLD field. As such, and given the historical reliance on this technique, reports employing this technique have been included in this review, where possible with more recent reports validating the findings. It is perhaps best that all findings previously based upon this technique should be revisited, using genetic knockdown, siRNA (or similar), or specific inhibition. The identification of highly specific PLD inhibitors has enabled functional analysis without the

concerns of off-target effects, inhibitor dose, or time course, associated with previous methods [184]. A wide-range of PLD inhibitors are reported, though many are currently poorly characterized [47]. A 2007 Novartis screen to isolate PLD2 inhibitors identified the psychotropic agent halopemide (also called R34301) [223], which inhibits both PLD1 (IC_{50} 21 nM in cells and IC_{50} 220 nM *in vitro*), and PLD2 (IC_{50} 300 nM in cells and IC_{50} 310 nM *in vitro*) [224]. The drug had previously been through clinical trials in which plasma concentrations sufficient for human PLD1 inhibition were used, demonstrating the clinical viability of PLD1 inhibition [225]. Following halopemide's identification, hundreds of analogs were synthesized and assayed in attempts to identify isoform specific inhibitors [47,224,226–228]. Notable inhibitors included FIPI, which inhibited PLD1 (IC_{50} 1 nM in cells, and IC_{50} 9.5 nM *in vitro*) and PLD2 (IC_{50} 44 nM in cells and IC_{50} 17 nM *in vitro*) with increased potency [224], FIPI acts by interacting with the second HKD motif and as such inhibits the catalytic sites of both PLD1 and PLD2 [229]. Isoform specific inhibitors also exist including: the PLD1 specific inhibitor: VU0155069 (approximately 163-fold selectivity over PLD2), and the PLD2 inhibitor: VU0155072 (approximately 10-fold selectivity over PLD1) [223,224,230–232]. Further optimization *via* medicinal chemistry approaches greatly improved isoform specificity and potency, resulting in the highly selective PLD1 inhibitor: VU0359595 (IC_{50} 3.7 nM, 1700-fold over PLD2), and an improved PLD2 inhibitor: VU0364739 (IC_{50} 20 nM, 75-fold preference over PLD1) [47,233–235].

4.10. Mammalian PLD1 and PLD2 regulation

Mammalian PLD enzymes are tightly regulated by multiple mechanisms including post-translational modification, cofactor availability, molecular interactions and signal-induced sub-cellular translocation (Fig. 2) [47,163]. PLD1, and PLD2 are differentially regulated with PLD2 being generally less agonist responsive. For example, PLD2 transfected cells are stimulated only 2-fold by phorbol 12-myristate 13-acetate (PMA), *versus* 10–15 fold for PLD1. Such observations led to suggestion that PLD2 is basally active (unlike PLD1) in unstimulated cells [89]. This was confirmed by the observation that PLD2 (but not PLD1) knockdown resulted in a reduction of basal PLD activity. PLD1 *in vitro* basal activity is activated directly by small G proteins and PKC, in conjunction with $PtdIns(4,5)P_2$ [88,236,237]. PLD2 displays constitutively high activity (1000-fold greater than PLD1) in the presence of $PtdIns(4,5)P_2$, but is insensitive to PLD1 activators such as Arf, Rho and PKC *in vitro* [34,89,236].

4.11. Regulation of mammalian PLD by phosphoinositides and other lipids

Early mammalian PLD studies identified a rat brain PLD activity which, was oleate-dependent and preferred neutral pH. It was inhibited by negatively-charged-phospholipid-binding aminoglycoside antibiotics, including neomycin, in a manner reversed by adding back $PtdIns(4,5)P_2$ [59,68,238–241]. Later, *in vitro* PLD assays using HL60 cell membranes revealed a $PtdIns(4,5)P_2$ requirement for choline release from $PtdCho$ [66], and that in the absence of sodium oleate, the partially purified oleate-dependent activity could also be stimulated by this phospholipid [68,69]. Cloning of mammalian PLD1 [34,138], and PLD2 [89,90,242] isoforms later revealed an obligate $PtdIns(4,5)P_2$ requirement for the activity of these isoforms. Several proteins involved in $PtdIns(4,5)P_2$ production, sequestration, and

dephosphorylation are implicated in PLD regulation. Over-expression of PtdIns4P 5-kinase increases PLD activity in mammalian cells, and both PLD1 and PLD2 bind to PtdIns4P 5-kinase I α [243]. PLD2 activity (but not that of PLD1) is increased when co-expressed with PtdIns4P 5-kinase I α and it is inhibited by over-expression of a catalytically inactive PtdIns4P 5-kinase I α mutant [243]. PtdIns4P 5-kinase I α activity is stimulated by PtdOH, providing a potential, positive feedback loop, or the possibility that one PLD isoform could stimulate another through stimulation of kinase activity. Dephosphorylation of PtdIns(4,5)P₂, or its sequestration, may also regulate PLD since the inositol phosphate 5-phosphatase synaptojanin [244,245] and the PtdIns(4,5)P₂⁻, and actin-binding protein gelsolin [246] inhibit PLD *in vitro*. Numerous studies demonstrate roles for the PH-domains and polybasic motifs of PLD1, and PLD2 in interaction with PtdIns(4,5)P₂. These lipid-binding domains play an important role in localization of these isoforms, and are reported to contribute to varying degrees in their obligate PtdIns(4,5)P₂ requirement for activity (see section 4.2). Other phosphoinositides also stimulate PLD activities, including PtdIns(3,4,5)P₃, a weak activator of the purified enzyme, which demonstrates greater activation in partly purified preparations [247]. PtdIns(3,4,5)P₃ stimulates human- [88,126] and rat PLD1 [138], activating and binding human PLD1 half as efficiently as PtdIns(4,5)P₂, suggesting a critical role of the phosphate position on the inositol ring [126]. Surface plasmon resonance analysis demonstrated only limited PtdIns(3,4,5)P₃ binding to intact PLD1 and none to the isolated PH- domain [126,247]. In contrast, the isolated PLD1 PX-domain bound PtdIns(3,4,5)P₃ with high affinity in a vesicle binding study. Binding required lysine (119,121) and arginine (179), and the PLD1 PX-domain also displayed modest affinity PtdIns3P as well as for PtdInsSP [139]. In addition to binding of these phosphoinositides, the PLD1 PX-domain can simultaneously bind PtdOH or PtdSer, and potentially other ionic lipids due to the presence of a second distinct lipid-binding pocket, dual occupancy of these pockets increases membrane association and likely plays a role in spatiotemporal PLD1 regulation [139]. The *in vivo* role of PI-3-kinase in regulation of PLD activity is complicated by the fact that while PI-3-kinase inhibitors such as wortmannin inhibit cellular PLD activity, they are non-specific and affect multiple other pathways [248]. In addition, PI-3-kinase may regulate PLD through indirect mechanisms, including lipid-binding proteins such as the cytohesin [249] and Tiam-1 [250] exchange factors regulating Arf-, and Rho, whose activity is controlled by PtdIns(3,4,5)P₃-dependent PH-domains.

Purification of multiple PLD activities from plants and mammals has indicated stimulation by unsaturated fatty acids [63,163,251]. These include one of the earliest purified mammalian PLDs, from porcine lung, which was stimulated by unsaturated oleic (18:1), linoleic (18:2), and arachidonic (20:4) fatty acids [63]. Study of oleate-dependent PLD activity has been hampered by the failure to conclusively identify the oleate-stimulated protein and it is likely that multiple isoforms can be oleate-stimulated depending on the assay system. For example, oleate stimulated PLD1 activity in Huh-7 cells through PI-3 kinase-mediated activation of Arf and Rho [252], while oleate stimulated PLD2 but not PLD1 in RBL-2H3 mast cells [172]. Several other studies suggested PLD2 is oleate-stimulated, and consistent with the early studies this isoform is enriched in lung [90,163], PLD activity was oleate-stimulated in Jurkat T-cells, only expressing PLD2, but not HL60's uniquely expressing PLD1 [90]. Similarly, oleate-stimulated activity in L1210 cells solely

expressing PLD2, but not in U937 cells only expressing PLD1 [253]. Oleate (18:1) also stimulated purified PLD2 (but not PLD1) *in vitro*, as did the other unsaturated fatty acids linoleate (18:2) and arachidonate (20:4), but not saturated fatty acids such as myristate (14:0), palmitate (16:0), stearate (18:0), or arachidate (20:0) [253].

5. Post-translational modification of mammalian PLDs

5.1. Palmitoylation, and ubiquitination

Both mammalian PLD1, and PLD2 are palmitoylated with important consequences for localization and regulation. The PLD1 [115,130], and PLD2 [254] PH-domains are palmitoylated on cysteine residues: a modification requiring a full-length, catalytically competent protein [255]. Mutation of cysteines –240 and –241 of human PLD1 didn't significantly alter *in vitro* activity, but decreased activity *in vivo*. This was associated with decreased perinuclear-localization, and a concomitant increase in plasma-membrane localization [130]. Mutation of corresponding rat PLD1 residues decreased basal activity and membrane localization, and also reduced levels of PLD1 serine and threonine phosphorylation [256]. Palmitoylation of rat PLD1 required association of the N- and C-termini of the PLD protein [256]. In addition to palmitoylation, PLD is also regulated by ubiquitination. The PLD1 (but not PLD2) PH-domain is multi-monoubiquitinated in a manner requiring catalytic activity and palmitoylation. Ubiquitination targets PLD to the proteasome for degradation likely serving to reduce lipase activity [231].

5.2. Phosphorylation

PLD1 and PLD 2 are phosphorylated on serine (S)-, tyrosine (Y)-, and threonine (T) residues [141,163,257–259]. Confusingly, basal *in vitro* and *in vivo* PLD activities are frequently insensitive to mutation of phosphorylation sites, suggesting phosphorylation alters localization and substrate/ regulator access, rather than activity. Many observations are also complicated by the failure of studies to address the possibility of intermediate kinases.

Casein kinase II, a serine-threonine-selective kinase, phosphorylates PLD1 (S911) [260] and PLD2 (on multiple sites *in vitro*) [261], but does not affect catalytic activity. The kinase complexes with both proteins and is suggested to stimulate U87 glioblastoma cell proliferation through a PLD-dependent mechanism [261]. PLD1 S505 is phosphorylated by AMP-activated protein kinase (AMPK), a modification required for *in vivo* glucose-stimulated PLD activity [262]. Similarly, cyclin-dependent kinase 5 (Cdk5)-mediated PLD2-S134 phosphorylation regulates EGF-stimulated insulin secretion in rat insulinoma cells [263]. PLD1 T147 is phosphorylated by the p90 ribosomal S6 kinase, an event required for stimulation of PLD activity in PC12 neuroendocrine cells by K^+ , a process in which PLD is stimulated following K^+ -mediated depolarization of membranes, and subsequent increase in cellular Ca^{2+} [264]. Association of the rat PLD1 N- and C-termini occurs *in vivo*, through conserved residues in the HKD domains. Association is required for palmitoylation of cysteine residues C240 and C241, which in turn is essential for widespread serine / threonine phosphorylation, possibly by direction of rat PLD1 to a kinase containing membrane fraction [103,256]. Serine/ threonine phosphorylation does not appear to be required rat-PLD1 activity, or for its stimulation by PKC, or small GTP-binding proteins but did localize

it exclusively to the membrane fraction [103]. An inhibitory role for phosphorylation may exist for PLD2. PLD2 over-expressed in HeLa cells was phosphorylated on serine and threonine residues, following treatment with the phosphatase inhibitor okadaic acid. This resulted in a concomitant inhibition of PtdIns(4,5)P₂-stimulated PLD2 which was not due to alteration of PtdIns(4,5)P₂ affinity [265].

Tyrosine phosphorylation also regulates PLD activity. The tyrosine phosphatase inhibitor vanadate increases PLD activity in HL60 granulocytes [266] and both fMLP-stimulated PLD activity and tyrosine phosphorylation are increased in neutrophils, in a manner inhibited by tyrosine kinase inhibitors [267]. PLD2 is tyrosine phosphorylated and confusingly dephosphorylation of PLD2 by tyrosine phosphatases is reported to both increase [268], and decrease [269] *in vitro* activity. PLD2 is tyrosine phosphorylated following EGF-stimulation [270–272], and since the mutations Y11A [272], or Y296F [270] increase EGF-stimulated PLD activity, phosphorylation of the residues appears to down-regulate activity. The tyrosine kinases Janus kinase 3 (JAK3), and Src phosphorylate PLD2 at Y415, and Y511 respectively [270]. Phosphorylation of Y415 stimulates PLD2 activity, while phosphorylation of Y511 is inhibitory [270]. Tyrosine phosphorylation of the PLD2 PX-domain residues Y169 and Y179 regulate SH2 domain-mediated binding to the adaptor protein Grb2 (Growth factor receptor bound protein 2). This in turn, recruits the proline rich C-terminus of the Ras GEF SOS (son of sevenless), *via* the Grb2 SH3-domain. This stimulates Ras, coupling EGF-stimulation to Ras activation, and increasing PLD2 activity. Y169 and Y179 act as Grb2 docking sites, with a level of redundancy. Mutation of either residue reduces Grb2 binding, while dual mutation abolishes it. The two residues appear to regulate distinct functions however, Y179 being dispensable for PLD2 activity while mutation of Y169F ablates it [273]. Furthermore, while both residues serve to bind Grb2, a Y179F but not a Y169F mutant could stimulate Ras activity. Transient over-expression of PLD2 Y179F additionally upregulates p21, Ras, Erk activity and increases cell proliferation, indicating that Y179 of PLD2 has a negative roll in Ras-mediated regulation of cell proliferation [273]. Interaction with Grb2 through PLD2 Y169, additionally plays an important role in regulation of PLD2 phospholipase activity, and localization. Cos 7 cells constitutively expressing Grb2 shRNA had significantly reduced PLD2 activity and PLD2 over-expressed in these cells localized to the cytoplasm and to a peri-nuclear localization to a lesser extent. Following co-transfection with an shRNA resistant Grb2 construct, PLD2 relocated to the perinuclear/ Golgi region upon EGF-stimulation. Endogenous PLD2 and Grb2 also co-localized in Huvec cells [274], Akt (protein kinase B) also phosphorylates PLD2 on threonine 175 and mutation of this residue (T175A) inhibits the PLD2 Y179F mutant from stimulating Ras, suggesting these residues allow PLD2 to fine-tune Ras signaling [275]. The phosphorylation state of PLDs may have relevance to disease. Tyrosine kinases are frequently upregulated in cancer, and a proteomic study examining global phosphotyrosine changes in cells overexpressing constitutively-active, transforming nucleophosmin-anaplastic lymphoma-kinase indicated increased phosphorylation of PLD 1 (Y711), and PLD2 (Y573) [276].

5.3. Regulation of mammalian PLDs by protein kinase C

Phorbol esters including Phorbol myristate acetate (PMA), which mimic the PKC-product DAG, stimulate PLD activity in a range of cell lines and tissues [277,278]. PLD1 is activated

by both PKC α , and PKC δ *in vitro* [279], and while the high basal activity of PLD2 appears unresponsive to PKC in some systems [89,101,280] in others it is inhibited by PKC-inhibitors, or stimulated by PKC, or PMA [163,281–283]. Over-expressed and endogenous PKC α and PKC δ co-immunoprecipitate with over-expressed PLD1 and PLD2, in SF9 cells, in a PMA potentiated manner [283]. Similarly, endogenous PKC α and over-expressed PLD1 co-immunoprecipitate in COS-1 cell lysates, and endogenous PLD1, and PKC α co-immunoprecipitate in NIH3T3 cell lysates [284]. Purified PKC α and PLD1 interact directly [178,284], and SPR indicates this occurs in the absence of exogenous phorbol ester, ATP, or GTP γ S [178]. The PLD1 PKC-binding site is N-terminal to the PX-domain [153], while PKC α requires both its regulatory and catalytic domains and the phenylalanine residue 663. The interaction is independent of PKC-kinase activity, occurring in the absence of ATP *in vitro*. Consistent with this, truncated PKC devoid of the catalytic domain activates PLD [247,286].

PKC phosphorylates PLD but the function *in vivo* is unclear, in many cases having little to no effect on activity [140,277]. Furthermore, many observations appear highly dependent on cell system, stimulus, and PKC-isoform, and the possibility exists of intermediate proteins [163]. In neutrophil membranes, PKC α stimulation of PLD requires ATP and is inhibited by staurosporine, a nonselective kinase inhibitor [257], suggesting PKC α directly phosphorylates PLD, or phosphorylates an intermediate PLD activator. However, in fibroblast membranes, PKC stimulated PLD1 activity through direct protein-protein interaction and not phosphorylation [277]. Proteomic analysis revealed PMA-stimulated PKC phosphorylates PLD1 on S2, S561, and T147, mutation of which results in slightly decreased PMA-stimulated PLD activity *in vivo*, but not *in vitro* [141]. Although dispensable for activity, S2 phosphorylation is required for receptor-stimulated actin association [259], PLD2 is phosphorylated at S134, S146, S243, T72, T99, T100, and T252 following COS-7 cell PMA-stimulation [258]. S243 and T252 were the predominantly phosphorylated residues but their mutation did not inhibit PMA-stimulated PLD activity [258]. Some studies suggest PKC phosphorylation of PLD is required for cell-surface receptor mediated PLD stimulation. For example, PLD1 T147 phosphorylation and activity increased rapidly following COS-7 cell EGF-stimulation, which is ablated by expression of dominant-negative PKC α , or mutation of the phosphorylation site [281]. In contrast, other studies suggest PKC-mediated PLD phosphorylation down-regulates PLD activity. For example, PMA rapidly stimulated PLD1 [285] and PLD2 [282] activities in COS-7 cells, but PLD phosphorylation only increased after a much longer period of stimulation, and this correlated with decreased activity [279,282,285]. Furthermore, phosphorylation of PLD2 serine and threonine residues following COS-7 cell PMA-stimulation was not required for PLD2 activity, since a kinase-dead PKC mutant acted as a more potent activator. Nor was it required for PMA-potentiated PLD2-PKC interaction, but rather served to down-regulate PLD2 activity [282]. Further evidence of PKC mediated PLD inhibition comes from the observation that the PKC-inhibitor staurosporine prolongs PMA-stimulated PLD activity [285], and PKC α / β inhibitors block phosphorylation, but not PMA-stimulated activity [282]. Furthermore, PLD inhibition by DGK ζ occurs through a mechanism that appears to involve it complexing with PKC α [234,287,288]. The dual, positive and negative regulation of PLD by PKC-mediated phosphorylation has led to suggestion that different PKC isoforms

perform these capacities, activated by different agonists [163]. For example, EGF may only activate positive regulators like PKC α , while PMA may activate multiple isoforms, including negative PLD1 regulators such as PKC δ [281,289]. Further complicating matters, individual PKC isoforms may behave differently depending on the PLD isoform. As an additional level of regulation, PKC also regulates PLD by influencing its expression levels. PMA selectively upregulated PLD1 but not PLD2 expression in HCT116 colorectal cancer cells, with upregulation being ablated following pre-treatment with PKC-inhibitors [280]. Regulation of PLD by PKC may also link PLD to Phospholipase C (PLC) signaling. PLD activation is frequently accompanied by stimulation of both PLC, and PKC is suggested as a potential link between these pathways [247], since PKC inhibition downstream of PLC blocks PLD stimulation [290].

6. Regulation of mammalian PLDs by small GTPases

6.1. PLD regulation by Arf proteins

Ras superfamily GTPases were the first proteins demonstrated to directly activate PLD. The first to be described was Arf, which was identified as a cytosolic factor capable of activating PLD in HL60 cell membranes, that was essential for GTP γ S-dependent stimulation [66]. The Arf inhibitor Brefeldin A, or over-expression of dominant negative Arf1, or Arf6, block PLD-stimulation [178,247,291]. Furthermore, numerous studies demonstrate *in vitro* stimulation of PLD activity by Arf1-[66,67,279,292], and both *in vitro* [66], and *in vivo* stimulation of PLD activity by Arf6 [178]. Early studies suggested Arf only stimulated PLD1 [89] however, later studies indicated a 2-fold stimulation of PLD2 above its high basal activity, with GTP γ S-activated Arf [90,130], compared with 4–6 fold stimulation of PLD1 [292].

ARF proteins are reported to bind PtdIns(4,5)P₂ [295], and PtdIns P₂ stimulates both ARF guanine nucleotide exchange, and ARF GAP activity [296]. A relationship between Arf6, PLD2 and PtdIns(4)P- 5-kinase I α is proposed [181], and several studies have indicated ARF-mediated PLD-stimulation is dependent on PtdIns(4,5)P₂, inciting speculation that Arf indirectly activates PLD by PtdIns(4,5)P₂-dependent membrane phospholipid head group rearrangement [47,297]. However, other studies report Arf-mediated PLD activation in the absence of PtdIns(4,5)P₂ [47,293,294], suggesting alternate or additional mechanisms of activation. PLD1b co-localizes with Arf6 at the plasma membrane in stimulated RBL-2H3 cells [178,247], and Arf1 in COS-1/-7 cell Golgi [298]. PLD1b bound Arf1 in an SPR study [178] and both Arf1 [299], and Arf6 [178] co-immunoprecipitate with PLD1. Since Arf activates N-terminally truncated PLD1 [292] and PLD2 [101] the Arf-binding site is likely elsewhere on the protein. The Arf N-terminus is believed to contain the PLD-interaction site, and Arf1 lacking the N-terminal 17aa no longer stimulates PLD1 activity [300,301]. Arf is myristoylated in this region and although PLD activation does not require this modification, stimulation is enhanced by it [66,69]. Arf myristoylation only appears to be required for certain PLD functions, being required for fMLP, but not GTP γ S-stimulated PLD activity [302,303]. Synergistic stimulation is also observed when Arf is combined with other Rho family GTPases and PKC [292], and PLD1b co-localizes with Arf6, Rac1, and PKC γ following plasma membrane translocation *in vivo* [178,247].

6.2. PLD regulation by Rho family members

Pretreatment with the Rho GTPase inhibitors *Clostridium difficile*- or *C. botulinum* C3 toxin blocks PLD activation [304], and RhoA, Cdc42, Rac1, and Rac2 stimulate PLD activity *in vitro* [71,178,247,279,305–307]. Rho, Cdc42, and Rac1 are proposed to be PLD 1-selective binding activators, stimulating substrate-binding affinity [292]. Direct binding of Rac1 to PLD1 has been demonstrated by SPR [178]. PLD1 lacks Cdc42 and Rac-interactive binding (CRIB)-, or Rho-binding Rho effector (REM) motifs [308], with Rho instead interacting *via* residues in the PLD1 C-terminus, within domains III and IV [100,237,309,310]. Rac2^{-/-} mice also show reduced PLD1 activity suggesting this isoform may also regulates PLD1 [311]. Rac2 regulates PLD2 through a dual, positive and negative, biphasic-mechanism during leukocyte chemotaxis [311]. GTP-bound Rac2 binds PLD2 through two poorly conserved Cdc42 and Rac-interactive binding (CRIB) motifs in the region of the PLD2 PH-domain [311–313]. PLD2 acts as a Rac2 GEF switching Rac2 from a GDP-bound inactive state to a GTP-bound active state, through a mechanism which requires the Rac2-binding, PLD2 CRIB motifs [146,313]. PLD also influences Rac activity through PtdOH-production aiding dissociation of the Rho-specific guanine nucleotide dissociation inhibitor (Rho GDI), facilitating Rac 1/2 plasma membrane association [314]. As such, a mechanism has been proposed in which rapid activation of a Rac2-PLD2 positive feedback loop occurs during onset of chemotaxis. This is followed by a second phase in which PLD2 activity is decreased, potentially by competitive binding of the PLD2 PH-domain region between GTP-bound Rac2 and PtdIn4,5P₂, or by limitation of PLD2's association with the membrane [311–313]. PtdOH additionally recruits and stabilizes interaction of the Rho family GEFs DOCK1/2 (dedicator of cytokinesis 1/2), and Tiam1 (T-lymphoma invasion and metastasis-inducing protein 1) to the plasma membrane, through their C-terminal PtdOH-binding polybasic motifs [208,313,315,316]. The Ras-GEF Sos (son of sevenless) also binds PtdOH and is recruited by PLD2 leading to Ras activation [273,317].

Other small GTPases play roles in PLD regulation and activity including Rheb (Ras-homology enriched in brain), which activates PLD1 *in vitro* [318] and RalA (Ras-related protein A), which increases PLD1 activity *in vitro*, and co-immunoprecipitates with PLD1, but not PLD2 [299,319]. The RalA interaction site maps to a site independent of Arf interaction, allowing synergistic PLD1 activation [299].

6.3. Proteolysis of mammalian PLD, and apoptotic signaling

Mammalian PLD1 and PLD2 are substrates for caspase cleavage, a process linked to apoptotic signaling [47,96]. Both isoforms are cleaved *in vitro*, and *in vivo* by caspases 3 and –8, with PLD1 additionally cleaved by caspase 7 [94,95]. Analysis of Alzheimer's patient brain tissue demonstrated caspase 3 activation and caspase-proteolyzed PLD1 fragments [95]. Caspase 3 cleaves PLD1 at aspartic acid residues D41, D545 and D581 *in vitro*, and at D545 *in vivo* where this is the dominant cleavage site [95,96]. D545 cleavage cuts PLD1 within the loop region yielding a 56-kDa C-terminal fragment (CF-PLD1), which localizes to the nucleus *via* an exposed nuclear localization sequence (NLS), and a 60-kDa cytosolic N-terminal fragment (NF-PLD1) [95,96,173]. Full-length PLD1 protects against apoptosis *via* suppression of p53 signaling, but *in vivo* PLD1 activity is suppressed by the dominant negative action of NF-PLD1, resulting in p53 de-repression and induction of

apoptotic signaling [96], The PLD1c splice variant which possesses an early stop codon at amino acid 513, is expressed in human brain and may also function in a pro-apoptotic mechanism, similar to NF-PLD1 [91]. CF-PLD1 generated during apoptosis is imported into the nucleus *via* association of its NLS with importin- β [95,170,173]. Residues in the N-terminal HKD motif target PLD1 to vesicles, and mutation studies have indicated that when the residues are absent the protein's association with importin- β increases [320]. Full-length PLD1 also possesses a NLS and is partially imported into the nucleus [96,173] where it mediates PKC α , and extracellular signal-regulated kinase (ERK) activation, a function which CF-PLD1 is unable to perform [173]. The ability of caspase-cleaved fragments to interact with each other, or the intact enzyme appeared likely given that separate PLD1 N- and C-terminal fragments can associate to form an active enzyme [102]. It is now known that the caspase-cleaved fragments interact *via* hydrophobic residues within the catalytic motifs and that this inhibits CF-PLD1's nuclear import [170,320].

Like PLD1, the PLD2 isoform is also anti-apoptotic, with PLD2 inhibition or knockdown increasing apoptotic signaling. This likely occurs *via* induction of anti-apoptotic protein expression (Bcl-2 and Bcl-XI), and down-regulation of pro-apoptotic proteins (Egr-1, and PTEN) [47]. Caspase-3 cuts PLD2 at multiple sites upstream of the PX domain (13–28aa), although the function of this is unclear, resulting in no significant changes in molecular weight, localization, apoptotic signaling, or catalytic activity [94,96].

7. Mammalian PLD function

Despite years of study, the precise nature of mammalian PLD function is still being elucidated. While largely believed to generate localized PtdOH pools, the observation that PLD can interact with over 30 different proteins has invited speculation of additional non-enzyme functions, including scaffolding roles [190,191]. PtdOH comprises about 1–4% of total cellular lipid [321] and plays both structural, and signaling roles. Complicating the study of PLD function is the fact that PtdOH can also be generated by *de novo* synthesis through: 1) sequential acylation of glycerol-3-phosphate [322–324], an important step in the Kennedy pathway for generation of glycerophospholipids [325]; 2) through the acylation of lysophosphatidic acid (LPA) by LPA acyltransferase (LPAAT), or 3) phosphorylation of DAG by DAG-kinase (DGK) [47]. For example, despite PLD activity being stimulated immediately following purinergic (P2Y₆) G-protein-coupled receptor (GPCR) stimulation, the majority of PtdOH generated is *via* DGK ζ [234]. The small negatively charged headgroup and resultant conical-shape of PtdOH intrinsically induce negative membrane curvature. This is believed to lower the activation energy for fission of membrane vesicles, and for their fusion with cell membranes [326]. Importantly, PtdOH acts as a signaling node, recruiting binding proteins including the GEFs: DOCK2 and SOS, which activate Rac1 and Ras, respectively [191,315,317], and the mammalian target of rapamycin (mTOR) [327]. PtdOH also mediates translocation and activation of the Raf-1 (c-Raf) serine/ threonine kinase [328–331]. Multiple cAMP-specific phosphor-diesterase (PDE) 4 family members are also regulated by PtdOH, with PDE4A5; PDE4D3 and PDE4EB1 being stimulated by PtdOH *in vitro* [332], and PDE4D3 binding PtdOH directly [333]. PDE4A1, while not activated *in vitro* by PtdOH [332] requires PtdOH-binding through its N-terminus for

membrane localization [298]. These interactions may indicate a PLD role in terminating G-protein coupled receptor signaling by metabolism of the second messenger cAMP [163].

While PtdOH production may represent a general PLD function, precise spatial and temporal regulation of this activity likely contributes to isoform specific functionalities. Mammalian PLD1, and PLD2 are implicated in a wide range of overlapping and isoform specific functions (see Fig. 3). PLD1 is implicated in vesicular trafficking [334,335] and exocytosis [175,336,337]. PLD1 and PLD2 are both implicated in anti-apoptosis [47,338], and PLD2 in endocytic recycling [339–341], PC 12 cell differentiation [342], actin-based membrane dynamics [181] and LI (neuronal cell adhesion molecule L1 or L1CAM)-dependent neurite outgrowth [343]. A PLD2 role as a guanine nucleotide exchange factor for Rac2 is now also recognized [146] (see Tables 1 and 2).

7.1. The role of mammalian PLDs in receptor signaling/ trafficking

PLD activity is stimulated by many receptor agonists including the receptor tyrosine kinase (RTK) agonists EGF [163,344] and PDGF [345], as well as by the cannabinoid type 1- [346]; D2 dopamine- [347]; endothelin-1 (ET-1) [345]; P2Y purinergic- [234,348–350]; formyl peptide- [41]; angiotensin II- (AngII) [345] and μ -opioid- [341] GPCRs. In turn, PLD activity and PtdOH are implicated in multiple aspects of receptor trafficking, including PtdOH's role in recruiting cellular machinery required to facilitate receptor endocytosis/exocytosis events [351], and induction of membrane curvature [5,134,352]. PLD activity is implicated in EGFR [353]; μ opioid- [341,354]; mGluR1a- (metabotropic glutamate) [355], angiotensin II type 1- [168] and FcyRI-receptor internalization [97,334]. The plasma membrane localizations of PLD2, and stimulated-PLD1, ideally posit them to influence vesicular trafficking at this location and both mammalian PLD1, [353,356,357], and PLD2 [168,339–341,358] regulate receptor endocytosis. EGF-receptor (EGFR) internalization and degradation are enhanced by overexpression of either isoform, and are inhibited by expression of catalytically inactive PLD1/2 mutants, the presence of primary alcohols, or inhibition of the RalA, or PKC PLD-activators [353,356,357]. PLD1 opposes the action of hypoxia-inducible factor 1 α (HIF1 α), a negative regulator of EGFR endocytosis [357]. Following EGF-stimulation, PLD1 promotes degradation of HIF1 α , in a manner requiring the PLD1 PH-domain. This increases expression of the Rab-effector Rabaptin 5 and accelerates EGFR internalization [357]. PLD2 co-immunoprecipitates with EGFR [272], and PLD2 over-expression increases EGFR mRNA and protein-levels, stabilizing mRNA and preventing it from decay, and inhibiting internalized-EGFR degradation [359]. Dynamin plays a vital role in endocytosis and both PLD1 and PLD2 bind to its GTP-bound form stimulating GTPase activity through PLD PX-domain dependent GAP activity [147]. Expression of either PLD1- or PLD2's isolated PX-domain stimulated EGFR endocytosis, similar to PLD1 or PLD2 overexpression [353,360]. Knockdown of both PLD isoforms with siRNA decreased EGFR endocytosis in a manner rescued by catalytically inactive PLD expression [147], suggesting PLD influences clathrin-endocytosis independently of PtdOH, or downstream DAG production. In addition to EGFR, PLD2 regulates endocytosis of the transferrin-receptor [339] and GPCRs [341,361,363] such as the angiotensin-[168], metabotropic glutamate –1 and –5 [355], β 2-adrenergic-, M3 muscarinic- and μ -opioid receptors [341,354,362,364]. PLD proteins likely regulate the endocytic process on multiple

levels, for example PLD derived PtdOH may induce negative membrane curvature at neck of endocytosing vesicles, while the PLD PX-domain acts to stimulate dynamin, facilitating vesicle scission [365]. In the case of the μ -opioid receptor, whose C-terminus interacts with PLD2, receptor endocytosis requires conversion of PLD2 derived PtdOH to DAG [341,354].

In addition to roles in endocytosis, PLD is also linked to Golgi/ TGN clathrin-coated vesicle formation [179] as well as COPI vesicle budding and tubulation [10]. PLD is also linked to clathrin-independent endocytic recycling, a process which requires Arf6 activation to recycle membrane proteins back to the PM [364,366–369]. Consistent with this, expression of an Arf6 effector domain mutant (N48R), which is unable to activate PLD activity, but is otherwise functional in terms of GEF/ GAP regulation and ability to activate PtdIns4P 5-kinase, caused an endosomal-tubule build-up in HeLa cells. This phenotype is consistent with a recycling defect, and is similar to that observed following inhibition of PtdOH production with butan-1-ol [211,352,370]. The Arf6 mutant (N48R) induced recycling block could be relieved by PMA treatment, (PLD being activated by PKC, bypassing the requirement for Arf6) [371]. Propranolol treatment which blocks PtdOH to DAG conversion, broke tubular recycling endosomes into vesicles, but didn't relieve blockage of vesicle fusion with the plasma membrane, suggesting a PtdOH-derived DAG role in vesicle fusion [365]. PLD2 has been linked to recycling, depletion of this isoform but not PLD1 inhibiting transferrin receptor recycling from the endocytic recycling compartment (ERC), but not receptor internalization in HeLa cells [339]. PLD2-mediated recycling required EFA6 (exchange factor for Arf6) an ARF6 GEF, which coordinatinates both this process, and membrane ruffling [372].

PLD is also required for exocytosis including: nascent secretory vesicle release from the TGN [175,373–377], exocytosis of myeloperoxidase (MPO) [378,379], IgE-receptor degranulation [380], and PLD1-regulated secretion of von Willebrand factor [381]. The exocytotic mechanism is reported to involve secretory carrier-associated membrane protein 2 (SCAMP2) interaction with Arf6 and PLD1, linking them to exocytotic fusion pore formation [382], in which the serine/ threonine kinase ribosomal protein s6 kinase (RSK2) and PtdOH are essential [199,383]. However, many studies linking PLD activity with the exocytotic process have been called in to question since the departure for using primary alcohols to block PtdOH production. More recent studies using the PLD1/2 inhibitor FIPI and PLD KO mice have indicated that PLD is not required for degranulation/ secretion from mast cells, or neutrophils [210,212].

In addition to roles in vesicular formation, PLD2 plays an important role in in structural maintenance of the Golgi, and lysosome, and PLD2 (but not PLD1) specific inhibitors [179], primary alcohols [8,179], PLD2 siRNA [10] or catalytically inactive PLD2 mutants [384], cause dramatic morphological changes to these organelles.

7.2. PLD's role in cell motility and cytoskeletal regulation

PLD activity and PtdOH are linked to mammalian cytoskeletal regulation and remodeling, and are key regulators of cell motility [13,14,89,385–389]. Mammalian PLD1 and PLD2 are both implicated in these processes. PLD activation stimulates actin stress fiber formation in fibroblasts [390] and endothelial cells [14], a PLD1 mediated event [391], while both PLD1

[392–394] and PLD2 [393] are involved in adhesion, cell spreading [395] and membrane ruffling [11,358] in leukocytes. The role of PLD in motility is evolutionarily conserved, being required for motility of algal monospores [396,397] and the slime mold *Dictyostelium* both of which are inhibited by primary alcohols, the latter being reversible by addition of exogenous PtdOH [398].

PLD's small GTPase regulators, such as Rho, Rac, and Arf6 have well established roles in actin rearrangement, cell motility, and wound healing [247,399]. Consequently, it is perhaps unsurprising that many of PLD's roles in these phenomena are tightly linked to GTP-binding protein activities, for example Arf6-stimulated MDCK cell migration occurs through Rac- and PLD activation [399], and antigen-stimulated mast cells exhibit Arf6-, and PLD2-dependent membrane ruffles [171]. Many PLD-mediated roles in cytoskeletal modulation and cell-motility occur through downstream effectors, and in addition to PLD activity being regulated by small GTPases, PLD has also been observed to act upstream of the small GTPase Rac, a major regulator of cytoskeletal rearrangement required for cell-spreading and migration. PLD-derived PtdOH targets and anchors Rac1-GTP to the plasma membrane [400], through the Rac C-terminal polybasic motif. Rac mutated in this region cannot translocate, nor initiate integrin-activated, downstream-activation of p21-activated kinase (PAK) proteins, which have known roles in cytoskeletal rearrangement, motility and filipodia formation [400]. The role of PLD2 in stimulation of membrane ruffling and subsequent motility have been closely linked to its relationship with Rac2, and the Grb2 (Growth receptor bound 2) adaptor protein [144,388,401]. The PLD2 PX-domain residues Y169, and Y179 interact with the Grb2 SH2 domain [274]. This interaction is reported to have major implications for PLD2 biology, being required for both PLD2 phospholipase activity, and its ability to re-localization to COS-7 cell Golgi, from the cytoplasm, following EGF-stimulation [274]. PLD2 and Grb2 co-localize in the actin-rich membrane-ruffles of macrophages, and play a role in the formation of these structures in resting and stimulated cells. PLD2 derived PtdOH was necessary but insufficient for the formation of these structures, requiring Rac-2 (Or Rac-1 to a lesser degree) for complete membrane ruffling induction [144]. Rac-2 is an activator of ARP2/3 which polymerizes actin and the three components coordinate to stimulate actin polymerization and membrane ruffling [144]. A model has been proposed in which PLD2 is targeted and activated at sites of membrane ruffling by Grb2, stimulating local PtdOH production. Rac2 a known PtdOH binding protein [580], associates with these proteins at the ruffle site enhancing membrane ruffle formation. In addition, Grb2 also links PLD2 to regulation of the actin nucleating Arp2/3 complex by promoting interaction of PLD2 with the Wiscott-Aldrich syndrome protein (WASP), which binds and activates Arp2/3, and is recruited to the plasma membrane during this process, enhancing phagocytic cup formation [401]. PLD2-and Grb2 also complex with the protein tyrosine phosphatase 1b (PTP1b), which serves to stimulate PLD2 activity [268]. PTP1b's role in cell adhesion and motility is complex, and seemingly dependent on cell type, and regulatory context, both positively, and negatively regulating these processes [402]. In general, PTP1b appears to positively affect cell motility associated with integrin-dependent signaling stimulation, and negatively regulates motility by antagonizing growth factor receptor tyrosine kinase signaling [402]. PLD2-, and to a lesser extent PLD1-derived PtdOH also bind and activate ribosomal S6 kinase (S6K) mediating actin polymerization, and

facilitating motility [388,389,403,404]. Mammalian PLD is also linked to cytoskeletal regulation and remodeling through PtdIns4P 5-kinase, a protein which both produces PtdIns(4,5)P₂ stimulating PLD activity, and is itself regulated by PtdOH [181,392]. The type I γ PtdIns4P 5-kinase isoform is implicated in cell motility, interacting with talin, and regulating focal adhesions [405,406]. Expression of dominant negative phosphatidylinositol PtdIns4P 5-kinase I γ b inhibited over-expressed PLD2's ability to stimulate cellular adhesion [392]. Antibodies against β_1 and β_2 integrins blocked PtdOH-, and PtdIns(4,5)P₂-stimulated adhesion inviting postulation that PLD-derived PtdOH stimulates PtdIns4P 5-kinase I γ b regulating integrins through PtdIns(4,5)P₂ production [392].

In addition to interacting with the cytoskeleton through binding partners and downstream effectors, PLDs also directly interact with cytoskeletal components. Furthermore, while PLD activity promotes cytoskeletal rearrangement, PLD itself can be regulated by cytoskeletal elements. Mammalian PLD activity is regulated bidirectionally by actin, with monomeric actin inhibiting activity and filamentous activity promoting it [407]. Stimulated PLD1 associates with actin, binding both monomeric and filamentous forms [407], and stimulated PLD2 translocates to filopodia [89], and membrane ruffles [171,181], co-localizing with cytoskeletal elements [92] including actin [176]. PLD2 activity is inhibited following actin binding, a process reversed by Arf1 *in vitro* [176].

7.3. The role of mammalian PLD in respiratory burst

Mammalian PLDs are implicated in pathogen induced reactive oxygen species (ROS) production, during which the membrane-bound nicotinamide adenine dinucleotide phosphate (NADPH) -oxidase is activated during respiratory burst, producing superoxide radicals in immune cells used by the host in pathogen defense [408]. Historically, many studies implicated PLD in this process [409], since primary alcohols blocked ROS production [184,378,410]. However, demonstration that: 1) the dual PLD1/ PLD2 inhibitor FIPI didn't affect respiratory burst stimulated by the GPCR fMLP, 2) that PtdOH generated in this process is through PLC/ DAG kinase, 3) that primary alcohols inhibit superoxide production through a mechanism independent of PLD activity [216], and 4) PLD^{-/-} neutrophils could also generate fMLP induced superoxide [210], resulted in PLDs role in this process being called into question. However, more recent experiments using bone marrow-derived primary neutrophils isolated from the PLD2^{-/-} knockout mouse, combined with use of isoform specific inhibitors, have demonstrated a role for PLD1 in regulation of phorbol ester-stimulated, adhesion-dependent, chemoattractant-, and Fc γ -receptor-stimulated ROS production, indicating a role for at least this isoform in these processes [184]. The precise mechanism by which PLD regulates ROS production however still remains to be elucidated, and is somewhat confusing since the response to FMLP is enhanced by removing PLD activity, compared to the results with PMA indicating that PLD activity may only regulate specific ROS pathways [184].

7.4. Mammalian PLD and mTOR activation

The target of rapamycin (TOR) is a serine/ threonine kinase, which is highly conserved throughout the eukaryotes. It controls cellular metabolism and growth, in response to nutrients, growth factors and stress [411]. PLD and PtdOH have been implicated in

mammalian TOR (mTOR) activation, and a PLD requirement has been demonstrated in serum, phenylephrine, and mechanically induced mammalian target of rapamycin (mTOR) signaling [327,412–415]. Following cell entry, rapamycin complexes with FK506-binding protein of 12 kDa (FKBP12) and binds the mTOR FKBP12-rapamycin binding (FRB) domain, inhibiting mTOR signaling [416–418]. PtdOH also interacts with this region and may compete for binding, being expected to increase resistance to rapamycin inhibition [327,419]. However, many studies addressing the role of PLD activity in mTOR regulation historically employed primary alcohols, and they should be viewed in the context of the caveats now known to be associated with that methodology. Furthermore, despite numerous studies implicating PtdOH's role in the mechanical induction of mTOR signaling, the role of PLD in this process is debated as the time courses of mechanically induced PLD activation and PtdOH production don't correspond [420]. PLD activity is elevated for the first 15 min following mechanical induction, before returning to, or decreasing below control levels. In contrast, PtdOH levels increase over the first 30 min ultimately reaching an elevated steady state. Specifically, PLD activity at 15–30 min post induction is 27% lower than in an unstimulated muscle control, while PtdOH levels are elevated 138% and 187% above the control at 15- and 30 min respectively [413]. These data do not rule out the possibility that PLD is involved in the early response to mechanical induction, but do indicate that PLD activity cannot account for the majority of the PtdOH response. Moreover, the observation that the dual mammalian PLD1/ PLD2 inhibitor FIPI blocked agonist-induced PLD activation, but didn't prevent mechanically induced PtdOH or mTOR signaling indicates a major role for these isoforms in mTOR induction is unlikely [415]. This is supported by the observation that while knockout of both PLD1 and PLD2 result in viable mice [42,184], knockout of mTOR is lethal [421,422]. As such, it seems increasingly likely that the PtdOH source required for mTOR activation primarily comes from sources other than PLD, primarily the LPAAT pathway [423]. However, interpretation of these findings is complicated by the observation that inhibition of PLD, can result in a compensatory elevation of PtdOH from undetermined sources [351]. It has also been speculated that the LPAAT pathway provides PtdOH required for nutrient sensing by mTOR, while PLD provides local PtdOH in response to growth factors, insulin and stress [423]. Since mTOR localizes to the lysosome under conditions of amino acid sufficiency [424], it has been postulated that PLD (particularly PLD1) may contribute to activation at this localization, particularly since the LPAAT pathway produces PtdOH at the ER, which is then moved by vesicular trafficking to other cellular locals [425]. Furthermore mTOR forced to localize to the lysosome in the absence of amino acids, could still be activated in the presence of the small GTPase Rheb [426], a known activator of PLD1 [318]. PLD has also been postulated to play a role in mTOR signaling in the context of cancer. Dysregulation of signaling pathways regulating mTOR are postulated to be the most common in a cancer setting and mTOR is critical for cancer cell survival [423,427]. The dysregulated pathways include the phosphatidylinositol-3 kinase/ AKT/ Rheb pathway [428]. PLD activity is upregulated in many cancers and is substantially increased in cells depleted of nutrients, particularly in cells harboring Ras mutations [423,429,430]. Mutation of Ras results in an increased requirement for exogenously supplied lipid due to compromised activity of stearyl-CoA desaturase-1, resulting in an inability of newly synthesized fatty acids to be desaturated, an essential requirement for membrane-targetted phospholipids [431,432]. Importantly, PLD

appears to supply PtdOH in the correct format for stabilization of mTOR. Dipalmitoyl - PtdOH containing two saturated fatty acids caused the mTORC2 complex to fall apart, in contrast to PtdOH containing palmitate (saturated) and oleate (mono-unsaturated), which stabilized mTORC1 and mTORC2 under conditions of PLD suppression [419]. As PLD produces its PtdOH from membrane PtdCho, the composition of the PtdOH produced would be more similar to the later condition, consisting of a saturated and unsaturated fatty acid. Elevation of PLD activity in the context of Ras mutation is therefore proposed to aid escape from a default apoptotic program, and since PLD is required for cell migration in the absence of serum, may also help them move to a more favorable environment [423,433].

7.5. PLD and lipid droplet formation

ARF-regulated PLD activity is linked to cell-free lipid droplet (LD) assembly [434], and assembly of very-low-density lipoproteins (VLDLs) [435,436], a process involving lipid droplet formation in the microsomal lumen [437]. PLD is also implicated in stimulation of LD-formation by fatty acids, particularly oleate. Fatty acids stimulate some PLD activities, and oleate is reported to stimulate LD-formation through activation of PLD and PI3kinase [172,252,253]. The PLD1 isoform (but not PLD2) is present in LDs, and increased PLD1 expression promotes LD formation, while PLD1 siRNA inhibits it [438,439]. PLD1 activity in LDs is reported to be stimulated by Arf1 [439], and in cell-free LD assembly PLD1 additionally required the extracellular signal-regulated kinase 2 (ERK2) [434,438,440]. PLD1 (but not PLD2) and ERK2 were essential factors for both basal and insulin-stimulated cytosolic lipid droplet production. Inhibition of ERK2 ablated PLD1's effect on lipid droplet formation, but did affect PLD1 activity. As such, PLD1 was proposed to act upstream of ERK2 [440]. ERK2 increases phosphorylation of the dynein cytoskeletal motor protein, increasing its translocation to adipose-differentiation related protein (ADRP)-containing LDs. Dynein plays a critical role in LD-formation, and microinjection of dynein antibodies strongly inhibits this process [438]. Excessive triglyceride accumulation in ADRP-containing LDs, especially in liver, and skeletal muscle, is associated with metabolic disorders including insulin resistance and type 2 diabetes [441,442], strong risk factors for cardiovascular disease. Lipid droplets are also linked to [443] arteriosclerosis and ADRP is the major LD associated protein in foam cells (lipid-loaded macrophages) associated with atherosclerotic lesions [444]. Consistent with a role in LD-formation, PLD activities are linked to obesity, diabetes [189] and to thrombotic disease [42,43,209].

8. Mammalian PLD isoforms and human health

As techniques for studying PLDs have improved, they have linked PLD activity to a number of disease states including thrombosis [42,43,209], Alzheimer's disease [37–41], multiple sclerosis [206,445] and a number of human cancers [162,446,447] (see Fig. 4). A finding perhaps unsurprising given the wide range of cellular processes in which PLD activities are implicated. The lack of severe phenotypes displayed by PLD knockout mice, and the apparent lack of overt toxicity of PLD1/2 inhibitors offers the hope that PLD specific inhibition may provide therapeutic potential [190].

8.1. PLD in vascular disease

Mammalian PLDs are linked to a number of vascular disease states including clotting disorders and atherosclerosis. Platelet aggregation is essential for hemostasis, and adhesion and activation of platelets at sites of vascular injury plays an essential role in limiting blood loss. These processes also form the mechanism underlying myocardial infarction and stroke [42], PLD1 and PLD2 are both expressed in platelets where they localize to ‘granule-like’ organelles. PLD1 being found through the platelet while PLD2 localizes to the platelet periphery, both isoforms redistributing to the plasma membrane upon activation and stimulation [42,448]. PLD1 is implicated in platelet activation, and stable thrombus formation under high shear forces, thrombi being unstable in PLD1’s absence, under rapid flow [42]. A key stage in platelet activation is activation of the integrin $\alpha_{IIb}\beta_3$ adhesion receptor, facilitating adhesion and aggregation. Mice lacking PLD1 display integrin $\alpha_{IIb}\beta_3$ activation, resulting in decreased fibrinogen binding and vascular thrombi formation [42]. PLD1’s role in this process is unclear but decreased integrin $\alpha_{IIb}\beta_{III}$ activation confers protection in stroke, pulmonary embolism and aortic thrombosis models [42,43]. Consistent with a role in regulation of the clotting process PLD activity is also linked to Von Willebrand disease, the most common inherited bleeding disorder, characterized by reduced blood-clotting which results from deficiency of the procoagulant and proinflammatory Von Willebrand clotting factor [449]. PLD1, (but not PLD2) regulates histamine-induced secretion of the prothrombotic Von Willebrand clotting factor from endothelial cells, which is inhibited by butan-1-ol or PLD1 RNAi [381]. The PLD2 isoform has also been linked to thrombus formation in a mouse, with both isoforms needing to be deleted for protection from FeCl₃-induced arteriolar thrombosis [209]. Dual deletion was also required to inhibit release of a granules, important factors in platelet biology with roles in clotting, and atherosclerosis [209]. PLD2 is also linked to blood pressure regulation, a key factor in thrombotic disease, facilitating endocytosis of the GPCR angiotensin [168] and subsequent release of the blood-pressure regulating hormone aldosterone in adrenal cortex cells [450,451]. The PLD2^{-/-} mouse displays increased blood pressure and decreased cardiac function due to decreased endothelial nitric oxide synthase (eNOS), resulting in decreased nitric oxide (NO), an important vasodilatory factor [581]. The decrease in eNOS appears to be a consequence of reduced free cholesterol in the PLD2^{-/-} mouse, resulting in an increase in HMG-CoA reductase, the rate limiting enzyme in cholesterol synthesis, and a negative regulator of eNOS [581]. Human PLD2 PX-domain small nucleotide polymorphisms (SNPs) were identified in a screen to identify polymorphisms associated with hypertension. R172C correlated with patients suffering from hypertension, while R98C was associated with decreased blood pressure and reduced hypertension risk [44]. Analysis of the R172C mutation has determined that this mutation likely results in partial loss of function, or altered function rather than complete PLD2 deficiency [581]. The role of mammalian PLDs in blood pressure regulation and thrombus formation makes them attractive drug targets for treatment of thrombotic disease, and inhibition of both PLD activities with the PLD1/2 inhibitor FIPI reduced occlusive thrombus formation following chemical injury in mice [452]. This was not associated with intracerebral hemorrhaging or increased duration of tail bleeding, suggesting pharmacological PLD-inhibition may provide a safe anti-thrombotic therapeutic strategy for ischemic stroke and arterial thrombosis [43,190]. However, it should be noted that hemostasis in mouse is less dependent on platelet activation than humans, and

this remains to be clinically tested [453]. Furthermore, application may be limited, since it was only effective when delivered prior to thrombosis, indicating inhibition may be useful for prophylactic treatment for high risk individuals, but less beneficial following thrombotic events such as stroke [190].

PLD is also implicated in atherosclerosis. During the atherosclerotic process exaggerated phagocytosis of lipids within the arterial wall leads to the accumulation of foam cells. Phagocytosis occurs through the uptake of low density lipoprotein (LDL). Foam cells containing LDL form atherosclerotic plaques which then act to restrict blood supply potentially resulting in stroke or peripheral arterial disease. Studies employing macrophages from PLD-deficient mice and specific PLD inhibitors have demonstrated that macrophage phagocytosis of cholesterol, and foam cell formation are less efficient in the absence of PLD2, demonstrating a role for this isoform in the formation of atherosclerotic plaques. PLD2 interacts with the Grb2-adaptor protein, actin, and WASP during macrophage phagocytosis of aggregated oxidized LDL (Agg-Ox-LDL) in the presence of CD36, and is proposed to act within this complex in the formation of the phagocytic cup, facilitating Agg-Ox-LDL uptake. PLD2 (but not PLD1), Grb2 and WASP are upregulated in diseased artery tissues indicating the potential *in vivo* relevance of these observations [454].

PLD activity has also been implicated in recovery following ischemia (reduced blood flow), which can occur as a result of multiple causes including vascular disease. In particular, PLD1 has been demonstrated to play an important role in tumor necrosis factor- α -mediated inflammation and scar formation following mouse myocardial ischemia, and reperfusion. Mice lacking PLD1 exhibited increased infarct size and reduced ventricular function, likely as a result of reduced tumor necrosis factor- α release, and altered interstitial collagen deposition [445].

8.2. PLD in viral pathogenesis

Host PLD activities are linked to pathogenesis associated with a number of human viruses [46,455–457]. Human PLD2 was identified in a whole genome RNAi screen for host genes required for influenza virus infection [457], a finding confirmed in cell culture models using isoform-selective PLD inhibitors [46]. Influenza infection stimulates PLD activity and PLD co-localizes with influenza virus during infection. PLD inhibition delayed viral entry and reduced viral titers with specific PLD2 inhibition correlating with significant increases in transcription of innate antiviral effectors. Reduction in viral titer following PLD2 inhibition was dependent on Rig-I (retinoic acid-inducible gene-1), IRF3 (Interferon regulatory factor 3) and MxA (myxovirus resistance gene A). Together these data suggest PLD facilitates rapid endocytosis of influenza virus, permitting viral escape from innate immune detection and effectors capable of limiting lethal infection. As such, PLD2 inhibition could potentially be used proactively, or subsequent to infection to limit disease progression [46]. PLD inhibitors also suppressed HIV-1 replication in activated T cells [455,456], and are proposed to block Ras/ERK signaling, activating the c-Myc transcription factor required to produce dNTPs required for viral replication during T cell activation [455,456]. These findings offer potential for therapeutic intervention for HIV-1 and other viral infections dependent on host nucleotide bio-synthesis [455].

8.3. PLD in cancer

Aberrant PLD/PtdOH signaling is observed in numerous human cancers, including those of breast, ovary, kidney and colon [162,446,447]. A range of PLD abnormalities have been observed including PLD mutation [458,459], increased abundance, and increased activity [47,162,447,458–464]. PLD is upregulated in cells transformed by oncogenes including v-Src [465], v-Raf [466], v-Ras [467] and V-Fps [468], and PLD activity was required for H-Ras transformation of Rat-2 fibroblasts [463]. PLD activity in cancer cells is linked to: increased metastasis and invasiveness [433,469–471], proliferative signaling [163,317,330,472], growth suppressor evasion [433,473–476], and resistance to cell death [477]. These findings are perhaps unsurprising, given the role of PLD activity in cancer-relevant processes such as cell motility, cytoskeletal rearrangement, [330], MMP-secretion [35,47,478] and regulation of mTOR [327,412–415]. While a consensus is emerging for PLD playing a pro-oncogenic role many older studies relied on inhibition of PtdOH production by primary alcohols and should be viewed with caution [163,190,479].

Mammalian PLD1 and PLD2 are both linked to cancer biology and isoform specific up-regulation is reported in a number of cancers including PLD1 in osteosarcoma [480], PLD2 in renal cancer [162], oleate-dependent PLD activity in breast cancer [460] and oleate-, and Arf-dependent activities in colon cancer [481]. PLD1 and PLD2 are linked to the prometastatic phenotype [482] with PLD1 in particular being implicated in metastasis and angiogenesis [43]. Isoform-specific PLD inhibitors decrease cancer cell invasion, migration, metastasis and angiogenesis [43,224,433,469], and specific inhibition of either PLD1, or PLD2, or both proteins inhibited invasion of highly metastatic breast cancer cells [224]. Furthermore, treatment of mice with the PLD1/ PLD2 dual inhibitor FIPI suppressed tumor growth and metastasis, and reduced growth of subcutaneously implanted B16F10 mouse melanoma cells into B16F10 tumors by 50% in PLD1^{-/-} but not PLD2^{-/-} mice [43]. PLD1 is required for metastatic tumor seeding and tumor vascularization with deficiency additionally impacting endothelial cell signaling [42]. Tumor platelet-interactions form an important stage in metastatic seeding, experimental metastasis being almost completely inhibited in a platelet-depleted host [483–486]. PLD1 deficiency impairs these interactions, reducing platelet-coating of tumor cells following stimulation by platelet-activating factors like PAR4-activating peptide or thrombin [43]. PLD1^{-/-} platelets, also display impaired $\alpha_{IIb}\beta_3$ integrin activation [42], and reduced metastasis was observed in PLD1^{-/-} mice after blocking $\alpha_{IIb}\beta_3$, suggesting a PLD role in facilitating $\alpha_{IIb}\beta_3$ mediated tumor cell-platelet contact [43]. Platelets release transforming growth factor- β 1 (TGF β 1) locally activating tumor cell signaling, facilitating the prometastatic phenotype [483], a process in which PLD is implicated [487].

In addition, to differences in platelet biology, PLD1-deficient mice possess endothelial cells with differences in angiogenic signaling pathways. The cells display: reduced basal phosphorylation of Akt at serine 473, and absence of VEGF-induced phosphorylation of this residue, they also exhibit a 50% reduction of ERK1/2 basal phosphorylation and diminished VEGF-induced p38 phosphorylation [43]. Consistent with PLD1's role in angiogenesis, the zebrafish PLD1 (zPLD1) isoform which is 64–68% identical to human and rodent PLD1

proteins at the amino acid level, is also required for angiogenesis, and both butan-1-ol and PLD1 morpholinos impair intersegmental blood vessel development [488].

Mammalian PLD2 is implicated in transformation, tumor metastasis and invasion [35,429,482]. Elevated PLD2 expression is observed in colorectal cancer patients [464,489] and a PLD2 polymorphism (C1814T) was identified in this group which remains of unclear significance since it does not effect PLD activity [458]. PLD2 is linked to *in vivo* EL4 lymphoma metastasis, with over-expression of catalytically inactive PLD2 reducing liver metastases [490], PLD2 is also linked invasion and metastasis of breast cancer [224,491]. Invasion of highly metastatic breast cancer cells is inhibited by a PLD2 specific inhibitor [224] and stable silencing of PLD2 in highly invasive breast cancer cells resulted in tumors with a mildly invasive capacity. In contrast, PLD2 over-expression in mildly invasive cells increased tumorigenicity following implantation into SCID (severe combined immunodeficient) mice. Furthermore, implantation of a micro-osmotic pump providing the PLD2-specific inhibitor NOPT reduced primary tumor volume and onset, and reduced axillary tumors by 50%, while a PLD 1/2-specific PLD inhibitor resulted in no axillary tumors suggesting an additional PLD1 role in this process [491]. PLD activity, including that of the PLD2 isoform has been linked to the epithelial-mesenchymal-transition (EMT), an important stage in breast cancer metastasis [492]. PLD2 is regulated by the zinc-finger transcription factors Slug (SNAI2) and Snail (SNAI1), which play key roles in EMT, cell survival and invasion. Their activity is reported to account for elevated PLD2 activity in breast cancers of larger size and poor prognosis. PLD2 is positively regulated by Slug which activates PLD2 gene expression, and negatively regulated by Snail which competitively binds the PLD2 promoter. Both PLD2 and Slug levels are elevated in highly aggressive cells, while Snail levels are reduced. An inverse pattern of expression is observed in cells displaying lower aggression [492]. Following the production of PtdOH, Snail activity is negated and Snail expression reduced in the highly invasive setting, while expression of the Slug positive regulator is increased [492]. PLD in breast cancer is also regulated by MicroRNAs (miRs). Breast cancer cells displaying low aggression, express low levels of PLD and high levels of four miRs, which decrease PLD-translation. Three of these (miR 203, -887, and -3619) target PLD2, while one targets PLD1 (miR 182). Combined expression of miR 887, and miR 3619 abolishes over 90% of PLD2 activity. These tumor-suppressor like miRs are down-regulated in postEMT, highly-aggressive cells, which display high levels of both PLD1 and PLD2, and tumor aggressiveness could be reversed by miR transfection. The junction proteins vimentin and E-cadherin play key roles in miR regulation. E-cadherin triggers miR expression in pre- EMT cells, down-regulating PLD activity, while vimentin reduces expression in invasive cells post-EMT transition, leading to higher PLD activation [493].

PLD2 is linked to vascular endothelial growth factor (VEGF) signaling [494], a key mediator of angiogenesis, embryonic development and pathophysiological repair [495–498]. VEGF is dramatically upregulated during pathogenic angiogenic events including diabetic retinopathy and cancer [499,500], PLD2 deficiency in immortalized human umbilical vein endothelial (iHUV) cells decreased VEGF mediated cell-survival, proliferation, migration, and tubulation [494]. Furthermore, *ex vivo* aortic sprouting assays using PLD2^{-/-} KO mouse tissue revealed PLD2 absence inhibits *ex vivo* angiogenesis [494]. Retinal

angiogenesis was also decreased in the absence of PLD2, as was both tumor growth and tumor angiogenesis in Lewis lung carcinoma cells subcutaneously implanted in PLD2 knockout mice *versus* wild type [501]. PLD2 is also linked to angiogenesis in clear cell renal carcinoma (ccRCC). PLD1 and PLD2 are both upregulated in ccRCC, with increased PLD levels corresponding with higher tumor stage and grade. Knockdown of PLD2 suppressed proliferation and invasion of ccRCC *in vitro* and growth, and invasion of tumors in a nude mouse xenograft model. Importantly elevated PLD2 expression was also found to be significantly associated with poor prognosis in 67 ccRCC patients. Expression of angiogenin (ANG), a protein involved in angiogenesis, invasion and metastasis is elevated in a number of human cancers, and inhibition of ANG significantly suppressed tumor invasion. PtdOH produced by PLD2 increases ANG expression, and treatment of renal cell carcinoma cells with PLD2 shRNA downregulated ANG mRNA, indicating a PLD2 role in regulating angiogenesis through regulation of ANG levels [502]. In addition to a role in angiogenesis, PLD2 is implicated in cancer cell migration and invasion [433,503], a role which is perhaps unsurprising since the isoform is linked to motility in numerous cell types including phagocytes [386,387,504,505], epithelial cells [506,507], and fibroblasts [508,509]. PLD2's role in increased proliferation of cancer cells appears tightly linked to the products of the oncogenes JAK (Janus kinase) and Fes (the human counterpart of feline sarcoma retrovirus protein associated with leukemia and sarcoma). These tyrosine kinases display elevated expression associated with tumor-growth, angiogenesis and metastasis. JAK and Fes physically interact, but binding appears to be reduced in transformed cells. PLD2 is phosphorylated on Y415, Y169 and Y179 following cell-stimulation, with JAK3 phosphorylating PLD2 at Y415 *in vitro* [270,503]. Fes interacts with these phosphorylated residues differentially binding to PLD2 on Y415 in non-transformed cells, and to Y415, and Y169 in transformed cells, at least in the later-case through the Fes SH2-domain [503]. JAK3 and PLD2 also interact although the binding remains to be fully characterized [503]. In transformed cells PLD2, JAK and Fes are over-expressed and the activity of all three proteins is elevated. The kinases activate PLD2 leading to increased PtdOH which further activates Fes (but not JAK3) forming a positive feedback loop [503]. In non-transformed cells, Fes negatively feeds back to JAK3 but this appears to be diminished in transformed cells, in which binding of the two proteins is reduced [503]. Silencing of any of the three proteins with siRNA reduced proliferation of highly proliferative breast cancer cells, and silencing of all three had a synergistic silencing effect [503]. Another aspect of cancer biology in which PLD2 plays an important role, is in anti-tumor immunity. Growth of tumors formed by subcutaneously transplanted cancer cells is enhanced in PLD2 knockout mice and is at least partly ascribable to the absence of PLD2 in bone marrow. Cytotoxic CD8⁺T cells were significantly reduced in tumors within the PLD2 knockout animal and division of cultured CD8⁺T cells was significantly suppressed indicating an important PLD2 role in T-lymphocyte proliferation [510].

8.4. PLD in neuronal physiology and pathology

PLD is expressed in brain tissue [511,512] and linked to both normal, and pathological brain function [39]. PLD isoforms mediate signaling, and trafficking of brain receptors including those of mito-genic growth factors [187,513], and opioid-, muscarinic-, and metabotropic glutamate receptors [341,354,355,514]. They play key roles in cell proliferation during brain

development [187,513,515,516]; and regulate neurite outgrowth, particularly axonal sprouting [165,343,517,518]. For example, stimulation of astrocytes with the muscarinic-receptor agonist carbachol results in axonal elongation and hippocampal neurite outgrowth, through PLD-dependent release of fibronectin, plasminogen, and laminin [519].

PLD1 and PLD2 are highly expressed in brain, particularly within the white matter. PLD1 expression changes only slightly during rat development (E15-P49), while PLD2 is upregulated in white and gray matter during the early postnatal stage [520]. Both isoforms are implicated in hippocampal mossy fiber sprouting, and neuronal plasticity [165]. PLD2 is also implicated in signaling by the neuronal L1 cell adhesion molecule (L1 CAM), and acts downstream of the L1-MAP Kinase pathway that regulates neurite outgrowth [343,518]. Highly sensitive analysis of PLD2 brain expression, using Locked Nucleotide Amplification (LNA) based *in situ* hybridization indicated PLD2 is expressed in hippocampus, cerebellum and olfactory bulb [164]. Loss of PLD2 from these regions could therefore impact function reflected in mouse behavior. Consistent with this, PLD2^{-/-} mice display learning and memory deficiencies, and reduced hippocampal acetylcholine release following behavioral stimulation [187]. PLD2^{-/-} mice also display behavioral abnormalities demonstrating decreased olfaction and potential anosmia, the inability to smell [164]. PLD2^{-/-} mice display abnormal cerebellar architecture, with ectopic Purkinje cells visible in the *arbor vitae* (cerebellar white matter) or clustered on the molecular layer surface, instead of being sandwiched between the molecular- and granular layers. Lipidomic analysis of the PLD2^{-/-} brain indicates that the quantitatively normal PtdOH-pool is qualitatively and regionally abnormal, with a general shift from shorter 32: and 34: PtdOH species to longer 36: and 38: species [39,164].

PLD2 [521,522] and the PLD family member PLD5 have both been linked to autism suggesting a potential common role for PLD family proteins in autism risk [522]. PLD2 was linked to autism in an Australian study which discovered an autism-linked SNP (rs4141463) within an intron of the mono-ADP ribosylhydrolase 2 (*MACROD2*) gene, a region linked to regulation of PLD2 expression [521,522]. *MACROD2* copy number variants are associated with schizophrenia [523], brain infarct [524], brain volume in multiple sclerosis [525] and deletion is reported in attention deficit hyperactivity disorder (ADHD) [526]. The *in vivo* relevance of this finding however, is currently unclear and another study looking at a European cohort failed to find an association between *MACROD2* and autism, suggesting the finding may be population dependent [527].

PLD is implicated in Alzheimer's disease (AD) [37–41], PLD activity being increased in AD brain homogenates [36,528]. Many facets of AD pathogenesis are mediated by cerebral Amyloid β (A β) accumulation, resulting from sequential cleavage of amyloid precursor protein (APP) by β -, and γ -secretases [39,529–532]. A β -stimulated PLD activity correlated with release of lactate dehydrogenase, a cell death indicator, suggesting amyloid neurotoxic actions are PLD mediated [47,533]. PLD activity was increased by APP in P19 mouse embryonic carcinoma cells [534] and oligomeric A β in cultured neurons [39]. PLD is also implicated in regulation of APP trafficking, as well as trafficking of pre-senilin-1 (PS1), a component of the γ -secretase which mediates APP cleavage to generate A β [36–41,188,528,535–539]. Both the PLD1 and PLD2 isoforms are linked to AD [37,39,188].

Studies using cell culture models suggest PLD1 is AD protective, and negatively regulates A β formation [37]. PLD1 (but not PLD2) is also implicated in APP- and PS1 trafficking, with important implications for APP metabolism and A β secretion [37–39]. PLD2 is activated by A β in cultured neurons, and reduction of PLD2 levels blocked A β -induced PLD activation [188]. PLD2 is predominantly localized to the cell-surface: a major site of A β action [168]. Oligomeric A β causes a partial internalization of PLD2 from the plasma membrane [188], in an extracellular Ca²⁺ dependent manner, re-localization being blocked by cPLA2 inhibition. This is consistent with studies indicating PLD2 activation occurs downstream of Ca²⁺ entry and cPLA2 stimulation [188]. PLD activity is elevated in a transgenic mouse AD model (SwAPP) and PLD2 deletion in this background blocked A β 42 oligomer synaptotoxicity. This resulted in synaptic protection, memory deficit rescue, and neuronal protection, despite significant levels of A β [188]. Liquid chromatography mass-spectrometry (LC-MS) analysis of ethanol-injected SwAPP mice *versus* control animals indicated increased PLD activity in the SwAPP AD background, with increases in phosphatidylethanol (PEtOH) (32:1, 34:2, and 34:1) and PtdOH 34:2 within the brain. PtdOH 34:2 accumulation was PLD-dependent and was not observed in SwAPP PLD2 knockout mice [188]. Profiling of PLD2^{-/-} knockout mouse brain lipids in an independent study revealed a similar decrease in shorter 32: and 34: PtdOH species and an increase in larger 36: and 38: species, suggesting compensation by other PtdOH producing enzymes [164]. The PtdOH 34:2 species was previously observed accumulating in *D. mela-nogaster* photoreceptors following PLD over-expression, which resulted in receptor degeneration, consistent with this lipid species playing a pathogenic role [540]. Taken together these data potentially suggest PLD2: 1) mediates signaling downstream of A β ; (2) regulates availability of putative A β receptors at synapses, or 3) alters A β to binding to putative receptors [188].

PLDs are implicated in the biology of synucleins a group of poorly characterized proteins that are enriched in nerve endings, and implicated in both AD and Parkinson's disease (PD). They are present in AD-associated amyloid plaques, and accumulate in PD Lewy bodies, with mutations in synuclein genes predisposing the PD condition [541–545]. The neurotoxic α -synuclein peptide co-immunoprecipitates with PLD1 and PLD2 [546], and α , β and γ synuclein inhibit PLD2 *in vitro* [545,547]. Activation of PLD2 by the muscarinic receptor in human dopaminergic cells is proposed to involve loss of PLD2-inhibition by α -synuclein [548]. Two α -synuclein point mutations associated with early-onset PD have been assayed for the ability to inhibit PLD2 activity *in vitro* [543–545]. While α -synuclein A30P displayed equal inhibition to wild-type α -synuclein, — A53T's ability to inhibit PLD2 was significantly enhanced [545]. Inhibition required residues in exon 4 and 6 of α -synuclein, a region required for the proteins a helical structure. Deletion or mutation of these regions rendered the protein unable to inhibit PLD2. This ability could also be blocked by phosphorylation of serine 129, or tyrosine 125, or 136 within α -synuclein exons 5 and 6 [545]. However, translation of *in vitro* findings to our understanding of the *in vivo* PLD-synuclein relationship is complicated, by contrasting reports that α -synuclein does not inhibit PLD activity [549], and that PLD does not contribute to α -synuclein mediated brain lesions [546].

PLD is also linked to fetal alcohol spectrum disorder (FASD) resulting from alcohol consumption during pregnancy [550]. A range of effects are observed within the spectrum depending on timing and extent of consumption during the developmental process [551]. PLD has long been known to produce phosphatidyl-alcohols in the presence of primary alcohols but the *in vivo* relevance of this has remained unclear. The consequence of transphosphatidylation are two-fold: 1) cellular phosphatidyl-alcohol accumulation; 2) inhibition of downstream PtdOH dependent pathways. There is a sparsity of evidence linking phosphatidyl-alcohol accumulation to *in vivo* toxicity. However, accumulation was associated with disruption of membrane function, including a reduction in Ins(1,4,5)P₃ levels [552] and reduced binding of ³H Ins(1,4,5)P₃ to cerebellar membranes [553]. Phosphatidyl-alcohol persisted in the brains of ethanol fed rats with a half-life of 8–10 h [553].

PLD activity is also linked to multiple sclerosis (MS) a disabling neurological autoimmune disease in which the immune system attacks the myelin nerve sheath. PLD1 reduces immune responses [206,445] and PLD1 ablation reduced symptoms in allergic encephalomyelitis (EAE) the murine MS model [45]. The CNS is ordinarily protected from lymphocyte incursions from the periphery preventing uncontrolled inflammation and tissue damage. However, during diseases of the CNS such as MS, lymphocytes readily cross the blood-brain barrier and induce demyelination and axonal damage. Inhibition of lymphocyte trafficking is therefore a major focus of research into treatment of CNS disorders. PLD1 is expressed in the lymphocytes of MS patients, during autoimmune CNS inflammation, but not in the lymphocytes of healthy individuals. Absence of PLD1 reduced chemokine static adhesion of lymphocytes to the endothelial adhesion molecules vascular cell adhesion molecule 1 (VCAM1) and Intercellular adhesion molecule 1 (ICAM1) *in vitro* with concomitant decreased motility in cell migration, and blood brain barrier models [45]. Absence of PLD1 resulted in attenuated disease severity in EAE mice indicating the relevancy of these findings to recruitment of the CNS *in vivo*.

8.5. PLD in insulin signaling and diabetes

Insulin stimulates mammalian PLD activity and numerous studies link PLD-derived PtdOH with the glucose uptake mechanism [213,291,554–556]. In-tum, mammalian PLD also regulates insulin signaling by regulating multiple aspects of vesicular-trafficking, [555], and potentially through regulation of mTOR (see previous section), a critical component of insulin signaling. Although the precise role of PLD in insulin signaling through mTOR and associated pathways is still being elucidated. Mammalian mTOR exists in two complexes defined by the nature of their primary accessory proteins, namely mTORC1, containing raptor (regulatory associated protein of Tor) and mTORC2, containing rictor (rapamycin insensitive component of TOR). The mechanisms by which these proteins regulate insulin signaling are still being fully resolved, but mTOR is known to activate AKT by phosphorylating it at ser473 enhancing insulin signaling [419,557]. Serum activation of PLD results in phosphorylation of AKT ser473, however this appears to be independent of mTORC2 [557].

PLD1 and PLD2 are both implicated in insulin signaling and PLD1 and PLD2 deficient mice exhibit insulin intolerance, characteristic of a pre-diabetic state [189]. PLD1, and PLD2 interact with PEA15 (phos-phoprotein enriched in diabetes/ astrocytes [also called PED]) [558], and alterations in the expression level are linked to diabetes and other disease states including Alzheimer's disease, polycystic ovary syndrome, cardiovascular disease, and cancer (PEA15 is a tumor suppressor) [559]. PLD1 interaction is dependent on a D- (also called DED [death effector domain])-peptide binding motif in the PEA15 N-terminus, and the D4-motif of PLD1 (which overlaps with its Rho activation site) [560,561]. The interaction is independent of PEA15 phosphorylation [562], and increases PLD1 activity [561]. This is potentially a result of increased PLD stability, since both PLD1- and PLD2 protein levels increase following PEA15 co-expression, suggesting it may act as a PLD chaperone [561]. PEA15 is upregulated in type 2 diabetics and may contribute to insulin resistance in glucose uptake. Cellular glucose transport at the plasma membrane occurs through the facilitative glucose transporter (Glut) family [563]. Glut1 resides at the plasma membrane and is thought to perform basal transport, while Glut4 is responsible for insulin-stimulated transport [564]. PEA15 overexpression in skeletal muscle, a major site of diabetic insulin resistance, increases cell-membrane Glut1 expression, and inhibits insulin-stimulated glucose transport, and Glut4 cell-surface recruitment [565]. Expansion of the Glut1 cell surface compliment, prevents further insulin-stimulated Glut1 translocation, and in cells uniquely expressing this transporter, may account for the lack of insulin-stimulated glucose transport, and increased basal glucose transport, which decreases insulin effectiveness, increasing insulin-resistance. In cells expressing both receptors a significant decrease in insulin responsiveness is additionally observed as Glut4 translocation to the plasma membrane is blocked [565]. Primary alcohols inhibit Glut-4 translocation and glucose uptake [566,567], and PLD1 RNAi, or catalytically inactive PLD1 mutant expression reduced plasma membrane Glut4 through delayed docking of Glut4 containing vesicles at the exocytic site [213]. Conversely, increased PLD-expression, increased insulin-stimulated Glut4 translocation [213,568]. In cell culture, or transgenic animal systems PEA15 over-expression impairs insulin-mediated glucose regulation in a PEA15-PLD1 interaction-dependent manner [560]. PEA15 over-expression also causes PLD-dependent PKC α -activation, preventing subsequent activation of PK ξ [569,570], which is a major Glut4 membrane translocation regulator [571]. Disruption of the PEA15-PLD1 interaction *in vitro* results in reduced PKC α activity and restoration of insulin sensitivity [560]. Furthermore, insulin sensitivity was restored in PEA15 over-expressing mice, following adenoviral expression of the PLD1 D4 PEA15-binding-domain. This disrupted the PEA15-PLD1 interaction, reduced PKC α activity and increased PKC ξ activation thereby enhancing insulin sensitivity [572]. PEA15 is also implicated in other aspects of the diabetic phenotype, PEA15 over-expression increasing mouse creatine levels and urine volume, and elevating transforming growth factor- α 1 (TGF β 1) in kidney, and serum [573]. Pharmacological PLD- or PKC β inhibition resulted in reduced TGF β 1 and the extra-cellular matrix component fibronectin, which could potentially result in diabetes-associated renal dysfunction and kidney damage [573]. TGF β 1 induces PEA15-mediated autophagy, and induces PEA15 transcription [574], Defects in autophagy are linked to the etiology of many diseases including type two diabetes (T2D), as well as cancer and neurodegenerative disease [579]. In T2D, impaired pancreatic beta cell function and development of insulin resistance

has been linked to autophagy. PLD1 is linked to autophagy modulation, and butan-1-ol, RNAi, PLD inhibitors and knockout of PLD1 in a mouse model all decreased macroautophagy [185]. Autophagy and the endocytic process are tightly linked [575] and it is perhaps unsurprising that PLD is implicated in regulation of autophagy given its links to endocytic trafficking [575–577]. PLD1's role in autophagy is required for cancer cell survival under conditions of prolonged glucose insufficiency [578].

9. Discussion

Since the initial discovery of PLD activity in plant tissue, activities have been detected across the genera. Improvements in scientific methodology have since resulted in cloning of PLD genes, identification of signature motifs, and an improved understanding of PLD structure and the catalytic mechanism. Improved detection of endogenous PLDs, has reduced dependency on over-expression constructs, allowing, with ever increasing accuracy, the precise localization of PLDs *in vivo*. The advent of RNA interference and in particular the evolution of isoform-specific PLD inhibitors to inhibit PLD expression or activities has facilitated a departure from our dependence on over-expression of mutant PLDs, and perhaps most importantly from use of primary alcohols to inhibit PtdOH production. These advances have greatly improved our understanding of the cellular functions of PLD enzymes. More recently technological advances including TALEN and CRISPR have enabled manipulation of DNA with increased ease, and fidelity, reducing off target effects, and promise to clarify the situation even further. The development and careful analysis of PLD knockout animal models, has vastly improved our understanding of the role of PLDs *in vivo* and are allowing for the first-time a thorough analysis of PLDs role in the context of whole organisms. As a result of these technological advances, PLD activities are now convincingly being linked to numerous diseases including Alzheimer's disease, thrombosis and numerous cancers. As our comprehension of PLDs role in the pathology of these diseases increases, and our understanding of PLDs potential for drugability grows, the hope that PLD proteins may provide drugable targets is becoming closer to reality.

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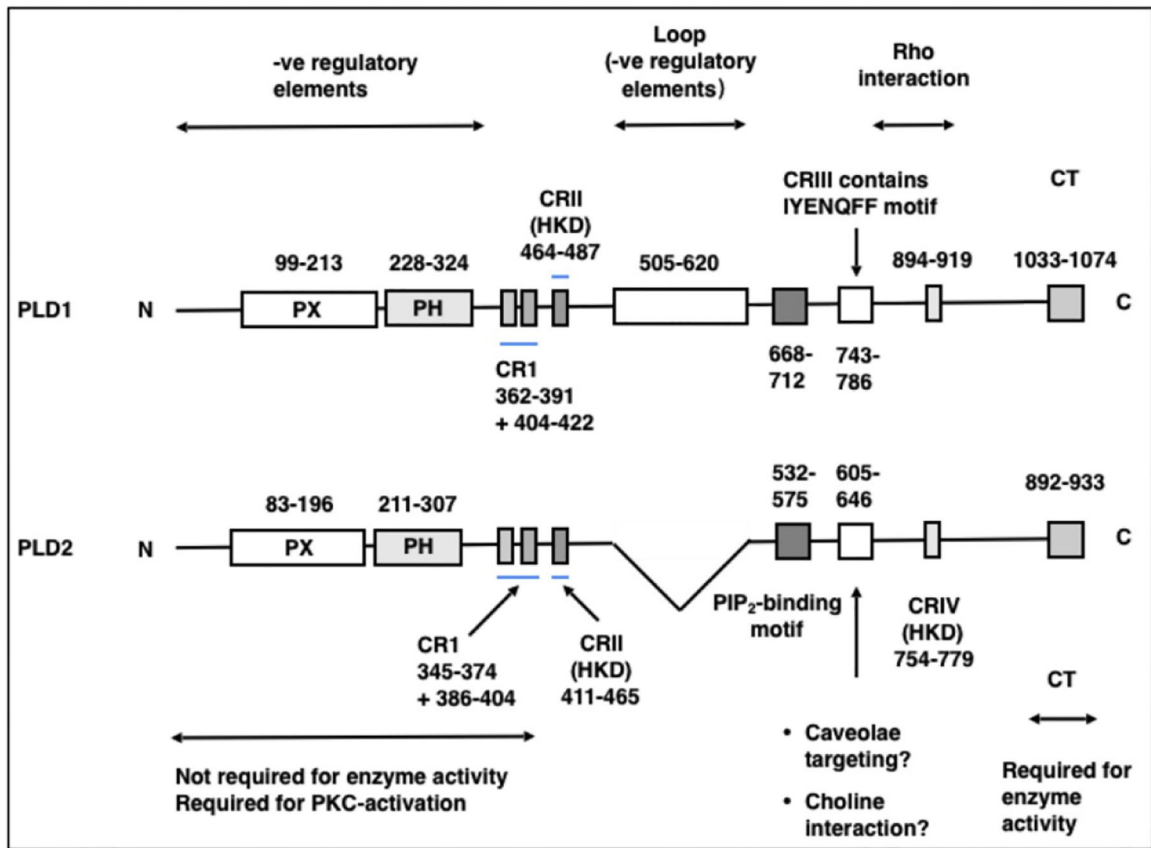


Fig. 1. A detailed comparison of PLD1 and PLD2 structure. PLD1 and PLD2 display 51% sequence homology and share a conserved structure with 4 conserved PLD regions (CR), of which CRII and IV contain the catalytic sequence HKD. They both contain PX- and PH-domains and a PIP₂ binding motif. PLD1 contains a loop sequence between CRII and CRIII absent in PLD2. Known and potential region-specific functions are indicated.

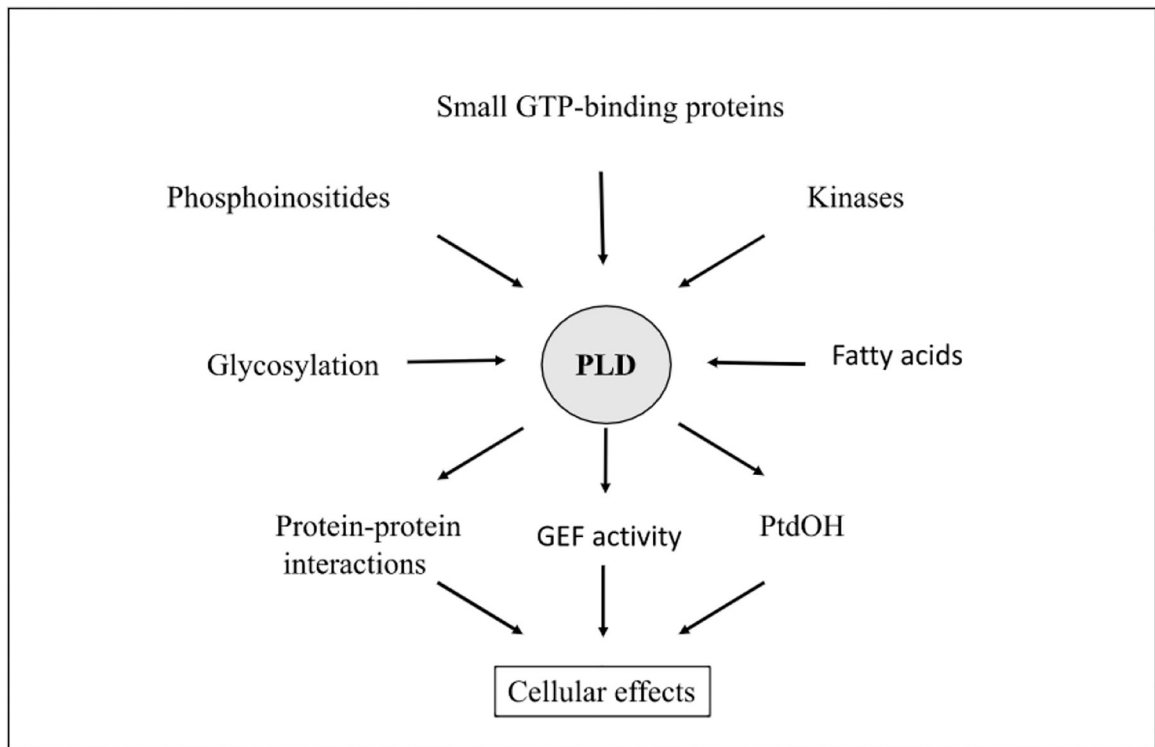


Fig. 2. PLD regulation and function. PLD activity is regulated by a multitude of factors including proteins and lipids. Its activity results in a diverse range of biological outcomes through production of PtdOH, GEF-activity, and protein-protein interactions.

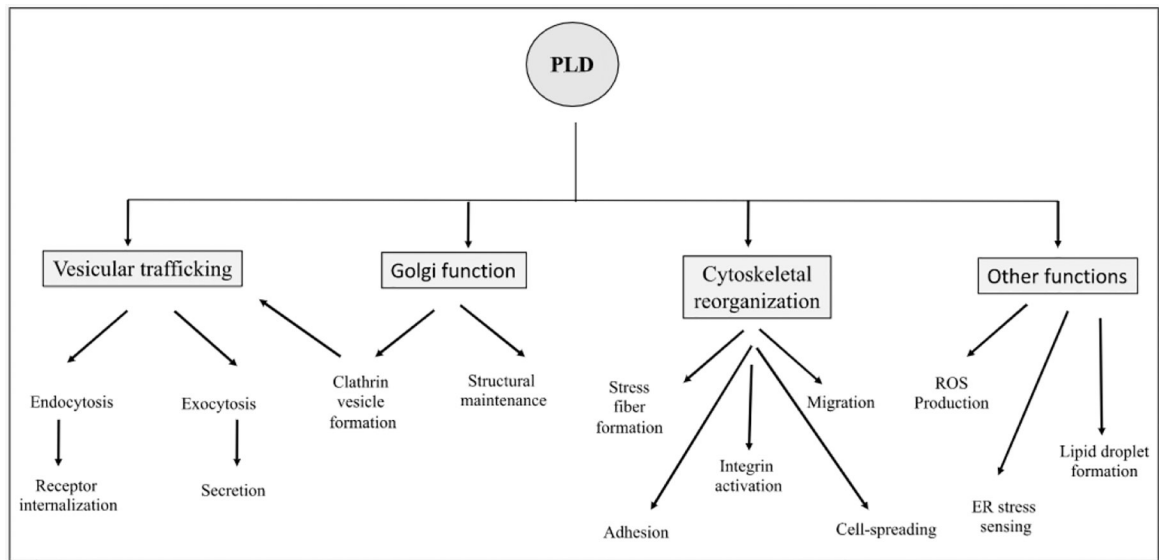


Fig. 3. Examples of mammalian PLD function. Mammalian PLDs are involved in a vast array of cellular processes, notably Vesicular trafficking, Golgi-function and cytoskeletal regulation.

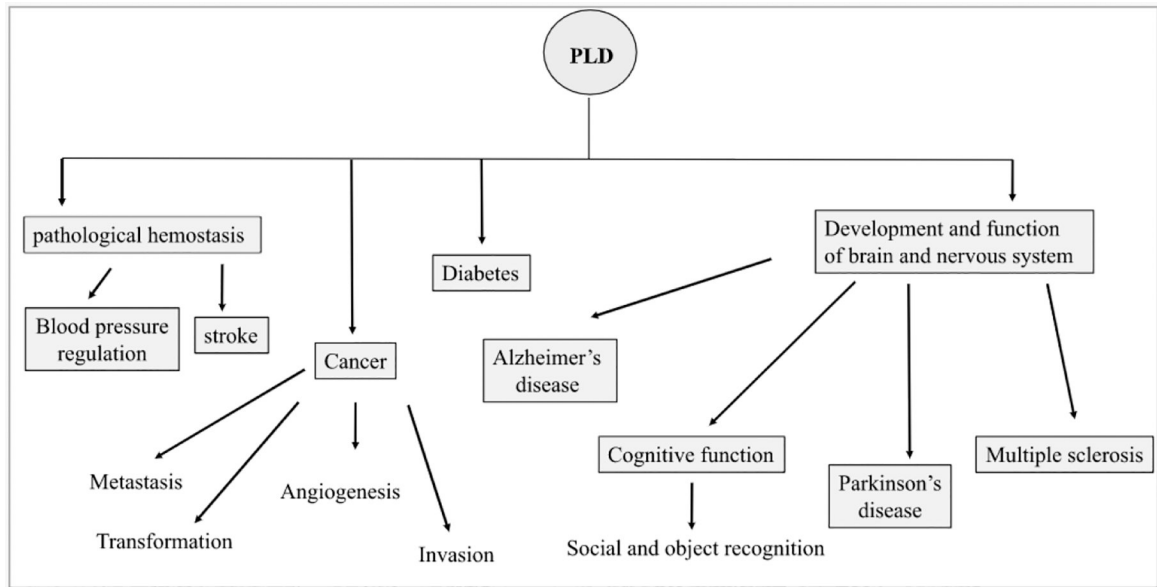


Fig. 4. The role of mammalian PLDs in disease. Mammalian PLDs have been implicated in a number of physiological processes and diseases, including brain function and development, Alzheimer’s disease, cancer, diabetes and stroke.

Table 1

Functions and disease relevance of mammalian PLD1.

Cancer (Melanoma), metastasis, angiogenesis.	[43,224,481]
Pathological hemostasis (e.g. strokes and pulmonary embolisms, autophagy, proteinopathies).	[42,185]
Brain development.	[187]
Behavioral stimulation response, cognitive function, social recognition.	
Receptor internalization.	[353]
Secretion/ exocytosis.	[373–377,381]
Actin Stress fiber formation, adhesion/ cell spreading.	[391,392,394]
ROS production.	[184]
Lipid droplet formation.	[439,440]
Integrin activation.	[42]
Diabetes.	[558,560]

A large number of studies have identified important roles for PLD1 in cellular and physiological processes as diverse as endocytosis, lipid droplet formation, cytoskeletal regulation, cognitive function and social recognition. PLD1 has also been implicated in numerous diseases including diabetes, strokes and cancer. Numbers in parentheses refer to reference number in manuscript bibliography.

Table 2**Functions and disease relevance of mammalian PLD2.**

Cancers including renal, breast, colorectal, bladder and lung. Tumor transformation, tumor metastasis and invasion. Angiogenesis.	[458,464,482,489,491,494]
Alzheimer's disease (AD), brain development, behavioral stimulation response, cognitive function, social and object recognition.	[39,187,188]
Receptor internalization, recycling and trafficking.	[41,97,168,334,339-341,353,354,364]
Golgi/TGN clathrin-coated vesicle formation, Golgi, and lysosome structural maintenance.	[8,10,179,384]
Adhesion.	[392,394]
Blood pressure regulation, thrombotic disease.	[44,168,196,452]

A large number of studies have indicated a diverse range of important cellular and physiological PLD2 functions including receptor internalization, Golgi function, cellular adhesion, behavioral stimulation response and blood pressure regulation. PLD2 has also been linked to a number of human diseases including Alzheimer's disease and cancer. Numbers in parentheses refer to reference number in manuscript bibliography.