>gnl|CDD|30941 COG0596, MhpC, Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [General function prediction only]
ASLLLAADGVRLAYREAGGGGPPLVLLHGFPGSSSVWRPVFKVLPALAARYRVIAPDLRG
HGRSDPAGYSLSAYADDLAALLDALGLEKVVLVGHSMGGAVALALALRHPDRVRGLVLIG
PAPPPGLLEAALRQPAGAAPLAALADLLLGLDAAAFAALLAALGLLAALAAAARAGLAEA
LRAPLLGAAAAAFARAARADLAAALLALLDRDLRAALARITVPTLIIHGEDDPVVPAELA
RRLAAALPNDARLVVIPGAGHFPHLEAPEAFAAALLAFLERL
>gnl|CDD|32968 COG3154, COG3154, Putative lipid carrier protein [Lipid metabolism]
RSRLVMRGPAALAAPARLLPFALQRQVLELVLSWQFRQALFDGLGEFLEGRWLFLPVRDL
PLRWFVEPVNGKLVVSRKAQADVSFSGDLFDLLALAEGKQDPDTLFFQRRLVIEGDTELG
LAVKNLLDAIELELPKDLGNALGQLAPVVEAGAGTARETALTGVAGGN
>gnl|CDD|33066 COG3255, COG3255, Putative sterol carrier protein [Lipid metabolism]
LNEDEEYRRAAKGWEGDLEQIVFEIPKENREKFGGKPAEGLAFKLQLSLGKCLGVEVIDG
GTVSKADAPDPPDFTLGASLDNWLDIITGKLNPTSAFMTGKLKVEGGMLSAMKLRYVIAA
FAMVKAAQRVPTGK
>gnl|CDD|34003 COG4281, ACB, Acyl-CoA-binding protein [Lipid metabolism]
DLSTRFEQAQTDVKELSEKPSNDELLKLYALFKQGSVGDNDGEKPGFFDIVGRYKYEAWA
GLKGKSQEDARQEYIALVEELKAKYGT
>gnl|CDD|28911 cd00029, C1, Protein kinase C conserved region 1 (C1) . Cysteine-rich zinc binding domain. Some members of this domain family bind phorbol esters and diacylglycerol, some are reported to bind RasGTP. May occur in tandem arrangement. Diacylglycerol (DAG) is a second messenger, released by activation of Phospholipase D. Phorbol Esters (PE) can act as analogues of DAG and mimic its downstream effects in, for example, tumor promotion. Protein Kinases C are activated by DAG/PE, this activation is mediated by their N-terminal conserved region (C1). DAG/PE binding may be phospholipid dependent. C1 domains may also mediate DAG/PE signals in chimaerins (a family of Rac GTPase activating proteins), RasGRPs (exchange factors for Ras/Rap1), and Munc13 isoforms (scaffolding proteins involved in exocytosis)
HRFVRKSFFKPTFCDVCRKSIWGLFKQGLRCSWCKVKCHKKCADKVPPSC
>gnl|CDD|28912 cd00030, C2, Protein kinase C conserved region 2 (CalB); Ca2+-binding motif present in phospholipases, protein kinases C, and synaptotagmins (among others). Some do not appear to contain Ca2+-binding sites. Particular C2s appear to bind phospholipids, inositol polyphosphates,and intracellular proteins. Synaptotagmin and PLC C2s are permuted in sequence with respect to N- and C-terminal beta strands
RLTVKIIEARNLPPKDKKGTSDPYVKVSLGGDKKQKKKTKVVKKTLNPVWNETFTFEVPP
PEESSLVIEVYDYDKFSRDDFIGEVTIPLSELLLDGKEGDRWFPL
>gnl|CDD|28947 cd00065, FYVE, FYVE domain; Zinc-binding domain; targets proteins to membrane lipids via interaction with phosphatidylinositol-3-phosphate, PI3P; present in Fab1, YOTB, Vac1, and EEA1;
DASSCMGCGKPFTLTRRRHHCRNCGRIFCSKCSSNRIPLPSMGGGKPVRVCDSCYEL
>gnl|CDD|28747 cd00113, PLAT, PLAT (Polycystin-1, Lipoxygenase, Alpha-Toxin) domain or LH2 (Lipoxygenase homology 2) domain. It consists of an eight stranded beta-barrel. The domain can be found in various domain architectures, in case of lipoxygenases, alpha toxin, lipases and polycystin, but also as a single domain or as repeats.The putative function of this domain is to facilitate access to sequestered membrane or micelle bound substrates
CRYTVTIKTGDKKGAGTDSNISLALYGENGNSSDIPILDGPGSFERGSTDTFQIDLKLDI
GDITKVYLRRDGSGLSDGWYCESITVQALGTKKVYTFPVNRWVLGGKWYTSVRSLK
>gnl|CDD|80302 cd00125, PLA2c, PLA2c: Phospholipase A2, a family of secretory and cytosolic enzymes; the latter are either Ca dependent or Ca independent. PLA2 cleaves the sn-2 position of the glycerol backbone of phospholipids (PC or phosphatidylethanolamine), usually in a metal-dependent reaction, to generate lysophospholipid (LysoPL) and a free fatty acid (FA). The resulting products are

either dietary or used in synthetic pathways for leukotrienes and prostaglandins. Often, arachidonic acid is released as a free fatty acid and acts as second messenger in signaling networks. Secreted PLA2s have also been found to specifically bind to a variety of soluble and membrane proteins in mammals, including receptors. As a toxin, PLA2 is a potent presynaptic neurotoxin which blocks nerve terminals by binding to the nerve membrane and hydrolyzing stable membrane lipids. The products of the hydrolysis (LysoPL and FA) cannot form bilayers leading to a change in membrane conformation and ultimately to a block in the release of neurotransmitters. PLA2 may form dimers or oligomers
NLLQFGKMIKCTTGRSALDYNGYGCYCGLGGSGTPVDDTDRCCQVHDCCYDRAEKGGCSP
YFTSYSYTCSDGQITCSDANDKCARALCECDRAAALCFARAPYNPKYRNYDKKRC
>gnl|CDD|73182 cd00137, PLCc, Phospholipase C, catalytic domain; Phosphoinositide-specific phospholipases C catalyze hydrolysis of phosphatidylinositol-4,5-bisphosphate (PIP2) to D-myo-inositol-1,4,5-trisphosphate (1,4,5-IP3) and sn-1,2-diacylglycerol (DAG). Both products function as second messengers in eukaryotic signal transduction cascades. 1,4,5-IP3 triggers inflow of calcium from intracellular stores; the membrane resident product DAG controls cellular protein phosphorylation states by activating various protein kinase C isozymes. The enzyme comprises 2 regions (X and Y) connected via a linker which may contain inserted domains, X and Y together form a TIM barrel-like structure containing the active site residues
MVAQDMSKPLSHYFIPSSHNTYLTGKQVWGESSIEGYIQALKHGCRCVELDCWDGPDNEP
VVYHGHTFTTPIKLSEVLEAIKDFAFVTSPYPVILSLEDHCSPDQQAKMADSFKETFGDL
LYTPPTFSSLNVLPSPEQLKGKILLKGKGYQSLQWKDGETFTTESNQSLNIFSQSEYKVL
LVKAIKETPLKLVKTNQNYLLRVYPSGTRGDSSNYNPQIAWNAGVQIVALNFQTYGEGMQ
LNLGMFRANG
>gnl|CDD|29051 cd00138, PLDc, Phospholipase D. Active site motifs; The PLD superfamily includes enzymes involved in signal transduction, lipid biosynthesis, endonucleases and open reading frames in pathogenic viruses and bacteria. PLD hydrolyzes the terminal phosphodiester bond of phospholipids to phosphatidic acid and a hydrophilic constituent. Phosphatidic acid is a compound that is heavily involved in signal transduction. The common features of the family members are that they can bind to a phosphodiester moiety, and that most of these enzymes are active as bi-lobed monomers or dimers
SVQLGESPSNNLDKKRVGGRSDLDALLEAISNAKKSIYIASFYLSPLITEYGPVILDALL
AAARRGVKVRILVDEWSNTDLKISSAYLDSLRALLDIGVRVFLIRTDKTYGGVLHTKLVI
VDDETAYIGSANLDGRSLTLNSEVGVVIYDPASLAADLKASLERDWNSTLRLKDYR
>gnl|CDD|29067 cd00148, PROF, Profilin binds actin monomers, membrane polyphosphoinositides such as PI(4,5)P2, and poly-L-proline. Profilin can inhibit actin polymerization into F-actin by binding to monomeric actin (G-actin) and terminal F-actin subunits, but - as a regulator of the cytoskeleton - it may also promote actin polymerization. It plays a role in the assembly of branched actin filament networks, by activating WASP via binding to WASP's proline rich domain. Profilin may link the cytoskeleton with major signalling pathways by interacting with components of the phosphatidylinositol cycle and Ras pathway
SWQAYVDDNLLGTGKVDSAAIVGHDDGSVWAASAGGFNLTPEEVGTLVAGFKDPDGVFST
GLTLGGQKYMVIRADDRSIYGKKGAGGVVIVKTKQALVIGMYEEGVQPGQANKVVEKLAD
YLRSQGY
>gnl|CDD|29115 cd00170, SEC14, Sec14p-like lipid-binding domain. Found in secretory proteins, such as S. cerevisiae phosphatidylinositol transfer protein (Sec14p), and in lipid regulated proteins such as RhoGAPs, RhoGEFs and neurofibromin (NF1). SEC14 domain of Dbl is known to associate with G protein beta/gamma subunits
LEELKELGKVGYLGGRDKEGRPVLIIRAGNKDLSKSLDSEELLRYLVYTLEKLLQEDDEQ
VEGFVVIIDLKGLSLSHLLPDPSLLKKILKILQDNYPERLKAVYIINPPWFFKVLWKIVK

PFLSEKTRKKIVFLGSDKEELLKYIDKEQLPEEYGGT
>gnl|CDD|29139 cd00177, START, START(STeroidogenic Acute Regulatory (STAR) related lipid Transfer) Domain. These domains are 200-210 amino acid in length and occur in proteins involved in lipid transport (phosphatidylcholine) and metabolism, signal transduction, and transcriptional regulation. The most striking feature of the START domain structure is a predominantly hydrophobic tunnel extending nearly the entire protein and used to binding a single molecule of large lipophilic compounds, like cholesterol
ESDKSVVLELAEEALEELLKLAEAEPGWVLSPEKKRGVEVYTRSFPDGGPGKEAKRETGV
VDVTAETLVDVLMDVEKRPEWDPNVKTLEVIETGDGGDLMIYELQAPSPGLVPPRDFVFL
RYCKRLEDGTYVIVDVSVDHPSVPPSPGYVRAENLPSGCLIQPLPPGYSKVTWVEHVDLK
GWGSLPRPLVNSGLAFGAARWVATLRRQCERL
>gnl|CDD|29555 cd00435, ACBP, Acyl CoA binding protein (ACBP) binds thiol esters of long fatty acids and coenzyme A in a one-to-one binding mode with high specificity and affinity. Acyl-CoAs are important intermediates in fatty lipid synthesis and fatty acid degradation and play a role in regulation of intermediary metabolism and gene regulation. The suggested role of ACBP is to act as a intracellular acyl-CoA transporter and pool former. ACBPs are present in a large group of eukaryotic species and several tissue-specific isoforms have been detected
LQEEFEAAAEKVKKLKTKPSNEEKLQLYSLYKQATVGDCNTERPGMFDLKGRAKWDAWNS
LKGMSKEDAMKAYIAKVEELIAKYA
>gnl|CDD|80303 cd00618, PLA2_like, PLA2_like: Phospholipase A2, a super-family of secretory and cytosolic enzymes; the latter are either Ca dependent or Ca independent. PLA2 cleaves the sn-2 position of the glycerol backbone of phospholipids (PC or phosphatidylethanolamine), usually in a metal-dependent reaction, to generate lysophospholipid (LysoPL) and a free fatty acid (FA). The resulting products are either dietary or used in synthetic pathways for leukotrienes and prostaglandins. Often, arachidonic acid is released as a free fatty acid and acts as second messenger in signaling networks. Secreted PLA2s have also been found to specifically bind to a variety of soluble and membrane proteins in mammals, including receptors. As a toxin, PLA2 is a potent presynaptic neurotoxin which blocks nerve terminals by binding to the nerve membrane and hydrolyzing stable membrane lipids. The products of the hydrolysis (LysoPL and FA) cannot form bilayers leading to a change in membrane conformation and ultimately to a block in the release of neurotransmitters. PLA2 may form dimers or oligomers
LPYGCYCGPGGSACPSGQPVDETDRCCRKHDCCYDQISDGGCCDGCLSYSFSEGGVTCLT
NSDLCTRSHCDCDRRLAICLARA
>gnl|CDD|29843 cd00821, PH, Pleckstrin homology (PH) domain. PH domains are only found in eukaryotes. They share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinases, regulators of G-proteins, endocytotic GTPases, adaptors, as well as cytoskeletal associated molecules and in lipid associated enzymes
KEGYLLKKTGKLRKGWKRRWFVLFNDLLLYYKKKSSKKSYKPKGSIPLSGAEVEESPDDS
GRKNCFEIRTPDGRSYLLQAESEEEREEWIEALQSA
>gnl|CDD|29848 cd00900, PH-like, Pleckstrin homology-like domain. This family includes the PH domain, both the Shc-like and IRS-like PTB domains, the ran-binding domain, the EVH1 domain, a domain in neurobeachin and the third domain of FERM. All of these domains have a PH fold, but lack significant sequence similarity. They are generally involved in targeting to protein to the appropriate cellular location or interacting with a binding partner. The PH

domain is commonly found in eukaryotic signaling proteins. This domain family possesses multiple functions including the ability to bind inositol phosphates and to other proteins
KEGYLLKLGSDDVSKGKRWKRRWFFLFDDGLLLYKSDDKKEIKPGSIPLSEISVEEDPDG
SDDPNCFAIVTKDRGRRVFVFQADSEEEAQEWVEALQQA
>gnl|CDD|29925 cd00912, ML, The ML (MD-2-related lipid-recognition) domain is present in MD-1, MD-2, GM2 activator protein, Niemann-Pick type C2 (Npc2) protein, phosphatidylinositol/phosphatidylglycerol transfer protein (PG/PI-TP), mite allergen Der p 2 and several proteins of unknown function in plants, animals and fungi. These single-domain proteins form two anti-parallel beta-pleated sheets stabilized by three disulfide bonds and with an accessible central hydrophobic cavity, and are predicted to mediate diverse biological functions through interaction with specific lipids
LVDCSDNSANIKEVLLSPCDPLPCPDHRGGNYNLSVTGTLREDIKSLYVDLALMSQGIKV
LNPDNSYDFCEAGLPKPSFCPLRKGQQYSYAKTVNVPEFTIPTIEYQVVLEDVTDKGEVL
ACAQATI
>gnl|CDD|29867 cd01218, PH_phafin2, Phafin2 Pleckstrin Homology (PH) domain. Phafin contains a PH domain and a FYVE domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinsases, regulators of G-proteins, endocytotic GTPases, adaptors, as well as cytoskeletal associated molecules and in lipid associated enzymes
GRVLVGEGVLTKMCRKKPKQRQFFLFNDILVYGNIVISKKKYNKQHILPLEGVQVESIED
DGIERNGWIIKTPTKSFAVYAATETEKREWMLHINKCVTDLLEK
>gnl|CDD|29868 cd01219, PH_FGD, FGD (faciogenital dysplasia protein) pleckstrin homology (PH) domain. FGD has a RhoGEF (DH) domain, followed by a PH domain, a FYVE domain and a C-terminal PH domain. FGD is a guanine nucleotide exchange factor that activates the Rho GTPase Cdc42. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinases, regulators of G-proteins, endocytotic GTPases, adaptors, as well as cytoskeletal associated molecules and in lipid associated enzymes
ELLKEGSVLKISSTTEKTEERYLFLFNDLLLYCVPRKMIGGSKFKVRARIDVSGMQVCEG
DNLERPHSFLVSGKQRCLELQARTQKEKNDWVQAIFSIIDE
>gnl|CDD|29869 cd01220, PH_CDEP, Chondrocyte-derived ezrin-like domain containing protein (CDEP) Pleckstrin homology (PH) domain. CDEP consists of a Ferm domain, a rhoGEF (DH) domain followed by two PH domains. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinases, regulators of G-proteins, endocytotic GTPases, adaptors, as well as cytoskeletal associated molecules and in lipid associated enzymes
EFIRQGCLLKLSKKGLQQRMFFLFSDLLLYTSKSPTDQNSFRILGHLPLRGMLTEESEHE

WGVPHCFTIFGGQCAITVAASTRAEKEKWLADLSKAIAD
>gnl|CDD|29870 cd01221, PH_ephexin, Ephexin Pleckstrin homology (PH) domain. Ephexin contains a RhoGEF (DH) followed by a PH domain and an SH3 domain. The ephexin PH domain is believed to act with the DH domain in mediating protein-protein interactions with the Eph receptor. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
RWLVKRGELTQLEERGSSNILRKKLKARTIYLFLFNDLLLITKKKLGSTFVVFDYAPRSF
LRVEKIEPDNQKIPLGSNLVGRPNLFLLTLLRNADDKQAELLLSADSQSDRERWLSALAP
PRRTN
>gnl|CDD|29871 cd01222, PH_clg, Clg (common-site lymphoma/leukemia guanine nucleotide exchange factor) pleckstrin homology (PH) domain. Clg contains a RhoGEF (DH) domain and a PH domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinsases, regulators of G-proteins, endocytotic GTPases, adaptors, a well as cytoskeletal associated molecules and in lipid associated enzymes
LGDLLLEGRFREHGGGKPRLLFLFQTMLLIAKPRGDKYQFKAYIPCKNLMLVEHLPGEPL
CFRVIPFDDPKGALQLTARNREEKRIWTQQLKRAMLQ
>gnl|CDD|29872 cd01223, PH_Vav, Vav pleckstrin homology (PH) domain. Vav acts as a guanosine nucleotide exchange factor(GEF) for Rho/Rac proteins. Mammalian Vav proteins consist of a calponin homology (CH) domain, an acidic region, a rho-GEF (DH)domain, a PH domain, a Zinc finger region and an SH2 domain, flanked by two SH3 domains. In invertebrates such as Drosophila and C.elegans, Vav is missing the N-terminal SH3 domain . PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
YGRPLLDGEVRIKASEDQKTKLRYIFLFDKAVIVCKALGDNTGDMQYTYKDIHDLADYKI
ENNPSRDTEGRDTRWKYGFYLAHKQGKTGFTFYFKTEHLRKKWLKALEMAMSNIRP
>gnl|CDD|29873 cd01224, PH_Collybistin, Collybistin pleckstrin homology (PH) domain. Collybistin is GEF which induces submembrane clustering of the receptor-associated peripheral membrane protein gephyrin. It consists of an SH3 domain, followed by a RhoGEF(dbH) and PH domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
ELFLQGEATRQKQNKGWNSSRVLFLFDHQMVLCKKDLIRRDHLYYKGRIDLDRCEVVNIR
DGKMFSSGHTIKNSLKIYSESTDEWYLFSFKSAERKHRWLSAFALERKF
>gnl|CDD|29874 cd01225, PH_Cool_Pix, Cool (cloned out of library)/Pix (PAK-interactive exchange factor) pleckstrin homology (PH) domain. Cool/Pix contains an N-terminal SH3 domain followed by a RhoGEF (DH) and PH domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display

strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
WEGQDIKTLGNVIHMSQVAVQYGAGEEKRERYLVLFPNVLLMLSASPRMSGFIYQGKLPL
TGIIVTRLEDTEALKNAFEISGPLIERIVVVCNNPQDAQEWVELLNANNPS
>gnl|CDD|29875 cd01226, PH_exo84, Exocyst complex 84-kDa subunit Pleckstrin Homology (PH) domain. Exo84 is a subunit of the exocyt complex, which is important in intracellular trafficking. In metazoa, Exo84 has a PH domain towards its N-terminus. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinsases, regulators of G-proteins, endocytotic GTPases, adaptors, a well as cytoskeletal associated molecules and in lipid associated enzymes
KVILYGELEEFDVETKKPVQRVMLFLLNDRLIVGNINAAGKYVMESTYSLNSVAVVNVKD
RENAKKVLKLLIFPESRIYQCESARIKTEWFEELEQAKRE
>gnl|CDD|29876 cd01227, PH_Dbs, Dbs (DBL's big sister) pleckstrin homology (PH) domain. Dbs is a guanine nucleotide exchange factor (GEF), which contains spectrin repeats, a rhoGEF (DH) domain and a PH domain. The Dbs PH domain participates in binding to both the Cdc42 and RhoA GTPases. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
GKLLMQGSFSVWTDHKKGHTKKELARFKPMQRHIFLHEKAVLFCKKREENGEGEKAPSYS
FKQSLKMTAVGITENVKGDTKKFEIWYNAREEVYILQAPTPEIKAAWVNEIRKVLTSQLQ
ACKEASQHRALEQ
>gnl|CDD|73249 cd01228, PH_BCR-related, BCR (breakpoint cluster region)-related pleckstrin homology (PH) domain. The BCR-related protein has a RhoGEF(DH) domain followed by a PH domain, a C2 domain and a RhoGAP domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinases, tyrosine kinases, regulators of G-proteins, endocytotic GTPAses, adaptors, a well as cytoskeletal associated molecules and in lipid associated enzymes
RQLVKDSFLVELVEGSRKLRHLFLFTDVLLCAKLKKTSRGKHQQYDCKWYIPLADLSFPS
EPFRIHNKNGKSYTFLLSSDYERSEWRESIQKLQKK
>gnl|CDD|29878 cd01229, PH_etc2, Epithelial cell transforming 2 (ECT2) pleckstrin homology (PH) domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinases, tyrosine kinases, regulators of G-proteins, endocytotic GTPases, adaptors, a well as cytoskeletal associated molecules and in lipid associated enzymes

LLSSHRSLVQRVETISLGEHLCDRGEQVTLFLFNDCLEIARKRHKVIGTFKSPHGSTRPP
ASLKHIHLMPLSQIKKVLDIRDTEDCHNAFALLVRPPTEQANVLLSFQMTSEELPKEVWL
KMLCRHVAN
>gnl|CDD|29879 cd01230, PH_EFA6, EFA6 Pleckstrin Homology (PH) domain. EFA6 is an guanine nucleotide exchange factor for ARF6, which is involved in membrane recycling. It consists of a SEC7 domain followed by a PH domain. The EFA6 PH domain regulates its association with the plasma membrane. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
YKHGALMRKVHADPDCRKTPFGKRSWKMFYGILRGLVLYLQKDEHKPGKSLSETELKNAI
SIHHALATRASDYSKKPHVFRLRTADWREFLFQTSSLKELQSWIERINVVAAAFSAP
>gnl|CDD|29880 cd01231, PH_Lnk, LNK-family Pleckstrin homology (PH) domain. The Lnk family of proteins consists of Lnk, APS and SH2B. They are adaptor proteins consisting of a PH domain and an SH2 domain, which mediates signaling through growth factor receptors. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. The lnk family PH domain is likely involved in targeting of the adaptor proteins to the plasma membrane
KEGVLRYSLADEADMDSGARWQRGRLVLRKAVGGYMLEFYLPLPPKSSKPKLQVACSSIS
EVRECTRLEMPDNLYTFVLKVDDNTDIIFEVGDEQQLNSWLAELRYC
>gnl|CDD|29881 cd01232, PH_TRIO, Trio pleckstrin homology (PH) domain. Trio is a multidomain signaling protein that contains two RhoGEF(DH)-PH domains in tandem. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
AQGKLLLQDTFQVWDPKAGLIQKGRERRVFLFEQSIIFAKEVKKKKQFGNPKYIYKSKLQ
VSKMGLTEHVEGDPCRFALWSGDPPISDNRIILKANSQETKQEWVKKIREILQE
>gnl|CDD|29883 cd01234, PH_CADPS, CADPS (Ca2+-dependent activator protein) Pleckstrin homology (PH) domain. CADPS is a calcium-dependent activator involved in secretion. It contains a central PH domain that binds to phosphoinositide 4,5 bisphosphate containing liposomes. However, membrane association may also be mediated by binding to phosphatidlyserine via general electrostatic interactions. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
NMKHCGYLYAIGKNVWKKWKKRFFVLVQVSQYTFAMCSYREKKAEPTEFIQLDGYTVDYM
PESDPDPNSELSLQGGRHFFNAVKEGDELKFATDDENERHLWVQAMYRATGQSHKPV
>gnl|CDD|29884 cd01235, PH_SETbf, Set binding factor Pleckstrin Homology (PH) domain. Set binding factor is a myotubularin-related pseudo-phosphatase consisting of a Denn domain, a Gram domain, an inactive phosphatase domain, a SID motif and a C-terminal PH domain. Its PH domain is predicted to bind lipids based upon its ability to respond to phosphatidylinositol 3-kinase
CEGYLYKRGALLKGWKPRWFVLDPDKHQLRYYDDFEDTAEKGCIDLAEVKSVNLAQPGMG
APKHTSRKGFFDLKTSKRTYNFLAENINEAQRWKEKIQQCI
>gnl|CDD|29885 cd01236, PH_outspread, Outspread Pleckstrin homology (PH) domain. Outspread contains two PH domains and a C-terminal coiled-coil region. PH domains share little sequence conservation, but all have a common fold, which is

electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinsases, regulators of G-proteins, endocytotic GTPAses, adaptors, a well as cytoskeletal associated molecules and in lipid associated enzymes
YCGWLLVAPDGTDFDNPVHRSKRWQRRWFILYDHGLLTYALDEMPTTLPQGTIDMNQCTD
VVDAEARTGQKFSICILTPDKEHFIKAETKEEISWWLNMLMVYP
>gnl|CDD|29887 cd01238, PH_Tec, Tec pleckstrin homology (PH) domain. Proteins in the Tec family of cytoplasmic protein tyrosine kinases that includes Bruton's tyrosine kinase (BTK), BMX, IL2-inducible T-cell kinase (Itk) and Tec. These proteins generally have an N-terminal PH domain, followed by a Tek homology (TH) domain, a SH3 domain, a SH2 domain and a kinase domain. Tec PH domains tether these proteins to membranes following the activation of PI3K and its subsequent phosphorylation of phosphoinositides. The importance of PH domain membrane anchoring is confirmed by the discovery of a mutation of a critical arginine residue in the BTK PH domain, which causes X-linked agammaglobulinemia (XLA) in humans and a related disorder is mice. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
ILEEIFIKRSQQKKKTSPLNYKERLFVLTKRKLSYYDVDAEKRKRERGSIDLEKIKCVET
VTPEGNGGDPPAPDGYPFQVVYDEGTLYVFAPSEKERSRWIKALKNV
>gnl|CDD|29888 cd01239, PH_PKD, Protein kinase D (PKD/PKCmu) pleckstrin homology (PH) domain. PKD consists of 2 C1 domains, followed by a PH domain and a kinase domain. While the PKD PH domain has not been shown to bind phosphorylated inositol lipids and is not required for membrane translocation, it is required for nuclear export. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
LKEGWMVHYTSSDNRRKKHYWRLDSKAITLYQEESGSRYYKEIPLAEILSVSSNNGDSVL
AKHPPHCFEIRTTTNVYFVGGEDYHAFSGGPPKKIPPSDSGRGSDNAQSWETAIRQA
>gnl|CDD|29889 cd01240, PH_beta-ARK, Beta adrenergic receptor kinase 1(beta ARK1)(GRK2) pleckstrin homology (PH) domain. Beta ARK1 is a G protein-coupled receptor kinase (GRK). It phosphorylates activated G-protein coupled receptors leading to the release of the previously bound heterotrimeric G protein agonist and thus signal termination. It consists of a domain found in regulators of G-protein signaling (RGS)(RH), a serine/threonine kinase domain and a C-terminal PH domain. The Beta-Ark 1 PH domain has an extended C-terminal helix, which mediates interactions with G beta gamma subunits. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
KDCIVHGYIKKLGGPFLSQWQTRYFKLYPNRLELYGESEANKPELITMDQIEDVSVEFQQ
IKEENCILLKIRDEKKIVLTNSDEIELKQWKKELRDAHRESQQLLQRMPKKANKIY
>gnl|CDD|29890 cd01241, PH_Akt, Akt pleckstrin homology (PH) domain. Akt (Protein Kinase B (PKB)) is a phosphatidylinositol 3'-kinase (PI3K)-dependent

Ser/Thr kinase. The PH domain recruits Akt to the plasma membrane by binding to phosphoinositides (PtdIns-3,4-P2) and is required for activation. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
VVKEGWLHKRGEYIKTWRPRYFLLKSDGSFIGYKEKPEDGDPFLPPLNNFSVAECQLMKT
ERPRPNTFIIRCLQWTTVIERTFHVESPEEREEWIHAIQTVA
>gnl|CDD|73250 cd01242, PH_ROK, Rok (Rho- associated kinase) pleckstrin homology (PH) domain. Rok is a serine/threonine kinase that binds GTP-rho. It consists of a kinase domain, a coiled coil region and a PH domain. The Rok PH domain is interrupted by a C1 domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
RMEGWLSLPNRTNKSRKPGWKKQYVVVSSRKILFYNDEQDKENSTPSMILDIDKLFHVRP
VTQGDVYRADAKEIPKIFQILYANEARDLLLLAPQTDEQNKWVSRLVKKIPK
>gnl|CDD|29892 cd01243, PH_MRCK, MRCK (myotonic dystrophy-related Cdc42-binding kinase) pleckstrin homology (PH) domain. MRCK consists of a serine/threonine kinase domain, a cysteine rich (C1) region, a PH domain and a p21 binding motif. It has been shown to promote cytoskeletal reorganization, which affects many biological processes. The MRCK PH domain is responsible for its targeting to cell to cell junctions. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
GTAYEGHVKIPKPGGVKKGWQRALVVVCDFKLFLYDIAEDRASQPSVVISQVLDMRDPEF
SVSSVLESDVIHASKKDIPCIFRVTTSQISASSSKCSTLMLADTEEEKSKWVGALSELHK
IL
>gnl|CDD|29893 cd01244, PH_RasGAP_CG9209, RAS_GTPase activating protein (GAP)_CG9209 pleckstrin homology (PH) domain. This protein consists of two C2 domains, followed by a RasGAP domain, a PH domain and a BTK domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinsases, regulators of G-proteins, endocytotic GTPases, adaptors, as well as cytoskeletal associated molecules and in lipid associated enzymes
KEGNLQQVDRSRLAWKKVLHFKKRYFQLTTTHLSWAKDVQCKKSALIKLAAIKGTEPLSD
KSFVNVDIITIVCEDDTMQLQFEAPVEATDWLNALEKQ
>gnl|CDD|29894 cd01245, PH_RasGAP_CG5898, RAS GTPase-activating protein (GAP) CG5898 Pleckstrin homology (PH) domain. This protein has a domain architecture of SH2-SH3-SH2-PH-C2-Ras_GAP. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH

domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinsases, regulators of G-proteins, endocytotic GTPAses, adaptors, a well as cytoskeletal associated molecules and in lipid associated enzymes
KKGNLLKRTKSVTKLWKTLYFALILDGSRSHESLLSSPKKTKPIGLIDLSDAYLYPVHDS
LFGRPNCFQIVERALPTVYYSCRSSEERDKWIESLQAQ
>gnl|CDD|29895 cd01246, PH_oxysterol_bp, Oxysterol binding protein (OSBP) Pleckstrin homology (PH) domain. Oxysterol binding proteins are a multigene family that is conserved in yeast, flies, worms, mammals and plants. They all contain a C-terminal oxysterol binding domain, and most contain an N-terminal PH domain. OSBP PH domains bind to membrane phosphoinositides and thus likely play an important role in intracellular targeting. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
VEGWLLKWTNYLKGWQKRWFVLDNGLLSYYKNKSSMRGKPRGTILLSGAVISEDDSDDKC
FTIDTGGDKTLHLRANSEEERQRWVDALELA
>gnl|CDD|29896 cd01247, PH_GPBP, Goodpasture antigen binding protein (GPBP) Pleckstrin homology (PH) domain. The GPBP protein is a kinase that phosphorylates an N-terminal region of the alpha 3 chain of type IV collagen , which is commonly known as the goodpasture antigen. It has has an N-terminal PH domain and a C-terminal START domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinsases, regulators of G-proteins, endocytotic GTPases, adaptors, as well as cytoskeletal associated molecules and in lipid associated enzymes
TNGVLSKWTNYINGWQDRYFVLKEGNLSYYKSEAEKSHGCRGSIFLKKAIIAAHEFDENR
FDISVNENVVWYLRAENSQSRLLWMDSVVRE
>gnl|CDD|29897 cd01248, PH_PLC, Phospholipase C (PLC) pleckstrin homology (PH) domain. There are several isozymes of PLC (beta, gamma, delta, epsilon. zeta). While, PLC beta, gamma and delta all have N-terminal PH domains, lipid binding specificity is not conserved between them. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
EVPEALQRGSVFIKWDDTSRERRRLFRLDEKGFFLYWKDEGKKEKKVLDISSIKEIRTGK
QPKDLKLRAELNQGNSLEERCFTIVYGTDLNLKSLDLVAPSEEEAKTWVSGLRKL
>gnl|CDD|29898 cd01249, PH_oligophrenin, Oligophrenin Pleckstrin homology (PH) domain. Oligophrenin is composed of a PH domain, a rhoGAP domain and a proline rich region. Closely related proteins have a C-terminal SH3 domain. PH domains a share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinsases, regulators of G-

proteins, endocytotic GTPases, adaptors, as well as cytoskeletal associated molecules and in lipid associated enzymes
KEGYLYMQEKSKFGGSWTKYYCTYSKETRIFTMVPFNQKTKTDMKGAVAQDETLTLKSCS
RRKTESIDKRFCFDVEVEEKPGVITMQALSEKDRRLWIEAMDGA
>gnl|CDD|29899 cd01250, PH_centaurin, Centaurin Pleckstrin homology (PH) domain. Centaurin beta and gamma consist of a PH domain, an ArfGAP domain and three ankyrin repeats. Centaurain gamma also has an N-terminal Ras homology domain. Centaurin alpha has a different domain architecture and its PH domain is in a different subfamily. Centaurin can bind to phosphatidlyinositol (3,4,5)P3. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
KQGYLYKRSSKSNKEWKKRWFVLKNGQLTYHHRLKDYDNAHVKEIDLRRCTVRHNGKQPD
RRFCFEVISPTKTWHFQADSEEERDDWISAIQES
>gnl|CDD|29900 cd01251, PH_centaurin_alpha, Centaurin alpha Pleckstrin homology (PH) domain. Centaurin alpha is a phophatidlyinositide binding protein consisting of an N-terminal ArfGAP domain and two PH domains. In response to growth factor activation, PI3K phosphorylates phosphatidylinositol 4,5-bisphosphate to phosphatidylinositol 3,4,5-trisphosphate. Centaurin alpha 1 is recruited to the plasma membrane following growth factor stimulation by specific binding of its PH domain to phosphatidylinositol 3,4,5-trisphosphate. Centaurin alpha 2 is constitutively bound to the plasma membrane since it binds phosphatidylinositol 4,5-bisphosphate and phosphatidylinositol 3,4,5-trisphosphate with equal affinity. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
KEGFMEKTGPKHTEGFKKRWFTLDDRRLMYFKDPLDAFAKGEVFLGSQEDGYEVREGLPP
GTQGNHWYGVTLVTPERKFLFACETEQDRREWIAAFQNVLSRP
>gnl|CDD|29901 cd01252, PH_cytohesin, Cytohesin Pleckstrin homology (PH) domain. Cytohesin is an ARF-Guanine nucleotide Exchange Factor (GEF), which has a Sec7-type Arf-GEFdomain and a pleckstrin homology domain. It specifically binds phosphatidylinositol-3,4,5-trisphosphate (PtdIns(3,4, 5)P3) via its PH domain and it acts as a PI 3-kinase effector mediating biological responses such as cell adhesion and membrane trafficking. PH domains are only found in eukaryotes. They share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
DREGWLLKQGGRVKTWKRRWFILTDNCLYYFEYTTDKEPRGIIPLENVSIREVEDPSKPF
CFELFSPSDKQQIKACKTESDGRVVEGNHSVYRISAANDEEMDEWIKSIKASISPNPFYE
MLAKR
>gnl|CDD|29902 cd01253, PH_beta_spectrin, Beta-spectrin pleckstrin homology (PH) domain. Beta spectrin binds actin and functions as a major component of the cytoskeleton underlying cellular membranes. Beta spectrin consists of multiple spectrin repeats followed by a PH domain, which binds to Inositol-1,4,5-Trisphosphate. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. PH domains are often involved in targeting proteins to the plasma membrane via lipid binding. PH domains are found in cellular signaling proteins

such as serine/threonine kinase, tyrosine kinsases, regulators of G-proteins, endocytotic GTPases, adaptors, as well as cytoskeletal associated molecules and in lipid associated enzymes
MEGSLERKHELESGGKKASNRSWDNVYGVLCGQSLSFYKDEKMAAENVHGEPPVDLTGAQ
CEVASDYTKKKHVFRLRLPDGAEFLFQAPDEEEMSSWVRALKSA
>gnl|CDD|29903 cd01254, PH_PLD, Phospholipase D (PLD) pleckstrin homology (PH) domain. PLD hydrolyzes phosphatidylcholine to phosphatidic acid (PtdOH), which can bind target proteins. PLD contains a PH domain, a PX domain and four conserved PLD signature domains. The PLD PH domain is specific for bisphosphorylated inositides. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
KEGYIMKRSGGKRSGSDDCSFGCCCFCRMCDRWQKRWFIVKESFLAYMDDPSSAQILDVI
LFDVDFKVNGGGKEDISLAVELKDITGLRHGLKITNSNRSLKLKCKSSRKLKQWMASIED
A
>gnl|CDD|29904 cd01255, PH_TIAM, TIAM Pleckstrin homology (PH) domain. TIAM (T-cell invasion and metastasis) is a guanine nucleotide exchange factor specific for RAC1. It consists of an N-terminal PH domain followed by Raf-like ras binding domain(RDB), a PDZ domain, a RhoGEF (DH) domain and a PH domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. This subfamily contains the alignment of the PH domain that follows the DH domain
YGAVFDQLFREHQKSCKQPIDLSPGDLLYHGGVEWLNPSDSLGKIKKELELMCFVFKSAV
VLVYKERLKQKKKLMGVSRKNATNEVDPFRFRVLIPVTALQVRASSAADMESNFLWELIH
LKSELEGRPEKVFVLCCSTAESRNAFLKTIRSILRESVRR
>gnl|CDD|29905 cd01256, PH_dynamin, Dynamin pleckstrin homology (PH) domain. Dynamin is a GTPase that regulates endocytic vesicle formation. It has an N-terminal GTPase domain, followed by a PH domain, a GTPase effector domain and a C-terminal proline arginine rich domain. Dynamin-like proteins, which are found in metazoa, plants and yeast have the same domain architecture as dynamin, but lack the PH domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
VIRKGWLSISNVGIMKGGSKDYWFVLTSESLSWYKDDEEKEKKYMLPLDGLKLRDIEGGF
MSRNHKFALFYPDGRNVYKDYKQLELGCETLEEVDSWKASFLRAGVYPEK
>gnl|CDD|29906 cd01257, PH_IRS, Insulin receptor substrate (IRS) pleckstrin homology (PH) domain. PH domains are only found in eukaryotes, and are often involved in targeting proteins to the plasma membrane via lipid binding. PH domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinsases, regulators of G-proteins, endocytotic GTPases, adaptors, a well as cytoskeletal associated molecules and in lipid associated enzymes. The IRS PH domain targets IRS molecules to the plasma membrane, usually in response to insulin stimulation
DVRKSGYLRKQKSMHKRFFVLRAESSGGPARLEYYENEKKFLQKGSAPKRVIPLESCFNI
NKRADAKHRHLIALYTRDEYFAVAAENEAEQDSWYQALLEL
>gnl|CDD|29907 cd01258, PH_syntrophin, Syntrophin pleckstrin homology (PH) domain. Syntrophins are peripheral membrane proteins, which associate with the

Duchenne muscular dystrophy protein dystrophin and other proteins to form the dystrophin glycoprotein complex (DGC). There are five syntrophin isoforms, alpha1, beta1, beta2, gamma1, and gamma2. They all contain two PH domains, with the N-teminal PH domain interupted by a PDZ domain. The N-terminal PH domain of alpha1syntrophin binds phosphatidylinositol 4,5-bisphosphate. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
HIGWVNEQLSGDDESSQRWRPRFLALKGSEFLFFETPPLSVEDWSRPLYVYKLYDVATRL
VKNSSTRRLNDQRDNCFLIRTGTQVENHYLRVETHRDLASWERALVRG
>gnl|CDD|29908 cd01259, PH_Apbb1ip, Apbb1ip (Amyloid beta (A4) Precursor protein-Binding, family B, member 1 Interacting Protein) pleckstrin homology (PH) domain. Apbb1ip consists of a Ras-associated domain and a PH domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
EMEGPLYLKADGKKSWKKYYFVLRSSGLYYFPKEKTKNTRDLACLNLLHGHNVYTGLGWR
KKYKSPTDYCFGFKAVGDQSKGSQSIKYLCAEDLPTLDRWLTAIRIAKYGKQLW
>gnl|CDD|29909 cd01260, PH_CNK, Connector enhancer of KSR (Kinase suppressor of ras) (CNK) pleckstrin homology (PH) domain. CNK is believed to regulate the activity and the subcellular localization of RAS activated RAF. CNK is composed of N-terminal SAM and PDZ domains along with a central or C-terminal PH domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinsases, regulators of G-proteins, endocytotic GTPAses, adaptors, a well as cytoskeletal associated molecules and in lipid associated enzymes
DCDGWLWKRKKPGGFMGQKWARRWFVLKGTTLYWYRSKQDEKAEGLIFLSGFTIESAKEV
KKKYAFKVCHPVYKSFYFAAETLDDLSQWVNHLITA
>gnl|CDD|29910 cd01261, PH_SOS, Son of Sevenless (SOS) Pleckstrin homology (PH) domain. SOS is a Ras guanine nucleotide exchange factor. It has a RhoGEF (DbH) domain, a PH domain, and a RasGEF domain. The SOS PH domain can bind to inositol 1,4,5-triphosphate. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
CNEFIMEGTLTRVGPSKKAKHERHVFLFDGLMVLCKSNHGQPRLPGASSAEYRLKEKFFM
RKVDINDKPDSSEYKNAFEIILKDGNSVIFSAKNAEEKNNWMAALISVQTKS
>gnl|CDD|29911 cd01262, PH_PDK1, 3-Phosphoinositide dependent protein kinase 1 (PDK1) pleckstrin homology (PH) domain. PDK1 contains an N-terminal serine/threonine kinase domain followed by a PH domain. Following binding of the PH domain to PtdIns(3,4,5)P3 and PtdIns(3,4)P2, PDK1 activates kinases such as Akt (PKB). PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane,

but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
ILKIGAVKKRKGLFAKKRQLILTNGPRLIYVDPVKKVVKGEIPWSDVELRVEVKNSSHFF
VHTPNKVYSFEDPKGRASQWKKAIEDLQK
>gnl|CDD|29912 cd01263, PH_anillin, Anillin Pleckstrin homology (PH) domain. Anillin is an actin binding protein involved in cytokinesis. It has a C-terminal PH domain, which has been shown to be necessary, but not sufficient for targetting of anillin to ectopic septin containing foci . PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinsases, regulators of G-proteins, endocytotic GTPAses, adaptors, a well as cytoskeletal associated molecules and in lipid associated enzymes
VEYHGFLTMFEDTSGFGAWHRRWCALEGGEIKYWKYPDDEKRKGPTGLIDLSTCTSSEGA
SAVRDICARPNTFHLDVWRPKMETDDETLVSQCRRGIERLRVMLSADTKEERQTWLSLLN
ST
>gnl|CDD|29913 cd01264, PH_melted, Melted pleckstrin homology (PH) domain. The melted protein has a C-terminal PH domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains. PH domains are found in cellular signaling proteins such as serine/threonine kinase, tyrosine kinsases, regulators of G-proteins, endocytotic GTPases, adaptors, as well as cytoskeletal associated molecules and in lipid associated enzymes
LIEGQLKEKKGRWRFIKRWKTRYFTLSGAQLLFQKGKSKDDPDDCSIDLSKIRSVKAVAK
KRRDRSLPKAFEIFTADKTYILKAKDEKNAEEWLQCLNIAV
>gnl|CDD|29914 cd01265, PH_PARIS-1, PARIS-1 pleckstrin homology (PH) domain. PARIS-1 contains a PH domain and a TBC-type GTPase catalytic domain. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
LCGYLHKIEGKGPLRGRRSRWFALDDRTCYLYYYKDSQDAKPLGRVDLSGAAFTYDPREE
KGRFEIHSNNEVIALKASSDKQMNYWLQALQSKRW
>gnl|CDD|29915 cd01266, PH_Gab, Gab (Grb2-associated binder) pleckstrin homology (PH) domain. The Gab subfamily includes several Gab proteins, Drosophila DOS and C. elegans SOC-1. They are scaffolding adaptor proteins, which possess N-terminal PH domains and a C-terminus with proline-rich regions and multiple phosphorylation sites. Following activation of growth factor receptors, Gab proteins are tyrosine phosphorylated and activate PI3K, which generates 3-phosphoinositide lipids. By binding to these lipids via the PH domain, Gab proteins remain in proximity to the receptor, leading to further signaling. While not all Gab proteins depend on the PH domain for recruitment, it is required for Gab activity. PH domains share little sequence conservation, but all have a common fold, which is electrostatically polarized. PH domains also have diverse functions. They are often involved in targeting proteins to the plasma membrane, but few display strong specificity in lipid binding. Any

specificity is usually determined by loop regions or insertions in the N-terminus of the domain, which are not conserved across all PH domains
LEGWLKKSPPYKLLFRTKWVRRYFVLHCGDRERNLFALEYYKTSRKFKLEFVIDLESCSQ
VDPGLLCTAGNCIFGYGFDIETIVRDLYLVAKNEEEMTLWVNCICKLC
>gnl|CDD|28748 cd01751, PLAT_LH2, PLAT/ LH2 domain of plant lipoxygenase related proteins. Lipoxygenases are nonheme, nonsulfur iron dioxygenases that act on lipid substrates containing one or more (Z,Z)-1,4-pentadiene moieties. In plants, the immediate products are involved in defense mechanisms against pathogens and may be precursors of metabolic regulators. The generally proposed function of PLAT/LH2 domains is to mediate interaction with lipids or membrane bound proteins
VKVKATVTVMKKNKLDLNDDGSGLDDLDDLLGRSLLLELVSSELDPKTGKGKKGKAAFLE
GWGKSLAGESAYEAEFEVPASFGPPGAVLVKNEHHSEFFLKSITLEGFGGSGTITFVCNS
WVYPKKDYPDKRIFFPN
>gnl|CDD|28749 cd01752, PLAT_polycystin, PLAT/LH2 domain of polycystin-1 like proteins. Polycystins are a large family of membrane proteins composed of multiple domains, present in fish, invertebrates, mammals, and humans that are widely expressed in various cell types and whose biological functions remain poorly defined. In human, mutations in polycystin-1 (PKD1) and polycystin-2 (PKD2) have been shown to be the cause for autosomal dominant polycystic kidney disease (ADPKD). The generally proposed function of PLAT/LH2 domains is to mediate interaction with lipids or membrane bound proteins
YLYLVTVFTGWRRGAGTTAKVTITLYGAEGESEPHHLRDPEKPIFERGSVDSFLLTTPFP
LGELQSIRLWHDNSGLSPSWYLSRVIVRDLQTGKKWFFLCNDWLSVEEGDGTVERTFPVA
>gnl|CDD|28750 cd01753, PLAT_LOX, PLAT domain of 12/15-lipoxygenase. As a unique subfamily of the mammalian lipoxygenases, they catalyze enzymatic lipid peroxidation in complex biological structures via direct dioxygenation of phospholipids and cholesterol esters of biomembranes and plasma lipoproteins. Both types of enzymes are cytosolic but need this domain to access their sequestered membrane or micelle bound substrates
AEYKVTVATGSSLFAGTDDYIYLTLVGTAGESEKQLLDRPGYDFERGAVDEYKVKVPEDL
GELLLVRLRKRKYLLFDAWFCNYITVTGPGGDEYHFPCYRWIEGYGTLELREG
>gnl|CDD|28751 cd01754, PLAT_plant_stress, PLAT/LH2 domain of plant-specific single domain protein family with unknown function. Many of its members are stress induced. In general, PLAT/LH2 consists of an eight stranded beta-barrel and it's proposed function is to mediate interaction with lipids or membrane bound proteins
CVYTIYVQTGSIWKAGTDSRISLQIYDADGPGLRIANLEAWGGLMGAGHDYFERGNLDRF
SGRGPCLPSPPCWMNLTSDGTGNHPGWYVNYVEVTQAGQHAPCMQHLFAVEQWLATDESP
YMLTAVRNN
>gnl|CDD|28752 cd01755, PLAT_lipase, PLAT/ LH2 domain present in connection with a lipase domain. This family contains two major subgroups, the lipoprotein lipase (LPL) and the pancreatic triglyceride lipase. LPL is a key enzyme in catabolism of plasma lipoprotein triglycerides (TGs). The central role of triglyceride lipases is in energy production. In general, PLAT/LH2 domain's proposed function is to mediate interaction with lipids or membrane bound proteins
WHYQVKVHLSGKKNLEVDGTFTVSLYGTKGETEQLPIVLGELKPNKTYSFLIDTEVDIGD
LLKVKFKWENNVINSNSGETLPKLGARKIRVKSGETQKKFTFCSQDTVRELEVLQTLVKC
>gnl|CDD|28753 cd01756, PLAT_repeat, PLAT/LH2 domain repeats of family of proteins with unknown function. In general, PLAT/LH2 consists of an eight stranded beta-barrel and it's proposed function is to mediate interaction with lipids or membrane bound proteins
VTYEVTVKTGDVKGAGTDANVFITLYGENGDTGKRKLKKSNNKNKFERGQTDKFTVEAVD
LGKLKKIRIGHDNSGLGAGWFLDKVEIREPGTGDEYTFPCNRWLDKDEDDGQIVRELYPS
>gnl|CDD|28754 cd01757, PLAT_RAB6IP1, PLAT/LH2 domain present in RAB6 interacting protein 1 (Rab6IP1)_like family. PLAT/LH2 domains consists of an

eight stranded beta-barrel. In RabIP1 this domain may participate in lipid-mediated modulation of Rab6IP1's function via it's generally proposed function of mediating interaction with lipids or membrane bound proteins
MPYHVVIVPSKKLGGSMFTANPWICVSGELGETPPLQIPKNSLEMTFDCQNLGKLTTVQI
GHDNSGLLAKWLVEYVMVRNEITGHTYKFPCGRWLGEGVDDGNGEDGSLERVLV
>gnl|CDD|28755 cd01758, PLAT_LPL, PLAT/ LH2 domain present in lipoprotein lipase (LPL). LPL is a key enzyme in catabolism of plasma lipoprotein triglycerides (TGs) and has therefeore has a profound influence on triglyceride and high-density lipoprotein (HDL) cholesterol levels in the blood. In general, PLAT/LH2 domain's proposed function is to mediate interaction with lipids or membrane bound proteins
FHYQLKIHFFNQTNRIETDPTFTISLYGTLGESENLPLTLPEGITGNKTNSFLITTEKDI
GDLLMLKLKWEGSSLWSNSWWTVQTIIPWSGWWRGSGLTIRKIRVKAGETQKKMTFCAED
PESSLLRPGQEKVFVKC
>gnl|CDD|28756 cd01759, PLAT_PL, PLAT/LH2 domain of pancreatic triglyceride lipase. Lipases hydrolyze phospholipids and triglycerides to generate fatty acids for energy production or for storage and to release inositol phosphates that act as second messengers. The central role of triglyceride lipases is in energy production. The proposed function of PLAT/LH2 domains is to mediate interaction with lipids or membrane bound proteins
WRYKVSVTLSGKKKVTGTILVSLYGNKGNTRQYEIFKGTLKPGNTYSAFIDVDVDVGPLT
KVKFIWNNNVINITLPKVGAEKITVQSGKDGKVFNFCSSETVRENVLQTLTPC
>gnl|CDD|28757 cd02899, PLAT_SR, Scavenger receptor protein. A subfamily of PLAT (Polycystin-1, Lipoxygenase, Alpha-Toxin) domain or LH2 (Lipoxygenase homology 2) domain. It consists of an eight stranded beta-barrel. The domain can be found in various domain architectures, in case of lipoxygenases, alpha toxin, lipases and polycystin, but also as a single domain or as repeats.The putative function of this domain is to facilitate access to sequestered membrane or micelle bound substrates. This subfamily contains Toxoplasma gondii Scavenger protein TgSR1
KTYTASVQTGKDKEAGTNGTIEITLLGSSGRSNPKTLSQGFYPGSLKRIRFRAADVGDIN
AIILSNTALNDPWYCDYVRIKSEDGKVFAFNVKRWIGYPYEQSVEVSLK
>gnl|CDD|79441 pfam00061, Lipocalin, Lipocalin / cytosolic fatty-acid binding protein family. Lipocalins are transporters for small hydrophobic molecules, such as lipids, steroid hormones, bilins, and retinoids. The family also encompasses the enzyme prostaglandin D synthase (EC:5.3.99.2). Alignment subsumes both the lipocalin and fatty acid binding protein signatures from PROSITE. This is supported on structural and functional grounds. The structure is an eight-stranded beta barrel
SGKWYLIASASNFEEFMKEKGPLRVYKPTIEITQEGNLEVTFTVKTNGTCKETTIVFKKG
EEPGEFTANYDGRKVKSVVTTDYDNYLILYQCKEKEGGHTRMAKLLGRGPDLSPEIKEEF
DKLVKTLGIDEENIVRLYKRD
>gnl|CDD|63956 pfam00068, Phospholip_A2_1, Phospholipase A2. Phospholipase A2 releases fatty acids from the second carbon group of glycerol. Perhaps the best known members are secreted snake venoms, but also found in secreted pancreatic and membrane-associated forms. Structure is all-alpha, with two core disulfide-linked helices and a calcium-binding loop. This alignment represents the major family of PLA2s. A second minor family, defined by the honeybee venom PLA2 PDB:1POC and related sequences from Gila monsters (Heloderma), is not recognised. This minor family conserves the core helix pair but is substantially different elsewhere. The PROSITE pattern PA2_HIS, specific to the first core helix, recognises both families
NLVQFGNMIQCATGKRPVLSYADYGCYCGWGGSGTPVDALDRCCFVHDCCYGEAEKPGCN
PKTTTYSYSCSNGDITCGGNDPCERFVCECDRAAAICFARNPYNKKYWNICTSERC
>gnl|CDD|79497 pfam00168, C2, C2 domain
LRVTVISAKNLPPKDLNGKSDPYVKVYLGGQPKDKKKTKVVKNTLNPVWNETFTFEVPLP
DLQELRIEVYDYDRFGKDDFIGEVT

>gnl|CDD|79498 pfam00169, PH, PH domain. PH stands for pleckstrin homology
VIKEGWLLKKGSGGKKSWKKRYFVLFDDVLLYYKDKKKSSSKPKGSIPLSGIQVTKVPDN
EGGKRKNVFEIRTGDRETLLLQAESEEERKEWVKALQSAIR
>gnl|CDD|79509 pfam00198, 2-oxoacid_dh, 2-oxoacid dehydrogenases acyltransferase (catalytic domain). These proteins contain one to three copies of a lipoyl binding domain followed by the catalytic domain
AGEEERVPLSGIRKAIAKRMTESKQTIPHFTLFDEVDMTKLLKLRKKLKEFAEKHGVKLT
FLDFIIKAVALALKKFPEVNASWDGDTNEIVYKKYVNIGVAVATPDGLVVPVIKNADKKS
LAEIAKEIKELAKKAREGKLKPEEMQGGTFTISNLGMFGGLFFTPIINPPQVAILGVGAI
VKRPVVVDGEIVVRPMMYLSLSFDHRVIDGADAARFLKDLKELLEDPALLL
>gnl|CDD|79528 pfam00235, Profilin, Profilin
SWQAYVDNLLMGTGKVQGAAIVGYDGSNVWAASAGFTFLKIGEIANIAAGFRNPANLPST
GIKLCGVKYMSLRGDGDRSIYGKKGAGGVVIVKTGQALVIGHYKETVQPGQANKVVEKLA
DYL
>gnl|CDD|64262 pfam00387, PI-PLC-Y, Phosphatidylinositol-specific phospholipase C, Y domain. This associates with pfam00388 to form a single structural unit
ELSSLVNYIQSIKFRSFSLPAEKNRSYEMSSFSERKAKRLLKESPVEFVKHNKRQLSRVY
PKGTRFDSSNFMPQPFWNAGCQMVALNFQTSDLPMQINLGMFEDNGGSGYVLKPEFLR
>gnl|CDD|79583 pfam00388, PI-PLC-X, Phosphatidylinositol-specific phospholipase C, X domain. This associates with pfam00387 to form a single structural unit
MSIPLSHYFISSSHNTYLTGKQLWGKSQVESYRQQLDHGCRCVELDCWDGPDDEPIIYHG
GTFTLEIKLKDVLEAIKDFLFKTSPYPIILSLENHCNSDQQRKMAKYFEEIFGDYLLTKP
LDSLTTKLPSLKDLRGKILLKNKK
>gnl|CDD|64477 pfam00614, PLDc, Phospholipase D Active site motif. Phosphatidylcholine-hydrolysing phospholipase D (PLD) isoforms are activated by ADP-ribosylation factors (ARFs). PLD produces phosphatidic acid from phosphatidylcholine, which may be essential for the formation of certain types of transport vesicles or may be constitutive vesicular transport to signal transduction pathways. PC-hydrolysing PLD is a homologue of cardiolipin synthase, phosphatidylserine synthase, bacterial PLDs, and viral proteins. Each of these appears to possess a domain duplication which is apparent by the presence of two motifs containing well-conserved histidine, lysine, and/or asparagine residues which may contribute to the active site. aspartic acid. An E. coli endonuclease (nuc) and similar proteins appear to be PLD homologues but possess only one of these motifs. The profile contained here represents only the putative active site regions, since an accurate multiple alignment of the repeat units has not been achieved
NDGRLHTKIVVVDDEVAYIGGANLDGGS
>gnl|CDD|64636 pfam00781, DAGK_cat, Diacylglycerol kinase catalytic domain (presumed). Diacylglycerol (DAG) is a second messenger that acts as a protein kinase C activator. The catalytic domain is assumed from the finding of bacterial homologues
LVIVNPKSGGGRGRKKVLEKLRKALNEAQVFETEEGGPAVALELARALGDFDLVVVAGGD
GTVNEVLNGLAGRELRAKPPLGIIPLGTGNDFARALGIPLDPDKAALLLILGQALRGDVV
VLDRW
>gnl|CDD|79702 pfam00787, PX, PX domain. PX domains bind to phosphoinositides
IVVVVDPEKSGDKKHTYYLYEVTTKTNLEEWSVKRRYSDFEELHKKLLRKFPLRILPPLP
PKKLFGSFSEEFIEKRRKGLEEYLQRLLQHPELSNSEVVLEFLESD
>gnl|CDD|64645 pfam00792, PI3K_C2, Phosphoinositide 3-kinase C2. Phosphoinositide 3-kinase region postulated to contain a C2 domain. Outlier of pfam00168 family
PYSDLYVECSLYHGGKPLCLPVQSTSYKPFSNPSIKWNEWLTFPIKISDLPRDARLVITL
WEISGKSKSESKVEPLGWVNLPLFDKKGILRQGPQLLSLWPSKEPDESFPTSTLEKLLKK
YERGDVQPNPRVDWLDFLTL
>gnl|CDD|64738 pfam00887, ACBP, Acyl CoA binding protein
LQEDFEAAAEKVKKLKKNPSNEEKLQLYSLYKQATVGDCNTSRPGMFDLKGRAKWDAWNE
LKGMSKEEAMKAYIAKVEELIAKYA

>gnl|CDD|64994 pfam01161, PBP, Phosphatidylethanolamine-binding protein
DAFDPSVPLPVKYSCGKGVNPGNPLTPSGVPSKPKVSWEGVDAQSYTLIMVDPDAPSRSN
PDLREWLHWIVVNIPGTNDATQGTNTSGENGYEGPCPPKGTGIHRYVFLVYRQPGRIDSD
EPNALDTVLDLGDGRPKFDVRKFAEKHILGLPVAGGFYNAQ
>gnl|CDD|65178 pfam01363, FYVE, FYVE zinc finger. The FYVE zinc finger is named after four proteins that it has been found in: Fab1, YOTB/ZK632.12, Vac1, and EEA1. The FYVE finger has been shown to bind two Zn++ ions. The FYVE finger has eight potential zinc coordinating cysteine positions. Many members of this family also include two histidines in a motif R+HHC+XCG, where + represents a charged residue and X any residue. We have included members which do not conserve these histidine residues but are clearly related
PHWVPDEEVSNCMRCGKPFTLTKRRHHCRACGRIFCSSCSSKTVPLPPMGERPVRVCDSC
YDLLN
>gnl|CDD|65231 pfam01417, ENTH, ENTH domain. The ENTH (Epsin N-terminal homology) domain is found in proteins involved in endocytosis and cytoskeletal machinery. The function of the ENTH domain is unknown
YSEAEIKVREATNNDPWGPSGKLMAEIAEATYNYVEFWEIMSVLWKRLNDKGKNWRHVYK
ALTLLEYLLRNGSERVVQDCRENIYNIRTLEDFQYVDENGKDQGINVRKKAKQLLELLND
DERL
>gnl|CDD|79820 pfam01477, PLAT, PLAT/LH2 domain. This domain is found in a variety of membrane or lipid associated proteins. It is called the PLAT (Polycystin-1, Lipoxygenase, Alpha-Toxin) domain or LH2 (Lipoxygenase homology) domain. The known structure of pancreatic lipase shows this domain binds to procolipase pfam01114, which mediates membrane association. So it appears possible that this domain mediates membrane attachment via other protein binding partners. The structure of this domain is known for many members of the family and is composed of a beta sandwich
VRYQVIVATGGSWGAGTTGKVGISLYGEEGESELIPLDKPLLAPGSTYSFTFDVDEDLGE
LGAVKIKNEHSGLNSPEWFLKRITVKDGGTQGKVHFPCNSWVYPKDETLSLRIF
>gnl|CDD|65360 pfam01553, Acyltransferase, Acyltransferase. This family contains acyltransferases involved in phospholipid biosynthesis and other proteins of unknown function. This family also includes tafazzin, the Barth syndrome gene
RVEVHGLENLPRKGPAIVVANHQSWLDPLVLSLLLYKRPRRPVFVAKDELFTVPLLGWLM
RLLGHIFIDRKKAKDARASLRELVELLLRAGKLVVIFPEGTRSRNGELLPFKKGAFRLAR
EAGVPIVPVAIS
>gnl|CDD|79862 pfam01764, Lipase_3, Lipase (class 3)
VVAFRGTNTILEWLADLDFSLVPFDLLFLGGGKVHKGFLDAYTSVRDQILEELKRLLEKY
PDYKIVVTGHSLGGALASLAAADLAENGLFPSSRIRVYTFGSPRVGNKAFAEYHDEQGPK
VYRVVNVNDIVPRLPPALL
>gnl|CDD|65632 pfam01852, START, START domain
ELAEEAAQELVKMALSDEPGWVLSSENENGDEVLQIFEPSHGEASRASGVVPMVLALLVE
ELLDDMEYRAQWDKDVRSAETLEVISSGGALQYYVAELQAPTPLSPRDFVFVRYWRELRD
GVYVIVDRSVDHPQFPPSSGYVRAERLPSGYLIEPCGNGPSKVTWVEHTDLKGWLPHWLI
RSLLKSGMAFGAKTWVATLQRLCER
>gnl|CDD|65792 pfam02036, SCP2, SCP-2 sterol transfer family. This domain is involved in binding sterols. It is found in the SCP2 protein, as well as the C terminus of the enzyme estradiol 17 beta-dehydrogenase EC:1.1.1.62. The UNC-24 protein contains an SPFH domain pfam01145
SAPLFQELEEALKELLEELVKKVGAILEFNVKDETGKEDAWTIDLKNGKGVVYGGGAAKA
DVTFTISDSDFLKILTGKLGPQTAFMQGKLKIKGNMMLAMKLMAVLKKFL
>gnl|CDD|65869 pfam02121, IP_trans, Phosphatidylinositol transfer protein. Along with the structurally unrelated Sec14p family (found in pfam00650), this family can bind/exchange one molecule of phosphatidylinositol (PI) or phosphatidylcholine (PC) and thus aids their transfer between different membrane compartments. There are three sub-families - all share an N-terminal PITP-like domain, whose sequence is highly conserved. It is described as consisting of three regions. The N-terminal region is thought to bind the lipid and contains

two helices and an eight-stranded, mostly antiparallel beta-sheet. An intervening loop region, which is thought to play a role in protein-protein interactions, separates this from the C-terminal region, which exhibits the greatest sequence variation and may be involved in membrane binding. PITP alpha has a 16-fold greater affinity for PI than PC. Together with PITP beta, it is expressed ubiquitously in all tissues
MLIKEYRILLPMSVQEYQVAQLYMIAKKSRNESHGEGSGVEILSNEPYEDGPGGKGQYTH
KIYHLGSKVPAWIRTLLPEGALEVHEEAWNAYPYTRTRYTNPMKEDFSIKIETWYKPDLG
TQENVFNLSPKDWKTRIIDYIDIVKDQVSSGDYKAEEDPKLFHSVKTGRGPLGPDWKAEL
VKTGDCPLMCAYKLCTVEFRYWGMQTKVENFIHDQALRRTMTRAHRQAWCWQDEWTGLTM
EDIRRLEEETQLHL
>gnl|CDD|66691 pfam03034, PSS, Phosphatidyl serine synthase. Phosphatidyl serine synthase is also known as serine exchange enzyme. This family represents eukaryotic PSS I and II which are membrane bound proteins which catalyses the replacement of the head group of a phospholipid (phosphotidylcholine or phosphotidylethanolamine) by L-serine
PHPALWRIVFGLSVLYLLFLQFLLFQNFDDIRQFLKWLDPKLGGATRLPEKEYGVNCSIY
SWDRIWSHFDIFAFAHFTGWAMKALLIRHWGLCWTISIMWELTELTFMHLLPNFAECWWD
SIILDVLICNGLGIWAGMKTCRFLEMRTYHWASIKDIPTTTGKIKRAVLQFTPASWSYFE
WFDPKSSLQRFAAVYLLVIIWLLTELNTFFLKHVFWMPPKHPLVLGRLIFIGLIAAPTVR
QYYVYLTDKPCKRVGTQCWVFGAICVLELLICIKFGQH
>gnl|CDD|66693 pfam03036, Perilipin, Perilipin family. The perilipin family includes lipid droplet-associated protein (perilipin) and adipose differentiation-related protein (adipophilin)
MATAVGDQPQQESVVDRVLHLPLVSRTYPLVSSAYTSTKDQYPKLNSVCEWAEKGVETIT
SAAVTSALPIVQKLEPQIAVANNYACKGLDKLEEKIPILYQPPEKIYSNAKDAVSSAKDS
VVQPILGRVDKVKGAGTASVESLKSVAWGSINTVLGTRVGQLASSGVDTALTKSEKLVEY
YLPLTKEELEMEAKKVEGFDDVAKPSAYVRLGSLSTKLSRRAYQQALRRVKAAKKKSQEV
IHQLHSVAPLSELARKNVYSAVQKLYVSWVEWKRSAGEDPEDQSHCAEQIEQRILLITRE
LTQQLVTALHTLLGNIQGIPQNIQDTTQHVGVMAGDIYSVFRTARSLKTTSDTALTSSKG
RLQALKDSLKGVTDYLVNNV
>gnl|CDD|66767 pfam03114, BAR, BAR domain. The BAR domain is found in amphiphysin and clathrin binding protein. However the function of this domain is unknown
LKKQFNRASQLLKEKVGKAEKTKLDEDFEELERRFDTTEKEIKKLVKDTKLYLQPNPGAR
AKQTLLAETMIEIGEELGDGSEFGKALEKYGEAMKQLAQLLEQLDDRLRSNFLDPLRNLL
KEFKEIQKHIKKLERKLLDYDAKRHRLKKAKSKKKLKKAEEELRQAQQKFEELNEELKEE
LPNLLALEVEFVVNCLQAFVEAQLDFHRQSYQLLEQLQQQLFK
>gnl|CDD|66801 pfam03149, Flotillin, Flotillin family. Flotillins are integral membrane proteins that have been shown to be present in several subcellular components, including caveolae (invaginated plasma membrane microdomains), lipid rafts (sphingolipid and cholesterol-rich, detergent-resistant plasma membrane microdomains), and the Golgi apparatus. The molecular function of flotillins remains uncertain. They are probably involved in organising the structure of caveolae and lipid rafts, and other detergent resistant membrane domains. They may also be involved in signal transduction. Flotillins have been shown to accumulate in brain cells with the development of Alzheimer's pathology. Also included in this family are Reggie proteins, which are expressed in non-caveolar neuronal plasma membrane domains
REAEAEKEAMDAKFLADTEIAEAQRDYELKKAEFDQEVNTAKAEAQLAYELQAAKAQQQI
REEEMQVEVVERKKQIAVEEQEIERREKELEATVKKPAEAERYRLEQLAEAEKQKQIAEA
EAEAEKIRKIGEAEAAAIEAKGKAEAEQMRKKAEAFQQYGEAAILDMLLEALPQ
>gnl|CDD|67419 pfam03803, Scramblase, Scramblase. Scramblase is palmitoylated and contains a potential protein kinase C phosphorylation site. Scramblase exhibits Ca2+-activated phospholipid scrambling activity in vitro. There are also possible SH3 and WW binding motifs. Scramblase is involved in the redistribution of phospholipids after cell activation or injury

MSGPLQPPANCPAGLEYLAQLDTLMVHQQIEPLEIFTGFETANRYVIKNMNGQPLYYAME
RSNCFARQCCGSQRPFVMHITDNFGAEVLTVKRPFRCCSCCCPCCLQECEIESPPGQTIG
TVLQRWHLWRRNFELQDGDGNQVLLVEGPGCKCSCGGDKEFPVKTADGGEVIGSISRKWG
GLGREAFTDADTYVVRFPLDLDVKLKAVLLGATFLIDFDYFER
>gnl|CDD|67689 pfam04083, Abhydro_lipase, ab-hydrolase associated lipase region
IDPEANLNVSQLIEKWGYPSEEHTVTTEDGYILTLHRIPRGKKNTELGKRPPVLLQHGLL
DSSSNWVVNL
>gnl|CDD|67791 pfam04191, PEMT, Phospholipid methyltransferase. The S. cerevisiae phospholipid methyltransferase (EC:2.1.1.16) has a broad substrate specificity of unsaturated phospholipids
FSLLGYVDPINPSFVAAVVTIAFNPLFWNIVARWEYNTRKLTKAFGGPKKACYMLAACIF
LLGIVRDHCYTQALKSQPTMEILDNPLVYGLGLALFGLGSVLVLSSMYKLGFTGTYLGDY
FGILKEERVTGFPFNVLDNPMYWGSTLNFLGWALMHGKPAGLLLTVVVAFVYRIALLYEE
PFTAEIYAQRDSKQAKKS
>gnl|CDD|80064 pfam04280, Tim44, Tim44-like domain. Tim44 is an essential component of the machinery that mediates the translocation of nuclear-encoded proteins across the mitochondrial inner membrane. Tim44 is thought to bind phospholipids of the mitochondrial inner membrane both by electrostatic interactions and by penetrating the polar head group region. This family includes the C-terminal region of Tim44 that has been shown to form a stable proteolytic fragment in yeast. This region is also found in a set of smaller bacterial proteins. The molecular function of the bacterial members of this family is unknown but transport seems likely. The crystal structure of the C terminal of Tim44 has revealed a large hydrophobic pocket which might play an important role in interacting with the acyl chains of lipid molecules in the mitochondrial membrane
AAALREIKSRDPNFDPKDFLRGAEEAYIPILEAYANGDLETLKKLVSEEVYSALAAEIKE
REARGVFVESRFVDIVKADLAEAKMEGGNDYAQVTVRFHAQQISRTRDKKGEVVEGDEDD
PKEVLELWTFERDPGNPDPNWRLVAIQA
>gnl|CDD|68543 pfam04972, BON, Putative phospholipid-binding domain. This domain is found in a family of osmotic shock protection proteins. It is also found in some Secretins and a group of potential haemolysins. Its likely function is attachment to phospholipid membranes
TTKVKAALLADPGLPGSDIKVTVENGVVTLSGTVDSEEEKEKAEEIARNVKGVKKVVNEI
TVAP
>gnl|CDD|69357 pfam05826, Phospholip_A2_2, Phospholipase A2. This family consists of several phospholipase A2 like proteins mostly from insects
IVPGTKWCGPGNIAANYSDLGREKETDKCCRAHDHCPDKISALENKHGLTNYRPYTISHC
DCDDRFRNCLKAANDSTANTVGKIYFNVVQVPCFGLEHPT
>gnl|CDD|70088 pfam06602, Myotub-related, Myotubularin-related. This family represents a region within eukaryotic myotubularin-related proteins that is sometimes found with pfam02893. Myotubularin is a dual-specific lipid phosphatase that dephosphorylates phosphatidylinositol 3-phosphate and phosphatidylinositol (3,5)-bi-phosphate. Mutations in gene encoding myotubularin-related proteins have been associated with disease
YELCPTYPAKLVVPKSISDDELKKVAKFRSRGRLPVLSWRHQENGAVIVRCSQPLVGFSG
KRCKEDEKLLQAIRKANAQSRKLYIVDARPRTNALANRAKGGGYENEENYPNAELVFL
>gnl|CDD|70467 pfam07002, Copine, Copine. This family represents a conserved region approximately 180 residues long within eukaryotic copines. Copines are Ca(2+)-dependent phospholipid-binding proteins that are thought to be involved in membrane-trafficking, and may also be involved in cell division and growth
SLHYISPRQPNPYEQAIRAVGEILQDYDSDKLFPAFGFGAKLPPDYSVSHDFPLNFNPED
PECNGLEGVLEAYREALPNVQLSGPTNFAPIINYAARIAEATQKGGQYHVLLIITDGQVT
DMKETIDAIVSASDLPLSIIIVGVG
>gnl|CDD|47395 smart00046, DAGKc, Diacylglycerol kinase catalytic domain (presumed); Diacylglycerol (DAG) is a second messenger that acts as a protein kinase C activator. DAG can be produced from the hydrolysis of

phosphatidylinositol 4,5-bisphosphate (PIP2) by a phosphoinositide-specific phospholipase C and by the degradation of phosphatidylcholine (PC) by a phospholipase C or the concerted actions of phospholipase D and phosphatidate phosphohydrolase. This domain is presumed to be the catalytic domain. Bacterial homologues areknown
PLLVFVNPKSGGGKGETLLRKFRSLLNPRQVFDLTKGGPDVALVIFRDVPSFDRVLVCGG
DGTVGWVLNALDKRELPLLTPPVAVLPLGTGNDLARSLGWGGGYDGEKLLKTLRDALEAD
TVKLDRW
>gnl|CDD|47412 smart00064, FYVE, Protein present in Fab1, YOTB, Vac1, and EEA1; Zinc-binding domain, possibly involved in endosomal targetting. Recent data indicates that these domains bind PtdIns(3)P
EKRPHWIPDEEVSNCMGCGKEFNLTKRRHHCRNCGRIFCSKCSSKKAPLPKLGNEKPVRV
CDDCYENLNG
>gnl|CDD|47430 smart00085, PA2c, Phospholipase A2;
NLWQFGNMIQCATGKRAWISYGDYGCYCGWGGSGTPVDATDRCCFVHDCCYGKAEKEGCN
PKTTTYSYSCDNGFITCGKNDNTSCLVFVCECDRAAAICFALNTYNKANYNIYTKKRC
>gnl|CDD|47453 smart00109, C1, Protein kinase C conserved region 1 (C1) domains (Cysteine-rich domains); Some bind phorbol esters and diacylglycerol. Some bind RasGTP. Zinc-binding domains
HHHVFRTFTGKPTYCCVCRKSIWGSFKQGLRCSWCKVKCHKKCAPKVPKPC
>gnl|CDD|47481 smart00142, PI3K_C2, Phosphoinositide 3-kinase, region postulated to contain C2 domain; Outlier of C2 family
VKIESLWDCNRPLVSTISLIHGIPLNWSSSYEDLYVEIQLYHGGKLLCLPVSTSYKAFFN
RVKWNEWLTFPIQISDLPREARLCITIYAVKDDSKKSEFGSSNLDLF
>gnl|CDD|47487 smart00148, PLCXc, Phospholipase C, catalytic domain (part); domain X; Phosphoinositide-specific phospholipases C. These enzymes contain 2 regions (X and Y) which together form a TIM barrel-like structure containing the active site residues. Phospholipase C enzymes (PI-PLC) act as signal transducers that generate two second messengers, inositol-1,4,5-trisphosphate and diacylglycerol. The bacterial enzyme appears to be a homologue of the mammalian PLCs
QDMSKPLSHYFINSSHNTYLTGKQLWGESSVEGYIQALKHGCRCVELDCWDGPDGEPVIY
HGHTFTLPIKLSEVLEAIKKFAFVTSPYPVILSLENHCSPDQQAKMAQMFKEIFGDLLYT
PPTTSSLEYLPSPEQLKGKILLKGK
>gnl|CDD|47488 smart00149, PLCYc, Phospholipase C, catalytic domain (part); domain Y; Phosphoinositide-specific phospholipases C. These enzymes contain 2 regions (X and Y) which together form a TIM barrel-like structure containing the active site residues. Phospholipase C enzymes (PI-PLC) act as signal transducers that generate two second messengers, inositol-1,4,5-trisphosphate and diacylglycerol. The bacterial enzyme appears to be a homologue of the mammalian PLCs
LSELVSYCAPVKFRSFELAEEKNPFYEMSSFSETKAKKLLEKAPTDFVRYNQRQLSRVYP
KGTRVDSSNYNPQVFWNHGCQMVALNFQTPDKAMQLNQGMFRANGGCGYVLKPDFLR
>gnl|CDD|47494 smart00155, PLDc, Phospholipase D. Active site motifs. Phosphatidylcholine-hydrolyzing phospholipase D (PLD) isoforms are activated by ADP-ribosylation factors (ARFs). PLD produces phosphatidic acid from phosphatidylcholine, which may be essential for the formation of certain types of transport vesicles or may be constitutive vesicular transport to signal transduction pathways. PC-hydrolysing PLD is a homologue of cardiolipin synthase, phosphatidylserine synthase, bacterial PLDs, and viral proteins. Each of these appears to possess a domain duplication which is apparent by the presence of two motifs containing well-conserved histidine, lysine, aspartic acid, and/or asparagine residues which may contribute to the active site. An E. coli endonuclease (nuc) and similar proteins appear to be PLD homologues but possess only one of these motifs. The profile contained here represents only the putative active site regions, since an accurate multiple alignment of the repeat units has not been achieved

YDGVLHTKLMIVDDETAYIGSANLDGRS
>gnl|CDD|47499 smart00162, SAPA, Saposin/surfactant protein-B A-type DOMAIN; Present as four and three degenerate copies, respectively, in prosaposin and surfactant protein B. Single copies in acid sphingomyelinase, NK-lysin amoebapores and granulysin. Putative phospholipid membrane binding domains
GPKRCTWGPSVWCQNLETASQCNAVKHCLQRVWS
>gnl|CDD|47562 smart00233, PH, Pleckstrin homology domain. Domain commonly found in eukaryotic signalling proteins. The domain family possesses multiple functions including the abilities to bind inositol phosphates, and various proteins. PH domains have been found to possess inserted domains (such as in PLC gamma, syntrophins) and to be inserted within other domains. Mutations in Brutons tyrosine kinase (Btk) within its PH domain cause X-linked agammaglobulinaemia (XLA) in patients. Point mutations cluster into the positively charged end of the molecule around the predicted binding site for phosphatidylinositol lipids
VIKEGWLLKKSSGGKKSWKKRYFVLFNGVLLYYKSKKKKSSSKPKGSIPLSGCTVREAPD
SDSDKKKNCFEIVTPDRKTLLLQAESEEEREEWVEALRKAIAKL
>gnl|CDD|47563 smart00234, START, in StAR and phosphatidylcholine transfer protein; putative lipid-binding domain in StAR and phosphatidylcholine transfer protein
EVAEEAAAELVKLALADGKGWVLSPEIENGDEYRSILEDGKFPGYASRLSGVVPMVSALL
VAELMDDSEYRKEWDKNFAKAEVVEVISPGGDIQYYVAAFVAPVSPRDFVFLRYWRKLDV
RGGYVIVSRSVTHETSPPSSGYVRAETLPSGLLIEPLGDGPSKVTWVSHADLKGWLPHWL
VRSLIKSGRAEFAKTWRATLQKNCEK
>gnl|CDD|47568 smart00239, C2, Protein kinase C conserved region 2 (CalB); Ca2+-binding motif present in phospholipases, protein kinases C, and synaptotamins (among others). Some do not appear to contain Ca2+-binding sites. Particular C2s appear to bind phospholipids, inositol polyphosphates, and intracellular proteins. Unusual occurrence in perforin. Synaptotagmin and PLC C2s are permuted in sequence with respect to N- and C-terminal beta strands. SMART detects C2 domains using one or both of two profiles
TLTVKIISARNLPPKDKGGKSDPYVKVSLDGDPREKKKTKVVKNTLNPVWNETFEFEVPP
PELSELEIEVYDKDRFSRDDFIGQVTIPLSDLLLGGRHEKL
>gnl|CDD|47602 smart00273, ENTH, Epsin N-terminal homology (ENTH) domain;
SDLEVKVRKATNNDEWGPKGKHLREIIQGTHNEKSSVAEIMAVLWRRLNDTKNWRVVYKA
LILLHYLLRNGSPNVVLEALRNRNRILTLSDFRDIDSRGKDQGANIRTYAKYLLERLEDD
GRLKKER
>gnl|CDD|47636 smart00308, LH2, Lipoxygenase homology 2 (beta barrel) domain;
AKYKVTVTTGVLDFAGTTASVSLSLIGAEGRGKESKLDYLERPLLFARGSTYSFTFDVDV
DFGELGAVKIKNEHAGLHPEWFLKSITVKDGPTGGKVHFPCNSWVYPKKKYPGERIFFAN
>gnl|CDD|47640 smart00312, PX, PhoX homologous domain, present in p47phox and p40phox. Eukaryotic domain of unknown function present in phox proteins, PLD isoforms, a PI3K isoform
DNILIVTVVEFETYGDGKHYYYVIEIETSTGLKEWTVKRRYSDFYELHSKLKRKFPRRIL
PPLPGKKLFVRSKLSEEFIEKRRRGLEKYLQKLLNHPELINHSEVVLEFLESS
>gnl|CDD|47705 smart00392, PROF, Profilin; Binds actin monomers, membrane polyphosphoinositides and poly-L-proline
MSWQAYVDNLLVGSGFVDGAAIGGKDGSVWAASAGRNFQIITPEEIAAIAALFNSLAGVF
SNGITLGGQKYMVIRADDRSIMGKKGAGGVVIVKTKQAIVIGMYEEGVQPGQANKTVEKL
ADYLRSSGY
>gnl|CDD|47803 smart00499, AAI, Plant lipid transfer protein / seed storage protein / trypsin-alpha amylase inhibitor domain family;
CPPVLLQLCAPCLSYLVGGSQRGAPPSQACCSQLRGLPSAAQCRCLALRAAVLGILIPGV
NAQNAASLPSACGVPVPPDC
>gnl|CDD|47819 smart00516, SEC14, Domain in homologues of a S. cerevisiae phosphatidylinositol transfer protein (Sec14p); Domain in homologues of a S. cerevisiae phosphatidylinositol transfer protein (Sec14p) and in RhoGAPs,

RhoGEFs and the RasGEF, neurofibromin (NF1). Lipid-binding domain. The SEC14 domain of Dbl is known to associate with G protein beta/gamma subunits
ELEVGKAYIPGGRYDKDGRPVLVFRAGRFDLKSVTLEELLRYLVYVLEKALQEEKKTGGI
EGFTVIFDLKGLSMSNPDLGVLRKILKILQDHYPERLGKVYIINPPWFFRVLWKIIKPFL
SEKTREKIRFVGPDSKEELLEYIDPEQLPEELGGTLD
>gnl|CDD|47989 smart00721, BAR, BAR domain
GLKKAFNRAKQKVGEKVGKAEKTKLDEDFEELERRFDTTEAEIEKLQKDTKLYLQPNPAL
RAKLASQKKLSKSLGEVYEGEDAGEGLGADSSYGKALDKLGEALKKLLQAKRSLDDQVKQ
TFILPLLNFLLSEFKEIKKARKKLERKRLDYDSARHKLKKAKKSKEKKKDEKLAKAEEEL
RKAKQEFEESNAQLVEELPQLVASRVDFFVNCLQALIEAQLRYHRQAYKLLQQLQQQLDG
>gnl|CDD|48004 smart00737, ML, Domain involved in innate immunity and lipid metabolism. ML (MD-2-related lipid-recognition) is a novel domain identified in MD-1, MD-2, GM2A, Npc2 and multiple proteins of unknown function in plants, animals and fungi. These single-domain proteins were predicted to form a beta-rich fold containing multiple strands, and to mediate diverse biological functions through interacting with specific lipids
FKDCDDDPGKVSEVSISPCPTSIHRGTTLTISIDFTPRQDISKLKVVVHGKIGGIEVPFP
GKTYDLCDVLLLKCPIKKGETVTYKNSFPVPKEFPPGKYTVEWELIDEDGGVLACINFTV
KIK
>gnl|CDD|48016 smart00749, BON, bacterial OsmY and nodulation domain;
TEKVKDALAKDGLIKADSIVVVTDGGVVVLLGGVVDNAEAAAAAAAAAVVGGVKVVVVNL
LIAV