Α

	APP1.1 NPI,05228.1 nduptor proston, phosphotyrousine interaction, PH domain and leacine zigner containing I	GO Process cell cycle cell proliferation signal transduction
HMMerhread	16,5pe	GO Function
2.0.0		protein binding
H sapiens	HMMerThread His	GO Component NuRD complex
Protein	Pfam Domain InterPro Domain HMMer e-value PDB ID SCOP ID n-value Z-Score Start End Ton Position Hits Count	cytoplasm early endosome membrane
Protein NP 036228.1 Transcript	PH IPR001849 5.6e-05 IFGX Ifgya 9.00649664486e-35 10.7648 278 375 1 45 BAR IPR004148 1 ILIRU Iurua 7.26029238822e-06 5.39926 4 224 1 1	endosome
NM 012096.2 Gene 20060	PID IPR006020 2.7e-07 IP3R 1p3ra 7.52005200536e-18 17.0381 502 633 1 7	membrane nucleus
	Domain Functions (GO) Pfam Domain GO ID GO Description	Synonyms
Orthologs DB Species of Ortholog HMMerThread Gene ID Link	BAR GO.000515 protein binding BAR GO.000577 vsroplasm	APPL DIP13alpha
DB Ortholog Gene ID Link HO Manascalus 72993 NP 660256.1	IBAR [CO3005757]cytopisem IDIMer Aligaments	iPfam Interactions
	BAR	Domain A Domain B
HPRD Interactions Interactor Gene ID Evidence	*->1k%ghCgffnRasqllko%VCkackTkvlDedFeolerrfdttcklv + X +++ +7 ++e+ +++ 4 Tott===================================	PH RhoGEF
DCC 1630 in vivo yeast 2-hybrid	kklyketklTigpnpaarakgkvlekiskrgqykrkgypq7etllaetm 1+ + + ++++++ m+ 1 ++ +	PH IRS PH PID
APPL2 55198 yeast 2-hybrid	38 KQLYQAMBRITDAGKELSAXYW qeigeelgddscdf/GkaLokygeamkqlaqlleqldervkunfidP 'ee+ +++ +lgddscdf/GkaLokygeamkqlaqlleqldervkunfidP	PH WD40 PH Ras
in vivo	66 KEYEKQT (PLOUDDEY-MESTLQQFSKVIDELSBORAVLSTQLADAMMYP 114 ltnllekefkolgkhikklerKEDypakrtrikkaktkaktokki	PH PH PH BTK
AKT2 208 in vitro in vivo yeast 2-hybrid	115 ITQFMERDIAWILTIAWVTQIASHKUDAAINRYGRIGHKHUNG 157 akAdgleeElrqAqqkfEelmeeLkeeEpnllelevefiunglq	BAR BAR
PSHR 2492 in vivo yeast 2-hybrid	<pre>->lipsgbdffftaballiefterdamstrukenter ->lipsgbdfftaballiefterdamstrukenter ->risticstoppe</pre>	BAR RhoGEF BAR IRS
PIK3CA 5290 in vivo	++ +44* f++ 0+1 +46 + 202 CYNDACISTIYNGSENIDEQLEE 224 PH	BAR PID BAR WD40
yeast 2-hybrid		BAR Ras
SILAZ 9219 in vivo	*********************************	BAR PH BAR BTK
ADIPOR1 51094 in vitro in vivo yeast 2-hybrid	14111111111111111111111111111111111111	
RAB5A 5868 in vitro in vivo	375 K 375	
RBBP7 5931 in vitro in vivo	PID	
IRAF2 7186 yeast 2-hybrid	TO ->	
Potential Domain-Domain Interactions	ikrikysrgerqpgtkidLsistdylklidektesekevlhdhplrkISP + $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$	
Domain A Interactor Domain B	iavogopdvälrtfayarr.s.qdiiaadgatykfaCiVFcokokyklas a + + ++r F++ r+a+ + ++ C++Fo+ +o	
PID APPL2 PID PH APPL2 PH	574 YAT-HQG-SHKLFG7VLRtSaGR-SESHLSSVCYIFESHNRGE 413 diaqavGqAFovaYqofIrs<-* j +0C A + a+ 1++	
PH RBBP7 WD40	614 KICDSVOLNKOIALEMELDR 633	
	InterPro Domains Name ID Database Start End External DB DB Name s-value	
	Pleckstrin-like IPR001849 ProfileScan 277 377 PS50003 PH_DOMAIN 0.0	
	Phosphotyrosine interaction region IPR006020 ProfileScan 502 638 PS01179 PID 0.0 Picekstrin homology-type IPR011993 Gene3D 261 389 G3DSA:2.30.29.20 PH_type 6.5999985252638E-4	
	Pleckstrin homology-type [PR011993] Geme3D 502 [629 G3DSA:2.30.29.30 [PH_type]] 3.4999985114892205E-8	
	CDD Domains Name ID Database Start End e-value	
	PTB 22849 CD 499 627 1.95035e-20	
	PTB 47768 SMART 500 636 2.60749e-11 CED-6 29922 CD 499 632 6.10087e-09	
	PID 89030 PFAM 502 632 3.7323e-06 CED6_AIDA1b 29216 CD 499 627 7.69998e-06	
	PH_centaurin 29899 CD 280 372 0.000447861	
	PH 98747 PFAM 279 375 0.00157939 PH 47362 SMART 278 376 0.00228739	
	PH_oligophrenin 23898 CD 314 367 0.00302726	
	IP 2866 CD S02 (no4) (nosm13)4 COG2005 5222 COG 126 222 (no11)973 PH-Bace 2686 CD 301 175 (nosm25)	
	PH-like 28845 CD 301 373 0.0155826 Numb 28917 CD 502 633 0.0937186	
	Summary	
	The protein encoded by this gene has been shown to be involved in the regulation of cell proliferation, and in the crosstalk between the adiponectin signalling and assume signalling pathways. The encoded proteins busis many other proteins, including RADSA, DCC, ARTZ, IRKECA, adjuscent mecropress, and proteins of the NADMCPT complex. This protein is found associated with encodermal mechanism, at can be released by DEF and translocated to the	1
	iand meanin signaling pathways. The encoded protein binds many other proteins, including KAB5A, DCC, AKT2, PIKSCA, adiponentin receptors, and proteins of the NuRD/MeCP1 complex. This protein is found associated with endosomal membranes, but can be released by EGF and translocated to the muckuts.	
	Associated Literature	3
	END/07/21 The findings suggest a role for APPL1 and APPL2 protein as dynamic scaffolds that modulate RAB5-associated signaling endosomal membranes by their ability to undergo domain-mediated oligomerization, membrane targeting and phosphoinosidde binding.	1
	16622416 APPL1 interacts with adiponectin receptors in mammalian cells and the interaction is stimulated by adiponectin.	
	17348559 These data suggest that APPL1 plays an important role in insulin-stimulated Glut4 translocation in muscle and adipose tissues and that its N- terminal portion may be critical for APPL1 function.	
	18307981. Thus, binding to APPL1 helps localize OCRL at specific cellular sites, and disruption of this interaction may play a role in disease. 17287461 APPL1 acts as a common downstream effector of Adiponectin receptors R1 and -R2, mediating adiponectin-evoked endothelial nitric oxide	
	production and endothelium-dependent vasodilation. [7490420 Observational study of gene-disease association. (HuGE Navigator)	
	17581628 The crystal structures of human APPL1 N-terminal BAR-PH domain motif, is reported.	
	17502038 The ability of APPL1 to interact with multiple signaling molecules and phospholipids supports an important role for this adaptor in cell signaling. 15016378 identification of a pathway directly linking the small GTPase Rab5, a key regulator of endocytosis, to signal transduction and mitogenesis via APPL 1 and APPL, 2 mo Rab5 Genetication.	
	APPL1 and APPL2, two Rab5 effectors 15070827 APPL1 is a potential interactor with FSHR	
	Complete HMMer Results]
	Pfam Domain e-value Start End	
	BAR 1 4 224	
	RRF 2.9 49 197 CsbD 47 609 651	
	Thymidylar_synt 47 84 275 5 3 exome N 49 581 662	
	Developed at the MPI-CBG Dresden, Germany, Please mail bradshaw@mpi-cbg.de for details	

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