

(A) Belongs to the CDP-alcohol phosphatidyltransferase class-I family.

1. **PIS1_ARATH** [*Arabidopsis thaliana* (thale cress)]
2. **CDIPT_HUMAN** [*Homo sapiens* (human)]
3. **PIS_YEAST** [*Saccharomyces cerevisiae* (baker's yeast)]
CDP-diacylglycerol--inositol 3-phosphatidyltransferase 1
(Phosphatidylinositol synthase 1) (PtdIns synthase 1) (PI synthase1) (AtPIS1). (**EC 2.7.8.11**)
FUNCTION: Catalyzes the biosynthesis of phosphatidylinositol (PtdIns) as well as PtdIns:inositol exchange reaction. May thus act to reduce an excessive cellular PtdIns content. The exchange activity is due to the reverse reaction of PtdIns synthase and is dependent on CMP, which is tightly bound to the enzyme.
CATALYTIC ACTIVITY: CDP-diacylglycerol + myo-inositol = CMP + phosphatidyl-1D-myo-inositol.
SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein. [5 TMSs]
INDUCTION: Inhibited by PtdIns (product inhibition), phosphatidylinositol phosphate, and nucleoside di- and tri-phosphates.
4. **PGSA_ECOLI** [*Escherichia coli*]
5. **PGSA_BACSU** [*Bacillus subtilis*]
6. **PGSA_HAEIN** [*Haemophilus influenzae*]
CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
(Phosphatidylglycerophosphate synthase) (PGP synthase). (**EC 2.7.8.5**)
FUNCTION: This protein catalyzes the committed step to the synthesis of the acidic phospholipids.
CATALYTIC ACTIVITY:
CDP-diacylglycerol + sn-glycerol 3-phosphate = CMP + 3(3-sn-phosphatidyl)-sn-glycerol 1-phosphate.
PATHWAY: Acidic phospholipids biosynthesis.
SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass membrane protein. [4 TMSs]
7. **PSS_BACSU** [*Bacillus subtilis*]
8. **PSS_YEAST** [*Saccharomyces cerevisiae* (baker's yeast)]
CDP-diacylglycerol--serine O-phosphatidyltransferase
(Phosphatidylserine synthase). (**EC 2.7.8.8**)
CATALYTIC ACTIVITY: CDP-diacylglycerol + L-serine = CMP + 3-O-sn-phosphatidyl-L-serine.
PATHWAY: Biosynthesis of phosphatidylcholine (Bremer-Greenberg pathway); committed step.
SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
9. **CPT1_YEAST** [*Saccharomyces cerevisiae* (baker's yeast)]
Diacylglycerol cholinephosphotransferase
(SN-1,2-diacylglycerol cholinephosphotransferase) (CHOPT). (**EC 2.7.8.2**)
FUNCTION: Involved in protein-dependent process of phospholipid transport to distribute phosphatidyl choline to the luminal surface. The multiple transmembrane domains and luminal hydrophilic domains of the cholinephosphotransferase might participate in the transport process.
CATALYTIC ACTIVITY: CDP-choline + 1,2-diacylglycerol = CMP + a phosphatidylcholine.
ENZYME REGULATION: Requires a divalent cation activator, and is inhibited by CMP.
SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
10. **EPT1_YEAST** [*Saccharomyces cerevisiae* (Baker's yeast)]
Ethanolaminephosphotransferase (**EC 2.7.8.1**) (ETHPT)
FUNCTION: Involved in protein-dependent process of phospholipid transport to distribute phosphatidyl ethanolamine to the luminal surface. The multiple transmembrane domains and luminal hydrophilic domains of the ethanolaminephosphotransferase might participate in the transport process. EPT1 catalyzes both choline- and ethanolamine-phosphotransferase reactions.
CATALYTIC ACTIVITY: CDP-ethanolamine + 1,2-diacylglycerol = CMP + a phosphatidylethanolamine

(B) Multiple alignment of the predicted DIP synthases and other characterized proteins from the CDP-alcohol phosphatidyltransferase class-I family.

DIPS signature

TM_DIPS					DG	sr	NR	s			tPnq			
Tnea_DIPS					MLRKST	DGWIS	SSLINRRFS	SRITN	-LILEKNWQI	TPNQ	MSFIS	SFLVGVLA	FPFYLLK	----
APE1516					MLRKTT	DGWIS	SSLNRRIS	STRITN	-FILKRNWNV	TPNQ	MSFVS	FLLGMI	AFFPYLIK	----
GZ13E1_32	(227aa of IMPCT)	-			MTVWRS	SWRLG	VGSGD	KPTD	CGPV	SRFLNRRIS	IASAIA	-AIALNLPL	TPNMLSLI	SFLTAAAAALFIAGG
Rxy1021259	(220aa of IMPCT)	-			KKA	EKLLQG	-DLAKSD	DGLI	SRHINREFS	TRIF	TPLLLK	MHRGI	TPNQ	VSILSFIIGLISL
17H9-22	(226aa of IMPCT)	-			RLSE	EMVLG	-WAAS	GNDCPV	SRHINRRIS	SRITR	---	RLDDTP	PLSDQ	VSLLSFLAALGAGLLAAG
PH1219	(210aa of IMPCT)	-			RE	AERLRMR	DQGRK	TRD	CGPV	SRHLNRP	VSRWLSR	---	YLVRTSV	TPNQ
PAB2433	(208aa of IMPCT)	-			KK	AKKLI	VAHSV	KVGV	DGFI	SRYLNR	KKVST	WISS	---	HLVDH
PF1058	(209aa of IMPCT)	-			KK	AKKLI	VYSSV	KVGV	DGFI	SRYLNR	KKVST	WISS	---	LLVHVT
TK2279	(214aa of IMPCT)	-			KR	ARMLVR	TAVK	TG	DGFI	SRHLNRRIS	STRVSE	---	LLVEK	
AF0263	(208aa of IMPCT)	-			R	ANRALV	SA-AV	KSGD	CGFI	SRKINRK	IS	TRISA	---	AIVNK
aq_1367	(216aa of IMPCT)	-			E	KAKYL	VKTA	IKGV	DGFI	SRNLNR	KKVST	TRISP	---	YLVDK
AF2299	(131aa of ?domain)	-			S	SLIKAK	RTGL	KPAY	DGWI	AREIN	RKVS	LRISR	---	LLADT
Saro3075	(106aa of ?domain)	-			L	EAGRA	ILRGT	AKPT	DCIV	SRHVNR	PLS	QAIST	---	VALR
PGSA_ECOLI														QFNIP
PGSA_BACSU														---
PSS_BACSU														---
PSS_YEAST														---
CDIPT_HUMAN														---
PIS_YEAST														---
PIS1_ARATH														---

DIPS signature

TM_DIPS	LPW	IAGIL	VQVS	S	DG	DGe	AR	s	G	D	Dr	d		sy
Tnea_DIPS	MPW	LAAIFI	IQIS	S	ILD	GVDGE	IAR	ARNMS	SNW	GAF	DTML	DRF	VDI	ILAVL
APE1516	QLLV	GGLLV	QLS	S	VL	DGVDG	I	VAR	ARL	RAA	SKAG	GF	DL	TML
GZ13E1_32	QAI	IGALL	IQIS	S	VL	DG	DGE	I	AR	LKH	MQS	SSL	DG	FV
Rxy1021259	RLR	LGGAL	VQLAS	S	IV	DG	DGE	I	AR	L	KHS	QSE	F	G
17H9-22	ALA	AGV	LAQLAS	S	IV	DG	DGE	I	AR	L	KHS	QSE	F	G
PH1219	-I	PLAG	L	YQIS	S	IL	DG	DGE	I	AR	ARM	QTS	K	F
PAB2433	-V	PI	AGIL	YQVS	S	IL	DG	DGE	I	AR	ARM	QTS	K	F
PF1058	-V	PL	AA	L	YQIS	S	IF	D	G	DGE	I	AR	ARM	QTS
TK2279	-L	PL	AG	L	YQIS	S	IL	DG	DGE	I	AR	ARM	QTS	K
AF0263	-I	PL	AG	L	YQIS	S	IL	DG	DGE	I	AR	ARM	QTS	K
aq_1367	-P	AL	G	L	L	YQIS	S	ML	D	G	DGE	I	AR	ARM
AF2299	T	L	L	A	G	V	I	Q	L	H	S	A	I	D
Saro3075	G	L	V	A	G	A	L	L	F	Q	A	A	S	I
PGSA_ECOLI	---	F	A	A	A	L	F	Q	A	A	V	A	A	V
PGSA_BACSU	---	G	I	L	F	I	A	S	T	D	W	V	D	G
PSS_BACSU	-I	H	S	A	V	L	F	I	F	T	G	M	F	L
PSS_YEAST	Y	Q	R	A	H	F	L	L	G	M	C	F	D	L
CDIPT_HUMAN	-P	L	T	A	S	S	F	L	L	S	G	L	L	D
PIS_YEAST	-P	T	A	F	T	W	L	Y	S	T	S	C	L	L
PIS1_ARATH	-K	P	L	F	S	V	L	Y	F	F	S	F	C	C

Family signature DxxDGxxARxxNxxxxGxxxxDxxD

DIPS signature

TM_DIPS	HSV	G	K	V	F	G	T	H	P	A	L	V	G	K	L	S	G	F	A	S	--	R	D	R	
Tnea_DIPS	HSV	G	K	V	F	G	T	H	P	A	L	V	G	K	L	S	G	F	A	S	--	R	D	R	
APE1516	H	T	R	G	E	R	D	A	G	V	H	P	S	L	V	G	P	L	S	L	S	--	R	D	R
GZ13E1_32	S	A	K	S	I	A	N	F	G	Y	K	G	L	I	A	A	G	R	--	R	D	R	L	L	L
Rxy1021259	R	A	R	W	E	A	L	G	R	M	P	S	-	R	F	T	G	L	A	T	--	R	D	R	
17H9-22	A	D	K	Y	D	G	L	M	A	R	R	L	S	-	G	A	S	F	R	L	G	--	R	D	R
PH1219	T	E	R	F	R	G	A	C	A	D	A	Y	K	V	P	A	L	R	K	I	P	G	R	D	E
PAB2433	T	E	R	F	R	G	A	C	A	D	A	Y	K	V	P	A	L	R	K	I	P	G	R	D	E
PF1058	T	E	R	F	R	G	A	C	A	D	A	Y	K	V	P	A	L	R	K	I	P	G	R	D	E
TK2279	T	E	R	F	R	G	A	C	A	D	A	Y	K	V	P	A	L	R	K	I	P	G	R	D	E
AF0263	S	E	K	Y	K	A	E	F	G	E	S	I	F	G	K	R	V	L	I	P	G	R	D	E	R
aq_1367	T	E	R	Y	K	A	G	A	C	A	D	A	Y	K	V	P	A	L	R	K	I	P	G	R	D
AF2299	G	D	K	F	V	A	A	M	R	T	Y	S	P	E	G	F	A	I	P	T	--	R	D	R	L
Saro3075	R	A	K	G	A	A	D	R	T	G	S	P	V	A	G	N	S	P	S	G	G	E	T	R	D
PGSA_ECOLI	L	R	E	W	M	A	E	L	K	R	S	S	V	A	S	W	I	G	K	T	T	A	Q	M	L
PGSA_BACSU	T	G	E	V	S	R	L	L	H	L	L	H	N	L	P	F	E	L	V	S	P	F	A	D	---
PSS_BACSU	F	N	I	E	Q	S	K	L	P	T	F	I	G	M	P	I	F	F	A	G	M	C	L	V	I
PSS_YEAST	F	N	V	T	V	A	Q	L	P	K	D	S	S	T	G	K	S	K	F	E	G	L	P	M	P
CDIPT_HUMAN	I	D	L	S	G	N	P	V	L	R	I	Y	T	S	R	P	A	L	T	C	A	G	N	E	L
PIS_YEAST	V	E	G	E	S	R	L	L	H	L	Y	T	R	D	V	L	T	I	C	A	F	N	E	L	F
PIS1_ARATH	V	K	D	S	T	S	W	L	F	R	L	Y	G	N	R	I	F	M	C	Y	C	C	S	C	

(C) Hydropathy profile of the putative DIP synthase DipB from *T. maritima*.

