

	1	10	20	30	40	50	60	70	80	90	100	110	118		
hPTPsiama D1 (NP 002841) PTPRS	(1)	ADVAEHTER	LKANDS	ESDPG	QFTWEH	SNLEVN	NRVAV	YDHSRVI	QPEGI				MGSDYINANV	VDGYRRQ	
mPTPsiama D1 (NP 035348(revised)) Ptpsr	(1)	TDAEHMER	LKANDS	ESDPG	QFTWEH	SNLEANK	NRVANV	YDHSRVI	QPEGI				MGSDYINANV	VDGYRRQ	
rPTPsiama D1 (NP 062013) Ptpord	(1)	TDAEHMER	LKANDS	ESDPG	QFTWEH	SNLEANK	NRVANV	YDHSRVI	QPEGI				MGSDYINANV	VDGYRRQ	
cPTPsiama D1 (I50212)	(1)	SELAEHTEH	LKANDN	ESDPG	QFTWEH	SNLEVN	NRVANV	YDHSRVI	LP	EGI			VGSDYINANV	VDGYRRQ	
xPTPsiama D1 (AC443607)	(1)	ADVAEHTEL	LKANDN	ESDPG	QFTWEH	SNLEVN	NRVANV	YDHSRVI	LP	EGI			IGSDYINANV	VDGYRRQ	
zPTPsiama D1 (CAC44759)	(1)	SELAEHTEL	LKANDN	ESDPG	QFTWEH	SNLEVN	NRVANV	YDHSRVI	LP	EGI			TGSDYINANV	VDGYRRQ	
hLAR D1 (NP 002831) PTPRF	(1)	TDADNTER	LKANDG	ESDPG	QFTWEN	SNLEVN	NRVANV	YDHSRVI	LP	DGV			PGSDYINANV	VDGYRRQ	
mLAR D1 (NP 035343) Ptprrf	(1)	TDADNTER	LKANDG	ESDPG	QFTWEN	SNSEVN	NRVANV	YDHSRVI	LP	DGV			PGSDYINANV	VDGYRRQ	
rLAR_D1 (NP 062122) Ptprrf	(1)	TDADNTER	LKANDG	ESDPG	QFTWEN	SNSEVN	NRVANV	YDHSRVI	LP	DGV			PGSDYINANV	VDGYRRQ	
xLAR D1 (AAF43606)	(1)	SDADNTER	LKANDG	ESDPG	QFTWEN	SNLEVN	NRVANV	YDHSRVI	LP	DAV			PGSDYINANV	VDGYRRQ	
hPTPdelta_D1 (NP 002830) PTPRD	(1)	LEADHIER	LKANDN	ESDPG	QFTWEH	SNLEVN	NRVANV	YDHSRVI	LP	DAV			PGSDYINANV	VDGYRRQ	
mPTPdelta D1 (D54689)	(1)	LEADHIER	LKANDN	ESDPG	QFTWEH	SNLEVN	NRVANV	YDHSRVI	LP	DAV			PGSDYINANV	VDGYRRQ	
xPTPdelta D1 (AAF43605)	(1)	LEADHIER	LKANDN	ESDPG	QFTWEH	SNLEVN	NRVANV	YDHSRVI	LP	DAV			PGSDYINANV	VDGYRRQ	
hPTPrho D1 (NP 573400) PTPRT	(1)	ADLLQHTI	QKRRGQ	YGFKE	VEALPEG	QASWDT	AKEDEN	NRGNIS	YDHSRVI	LV	DGD		PHSDYINANV	VDGYRRQ	
mPTPrho D1 (NP 067439) Ptprrt	(1)	ADLLQHTI	QKRRGQ	YGFKE	VEALPEG	QASWDT	AKEDEN	NRGNIS	YDHSRVI	LV	DGD		PHSDYINANV	VDGYRRQ	
xPTPrho D1 (AAD50295)	(1)	ADLLQHTI	QKRRGQ	YGFKE	VEALPEG	QASWDT	AKEDEN	NRGNIS	YDHSRVI	LV	DGD		PHSDYINANV	VDGYRRQ	
hPTPmu D1 (NP 002836) PTPRM	(1)	ADLLQHTI	QKCAEG	YGFKE	ESFFEG	QSAPWDS	AKDENR	NRGNIS	YDHSRVI	LV	DGD		TNSDYINANV	VDGYRRQ	
mPTPmu D1 (NP 033010) Ptprrm	(1)	ADLLQHTI	QKCAEG	YGFKE	ESFFEG	QSAPWDS	AKDENR	NRGNIS	YDHSRVI	LV	DGD		NNSDYINANV	VDGYRRQ	
hPTPkappa D1 (NP 002835) PTPRK	(1)	ADLLQHTI	NLKTSDS	YGFKE	ESFFEG	QSASWDV	AKKQNR	NRGNIS	YDHSRVI	LV	DGD		PSSDYINANV	VDGYRRQ	
mPTPkappa D1 (NP 033009 (revised)) Ptprrk	(1)	ADLLQHTI	NLKTSDS	YGFKE	ESFFEG	QSASWDV	AKKQNR	NRGNIS	YDHSRVI	LV	DGD		PSSDYINANV	VDGYRRQ	
hPTPlamda D1 (NP 005695) PTPRU	(1)	ADLLQHTI	NLKTAE	YGFKE	ESFFEG	WD	ATKKDK	NRGNIS	YDHSRVI	LV	DGD		PNSDYINANV	VDGYRRQ	
mPTPlamda D1 (NP 035344) Ptprrl	(1)	ADLLQHTI	NLKTAE	YGFKE	ESFFEG	WD	ATKKDK	NRGNIS	YDHSRVI	LV	DGD		PDSDYINANV	VDGYRRQ	
rPTPpsi_D1 (AAB42210) Ptprru	(1)	ADLLQHTI	NLKTAE	YGFKE	ESFFEG	WD	ATKKDK	NRGNIS	YDHSRVI	LV	DGD		PDSDYINANV	VDGYRRQ	
cPTPaloha D1 (AAB04150)	(1)	DKLEEN	NRRIADDN	KLFRE	ESNALP	ACPIQAT	CEAA	SKEEN	NRVNL	YDHSRVI	LV	DGD	PDSDYINANV	VDGYRRQ	
hPTPaloha D1 (NP 002827) PTPRA	(1)	DKLEEN	NRRIADDN	KLFRE	ESNALP	ACPIQAT	CEAA	SKEEN	NRVNL	YDHSRVI	LV	DGD	PDSDYINANV	VDGYRRQ	
mPTPaloha D1 (AAK56109) Ptpora	(1)	DKLEEN	NRRIADDN	KLFRE	ESNALP	ACPIQAT	CEAA	SKEEN	NRVNL	YDHSRVI	LV	DGD	PDSDYINANV	VDGYRRQ	
rPTPaloha D1 (NP 036895) Ptpora	(1)	DKLEEN	NRRIADDN	KLFRE	ESNALP	ACPIQAT	CEAA	SKEEN	NRVNL	YDHSRVI	LV	DGD	PDSDYINANV	VDGYRRQ	
zPTPaloha D1 (NP 571963) Ptpora	(1)	DKLEEN	NRRIADDN	KLFRE	ESNALP	VCPIQAS	CDAA	SKEES	NRVNL	YDHSRVI	LV	DGD	PDSDYINANV	VDGYRRQ	
xPTPaloha D1 (AAA17990)	(1)	DKLEEN	NRRIADDN	KLFRE	ESNALP	ACPIQAT	CEAA	SKEEN	NRVNL	YDHSRVI	LV	DGD	PDSDYINANV	VDGYRRQ	
hPTPpsilon D1 (NP 006495) PTPRE	(1)	EHLEEN	NRVRSADD	KRFRE	ESNALP	SGHIQGT	FEL	ANKEN	NRVNL	YDHSRVI	LV	DGD	PCSDYINANV	VDGYRRQ	
mPTPpsilon D1 (NP 035342) Ptpre	(1)	EHLEEN	NRVRSADD	KRFRE	ESNALP	SGHIQGT	FEL	ANKEN	NRVNL	YDHSRVI	LV	DGD	PCSDYINANV	VDGYRRQ	
rPTPpsilon D1 (XP 215102) Ptprr	(1)	EHLEEN	NRVRSADD	KRFRE	ESNALP	SGHIQGT	FEL	ANKEN	NRVNL	YDHSRVI	LV	DGD	PCSDYINANV	VDGYRRQ	
hPTPqamma D1 (NP 002832) PTPRG	(1)	KQFVKH	IGELYSNNQ	HGFSE	EEVQRC	TADMNIT	AEHSNH	DNKHK	NRVIN	LAYDHSRVI	LV	DGD	PGKDS	KHSDYINANV	VDGYRRQ
mPTPqamma D1 (NP 033007) Ptprrg	(1)	KQFVKH	IGELYSNNQ	HGFSE	EEVQRC	TADMNIT	AEHSNH	DNKHK	NRVIN	LAYDHSRVI	LV	DGD	PGKDS	KHSDYINANV	VDGYRRQ
rPTPqamma D1 (NP 599183) Ptprrg	(1)	KQFVKH	IGELYSNNQ	HGFSE	EEVQRC	TADMNIT	AEHSNH	DNKHK	NRVIN	LAYDHSRVI	LV	DGD	PGKDS	KHSDYINANV	VDGYRRQ
cPTPqamma D1 (Q98936)	(1)	KQFVKH	IGELYSNNQ	HGFSE	EEVQRC	TADMNIT	AEHSNH	DNKHK	NRVIN	LAYDHSRVI	LV	DGD	PGKDS	KHSDYINANV	VDGYRRQ
hPTPzeta D1 (NP 002842) PTPRZ1	(1)	KHFPPKH	VADLHASNG	FTEEFET	KEFQ	VEVQSC	TVDLGIT	ADS	NH	DNKHK	NRVIN	LAYDHSRVI	LV	QAEKDG	
rPTPzeta D1 (NP 037212) Ptprrz1	(1)	KHFPPKH	VADLHASNG	FTEEFET	KEFQ	VEVQSC	TVDLGIT	ADS	NH	DNKHK	NRVIN	LAYDHSRVI	LV	QAEKDG	
cPTPzeta D1 (AAA49015)	(1)	KHFPPKH	VADLHASNG	FTEEFET	KEFQ	VEVQSC	TVDLGIT	ADS	NH	DNKHK	NRVIN	LAYDHSRVI	LV	QAEKDG	
xPTPzeta D1 (BAA97445)	(1)	KQFHKH	VEDLHSRNG	FTEEFET	KEFQ	VEVQSC	TVDLGIT	ADS	NH	DNKHK	NRVIN	LAYDHSRVI	LV	QAEKDG	
hCD45 D1 (NP 002829) PTPRC	(1)	DLLETY	KRKIADEG	RLFLA	FQSP	RVFSK	FPIK	ARK	HNQNK	NRV	VDL	LPYD	YNRV	SENGD	
mCD45 D1 (NP 035340) Ptprrc	(1)	DLLETY	KRKIADEG	RLFLA	FQSP	RVFSK	FPIK	ARK	HNQNK	NRV	VDL	LPYD	YNRV	SENGD	
rCD45_D1 (XP 213985) Ptprrc	(1)	DLLETY	KRKIADEG	RLFLA	FQSP	RVFSK	FPIK	ARK	HNQNK	NRV	VDL	LPYD	YNRV	SENGD	
cCD45 D1 (A54008)	(1)	EKLETY	KRKIADEG	RLFLD	FQSP	RIFTK	FPK	AKR	SH	QNK	NRV	IDL	LPYD	HN	
cypcCD45 D1 (BAA92179)	(1)	GGV	VEAYK	NNKIADEG	RLFMD	FQSP	RIFSN	YTI	KE	AK	SS	NOYK	NRV	VDL	
fuCD45 D1 (CAB96211)	(1)	ETL	LDA	YK	KKIADEG	RLFLA	FQSP	RVFSK	FV	SV	KE	ARR	GC	VD	
sharkCD45 D1 (T43148)	(1)	EQ	L	VD	YK	KKIADEG	RLFLA	FQSP	RVFSK	FV	SV	KE	ARR	GC	
hDEP1 D1 (NP 002834) PTPRJ	(1)	ENFEAY	FKKQ	QADSN	CGFAE	VEDK	LVGIS	QPK	YAE	ELAE	NR	GNV	LPYD	IS	
rDEP1 D1 (NP 058965) Ptprrj	(1)	ENFEAY	FKKQ	QADSN	CGFAE	VEDK	LVGIS	QPK	YAE	ELAE	NR	GNV	LPYD	IS	
mDEP1 D1 (NP 033008) Ptprrj	(1)	ENFEAY	FKKQ	QADSN	CGFAE	VEDK	LVGIS	QPK	YAE	ELAE	NR	GNV	LPYD	IS	
hGLEPP1 D1 (NP 109592) PTPRO	(1)	DDFDAY	LK	DAK	SS	YKFS	LQ	FEEL	KL	GLD	IP	HF	ADL	LN	
rGLEPP1 D1 (NP 059032) Ptprr	(1)	DDFDAY	LK	DAK	SS	YKFS	LQ	FEEL	KL	GLD	IP	HF	ADL	LN	
mPTPphi D1 (NP 035346) Ptprr	(1)	DDFDAY	LK	DAK	SS	YKFS	LQ	FEEL	KL	GLD	IP	HF	ADL	LN	
rabPTPoc D1 (AAB16824)	(1)	DDFDAY	LK	DAK	SS	YKFS	LQ	FEEL	KL	GLD	IP	HF	ADL	LN	
hPTPbeta D1 (NP 002828) PTPRB	(1)	NQFE	EGH	FMK	LQ	ADSN	YL	SK	VE	EELK	DVGR	NS	QCDI	ALL	
mPTPbeta D1 (NP 084204) Ptprrb	(1)	NQFE	EGH	FMK	LQ	ADSN	YL	SK	VE	EELK	DVGR	NS	QCDI	ALL	
rPTPbeta D1 (XP 235156 (revised))	(1)	NQFE	EGH	FMK	LQ	ADSN	YL	SK	VE	EELK	DVGR	NS	QCDI	ALL	
hPTSP31 D1 (AR073855) PTPGMCI	(1)	KSF	LQ	H	VE	LCTN	NN	LKFQ	E	SE	L	P	KFLQ	DL	
rPTPGMC1 D1 (NP 075214) Ptprrg	(1)	KSF	LQ	H	VE	LCTN	NN	LKFQ	E	SE	L	P	KFLQ	DL	
hSAP1_D1 (NP 002833) PTPRH	(1)	EDF	ADH	V	R	NR	ER	DSN	CGFAE	VEDK	LVG	H	S	Q	
mSAP1 D1 (BAC37443)	(1)	KDF	ADH	V	R	NR	ER	DSN	CGFAE	VEDK	LVG	H	S	Q	
rPTPBEM2 D1 (NP 598276)	(1)	KDF	ADH	V	R	NR	ER	DSN	CGFAE	VEDK	LVG	H	S	Q	
mPTPESP_D1 (NP_031981) Esp	(1)	HSF	R	S	Y	E	A	K	S	A	R	A	H	H	

Alignment_195_Vert_PTP_Domains_D1_and_D2_Updated (VNTI 8.0).apcr

	blA2 D1 (P56722) Ptdrn (179)	HFLSWEAECTEAS--TRP	LDLRRKVNKCYR-----	GRSC	ILVHCS	DGAGRTGTYV	ILDMV	LNRAK	--VKE	LDIAAT	LEHVRD	DORPGL	LVRSK	QDFE	FALT	VAEEN
	hIA2beta D1 (NP 002838) PTPRN2 (179)	HFLSNYDRGVSS--SRSL	LDLRRKVNKCYR-----	GRSC	ILVHCS	DGAGRTGTYV	ILDMV	LNRAK	--AKE	LDIAAT	LEHVRD	DORPGL	LVRSK	QDFE	FALT	VAEEN
	macnelA2beta D1 (O02695) (179)	HFLSNYDRGVSS--SRSL	LDLRRKVNKCYR-----	GRSC	ILVHCS	DGAGRTGTYV	ILDMV	LNRAK	--AKE	LDIAAT	LEHVRD	DORPGL	LVRSK	QDFE	FALT	VAEEN
	mPTPNP D1 (P80560) Ptdrn2 (179)	HFLSNYDQGVSS--TRSL	LDLRRKVNKCYR-----	GRSC	ILVHCS	DGAGRTGTYV	ILDMV	LNRAK	--AKE	LDIAAT	LEHVRD	DORPGL	LVRSK	QDFE	FALT	VAEEN
	rPTPNE6 D1 (NP 113788) Ptdrn2 (179)	HFLSNYDQGVSS--TRSL	LDLRRKVNKCYR-----	GRSC	ILVHCS	DGAGRTGTYV	ILDMV	LNRAK	--AKE	LDIAAT	LEHVRD	DORPGL	LVRSK	QDFE	FALT	VAEEN
	hCD45 D2 (NP 002829) PTPRC (199)	QNTNNSVVEQFAE--PKEL	ISMVQVVKQKLPKQNS	EGM	---	KYHKS	SLVHR	DRDS	SQQTGL	CA	FNLL	ESAET	---	EDV	VDFV	VKLVKAR
	mCD45 D2 (NP 035340) Ptdrc (199)	QCTTWKGEELFAE--PKDL	VTLIQNKQKLPKQNS	EGM	---	KYHKS	SLVHR	DRDS	SQQTGL	CA	FNLL	ESAET	---	EDV	VDFV	VKLVKAR
	rCD45_D2 (XP 213985) Ptdrc (199)	QCTTWKGEELFAE--PKDL	VTLIQNKQKLPKQNS	EGM	---	KYHKS	SLVHR	DRDS	SQQTGL	CA	FNLL	ESAET	---	EDV	VDFV	VKLVKAR
	cCD45 D2 (A54080) (199)	QYHKNGLDVPEE--PKDL	VDMVLSKQKVPSPASE	S	---	RNSRS	YFV	IHC	CDSSQ	Q	WCV	CM	NTL	LSAET	---	EMV
	fuCD45 D2 (CAB96211) (199)	QFLKMGKVEVPEE--PKDL	ADLKEAKHRCGY	---	---	TWPR	STV	I	VHC	NS	GS	RS	GAF	CA	WNL	LDNAEK
	cypcaCD45 D2 (BAA92179) (197)	QFLKMGRELVPEE--AQEL	VMASIRRENGHYD	NS	---	KTNRN	V	I	VHC	NS	GS	RS	GAF	CA	WNL	LDNAEK
	aotvoCD45 D2 (AAM48512) (3') (191)	QYTNNSVXXLFAE--PKEL	ISMVQVVKQKLPKQNS	EGM	---	KXHK	X	L	L	H	RD	S	Q	T	G	L
	sharkCD45 D2 (T43148) (198)	HFHDWASELVEE--PSNF	TKMLRSKELKSL	LQ	EP	---	SSL	SP	S	L	V	H	C	S	A	G
	cPTPaloha D2 (AAB04150) (181)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	---	QSGNH	PI	V	H	C	S	A	G	R	T	G
	hPTPaloha D2 (NP 002827) PTPRA (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	---	QSGNH	PI	V	H	C	S	A	G	R	T	G
	mPTPaloha D2 (NP 033006) Ptdra (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	---	QSGNH	PI	V	H	C	S	A	G	R	T	G
	rPTPaloha D2 (NP 036895) Ptdra (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	---	QSGNH	PI	V	H	C	S	A	G	R	T	G
	xPTPaloha D2 (AAA17990) (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	---	QSGNH	PI	V	H	C	S	A	G	R	T	G
	zPTPaloha D2 (NP 571963) ptdra (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	---	QSGNH	PI	V	H	C	S	A	G	R	T	G
	rvPTPR4b D2 (BAA95196) (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	---	QSGNH	PI	V	H	C	S	A	G	R	T	G
	hPTPepsilon D2 (NP 006495) PTPRE (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	---	QSGNH	PI	V	H	C	S	A	G	R	T	G
	mPTPepsilon D2 (NP 035342) Ptdre (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	---	QSGNH	PI	V	H	C	S	A	G	R	T	G
	rPTPepsilon D2 (XP 215102) Ptdre (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	---	QSGNH	PI	V	H	C	S	A	G	R	T	G
	orylaPTPepsilon D2 (BAC06424) (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	---	QSGNH	PI	V	H	C	S	A	G	R	T	G
	hPTPkappa D2 (NP 002835) PTPRK (180)	QNLGASREVPVGS--KRSF	LKLLQLEK	WQ	EE	---	E	G	E	R	T	L	H	C	S	A
	mPTPkappa D2 (NP 033009) Ptdrk (180)	QNLGASREVPVGS--KRSF	LKLLQLEK	WQ	EE	---	E	G	E	R	T	L	H	C	S	A
	rvPTPR2B D2 (BAA95194) (180)	QNLGASREVPVGS--KRSF	LKLLQLEK	WQ	EE	---	E	G	E	R	T	L	H	C	S	A
	hPTPlamda D2 (NP 005695) PTPRU (183)	QFLRNSARDTPDS--KRAF	LHLILAE	DK	WA	---	G	B	E	R	T	L	H	C	S	A
	mPTPlamda D2 (NP 035344) Ptdrl (183)	QFLRNSARDTPDS--KRAF	LHLILAE	DK	WA	---	G	B	E	R	T	L	H	C	S	A
	mPTPmu D2 (NP 002836) PTPRM (180)	QFLGWMRDTPVPS--KRSF	LKLLQLEK	WQ	EE	---	G	G	E	R	T	L	H	C	S	A
	mPTPmu D2 (NP 033010) Ptdrm (180)	QFLGWMRDTPVPS--KRSF	LKLLQLEK	WQ	EE	---	G	G	E	R	T	L	H	C	S	A
	rPTPmu D2 (XP 237546 (revised)) (180)	QFLGWMRDTPVPS--KRSF	LKLLQLEK	WQ	EE	---	G	G	E	R	T	L	H	C	S	A
	hPTPrho D2 (NP 573400) PTPRT (180)	QILGWARDTPPS--KRSF	LKVVRREK	WQ	EQ	---	G	R	E	R	T	L	H	C	S	A
	mPTPrho D2 (NP 067439) Ptdrr (180)	QILGWARDTPPS--KRSF	LKVVRREK	WQ	EQ	---	G	R	E	R	T	L	H	C	S	A
	cPTPsiama D2 (I50212) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	hLAR D2 (NP 002831) PTPRF (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	mLAR D2 (NP 035343) Ptdrf (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	rLAR D2 (NP 062122) Ptdrf (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	xLAR D2 (AAF43606) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	zLAR D2 (CAC44758) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	rvPTPR2Aa D2 (BAA95188) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	hPTPdelta D2 (NP 002830) PTPRD (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	mPTPdelta D2 (D54689) (181)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	xPTPdelta D2 (AAF43605) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	rvPTPR2Ab D2 (BAA95191) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	hPTPsiama D2 (NP 002841) PTPRS (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	mPTPsiama D2 (NP 035348) Ptdrs (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	xPTPsiama D2 (AAF43607) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	zPTPsiama D2 (CAC44759) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	rPTPsiama D2 (NP 062013) Ptdrd (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	rvPTPR2Ac D2 (BAA95193) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG	---	QD	GP	I	V	H	C	S	A	G	R	T
	hPTPaamma D2 (NP 002832) PTPRG (186)	QCPKWFNPDAFIS--STFEL	LVNFK	KE	EA	---	R	D	GP	I	V	H	C	S	A	G
	mPTPaamma D2 (NP 033007) Ptdra (186)	QCPKWFNPDAFIS--STFEL	LVNFK	KE	EA	---	R	D	GP	I	V	H	C	S	A	G
	rPTPaamma D2 (NP 599183) Ptdra (178)	YVLEVRHGFQAFIS--STFEL	LVNFK	KE	EA	---	R	D	GP	I	V	H	C	S	A	G
	rvPTPR5b D2 (BAA95197) (186)	QCPKWFNPDAFIS--STFEL	LVNFK	KE	EA	---	R	D	GP	I	V	H	C	S	A	G
	cPTPaamma D2 (Q98936) (186)	QCPKWFNPDAFIS--STFEL	LVNFK	KE	EA	---	R	D	GP	I	V	H	C	S	A	G
	hPTPzeta D2 (NP 002842) PTPRZ1 (185)	QCPKWFNPDSFIS--KTFEL	LVNFK	KE	EA	---	R	D	GP	I	V	H	C	S	A	G
	cPTPzeta D2 (AAA49015) (185)	QCPKWFNPDSFIS--KTFEL	LVNFK	KE	EA	---	R	D	GP	I	V	H	C	S	A	G
	mPTPzeta D2 (XP 133090) Ptdrz1 (185)	QCPKWFNPDSFIS--KTFEL	LVNFK	KE	EA	---	R	D	GP	I	V	H	C	S	A	G
	rPTPzeta D2 (NP 037212) Ptdrz1 (185)	QCPKWFNPDSFIS--KTFEL	LVNFK	KE	EA	---	R	D	GP	I	V	H	C	S	A	G
	xPTPzeta D2 (BAA97445) (185)	QCPKWFNPDSFIS--KTFEL	LVNFK	KE	EA	---	R	D	GP	I	V	H	C	S	A	G
	rvPTPR5a D2 (BAA95195) (181)	QSPRWFNPDSFIS--KTFEL	LVNFK	KE	EA	---	R	D	GP	I	V	H	C	S	A	G
	Consensus (237)	QFT WPDHGVV	LL F I V				GP	I	V	H	C	S	A	G	R	T