

	1	10	20	30	40	50	60	70	80	90	100	110	118																											
hPTPsiama D1 (NP 002841) PTPRS	(1)	ADVAEHTERL	KANDS	---	LKLSQVES	DPG	---	QQFTWEH	---	SNLEVN	NRPK	NRVANV	IAYDHSRVI	QP	EGI	---	MG	SDYINAN	VDGYRRQ																					
mPTPsiama D1 (NP 035348(revised)) Ptpsr	(1)	TDAEHEMERL	KANDS	---	LKLSQVES	DPG	---	QQFTWEH	---	SNLEANK	NRPK	NRVANV	IAYDHSRVI	LP	EGI	---	MG	SDYINAN	VDGYRRQ																					
rPTPsiama D1 (NP 062013) Ptpord	(1)	TDAEHEMERL	KANDS	---	LKLSQVES	DPG	---	QQFTWEH	---	SNLEANK	NRPK	NRVANV	IAYDHSRVI	LP	EGI	---	MG	SDYINAN	VDGYRRQ																					
cPTPsiama D1 (I50212)	(1)	SELAEHTERL	KANDN	---	LKLSQVES	DPG	---	QQFTWEH	---	SNLEVN	NRPK	NRVANV	IAYDHSRVI	LP	EGI	---	VG	SDYINAN	VDGYRRQ																					
xPTPsiama D1 (CAC43607)	(1)	ADVAEHTERL	KANDN	---	LKLSQVES	DPG	---	QQFTWEH	---	SNLEVN	NRPK	NRVANV	IAYDHSRVI	LP	EGI	---	IG	SDYINAN	VDGYRRQ																					
zPTPsiama D1 (CAC44759)	(1)	SELAEHTERL	KANDN	---	LKLSQVES	DPG	---	QQFTWEH	---	SNLEVN	NRPK	NRVANV	IAYDHSRVI	LP	EGI	---	TG	SDYINAN	VDGYRRQ																					
hLAR D1 (NP 002831) PTPRF	(1)	TDAADNERL	KANDG	---	LKFSQVES	DPG	---	QQFTWEN	---	SNLEVN	NRPK	NRVANV	IAYDHSRVI	LP	EGI	---	PG	SDYINAN	VDGYRRQ																					
mLAR D1 (NP 035343) Ptprrf	(1)	TDADNERL	KANDG	---	LKFSQVES	DPG	---	QQFTWEN	---	SNSEVN	NRPK	NRVANV	IAYDHSRVI	LP	EGI	---	PG	SDYINAN	VDGYRRQ																					
rLAR_D1 (NP 062122) Ptprrf	(1)	TDADNERL	KANDG	---	LKFSQVES	DPG	---	QQFTWEN	---	SNSEVN	NRPK	NRVANV	IAYDHSRVI	LP	EGI	---	PG	SDYINAN	VDGYRRQ																					
xLAR D1 (AAF43606)	(1)	SDADNERL	KANDG	---	LKFSQVES	DPG	---	QQFTWEN	---	SNLEVN	NRPK	NRVANV	IAYDHSRVI	LP	EGI	---	PG	SDYINAN	VDGYRRQ																					
hPTPdelta_D1 (NP 002830) PTPRD	(1)	LEADHERL	KANDN	---	LKFSQVES	DPG	---	QQFTWEH	---	SNLEVN	NRPK	NRVANV	IAYDHSRVI	LP	EGI	---	PG	SDYINAN	VDGYRRQ																					
mPTPdelta D1 (D54689)	(1)	LEADHERL	KANDN	---	LKFSQVES	DPG	---	QQFTWEH	---	SNLEVN	NRPK	NRVANV	IAYDHSRVI	LP	EGI	---	PG	SDYINAN	VDGYRRQ																					
xPTPdelta D1 (AAF43605)	(1)	LELEDHERL	KANDN	---	LKFSQVES	DPG	---	QQFTWEH	---	SNLEVN	NRPK	NRVANV	IAYDHSRVI	LP	EGI	---	PG	SDYINAN	VDGYRRQ																					
hPTPrho D1 (NP 573400) PTPRT	(1)	ADLLQHTITQ	KRRGQG	---	YGFKEVEAL	PEG	---	QTASWDT	---	AKEDEN	NRNK	NRGNLI	SYDHSRVI	LV	DGD	---	PH	SDYINAN	VDGYHPR																					
mPTPrho D1 (NP 067439) Ptprrt	(1)	ADLLQHTITQ	KRRGQG	---	YGFKEVEAL	PEG	---	QTASWDT	---	AKEDEN	NRNK	NRGNLI	SYDHSRVI	LV	DGD	---	PH	SDYINAN	VDGYHPR																					
xPTPrho D1 (AAD50295)	(1)	ADLLQHTITQ	KRRGQG	---	YGFKEVEAL	PEG	---	QTASWDT	---	AKEDEN	NRNK	NRGNLI	SYDHSRVI	LV	DGD	---	PH	SDYINAN	VDGYHPR																					
hPTPmu D1 (NP 002836) PTPRM	(1)	ADLLQHTITQ	KCAEG	---	YGFKEVEAL	PEG	---	QSAPWDS	---	AKEDEN	NRNK	NRGNLI	SYDHSRVI	LV	DGD	---	TN	SDYINAN	VDGYHPR																					
mPTPmu D1 (NP 033010) Ptprrm	(1)	ADLLQHTITQ	KCAEG	---	YGFKEVEAL	PEG	---	QSAPWDS	---	AKEDEN	NRNK	NRGNLI	SYDHSRVI	LV	DGD	---	NN	SDYINAN	VDGYHPR																					
hPTPkappa D1 (NP 002835) PTPRK	(1)	ADLLQHTINL	KTKTSDS	---	YGFKEVEAL	PEG	---	QSASWDV	---	AKKQNR	NRNK	NRGNLI	SYDHSRVI	LV	DGD	---	PS	SDYINAN	VDGYQRP																					
mPTPkappa D1 (NP 033009 (revised)) Ptprrk	(1)	ADLLQHTINL	KTKTSDS	---	YGFKEVEAL	PEG	---	QSASWDV	---	AKKQNR	NRNK	NRGNLI	SYDHSRVI	LV	DGD	---	PS	SDYINAN	VDGYQRP																					
hPTPlamda D1 (NP 005695) PTPRU	(1)	ADLLQHTINQ	KTAEG	---	YGFKEVEAL	PEG	---	WD	---	ATKKDK	NRNK	NRGNLI	SYDHSRVI	LV	DGD	---	PN	SDYINAN	VDGYHRS																					
mPTPlamda D1 (NP 035344) Ptprrl	(1)	ADLLQHTINQ	KTAEG	---	YGFKEVEAL	PEG	---	WD	---	ATKKDK	NRNK	NRGNLI	SYDHSRVI	LV	DGD	---	PD	SDYINAN	VDGYHRS																					
rPTPpsi_D1 (AAB42210) Ptprru Fraam	(1)	ADLLQHTINQ	KTAEG	---	YGFKEVEAL	PEG	---	WD	---	ATKKDK	NRNK	NRGNLI	SYDHSRVI	LV	DGD	---	PD	SDYINAN	VDGYHRS																					
cPTPaloha D1 (AAB04150)	(1)	DKLEEEIN	RRI	GDDN	---	KLFRE	ENALP	---	ACPIQAT	CEAA	SKEE	NRK	NRVNI	LPYDHSRVI	TP	EGV	---	PD	SDYINAN	VDGYQEK																				
hPTPaloha D1 (NP 002827) PTPRA	(1)	DKLEEEIN	RNR	MADDN	---	KLFRE	ENALP	---	ACPIQAT	CEAA	SKEE	NRK	NRVNI	LPYDHSRVI	TP	EGV	---	PD	SDYINAN	VDGYQEK																				
mPTPaloha D1 (AAK56109) Ptpora	(1)	DKLEEEIN	RNR	MADDN	---	KLFRE	ENALP	---	ACPIQAT	CEAA	SKEE	NRK	NRVNI	LPYDHSRVI	TP	EGV	---	PD	SDYINAN	VDGYQEK																				
rPTPaloha D1 (NP 036895) Ptpora	(1)	DKLEEEIN	RNR	MADDN	---	KLFRE	ENALP	---	ACPIQAT	CEAA	SKEE	NRK	NRVNI	LPYDHSRVI	TP	EGV	---	PD	SDYINAN	VDGYQEK																				
zPTPaloha D1 (NP 571963) Ptpora	(1)	DKLEEEIN	RNR	MADDN	---	KLFRE	ENALP	---	VCPIQAS	CDAA	SKEE	NRK	NRVNI	LPYDHSRVI	TP	EGV	---	PD	SDYINAN	VDGYQEK																				
xPTPaloha D1 (AAA17990)	(1)	DKLEEEIN	RNR	MADDN	---	KLFRE	ENALP	---	ACPIQAT	CEAA	SKEE	NRK	NRVNI	LPYDHSRVI	TP	EGV	---	PD	SDYINAN	VDGYQEK																				
hPTPpsilon D1 (NP 006495) PTPRE	(1)	EHLEEEIR	VR	SADDC	---	KRFRE	ENSP	---	SGHIQGT	FEL	ANK	ENR	NRK	NRVNI	LPYDHSRVI	TP	DGI	---	PC	SDYINAN	VDGYKEK																			
mPTPpsilon D1 (NP 035342) Ptpre	(1)	EHLEEEIR	VR	SADDC	---	KRFRE	ENSP	---	SGHIQGT	FEL	ANK	ENR	NRK	NRVNI	LPYDHSRVI	TP	DGI	---	PC	SDYINAN	VDGYKEK																			
rPTPpsilon D1 (XP 215102) Ptprr	(1)	EHLEEEIR	VR	SADDC	---	KRFRE	ENSP	---	SGHIQGT	FEL	ANK	ENR	NRK	NRVNI	LPYDHSRVI	TP	DGI	---	PC	SDYINAN	VDGYKEK																			
hPTPqamma D1 (NP 002832) PTPRG	(1)	KQFVKHIG	E	LYSNQ	---	HGFSE	VEE	QRC	---	TADMN	ITAEH	SNH	DN	RHK	NRVNI	LPYDHSRVI	TP	PKG	DS	YINAN	VDGYNKA																			
mPTPqamma D1 (NP 033007) Ptprrg	(1)	KQFVKHIG	E	LYSNQ	---	HGFSE	VEE	QRC	---	TADMN	ITAEH	SNH	DN	RHK	NRVNI	LPYDHSRVI	TP	PKG	DS	YINAN	VDGYNKA																			
rPTPqamma D1 (NP 591833) Ptprrg	(1)	IFPDDME	A	LPVKQF	---	GKSQHG	SG	VEE	QRC	---	TADMN	ITAEH	SNH	DN	RHK	NRVNI	LPYDHSRVI	TP	PKG	DS	YINAN	VDGYNKA																		
cPTPqamma D1 (Q98936)	(1)	KQFVKHIG	E	LYSNQ	---	HGFSE	VEE	QRC	---	TADMN	ITAEH	SNH	DN	RHK	NRVNI	LPYDHSRVI	TP	PKG	DS	YINAN	VDGYNKA																			
hPTPzeta D1 (NP 002842) PTPRZ1	(1)	KHFPPKHV	ADL	HASSG	---	FTEEFET	KEF	QEQ	QSC	---	TVDLG	ITADS	SNH	DN	RHK	NRVNI	LPYDHSRVI	TP	AEK	DG	YINAN	VDGYNRP																		
rPTPzeta D1 (NP 037122) Ptprrz1	(1)	KHFPPKHV	ADL	HASNG	---	FTEEFET	KEF	QEQ	QSC	---	TVDLG	ITADS	SNH	DN	RHK	NRVNI	LPYDHSRVI	TP	AEK	DG	YINAN	VDGYNRP																		
cPTPzeta D1 (AAA49015)	(1)	KHFPPKHV	ADL	HASNG	---	FSE	EE	QEQ	QSC	---	TVDLG	ITSDS	SNH	DN	RNK	NRVNI	LPYDHSRVI	TP	AEK	DG	YINAN	VDGYNRP																		
xPTPzeta D1 (BAA97445)	(1)	KQFHKH	EDL	HSRNG	---	FTE	EE	QEQ	QSC	---	TTDLG	ITYEN	SNH	DN	RNK	NRVNI	LPYDHSRVI	TP	AEK	DG	YINAN	VDGYNRP																		
hCD45 D1 (NP 002829) PTPRC	(1)	DI	LETYKR	KIAD	DEG	---	RLF	LA	EQS	TP	---	RVFSK	FP	IK	ARK	HN	QNK	NRVNI	LPYDHSRVI	TP	SE	NGD	YINAN	VDGFKFP																
mCD45 D1 (NP 035340) Ptprrc	(1)	DI	LETYKR	KIAD	DEG	---	RLF	LA	EQS	TP	---	RVFSK	FP	IK	ARK	HN	QNK	NRVNI	LPYDHSRVI	TP	SE	NGD	YINAN	VDGFKFP																
rCD45_D1 (XP 213985) Ptprrc	(1)	DI	LETYKR	KIAD	DEG	---	RLF	LA	EQS	TP	---	RVFSK	FP	IK	ARK	HN	QNK	NRVNI	LPYDHSRVI	TP	SE	NGD	YINAN	VDGFKFP																
cCD45 D1 (A54008)	(1)	EKL	LETYKR	KIAD	DEG	---	RLF	LD	EQS	TP	---	RIF	TK	FP	M	K	AK	RS	HN	QNK	NRVNI	LPYDHSRVI	TP	SE	PGD	YINAN	VDGFKFP													
cypcCD45 D1 (BAA92179)	(1)	GG	VEAY	KNK	IAD	DEG	---	RLF	MD	EQS	TP	---	RIF	SN	Y	T	I	K	E	AK	RS	HN	QNK	NRVNI	LPYDHSRVI	TP	SE	STGGED	YINAN	VDGFKFP										
fuCD45 D1 (CAB96211)	(1)	ET	L	DAY	KR	KIAD	DEG	---	RLF	LA	EQS	TP	---	RIF	SK	Y	T	V	K	E	AK	RS	HN	QNK	NRVNI	LPYDHSRVI	TP	SE	VTGNGS	YINAN	VDGFKFP									
sharkCD45 D1 (T43148)	(1)	EQ	L	IV	YR	RR	Q	A	D	EQS	TP	---	RV	FS	K	F	S	V	K	E	AK	RS	HN	QNK	NRVNI	LPYDHSRVI	TP	SE	VTGAGE	YINAN	VDGFKFP									
hDEP1 D1 (NP 002834) PTPRJ	(1)	ENFEAY	FKK	Q	A	D	S	N	---	CGFAE	VED	K	---	LVG	I	S	Q	P	K	Y	A	E	L	A	E	NRGK	NRVNI	LPYDHSRVI	TP	SV	Q	T	H	S	YINAN	VDGYHSK				
rDEP1 D1 (NP 058965) Ptprrj	(1)	ENFEAY	FKK	Q	A	D	S	N	---	CGFAE	VED	K	---	L	I	G	I	S	L	P	K	Y	A	E	L	A	E	NRGK	NRVNI	LPYDHSRVI	TP	SV	Q	T	H	S	YINAN	VDGYHSK		
mDEP1 D1 (NP 033008) Ptprrj	(1)	ENFEAY	FKK	Q	A	D	S	N	---	CGFAE	VED	K	---	L	I	G	I	S	L	P	K	Y	T	A	E	L	A	E	NRGK	NRVNI	LPYDHSRVI	TP	SV	Q	T	H	S	YINAN	VDGYHSK	
hGLEPP1 D1 (NP 109592) PTPRO	(1)	DDFDAY	L	KD	AK	D	S	D	---	YKFS	LQ	EE	L	---	L	I	G	L	D	I	P	H	F	A	D	L	NRCK	NRVNI	LPYDHSRVI	TP	LS	N	E	E	YINAN	VDGYNSP				
rGLEPP1 D1 (NP 059032) Ptprr	(1)	DDFDAY	L	KD	AK	D	S	D	---	YKFS	LQ	EE	L	---	L	I	G	L	D	I	P	H	F	A	D	L	NRCK	NRVNI	LPYDHSRVI	TP	LS	N	E	E	YINAN	VDGYNSP				
mPTPphi D1 (NP 035346) Ptprr	(1)	DDFDAY	L	KD	AK	D	S	D	---	YKFS	LQ	EE	L	---	L	I	G	L	D	I	P	H	F	A	D	L	NRCK	NRVNI	LPYDHSRVI	TP	LS	N	E	E	YINAN	VDGYNSP				
rabPTPoc D1 (AAB16824)	(1)	DDFDAY	L	KD	AK	D	S	D	---	YKFS	LQ	EE	L	---	L	I	G	L	D	I	P	H	F	A	D	L	NRCK	NRVNI	LPYDHSRVI	TP	LS	N	E	E	YINAN	VDGYNSP				
hPTPbeta D1 (NP 002828) PTPRB	(1)	NQ	EGH	FM	L	Q	A	D	S	N	---	YL	SK	E	VE	D	K	---	D	V	G	R	S	Q	C	D	I	A	L	L	E	NRGK	NRVNI	LPYDHSRVI	TP	VS	D	D	YINAN	VDGYNSP
mPTPbeta D1 (NP 084204) Ptprrb	(1)	NQ	EGH	FM	L	Q	A	D	S	N	---	YL	SK	E	VE	D	K	---	D	V	G	R	S	Q	C	D	I	A	L	L	E	NRGK	NRVNI	LPYDHSRVI	TP	VS	D	D	YINAN	VDGYNSP
rPTPbeta D1 (XP 235156 (revised))	(1)	NQ	EGH	FM	L	Q	A	D	S	N	---	YL	SK	E	VE	D	K	---	D	V	G	R	S																	

Alignment_195_Vert_PTP_Domains_D1_and_D2_Updated (VNTI 8.0).apc

blA2 D1 (P56722) Ptdrn (179)	HFLSWEAECTEAS--TRP	LDLRRKVNKCYR-----	GRSCILVHCS	DGAGRTGTYV	LDLDMVNLNR	AKG--VKE	LDIAATLEHVRDORPGLVRSKQ	QEF	FALTVA	AEE	N			
hIA2beta D1 (NP 002838) PTPRN2 (179)	HFLSNYDRGVSS--SRSL	LDLRRKVNKCYR-----	GRSCILVHCS	DGAGRTGTYV	LDLDMVNLNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQ	QEF	FALTVA	AEE	N			
macnelA2beta D1 (O02695) (179)	HFLSNYDRGVSS--SRSL	LDLRRKVNKCYR-----	GRSCILVHCS	DGAGRTGTYV	LDLDMVNLNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQ	QEF	FALTVA	AEE	N			
mPTPNP D1 (P80560) Ptdrn2 (179)	HFLSNYDRGVSS--TRSL	LDLRRKVNKCYR-----	GRSCILVHCS	DGAGRTGTYV	LDLDMVNLNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQ	QEF	FALTVA	AEE	N			
rPTPNE6 D1 (NP 113788) Ptdrn2 (179)	HFLSNYDRGVSS--TRSL	LDLRRKVNKCYR-----	GRSCILVHCS	DGAGRTGTYV	LDLDMVNLNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQ	QEF	FALTVA	AEE	N			
hCD45 D2 (NP 002829) PTPRC (199)	QNTNNSVVEQFAE--PKEL	ISMVQVVKQKLPKQNS	EGM---KHHKST	LLLRDRD	CSQQGTG	LCALN	LLLSAET--	EV	VDFVQVVKALRKARPGM	VSTF	QYQFLVDVASTYP			
mCD45 D2 (NP 035340) Ptdrc (199)	QCTTWKGEELFAE--PKDL	VTLQKQKLPKQNS	EGM---KYHKKH	SLVLRDRD	CSQQGTG	LCALN	LLLSAET--	ED	VDFVQVVKALRKARPGM	VCSY	QYQFLVDIASIYP			
rCD45 D2 (XP 213985) Ptdrc (199)	QCTTWKGEELFAE--PKDL	VTLQKQKLPKQNS	EGM---KYHKKH	SLVLRDRD	CSQQGTG	LCALN	LLLSAET--	ED	VDFVQVVKALRKARPGM	VCSY	QYQFLVDIASIYP			
cCD45 D2 (A54080) (199)	QYHKHNGLDVPE--PKDL	VDMVLSKQKVPSPASE	SDS---RNSRSY	FVLRD	CSQQGTG	LCALN	LLLSAET--	EM	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIARTYP			
fuCD45 D2 (CAB96211) (199)	QFLKMGKVEVPE--PKDL	ADLKEKHKRCGY---	TWPRST	IVLH	CNDSGSRGAF	CAW	NLLD	NAEK---	EM	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIEVYYP		
cypcaCD45 D2 (BAA92179) (197)	QFLKMGKVEVPE--PKDL	VDMVLSKQKVPSPASE	SDS---RNSRSY	FVLRD	CSQQGTG	LCALN	LLLSAET--	EM	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIARTYP			
aotvoCD45 D2 (AAM48512) (3') (191)	QYTNNSVXXLFAE--PKEL	ISMVQVVKQKLPKQNS	EGM---KXHKX	SLVLRDRD	CSQQGTG	LCALN	LLLSAET--	EV	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIARTYP			
sharkCD45 D2 (T43148) (198)	HFHDAWASELFAE--PSNF	TKMLRSKELKSL	LQEP---SSLS	PSLIVH	CNDSGAK	TGVFYA	WILL	DNADT---	ENV	LDVLTQVVKALRKARPGM	VSTF	QYQFLVDIARTYP		
cPTPaloha D2 (AAB04150) (181)	HFHGWPEVGLSD--GKGN	INLIAAQKQQQ---	QSGNH	PIVH	CSAGAGRTGTF	CAL	STVLR	KA--	EG	LDVFTVKSRLRQRPHMVQTL	QYEF	CKVVOBYID		
hPTPaloha D2 (NP 002827) PTPRA (182)	HFHGWPEVGLSD--GKGN	INLIAAQKQQQ---	QSGNH	PIVH	CSAGAGRTGTF	CAL	STVLR	KA--	EG	LDVFTVKSRLRQRPHMVQTL	QYEF	CKVVOBYID		
mPTPaloha D2 (NP 033006) Ptdra (182)	HFHGWPEVGLSD--GKGN	INLIAAQKQQQ---	QSGNH	PIVH	CSAGAGRTGTF	CAL	STVLR	KA--	EG	LDVFTVKSRLRQRPHMVQTL	QYEF	CKVVOBYID		
rPTPaloha D2 (NP 036895) Ptdra (182)	HFHGWPEVGLSD--GKGN	INLIAAQKQQQ---	QSGNH	PIVH	CSAGAGRTGTF	CAL	STVLR	KA--	EG	LDVFTVKSRLRQRPHMVQTL	QYEF	CKVVOBYID		
xPTPaloha D2 (AAA17990) (182)	HFHGWPEVGLSD--GKGN	INLIAAQKQQQ---	QSGNH	PIVH	CSAGAGRTGTF	CAL	STVLR	KA--	EG	LDVFTVKSRLRQRPHMVQTL	QYEF	CKVVOBYID		
zPTPaloha D2 (NP 571963) ptdra (182)	HFHGWPEVGLSD--GKGN	INLIAAQKQQQ---	QSGNH	PIVH	CSAGAGRTGTF	CAL	STVLR	KA--	EG	LDVFTVKSRLRQRPHMVQTL	QYEF	CKVVOBYID		
rvPTPR4b D2 (BAA95196) (182)	HFHGWPEVGLSD--GKGN	INLIAAQKQQQ---	QSGNH	PIVH	CSAGAGRTGTF	CAL	STVLR	KA--	EG	LDVFTVKSRLRQRPHMVQTL	QYEF	CKVVOBYID		
hPTPepsilon D2 (NP 006495) PTPRE (187)	HFHGWPEVGLSD--GKGN	INLIAAQKQQQ---	QSGNH	PIVH	CSAGAGRTGTF	CAL	STVLR	KA--	EG	LDVFTVKSRLRQRPHMVQTL	QYEF	CKVVOBYID		
mPTPepsilon D2 (NP 035342) Ptdre (187)	HFHGWPEVGLSD--GKGN	INLIAAQKQQQ---	QSGNH	PIVH	CSAGAGRTGTF	CAL	STVLR	KA--	EG	LDVFTVKSRLRQRPHMVQTL	QYEF	CKVVOBYID		
rPTPepsilon D2 (XP 215102) Ptdre (187)	HFHGWPEVGLSD--GKGN	INLIAAQKQQQ---	QSGNH	PIVH	CSAGAGRTGTF	CAL	STVLR	KA--	EG	LDVFTVKSRLRQRPHMVQTL	QYEF	CKVVOBYID		
orylaPTPepsilon D2 (BAC06424) (187)	HFHGWPEVGLSD--GKGN	INLIAAQKQQQ---	QSGNH	PIVH	CSAGAGRTGTF	CAL	STVLR	KA--	EG	LDVFTVKSRLRQRPHMVQTL	QYEF	CKVVOBYID		
hPTPalpha D2 (AAB04150) (181)	HFHGWPEVGLSD--GKGN	INLIAAQKQQQ---	QSGNH	PIVH	CSAGAGRTGTF	CAL	STVLR	KA--	EG	LDVFTVKSRLRQRPHMVQTL	QYEF	CKVVOBYID		
hPTPbeta D2 (NP 002835) PTPRK (180)	QNLGASREVPVGS--KRSF	LKLLQLEK	WQEEEC---E	EGE	RTLVH	CLNGGRR	GMFCAL	GI	VMMKR--	QNV	VDFHVAKTLRNSP	MVEAP	QYRRCVDVALEYE	
mPTPbeta D2 (NP 033009) Ptdrk (180)	QNLGASREVPVGS--KRSF	LKLLQLEK	WQEEEC---E	EGE	RTLVH	CLNGGRR	GMFCAL	GI	VMMKR--	QNV	VDFHVAKTLRNSP	MVEAP	QYRRCVDVALEYE	
rvPTPR2B D2 (BAA95194) (180)	QNLGASREVPVGS--KRSF	LKLLQLEK	WQEEEC---E	EGE	RTLVH	CLNGGRR	GMFCAL	GI	VMMKR--	QNV	VDFHVAKTLRNSP	MVEAP	QYRRCVDVALEYE	
hPTPlamda D2 (NP 005695) PTPRU (183)	QFLRNSARDTPDS--KRAF	LHLHLA	DRKWAES---D	GB	RTLVH	CLNGGRR	GMFCAL	GI	VMMKR--	QNV	VDFHVAKTLRNSP	MVEAP	QYRRCVDVALEYE	
mPTPlamda D2 (NP 035344) Ptdrl (183)	QFLRNSARDTPDS--KRAF	LHLHLA	DRKWAES---D	GB	RTLVH	CLNGGRR	GMFCAL	GI	VMMKR--	QNV	VDFHVAKTLRNSP	MVEAP	QYRRCVDVALEYE	
mPTPmu D2 (NP 002836) PTPRM (180)	QFLGWMRDRTPVS--KRSF	LKLLQLEK	WQEEYN---G	EGE	RTLVH	CLNGGRR	GMFCAL	GI	VMMKR--	QNV	VDFHVAKTLRNSP	MVEAP	QYRRCVDVALEYE	
mPTPmu D2 (NP 033010) Ptdrm (180)	QFLGWMRDRTPVS--KRSF	LKLLQLEK	WQEEYN---G	EGE	RTLVH	CLNGGRR	GMFCAL	GI	VMMKR--	QNV	VDFHVAKTLRNSP	MVEAP	QYRRCVDVALEYE	
rPTPmu D2 (XP 237546 (revised)) (180)	QFLGWMRDRTPVS--KRSF	LKLLQLEK	WQEEYN---G	EGE	RTLVH	CLNGGRR	GMFCAL	GI	VMMKR--	QNV	VDFHVAKTLRNSP	MVEAP	QYRRCVDVALEYE	
hPTPrho D2 (NP 573400) PTPRT (180)	QFLGWMRDRTPVS--KRSF	LKLLQLEK	WQEEQYD---G	EGE	RTLVH	CLNGGRR	GMFCAL	GI	VMMKR--	QNV	VDFHVAKTLRNSP	MVEAP	QYRRCVDVALEYE	
mPTPrho D2 (NP 067439) Ptdrt (180)	QFLGWMRDRTPVS--KRSF	LKLLQLEK	WQEEQYD---G	EGE	RTLVH	CLNGGRR	GMFCAL	GI	VMMKR--	QNV	VDFHVAKTLRNSP	MVEAP	QYRRCVDVALEYE	
cPTPsiama D2 (I50212) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
hLAR D2 (NP 002831) PTPRF (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
mLAR D2 (NP 035343) Ptdrf (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
rLAR D2 (NP 062122) Ptdrf (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
xLAR D2 (AAF43606) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
zLAR D2 (CAC44758) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
rvPTPR2Aa D2 (BAA95188) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
hPTPdelta D2 (NP 002830) PTPRD (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
mPTPdelta D2 (D54689) (181)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
xPTPdelta D2 (AAF43605) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
rvPTPR2Ab D2 (BAA95191) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
hPTPsiama D2 (NP 002841) PTPRS (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
mPTPsiama D2 (NP 035348) Ptdrs (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
xPTPsiama D2 (AAF43607) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
zPTPsiama D2 (CAC44759) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
rvPTPsiama D2 (NP 062013) Ptdrd (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
rvPTPR2Ac D2 (BAA95193) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQ	FG---Q	QP	ITVH	CSAGAGRTG	VFTLS	SIV	LRRY--	EG	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG	
hPTPaamma D2 (NP 002832) PTPRG (186)	QCPKWFNPDAFIS--STFEL	LVNFK	KEEALT---R	DP	ITVH	DEHFGV	GTAGT	LCAL	TTL	HQEK--	ENS	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG
mPTPaamma D2 (NP 033007) Ptdra (186)	QCPKWFNPDAFIS--STFEL	LVNFK	KEEALT---R	DP	ITVH	DEHFGV	GTAGT	LCAL	TTL	HQEK--	ENS	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG
rvPTPaamma D2 (NP 599183) Ptdra (178)	YVLEVRHFGAFIS--STFEL	LVNFK	KEEALA---R	DP	ITVH	DEHFGV	GTAGT	LCAL	TTL	HQEK--	ENS	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG
rvPTPR5b D2 (BAA95197) (186)	QCPKWFNPDAFIS--STFEL	LVNFK	KEEAST---R	DP	ITVH	DEHFGV	GTAGT	LCAL	TTL	HQEK--	ENS	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG
cPTPaamma D2 (Q98936) (186)	QCPKWFNPDAFIS--STFEL	LVNFK	KEEALT---R	DP	ITVH	DEHFGV	GTAGT	LCAL	TTL	HQEK--	ENS	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG
hPTPzeta D2 (NP 002842) PTPRZ1 (185)	QCPKWFNPDSFIS--KTFEL	LVNFK	KEEAAAN---R	DP	ITVH	DEHFGV	GTAGT	LCAL	TTL	HQEK--	ENS	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG
cPTPzeta D2 (AAA49015) (185)	QCPKWFNPDSFIS--KTFEL	LVNFK	KEEAAAN---R	DP	ITVH	DEHFGV	GTAGT	LCAL	TTL	HQEK--	ENS	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG
rvPTPzeta D2 (NP 033009) Ptdrz1 (185)	QCPKWFNPDSFIS--KTFEL	LVNFK	KEEAAAN---R	DP	ITVH	DEHFGV	GTAGT	LCAL	TTL	HQEK--	ENS	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG
rvPTPzeta D2 (NP 037212) Ptdrz1 (185)	QCPKWFNPDSFIS--KTFEL	LVNFK	KEEAAAN---R	DP	ITVH	DEHFGV	GTAGT	LCAL	TTL	HQEK--	ENS	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG
xPTPzeta D2 (BAA97445) (185)	QCPKWFNPDSFIS--KTFEL	LVNFK	KEEAAAN---R	DP	ITVH	DEHFGV	GTAGT	LCAL	TTL	HQEK--	ENS	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG
rvPTPR5a D2 (BAA95195) (181)	QSPRWFNPDSFIS--KTFEL	LVNFK	KEEAAAN---R	DP	ITVH	DEHFGV	GTAGT	LCAL	TTL	HQEK--	ENS	VDFVQVVKALRKARPGM	VSTF	QYQFLVDIAALEYIG
Consensus (237)	QFT WPDHGVV	LL F I V			GPIV	VHCSAGV	GRGTGTFI	ID	M L E L	E	VDFV	VK LR QR	MVQT	EQY FIY ALLE L