

	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	NPKP	NRVANV	IAYDHSRVI	QPEGI
mPTPsiama D1 (NP 035348(revised)) Ptpsr	(1)	TDAEHEMERL	KANDS	---	LKLSQVES	DPG	---	QQFTWEH	---	SNLEANKP	NRVANV	IAYDHSRVI	QPEGI	---
rPTPsiama D1 (NP 062013) Ptpord	(1)	TDAEHEMERL	KANDS	---	LKLSQVES	DPG	---	QQFTWEH	---	SNLEANKP	NRVANV	IAYDHSRVI	QPEGI	---
cPTPsiama D1 (I50212)	(1)	SELAEHTERL	KANDN	---	LKLSQVES	DPG	---	QQFTWEH	---	SNLEVNPKP	NRVANV	IAYDHSRVI	LP	EGE
xPTPsiama D1 (AC443607)	(1)	ADVAEHTERL	KANDN	---	LKLSQVES	DPG	---	QQFTWEH	---	SNLEVNRAK	NRVANV	IAYDHSRVI	LP	EGE
zPTPsiama D1 (CAC44759)	(1)	SELAEHTERL	KANDN	---	LKLSQVES	DPG	---	QQFTWEH	---	SNLEVNPKP	NRVANV	IAYDHSRVI	LAP	EGE
hLAR D1 (NP 002831) PTPRF	(1)	TDADNTERL	KANDG	---	LKFSQVES	DPG	---	QQFTWEN	---	SNLEVNPKP	NRVANV	IAYDHSRVI	LTS	DGV
mLAR D1 (NP 035343) Ptprrf	(1)	TDADNTERL	KANDG	---	LKFSQVES	DPG	---	QQFTWEN	---	SNSEVNPKP	NRVANV	IAYDHSRVI	LTS	DGV
rLAR_D1 (NP 062122) Ptprrf	(1)	TDADNTERL	KANDG	---	LKFSQVES	DPG	---	QQFTWEN	---	SNSEVNPKP	NRVANV	IAYDHSRVI	LTS	DGV
xLAR D1 (AAF43606)	(1)	SDADNTERL	KANDG	---	LKFSQVES	DPG	---	QQFTWEN	---	SNLEVNPKP	NRVANV	IAYDHSRVI	LTS	DAV
hPTPdelta_D1 (NP 002830) PTPRD	(1)	LEADHIERL	KANDN	---	LKFSQVES	DPG	---	QQFTWEH	---	SNLEVNPKP	NRVANV	IAYDHSRVI	LSA	EGE
mPTPdelta D1 (D54689)	(1)	LEADHIERL	KANDN	---	LKFSQVES	DPG	---	QQFTWEH	---	SNLEVNPKP	NRVANV	IAYDHSRVI	LSA	EGE
xPTPdelta D1 (AAF43605)	(1)	LELEDHIERL	KANDN	---	LKFSQVES	DPG	---	QQFTWEH	---	SNLEVNPKP	NRVANV	IAYDHSRVI	LSDGI	---
hPTPrho D1 (NP 573400) PTPRT	(1)	ADLLQHTITQ	KRRGQG	---	YGFKEVEAL	PEG	---	QTASWDT	---	AKEDENR	NK	NRGNL	ISYDHSRVI	LVDGD
mPTPrho D1 (NP 067439) Ptprrt	(1)	ADLLQHTITQ	KRRGQG	---	YGFKEVEAL	PEG	---	QTASWDT	---	AKEDENR	NK	NRGNL	ISYDHSRVI	LVDGD
xPTPrho D1 (AAD50295)	(1)	ADLLQHTITQ	KRRGQG	---	YGFKEVEAL	PEG	---	QTASWDT	---	AKEDENR	NK	NRGNL	ISYDHSRVI	QTEED
hPTPmu D1 (NP 002836) PTPRM	(1)	ADLLQHTITQ	KCAEG	---	YGFKEVEAL	PEG	---	QSAPWDS	---	AKEDENR	NK	NRGNL	ISYDHSRVI	LQTEGD
mPTPmu D1 (NP 033010) Ptprrm	(1)	ADLLQHTITQ	KCAEG	---	YGFKEVEAL	PEG	---	QSAPWDS	---	AKEDENR	NK	NRGNL	ISYDHSRVI	QTEGD
hPTPkappa D1 (NP 002835) PTPRK	(1)	ADLLQHTINL	KTKTSDS	---	YGFKEVES	PFEG	---	QSASWDV	---	AKKQNR	AK	NRGNL	ISYDHSRVI	QTEDD
mPTPkappa D1 (NP 033009 (revised)) Ptprrk	(1)	ADLLQHTINL	KTKTSDS	---	YGFKEVES	PFEG	---	QSASWDV	---	AKKQNR	AK	NRGNL	ISYDHSRVI	QTEDD
hPTPlamda D1 (NP 005695) PTPRU	(1)	ADLLQHTINQ	KTAEG	---	YGFKEVES	PFEG	---	WD	---	ATKKDK	DL	GGQ	QEP	SPAYDRH
mPTPlamda D1 (NP 035344) Ptprrl	(1)	ADLLQHTINQ	KTAEG	---	YGFKEVES	PFEG	---	WD	---	ATKKDK	DL	GGQ	QEP	SPAYDRH
rPTPpsi_D1 (AAB42210) Ptprru	(1)	ADLLQHTINQ	KTAEG	---	YGFKEVES	PFEG	---	WD	---	ATKKDK	DL	GGQ	QEP	SPAYDRH
cPTPaloha D1 (AAB04150)	(1)	DKLEEEIN	RRI	GDDN	---	KLFRE	EN	ALP	---	ACPIQAT	CEAA	SKEE	NK	NRV
hPTPaloha D1 (NP 002827) PTPRA	(1)	DKLEEEIN	RNR	MADDN	---	KLFRE	EN	ALP	---	ACPIQAT	CEAA	SKEE	NK	NRV
mPTPaloha D1 (AAK56109) Ptpora	(1)	DKLEEEIN	RNR	MADDN	---	KLFRE	EN	ALP	---	ACPIQAT	CEAA	SKEE	NK	NRV
rPTPaloha D1 (NP 036895) Ptpora	(1)	DKLEEEIN	RNR	MADDN	---	KLFRE	EN	ALP	---	ACPIQAT	CEAA	SKEE	NK	NRV
zPTPaloha D1 (NP 571963) ptpora	(1)	DKLEEEIN	RNR	MADDN	---	KLFRE	EN	ALP	---	VCPIQAS	CDAA	SKEE	NK	NRV
xPTPaloha D1 (AAA17990)	(1)	DKLEEEIN	RNR	MADDN	---	KLFRE	EN	ALP	---	ACPIQAT	CEAA	SKEE	NK	NRV
hPTPpsilon D1 (NP 006495) PTPRE	(1)	EHLEEEIR	VR	SADDC	---	KRFRE	EN	SP	---	SGHIQGT	FEL	ANKE	NK	NRV
mPTPpsilon D1 (NP 035342) Ptpre	(1)	EHLEEEIR	VR	SADDC	---	KRFRE	EN	SP	---	SGHIQGT	FEL	ANKE	NK	NRV
rPTPpsilon D1 (XP 215102) Ptprr	(1)	EHLEEEIR	VR	SADDC	---	KRFRE	EN	SP	---	SGHIQGT	FEL	ANKE	NK	NRV
hPTPqamma D1 (NP 002832) PTPRG	(1)	KQFVKH	IG	LY	SNQ	---	HGFSE	EE	VQRC	---	TADMN	ITAEH	SNH	DN
mPTPqamma D1 (NP 033007) Ptprrg	(1)	KQFVKH	IG	LY	SNQ	---	HGFSE	EE	VQRC	---	TADMN	ITAEH	SNH	DN
rPTPqamma D1 (NP 599183) Ptprrg	(1)	KQFVKH	IG	LY	SNQ	---	HGFSE	EE	VQRC	---	TADMN	ITAEH	SNH	DN
cPTPqamma D1 (Q98936)	(1)	KQFVKH	IG	LY	SNQ	---	HGFSE	EE	VQRC	---	TADMN	ITAEH	SNH	DN
hPTPzeta D1 (NP 002842) PTPRZ1	(1)	KHFPPKH	VAD	L	HAS	SG	---	FTEEFET	---	KEF	Q	EV	Q	SC
rPTPzeta D1 (NP 037212) Ptprrz1	(1)	KHFPPKH	VAD	L	HAS	SG	---	FTEEFET	---	KEF	Q	EV	Q	SC
cPTPzeta D1 (AAA49015)	(1)	KHFPPKH	VAD	L	HAS	SG	---	FTEEFET	---	KEF	Q	EV	Q	SC
xPTPzeta D1 (BAA97445)	(1)	KQFHKK	ED	L	HS	R	SG	---	---	FTDE	EE	Q	SC	---
hCD45 D1 (NP 002829) PTPRC	(1)	DI	LE	TY	KR	KI	AD	EG	---	---	RF	LA	FL	QS
mCD45 D1 (NP 035340) Ptprrc	(1)	DI	LE	TY	KR	KI	AD	EG	---	---	RF	LA	FL	QS
rCD45_D1 (XP 213985) Ptprrc	(1)	DI	LE	TY	KR	KI	AD	EG	---	---	RF	LA	FL	QS
cCD45 D1 (A54008)	(1)	EK	LE	TY	KR	KI	AD	EG	---	---	RF	LD	FL	QS
cypcCD45 D1 (BAA92179)	(1)	GG	LV	EAY	K	N	KI	AD	EG	---	---	RF	MD	FL
fuCD45 D1 (CAB96211)	(1)	ET	LD	AY	KR	KI	AD	EG	---	---	RF	LA	FL	QS
sharkCD45 D1 (T43148)	(1)	EQ	LD	VY	RR	KQ	AD	EG	---	---	RF	LA	FL	QS
hDEP1 D1 (NP 002834) PTPRJ	(1)	ENFEAY	F	KKQ	Q	AD	SN	---	---	CG	FA	E	ED	K
rDEP1 D1 (NP 058965) Ptprrj	(1)	ENFEAY	F	KKQ	Q	AD	SN	---	---	CG	FA	E	ED	K
mDEP1 D1 (NP 033008) Ptprrj	(1)	ENFEAY	F	KKQ	Q	AD	SN	---	---	CG	FA	E	ED	K
hGLEPP1 D1 (NP 109592) PTPRO	(1)	DDFDAY	L	KD	AK	D	SS	---	---	YK	FL	S	LQ	EE
rGLEPP1 D1 (NP 059032) Ptprr	(1)	DDFDAY	L	KD	AK	D	SS	---	---	YK	FL	S	LQ	EE
mPTPphi D1 (NP 035346) Ptprr	(1)	DDFDAY	L	KD	AK	D	SS	---	---	YK	FL	S	LQ	EE
rabPTPoc D1 (AAB16824)	(1)	DDFDAY	L	KD	AK	D	SS	---	---	YK	FL	S	LQ	EE
hPTPbeta D1 (NP 002828) PTPRB	(1)	NQ	EG	H	F	M	L	Q	AD	SN	---	---	Y	L
mPTPbeta D1 (NP 084204) Ptprrb	(1)	NQ	EG	H	F	M	L	Q	AD	SN	---	---	Y	L
rPTPbeta D1 (XP 235156 (revised))	(1)	NQ	EG	H	F	M	L	Q	AD	SN	---	---	Y	L
hPTSP31 D1 (AR073855) PTPGMC1	(1)	KS	F	LQ	H	V	E	L	C	T	N	N	---	---
rPTPGMC1 D1 (NP 075214) Ptprrg	(1)	KS	F	LQ	H	V	E	L	C	T	N	N	---	---
hSAP1_D1 (NP 002833) PTPRH	(1)	ED	F	A	D	H	V	R	N	E	K	D	S	---
mSAP1 D1 (BAC37443)	(1)	KD	F	A	D	H	V	R	N	E	K	D	S	---
rPTPBEM2 D1 (NP 598276)	(1)	KD	F	A	D	H	V	R	N	E	K	D	S	---
mPTPESP_D1 (NP_031981) Esp	(1)	HS	F	R	S	Y	E	A	K	S	A	R	A	---

Alignment_195_Vert_PTP_Domains_D1_and_D2_Updated (VNTI 8.0).apcr

	blA2 D1 (P56722) Ptdrn (179)	HFLSWEAECTEAS--TRPFLDRLRRKYNKCYR-----GRSCPIVHVCSDGAGRTGTVLIDMVNLRNAKAG--VKEIDIAATLEHVRDORPGLVRSKQGFQEFALTAAAEEN
	hiA2beta D1 (NP 002838) PTPRN2 (179)	HFLSNYDRGVGSS--SRSLDLRRLRRKYNKCYR-----GRSCPIVHVCSDGAGRTGTVLIDMVNLRNAKAG--AKEIDIAATLEHVRDORPGLVRSKQGFQEFALTAAAEEN
	macnelA2beta D1 (O02695) (179)	HFLSNYDRGVGSS--SRSLDLRRLRRKYNKCYR-----GRSCPIVHVCSDGAGRTGTVLIDMVNLRNAKAG--AKEIDIAATLEHVRDORPGLVRSKQGFQEFALTAAAEEN
	mPTPNP D1 (P80560) Ptdrn2 (179)	HFLSNYDQGVVSS--TRSLDLRRLRRKYNKCYR-----GRSCPIVHVCSDGAGRTGTVLIDMVNLRNAKAG--AKEIDIAATLEHVRDORPGLVRSKQGFQEFALTAAAEEN
	rPTPNE6 D1 (NP 113788) Ptdrn2 (179)	HFLSNYDQGVVSS--TRSLDLRRLRRKYNKCYR-----GRSCPIVHVCSDGAGRTGTVLIDMVNLRNAKAG--AKEIDIAATLEHVRDORPGLVRSKQGFQEFALTAAAEEN
	hCD45 D2 (NP 002829) PTPRC (199)	QKTNNSVVEQFAE--PKELISMVQVVKQLPKQKNSSEG---KHKHSTLLHTRDGSQQGTGFCALNLLLSAET--EVDVDFVQVVKLRKARPGMVSTFFQYQFLVDVASTYP
	mCD45 D2 (NP 035340) Ptdrc (199)	QCTTKGEEFAE--PKDLVSMVQDDKQLPKASPEGM---KYHKHSLVHTRDGSQQGTGFCALNLLLSAET--EVDVDFVQVVKLRKARPGMVSTFFQYQFLVDVASTYP
	rCD45_D2 (XP 213985) Ptdrc (199)	QCTTKGEEFAE--PKDLVTLIQNKQLPKPSGSEG---KYHKHSLVHTRDGSQQGTGFCALNLLLSAET--EVDVDFVQVVKLRKARPGMVSTFFQYQFLVDVASTYP
	ccD45 D2 (A54080) (199)	QCHKNGLDVPEE--PKDLVDMVLSKQKVPSPASEDS---RNSRSYFVHTRDGSQQGTGFCALNLLLSAET--EVDVDFVQVVKLRKARPGMVSTFFQYQFLVDVASTYP
	fuCD45 D2 (CAB96211) (199)	QFLKMGDKVEPK--PQDADLKEKHKRGGY---TWPRSTVIVHTRDGSRRGAFCAWNLNDNAEK---EKMVDVFQVVKLRKERQKGCPSLQYQFLVDVASTYP
	cypcaCD45 D2 (BAA92179) (197)	QFLKMGRELEN--AQELVEMASIRRENGHYDNS---KTRNRVPIVHTRDGSRRGAFCAWNLNDNAEK---EKLVDVLEQVNRKLRKQGMVETIROYQFLVLTAEAFPP
	aotvoCD45 D2 (AAM48512) (3') (191)	QYTNNSVXXLAX--PKELISMVQVXKQKLPQKNSSEG---KXHKSLVHTRDGSQQGTGFCALNLLLSAET--EVDVDFVQVVKLRKARPGMVSTFFQYQFLVDVASTYP
	sharkCD45 D2 (T43148) (198)	HFHDMASELED--PSNFTKMLRSKELKSTLQEPPE---SSLSPSLVHTRDGSAGKTVGFYAWILLDNADT---NVLVDLQTVKLRKARPGMVSTFFQYQFLVDVASTYP
	cPTPaloha D2 (AAB04150) (181)	HFHGWFEVGLSD--GKGNINLIIAAQKQQQ---QSGNHPIVHCHCSAGAGRTGTFICALSTVLERKA--EGLDVFQTVKSLRQRPHMVQTLROYEFCYKVVQBYID
	hPTPaloha D2 (NP 002827) PTPRA (182)	HFHGWFEVGLSD--GKGNINLIIAAQKQQQ---QSGNHPIVHCHCSAGAGRTGTFICALSTVLERKA--EGLDVFQTVKSLRQRPHMVQTLROYEFCYKVVQBYID
	mPTPaloha D2 (NP 033006) Ptdra (182)	HFHGWFEVGLSD--GKGNINLIIAAQKQQQ---QSGNHPIVHCHCSAGAGRTGTFICALSTVLERKA--EGLDVFQTVKSLRQRPHMVQTLROYEFCYKVVQBYID
	rPTPaloha D2 (NP 036895) Ptdra (182)	HFHGWFEVGLSD--GKGNINLIIAAQKQQQ---QSGNHPIVHCHCSAGAGRTGTFICALSTVLERKA--EGLDVFQTVKSLRQRPHMVQTLROYEFCYKVVQBYID
	xPTPaloha D2 (AAA17990) (182)	HFHGWFEVGLTD--GKGNINLIIAAQKQQQ---QSGNHPIVHCHCSAGAGRTGTFICALSTVLERKA--EGLDVFQTVKSLRQRPHMVQTLROYEFCYKVVQBYID
	zPTPaloha D2 (NP 571963) ptdra (182)	HFHGWFEVGLSD--GKGNINLIIAAQKQQQ---QSGNHPIVHCHCSAGAGRTGTFICALSTVLERKA--EGLDVFQTVKSLRQRPHMVQTLROYEFCYKVVQBYID
	rvPTPR4b D2 (BAA95196) (182)	HFHGWFEVGLAD--GKGNINLIIAAQKQQQ---QSGNHPIVHCHCSAGAGRTGTFICALSTVLERKA--EGLDVFQTVKSLRQRPHMVQTLROYEFCYKVVQBYID
	hPTPepsilon D2 (NP 006495) PTPRE (187)	HFHGWFEVGLAE--GKGNIDLIIAAQKQQQ---QTNGNHPIVHCHCSAGAGRTGTFICALSNILERKA--EGLDVFQTVKSLRQRPHMVQTLROYEFCYKVVQBYID
	mPTPepsilon D2 (NP 035342) Ptdre (187)	HFHGWFEVGLAE--GKGNIDLIIAAQKQQQ---QTNGNHPIVHCHCSAGAGRTGTFICALSNILERKA--EGLDVFQTVKSLRQRPHMVQTLROYEFCYKVVQBYID
	rPTPepsilon D2 (XP 215102) Ptdre (187)	HFHGWFEVGLTE--GKGNIDLIIAAQKQQQ---QTNGNHPIVHCHCSAGAGRTGTFICALSNILERKA--EGLDVFQTVKSLRQRPHMVQTLROYEFCYKVVQBYID
	orylaPTPepsilon D2 (BAC06424) (187)	HFHGWFEVGLVD--GRGNIDLIIAAQKQQQ---QSGNRPVHCHCSAGAGRTGTFICALSNILERKA--EGLDVFQTVKSLRQRPHMVQTLROYEFCYKVVQBYID
	rPTPR4a D2 (BAA95190) (182)	HFHDMFEIGLEAE--GKGNIDLIIAAQKQQQ---KSGNHPIVHCHCSAGAGRTGTFICALSNILERKA--EGLDVFQTVKSLRQRPHMVQTLROYEFCYKVVQBYID
	hPTPkappa D2 (NP 002835) PTPRK (180)	QLGLWASREVPGS--KRSLKLLKLEKQWQEEC---EEGERTLVHCLNGGRRGMFCALGIVLMKRR--QNVVDVFAVKTLRNSPVEAPQYRRCVDVALEYE
	mPTPkappa D2 (NP 033009) Ptdrk (180)	QLGLWASREVPGS--KRSLKLLKLEKQWQEEC---EEGERTLVHCLNGGRRGMFCALGIVLMKRR--QNVVDVFAVKTLRNSPVEAPQYRRCVDVALEYE
	rvPTPR2B D2 (BAA95194) (180)	QLGLWASREVPGS--KRSLKLLKLEKQWQEEC---EEGERTLVHCLNGGRRGMFCALGIVLMKRR--QNVVDVFAVKTLRNSPVEAPQYRRCVDVALEYE
	QLGLWASREVPGS--KRSLKLLKLEKQWQEEC---EEGERTLVHCLNGGRRGMFCALGIVLMKRR--QNVVDVFAVKTLRNSPVEAPQYRRCVDVALEYE	
	hPTPlamda D2 (NP 005695) PTPRU (183)	QLRLWSARLDPDS--KRAFLLHLLAEKQWQAES---GDERTVHCLNGGRRGTCACATVLEMR--HNLVDVFFAAKTLRNYKSPVETMDFHFCVDVALEYE
	mPTPlamda D2 (NP 035344) Ptdrl (183)	QLRLWSARLDPDS--KRAFLLHLLAEKQWQAES---GDERTVHCLNGGRRGTCACATVLEMR--HNLVDVFFAAKTLRNYKSPVETMDFHFCVDVALEYE
	mPTPmu D2 (NP 002836) PTPRM (180)	QLGLWEMRDLTTPS--KRSLKLLKLEKQWQEEY---GGEPTVHCLNGGRRGTFICALSIVCMRHH--QRTVDVFAVKTLRNKKNSMVDLLQYKFCVDVALEYE
	mPTPmu D2 (NP 033010) Ptdrm (180)	QLGLWEMRDLTTPS--KRSLKLLKLEKQWQEEY---GGEPTVHCLNGGRRGTFICALSIVCMRHH--QRTVDVFAVKTLRNKKNSMVDLLQYKFCVDVALEYE
	rPTPmu D2 (XP 237546 (revised)) (180)	QLGLWEMRDLTTPS--KRSLKLLKLEKQWQEEY---GGEPTVHCLNGGRRGTFICALSIVCMRHH--QRTVDVFAVKTLRNKKNSMVDLLQYKFCVDVALEYE
	hPTPrho D2 (NP 057400) PTPRT (180)	QLIGWEMRDLTTPS--KRSLKLVVRRLEKQWQEQYD--GREERTVHCLNGGRRGTFICALCSVCMRQQ--QNIIDVFHLVKTLRNKKNSMVEETLQYKFCVDVALEYE
	mPTPrho D2 (NP 067439) Ptdrr (180)	QLIGWEMRDLTTPS--KRSLKLVVRRLEKQWQEQYD--GREERTVHCLNGGRRGTFICALCSVCMRQQ--QNIIDVFHLVKTLRNKKNSMVEETLQYKFCVDVALEYE
	cPTPsiama D2 (I50212) (182)	QFTDWFEEGVVFKS--GEGFIDTIGOVHKTKEQFG---QDGPITVHCHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	hLAR D2 (NP 002831) PTPRF (182)	QFTDWFEEGVVFKT--GEGFIDTIGOVHKTKEQFG---QDGPITVHCHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	mLAR D2 (NP 035343) Ptdrr (182)	QFTDWFEEGVVFKT--GEGFIDTIGOVHKTKEQFG---QDGPITVHCHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	rLAR_D2 (NP 062122) Ptdrr (182)	QFTDWFEEGVVFKT--GEGFIDTIGOVHKTKEQFG---QDGPITVHCHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	xLAR D2 (AAF43606) (182)	QFTDWFEEGVVFKT--GEGFIDTIGOVHKTKEQFG---QDGPITVHCHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	zLAR D2 (CAC44758) (182)	QFTDWFEEGVVFKT--GEGFIDTIGOVHKTKEQFG---QDGPITVHCHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	rvPTPR2Aa D2 (BAA95188) (182)	HFIDWFEQGVVFKT--GEGFIDTIGOVHKTKEQFG---QDGPITVHCHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	hPTPdelta D2 (NP 002830) PTPRD (182)	QFTDWFEEGVVFKS--GEGFIDTIGOVHKTKEQFG---QDGPISVHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	mPTPdelta D2 (D54689) (181)	QFTDWFEEGVVFKS--GEGFIDTIGOVHKTKEQFG---QDGPISVHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	xPTPdelta D2 (AAF43605) (182)	QFTDWFEEGVVFKS--GEGFIDTIGOVHKTKEQFG---QDGPISVHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	rvPTPR2Ab D2 (BAA95191) (182)	QFTDWFEEGVVFKS--GEGFIDTIGOVHKTKEQFG---QDGPISVHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	hPTPsiama D2 (NP 002841) PTPRS (182)	QFTDWFEEGVVFKS--GEGFIDTIGOVHKTKEQFG---QDGPISVHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	mPTPsiama D2 (NP 035348) Ptdrs (182)	QFTDWFEEGVVFKS--GEGFIDTIGOVHKTKEQFG---QDGPISVHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	xPTPsiama D2 (AAF43607) (182)	QFTDWFEEGVVFKS--GEGFIDTIGOVHKTKEQFG---QDGPISVHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	zPTPsiama D2 (CAC44759) (182)	QFTDWFEEGVVFKS--GEGFIDTIGOVHKTKEQFG---QDGPISVHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	rPTPsiama D2 (NP 062013) Ptdrd (182)	QFTDWFEEGVVFKS--GEGFIDTIGOVHKTKEQFG---QDGPISVHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	rvPTPR2Ac D2 (BAA95193) (182)	QFTDWFEEGVVFKS--GEGFIDTIGOVHKTKEQFG---QDGPISVHCSAGAGRTGTFICALSIVLERRY--EGVDMFQTVKMLRTORPAMVQTEIYQQLCVRAALEYG
	hPTPaamma D2 (NP 002832) PTPRG (186)	QCPKWFNPDPAPIS---STFELNIVKKEEALT---RDGPTVHVDYEGAVSAGMLCATLTSQQEN--NAVDVYQVAKMNLNMRPGVFTDIROYQFLKAVLSLIS
	mPTPaamma D2 (NP 033007) Ptdra (186)	QCPKWFNPDPAPIS---STFELNIVKKEEALT---RDGPTVHVDYEGAVSAGMLCATLTSQQEN--NAVDVYQVAKMNLNMRPGVFTDIROYQFLKAVLSLIS
	rPTPaamma D2 (NP 599183) Ptdra (178)	YVLEVRHFQAPIS---STFELNIVKKEEALA---RDGPTVHVDYEGAVSAGMLCATLTSQQEN--NAVDVYQVAKMNLNMRPGVFTDIROYQFLKAVLSLIS
	rvPTPR5b D2 (BAA95197) (186)	QCPKWFNPDPAPIS---STFELNIVKKEEAST---RDGPTVHDFEGVVSAGLCCGTLTSQQEC--SADVYQVAKMNLNMRPGVFTDIROYQFLKAVLSLIS
	cPTPaamma D2 (Q98936) (186)	QCPKWFNPDPAPIS---STFELNIVKKEEALT---RDGPTVHVDYEGAVSAGMLCATLTSQQEN--NAVDVYQVAKMNLNMRPGVFTDIROYQFLKAVLSLIS
	hPTPzeta D2 (NP 002842) PTPRZ1 (185)	QCPKWFNPDPAPIS---STFELNIVKKEEAAAN---RDGPMIVDEHGGVGTAGTCALTTLHQEK--NSVDVYQVAKMNLNMRPGVFTDIROYQFLKAVLSLIS
	cPTPzeta D2 (AAA49015) (185)	QCPKWFNPDPAPIS---STFELNIVKKEEAAAN---RDGPMIVDEHGGVGTAGTCALTTLHQEK--NSVDVYQVAKMNLNMRPGVFTDIROYQFLKAVLSLIS
	mPTPzeta D2 (XP 133090) Ptdrz1 (185)	QCPKWFNPDPAPIS---KTFEELSIKKEEAAAN---RDGPMIVDEHGGVGTAGTCALTTLHQEK--NSVDVYQVAKMNLNMRPGVFTDIROYQFLKAVLSLIS
	rPTPzeta D2 (NP 037212) Ptdrz1 (185)	QCPKWFNPDPAPIS---KTFEELSIKKEEAAAN---RDGPMIVDEHGGVGTAGTCALTTLHQEK--NSVDVYQVAKMNLNMRPGVFTDIROYQFLKAVLSLIS
	xPTPzeta D2 (BAA97445) (185)	QCPKWFNPDPAPIS---KTFEELSIKKEEAAAN---RDGPMIVDEHGGVGTAGTCALTTLHQEK--NSVDVYQVAKMNLNMRPGVFTDIROYQFLKAVLSLIS
	rvPTPR5a_D2 (BAA95195) (181)	QSPRWENPDGAPIS---KTFELNIVKKEEAAAN---RDGPTVHDEHGGVGTAGTCALTTLHQEK--NSVDVYQVAKMNLNMRPGVFTDIROYQFLKAVLSLIS
	Consensus (237)	QFTWFDHGVVPLLLFIIVGPIVVHCSAGVGRGTGTFIDMLELEVDVDFVKLRQRMVQTEIQYFIYALLEL