

PTP domains (excluding domains D2)

	$\alpha 1'$	$\alpha 2'$	$\alpha 1$	$\beta 1$	$\beta 2$	$\beta 3$																																																																												
Amino acid in hPTP1B	#10	#20	#30	#40	#50	#60	#70	#80																																																																										
hPTPalpha	DKLEEEINRRMADDN	KLFRREFFNAL	PAACPIQA	TCEAASKEENKEK	RYVNI	LPYDHSRV	H LTPVEGV	PDSDYINASFINGY	-----QEKKNFIAAQGP																																																																									
hPTPepsilon	EHLEEEIRIRSAADD	KQFRREFFNLS	PSGHIQG	TFELANKEENREK	RYVNI	LPNDHSRV	LSQLDGI	PCSDYINASYIDGY	-----KEKNKFAAQGP																																																																									
hPTPkappa	ADLLQHINLMKTSDS	YGFKEEYESF	FEQGS	SWDVAKKQNR	AKNR	RYGN	IAYDHSRV	VLQPVEDD	PCSDYINASYIDGY	-----QRP SHYIAAQGP																																																																								
hPTPmu	ADLLQHITQMKCAEG	YGFKEEYESF	FEQGS	PWDSAKKDENR	MKN	RYGN	IAYDHSRV	VLQPIEGD	TNSDYINGNYIDGY	-----HRPNHYIAAQGP																																																																								
hPTPrho	ADLLQHITQMKRGG	YGFKEEYEA	LEGTA	SWDTAKEDENR	NKN	RYGN	IISYDHSRV	RLVLDGD	PHSDYINASYIDGY	-----HRPRHYIAAQGP																																																																								
hPTPlamda	ADLLQHINQMKTAE	YGFKEEYESF	FEGWDA	T	-----	KKKDKVKGS	QEPMPAYDRH	RVK LHPMLGD	PNADYINASYIDGY	-----HRSNHFAAQGP																																																																								
hPTPdelta	LELADHIERLKANDN	LKFSQEYESI	D	PGQQF	-----	TWEHSNLEVN	KPKRYAN	VIAYDHSRV	LISAIEGI	PGSDYINASYIDGY	-----RKQNAZIAAQGP																																																																							
hPTPsigma	ADMAEHTERLKANDS	LKLSQEYESI	D	PGQQF	-----	TWEHSNLEVN	KPKRYAN	VIAYDHSRV	LQPIEGI	MGSDYINASYIDGY	-----RQNAZIAAQGP																																																																							
hPTPgamma	KQFVKHIGELYSNNQ	HGFSDFEEV	Q	RCTADMN	I	TAEHSNHPEN	KHKRYIN	I	LAYDHSRV	KLRLPGKDS	KHSDYINASYIDGY	-----NKAKAYIAAQGP																																																																						
hPTPzeta	KHFPKHVADLHASSG	TEEFETLKEFYQE	V	QSCSTVDLGI	-----	TADSSNHPDN	KHKRYIN	I	IVAYDHSRV	KLQAIAEKDG	KLTDYINASYIDGY	-----NRPKAYIAAQGP																																																																						
hLAR	TDLADNIERLKANDG	LKFSQEYESI	D	PGQQF	-----	TWENSNLEVN	KPKRYAN	VIAYDHSRV	LTSIDGV	PGSDYINASYIDGY	-----RKQNAZIAAQGP																																																																							
hCD45	DILLETYKRKIADEG	RLFLAEFQSI	PRVFSKF	-----	PIKEAR	KPFN	KRYAN	VIAYDHSRV	VELSEINGD	AGSNYINASYIDGY	-----KEPRKYIAAQGP																																																																							
hGLEPP1	DDFDAYIKDMAKSD	YKFSLQFEEL	KLIGLDI	-----	PHFAAD	PLNRCK	RYTN	I	LPYDFSR	VLVSMNEE	EGADYINASYIDGY	-----NSPQEYIAAQGP																																																																						
hTPS31	KSFLQHVEELCTNNN	LKFSQEYESI	D	PGQQF	-----	SSTAD	ADLPWNR	AKNR	RYFN	I	KPYNNR	VKL IADASV	PGSDYINASYIDGY	-----LCPNEFAAQGP																																																																				
hDEP1	ENFEAYFKKQADS	CGFAEEYED	L	KLVGISQ	-----	PKYAAEL	AENR	GKN	RYNN	VL	YDHSRV	KL	SVQTHS	-----	DDYINASYIDGY	-----HKKDFIAAQGP																																																																		
hPTPbeta	NQFEGHFMKLAQDS	YLLSKEYEEL	KD	VGRRNQ	-----	SCD	IALLPEN	RGN	RYNN	I	LPYD	AT	RV	KL	SNVDDD	PCSDYINASYIDGY	-----NFRREYIAAQGP																																																																	
hSAP1	EDFADHVRKNERDS	CGFADEYQQL	SLVGH	SQ	-----	SQMVAS	ASENN	AKNR	RYRN	VL	YDHSRV	PL	KPIHEE	-----	PGSDYINASYIDGY	-----WSPQEYIAAQGP																																																																		
hSTEP	SRVLQAEELHDEKALD	FLLQAEFF	E	PMNFVD	-----	PKEYD	IPLGR	VKN	RYKT	I	LPN	HSRV	CL	TS	PPDD	PLSSYINASYIDGY	-----GEEKYIAAQGP																																																																	
hPCPTP1	SRILLTRSLRDHVASS	HLLQSEFMEI	PMNFVD	-----	PKEYD	IPLGR	VKN	RYKT	I	LPN	HSRV	CL	TS	PPDD	PLSSYINASYIDGY	-----GEEKYIAAQGP																																																																		
hHePTP	GHPLTRWALQRQPPSP	KLLEEF	FLK	I	PSNFVS	-----	PEDLD	IPGH	ASK	RYKT	I	LPN	QSRV	CL	GRAQ	SQE	-----	DGDYINASYIDGY	-----GKEKVIYIAAQGP																																																															
hSHP1	ADINRVLELNKKQES	EDTAKAG	FWE	FESL	Q	QKQEV	KNLH	-----	QRLEG	QR	PN	KGK	RYKN	I	LP	FDHSRV	VL	QGRDSN	-----	PGSDYINASYIDGY	-----NANYIKN	-----	QLL	GPD	-----	ENAKTYIASQGP																																																								
hSHP2	AEIESRVRELSKLA	ETTDKVKQGF	WEE	FETL	Q	QKQEC	LLY	-----	SRKEG	QR	EN	KN	KN	RYKN	I	LP	FDHSRV	VL	HDGDP	NE	-----	PVSDYINASYIDGY	-----NAN	IM	PE	FET	KCN	NSKPK	KSYIAAQGP																																																					
hPEST	EILRKFIQRVQAMK	SPDHNGED	FARD	FMR	RL	ST	KYRTE	KI	YPT	AT	GE	KE	EN	V	K	RYKD	I	LP	FDHSRV	VL	LKT	PT	-----	QDSDYINASYIDGY	-----NAN	F	I	KG	-----	YGP	KAYIAAQGP																																																			
hLyPTP	EILQKFLDEAKKGI	TK	-----	EE	FAN	FLK	LR	QST	KYK	ADK	TYPT	VA	E	K	P	K	RYKD	I	LP	YDHSRV	VL	S	L	IT	SD	-----	EDSSYINASYIDGY	-----NAN	F	I	KG	-----	YGP	KAYIAAQGP																																																
hBDP1	DSARSFLERLEARG	REG	-----	AV	LAGE	FSD	I	Q	AS	A	AW	K	AD	G	V	C	S	VR	PN	RYKD	I	LP	YDHSRV	VL	S	L	L	Q	EE	-----	GHSDYINASYIDGY	-----NAN	F	I	RG	-----	DG	S	L	YIAAQGP																																										
hTPD1	ATNDERCKILEQR	LEQG	-----	MV	FTE	YER	I	KL	RL	VDG	-----	EC	STAR	L	P	EN	AER	RF	Q	ED	VL	YD	HSRV	VL	VP	T	KE	-----	NTGYINASHIKVSV	-----	SG	I	E	WDYIAAQGP																																																
hTPD2	VPMDERFRTLKK	LEEG	-----	MV	FTE	YER	I	KL	K	ANG	-----	I	F	TA	A	L	P	EN	AER	RF	Q	ED	VL	YD	HSRV	VL	VP	T	KE	-----	NTGYINASHIKVSV	-----	GA	E	WHYIAAQGP																																															
hMEG1	HSLESMIQLAEG	LITG	-----	TV	L	Q	FD	Q	LY	R	K	P	G	M	-----	TM	S	C	A	K	L	P	Q	N	I	S	K	RYRD	I	SP	YD	AT	RV	L	KG	-----	NEDYINASYIDGY	-----NAN	Y	N	M	E	I	P	-----	SSS	I	N	QYIAAQGP																																	
hTPPH1	DTLEGSMALKKGL	ESG	-----	TV	L	Q	FD	Q	LY	R	K	P	G	M	-----	A	I	F	A	K	L	P	Q	N	I	S	K	RYRD	I	SP	YD	AT	RV	L	KG	-----	NEDYINASYIDGY	-----NAN	Y	N	M	E	I	P	-----	AAN	L	V	N	KYIAAQGP																																
hPTPBAS	KSVIRVLRGLDQ	GI	-----	PS	K	E	L	E	N	Q	L	E	L	P	L	-----	Q	C	L	I	G	O	T	K	R	R	K	RYRD	I	SP	YD	AT	RV	L	KG	-----	NEDYINASYIDGY	-----NAN	Y	N	M	E	I	P	-----	K	E	E	F	YIAAQGP																																
hPTP1B	MEMEKFEFGLDK	SGS	-----	WA	A	I	Q	D	I	HE	A	S	D	F	-----	P	C	R	V	A	K	L	P	K	N	R	RYRD	I	SP	YD	AT	RV	L	KG	-----	NEDYINASHIKVSV	-----	D	N	Y	I	N	A	S	L	I	K	M	E	-----	E	A	Q	R	S	YIAAQGP																										
hTCPTP	TTIEREFEE	LDTQRR	-----	W	P	L	Y	L	E	I	R	N	E	S	H	Y	-----	P	H	R	V	A	K	F	P	E	N	R	RYRD	I	SP	YD	AT	RV	L	KG	-----	NEDYINASHIKVSV	-----	D	N	Y	I	N	A	S	L	V	D	I	E	-----	E	A	Q	R	S	YIAAQGP																								
hMEG2	MTIQELVDYV	NARQK	-----	G	I	E	E	Y	E	D	I	R	E	N	P	V	G	-----	T	F	H	C	S	M	P	G	N	L	E	K	RYGD	I	V	P	C	L	D	Q	T	RV	L	K	T	R	S	G	H	T	-----	Q	T	D	Y	I	N	A	S	F	M	D	G	Y	-----	K	K	N	A	Y	I	G	T	Q	G									
hIA2	HMILAYMDHL	LRNRDR	-----	L	A	K	E	W	A	L	C	A	Y	Q	A	E	P	N	-----	T	C	A	T	A	Q	G	E	G	N	I	K	RYPD	I	F	L	P	Y	D	H	A	R	I	K	L	K	V	E	S	S	P	S	-----	R	S	D	Y	I	N	A	S	P	I	E	H	D	-----	P	R	M	A	Y	I	T	Q	G							
hIA2beta	HMILSYMEDHL	KNKRN	-----	L	E	K	E	W	A	L	C	A	Y	Q	A	E	P	N	-----	S	S	F	V	A	Q	R	E	N	V	P	K	RYSL	A	V	L	T	Y	D	H	S	R	V	L	L	K	A	E	N	S	H	S	-----	H	S	D	Y	I	N	A	S	P	I	M	D	H	-----	P	R	N	P	A	Y	I	T	Q	G						
hPTPTyp	TAIKDCLKL	LEEKTA	-----	Y	D	I	M	Q	E	F	A	L	E	L	K	N	L	P	G	-----	E	F	Y	S	G	N	Q	P	S	R	E	K	RYRD	I	L	P	Y	D	S	T	R	V	P	L	G	-----	S	K	D	Y	I	N	A	S	Y	I	R	I	V	N	-----	C	G	E	E	F	YIAAQGP															
hHDTP	ERLRLQQLQEL	EA	FRGLQ	GDV	-----	G	A	L	D	T	V	W	R	E	L	Q	-----	D	A	Q	E	H	D	A	R	-----	G	R	S	I	A	I	A	R	C	Y	S	L	K	N	R	H	Q	D	V	M	P	Y	D	S	N	V	L	R	S	G	-----	K	D	D	Y	I	N	A	S	C	V	E	G	L	S	-----	P	Y	C	P	L	V	A	T	Q	G

Consensus - (amino acid identity 100%, 90%, 80%): E N KRY D R L D Y I N A Y I A T QGP
 Motif 1 Motif 2 Motif 3 Motif 4

PTP domains D2

hPTPalpha	T	S	L	E	T	H	L	Q	K	I	Y	N	K	I	P	G	-----	T	S	N	G	L	E	E	F	K	L	T	S	I	K	I	Q	N	-----	D	K	M	R	T	G	N	L	P	A	N	M	K	K	N	R	V	L	Q	I	P	Y	E	F	N	R	V	I	P	V	K	R	G	E	-----	E	N	T	D	Y	V	N	A	S	F	I	D	G	Y	-----	R	Q	K	D	S	Y	I	A	S	Q	G	
hPTPepsilon	S	S	L	E	K	H	L	Q	T	M	H	G	T	T	H	-----	F	D	K	I	G	L	E	E	F	K	L	T	N	V	R	I	M	K	-----	E	N	M	R	T	G	N	L	P	A	N	M	K	K	A	R	V	I	P	Y	D	F	N	R	V	I	L	S	M	K	R	G	-----	E	Y	T	D	Y	V	N	A	S	F	I	D	G	Y	-----	R	Q	K	D	S	Y	I	A	S	Q	G			
hCD45	S	E	L	H	P	Y	L	H	N	M	K	K	R	D	P	-----	S	E	P	S	L	E	A	E	F	Q	R	L	P	S	R	S	R	W	-----	T	Q	H	I	G	N	Q	E	E	N	K	R	N	S	N	V	I	P	Y	D	N	R	V	L	S	M	K	H	E	M	(19)	E	P	S	K	Y	I	N	A	S	F	I	M	S	Y	-----	W	K	P	E	V	M	I	A	A	Q	G					
hPTPgamma	N	Q	L	H	S	Y	V	N	S	I	L	I	P	G	V	-----	G	K	T	R	L	E	K	Q	F	K	L	V	T	Q	C	N	A	K	Y	-----	V	E	C	F	S	A	Q	K	E	C	N	K	E	K	R	N	S	S	V	P	S	E	R	A	R	V	G	L	A	P	L	P	G	M	-----	K	G	T	D	Y	V	N	A	S	F	I	M	G	Y	-----	Y	R	S	N	E	F	I	I	T	Q	H
hPTPzeta	S	H	I	H	A	Y	V	N	A	L	I	P	G	P	-----	G	K	T	K	L	E	K	Q	F	L	V	T	S	Q	N	I	Q	Q	-----	S	D	Y	S	A	A	L	K	Q	C	N	R	E	K	R	T	S	S	I	P	E	R	S	R	V	G	I	S	S	L	S	G	-----	E	G	T	D	Y	V	N	A	S	F	I	M	G	Y	-----	Y														

PTP domains (excluding domains D2)

Amino acid	α3		β12	α4		α5		α6						
	#190	#200	#210	#220	#230	#240	#250	#260	#270	#280				
hPTPalpha	--PIGMLKFLKKVKACNPQYA	-----	GAIIVVHCSAGVGRGTGF	VVIDAMLDMHTE	ERK	---VDVYGFVSRIR	RAQR	CCQMV	QTD	MQYVF	IYQALEHYLY	GDTEL		
hPTPepsilon	--PIGMLKFLKKVKTLNPVHA	-----	GPVVVHCSAGVGRGTGF	VVIDAMMAMHAE	QK	---VDVFEFVSRIR	RNR	PQMV	QTD	MQYTF	IYQALEYYLY	GDTEL		
hPTPkappa	--ATGLLSFIRRVKLSNPPSA	-----	GPVVVHCSAGAGRTGCF	VVIDIMLDMAER	EGV	---VDIYNCVKAL	RSRR	INMV	QTE	EQYIF	IHDAL	LEACLG	GETAI	
hPTPmu	--ATGLLGfVfRQVKSKSPSPA	-----	GPLVVHCSAGAGRTGCF	VVIDIMLDMAER	EGV	---VDIYNCVREL	RSRR	VNMV	QTE	EQYVF	IHDAL	LEACLG	GDTSV	
hPTPrho	--ATGLLGfVfRQVKFLNPPEA	-----	GPVVVHCSAGAGRTGCF	VVIDIMLDMAEN	EGV	---VDIFNCVREL	RAQR	VNLV	QTE	EQYVF	VHDA	LEACLG	GNIAI	
hPTPlamda	--ATGLLAFIRRVKASTPPDA	-----	GPVVVHCSAGAGRTGCF	VVIDIMLDMAEC	EGV	---VDIYNCVKT	LSRR	VNMV	QTE	EQYIF	IHDAL	LEACLG	GETTI	
hPTPdelta	--PTPFLAFLRRVKTGNPPDA	-----	GPMVVHCSAGVGRGTGF	VVIDAMLERIK	KEKT	---LDIYGHVTL	MRQR	NYMV	QTE	EQYIF	IHDAL	LEAVTG	GNTEV	
hPTPsigma	--PTPFLAFLRRVKTGNPPDA	-----	GPVVVHCSAGVGRGTGF	VVIDAMLERIK	KEKT	---LDIYGHVTL	MRQR	NYMV	QTE	EQYIF	IHDAL	LEAVTG	GNTEV	
hPTPgamma	--ALPVLTFVRRSSAARMPET	-----	GPLVVHCSAGVGRGTGF	VVIDSMLQQIK	KDST	---VNVLGF	LKHIRT	QRNY	LV	QTE	EQYIF	IHDAL	LEA	ILGKETEV
hPTPzeta	--SLPVLTFVRRSSAARMPET	-----	GPVVVHCSAGVGRGTGF	VVIDSMLQQIK	QHEGT	---VNTFGFLKH	IRSR	QNYL	LV	QTE	EQYVF	IHDTL	EA	ILSKETEV
hLAR	--PTPFLAFLRRVKTGNPPDA	-----	GPMVVHCSAGVGRGTGF	VVIDAMLERIK	KEKT	---VDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hCD45	--PHLLKFLRRVNAFSNFFS	-----	GPVVVHCSAGVGRGTGF	VVIDAMLERIK	KEKT	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hGLEPP1	NAAESILQFVHMVRQATKSK	-----	GPMIVHCSAGVGRGTGF	VVIDALDRL	LQHIRDHEF	---VDILGLV	SEMRSY	RMSV	QTE	EQYIF	IHQCV	QLMWM	KKKQF	
hTPS31	--SAPLIFHFVKLVRASRAHDT	-----	TPMIVHCSAGVGRGTGF	VVIDALDHL	TQHINDHDF	---VDIYGLV	AELE	RSMC	MV	QNL	AAQYF	ILHQCI	L	DLLSNKG
hDEP1	TDLLINFRYLVRDYMKQSPPE	-----	SPVVVHCSAGVGRGTGF	VVIDRLI	YQIENENT	---VDVYGI	VYDL	LRMH	PL	QTE	EQYVF	LNQC	VD	ILVRSQK
hPTPbeta	--TQSLIQFVRTVDYINRSPGA	-----	GPTVVHCSAGVGRGTGF	VVIDALDRI	LQQLDSKDS	---VDIYGA	VDL	LRH	VHM	QTE	EQYVF	ILHQ	CV	DR
hSAP1	PDTLAFWRMLRQWLDQTMEG	-----	GPMVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hSTEP	--APPVLLHLVREVEEAQQEGPHC	-----	APVVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hPCPTP1	--AQLPLQLMLDVEEDRLASQGR	-----	GPVVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hHePTP	--AGPLLRLVAEVEESPETAHP	-----	GPVVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hSHP1	--PGGVLSFLDQINQRQESLPHA	-----	GPVVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hSHP2	--PGVLDLLEEYHHKQESIMDA	-----	GPVVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hPEST	--FDSILDMISLMRKYQEHED	-----	VVICIHCSAGCGRTGA	ICADY	TWMLLKAGI	PEEFNFV	NLIQEM	RTQR	HS	AV	QTE	EQYEL	VHRA	IAQLFEK
hLyPTP	--IDPILLELIDWVRCYQEDDS	-----	VVICIHCSAGCGRTGA	ICADY	TWMLLKAGI	PEEFNFV	NLIQEM	RTQR	HS	AV	QTE	EQYEL	VHRA	IAQLFEK
hBDP1	--PDHMLAMVEEAARRLQSGSP	-----	EPVHVHCSAGCGRTGA	ICADY	TWMLLKAGI	PEEFNFV	NLIQEM	RTQR	HS	AV	QTE	EQYEL	VHRA	IAQLFEK
hTPD1	--LKGFLSYLEEQVRRHTNSTSDPQSPN	-----	PPLLVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hTPD2	--VQGFLSYLEEQVRRHTNSTSDPQSPN	-----	PPLLVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hMEG1	--SSDFLDFVCHVRNKRAGKE	-----	EPVHVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hTPPH1	--SSDFLDFVCHVRNKRAGKE	-----	EPVHVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hTPBAS	--PDDLLTFISYMRH IHR	-----	GPVVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hTP1B	--PASFLNLFKVRRESGSLSPHE	-----	GPVVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hTCPTP	--PASFLNLFKVRRESGSLSPHE	-----	GPVVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hMEG2	--AASLIDFLRVVRNQQSLAVSNMGARSKGQCEP	-----	PVVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hIA2	--TRPLDFRRKVNKCYGRS	-----	CPVVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hIA2beta	--SRSLDFRRKVNKCYGRS	-----	CPVVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hPTPTyp	--ADSFIKYIRYARKSHLT	-----	GPMVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
hHDPTP	--PSNLLRFIQEVHAHYLHQRPLH	-----	TPVVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV	
Consensus	L		P	VHCSAG	GRTG		R	R	Q	T	Q	Y	F	
				Motif 9					Motif 10					

PTP domains D2

hPTPalpha	--GKGMISIIAAVQKQKQSGN	-----	HPITVHCSAGAGRTGTF	CALSTV	LERVKA	EGI	---LDVFQTVKSL	LRQR	PHMV	QTE	EQYEF	FCYKVV	QVEY	IDA	FS
hPTPepsilon	--GKGMIDLIAAVQKQKQQTGN	-----	HPITVHCSAGAGRTGTF	CALSTV	LERVKA	EGL	---LDVFQAVKSL	LRQR	PHMV	QTE	EQYEF	FCYKVV	QDF	IDI	FS
hCD45	--PKELISMIQVVKQLPKNSSEGNKHHKS	-----	TPLLHCRDGSQQTGI	CALLNL	LSAETEEV	---	VDIFQVVKAL	RKAR	PGV	ST	F	EQYQ	FLY	DVIA	STYPA
hPTPgamma	--STFELINVIKEEALTRD	-----	GPVVVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV		
hPTPzeta	--KTFELISVIEEAAARND	-----	GPMIVHDEHGGVTA	GTFCAL	TLMHQLEKENS	---	VDVYQVAKMI	NLMR	PGV	FAD	I	EQYQ	FLY	KVIL	SLVSTR
hPTPsigma	--GEGFIDFIGQVHKTKEQFGQD	-----	GPISVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV		
hPTPdelta	--GEGFIDFIGQVHKTKEQFGQD	-----	GPISVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV		
hLAR	--GEGFIDFIGQVHKTKEQFGQD	-----	GPISVHCSAGVGRGTGF	VVIDALDVL	LRQLQSEGL	---LDIYGHVTL	MRQR	NYMV	QTE	EQYVF	IHDAL	LEAVTG	GNTEV		
hPTPrho	--SKRSLLKVVRRLEKQEQYDGRE	-----	GRTVVHCLNGGGRSGT	FCAL	ISVCEMI	QQNI	---	IDVFHIVK	TLRN	KN	SN	VM	ET	LE	YLS
hPTPmu	--SKRSFLKLIHQVQKQEEYNGGE	-----	GPTVVHCLNGGGRSGT	FCAL	ISVCEMI	RHRT	---	VDVFHAVK	TLRN	KN	KN	PM	VD	LD	QYK
hPTPkappa	--SKRSFLKLIHQVQKQEEYNGGE	-----	GRTIVHCLNGGGRSGT	FCAL	ISVCEMI	RHRT	---	VDVFHAVK	TLRN	KN	KN	PM	VE	AP	EQYR
hPTPlamda	--SKKAFLLLAEDVQWQAESGD	-----	GRTIVHCLNGGGRSGT	FCAL	ISVCEMI	RHRT	---	VDVFHAVK	TLRN	KN	KN	PM	VE	AP	EQYR

Color code: N 100 % amino acid identity E 80 % amino acid identity S 40 % amino acid identity
 L 90 % amino acid identity P 60 % amino acid identity

VectorNTI Screen View - Alignment_195_Vert_PTP_Domains_D1_and_D2 (VNTI 8.0).ap

blA2 D1 (P56722) Ptdn	(1) HMLAYMEDHLNRND-----RLAKBQALCAY----QAEPNTCATAQEGEIKK--NRSLPDFPYDHAHAKIKVVESSP-----SRSDYINAFPIEIDPR
hIA2beta D1 (NP 002838) PTPRN2	(1) HMLSYMEDHLNKNK-----RLKKEEALCAY----QAEPNSFVYQREEVVPK--NRSLAVITDHSRVLKKAENSH-----SHSDYINAFIMDHDR
macnelA2beta D1 (O02695)	(1) HMLSYMEDHLNKNK-----RLKKEEALCAY----QAEPNSSLVAQREENVPK--NRSLAVITDHSRVLKKAENSH-----SHSDYINAFIMDHDR
mPTPNP D1 (P80560) Ptdn2	(1) HMLAYMEDHLNKNK-----RLKKEEALCAY----QAEPNSSLVAQREENAPK--NRSLAVITDHSRVLKKAENSH-----SSSDYINAFIMDHDR
rPTNE6 D1 (NP 113788) Ptdn2	(1) HMLAYMEDHLNKNK-----RLKKEEALCAY----QAEPNSSLVAQREENAPK--NRSLAVITDHSRVLKKAENSH-----SNSDYINAFIMDHDR
hCD45 D2 (NP 002829) PTPRC	(1) SEHPYIHNKKRRDP--SEPSPEAEQRPL----SYRSWRQTQHQEQEENKSK--NRNSVLPYDFNRPVKHELEMS--KESEHSDSDSDSDSDSEEPKVINASLMSYWKP
mCD45 D2 (NP 035340) Ptdrc	(1) SEHSCILHNKKRRDP--SDPSPEAEQRPL----SYRSWRQTQHQEQEENKSK--NRNSVLPYDFNRPVKHELEMS--KESEPESDSDSDSDSDSEETKVINASLMSYWKP
rCD45_D2 (XP 213985) Ptdrc	(1) SEHSLQNLNKKRRDP--SDPSPEAEQRPL----SYRSWRQTQHQEQEENKSK--NRNSVLPYDFNRPVKHELEMS--KESEAESDSDSDSDSDSEETKVINASLMSYWKP
ccCD45 D2 (A54080)	(1) SEHSLYNNLKKRRDP--SEPSLEAEQRPL----SYKGWRVTQNTQNEENKSK--NRNSANTVPYDFNRPVKHELEMS--KESEHSDSDSDSDSDSEESKVINASLMSYWKP
fuCD45 D2 (CAB96211)	(1) QELHSTLNTLQQRSSD--NEPTLLEDFERLP----NFKNWRFTNTGVTENKSKK--NRSSVLPYDFNRPVKHELEMS--KESEHSDSDSDSDSDSEESKVINASLMSYWKP
cypcaCD45 D2 (BAA92179)	(1) SEFHVSVNTLQKNG--SDPSLEAEQRPL----KFKKWRMTMTGSSDENKSK--NRDSAVLPYDFNRPVKHELEMS--QTSDEPEDEEYSSDSEESKVINASLMSYWKP
aotvoCD45 D2 (AAM48512) (3')	(1) -----NKKRRDP--SEPSPEAEQRPL----SYRSWRQTQHQEQEENKSK--NRNSVLPYDFNRPVKHELEMS--KESEHSDSDSDSDSDSEESKVINASLMSYWKP
sharkCD45 D2 (T43148)	(1) SELPKHINFKKNDPP--SEPSMGEFQRPL----PYTDWRQTQTRRGEQSK--NRSLVLPYDFNRPVKHELEMS--KDSHSDSDSDSDSDSEESKVINASLMSYWKP
cPTPaloha D2 (AAB04150)	(1) TSEIHLQKLYNKVP--GTSSNGEEFKKLT--IKIQNDKMRTNLPAANMKK--NRVLOLPYDFNRPVKRGE--ENSDYINAFIDGYRRR
hPTPaloha D2 (NP 002827) PTPRA	(1) TSETHLQKLYNKIP--GTSNNGEEFKKLT--IKIQNDKMRTNLPAANMKK--NRVLOLPYDFNRPVKRGE--ENSDYINAFIDGYRQK
mPTPaloha D2 (NP 033006) Ptdra	(1) TSETHLQKLYNKIP--GTSNNGEEFKKLT--IKIQNDKMRTNLPAANMKK--NRVLOLPYDFNRPVKRGE--ENSDYINAFIDGYRQK
rPTPaloha D2 (NP 036895) Ptdra	(1) TSDTHLQKLYNKIP--GTSNNGEEFKKLT--IKIQNDKMRTNLPAANMKK--NRVLOLPYDFNRPVKRGE--ENSDYINAFIDPYRQK
xPTPaloha D2 (AAA17990)	(1) TSETHLQKLYSKFP--GTNSTGEEFKKLT--IKIQNDKMRTNLPAANMKK--NRVLOLPYDFNRPVKRGE--ENSDYINAFIDGYRQK
zPTPaloha D2 (NP 571963) ptdra	(1) TSETHMNLKLYPLP--GAGCGGLEAEFKKLT--IKIQNDKMRTNLPAANMKK--NRVLOLPYDFNRPVKRGE--ENSDYINAFIDGYRQK
rvPTPR4b D2 (BAA95196)	(1) TSESHLQKLYNRVS--GSGCGNGEEFKKLT--IKIQNDKMRTNLPAANMKK--NRVLOLPYDFNRPVKRGE--ENSDYINAFIDGYRQK
hPTPepsilon D2 (NP 006495) PTPRE	(1) SSELKHLQTLHGT--HFDKIGEEFKKLTN--VRIMKENMRTGNLPAANMKK--ARVIOILPYDFNRPVKRGE--EYSDYINAFIDGYRQK
mPTPepsilon D2 (NP 035342) Ptdre	(1) SSELERHLQTLHSTAT--HFDKIGEEFKKLTN--VRIMKENMRTGNLPAANMKK--ARVIOILPYDFNRPVKRGE--EYSDYINAFIDGYRQK
rPTPepsilon D2 (XP 215102) Ptdre	(1) SSELERHLQTLHGTAT--HFDKIGEEFKKLTN--VRIMKENMRTGNLPAANMKK--ARVIOILPYDFNRPVKRGE--EYSDYINAFIDGYRQK
orylaPTPepsilon D2 (BAC06424)	(1) CSELGHLHRLHNRTA--PNDRLIGEEFKKLTN--VRIMKENMRTGNLPAANMKK--ARVIOILPYDFNRPVKRGE--EYSDYINAFIDGYRQK
rvPTPR4a D2 (BAA95190)	(1) SSELKHLQKLRNKTG--HFDITGEEFKKLTN--VRIRKDNMRTGNLPAANMKK--ARVIOILPYDFNRPVKRGE--EYSDYINAFIDGYRQK
hPTPkappa D2 (NP 002835) PTPRK	(1) KAAYPDMIRLDSQTN--SSHKDEPQTLNS--VTPRLQAEDCSIALFRNHDK--NRSMDLPPRCLPFLITDGD--ESNRYINAFIDMSYRQP
mPTPkappa D2 (NP 033009) Ptdrk	(1) KAAYPDMIRLDSQTN--SSHKDEPQTLNS--VTPRLQAEDCSIALFRNHDK--NRSMDLPPRCLPFLITDGD--ESNRYINAFIDMSYRQP
rvPTPR2B D2 (BAA95194)	(1) KQAYYEMIRLDSQSN--SSQLKDEPQTLNS--VSSQLQPEDCSIALFRNHDK--NRSMDLPPRCLPFLITDGD--ESNRYINAFIDMSYRQP
hPTPlamda D2 (NP 005695) PTPRU	(1) KATYKEMIRLDPQSN--SSQLREBPQTLNS--VTPPLDVEECSIALFRNHDK--NRSMDLPPRCLPFLITDGD--DSNNRYINAFIDMSYRQS
mPTPlamda D2 (NP 035344) Ptdrl	(1) RATYREMIRLDPQSN--SSQLREBPQTLNS--VTPPLDVEECSIALFRNHDK--NRSMDLPPRCLPFLITDGD--DNRYINAFIDMSYRQS
hPTPmu D2 (NP 002836) PTPRM	(1) RSLYDMNKLDPQTN--SSQKEBPRTNLM--VTPTLRVEDCSIALFRNHDK--NRNCDMLPPRCLPFLITDGD--ESNRYINAFIDMSYKQP
mPTPmu D2 (NP 033010) Ptdrm	(1) RSLYDMNKLDPQTN--SSQKEBPRTNLM--VTPTLRVEDCSIALFRNHDK--NRNCDMLPPRCLPFLITDGD--ESNRYINAFIDMSYKQP
rPTPmu D2 (XP 237546 (revised))	(1) RSLYDMNKLDPQTN--SSQKEBPRTNLM--VTPTLRVEDCSIALFRNHDK--NRNCDMLPPRCLPFLITDGD--ESNRYINAFIDMSYKQP
hPTPrho D2 (NP 573400) PTPRT	(1) RSLYNYNISRLLDPQTN--SSQKDEPQTLNI--VTPVRPVEDCSIALFRNHDK--NRSMDLVLELPPRCLPFLITDGD--ESNRYINAFIDMSYKQP
mPTPrho D2 (NP 067439) Ptdrt	(1) RSLYNYNISRLLDPQTN--SSQKDEPQTLNI--VTPVRPVEDCSIALFRNHDK--NRSMDLVLELPPRCLPFLITDGD--ESNRYINAFIDMSYKQP
cPTPsiama D2 (I50212)	(1) RNLYTYIQKLAQIEVGG--EHVTGMLEFKRLAN--SKAHTSRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
hLAR D2 (NP 002831) PTPRF	(1) RNLYAHYIQLGQVPPG--ESVTAMELEFKRLAN--SKAHTSRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
mLAR D2 (NP 035343) Ptdrf	(1) RNLYAHYIQLGQVPPG--ESVTAMELEFKRLAN--SKAHTSRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
rLAR_D2 (NP 062122) Ptdrf	(1) RNLYAHYIQLGQVPPG--ESVTAMELEFKRLAG--SKARASRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
xLAR D2 (AAF43606)	(1) RSLYAHYIQLGQVPPG--ESVTSMLEFKRLAN--SKAHTSRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
rvPTPR2Ac D2 (CAC44758)	(1) RSLYTHYIQLTQAPPG--DVTAMELEFKRLAN--SKAHTSRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
rvPTPR2Aa D2 (BAA95188)	(1) RSLFAHYIQLGQVPPA--ETVTAMELEFKRLAN--SKAHTSRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
hPTPdelta D2 (NP 002830) PTPRD	(1) RNLYAYIQKLTQIETG--ENVTGMLEFKRLAS--SKAHTSRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
mPTPdelta D2 (D54689)	(1) RNLYAYIQKLTQIETG--ENVTGMLEFKRLAS--SKAHTSRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
xPTPdelta D2 (AAF43605)	(1) RNLYAYIQKLTQIEPG--ENVTGMLEFKRLAS--FKAHTSRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
rvPTPR2Ab D2 (BAA95191)	(1) RNLYAYIQKLTQVEPG--ENVTGMLEFKRLAN--TKAHTSRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
hPTPsiama D2 (NP 002841) PTPRS	(1) RSNLYAYIQKLAQVEPG--EHVTGMLEFKRLAN--SKAHTSRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
mPTPsiama D2 (NP 035348) Ptdrs	(1) RSNLYTYIQKLAQVEPG--EHVTGMLEFKRLAS--SKAHTSRFITASLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
xPTPsiama D2 (AAF43607)	(1) RNLYTYIQNLAQIDVG--EHVIGMLEFKRLAN--SKAHTSRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
zPTPsiama D2 (CAC44759)	(1) RSLFSYIQLKLAQVEAG--EHVSGMLEFKRLAN--SKAHTSRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--LEGSDYINAFIDGYRQK
rPTPsiama D2 (NP 062013) Ptdrd	(1) RSLYTYIQKLAQVEPG--EHVTGMLEFKRLAS--SKAHTSRFITASLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
rvPTPR2Ad D2 (BAA95193)	(1) RNLYSYIQLKLTQVETG--EHVTGMLEFKRLAN--SKAHTSRFISANLFCNRFK--NRLVNIMPYESTRVCQPGRG--VEGSDYINAFIDGYRQK
hPTPgamma D2 (NP 002832) PTPRG	(1) NQLHSYVNSLIPGVG--GKTRLEKQKFLVQ--CNAKYVECFSAQKECNREK--NRNSVVPARARVGLAPPG--MKGSDYINAFIDGYRQS
mPTPgamma D2 (NP 033007) Ptdrg	(1) NQLHSYVNSLIPGVG--GKTRLEKQKFLVQ--CNAKYVECFSAQKECNREK--NRNSVVPARARVGLAPPG--MKGSDYINAFIDGYRQS
rPTPgamma D2 (NP 599183) Ptdrg	(1) NQLHSYVNSLIPGVG--GKTRLEKQKFLVQ--CNAKYVECFSAQKECNREK--NRNSVVPARARVGLAPPG--MKGSDYINAFIDGYRQS
rvPTPR5b D2 (BAA95197)	(1) NQLHSYVNSLIPGLS--GKMRLEKQKFLVQ--CNAKFIECFSAQKECNREK--NRNSVVPARARVGLAPPG--TKGSDYINAFIDGYRQS
cPTPgamma D2 (Q98936)	(1) NQLHSYVNSLIPGGI--GKTRLEKQKFLVQ--CNAKYVECFSAQKDCNREK--NRNSVVPARARVGLAPPG--MKGSDYINAFIDGYRQS
hPTPzeta D2 (NP 002842) PTPRZ1	(1) SHHAYYNALLIPGPA--GKTKLEKQLLSQ--SNIQSDYSALKQCNRK--NRSSLLPVRSRVGLSSSG--EGSDYINAFIDGYRQS
cPTPzeta D2 (AAA49015)	(1) THHAYYNALLIPGPT--GKTRLEKQKFLLSQ--SNTQQCDYSTALKQCNRK--NRSSLLPVRSRVGLSSSG--EGSDYINAFIDGYRQS
mPTPzeta D2 (XP 133009) Ptdrz1	(1) SHHHSYVNTLIPGPT--GKTKLEKQLLSQ--SNILQSDYSTALKQCNRK--NRSSLLPVRSRVGLSSSG--EGSDYINAFIDGYRQS
rPTPzeta D2 (NP 037212) Ptdrz1	(1) SHHHSYVNTLIPGFS--GKTKLEKQLLSQ--SNILQSDYSTALKQCNRK--NRSSLLPVRSRVGLSSSG--EGSDYINAFIDGYRQS
xPTPzeta D2 (BAA97445)	(1) THHGYVNTLITMGPS--GKSRLEKQKFLSSE--PNILQCDYSTALKQCNRK--NRSSLLPVRSRVGLSSSG--EGSDYINAFIDGYRQS
rvPTPR5a_D2 (BAA95195)	(1) NHHTYVNTLITPGFS--GKTKLEKQLLSQ--PHAKQCDYSALKQCNRK--NRSSLLPVRSRVGLSSSG--EGSDYINAFIDGYRQS
Consensus	(1) L I L L E F L A P N K K NRY NILPYD SRV L I SDYINASYI GY

	(119)	119	130	140	150	160	170	180	190	200	210	220	236	
hPTPsiama D1 (NP 002841) PTPRS	(84)	N	---	A	Y	I	A	T	G	G	P	E	T	---
mPTPsiama D1 (NP 035348(revised)) Ptpsr	(84)	N	---	A	Y	I	A	T	G	G	P	E	T	---
rPTPsiama D1 (NP 062013) Ptpsr	(84)	N	---	A	Y	I	A	T	G	G	P	E	T	---
cPTPsiama D1 (I50212)	(84)	N	---	A	Y	I	A	T	G	G	P	E	T	---
xPTPsiama D1 (AAC43607)	(84)	N	---	A	Y	I	A	T	G	G	P	E	T	---
zPTPsiama D1 (CAC44759)	(84)	N	---	A	Y	I	A	T	G	G	P	E	T	---
hLAR_D1 (NP 002831) PTPRF	(84)	N	---	A	Y	I	A	T	G	G	P	E	T	---
mLAR_D1 (NP 035343) Ptpfr	(84)	N	---	A	Y	I	A	T	G	G	P	E	T	---
rLAR_D1 (NP 062122) Ptpfr	(84)	N	---	A	Y	I	A	T	G	G	P	E	T	---
xLAR_D1 (AAF43606)	(84)	N	---	A	Y	I	A	T	G	G	P	E	T	---
hPTPdelta_D1 (NP 002830) PTPRD	(84)	N	---	A	Y	I	A	T	G	G	P	E	T	---
mPTPdelta_D1 (D54689)	(84)	N	---	A	Y	I	A	T	G	G	P	E	T	---
xPTPdelta_D1 (AAC43605)	(84)	N	---	A	Y	I	A	T	G	G	P	E	T	---
hPTPrho_D1 (NP 573400) PTPRT	(84)	R	---	H	Y	I	A	T	G	G	P	E	T	---
mPTPrho_D1 (NP 067439) Ptprr	(84)	R	---	H	Y	I	A	T	G	G	P	E	T	---
xPTPrho_D1 (AAD50295)	(84)	R	---	H	Y	I	A	T	G	G	P	E	T	---
hPTPmu_D1 (NP 002836) PTPRM	(84)	N	---	H	Y	I	A	T	G	G	P	E	T	---
mPTPmu_D1 (NP 033010) Ptprm	(84)	N	---	H	Y	I	A	T	G	G	P	E	T	---
hPTPkappa_D1 (NP 002835) PTPRK	(84)	S	---	H	Y	I	A	T	G	G	P	E	T	---
mPTPkappa_D1 (NP 033009 (revised)) Ptprk	(84)	S	---	H	Y	I	A	T	G	G	P	E	T	---
hPTPlamda D1 (NP 005695) PTPRU	(80)	N	---	H	Y	I	A	T	G	G	P	E	T	---
mPTPlamda D1 (NP 035344) Ptprr	(80)	N	---	H	Y	I	A	T	G	G	P	E	T	---
rPTPpsi_D1 (AAB42210) Ptprr Fraam	(80)	N	---	H	Y	I	A	T	G	G	P	E	T	---
cPTPaloha D1 (AAF04150)	(85)	N	---	K	F	I	A	A	G	G	P	E	T	---
hPTPaloha D1 (NP 002827) PTPRA	(85)	N	---	K	F	I	A	A	G	G	P	E	T	---
mPTPaloha D1 (AAK56109) Ptora	(85)	N	---	K	F	I	A	A	G	G	P	E	T	---
rPTPaloha D1 (NP 036895) Ptora	(85)	N	---	K	F	I	A	A	G	G	P	E	T	---
zPTPaloha D1 (NP 571963) Ptora	(85)	N	---	K	F	I	A	A	G	G	P	E	T	---
xPTPaloha D1 (AAA17990)	(85)	N	---	K	F	I	A	A	G	G	P	E	T	---
hPTPpsilon D1 (NP 006495) PTPRE	(85)	N	---	K	F	I	A	A	G	G	P	E	T	---
mPTPpsilon D1 (NP 035342) Ptpre	(85)	N	---	K	F	I	A	A	G	G	P	E	T	---
rPTPpsilon D1 (XP 215102) Ptpre	(85)	N	---	K	F	I	A	A	G	G	P	E	T	---
hPTPgamma D1 (NP 002832) PTPRG	(89)	K	---	A	Y	I	A	T	G	G	P	E	T	---
mPTPgamma D1 (NP 033007) Ptprr	(89)	K	---	A	Y	I	A	T	G	G	P	E	T	---
rPTPgamma D1 (NP 599183) Ptprr	(93)	K	---	A	Y	I	A	T	G	G	P	E	T	---
cPTPgamma D1 (Q98936)	(89)	K	---	A	Y	I	A	T	G	G	P	E	T	---
hPTPzeta D1 (NP 002842) PTPRZ1	(94)	K	---	A	Y	I	A	A	G	G	P	E	T	---
rPTPzeta D1 (NP 037212) Ptprr2	(94)	K	---	A	Y	I	A	A	G	G	P	E	T	---
cPTPzeta D1 (AAA49015)	(87)	K	---	A	Y	I	A	A	G	G	P	E	T	---
xPTPzeta D1 (BAA97445)	(87)	K	---	A	Y	I	A	A	G	G	P	E	T	---
hCD45 D1 (NP 002829) PTPRC	(85)	R	---	K	Y	I	A	A	G	G	P	E	T	---
mCD45 D1 (NP 035340) Ptprc	(85)	R	---	K	Y	I	A	A	G	G	P	E	T	---
rCD45_D1 (XP 213985) Ptprc	(85)	R	---	K	Y	I	A	A	G	G	P	E	T	---
cCD45 D1 (A54080)	(85)	R	---	K	Y	I	A	A	G	G	P	E	T	---
cypcCD45 D1 (BAA92179)	(82)	K	---	K	Y	I	A	A	G	G	P	E	T	---
fuCD45 D1 (CAB96211)	(85)	K	---	K	Y	I	A	A	G	G	P	E	T	---
sharkCD45 D1 (T43148)	(85)	R	---	K	Y	I	A	A	G	G	P	E	T	---
hDEP1_D1 (NP 002834) PTPRJ	(84)	K	---	D	E	L	A	T	G	G	P	E	T	---
rDEP1_D1 (NP 058965) Ptprr	(84)	K	---	D	E	L	A	T	G	G	P	E	T	---
mDEP1_D1 (NP 033008) Ptprr	(84)	K	---	D	E	L	A	T	G	G	P	E	T	---
hGLEPP1_D1 (NP 109592) PTPRO	(85)	Q	---	E	Y	I	A	T	G	G	P	E	T	---
rGLEPP1_D1 (NP 059032) Ptprr	(85)	Q	---	E	Y	I	A	T	G	G	P	E	T	---
mPTPphi D1 (NP 035346) Ptprr	(85)	Q	---	E	Y	I	A	T	G	G	P	E	T	---
rabPTPoc D1 (AAB16824)	(85)	Q	---	E	Y	I	A	T	G	G	P	E	T	---
hPTPbeta D1 (NP 002828) PTPRB	(85)	R	---	E	Y	I	A	T	G	G	P	E	T	---
mPTPbeta D1 (NP 084204) Ptprr	(85)	R	---	E	Y	I	A	T	G	G	P	E	T	---
rPTPbeta D1 (XP 235156 (revised))	(85)	R	---	E	Y	I	A	T	G	G	P	E	T	---
hPTPS31 D1 (AR073855) PTPGMC1	(85)	N	---	E	F	I	A	T	G	G	P	E	T	---
rPTPGMC1 D1 (NP 075214) Ptprr	(85)	N	---	E	F	I	A	T	G	G	P	E	T	---
hSAP1_D1 (NP 002833) PTPRH	(85)	Q	---	E	F	I	A	T	G	G	P	E	T	---
mSAP1_D1 (BAC37443)	(85)	K	---	E	F	I	A	T	G	G	P	E	T	---
rPTPBEM2 D1 (NP 598276)	(85)	K	---	E	F	I	A	T	G	G	P	E	T	---
mPTPESP_D1 (NP_031981) Esp	(85)	Q	---	E	I	A	T	G	G	P	E	T	---	

	(237)	237	250	260	270	280	290	300	310	320	330	340	354										
hPTPsiama D1 (NP 002841) PTPRS (176)	QPTAWP	DHGVPEY	-PTPFLA	LRRVKTCN				PPDA	GPIV	VHCSAGV	GRGTCF	IVDAMLER	KP---	EKTVDV	YGHV	TLMS	SQRNY	MQVTE	QVYSF	IHE	ADLEAMG		
mPTPsiama D1 (NP 035348(revised)) Ptprs (176)	QPTAWP	DHGVPEY	-PTPFLA	LRRVKTCN				PPDA	GPIV	VHCSAGV	GRGTCF	IVDAMLER	KT---	EKTVDV	YGHV	TLMS	SQRNY	MQVTE	QVYSF	IHE	ADLEAMG		
rPTPsiama D1 (NP 062013) Ptpord (176)	QPTAWP	DHGVPEY	-PTPFLA	LRRVKTCN				PPDA	GPIV	VHCSAGV	GRGTCF	IVDAMLER	RT---	EKTVDV	YGHV	TLMS	SQRNY	MQVTE	QVYSF	IHE	ADLEAMG		
cPTPsiama D1 (I50212) (176)	QPTAWP	DHGVPEY	-PTPFLA	LRRVKTCN				PPDA	GPIV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDV	YGHV	TLMS	SQRNY	MQVTE	QVYSF	IHE	ADLEAMG		
xPTPsiama D1 (AAF43607) (176)	QPTAWP	DHGVPEY	-PTPFLA	LRRVKTCN				PPDA	GPIV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDV	YGHV	TLMS	SQRNY	MQVTE	QVYSF	IHE	ADLEAMG		
zPTPsiama D1 (CAC44759) (176)	QPTAWP	DHGVPEY	-PTPFLA	LRRVKTCN				PPDA	GPIV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDV	YGHV	TLMS	SQRNY	MQVTE	QVYSF	IHE	ADLEAMG		
hLAR D1 (NP 002831) PTPRF (176)	QPMWPD	HGVPEY	-PTPFLA	LRRVKACN				PLDA	GPMV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDV	YGHV	TLMS	SQRNY	MQVTE	QVYSF	IHE	ADLEAMG		
mLAR D1 (NP 035343) Ptprf (176)	QPMWPD	HGVPEY	-PTPFLA	LRRVKACN				PLDA	GPMV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDV	YGHV	TLMS	SQRNY	MQVTE	QVYSF	IHE	ADLEAMG		
rLAR_D1 (NP 062122) Ptorf (176)	QPMWPD	HGVPEY	-PTPFLA	LRRVKACN				PLDA	GPMV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDV	YGHV	TLMS	SQRNY	MQVTE	QVYSF	IHE	ADLEAMG		
xLAR D1 (AAF43606) (176)	QPMWPD	HGVPEY	-PTPFLA	LRRVKACN				PPDA	GPMF	VHCSAGV	GRGTCF	IVDAMLER	KL---	EKTVDV	YGHV	TLMS	SQRNY	MQVTE	QVYSF	IHE	ADLEAMG		
hPTPdelta_D1 (NP 002830) PTPRD (176)	QPTAWP	DHGVPEH	-PTPFLA	LRRVKTCN				PPDA	GPMV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDV	YGHV	TLMS	SQRNY	MQVTE	QVYSF	IHE	ADLEAMG		
mPTPdelta D1 (D54689) (174)	QPTAWP	DHGVPEH	-PTPFLA	LRRVKTCN				PPDA	GPMV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDV	YGHV	TLMS	SQRNY	MQVTE	QVYSF	IHE	ADLEAMG		
xPTPdelta D1 (AAF43605) (176)	QPTAWP	DHGVPEH	-PTPFLA	LRRVKTCN				PPDA	GPMV	VHCSAGV	GRGTCF	NVIDAMLER	RH---	EKTVDV	YGHV	TLMS	SQRNY	MQVTE	QVYSF	IHE	ADLEAMG		
hPTPrho D1 (NP 573400) PTPRT (175)	HFTSWPD	HGVPEY	-ATGFLG	VRQVKFLN				PEEA	GPIV	VHCSAGV	GRGTCF	IAIDIMLDM	MAEN---	EGVVDI	YNCV	ELR	AQRVN	LVQTE	QVYVF	IHE	ADLEACL		
mPTPrho D1 (NP 067439) Ptprt (175)	HFTSWPD	HGVPEY	-ATGFLG	VRQVKFLN				PEEA	GPIV	VHCSAGV	GRGTCF	IAIDIMLDM	MAEN---	EGVVDI	YNCV	ELR	AQRVN	LVQTE	QVYVF	IHE	ADLEACL		
xPTPrho D1 (AAD50295) (175)	HFTSWPD	HGVPEY	-ATGFLG	VRQVKFLN				PPDA	GPIV	VHCSAGV	GRGTCF	IAIDIMLDM	MAEN---	EGVVDI	YNCV	ELR	AQRVN	LVQTE	QVYVF	IHE	ADLEACL		
hPTPmu D1 (NP 002836) PTPRM (175)	HFTGWP	DHGVPEY	-ATGFLG	VRQVKSKS				PPSA	GPLV	VHCSAGV	GRGTCF	IVDIMLDM	MAER---	EGVVDI	YNCV	ELR	AQRVN	LVQTE	QVYVF	IHE	ADLEACL		
mPTPmu D1 (NP 033010) Pterm (175)	HFTGWP	DHGVPEY	-ATGFLG	VRQVKSKS				PPNA	GPLV	VHCSAGV	GRGTCF	IVDIMLDM	MAER---	EGVVDI	YNCV	ELR	AQRVN	LVQTE	QVYVF	IHE	ADLEACL		
hPTPkappa D1 (NP 002835) PTPRK (175)	HFTGWP	DHGVPEY	-ATGFLS	VRRLKLSN				PPSA	GPIV	VHCSAGV	GRGTCF	IVDIMLDM	MAER---	EGVVDI	YNCV	ELR	AQRVN	LVQTE	QVYVF	IHE	ADLEACL		
mPTPkappa D1 (NP 033009 (revised)) Ptok (175)	HFTGWP	DHGVPEY	-ATGFLS	VRRLKLSN				PPSA	GPIV	VHCSAGV	GRGTCF	IVDIMLDM	MAER---	EGVVDI	YNCV	ELR	AQRVN	LVQTE	QVYVF	IHE	ADLEACL		
hPTPlamda D1 (NP 005695) PTPRU (171)	HFTAWP	HGVPEY	-ATGFLA	LRRVKAST				PPDA	GPIV	VHCSAGV	GRGTCF	IVDVMLDMA	EAC---	EGVVDI	YNCV	TLCS	SRRVNM	QVTE	QVYVF	IHE	ADLEACL		
mPTPlamda D1 (NP 035344) Ptprl (171)	HFTAWP	HGVPEY	-ATGFLA	LRRVKAST				PPDA	GPIV	VHCSAGV	GRGTCF	IVDVMLDMA	EAC---	EGVVDI	YNCV	TLCS	SRRVNM	QVTE	QVYVF	IHE	ADLEACL		
rPTPpsi_D1 (AAB42210) Ptpru Fraam (171)	HFTAWP	HGVPEY	-ATGFLA	LRRVKAST				PPDA	GPIV	VHCSAGV	GRGTCF	IVDVMLDMA	EAC---	EGVVDI	YNCV	TLCS	SRRVNM	QVTE	QVYVF	IHE	ADLEACL		
cPTPaloha D1 (AAB04150) (181)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				POYA	GAIV	VHCSAGV	GRGTCF	IVDAMDM	MHT---	ERKVDV	YGFV	SR	RAQR	CMQV	TD	MOYVF	IHE	QALLEHYL	
hPTPaloha D1 (NP 002827) PTPRA (181)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				POYA	GAIV	VHCSAGV	GRGTCF	IVDAMDM	MHT---	ERKVDV	YGFV	SR	RAQR	CMQV	TD	MOYVF	IHE	QALLEHYL	
mPTPaloha D1 (AAK56109) Ptora (181)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				POYA	GAIV	VHCSAGV	GRGTCF	IVDAMDM	MHT---	ERKVDV	YGFV	SR	RAQR	CMQV	TD	MOYVF	IHE	QALLEHYL	
rPTPaloha D1 (NP 036895) Ptora (181)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				POYA	GAIV	VHCSAGV	GRGTCF	IVDAMDM	MHT---	ERKVDV	YGFV	SR	RAQR	CMQV	TD	MOYVF	IHE	QALLEHYL	
zPTPaloha D1 (NP 571963) pтора (181)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				POYA	GAIV	VHCSAGV	GRGTCF	IVDAMDM	MHT---	ERKVDV	YGFV	SR	RAQR	CMQV	TD	MOYVF	IHE	QALLEHYL	
xPTPaloha D1 (AAA17990) (181)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				POYA	GAIV	VHCSAGV	GRGTCF	IVDAMDM	MNT---	EKKVDV	YGFV	SR	RAQR	CMQV	TD	MOYVF	IHE	QALLEHYL	
hPTPension D1 (NP 006495) PTPRE (180)	HFTSWPD	FVGPFT	-PIGLK	LKKVKTLN				PVHA	GPV	VHCSAGV	GRGTCF	IVDAMDM	MHA---	QKVDV	YGFV	SR	RAQR	CMQV	TD	MOYVF	IHE	QALLEHYL	
mPTPension D1 (NP 035342) Ptpre (180)	HFTSWPD	FVGPFT	-PIGLK	LKKVKTLN				PVHA	GPV	VHCSAGV	GRGTCF	IVDAMDM	MHA---	QKVDV	YGFV	SR	RAQR	CMQV	TD	MOYVF	IHE	QALLEHYL	
rPTPension D1 (XP 215102) Ptpre (180)	HFTSWPD	FVGPFT	-PIGLK	LKKVKTLN				PSHA	GPIV	VHCSAGV	GRGTCF	IVDAMDM	MHS---	QKVDV	YGFV	SR	RAQR	CMQV	TD	MOYVF	IHE	QALLEHYL	
hPTPqamma D1 (NP 002832) PTPRG (192)	HNTQWPD	MGVPEY	-ALPVL	TVRRSSAA				MPET	GPV	VHCSAGV	GRGTCF	IVDMSL	QQK---	KSTVNV	LGLF	LKH	HTORN	LVQTE	QVYVF	IHE	ADLEACL		
mPTPqamma D1 (NP 033007) Ptprq (192)	HNTQWPD	MGVPEY	-ALPVL	TVRRSSAA				MPDM	GPV	VHCSAGV	GRGTCF	IVDMSL	QQK---	KSTVNV	LGLF	LKH	HTORN	LVQTE	QVYVF	IHE	ADLEACL		
rPTPqamma D1 (NP 599183) Ptprq (196)	HNTQWPD	MGVPEY	-ALPVL	TVRRSSAA				MPDM	GPV	VHCSAGV	GRGTCF	IVDMSL	QQK---	KSTVNV	LGLF	LKH	HTORN	LVQTE	QVYVF	IHE	ADLEACL		
cPTPqamma D1 (Q98936) (192)	HNTQWPD	MGVPEY	-ALPVL	TVRRSSAA				TPHM	GPV	VHCSAGV	GRGTCF	IVDMSL	QQK---	KSTVNV	LGLF	LKH	HTORN	LVQTE	QVYVF	IHE	ADLEACL		
hPTPzeta D1 (NP 002842) PTPRZ1 (194)	HNTQWPD	MGVPEY	-SLPVL	TVRRKAAAYAK				RHAV	GPV	VHCSAGV	GRGTCF	IVDMSL	QQH---	GTVNV	LFGF	LKH	HTORN	LVQTE	QVYVF	IHE	ADLEACL		
rPTPzeta D1 (NP 037212) Ptporz1 (194)	HNTQWPD	MGVPEY	-SLPVL	TVRRKAAAYAK				RHAV	GPV	VHCSAGV	GRGTCF	IVDMSL	QQH---	GTVNV	LFGF	LKH	HTORN	LVQTE	QVYVF	IHE	ADLEACL		
cPTPzeta D1 (AAA49015) (187)	HNTQWPD	MGVPEY	-TLPVL	TVRRKASHAK				RHAV	GPV	VHCSAGV	GRGTCF	IVDMSL	QQH---	GTVNV	LFGF	LKH	HTORN	LVQTE	QVYVF	IHE	ADLEACL		
xPTPzeta D1 (BAA97445) (187)	HNTQWPD	MGVPEY	-TLPVL	TVRRKASHAK				KLN	GPV	VHCSAGV	GRGTCF	IVDMSL	QQH---	GTVNV	LFGF	LKH	HTORN	LVQTE	QVYVF	IHE	ADLEACL		
hCD45 D1 (NP 002829) PTPRC (180)	QPTSWPD	HGVPEE	-PHLLK	LRRVNAFS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLE	GEA---	EGKVDV	YGVV	VKL	RRQR	CLMV	VEAQ	YILL	IQAL	VEYHQ	
mCD45 D1 (NP 035340) Ptprc (180)	QPTSWPD	HGVPEE	-PHLLK	LRRVNAFS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLE	GEA---	EGKVDV	YGVV	VKL	RRQR	CLMV	VEAQ	YILL	IQAL	VEYHQ	
rCD45_D1 (XP 213985) Ptprc (180)	QPTSWPD	HGVPEE	-PHLLK	LRRVNAFS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLE	GEA---	EGKVDV	YGVV	VKL	RRQR	CLMV	VEAQ	YILL	IQAL	VEYHQ	
cCD45 D1 (A54080) (180)	QPTSWPD	HGVPEE	-PHLLK	LRRVNAFS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLE	GEA---	EGKVDV	YGVV	VKL	RRQR	CLMV	VEAQ	YILL	IQAL	VEYHQ	
cypcCD45 D1 (BAA92179) (177)	QPTSWPD	HGVPEE	-PHLLK	LRRVNAFS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLE	GEA---	EGKVDV	YGVV	VKL	RRQR	CLMV	VEAQ	YILL	IQAL	VEYHQ	
fuCD45 D1 (CAB96211) (180)	QPTSWPD	HGVPEE	-PHLLK	LRRVNAFS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLE	GEA---	EGKVDV	YGVV	VKL	RRQR	CLMV	VEAQ	YILL	IQAL	VEYHQ	
sharkCD45 D1 (T43148) (180)	QPTSWPD	HGVPEE	-PHLLK	LRRVNAFS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLE	GEA---	EGKVDV	YGVV	VKL	RRQR	CLMV	VEAQ	YILL	IQAL	VEYHQ	
hDEP1 D1 (NP 002834) PTPRJ (176)	HFTSWPD	HGVPEE	-TDLIN	RYLVRDYMKQ				SPPES	PIV	VHCSAGV	GRGTCF	IAIDRL	LYQEN---	ENTVDV	YGLV	YD	MHR	PLMV	QTE	QVYVF	IHE	ADLEACL	
rDEP1 D1 (NP 058965) Ptpri (176)	HFTSWPD	HGVPEE	-TDLIN	RYLVRDYMKQ				IPPE	SPIL	VHCSAGV	GRGTCF	IAIDRL	LYQEN---	ENTVDV	YGLV	YD	MHR	PLMV	QTE	QVYVF	IHE	ADLEACL	
mDEP1 D1 (NP 033008) Ptpri (176)	HFTSWPD	HGVPEE	-TDLIN	RYLVRDYMKQ				IPPE	SPIL	VHCSAGV	GRGTCF	IAIDRL	LYQEN---	ENTVDV	YGLV	YD	MHR	PLMV	QTE	QVYVF	IHE	ADLEACL	
hGLEPP1_D1 (NP 109592) PTPRO (176)	NVTAWP	DHGVPEE	-TANAAES	LQVYVHM	RQQAT			KSK	GPMI	VHCSAGV	GRGTCF	IALDRL	LQHRD---	HEFVDI	LGLV	SE	EM	SRYS	MS	MQVTE	QVYVF	IHE	ADLEACL
rGLEPP1_D1 (NP 059032) Ptpro (176)	NVTAWP	DHGVPEE	-TANAAES	LQVYVHM	RQQAT			KSK	GPMI	VHCSAGV	GRGTCF	IALDRL	LQHRD---	HEFVDI	LGLV	SE	EM	SRYS	MS	MQVTE	QVYVF	IHE	ADLEACL
mPTPphi D1 (NP 035346) Ptpro (176)	NVTAWP	DHGVPEE	-TANAAES	LQVYVHM	RQQAT			KSK	GPMI	VHCSAGV	GRGTCF	IALDRL	LQHRD---	HEFVDI	LGLV	SE	EM	SRYS	MS	MQVTE	QVYVF	IHE	ADLEACL
rabPTPoc D1 (AAB16824) (176)	NVTAWP	DHGVPEE	-TANAAES	LQVYVHM	RQQAT			KSK	GPMI	VHCSAGV	GRGTCF	IALDRL	LQHRD---	HEFVDI	LGLV	SE	EM	SRYS	MS	MQVTE	QVYVF	IHE	ADLEACL
hPTPbeta D1 (NP 002828) PTPRB (179)	HNTVWP	DHGVPEE	-TQSLQ	IQVRR	VDYINR			SPGA	GTV	VHCSAGV	GRGTCF	IALDRL	LQDS---	KDSVDI	YGAV	HD	LHR	VH	MQVTE	QVYVF	IHE	ADLEACL	
mPTPbeta D1 (NP 084204) Ptprb (179)	HNTVWP	DHGVPEE	-TQSLQ	IQVRR	VDYINR			SPGA	GTV	VHCSAGV	GRGTCF	IALDRL	LQDS---	KDSVDI	YGAV	HD	LHR	VH	MQVTE	QVYVF	IHE	ADLEACL	
rPTPbeta D1 (XP 235156 (revised)) (179)	HNTVWP	DHGVPEE	-TQSLQ	IQVRR	VDYINR			SPGA	GTV														

VectorNTI Screen View - Alignment_195_Vert_PTP_Domains_D1_and_D2 (VNTI 8.0).apr

rOSTPTP D1 (NP 149090) Eso (178)	QPTWDFDSVPEA--PSSLLAVLVEVQEQVQA-----TQGKGLIIVHCSAGVGRGTGFIATSLRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hPCPTP1 D1 (NP 002840) PTPRR (174)	WVTSWDFDKTDS--AQPQLQLMLDVEDRDLA-----SQGRGFLVVHCSAGVGRGTGFIATSLRIGCQKE---EGVVDALSLVCOQLRMDRGGMVGTSQYEFVHHAALCLYES
rPCPTP1 D1 (NP 446046) Ptprr (174)	WVTSWDFDKTDS--AQPQLQLMLDVEDRDLA-----SEGRGFLVVHCSAGVGRGTGFIATSLRIGCQKE---EGVVDALSLVCOQLRMDRGGMVGTSQYEFVHHAALCLFES
mPTPSL D1 (NP 035347) Ptprr (174)	WVTSWDFDKTDS--AQPQLQLMLDVEDRDLA-----SEGRGFLVVHCSAGVGRGTGFIATSLRIGCQKE---EGVVDALSLVCOQLRMDRGGMVGTSQYEFVHHAALCLFES
hSTEP D1 (NP 116710) PTPN5 (174)	WFTSWDFDKTDR--APPPLHLHLMREVEAAQQQE-----GPHCSFLIIVHCSAGVGRGTGFIATSLRIGCQRR---EGVVDLTKTTCQLRQDRGGMVGTSQYEFVHHAALCLYESK
mSTEP D1 (NP 038671) Pton5 (174)	WFTSWDFDKTDR--APPPLHLHLMREVEAAQQQE-----GPHCSFLIIVHCSAGVGRGTGFIATSLRIGCQRR---EGVVDLTKTTCQLRQDRGGMVGTSQYEFVHHAALCLYESK
rSTEP D1 (NP 062126) Pton5 (174)	WFTSWDFDKTDR--APPPLHLHLMREVEAAQQQE-----GPHCSFLIIVHCSAGVGRGTGFIATSLRIGCQRR---EGVVDLTKTTCQLRQDRGGMVGTSQYEFVHHAALCLYESK
hHePTP D1 (NP 002823) PTPN7 (172)	LPSAWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mHePTP D1 (NP 796055) Pton7 (172)	LPSAWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
rLCPTP D1 (P49445) Pton7 (172)	LPSAWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hLyPTP D1 (NP 057051) PTPN22 (185)	HVKNWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mPEP D1 (NP 033005) Pton8 (185)	HVKNWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hPEST D1 (NP 002826) PTPN12 (189)	HVYVWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
rRKPTP D1 (NP 476456) Pton12 (189)	HVYVWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mPEST D1 (NP 035333) Pton12 (189)	HVYVWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hBDP1 D1 (NP 055184) PTPN18 (186)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mPTPK1_D1 (NP 035336) Pton18 (186)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
rPTP20 D1 (AAC52896) (186)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hSHP1 D1 (NP 002822) PTPN6 (193)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mSHP1 D1 (NP 038573) Hcph (193)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
rSHP1_D1 (NP 446360) Ptoh6 (193)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
zSHP1 D1 (AAH44414) (193)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
rVPTPN6c D1 (BAA95199) (162)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hSHP2 D1 (NP 002825) PTPN11 (196)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mSHP2 D1 (NP 035332) Pton11 (200)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
rSHP2_D1 (NP 037220) Pton11 (196)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
cSHP2 D1 (JCS167) (196)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
zSHP2 D1 (AAH45328) (196)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
xSHP2 D1 (A56561) (196)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
rVPTPN6b D1 (BAA95198) (167)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hPTPD1 D1 (NP 008970) PTPN21 (184)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mPTPRL10 D1 (NP 036007) Pton21 (184)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
rPTP2E D1 (NP 598229) Pto2E (184)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hPTP2E D1 (NP 005392) PTPN14 (183)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mPTP36 D1 (NP 033002) Pton14 (183)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
rPTP2E D1 (XP 223062 (revised)) (183)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hMEG1 D1 (NP 002821) PTPN4 (178)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mMEG1 D1 (NP 064317) Pton4 (178)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
zMEG1 D1 (CAD43435) (173)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hPTPH1 D1 (NP 002820) PTPN3 (178)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mPTPH1 D1 (XP 143789) Pton3 (178)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hPTPBAS D1 (NP 006255) PTPN13 (178)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mPTPBAS D1 (NP 035334) Pton13 (178)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
bPTPA14 D1 (NP 777015) PTPN13 (178)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hPTP1A D1 (AL050040) PTPN20 (177)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mPTP1Typ_D1 (NP 033004) Pton20 (176)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
cPTP1B D1 (O13016) (175)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hPTP1B D1 (NP 002818) PTPN1 (175)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mPTP1B D1 (NP 035331) Pton1 (175)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
rPTP1B D1 (NP 036769) Pton1 (175)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
zPTP1B D1 (NP 570999) pto1b (173)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hTCTPT D1 (NP 002819) PTPN2 (174)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mTCTPT D1 (NP 033003) Pton2 (174)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
rTCTPT D1 (NP 446442) Pton2 (174)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
zTCTPT D1 (AAH44373) (173)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hMEG2 D1 (NP 002824) PTPN9 (179)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mMEG2_D1 (NP 062625) Pton9 (179)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
xPTPX10 D1 (B53978) (179)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
xPTPX1 D1 (AAH43621) (179)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hHDPTP D1 (NP 056281) PTPN23 (183)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mHDPTP D1 (AAH22721) (183)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
rPTPTD14 D1 (T14355) (183)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hIA2 D1 (NP 002837) PTPRN (179)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
mIA2 D1 (NP 033011) Ptprr (179)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG
hIA2_D1 (NP 446333) Ptprr (179)	QVMSWDFDQTPES--AGPPLRLVAEVEETP-ET-----AAHPGFLIIVHCSAGVGRGTGFIATSLRIGCQKKA---RGEVVDLGLVCOQLRDRGGMVGTSQYEFVHHAALCLYAG

VectorNTI Screen View - Alignment_195_Vert_PTP_Domains_D1_and_D2 (VNTI 8.0).apr

blA2 D1 (P56722) Ptdrn (179)	HFLSWEAECTFAS--TRP	LDLRRKVNKCYR-----	GRSC	ILVHCS	DGAGRTGTYV	LDLDMVNNR	AKG--VKE	LDIAATLEHVRDORPGLVRSKQDFE	FALTAAAEEN
hIA2beta D1 (NP 002838) PTPRN2 (179)	HFLSNYDRGVSS--SRSL	LDLRRKVNKCYR-----	GRSC	ILVHCS	DGAGRTGTYV	LDLDMVNNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQDFE	FALTAAAEEN
macnelA2beta D1 (O02695) (179)	HFLSNYDRGVSS--SRSL	LDLRRKVNKCYR-----	GRSC	ILVHCS	DGAGRTGTYV	LDLDMVNNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQDFE	FALTAAAEEN
mPTPNP D1 (P80560) Ptdrn2 (179)	HFLSNYDRGVSS--TRSL	LDLRRKVNKCYR-----	GRSC	ILVHCS	DGAGRTGTYV	LDLDMVNNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQDFE	FALTAAAEEN
rPTPNE6 D1 (NP 113788) Ptdrn2 (179)	HFLSNYDRGVSS--TRSL	LDLRRKVNKCYR-----	GRSC	ILVHCS	DGAGRTGTYV	LDLDMVNNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQDFE	FALTAAAEEN
hCD45 D2 (NP 002829) PTPRC (199)	QNTNNSVEQFAE--PKEL	ISMVQVKKQLPKQNSSEG	---	KYHKS	SLVHR	RDSSQQTGL	CAFLNLL	LSAET--	EDVDFVQVVKALRKARPGMVSFTFQYQFLVDVASTYP
mCD45 D2 (NP 035340) Ptdrc (199)	QCTTWKGEFAE--PKDL	VTLQNKQKLPKSGSEG	---	KYHKS	SLVHR	RDSSQQTGL	CAFLNLL	LSAET--	EDVDFVQVVKALRKARPGMVSFTFQYQFLVDVASTYP
rCD45_D2 (XP 213985) Ptdrc (199)	QCTTWKGEFAE--PKDL	VTLQNKQKLPKSGSEG	---	KYHKS	SLVHR	RDSSQQTGL	CAFLNLL	LSAET--	EDVDFVQVVKALRKARPGMVSFTFQYQFLVDVASTYP
cCD45 D2 (A54080) (199)	QYHKNGLDVPE--PKDL	VDMVLSKQKVPSPASEDS	---	RNSRS	YFVH	CDSSQQTGL	CAFLNLL	LSAET--	EDVDFVQVVKALRKARPGMVSFTFQYQFLVDVASTYP
fuCD45 D2 (CAB96211) (199)	QFLKMGKVEPE--PKDL	ADLKEKHKRCGY	---	TWPR	STV	IVH	CNDSGSRGAF	CAFLNLL	LSAET--
cypcaCD45 D2 (BAA92179) (197)	QFLKMGRELEN--AQEL	VMASIRRENGHYDNS	---	KTRN	RVF	IVH	CNDSGSRGAF	CAFLNLL	LSAET--
aotvoCD45 D2 (AAM48512) (3') (191)	QYTNNSVXXLAX--PKEL	ISMVQVKKQLPKQNSSEG	---	KXHK	SLV	HR	RDSSQQTGL	CAFLNLL	LSAET--
sharkCD45 D2 (T43148) (198)	HFHDWASELED--PSNF	TMRSEKELSLTQPEE	---	SSL	SP	SLV	H	RDSSQQTGL	CAFLNLL
cPTPaloha D2 (AAB04150) (181)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGN	H	ITV	H	CSAGAGRTGTF	CALSTVLER
hPTPaloha D2 (NP 002827) PTPRA (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGN	H	ITV	H	CSAGAGRTGTF	CALSTVLER
mPTPaloha D2 (NP 033006) Ptdra (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGN	H	ITV	H	CSAGAGRTGTF	CALSTVLER
rPTPaloha D2 (NP 036895) Ptdra (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGN	H	ITV	H	CSAGAGRTGTF	CALSTVLER
xPTPaloha D2 (AAA17990) (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGN	H	ITV	H	CSAGAGRTGTF	CALSTVLER
zPTPaloha D2 (NP 571963) ptdra (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGN	H	ITV	H	CSAGAGRTGTF	CALSTVLER
rvPTPR4b D2 (BAA95196) (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGN	H	ITV	H	CSAGAGRTGTF	CALSTVLER
hPTPepsilon D2 (NP 006495) PTPRE (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGN	H	ITV	H	CSAGAGRTGTF	CALSTVLER
mPTPepsilon D2 (NP 035342) Ptdre (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGN	H	ITV	H	CSAGAGRTGTF	CALSTVLER
rPTPepsilon D2 (XP 215102) Ptdre (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGN	H	ITV	H	CSAGAGRTGTF	CALSTVLER
orylaPTPepsilon D2 (BAC06424) (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGN	H	ITV	H	CSAGAGRTGTF	CALSTVLER
hPTPalpha D2 (AAB95190) (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGN	H	ITV	H	CSAGAGRTGTF	CALSTVLER
hPTPkappa D2 (NP 002835) PTPRK (180)	QNLGASREVPVGS--KRSF	LKLLQLEKQWEEC	---	EGER	RTL	HL	CLNGGRRGM	CAFLIVM	MKR--
mPTPkappa D2 (NP 033009) Ptdrk (180)	QNLGASREVPVGS--KRSF	LKLLQLEKQWEEC	---	EGER	RTL	HL	CLNGGRRGM	CAFLIVM	MKR--
rvPTPR2B D2 (BAA95194) (180)	QNLGASREVPVGS--KRSF	LKLLQLEKQWEEC	---	EGER	RTL	HL	CLNGGRRGM	CAFLIVM	MKR--
hPTPlamda D2 (NP 005695) PTPRU (183)	QFLRNSARDTPDS--KRAF	LHLDAEDKWAQES	---	GDERT	V	HL	CLNGGRRGT	CACATV	EMRC--
mPTPlamda D2 (NP 035344) Ptdrl (183)	QFLRNSARDTPDS--KRAF	LHLDAEDKWAQES	---	GDERT	V	HL	CLNGGRRGT	CACATV	EMRC--
mPTPmu D2 (NP 002836) PTPRM (180)	QFLGWMRDTPVPS--KRSF	LKLLQLEKQWEEYN	---	GGE	RT	V	HL	CLNGGRRGT	CALISVCM
mPTPmu D2 (NP 033010) Ptdrm (180)	QFLGWMRDTPVPS--KRSF	LKLLQLEKQWEEYN	---	GGE	RT	V	HL	CLNGGRRGT	CALISVCM
rPTPmu D2 (XP 237546 (revised)) (180)	QFLGWMRDTPVPS--KRSF	LKLLQLEKQWEEYN	---	GGE	RT	V	HL	CLNGGRRGT	CALISVCM
hPTPrho D2 (NP 573400) PTPRT (180)	QILGWARDTPPS--KRSF	LKVVRREKQWQEQYD	---	GRE	RT	V	HL	CLNGGRRGT	CALISVCM
mPTPrho D2 (NP 067439) Ptdrr (180)	QILGWARDTPPS--KRSF	LKVVRREKQWQEQYD	---	GRE	RT	V	HL	CLNGGRRGT	CALISVCM
cPTPsiama D2 (I50212) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
hLAR D2 (NP 002831) PTPRF (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
mLAR D2 (NP 035343) Ptdrf (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
rLAR D2 (NP 062122) Ptdrf (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
xLAR D2 (AAF43606) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
zLAR D2 (CAC44758) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
rvPTPR2Aa D2 (BAA95188) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
hPTPdelta D2 (NP 002830) PTPRD (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
mPTPdelta D2 (D54689) (181)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
xPTPdelta D2 (AAF43605) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
rvPTPR2Ab D2 (BAA95191) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
hPTPsiama D2 (NP 002841) PTPRS (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
mPTPsiama D2 (NP 035348) Ptdrs (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
xPTPsiama D2 (AAF43607) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
zPTPsiama D2 (CAC44759) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
rPTPsiama D2 (NP 062013) Ptdrd (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
rvPTPR2Ac D2 (BAA95193) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QD	GP	ITV	H	CSAGAGRTGTF	ITLSIVL
hPTPaamma D2 (NP 002832) PTPRG (186)	QCPKWFNPDPAPIS--STFEL	LVNFKKEALT	---	RD	GP	ITV	H	DEHGAVSAGML	CALTTLS
mPTPaamma D2 (NP 033007) Ptdra (186)	QCPKWFNPDPAPIS--STFEL	LVNFKKEALT	---	RD	GP	ITV	H	DEHGAVSAGML	CALTTLS
rPTPaamma D2 (NP 599183) Ptdra (178)	YVLEVRHFQAPIS--STFEL	LVNFKKEALA	---	RD	GP	ITV	H	DEHGAVSAGML	CALTTLS
rvPTPR5b D2 (BAA95197) (186)	QCPKWFNPDPAPIS--STFEL	LVNFKKEAST	---	RD	GP	ITV	H	DEHFGVVSAGL	CGTTL
cPTPaamma D2 (Q98936) (186)	QCPKWFNPDPAPIS--STFEL	LVNFKKEALT	---	RD	GP	ITV	H	DEHGAVSAGML	CALTTLS
hPTPzeta D2 (NP 002842) PTPRZ1 (185)	QCPKWFNPDPAPIS--STFEL	LVNFKKEAAN	---	RD	GP	ITV	H	DEHDEHGAVTAT	CALTTL
cPTPzeta D2 (AAA49015) (185)	QCPKWFNPDPAPIS--STFEL	LVNFKKEAAN	---	RD	GP	ITV	H	DEHDEHGAVTAT	CALTTL
mPTPzeta D2 (XP 133090) Ptdrz1 (185)	QCPKWFNPDPAPIS--STFEL	LVNFKKEAAN	---	RD	GP	ITV	H	DEHDEHGAVTAT	CALTTL
rPTPzeta D2 (NP 037212) Ptdrz1 (185)	QCPKWFNPDPAPIS--STFEL	LVNFKKEAAN	---	RD	GP	ITV	H	DEHDEHGAVTAT	CALTTL
xPTPzeta D2 (BAA97445) (185)	QCPKWFNPDPAPIS--STFEL	LVNFKKEAAN	---	RD	GP	ITV	H	DEHDEHGAVTAT	CALTTL
rvPTPR5a_D2 (BAA95195) (181)	QSPRWFNPDPAPIS--STFEL	LVNFKKEAAN	---	RD	GP	ITV	H	DEHDEHGAVTAT	CALTTL
Consensus (237)	QFTWPDHGVV	LLFI	V					GPVVHCSAGVGRGTGTF	IDMLEL