

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	RNVNLPYDHSRV	HLTPVEGV	PDSDYINASFINGY	-----QEKKNFIAAQGP							
hPTPepsilon	EHLEEEIRIRSADD	KQFRREFFNLS	PSGHIQG	TFELANKEENREK	RVPNLPNDHSRV	LSQLDGI	PCSDYINASYIDGY	-----KEKNKFAAQGP							
hPTPkappa	ADLLQHINLMKTSDS	YGFKEEYESF	FEQGS	SWDVAKKQNR	RKRYGNIIAYDHSRV	VLQPVEDD	PSSDYINANYIDGY	-----QRPSHYIAAQGP							
hPTPmu	ADLLQHITQMKCAEG	YGFKEEYESF	FEQGS	PWDSAKKDENR	MKNRYGNIIAYDHSRV	VLQTIIEGD	TNSDYINGNYIDGY	-----HRPNHYIAAQGP							
hPTPrho	ADLLQHITQMKRGG	YGFKEEYEAL	PEGTA	SWDTAKEDENR	NKNRYGNIIISYDHSRV	RLVLDGD	PHSDYINANYIDGY	-----HRPRHYIAAQGP							
hPTPlambda	ADLLQHINQMKTAE	YGFKEEYESF	FEGWDA	T-----K	KKDKVKKGS	RQEPMPAYDRH	RVKLHPMLGD	PNADYINANYIDGY	-----HRSNHFAAQGP						
hPTPdelta	LELADHIERLKAND	N-----L	KFSQEYESI	DPGQQF	-----T	WEHSNLEVN	KPKRYANVIA	YDHSRVLLSAIEGI	PGSDYINANYIDGY	-----RKQNAFAAQGP					
hPTPsigma	ADMAEHTERLKAND	S-----L	KLSQEYESI	DPGQQF	-----T	WEHSNLEVN	KPKRYANVIA	YDHSRVLLQPIE	MGSDYINANYIDGY	-----RRQNAFAAQGP					
hPTPgamma	KQFVKHIGELYSN	N-----H	GFSEDFEEV	QRCTADMN	I-----T	AEHSNHPEN	KHKRYINIL	AYDHSRVKLRPL	PGKDSKHSY	INANYVDGY	-----NKAKAYIAAQGP				
hPTPzeta	KHFPKHVADLHASS	F-----T	TEEFETL	KEFYQEV	QSCSTVDLGI	-----T	ADSSNHPDN	KHKRYINIV	AYDHSRVKLAQLA	EKGKLTDY	INANYVDGY	-----NRPKAYIAAQGP			
hLAR	TDLADNIERLKAND	G-----L	KFSQEYESI	DPGQQF	-----T	WEHSNLEVN	KPKRYANVIA	YDHSRVLLTSIDG	V-----P	GSDDYINANYIDGY	-----RKQNAFAAQGP				
hCD45	DILLETYKRKIADE	G-----R	LFLAEFQSI	PRVFSKF	-----P	IKEARKPFN	QKNRYADV	LPYDHSRVV	ELSEINGD	-----A	GSNYINASYIDGF	-----KEPRKYIAAQGP			
hGLEPP1	DDFDAYIKDMAKDS	D-----Y	KFSLQFEEL	KLIGLDI	-----P	HFAADPL	LNRCRYTN	ILPYDFSRV	RLVSMNEE	-----E	GADYINANYIPGY	-----NSPQEYIAAQGP			
hTPS31	KSFLQHVEELCTNN	N-----L	KFQEEFSEL	PKFLQDL	-----S	TADADLPWN	RAKRYFPN	IKPYNNR	VKL	IADASV	-----P	GSDDYINASYISGY	-----LCPNEFAAQGP		
hDEP1	ENFEAYFKKQADS	N-----C	FAEEYEDL	KLVGISQ	-----P	KYAAELAE	NRGKRYNN	VLPIISR	VKLSVQTH	-----S	DDYINANYMPGY	-----HSKKDFIAAQGP			
hPTPbeta	NQFEGHFMKLDADS	N-----Y	LLSKEYEEL	KDVGRRN	-----S	CDIALLPEN	RKRYNN	ILPYDSTRV	VKLSNVDD	-----S	PCSDYINASYIPGN	-----NFRREYIAAQGP			
hSAP1	EDFADHVRKNERDS	N-----C	GFADEYQQL	SLVGHSS	-----S	QMVASASE	NNAKRYRN	VLPIYDWSRV	VLPKPIHEE	-----P	GSDDYINASFMPGL	-----WSPQEYIAAQGP			
hSTEP	SRVLQAEELHDEKAL	D-----F	LLQAEFFEL	PMNFVD	-----P	KEYDIPGL	VRYKTY	ILPNPHSRV	VCLTSPDD	-----P	LSSYINANYIRGYG	-----GEEKYIAAQGP			
hPCPTP1	SRLLTRSQLRDVASS	N-----H	LLQSEFMEI	PMNFVD	-----P	KEIDIPRH	GKRYKT	ILPNPLSRV	VCLTRPKNDD	-----S	LSTYINANYIRGS	-----GKEKAFIAAQGP			
hHePTP	GHPLTRWALQRQPP	S-----K	LEEFELKI	PSNFVS	-----P	EDLDIPGH	ASKRYKT	ILPNPQSRV	VCLGRAQS	-----Q	E	-----D	GDYINANYIRGYD	-----GKEKVIYIAAQGP	
hSHP1	ADIENTRVLELNKK	QES	EDTAKAG	FWEFESL	-----Q	QEVKLNH	-----Q	RLEGQR	PNKGRYKNI	LPFDHSRV	ILQGRDSN	-----P	GSDDYINANYIKN	-----QLLGP	ENAKTYIASQGP
hSHP2	AEIESRVRELSKLA	ETTDKVKQGF	WEEFETL	QEQECKLLY	-----S	RKEGQR	ENKRYKNI	LPFDHTRV	VLDHGD	-----P	NSVSDYINANYIMPE	-----FETKCN	NSKPKKSYIAAQGP		
hPEST	EILRKFIQRVQAMK	SPDHNGED	FARDFMR	RLRSTKYRTEKI	YPTATGEKEEN	VYKRYKDI	LPFDHSRV	VLTKLTPS	-----Q	DSDDYINANFIKGV	-----Y	YGPKAYIAAQGP			
hLyPTP	EILQKFLDEAKKGI	TK-----E	EFLNEFLKL	KRQSTKYKADKTY	PTVAEKPKNI	KRYKDI	LPYDYSRV	VLESLITSD	-----E	SSYINANFIKGV	-----Y	YGPKAYIAAQGP			
hBDP1	DSARSFLERLEARG	REG---AV	LAGEFSDI	QACSAAWKADG	VCSTVAGSR	PNRKYKDI	LPYDSTRV	ILSLLQEE	-----G	HSDDYINGNIRGV	-----D	GSLEYIAAQGP			
hTPD1	ATNDERCKILEQR	LEQG---MV	FTEYERI	LKKRLVDG	-----E	STARLPENA	ERFQDV	VLPIYDSTRV	ELVPTKEN	-----N	TGYINASHIKVSV	-----S	GIEWDYIAAQGP		
hTPD2	VPMDERFRTLKKK	LEEG---MV	FTEYEQI	PKKKANG	-----I	FSTAALPEN	EAERSR	IREVVPYEEN	RVELIPTKEN	-----N	TGYINASHIKVVV	-----G	AEWHYIAAQGP		
hMEG1	HSLERESMIQLAEG	LITG---TV	LTFDQDLY	YRKKPGM	-----T	MSCAKLPQ	NI SKRYRDI	ISPYDSTRV	ILKGV	-----N	EDYINANYINMEIP	-----S	SIINQYIAAQGP		
hTPPH1	DTLEGSMALKKGL	ESG---TV	LQFEQLY	YRKKPGL	-----A	ITFAKLPQ	NLDKNRYKDI	VLPIYDSTRV	LLQSG	-----N	EDYINASYNMEIP	-----A	ANLVNKYIAAQGP		
hPTPBAS	KSVIRVLRGLDQGI	S-----P	SKELENL	QELKPLD	-----Q	LIGQTKR	RRRKYKDI	LPYDSTRV	PLGD	-----E	GGYINASFIIKIPV	-----K	EEFYIAAQGP		
hPTP1B	MEMEKFEFGLDKGS	I-----W	AAYQDI	RHEASDF	-----P	CRVAKLP	KNRNRKYRDN	VSPFDHSR	IKLHQE	-----D	NDYINASLTKME	-----E	EAQRSYIAAQGP		
hTCPTP	TTIEREFEELED	TQRR---W	PLYLEI	RNESHDY	-----P	HRVAKFP	ENRNRKYRDS	VSPYDHSR	VKLQNA	-----E	NDYINASLVDIE	-----E	EAQRSYIAAQGP		
hMEG2	MTIQELVDYVVARQ	K-----G	YEEYEDI	RRENVPV	-----T	FHCSMSP	GNLEKNRYGD	VPCLDQTRV	KLTKRSGH	-----Q	TDYINASFMDGY	-----K	KQNAFYIAAQGP		
hIA2	HMILAYMEDHLRNR	DR---S	EPAEQAL	CAYQAEPN	-----T	CATAQGEG	NKKNRHPD	FLPYDHSR	IKLVHESS	-----R	SDYINASPIEHD	-----P	PRPAYIAAQGP		
hIA2beta	HMILSYMEDHLKKN	R-----L	EKEWAL	CAYQAEPN	-----S	SFVAQRE	ENVPKRYSL	AVLTYDHSR	VLLKAENSH	-----H	SDYINASPIMDH	-----P	PRPAYIAAQGP		
hPTPTyp	TAIKDCLKLLEEK	TAA---Y	IQEFMAL	EELKLPG	-----E	FYSVGN	QPSNREKNRYRDI	ILPYDSTRV	PLGK	-----S	KDYINASYIRIVN	-----C	GEEFYIAAQGP		
hHDPTP	ERLRLQQLQELAE	FRGQLGDV	GALD	TVWRE	LELQDAQEH	DAR...GRS	IAIARCYSL	KNRHQD	VMPYD	NSRV	VLLRSG	-----K	DDYINASCVEGLS	-----P	YCPLVATQAP

Consensus - (amino acid identity 100%, 90%, 80%): E N KNRV D RVL DYINA YIATQGP
 Motif 1 Motif 2 Motif 3 Motif 4

PTP domains D2

hPTPalpha	TSLLETHLQKIYNKIPG	-----TS	NGLLEEFKFK	LSIKIQN	-----D	KMRTGNL	PANMKK	NRVLQII	PYEFNR	VII	IPVKG	RG	-----E	NTDYVNASFIDGY	-----R	QKDSYIASQGP				
hPTPepsilon	SLEKHLQTMHGTTTH	-----F	DKIGLEEFKFK	LTVRIMK	-----E	NMRTGNL	PANMKK	KARVIQII	PYDFNR	VII	ILSMK	RQ	-----E	YTDYVNASFIDGY	-----R	QKDYFIAAQGP				
hCD45	SELHPYLLHNMKKRDP	-----N	SESPLEAEFQR	LTVRSWR	-----T	QHIGNQ	EEKNRNSNVI	PYDYNRV	PLKHELE	M(19)	EP	SKYI	-----N	ASFIMSY	-----W	KPEVYIAAQGP				
hPTPgamma	NQLHSYVNSILLIPGVG	-----G	KTRLEKQFKLV	TQCNAKY	-----V	CFSAQKE	CNKEKNRNSSVV	PSEARAR	VGLAPL	PGM	-----K	GTDYINASYIMGY	-----Y	RSNEFIITQHP						
hPTPzeta	SHIHAYVNALLIPGPA	-----G	KTKLEKQFKLV	LSQSNIQ	-----S	SAALKQC	NREKNRTSSI	IPVERSR	VGISSLS	G	-----E	GTDYINASYIMGY	-----Y	QSNEFIITQHP						
hPTPsigma	RSLYAYIQKLAQVE	ETG---E	HVTGMELEFKR	LANSKAHT	-----S	RIFANLPC	NKFKNRLVNIM	PYESTR	VCLQPI	IRGV	-----E	GSDDYINASFIDGY	-----R	QKAYIAAQGP						
hPTPdelta	RNLAYAIQKLTQIETG	-----E	NTGMELEFKR	LANSKAHT	-----S	RIFANLPC	NKFKNRLVNIM	PYESTR	VCLQPI	IRGV	-----E	GSDDYINASFIDGY	-----R	QKAYIAAQGP						
hLAR	RNLAYAIQKLGQVPPG	-----E	SVTAMELEFKL	LASSKAHT	-----S	RIFANLPC	NKFKNRLVNIM	PYELTR	VCLQPI	IRGV	-----E	GSDDYINASFIDGY	-----R	QKAYIAAQGP						
hPTPrho	CEFRSLYYNI	SRLD	DPQ	-----T	NSSQIKDE	FQTLN	IVTPRV	RP	-----E	DCS	IGLLPR	NHDKNR	SMVD	PLDRCL	PFLISVD	-----E	SSNYINAAALMDSH	-----K	QPAAFVITQHP	
hPTPmu	SQVRSLYYDMKLD	DPQ	-----T	NSSQIKDE	FQTLN	IVTPRV	RP	-----E	DCS	IGLLPR	NHDKNR	SMVD	PLDRCL	PFLIT	IDG	-----E	SSNYINAAALMDSY	-----K	QPSAFITQHP	
hPTPkappa	CEFKAAAYFDMIR	IRID	DSQ	-----T	NSSHLKDE	FQTLN	IVTPRV	RP	-----E	DCS	IAACLR	NHDKNR	FM	PLDRCL	PFLIT	IDG	-----E	SSNYINAAALMDSY	-----R	QPSAFITQHP
hPTPlambda	SEFKATYKEMIRID	DPQ	-----S	NSSQLREEFQTL	LSNV	TPPLDV	-----E	EC	SIALPR	NHDKNR	SMVD	PLDRCL	PFLISTD	IG	-----D	SSNYINAAALTD	SY	-----T	RSAAFI	VTLHP

Color code: N 100% amino acid identity E 80% amino acid identity S 40% amino acid identity (19) amino acid insert - conserved among vertebrate CD45 orthologs
 L 90% amino acid identity L 60% amino acid identity SKSEHSDSDSSDDSDSE

PTP domains (excluding domains D2)

Amino acid	α3		β12	α4		α5		α6					
	#190	#200	#210	#220	#230	#240	#250	#260	#270	#280			
hPTPalpha	--PIGMLKFLKKVKACNPQYA	-----	GAIIVVHCSAGVGRGTGTFVVIDAMLDMMHTERK	---	VDVYGFVSRIRRAQR	CCQMV	QTD	MQYVF	IYQAL	LEHYLY	GDTEL		
hPTPepsilon	--PIGMLKFLKKVKTLNPVHA	-----	GPVVVHCSAGVGRGTGTFVIDAMMAMMHA	EQK	---	VDVFEFVSRIRNR	QPMV	QTD	MQYTF	IYQAL	LEYLY	GDTEL	
hPTPkappa	--ATGLLSFIRRVKLSNPSSA	-----	GPVVVHCSAGAGRTGCFVIDIMLDMAEREGV	---	VDIYNCVKALRSR	RIN	QMV	QTE	EQYIF	IHDAL	LEACLG	GETAI	
hPTPmu	--ATGLLGfVfRQVKSKSPSSA	-----	GPLVVHCSAGAGRTGCFVIDIMLDMAEREGV	---	VDIYNCVRELRSR	RVM	QTE	EQYVF	IHDAL	LEACLG	GDTSV		
hPTPrho	--ATGLLGfVfRQVKFLNPPEA	-----	GPVVVHCSAGAGRTGCFVIDIMLDMAENEGV	---	VDIFNCVRELRAQR	VNL	QTE	EQYVF	VHDA	LEACLG	GNATA		
hPTPlamda	--ATGLLAFIRRVKASTPPDA	-----	GPVVVHCSAGAGRTGCFVIDIMLDMAEENEGV	---	VDIYNCVKTLSR	RVM	QTE	EQYIF	IHDAL	LEACLG	GETTI		
hPTPdelta	--PTPFLAFLRRVKTCPNPPDA	-----	GPMVVHCSAGVGRGTGCFVIDAMLERIKHEKT	---	LDIYGHVTLMR	RAQR	N	QTE	EQYIF	IHDAL	LEAVT	QNTFV	
hPTPsigma	--PTPFLAFLRRVKTCPNPPDA	-----	GPVVVHCSAGVGRGTGCFVIDAMLERIKHEKT	---	VDVYGHVTLMR	SQR	N	QTE	EQYIF	IHEAL	LEAVG	GNTEV	
hPTPgamma	--ALPVLTFVRRSSAARMPET	-----	GPLVVHCSAGVGRGTGTYVIDSMLQKIKDKST	---	VNVLGFLKHIRT	QR	N	QTE	EQYIF	IHDAL	LEA	ILGKETEV	
hPTPzeta	--SLPVLTFVRRKAAAYAKRHAV	-----	GPVVVHCSAGVGRGTGTYVIDSMLQKIQHEGT	---	VNIFGFLKHISQR	N	QTE	EQYVF	IHDTL	EA	ILSKETEV		
hLAR	--PTPILAFLLRRVKACNPLDA	-----	GPMVVHCSAGVGRGTGCFVIDAMLERMKHEKT	---	VDIYGHVTCMR	SQR	N	QTE	EQYVF	IHEAL	LEAAT	CGHTEV	
hCD45	--PHLLKFLRRVNAFSNFFS	-----	GPVVVHCSAGVGRGTGTYVIDAMLEGLEAENK	---	VDVYGVVVKLR	RQR	N	QTE	EQYIF	IHQAL	VEYNQF	GETEV	
hGLEPP1	NAAESILQFVHMVRQATKSK	-----	GPMIVHCSAGVGRGTGTFIALDRLQLQHIRDHEF	---	VDILGLVSEMR	RSY	R	QTE	EQYIF	IHQCV	QLMWM	KKKQF	
hTPS31	--SAPLIFHFVKLVRASRAHDT	-----	TPMIVHCSAGVGRGTGTFIALDHLTQHIENDHF	---	VDIYGLVAELR	SE	R	QTE	EQYIF	FLHQC	LDLLS	NKGSNQ	
hDEP1	TDLLINFRYLVRDYMKQSPPE	-----	SPVVVHCSAGVGRGTGTFIALDRLIYQIENENT	---	VDVYGVVYDLR	MHR	N	QTE	EQYVF	FLNQC	VDL	VR	SQKDSK
hPTPbeta	--TQSLIQFVRTVDYINRSPGA	-----	GPTVVHCSAGVGRGTGTFIALDRLIQLQLSDKDS	---	VDIYGAHDLR	LHR	V	QTE	EQYVF	LHQCV	RD	LR	AKLR
hSAP1	PDTLAFWRMLRQWLDQTMEG	-----	GPMVVHCSAGVGRGTGTFIALDVLRLRQLQSEGL	---	LDIYGHVTCMR	SQR	N	QTE	EQYVF	IHQAL	VEYNQF	GETEV	
hSTEP	--APPLLHLVREVEEAQQEGPHC	-----	APIIVHCSAGIGRTGCFIATSICCCQLRQEGV	---	VDILKTTCCQL	RQD	R	QTE	EQYVF	VHVM	SLY	EK	QLSHQS
hPCPTP1	--AQLPLQLMLDVEEDRLASQGR	-----	GPVVVHCSAGIGRTGCFIATSIGCQQLKEEGV	---	VDALSI	V	QTE	EQYVF	VHHA	LCL	YES	R	LSAET
hHePTP	--AGPLLRLVAEVEESPETAHP	-----	GPVVVHCSAGIGRTGCFIATRIGCQQLKARGE	---	VDILGIV	QTE	EQYVF	VHHA	LCL	YES	R	LSAET	
hSHP1	--PGGVLDFLQVIRNQRQESLPH	-----	GPVVVHCSAGIGRTGTFIATSDMLNENK	---	VDIYGHVTCMR	SQR	N	QTE	EQYVF	IHQAL	VEYNQF	GETEV	
hSHP2	--PGGVLDFLQVIRNQRQESLPH	-----	GPVVVHCSAGIGRTGTFIATSDMLNENK	---	VDIYGHVTCMR	SQR	N	QTE	EQYVF	IHQAL	VEYNQF	GETEV	
hPEST	--FDSILDMISLMRKYQEHED	-----	VPICIHCSAGCGRTGAICADYTWMLLKAGKIP	EEFN	VN	LI	QTE	EQYVF	VHHA	LCL	YES	R	LSAET
hLyPTP	--IDPILLELIDWVRCYQEDDS	-----	VPICIHCSAGCGRTGAICADYTWMLLKAGKIP	EEFN	VN	LI	QTE	EQYVF	VHHA	LCL	YES	R	LSAET
hBDP1	--PDHMLAMVEEAARRLQSGSP	-----	EPLCVHCSAGCGRTGVLCTVDYVRRQLLLTQMI	PPDF	SL	FD	QTE	EQYVF	VHHA	LCL	YES	R	LSAET
hTPD1	--LKGFLSYLEEIQSVRRHTNSTSDPQSPN	-----	PPLLHCSAGVGRGTGVLISELMIACLEHNEV	---	LDIPRVL	QTE	EQYVF	VHHA	LCL	YES	R	LSAET	
hTPD2	--VQGFLSYLEEIQSVRRHTNSMLEGKTRH	-----	PVVVHCSAGVGRGTGVLISELMIACLEHNEV	---	LDIPRVL	QTE	EQYVF	VHHA	LCL	YES	R	LSAET	
hMEG1	--SSDFLDFVCHVRNKRAGKE	-----	EPVVVHCSAGIGRTGVLIMETAMCLIECNQP	---	VYPLDI	QTE	EQYVF	VHHA	LCL	YES	R	LSAET	
hTPPH1	--SSDFLEFVNYVRS LRVD	-----	EPLLVHCSAGIGRTGVLIMETAMCLTERNL	---	IYPLDI	QTE	EQYVF	VHHA	LCL	YES	R	LSAET	
hTPBAS	--PDDLTFISYMRH IHR	-----	GPVVVHCSAGIGRTGVLIMETAMCLTERNL	---	IYPLDI	QTE	EQYVF	VHHA	LCL	YES	R	LSAET	
hTP1B	--PASFLNLFKVRRESGSLSPEH	-----	GPVVVHCSAGIGRTGVLIMETAMCLTERNL	---	IYPLDI	QTE	EQYVF	VHHA	LCL	YES	R	LSAET	
hTCPTP	--PASFLNLFKVRRESGSLNPDH	-----	GPVVVHCSAGIGRTGVLIMETAMCLTERNL	---	IYPLDI	QTE	EQYVF	VHHA	LCL	YES	R	LSAET	
hMEG2	--AASLIDFLRVVRNQQSLAVSNMGARSKGQCEP	-----	PVVVHCSAGIGRTGVLIMETAMCLTERNL	---	IYPLDI	QTE	EQYVF	VHHA	LCL	YES	R	LSAET	
hIA2	--TRPLDFRRKVNKCYGRS	-----	CPVVVHCSAGIGRTGTYLIDMVLNRMAKGVK	---	EIDIAAT	QTE	EQYVF	VHHA	LCL	YES	R	LSAET	
hIA2beta	--SRSLDFRRKVNKCYGRS	-----	CPVVVHCSAGIGRTGTYLIDMVLNRMAKGVK	---	EIDIAAT	QTE	EQYVF	VHHA	LCL	YES	R	LSAET	
hPTPTyp	--ADSFIKYIRYARKSHLT	-----	GPMVVHCSAGIGRTGTYLIDMVLNRMAKGVK	---	EIDIAAT	QTE	EQYVF	VHHA	LCL	YES	R	LSAET	
hHDPTP	--PSNLLRFIQEVHAHYLHQRPLH	-----	TPVVVHCSAGVGRGTGAFALLYAAVQVEEAGNG	---	IPELP	QTE	EQYVF	VHHA	LCL	YES	R	LSAET	

PTP domains D2

hPTPalpha	--GKGMISIIAAVQKQKQSGN	-----	HPITVHCSAGAGRTGTFICALSTVLERVKAEGI	---	LDVFQTVKSLRL	QRP	QTE	EQYVF	FCYKVVQ	EYIDA	FS	SDYA
hPTPepsilon	--GKGMIDLIAAVQKQKQQTGN	-----	HPITVHCSAGAGRTGTFICALSNILERVKAEG	---	LDVFQAVKSLRL	QRP	QTE	EQYVF	FCYKVVQ	DFIDI	FS	SDYA
hCD45	--PKELISMIQVVKQLPKNSSEGNKHHKS	-----	TPLLHCRDGSQQTGIFCALLNLLESAAETEEV	---	VDIFQVVKALR	KAR	QTE	EQYVF	FLYDV	I	ASTY	PAQNGQV
hPTPgamma	--STFELINVIKEEALTRD	-----	GPVVVHCSAGAGRTGTFICALNLSQLENAEN	---	VDIFQVVKALR	KAR	QTE	EQYVF	FLYDV	I	ASTY	PAQNGQV
hPTPzeta	--KTFELISVIEEAAARD	-----	GPMIVDEHGGVTAAGTFICALTLMHQLEKENS	---	VDVYQVAKMI	NLM	QTE	EQYVF	FLYKV	ILSL	V	STRQEN
hPTPsigma	--GEGFIDFIGQVHKTKEQFGQD	-----	GPISVHCSAGVGRGTGVTLSIVLERMR	YEGV	---	VDIFQTVKMLRT	QRP	QTE	EQYVF	FCYQA	ALEY	LSFDHYA
hPTPdelta	--GEGFIDFIGQVHKTKEQFGQD	-----	GPISVHCSAGVGRGTGVTLSIVLERMR	YEGV	---	VDIFQTVKMLRT	QRP	QTE	EQYVF	FCYQA	ALEY	LSFDHYA
hLAR	--GEGFIDFIGQVHKTKEQFGQD	-----	GPISVHCSAGVGRGTGVTLSIVLERMR	YEGV	---	VDIFQTVKMLRT	QRP	QTE	EQYVF	FCYQA	ALEY	LSFDHYA
hPTPrho	--SKRSLLKVVRRLEKQEQYDGRE	-----	GRTVVHCLNGGGRSGTFCALISVCEMLIQQNI	---	IDVFHIVKTL	LRN	QTE	EQYVF	FCYQA	ALEY	LS	FDHYA
hPTPmu	--SKRSFLKLIQVQKQEEYNGGE	-----	GPTVVHCLNGGGRSGTFCALISVCEMLIQQNI	---	IDVFHIVKTL	LRN	QTE	EQYVF	FCYQA	ALEY	LS	FDHYA
hPTPkappa	--SKRSFLKLIQVQKQEEYNGGE	-----	GRTIVHCLNGGGRSGTFCALISVCEMLIQQNI	---	IDVFHIVKTL	LRN	QTE	EQYVF	FCYQA	ALEY	LS	FDHYA
hPTPlamda	--SKKAFLLLAEDVQWQAESGD	-----	GRTIVHCLNGGGRSGTFCACATVLEMI	---	VDVF	FAA	QTE	EQYVF	FCYQA	ALEY	LE	GLESR

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).apr

rOSTPTP D1 (NP 149090) Eso	(1) HSF	RQSYEAKSAHAH	----	QT	FP	EQ	EE	EK	----	EV	GKDQ	PR	LE	EH	DN	IK	NR	PH	VP	YD	HS	SR	V	TQ	PG	----	PH	SD	YIN	AN	TP	GS	HT								
hPCPTP1 D1 (NP 002840) PTPRR	(1) SR	LTRS	QL	RD	VV	AS	----	HL	QS	FE	ME	FP	----	MM	FV	DP	PK	ED	IR	PH	GT	NR	KT	IL	PN	PL	SR	VR	CP	RP	KN	V	TD								
rPCPTP1 D1 (NP 446046) Ptprr	(1) SR	LTS	PQ	LR	DV	VV	AS	----	HL	QS	FE	ME	FP	----	MM	FV	DP	PK	ED	IR	PH	GT	NR	KT	IL	PN	PL	SR	VR	CP	RP	KN	V	TD							
mPTPSL D1 (NP 035347) Ptprr	(1) SR	LTRS	QL	RD	VV	AS	----	HL	QS	FE	ME	FP	----	MM	FV	DP	PK	ED	IR	PH	GT	NR	KT	IL	PN	PL	SR	VR	CP	RP	KN	V	TD								
hSTEP D1 (NP 116710) PTPN5	(1) SR	LQAE	EEL	HE	KA	LD	PD	----	FL	QA	EF	FE	FP	----	MM	FV	DP	PK	EY	DI	GL	VR	NR	KT	IL	PN	PH	SR	VR	TS	PD	DD	----								
mSTEP D1 (NP 038671) Pton5	(1) SR	LRAE	EEL	HE	KA	LD	PD	----	FL	QA	EF	FE	FP	----	MM	FV	DP	PK	EY	DI	GL	VR	NR	KT	IL	PN	PH	SR	VR	TS	PD	DD	----								
rSTEP D1 (NP 062126) Pton5	(1) SR	LRAE	EEL	HE	KA	LD	PD	----	FL	QA	EF	FE	FP	----	MM	FV	DP	PK	EY	DI	GL	VR	NR	KT	IL	PN	PH	SR	VR	TS	PD	DD	----								
hHePTP D1 (NP 002823) PTPN7	(1) HP	TRW	LQ	RQ	PP	SS	----	KQ	EE	FL	PK	FP	----	SN	FV	NP	ED	LD	IG	H	AS	DR	KT	IL	PN	PQ	SR	VR	CP	GR	AQ	SQ	----								
mHePTP D1 (NP 796055) Pton7	(1) HP	TRW	LQ	RQ	PP	SS	----	KQ	EE	FL	PK	FP	----	SN	FV	NP	ED	LD	IG	H	AS	DR	KT	IL	PN	PQ	SR	VR	CP	GR	AQ	SQ	----								
rLCPTP D1 (P49445) Pton7	(1) HP	TRW	LQ	RQ	PP	SS	----	KQ	EE	FL	PK	FP	----	SN	FV	NP	ED	LD	IG	H	AS	DR	KT	IL	PN	PQ	SR	VR	CP	GR	AQ	SQ	----								
hLyPTP D1 (NP 057051) PTPN22	(1) EI	LQ	KF	IDE	AQ	SK	KI	----	TK	EE	FAN	FL	PK	KR	Q	ST	K	Y	K	A	D	T	Y	P	T	V	AK	E	K	IK	NR	KD	IL	PD	YS	RV	SL	TS			
mPEP D1 (NP 033005) Pton8	(1) EI	LQ	LK	E	AQ	SK	KL	----	NS	EE	FAS	FL	PK	KR	Q	ST	K	Y	K	A	D	T	Y	P	T	V	AK	E	K	IK	NR	KD	IL	PD	YS	RV	SL	TS			
hPEST D1 (NP 002826) PTPN12	(1) EI	L	R	R	F	I	Q	R	Y	Q	A	M	S	P	D	H	N	G	E	D	N	F	A	R	Y	M	R	R	L	S	T	K	Y	R	T	E	K	I	Y	P	T
rRKPTP D1 (NP 035332) Pton12	(1) EI	L	R	R	F	I	Q	R	Y	Q	A	M	S	P	D	H	N	G	E	D	N	F	A	R	Y	M	R	R	L	S	T	K	Y	R	T	E	K	I	Y	P	T
mPEST D1 (NP 035333) Pton12	(1) EI	L	R	R	F	I	Q	R	Y	Q	A	M	S	P	D	H	N	G	E	D	N	F	A	R	Y	M	R	R	L	S	T	K	Y	R	T	E	K	I	Y	P	T
hBDP1 D1 (NP 055184) PTPN18	(1) DS	ARS	F	ER	E	ARGG	----	REG	AV	AGE	FS	DR	Q	ACS	A	A	N	K	D	G	V	C	S	T	V	AS	SR	EN	VR	NR	KD	IL	PD	YS	RV	SL	QEE				
mPTPK1_D1 (NP 035336) Pton18	(1) DL	RS	L	E	Q	E	ARDY	----	REG	AV	AGE	FS	DR	Q	ACS	A	A	N	K	D	G	V	C	S	T	V	AS	SR	EN	VR	NR	KD	IL	PD	YS	RV	SL	QEE			
rPTP20 D1 (AAC52896)	(1) DL	RS	F	L	E	Q	E	ARDH	----	R	K	GA	L	AR	F	SD	K	A	R	S	V	A	N	K	D	G	V	C	S	T	V	AS	SR	EN	VR	NR	KD	IL	PD	YS	RV
hSHP1 D1 (NP 002822) PTPN6	(1) AD	EN	R	V	L	E	N	KK	Q	E	S	E	D	T	R	K	A	G	F	W	E	B	E	S	L	Q	K	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q			
mSHP1 D1 (NP 038573) Hcpb	(1) AD	EN	R	V	L	E	N	KK	Q	E	S	E	D	T	R	K	A	G	F	W	E	B	E	S	L	Q	K	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q			
rSHP1_D1 (NP 446360) Ptoh6	(1) AD	EN	R	V	L	E	N	KK	Q	E	S	E	D	T	R	K	A	G	F	W	E	B	E	S	L	Q	K	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q			
zSHP1 D1 (AAH44414)	(1) V	N	L	Q	D	T	S	R	E	K	M	D	G	A	D	K	I	K	A	G	F	W	E	B	E	S	L	Q	K	Q	Q	Q	Q	Q	Q	Q	Q				
rPTPN6c D1 (BAA95199)	(1) --	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---					
hSHP2 D1 (NP 002825) PTPN11	(1) AE	ES	R	V	R	E	L	S	K	L	A	E	T	T	D	K	V	K	Q	G	F	W	E	B	E	S	L	Q	K	Q	Q	Q	Q	Q	Q	Q					
rSHP2_D1 (NP 035332) Pton11	(1) AE	ES	R	V	R	E	L	S	K	L	A	E	T	T	D	K	V	K	Q	G	F	W	E	B	E	S	L	Q	K	Q	Q	Q	Q	Q	Q	Q					
rSHP2_D1 (NP 037220) Pton11	(1) AE	ES	R	V	R	E	L	S	K	L	A	E	T	T	D	K	V	K	Q	G	F	W	E	B	E	S	L	Q	K	Q	Q	Q	Q	Q	Q	Q					
cSHP2 D1 (JC5167)	(1) AE	ES	R	V	R	E	L	S	K	L	A	E	T	T	D	K	V	K	Q	G	F	W	E	B	E	S	L	Q	K	Q	Q	Q	Q	Q	Q	Q					
zSHP2 D1 (AAH45328)	(1) AE	ES	R	V	R	E	L	S	K	L	A	E	T	T	D	K	V	K	Q	G	F	W	E	B	E	S	L	Q	K	Q	Q	Q	Q	Q	Q	Q					
xSHP2 D1 (A56561)	(1) AE	ES	R	V	R	E	L	S	K	L	A	E	T	T	D	K	V	K	Q	G	F	W	E	B	E	S	L	Q	K	Q	Q	Q	Q	Q	Q	Q					
rPTPN6b D1 (BAA95198)	(1) --	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
hPTPD1 D1 (NP 008970) PTPN21	(1) A	N	D	E	R	C	K	I	L	E	Q	R	L	E	----	Q	M	F	T	B	E	R	L	K	----	K	R	L	V	D	G	E	C	S	T	A	R	L			
mPTPRL10 D1 (NP 036007) Pton21	(1) A	N	D	E	R	C	K	V	L	E	Q	R	L	E	----	Q	M	F	T	B	E	R	L	K	----	K	R	L	V	D	G	E	C	S	T	A	R	L			
rPTP2E D1 (NP 598229) Pto2E	(1) A	N	D	E	R	C	K	V	L	E	Q	R	L	E	----	Q	M	F	T	B	E	R	L	K	----	K	R	L	V	D	G	E	C	S	T	A	R	L			
hPTPD2 D1 (NP 005392) PTPN14	(1) V	P	D	E	R	F	R	L	K	K	K	L	E	----	E	G	M	F	T	B	E	R	L	K	----	K	K	K	A	N	G	I	F	S	T	A	L				
mPTP36 D1 (NP 033002) Pton14	(1) V	P	D	E	R	F	R	L	K	K	K	L	E	----	E	G	M	F	T	B	E	R	L	K	----	K	K	K	A	N	G	I	F	S	T	A	L				
rPTPD2 D1 (XP 223062 (revised))	(1) V	P	D	E	R	F	R	L	K	K	K	L	E	----	E	G	M	F	T	B	E	R	L	K	----	K	K	K	A	N	G	I	F	S	T	A	L				
hMEG1 D1 (NP 002821) PTPN4	(1) H	S	R	E	S	N	I	Q	A	E	G	L	I	----	T	G	T	L	A	Q	D	L	Y	----	R	K	P	G	M	T	M	S	C	K	L	Q					
mMEG1 D1 (NP 064317) Pton4	(1) H	S	R	E	S	N	I	Q	A	E	G	L	I	----	T	G	T	L	A	Q	D	L	Y	----	R	K	P	G	M	T	M	S	C	K	L	Q					
zMEG1 D1 (CAD43435)	(1) D	A	W	R	D	S	L	Y	L	K	E	G	L	----	S	G	T	L	A	Q	D	L	Y	----	R	K	P	G	M	T	M	S	C	K	L	Q					
hPTPH1 D1 (NP 002820) PTPN3	(1) D	T	E	G	S	M	A	L	K	K	G	L	E	----	S	G	T	L	A	Q	D	L	Y	----	R	K	P	G	L	A	I	T	A	K	L						
mPTPH1 D1 (XP 143789) Pton3	(1) D	S	L	E	G	S	M	E	L	K	K	G	L	E	----	S	G	T	L	A	Q	D	L	Y	----	R	K	P	G	L	A	V	S	P	A						
hPTPBAS D1 (NP 006255) PTPN13	(1) A	N	L	K	S	V	I	R	L	G	L	L	D	----	Q	G	I	P	S	K	E	L	E	N	Q	----	E	L	K	P	L	D	Q	C	L						
mPTPBL D1 (NP 035334) Pton13	(1) T	Q	L	A	T	I	R	T	L	Q	L	L	D	----	Q	G	I	P	S	K	E	L	E	N	Q	----	E	L	K	P	L	D	Q	C	L						
bPTPA14 D1 (NP 777015) PTPN13	(1) A	K	L	K	S	V	I	R	L	G	L	L	D	----	Q	G	I	P	S	K	E	L	E	N	Q	----	E	L	K	P	L	D	Q	C	L						
hPTPD2 D1 (AL050040) PTPN20	(1) T	A	K	D	C	L	K	I	L	E	K	T	A	----	A	Y	D	W	E	F	M	A	L	E	----	L	K	N	L	P	G	E	F	Y							
mPTPTyp_D1 (NP 033004) Pton20	(1) S	A	R	D	C	L	N	T	L	Q	K	E	E	----	L	D	T	R	F	L	E	L	E	----	Q	M	T	L	P	D	D	F	N								
cPTP1B D1 (O13016)	(1) M	E	K	E	F	H	R	L	D	Q	A	S	----	W	A	A	I	Q	D	R	----	H																			

VectorNTI Screen View - Alignment_195_Vert_PTP_Domains_D1_and_D2 (VNTI 8.0).ap

blA2 D1 (P56722) Ptdrn	(1) HMLAYMEDHLNRND-----RLAKBQALCAY----QAEPNTCATAQEGEIKKK--NRSLPDFPYDHAHAKIKVVESSP-----SRSDYINAFPTIEHDPDR
hIA2beta D1 (NP 002838) PTPRN2	(1) HMLSYMEDHLKNKN-----RLKKEWEALCAY----QAEPNSFVYQREEVVPK--NRSLAVITVDHSSVLLKAENSH-----SHSDYINAFPTIMHDPDR
macnelA2beta D1 (O02695)	(1) HMLSYMEDHLKNKN-----RLKKEWEALCAY----QAEPNSSLVAQREENVPK--NRSLAVITVDHSSVLLKAENSH-----SHSDYINAFPTIMHDPDR
mPTPNP D1 (P80560) Ptdrn2	(1) HMLAYMEDHLKNKN-----RLKKEWEALCAY----QAEPNSSLVAQREENAPK--NRSLAVITVDHSSVLLKXSNH-----SSSDYINAFPTIMHDPDR
rPTNE6 D1 (NP 113788) Ptdrn2	(1) HMLAYMEDHLKNKN-----RLKKEWEALCAY----QAEPDSSLVAQREENAPK--NRSLAVITVDHSSVLLKXSNH-----SNSDYINAFPTIMHDPDR
hCD45 D2 (NP 002829) PTPRC	(1) SEHPYIHNKRRKDDP--SEPSPEAEQRQLP----SYRSWRQTQHIQNGEENKSK--NRNSNVIPYDFNRRVPLKHELEMS--KESEHSDSESSDDSDSEEPKRYINAFPTMSYWKFP
mCD45 D2 (NP 035340) Ptdrc	(1) SEHSCILHNKRRKDDP--SDPSPEAEQRQLP----SYRSWRQTQHIQNGEENKSK--NRNSNVIPYDFNRRVPLKHELEMS--KESEPEDESSESSDDSDSEETKRYINAFPTMSYWKFP
rCD45_D2 (XP 213985) Ptdrc	(1) SEHSHYLNKRRKDDP--SEPSLEAEQRQLP----SYKGRWTQNTQNGEENKSK--NRNSANTVYDFNRRVPLRSEEEQ--KEGEHSDSESSDSDSEESKRYINAFPTITYGWGP
cdCD45 D2 (A54080)	(1) QELHSTLNTLQQRSSD--NEPTLLEDFERLP----NFKNWRFTNTGVTENKMKK--NRSSSVIPYDFNRRVLLKLEDEKSHESDPPDDDDYDTSSYDDIEDSKRYINAFPTISYWGFP
fuCD45 D2 (CAB96211)	(1) SEFHVSVNTLQKNG--SDPSLEKFEQKLP----KFKKWRMTMTGSSDEDKSK--NRDSAVIPYDFNRRVIFRLDIEGN---QTSDPDEDEEYSSDEEESNQYINAFPTIDGYWCN
cypcaCD45 D2 (BAA92179)	(1) -----NKKRDRPP--SEPSPEAEQRQLP----SYRSWRQTQHIQNGEENKSK--NRNSNVIPYDFNRRVPLKHELEMS--KESEHSDSESSDDSDSEEXKRYINAFPTIMXWKP
aotvoCD45 D2 (AAM48512) (3')	(1) -----NKKRDRPP--SEPSPEAEQRQLP----PYTDWRQTQTRRGEQSK--NRSLSVIAYDFNRRVTKLEDEKS--KDSHSDSDSLLSDDSDSEESKRYINAFPTIDGYWHS
sharkCD45 D2 (T43148)	(1) SELPKHINFKKNDPP--SEPSMREGFORLP----PYTDWRQTQTRRGEQSK--NRSLSVIAYDFNRRVTKLEDEKS--KDSHSDSDSLLSDDSDSEESKRYINAFPTIDGYWHS
cPTPaloha D2 (AAB04150)	(1) TSEIHLQKLYNKVP--GTSSNGEEFKKLT--IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRRVLPVKRGE-----ENSDYINAFPTIDGYRRR
hPTPaloha D2 (NP 002827) PTPRA	(1) TSEIHLQKLYNKIP--GTSNNGEEFKKLT--IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRRVLPVKRGE-----ENSDYINAFPTIDGYRQK
mPTPaloha D2 (NP 033006) Ptdra	(1) TSEIHLQKLYNKIP--GTSNNGEEFKKLT--IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRRVLPVKRGE-----ENSDYINAFPTIDGYRQK
rPTPaloha D2 (NP 036895) Ptdra	(1) TSEIHLQKLYNKIP--GTSNNGEEFKKLT--IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRRVLPVKRGE-----ENSDYINAFPTIDGYRQK
xPTPaloha D2 (AAA17990)	(1) TSEIHLQKLYSKFP--GTNSTGEEFKKLT--IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRRVLPVKRGE-----ENSDYINAFPTIDGYRQK
zPTPaloha D2 (NP 571963) ptdra	(1) TSEIHLQKLYSKFP--GTNSTGEEFKKLT--IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRRVLPVKRGE-----ENSDYINAFPTIDGYRQK
rVTPR4b D2 (BAA95196)	(1) TSEIHLQKLYNRVS--GSGCGNGEEFKKLT--IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRRVLPVKRGE-----ENSDYINAFPTIDGYRQK
hPTPepsilon D2 (NP 006495) PTPRE	(1) SSELKHLQTLHGTTT--HFDKIGEEFKKLTN--VRIMKENMRTGNLPAANMKK--ARVIOIIPYDFNRRVLSMKRGG-----EYSDYINAFPTIDGYRQK
mPTPepsilon D2 (NP 035342) Ptdre	(1) SSELKHLQTLHGTAT--HFDKIGEEFKKLTN--VRIMKENMRTGNLPAANMKK--ARVIOIIPYDFNRRVLSMKRGG-----EYSDYINAFPTIDGYRQK
rPTPepsilon D2 (XP 215102) Ptdre	(1) SSELKHLQTLHGTAT--HFDKIGEEFKKLTN--VRIMKENMRTGNLPAANMKK--ARVIOIIPYDFNRRVLSMKRGG-----EYSDYINAFPTIDGYRQK
orylaPTPepsilon D2 (BAC06424)	(1) CSLEGHILHRLHNTRA--PNDRLIGEEFKKLTN--VRIMKENMRTGNLPAANMKK--ARVIOIIPYDFNRRVLSMRGG-----EYSDYINAFPTIDGYRQK
orylaPTPepsilon D2 (BAA95190)	(1) CSLEGHILHRLHNTRG--PNDRLIGEEFKKLTN--VRIRKDNMRTGNLPAANMKK--ARVIOIIPYDFNRRVLSMRGG-----EYSDYINAFPTIDGYRQK
hPTPkappa D2 (NP 002835) PTPRK	(1) KAAYPDIRHDSQTN-----SSHKDEPQTLS--VTPRLQAEDCSIALCLRNHDK--NRSMMDLPPRCLPFLITDGD-----ESNRYINAFPTIDGYRQP
mPTPkappa D2 (NP 033009) Ptdrk	(1) KAAYPDIRHDSQTN-----SSHKDEPQTLS--VTPRLQAEDCSIALCLRNHDK--NRSMMDLPPRCLPFLITDGD-----ESNRYINAFPTIDGYRQP
rVTPR2B D2 (BAA95194)	(1) KQAYYEMIRHDSQSN-----SSQLKDEPQTLS--VSSQLQPEDCSIALCLRNHDK--NRSMMDLPPRCLPFLITDGD-----ESNRYINAFPTIDGYRQP
hPTPlamda D2 (NP 005695) PTPRU	(1) KATYEMIRHDSQSN-----SSQLREBPQTLS--VTPPLDVEECSIALCLRNHDK--NRSMMDLPPRCLPFLITDGD-----DSNRYINAFPTIDGYRQK
mPTPlamda D2 (NP 035344) Ptdrl	(1) RATYEMIRHDSQSN-----SSQLREBPQTLS--VTPPLDVEECSIALCLRNHDK--NRSMMDLPPRCLPFLITDGD-----DSNRYINAFPTIDGYRQK
hPTPmu D2 (NP 002836) PTPRM	(1) RSLYDMNKLDPQTN-----SSQKEPRTLNM--VTPTLRVEDCSIALCLRNHDK--NRNCDMLPPRCLPFLITDGD-----ESNRYINAFPTIDGYRQP
mPTPmu D2 (NP 033010) Ptdrm	(1) RSLYDMNKLDPQTN-----SSQKEPRTLNM--VTPTLRVEDCSIALCLRNHDK--NRNCDMLPPRCLPFLITDGD-----ESNRYINAFPTIDGYRQP
rPTPmu D2 (XP 237546 (revised))	(1) RSLYDMNKLDPQTN-----SSQKEPRTLNM--VTPTLRVEDCSIALCLRNHDK--NRNCDMLPPRCLPFLITDGD-----ESNRYINAFPTIDGYRQP
hPTPrho D2 (NP 573400) PTPRT	(1) RSLYDNISRLDPQTN-----SSQKDEPQTNI--VTPVRPVEDCSIALCLRNHDK--NRSMMDLPPRCLPFLITDGD-----ESNRYINAFPTIDGYRQP
mPTPrho D2 (NP 067439) Ptdrt	(1) RSLYDNISRLDPQTN-----SSQKDEPQTNI--VTPVRPVEDCSIALCLRNHDK--NRSMMDLPPRCLPFLITDGD-----ESNRYINAFPTIDGYRQP
cPTPsiama D2 (I50212)	(1) RNLYTYIQKLAQIEVGG--EHVTGMLEFKRLAN--SKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
hLAR D2 (NP 002831) PTPRF	(1) RNLYAHYIQLGQVPPG--ESVTAMELEFKRLAN--SKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
mLAR D2 (NP 035343) Ptdrf	(1) RNLYAHYIQLGQVPPG--ESVTAMELEFKRLAN--SKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
rLAR_D2 (NP 062122) Ptdrf	(1) RNLYAHYIQLGQVPPG--ESVTAMELEFKRLAG--SKARASRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
xLAR D2 (AAF43606)	(1) RSLYAHYIQLGQVPPG--ESVTAMELEFKRLAN--SKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
rLAR D2 (CAC44758)	(1) RSLYTHYIQLGQAPPG--DVTAMELEFKRLAN--SKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
rVTPR2Aa D2 (BAA95188)	(1) RSLFAHYIQLGQVPPA--ETVTAMELEFKRLAN--SKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
hPTPdelta D2 (NP 002830) PTPRD	(1) RNLYAYIYIQLGQVPPG--ENVTGMLEFKRLAS--SKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
mPTPdelta D2 (D54689)	(1) RNLYAYIYIQLGQVPPG--ENVTGMLEFKRLAS--SKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
xPTPdelta D2 (AAF43605)	(1) RNLYAYIYIQLGQVPPG--ENVTGMLEFKRLAS--FKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
rVTPR2Ab D2 (BAA95191)	(1) RNLYAYIYIQLGQVPPG--ENVTGMLEFKRLAN--TKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
hPTPsiama D2 (NP 002841) PTPRS	(1) RSLYAYIYIQLGQVEPG--EHVTGMLEFKRLAN--SKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
mPTPsiama D2 (NP 035348) Ptdrs	(1) RSLYTYIYIQLGQVEPG--EHVTGMLEFKRLAN--SKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
xPTPsiama D2 (AAF43607)	(1) RNLYTYIYIQLGQVDPG--EHVIGMELFKRLAN--SKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
rPTPsiama D2 (CAC44759)	(1) RSLFSYIYIQLGQVEAG--EHVSGMELFKRLAN--SKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----LEGSDYINAFPTIDGYRQK
rPTPsiama D2 (NP 062013) Ptdrd	(1) RSLYTYIYIQLGQVEPG--EHVTGMELFKRLAN--SKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
rVTPR2Ac D2 (BAA95193)	(1) RNLYSYIYIQLGQVETG--EHVTGMELFKRLAN--SKAHSRFISANLCLNFKF--NRLVNIPYESTRVCQPGRG-----VEGSDYINAFPTIDGYRQK
hPTPgamma D2 (NP 002832) PTPRG	(1) NQLHSYVNSLIPGVG--GKTRLEKQKFLVQ--CNAKYVECFSAQKECNK--NRNSVVPARARVGLAPPG-----MKGSDYINAFPTIDGYRYS
mPTPgamma D2 (NP 033007) Ptdrg	(1) NQLHSYVNSLIPGVG--GKTRLEKQKFLVQ--CNAKYVECFSAQKECNK--NRNSVVPARARVGLAPPG-----MKGSDYINAFPTIDGYRYS
rPTPgamma D2 (NP 599183) Ptdrg	(1) NQLHSYVNSLIPGVG--GKTRLEKQKFLVQ--CNAKYVECFSAQKECNK--NRNSVVPARARVGLAPPG-----MKGSDYINAFPTIDGYRYS
rVTPR5b D2 (BAA95197)	(1) NQLHSYVNSLIPGLS--GKMRLEKQKFLVQ--CNAKFIECFSAQKECNK--NRNSVVPARARVGLAPPG-----TKGSDYINAFPTIDGYRYS
cPTPgamma D2 (Q98936)	(1) NQLHSYVNSLIPGGI--GKTRLEKQKFLVQ--CNAKYVECFSAQKDCNK--NRNSVVPARARVGLAPPG-----MKGSDYINAFPTIDGYRYS
hPTPzeta D2 (NP 002842) PTPRZ1	(1) SHHAYYNALLIPGPA--GKTKLEKQQLSQ--SNIQSDYSALKQCNR--NRSSLLPVRSRVGLSSSG-----EGSDYINAFPTIDGYYS
cPTPzeta D2 (AAA49015)	(1) THHAYYNALLIPGPT--GKTRLEKQKFLSQ--SNTQQCDYSTLKCNR--NRSSLLPVRSRVGLSSSG-----EGSDYINAFPTIDGYYS
mPTPzeta D2 (XP 133009) Ptdrz1	(1) SHHSHYVNTLIPGPT--GKTKLEKQQLSQ--SNILQSDYSTLKCNR--NRSSLLPVRSRVGLSSSG-----EGSDYINAFPTIDGYYS
rPTPzeta D2 (NP 037212) Ptdrz1	(1) SHHSHYVNTLIPGFS--GKTKLEKQQLSQ--SNILQSDYSTLKCNR--NRSSLLPVRSRVGLSSSG-----EGSDYINAFPTIDGYYS
xPTPzeta D2 (BAA97445)	(1) THHSHYVNTLTMGFS--GKSRLEKQKFLSE--PNILQCDYSTALKQNR--NRSSLLPVRSRVGLSSSG-----EGSDYINAFPTIDGYHES
rVTPR5a_D2 (BAA95195)	(1) NHHTYVNTLTPGFS--GKTKLEKQKFLSQ--PHAKQCDYSALKQCNR--NRSSLLPVRSRVGLSSSG-----EGSDYINAFPTIDGYHRI
Consensus	(1) L I L L E F L A P N K K NRY NILPYD SRV L I SDYINAFPTIDGYYS

	(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 (AAB04150)	(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	---
hPTPqamma D1 (NP 002832) PTPRG	(89)	K	---	A	Y	I	A	T	G	G	P	E	T	---
mPTPqamma D1 (NP 033007) Ptprr	(89)	K	---	A	Y	I	A	T	G	G	P	E	T	---
rPTPqamma D1 (NP 599183) Ptprr	(93)	K	---	A	Y	I	A	T	G	G	P	E	T	---
cPTPqamma 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	F	I	A	A	G	G	P	E	T	---
mCD45 D1 (NP 035340) Ptprc	(85)	R	---	K	F	I	A	A	G	G	P	E	T	---
rCD45_D1 (XP 213985) Ptprc	(85)	R	---	K	F	I	A	A	G	G	P	E	T	---
cCD45 D1 (A54080)	(85)	R	---	K	F	I	A	A	G	G	P	E	T	---
cypcCD45 D1 (BAA92179)	(82)	K	---	K	F	I	A	A	G	G	P	E	T	---
fuCD45 D1 (CAB96211)	(85)	K	---	K	F	I	A	A	G	G	P	E	T	---
sharkCD45 D1 (T43148)	(85)	R	---	K	F	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	---	

VectorNTI Screen View - Alignment_195_Vert_PTP_Domains_D1_and_D2 (VNTI 8.0).apr

rOSTPTP D1 (NP 149090) Eso (85) Q-----EI IATQGPLKKTIEDPWRVWEQVHVHMLVGMENGRVLCHEHYWFPANS---TPVTHGHITHHLAIEP--EDEMTRREQLQHGT-----EQQRVVKQL
hPCPTP1 D1 (NP 002840) PTPRR (85) E-----KA IATQGPLINTVDDPFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
rPCPTP1 D1 (NP 446064) PTPrr (85) E-----KA IATQGPLINTVDDPFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
mPTPSL D1 (NP 035347) PTPrr (85) E-----KA IATQGPLINTVDDPFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
hSTEP D1 (NP 116710) PTPN5 (85) E-----KVYIATQGPLVSTVADPFRMWVQEREPVIMYINIEE--MNEKCTEYWE--EQVADGGETVQKVIH--TEDYRRLALISKS-----GTEERGLKHHY
mSTEP D1 (NP 038671) Pton5 (85) E-----KVYIATQGPLVSTVADPFRMWVQEREPVIMYINIEE--MNEKCTEYWE--EQVADGGETVQKVIH--TEDYRRLALISRR-----GTEERGLKHHY
rSTEP D1 (NP 062126) Pton5 (85) E-----KVYIATQGPLVSTVADPFRMWVQEREPVIMYINIEE--MNEKCTEYWE--EQVADGGETVQKVIH--TEDYRRLALISRR-----GTEERGLKHHY
hHePTP D1 (NP 002823) PTPN7 (83) E-----KVIYATQGPLPNTVADPFWVWVQEDVSVIYMLIQLR--GSEKCVHYWPT---EEETVGPQIRIQDMKE--CEPYTRQLTQY-----QBERSVKHHI
mHePTP D1 (NP 796055) Pton7 (83) E-----KVIYATQGPLPNTVADPFWVWVQEDVSVIYMLIQLR--GSEKCVHYWPT---EEEAVGPQIRIQDMKE--HPBYTRQLTQY-----QBERSVKHHI
rLCPTP D1 (P49445) Pton7 (83) E-----KVIYATQGPLPNTVADPFWVWVQEDVSVIYMLIQLR--GSEKCVHYWPT---EEEAVGPQIRIQDMKE--HPBYTRQLTQY-----QBERSVKHHI
hLyPTP D1 (NP 057051) PTPN22 (93) K-----AYIATQGPLSTLTLDFPWRMVEYSVLLIGMACMEYEMGKKKQERYWAEFPV--EMQLEGGPFSVSCAARKKK--SDYIIRTLKVKFN-----SETRTLYQF
mPEP D1 (NP 033005) Pton8 (93) K-----AYIATQGPLSTLTLDFPWRMVEYSVLLIGMACMEYEMGKKKQERYWAEFPV--EMQLEGGPFSVSCAARKKK--SDYIIRTLKVKFN-----SETRTLYQF
hPEST D1 (NP 002826) PTPN12 (97) K-----AYIATQGPLANTVIDPFRMWVEYNVVVIVMACREFEMGKKKQERYWLYG--EDPITFAPFKISCEDEQAR--TDYFARTLLLEFQ-----NESRRLYQF
rRKPTP D1 (NP 476456) Pton12 (97) R-----AYIATQGPLANTVIDPFRMWVEYNVVVIVMACREFEMGKKKQERYWLYG--EDPITFAPFKISCEDEQAR--TDYFARTLLLEFQ-----NESRRLYQF
mPEST D1 (NP 035333) Pton12 (97) K-----AYIATQGPLRNTVIDPFRMWVEYNVVVIVMACREFEMGKKKQERYWLYG--EDPITFAPFKISCEDEQAR--TDYFARTLLLEFQ-----NESRRLYQF
hBDP1 D1 (NP 055184) PTPN18 (94) L-----AYIATQGPLPHTLLDFPRLVWEPGVKILEMACQETENGRKQERYWAE--QEPLOTGLPFCITIKKKWL--NEDIMARTLKVTFQ-----KEFSPVHLQ
mPTPK1_D1 (NP 035336) Pton18 (94) Q-----AYIATQGPLPHTLLDFPRLVWEPGVKILEMACQETENGRKQERYWAE--QEPLOTGLPFCITIKKKWL--NEDIMARTLKVTFQ-----KEFSPVHLQ
rPTP20 D1 (AAC52896) (94) Q-----AYIATQGPLPHTLLDFPRLVWEPGVKILEMACQETENGRKQERYWAE--QEPLOTGLPFCITIKKKWL--NEDIMARTLKVTFQ-----KEFSPVHLQ
hSHP1 D1 (NP 002822) PTPN6 (94) PDEN--AKTYIASQGCLEATVNDPFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
mSHP1 D1 (NP 038573) Hcpn (94) PDEN--SKTYIASQGCLEATVNDPFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
rSHP1_D1 (NP 446360) Ptoh6 (94) PDEN--SKTYIASQGCLEATVNDPFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
zSHP1 D1 (AAH44414) (94) TNPQ--KTYIACQGCLEATVNDPFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
rvPTPN6c D1 (BAA95199) (65) DD--CKNYIATQGCLEATVNDPFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
hSHP2 D1 (NP 002825) PTPN11 (94) KCNNSKPKKSYIATQGCLEATVNDPFRMVQENSRVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
mSHP2 D1 (NP 035332) Pton11 (94) KCNNSKPKKSYIATQGCLEATVNDPFRMVQENSRVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
rSHP2_D1 (NP 037220) Pton11 (94) KCNNSKPKKSYIATQGCLEATVNDPFRMVQENSRVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
cSHP2 D1 (JCS167) (94) KCNNSKPKKSYIATQGCLEATVNDPFRMVQENSRVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
zSHP2 D1 (AAH45328) (94) KSNNSKPKKSYIATQGCLEATVNDPFRMVQENSRVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
xSHP2 D1 (AA56511) (94) KCINPKPKKSYIATQGCLEATVNDPFRMVQENSRVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
nrTTTKPKK6 YIATQGCLEATVNDPFRMVQENSRVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
hPTPD1 D1 (NP 008970) PTPN21 (86) IE----WDYIATQGPLQNTCQDFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
mPTPRL10 D1 (NP 036007) Pton21 (86) IE----WDYIATQGPLQNTCQDFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
rPTP2E D1 (NP 598229) Pto2E (86) IE----WDYIATQGPLQNTCQDFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
hPTPD2 D1 (NP 005392) PTPN14 (85) AE----WHYIATQGPLPHTCHDFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
mPTP36 D1 (NP 033002) Pton14 (85) SE----WHYIATQGPLPHTCHDFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
rPTPD2 D1 (XP 223062 (revised)) (85) SE----WHYIATQGPLPHTCHDFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
hMEG1 D1 (NP 002821) PTPN4 (81) SS----IINQYIACQGPLPHTCCKDFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
mMEG1 D1 (NP 064317) Pton4 (81) SS----IINQYIACQGPLPHTCCKDFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
zMEG1 D1 (CAD43435) (81) CS----LINRYIACQGPLPHTCCKDFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
hPTPH1 D1 (NP 002820) PTPN3 (81) AN----LVNKYIATQGPLPHTCAQFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
mPTPH1 D1 (XP 143789) Pton3 (81) AN----LVNKYIATQGPLPHTCAQFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
hPTPBAS D1 (NP 006255) PTPN13 (81) EE----FVYIACQGPLPHTVGFDFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
mPTPBAS D1 (NP 035334) Pton13 (81) EE----FVYIACQGPLPHTVGFDFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
bPTPB14 D1 (NP 777015) PTPN13 (81) EE----FVYIACQGPLPHTVGFDFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
hPTPD2 D1 (AL050040) PTPN20 (81) EE----YFYIATQGPLSTHDFDFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
mPTPTyp_D1 (NP 033004) Pton20 (80) EE----YFYIATQGPLSTHDFDFWQVWQEDSPVIMYIKLKE--KNEKCVLWYWE----KRGIVGKVEVLVIGVNE--CDNYTIRNLVLR-----GSHTOHVKKHY
cPTP1B D1 (O13016) (79) R-----SYILLTQGPLPNTCGHPFWVWVQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
hPTP1B D1 (NP 002818) PTPN1 (79) R-----SYILLTQGPLPNTCGHPFWVWVQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
mPTP1B D1 (NP 035331) Pton1 (79) R-----SYILLTQGPLPNTCGHPFWVWVQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
rPTP1B D1 (NP 036769) Pton1 (79) R-----SYILLTQGPLPNTCGHPFWVWVQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
zPTP1B D1 (NP 570999) pto1b (77) R-----KYILLTQGPLPNTCGHPFWVWVQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
hTCTP1 D1 (NP 002819) PTPN1 (79) R-----SYILLTQGPLPNTCGHPFWVWVQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
mTCTP1 D1 (NP 033003) Pton2 (79) R-----SYILLTQGPLPNTCGHPFWVWVQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
rTCTP1 D1 (NP 446442) Pton2 (79) R-----SYILLTQGPLPNTCGHPFWVWVQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
zTCTP1 D1 (AAH44373) (77) R-----KYILLTQGPLPNTCGHPFWVWVQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
hMEG2 D1 (NP 002824) PTPN9 (85) N-----AYISLQGPLPNTYRDFPWLWVWQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
mMEG2 D1 (NP 062625) Pton9 (85) N-----AYISLQGPLPNTYRDFPWLWVWQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
xPTPX10 D1 (B53978) (85) N-----AYISLQGPLPNTYRDFPWLWVWQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
xPTPX1 D1 (AAH43621) (85) N-----AYISLQGPLPNTYRDFPWLWVWQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
hHDPTP D1 (NP 056281) PTPN23 (88) CP----PLMATQGPLPHTAADFVWVWQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
mHDPTP D1 (AAH22721) (88) CP----PLMATQGPLPHTAADFVWVWQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
rPTPTD14 D1 (T14355) (88) CP----PLMATQGPLPHTAADFVWVWQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
hIA2 D1 (NP 002837) PTPRN (85) MP----AYIATQGPLSHTADFVWVWQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
mIA2 D1 (NP 033011) Ptprr (85) MP----AYIATQGPLSHTADFVWVWQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF
rIA2 D1 (NP 446333) Ptprr (85) MP----AYIATQGPLSHTADFVWVWQKSRGVMLNRMVKK--GSLKCAQYWPQKEEKEMVFDNTEKLTISIDV--KSYITVWQLEENLTTQ--ETRELLHF

	(237)	237	250	260	270	280	290	300	310	320	330	340	354
hPTPsiama D1 (NP 002841) PTPRS (176)	Q PTAWP D H G V P EY--PT P LA L RRV K T C N												
mPTPsiama D1 (NP 035348(revised)) Ptprs (176)	Q PTAWP D H G V P EY--PT P LA L RRV K T C N												
rPTPsiama D1 (NP 062013) Ptpord (176)	Q PTAWP D H G V P EY--PT P LA L RRV K T C N												
cPTPsiama D1 (I50212) (176)	Q PTAWP D H G V P EY--PT P LA L RRV K T C N												
xPTPsiama D1 (AAF43607) (176)	Q PTAWP D H G V P EY--PT P LA L RRV K T C N												
zPTPsiama D1 (CAC44759) (176)	Q PTAWP D H G V P EY--PT P LA L RRV K T C N												
hLAR D1 (NP 002831) PTPRF (176)	Q PTAWP D H G V P EY--PT P LA L RRV K K A C N												
mLAR D1 (NP 035343) Ptprf (176)	Q PTAWP D H G V P EY--PT P LA L RRV K K A C N												
rLAR_D1 (NP 062122) Ptporf (176)	Q PTAWP D H G V P EY--PT P LA L RRV K K A C N												
xLAR D1 (AAF43606) (176)	Q PTAWP D H G V P EY--PT P LA L RRV K K A C N												
hPTPdelta_D1 (NP 002830) PTPRD (176)	Q PTAWP D H G V P EH--PT P LA L RRV K T C N												
mPTPdelta D1 (D54689) (174)	Q PTAWP D H G V P EH--PT P LA L RRV K T C N												
xPTPdelta D1 (AAF43605) (176)	Q PTAWP D H G V P EH--PT P LA L RRV K T C N												
hPTPrho D1 (NP 573400) PTPRT (175)	H FTSW D F G V P CY--AT G L G V R Q K FL N												
mPTPrho D1 (NP 067439) Ptprt (175)	H FTSW D F G V P CY--AT G L G V R Q K FL N												
xPTPrho D1 (AAD50295) (175)	H FTSW D F G V P CY--AT G L G V R Q K FL N												
hPTPmu D1 (NP 002836) PTPRM (175)	H FTGW D F G V P YH--AT G L G V R Q K SK S												
mPTPmu D1 (NP 033010) Pterm (175)	H FTGW D F G V P YH--AT G L G V R Q K SK S												
hPTPkappa D1 (NP 002835) PTPRK (175)	H FTGW D F G V P YH--AT G L S V R R K LS N												
mPTPkappa D1 (NP 033009 (revised)) Ptokr (175)	H FTGW D F G V P YH--AT G L S V R R K LS N												
hPTPlamda D1 (NP 005695) PTPRU (171)	H PTAWP E H G V P YH--AT G LA L RRV K AS T												
mPTPlamda D1 (NP 035344) Ptprl (171)	H PTAWP E H G V P YH--AT G LA L RRV K AS T												
rPTPpsi_D1 (AAB42210) Ptpru Fraam (171)	H PTAWP E H G V P YH--AT G LA L RRV K AS T												
cPTPaloha D1 (AAB04150) (181)	H PTSW D F G V P FT--P I GL L K L KK V K A C N												
hPTPaloha D1 (NP 002827) PTPRA (181)	H PTSW D F G V P FT--P I GL L K L KK V K A C N												
mPTPaloha D1 (AAK56109) Ptora (181)	H PTSW D F G V P FT--P I GL L K L KK V K A C N												
rPTPaloha D1 (NP 036895) Ptora (181)	H PTSW D F G V P FT--P I GL L K L KK V K A C N												
zPTPaloha D1 (NP 571963) pтора (181)	H PTSW D F G V P FT--P I GL L K L KK V K A C N												
xPTPaloha D1 (AAA17990) (181)	H PTSW D F G V P FT--P I GL L K L KK V K A C N												
hPTPension D1 (NP 006495) PTPRE (180)	H PTSW D F G V P FT--P I GL L K L KK V K T LN												
mPTPension D1 (NP 035342) Ptpre (180)	H PTSW D F G V P FT--P I GL L K L KK V K T LN												
rPTPension D1 (XP 215102) Ptpore (180)	H PTSW D F G V P FT--P I GL L K L KK V K T LN												
hPTPqamma D1 (NP 002832) PTPRG (192)	H PTQW D M G V P EY--AL P LT V RR S SA R												
mPTPqamma D1 (NP 033007) Ptpoq (192)	H PTQW D M G V P EY--AL P LT V RR S SA R												
rPTPqamma D1 (NP 599183) Ptpoq (196)	H PTQW D M G V P EY--AL P LT V RR S SA R												
cPTPqamma D1 (Q98936) (192)	H PTQW D M G V P EY--AL P LT V RR S SA R												
hPTPzeta D1 (NP 002842) PTPRZ1 (194)	H PTQW D M G V P EY--SL P L T V R KA AY A K												
rPTPzeta D1 (NP 037212) Ptporz1 (194)	H PTQW D M G V P EY--SL P L T V R KA AY A K												
cPTPzeta D1 (AAA49015) (187)	H PTQW D M G V P EY--SL P L T V R KA AY A K												
xPTPzeta D1 (BAA97445) (187)	H PTQW D M G V P EY--SL P L T V R KA AY A K												
hCD45 D1 (NP 002829) PTPRC (180)	Q PTSW D H G V P ED--P H LL L K L RR R NA F S												
mCD45 D1 (NP 035340) Ptporc (180)	Q PTSW D H G V P ED--P H LL L K L RR R NA F S												
rCD45_D1 (XP 213985) Ptporc (180)	Q PTSW D H G V P ED--P H LL L K L RR R NA F S												
cCD45 D1 (A54080) (180)	Q PTSW D H G V P ED--P H LL L K L RR R NA F S												
cypcCD45 D1 (BAA92179) (177)	Q PTSW D H G V P ED--P S LL L K L RR R NS F K												
fuCD45 D1 (CAB96211) (180)	Q PTSW D H G V P ED--P H LL L K L RR R NS F K												
sharkCD45 D1 (T43148) (180)	Q PTSW D H G V P ED--P H LL L K L RR R NS F K												
hDEP1 D1 (NP 002834) PTPRJ (176)	H FTSW D F G V P DT--T D LL I N R Y L RD Y M K Q												
rDEP1 D1 (NP 058965) Ptpri (176)	H FTSW D F G V P DT--T D LL I N R Y L RD Y M K Q												
mDEP1 D1 (NP 033008) Ptpri (176)	H FTSW D F G V P DT--T D LL I N R Y L RD Y M K Q												
hGLEPP1_D1 (NP 109592) PTPRO (176)	N YTA W P D H G V P TANA A ES L Q V Y V HM R Q Q AT												
rGLEPP1_D1 (NP 059032) Ptpro (176)	N YTA W P D H G V P TANA A ES L Q V Y V HM R Q Q AT												
mPTPphi D1 (NP 035346) Ptpro (176)	N YTA W P D H G V P TANA A ES L Q V Y V HM R Q Q AT												
rabPTPoc D1 (AAB16824) (176)	N YTA W P D H G V P TANA A ES L Q V Y V HM R Q Q AT												
hPTPbeta D1 (NP 002828) PTPRB (179)	H YTV D P D H G V P ET--T Q S L I Q VR T Y D Y I N R												
mPTPbeta D1 (NP 084204) Ptprb (179)	H YTV D P D H G V P ET--T Q S L I Q VR T Y D Y I N R												
rPTPbeta D1 (XP 235156 (revised)) (179)	H YTV D P D H G V P ET--T Q S L I Q VR T Y D Y I N R												
hPTPS31 D1 (AR073855) PTPGMC1 (177)	N YTA W P E H G V P EN--S A PL I H V K L W R AS R												
rPTPGMC1 D1 (NP 075214) Ptpoq (177)	N YTA W P E H G V P EN--S A PL I H V K L W R AS R												
hSAP1_D1 (NP 002833) PTPRH (178)	H YQ A W D H G V P SS--P D T L LA R WM R Q W L D Q												
mSAP1 D1 (BAC37443) (178)	H YQ A W D H G V P SS--P D T L LA R WM R Q W L D Q												
rPTPBEM2 D1 (NP 598276) (178)	H YQ A W D H G V P SS--P D T L LA R WM R Q W L D Q												
mPTPESP_D1 (NP_031981) Esp (178)	Q PT T W D H S V P EA--P S S L A L Y E LV Q EV K A												

VectorNTI Screen View - Alignment_195_Vert_PTP_Domains_D1_and_D2 (VNTI 8.0).apr

rOSTPTP D1 (NP 149090) Eso (178)	QPTWDFDSVPEA--PSSLLAVLVEQEQVQA-----TQGKGLIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hPCPTP1 D1 (NP 002840) PTPRR (174)	WVTSWDFDKTDS--AQPQLQMLDVEDRDLA-----SQGRGVVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rPCPTP1 D1 (NP 446046) Ptprr (174)	WVTSWDFDKTDS--AQPQLQMLDVEDRDLA-----SEGRGVVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mPTPSL D1 (NP 035347) Ptprr (174)	WVTSWDFDKTDS--AQPQLQMLDVEDRDLA-----SEGRGVVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hSTEP D1 (NP 116710) PTPN5 (174)	WFTSWDFDKTDR--APPPLHLHREVEEAAQQE-----GPHCSPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mSTEP D1 (NP 038671) Pton5 (174)	WFTSWDFDKTDR--APPPLHLHREVEEAAQQE-----GPHCSPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rSTEP D1 (NP 062126) Pton5 (174)	WFTSWDFDKTDR--APPPLHLHREVEEAAQQE-----GPHCSPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hHePTP D1 (NP 002823) PTPN7 (172)	LPSAWDFDQTES--AGPPLRLVAEVEETP-ET-----AAHPGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mHePTP D1 (NP 796055) Pton7 (172)	LPSAWDFDQTES--AGPPLRLVAEVEETP-ET-----AAHPGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rLCPTP D1 (P49445) Pton7 (172)	LPSAWDFDQTES--AGPPLRLVAEVEETP-ET-----AAHPGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hLyPTP D1 (NP 057051) PTPN22 (185)	HVKNWDFDVPSS----DPILQLLWDMRCYQ-----EDDSVVICVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mPEP D1 (NP 033005) Pton8 (185)	HVKNWDFDVPSS----DPILQLLWDMRCYQ-----EDDSVVICVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hPEST D1 (NP 002826) PTPN12 (189)	HVVNWDFDVPSS----FDSLDMMLSMRKYQ-----EHEDVICVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rRKPTP D1 (NP 476456) Pton12 (189)	HVVNWDFDVPSS----FDSLDMMLSMRKYQ-----EHEDVICVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mPEST D1 (NP 035333) Pton12 (189)	HVVNWDFDVPSS----FDSLDMMLSMRKYQ-----EHEDVICVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hBDP1 D1 (NP 055184) PTPN18 (186)	QVMSWDFDGVFSS--PDHLLMVEEARLQGG-----SGPFLCIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mPTPK1_D1 (NP 035336) Pton18 (186)	QVMSWDFDGVFSS--SDHLLTMVEEARCLQG-----LGPFLCIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rPTP20 D1 (AAC52896) (186)	QVMSWDFDGVFSS--SDHLLTMVEEARCLQG-----LGPFLCIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hSHP1 D1 (NP 002822) PTPN6 (193)	QVLSWDFDGVFSE--PGGGLSLDQINQRQES-----LPHAGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mSHP1 D1 (NP 038573) Hcph (193)	QVLSWDFDGVFSE--PGGGLSLDQINQRQES-----LPHAGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rSHP1_D1 (NP 446360) Ptoh6 (193)	QVLSWDFDGVFSE--PGGGLSLDQINQRQES-----LPHAGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
zSHP1 D1 (AAH44414) (193)	QVLSWDFDGVFQE--PGGGLSLDQINQRQEE-----LRSSGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rVPTPN6c D1 (BAA95199) (162)	QVLSWDFDGVFNE--PGGGLSLDQINQRQES-----IPDTPGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hSHP2 D1 (NP 002825) PTPN11 (196)	HFRWDFDGVFSD--PGGLLDLLEEHKQES-----IMDAGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mSHP2 D1 (NP 035332) Pton11 (200)	HFRWDFDGVFSD--PGGLLDLLEEHKQES-----IVDAGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rSHP2_D1 (NP 037220) Pton11 (196)	HFRWDFDGVFSD--PGGLLDLLEEHKQES-----IVDAGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
cSHP2 D1 (JCS167) (196)	HFRWDFDGVFSD--PGGLLDLLEEHKQES-----ISDAGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
zSHP2 D1 (AAH45328) (196)	HFRWDFDGVFSD--PGGLLDLLEEHKQES-----ITDAGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
xSHP2 D1 (A56561) (196)	HFRWDFDGVFSD--PGGLLDLLEEHKQES-----ITDAGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rVPTPN6b D1 (BAA95198) (167)	HFKTWDFDGVFSD--PGGLLDLLEEHKQES-----IPEAGPIIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hPTPD1 D1 (NP 008970) PTPN21 (184)	QVTDWDFEHCEDD--LKGFLSLLEEQSVRRHTNSTS--D-PQSPNPLVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mPTPRL1 D1 (NP 036007) Pton21 (184)	QVTDWDFEHCEDD--LKGFLSLLEEQSVRRHTNSTS--E-PKSHNPLVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rPTP2E D1 (NP 598229) Pto2E (184)	QVTDWDFEHCEDD--LKGFLSLLEEQSVRRHTNSTS--E-PRSPNPLVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hPTPD2 D1 (NP 005392) PTPN14 (183)	QVTDWDFEHCEDD--VQGFSLLEEQSVRRHTNSML--EGTKNRHPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mPTP36 D1 (NP 033002) Pton14 (183)	QVTDWDFEHCEDD--VQGFSLLEEQSVRRHTNSML--EGTKNRHPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rPTPD2 D1 (XP 223062 (revised)) (183)	QVTDWDFEHCEDD--VQGFSLLEEQSVRRHTNSVL--EGVKTRHPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hMEG1 D1 (NP 002821) PTPN4 (178)	QVLAWDFDGVFDD--SSDFLDFVCHRNKR-----ACKKEPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mMEG1 D1 (NP 064317) Pton4 (178)	QVLAWDFDGVFDD--SSDFLDFVCHRNKR-----AGKDEPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
zMEG1 D1 (CAD43435) (173)	QVLAWDFDGVFDD--STDFLDFVAVLNKR-----AGKDEPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hPTPH1 D1 (NP 002820) PTPN3 (178)	QVVAWDFDGVFDD--SSDFLDFVNYRSLR-----VDSGPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mPTPH1 D1 (XP 143789) Pton3 (178)	QVVAWDFDGVFDD--SSDFLDFVNYRSLR-----VDGEPVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hPTPBAS D1 (NP 006255) PTPN13 (178)	NFTAWDFDHTSQ--PDDLTFISYRHI-----HRSGPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mPTPBAS D1 (NP 035334) Pton13 (178)	NFTAWDFDHTSQ--PDDLTFISYRHI-----RRSGPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
bPTPA14 D1 (NP 777015) PTPN13 (178)	NFTAWDFDHTSQ--PDDLTFISYRHI-----HRSGPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hPTP1A D1 (AL050040) PTPN20 (177)	QFTKWDFDGTAS--ADSFLLKRYRKS-----HITGPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mPTP1Typ_D1 (NP 033004) Pton20 (176)	QFTKWDFDGTAS--ADSFLLKRYRKS-----HITGPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
cPTP1B D1 (O13016) (175)	HVTTWDFDGVFES--PASFLLFKVRESGS-----LNPEYGVVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hPTP1B D1 (NP 002818) PTPN1 (175)	HVTTWDFDGVFES--PASFLLFKVRESGS-----LSPHGGPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mPTP1B D1 (NP 035331) Pton1 (175)	HVTTWDFDGVFES--PASFLLFKVRESGS-----LSPHGGPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rPTP1B D1 (NP 036769) Pton1 (175)	HVTTWDFDGVFES--PASFLLFKVRESGS-----LSPHGGPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
zPTP1B D1 (NP 570999) pto1b (173)	HVTTWDFDGVFES--PASFLLFKVRESGS-----LSPHGGPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hTCTPT D1 (NP 002819) PTPN2 (174)	HVTTWDFDGVFES--PASFLLFKVRESGS-----LNPDHGPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mTCTPT D1 (NP 033003) Pton2 (174)	HVTTWDFDGVFES--PASFLLFKVRESGS-----LNPDHGPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rTCTPT D1 (NP 446442) Pton2 (174)	HVTTWDFDGVFES--PASFLLFKVRESGS-----LNPDHGPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
zTCTPT D1 (AAH44373) (173)	HVTTWDFDGVFES--PASFLLFKVRESGS-----LGMGQPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hMEG2 D1 (NP 002824) PTPN9 (179)	QVLSWDFDGVFSS--AASLIDFVRVNRQSLAVSNMGRSKGQCPPEPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mMEG2_D1 (NP 062625) Pton9 (179)	QVLSWDFDGVFSS--AASLIDFVRVNRQSLAVSNMGRSKGQCPPEPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
xPTPX10 D1 (B53978) (179)	QVMSWDFDGVFSS--ASALIDFVRVNRQSLAVSNMGRSKGQCPPEPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
xPTPX1 D1 (AAH43621) (179)	QVMSWDFDGVFSS--ASALIDFVRVNRQSLAVSNMGRSKGQCPPEPIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hHDPTP D1 (NP 056281) PTPN23 (183)	HFFTWFELGLDS--PNSNLRDQEQHAHYLHQR-----PLHTFIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mHDPTP D1 (AAH22721) (183)	HFFTWFELGLDS--PNSNLRDQEQHAHYLHQR-----PLHTFIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rPTPTD14 D1 (T14355) (183)	HFFTWFELGLDS--PNSNLRDQEQHAHYLHQR-----PLHTFIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hIA2 D1 (NP 002837) PTPRN (179)	HFLSWFACETAS--TRPFLDRRKNKCYR-----GRSCIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
mIA2 D1 (NP 033011) Ptprr (179)	HFLSWFACETAS--TRPFLDRRKNKCYR-----GRSCIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
rIA2_D1 (NP 446333) Ptprr (179)	HFLSWFACETAS--TRPFLDRRKNKCYR-----GRSCIVHCSAGVGRGTGFIATSLRRLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL

VectorNTI Screen View - Alignment_195_Vert_PTP_Domains_D1_and_D2 (VNTI 8.0).apr

blA2 D1 (P56722) Ptdrn (179)	HFLSWEAECTFAS--TRP	LDLRRKVNKCYR-----	GRSCILVHCS	DGAGRTGTYV	LDLDMVNNR	AKG--VKE	LDIAATLEHVRDORPGLVRSKQ	QEF	FALTAAAEEN
hIA2beta D1 (NP 002838) PTPRN2 (179)	HFLSNYDRGVSS--SRSL	LDLRRKVNKCYR-----	GRSCILVHCS	DGAGRTGTYV	LDLDMVNNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQ	QEF	FALTAAAEEN
macnelA2beta D1 (O02695) (179)	HFLSNYDRGVSS--SRSL	LDLRRKVNKCYR-----	GRSCILVHCS	DGAGRTGTYV	LDLDMVNNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQ	QEF	FALTAAAEEN
mPTPNP D1 (P80560) Ptdrn2 (179)	HFLSNYDRGVSS--TRSL	LDLRRKVNKCYR-----	GRSCILVHCS	DGAGRTGTYV	LDLDMVNNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQ	QEF	FALTAAAEEN
rPTPNE6 D1 (NP 113788) Ptdrn2 (179)	HFLSNYDRGVSS--TRSL	LDLRRKVNKCYR-----	GRSCILVHCS	DGAGRTGTYV	LDLDMVNNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQ	QEF	FALTAAAEEN
hCD45 D2 (NP 002829) PTPRC (199)	QNTNNSVEQFAE--PKEL	ISMVQVKKQLPKQNSSEG	---KHHKST	LLHHRD	CSQQQTGL	CAFLNLL	LSAET--	EVVDV	QVVKALRKARPGMVS
mCD45 D2 (NP 035340) Ptdrc (199)	QCTTWKGEFAE--PKDL	VLTQNKQKLPKSPSEG	---KYHKS	SLVHRD	CSQQQTGL	CAFLNLL	LSAET--	EDVDV	QVVKALRKARPGMVS
rcD45_D2 (XP 213985) Ptdrc (199)	QCTTWKGEFAE--PKDL	VLTQNKQKLPKSPSEG	---KYHKS	SLVHRD	CSQQQTGL	CAFLNLL	LSAET--	EDVDV	QVVKALRKARPGMVS
ccD45 D2 (A54080) (199)	QCHKNGLDVPE--PKDL	VDMVLSKQKVPSPASEDS	---RNSRS	VFLVHC	CDSSQQQ	WCVL	CMNTLL	LSAET--	EMVDV
fuCD45 D2 (CAB96211) (199)	QFLKMGKVEPEK--PQDL	ADLKEKHKRCGY	---TWRST	VIVHC	CDSSRRGAF	CAFLNLL	LSAET--	EMVDV	
cypcaCD45 D2 (BAA92179) (197)	QFLKMGRELEEN--AQEL	VMASIRRENGHYDNS	---KTRNR	VIVHC	CDSSRRGAF	CAFLNLL	LSAET--	EKL	
aotvoCD45 D2 (AAM48512) (3') (191)	QYTNNSVXXLAX--PKEL	ISMVQVKKQLPKQNSSEG	---KXHKX	SLVHRD	CSQQQTGL	CAFLNLL	LSAET--	EVVDV	
sharkCD45 D2 (T43148) (198)	HFHDWASELEED--PSNF	TMRSEKELSLTQPEE	---SSLSP	SLVHC	CDGAKTGV	YAWILL	DNADT--	ENVL	
cPTPaloha D2 (AAB04150) (181)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---QSGNH	PIVHC	SAGAGRTGTF	CAFLNLL	LSAET--	EGL	
hPTPaloha D2 (NP 002827) PTPRA (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---QSGNH	PIVHC	SAGAGRTGTF	CAFLNLL	LSAET--	EGL	
mPTPaloha D2 (NP 033006) Ptdra (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---QSGNH	PIVHC	SAGAGRTGTF	CAFLNLL	LSAET--	EGL	
rPTPaloha D2 (NP 036895) Ptdra (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---QSGNH	PIVHC	SAGAGRTGTF	CAFLNLL	LSAET--	EGL	
xPTPaloha D2 (AAA17990) (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---QSGNH	PIVHC	SAGAGRTGTF	CAFLNLL	LSAET--	EGL	
zPTPaloha D2 (NP 571963) ptdra (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---QSGNH	PIVHC	SAGAGRTGTF	CAFLNLL	LSAET--	EGL	
rvPTPR4b D2 (BAA95196) (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---QSGNH	PIVHC	SAGAGRTGTF	CAFLNLL	LSAET--	EGL	
hPTPepsilon D2 (NP 006495) PTPRE (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---QSGNH	PIVHC	SAGAGRTGTF	CAFLNLL	LSAET--	EGL	
mPTPepsilon D2 (NP 035342) Ptdre (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---QSGNH	PIVHC	SAGAGRTGTF	CAFLNLL	LSAET--	EGL	
rPTPepsilon D2 (XP 215102) Ptdre (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---QSGNH	PIVHC	SAGAGRTGTF	CAFLNLL	LSAET--	EGL	
orylaPTPepsilon D2 (BAC06424) (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---QSGNH	PIVHC	SAGAGRTGTF	CAFLNLL	LSAET--	EGL	
rvPTPR4a D2 (BAA95190) (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---QSGNH	PIVHC	SAGAGRTGTF	CAFLNLL	LSAET--	EGL	
hPTPkappa D2 (NP 002835) PTPRK (180)	QNLGASREVPGS--KRSF	LKLLQLEKQWEEC	---EEGE	RTLHL	CLNGGRRGM	CAFLNLL	LSAET--	QNV	
mPTPkappa D2 (NP 033009) Ptdrk (180)	QNLGASREVPGS--KRSF	LKLLQLEKQWEEC	---EEGE	RTLHL	CLNGGRRGM	CAFLNLL	LSAET--	QNV	
rvPTPR2B D2 (BAA95194) (180)	QNLGASREVPGS--KRSF	LKLLQLEKQWEEC	---EEGE	RTLHL	CLNGGRRGM	CAFLNLL	LSAET--	QNV	
hPTPlamda D2 (NP 005695) PTPRU (183)	QFLRNSARDTPDS--KRAF	LHLDAEDKWAQES	---GDERT	VHLCL	NGGRRGT	CACATV	LEMRC--	HNL	
mPTPlamda D2 (NP 035344) Ptdrl (183)	QFLRNSARDTPDS--KRAF	LHLDAEDKWAQES	---GDERT	VHLCL	NGGRRGT	CACATV	LEMRC--	HNL	
mPTPmu D2 (NP 002836) PTPRM (180)	QFLGWMRDTPVPS--KRSF	LKLLQLEKQWEEYN	---GGEPT	VHLCL	NGGRRGT	CALISV	ICMRH--	QRT	
mPTPmu D2 (NP 033010) Ptdrm (180)	QFLGWMRDTPVPS--KRSF	LKLLQLEKQWEEYN	---GGEPT	VHLCL	NGGRRGT	CALISV	ICMRH--	QRT	
rPTPmu D2 (XP 237546 (revised)) (180)	QFLGWMRDTPVPS--KRSF	LKLLQLEKQWEEYN	---GGEPT	VHLCL	NGGRRGT	CALISV	ICMRH--	QRT	
hPTPrho D2 (NP 057400) PTPRT (180)	QILGWARDTPPS--KRSF	LKVVRREKQWQEQYD	---GREGR	VHLCL	NGGRRGT	CALISV	ICMRH--	QNI	
mPTPrho D2 (NP 067439) Ptdrt (180)	QILGWARDTPPS--KRSF	LKVVRREKQWQEQYD	---GREGR	VHLCL	NGGRRGT	CALISV	ICMRH--	QNI	
cPTPsiama D2 (I50212) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
hLAR D2 (NP 002831) PTPRF (182)	QFTDWEQGVVFKT--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
mLAR D2 (NP 035343) Ptdrf (182)	QFTDWEQGVVFKT--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
rLAR D2 (NP 062122) Ptdrf (182)	QFTDWEQGVVFKT--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
xLAR D2 (AAF43606) (182)	QFTDWEQGVVFKT--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
zLAR D2 (CAC44758) (182)	QFTDWEQGVVFKT--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
rvPTPR2Aa D2 (BAA95188) (182)	QFTDWEQGVVFKT--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
hPTPdelta D2 (NP 002830) PTPRD (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
mPTPdelta D2 (D54689) (181)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
xPTPdelta D2 (AAF43605) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
rvPTPR2Ab D2 (BAA95191) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
hPTPsiama D2 (NP 002841) PTPRS (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
mPTPsiama D2 (NP 035348) Ptdrs (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
xPTPsiama D2 (AAF43607) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
zPTPsiama D2 (CAC44759) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
rPTPsiama D2 (NP 062013) Ptdrd (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
rvPTPR2Ac D2 (BAA95193) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---QDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
hPTPaamma D2 (NP 002832) PTPRG (186)	QCPKWFNPDAFIS--STFEL	LVNFKKEALT	---RDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
mPTPaamma D2 (NP 033007) Ptdra (186)	QCPKWFNPDAFIS--STFEL	LVNFKKEALT	---RDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
rPTPaamma D2 (NP 599183) Ptdra (178)	YVLEVRHFQAFIS--STFEL	LVNFKKEALA	---RDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
rvPTPR5b D2 (BAA95197) (186)	QCPKWFNPDAFIS--STFEL	LVNFKKEAST	---RDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
cPTPaamma D2 (Q98936) (186)	QCPKWFNPDAFIS--STFEL	LVNFKKEALT	---RDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
hPTPzeta D2 (NP 002842) PTPRZ1 (185)	QCPKWFNPDSFIS--KTFEL	LSIKKEEAA	---RDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
cPTPzeta D2 (AAA49015) (185)	QCPKWFNPDSFIS--KTFEL	LSIKKEEAA	---RDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
mPTPzeta D2 (XP 133090) Ptdrz1 (185)	QCPKWFNPDSFIS--KTFEL	LSIKKEEAA	---RDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
rPTPzeta D2 (NP 037212) Ptdrz1 (185)	QCPKWFNPDSFIS--KTFEL	LSIKKEEAA	---RDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
xPTPzeta D2 (BAA97445) (185)	QCPKWFNPDSFIS--KTFEL	LSIKKEEAA	---RDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
rvPTPR5a D2 (BAA95195) (181)	QSPRWFNPDSFIS--KTFEL	LSIKKEEAA	---RDGP	ITVHC	SAGAGRTGTF	ITLSIVL	RRY--	EGV	
Consensus (237)	QFTWPDHGVV	LLFI	V	GP	IVVHCSAGVGRGTGTF	IDMLE	L	E	VDFV