

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	HLTPVEGV	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	VLQTI EGD	TNSDYINGNYIDGY	-----HRPNHYIAAQGP																																																																															
hPTPrho	ADLLQHITQMKRGG	YGFKEEYEA	LEGTA	SWDTAKEDENR	NKN	RYGN	IISYDHSRV	RLVLDGD	PHSDYINASYIDGY	-----HRPRHYIAAQGP																																																																															
hPTPlamda	ADLLQHINQMKTAE	YGFKEEYESF	FEGWDA	T	-----	KKKDKVKGS	QEPMPAYDRH	RVKLLHPLMG	PNADYINASYIDGY	-----HRSNHFAAQGP																																																																															
hPTPdelta	LELADHIERLKANDN	LKFSQEYESI	D	PGQQF	-----	TWEHSNLEVN	KPKRYAN	VIAYDHSRV	LSAIEGI	PGSDYINASYIDGY	-----RKQNAZIAAQGP																																																																														
hPTPsigma	ADMAEHTERLKANDS	LKLSQEYESI	D	PGQQF	-----	TWEHSNLEVN	KPKRYAN	VIAYDHSRV	LQPIEGI	MGSDYINASYIDGY	-----RQNAZIAAQGP																																																																														
hPTPgamma	KQFVKHIGELYSNNQ	HGFSDFEEV	Q	RCTADMN	I	TAEHSNHPEN	KHKRYIN	I	LAIDHSRV	KLRLPLGKDS	KHSDYINASYIDGY	-----NKAKAZIAAQGP																																																																													
hPTPzeta	KHFPKHVADLHASSGF	TEEFETLKEFYQE	V	QSCSTVDLGI	-----	TADSSNHPDN	KHKRYIN	I	IVAYDHSRV	KLQAIAEKDG	KLTDYINASYIDGY	-----NRPKAZIAAQGP																																																																													
hLAR	TDLADNIERLKANDG	LKFSQEYESI	D	PGQQF	-----	TWENSNLEVN	KPKRYAN	VIAYDHSRV	LTSIDGV	PGSDYINASYIDGY	-----RKQNAZIAAQGP																																																																														
hCD45	DILLETYKRIADG	RLFLAEFQSI	PRVFSKF	-----	PIKEAR	KPFN	KNR	RYAN	IVAYDHSRV	VLSEINGD	AGSNYINASYIDGF	-----KEPRKZIAAQGP																																																																													
hGLEPP1	DDFDAYIKDMAKSD	YKFSLQFEEL	KLIGLDI	-----	PHFAAD	PLNRCK	RYTN	ILPYDFSR	VLVSMNEE	EGADYINASYIPGY	-----NSPQEZIAAQGP																																																																														
hTPS31	KSLFQHVVEELCTNNN	LKFSQEEFSEL	KFLQLD	-----	SSTAD	PLWNR	AKN	RYFN	IKPYNNR	VKL	IADASV	PGSDYINASYISGY	-----LCPNEZIAAQGP																																																																												
hDEP1	ENFEAYFKKQADS	CGFAEEYEDL	KLVGISQ	-----	PKYAAEL	AENR	GKN	RYNN	VLPI	DSRV	KL	SVQTHS	-----	DDYINASYMPGY	-----HSKKDFIAAQGP																																																																										
hPTPbeta	NQFEGHFMKLQADS	YLLSKEYEEL	KDVG	RNQ	-----	SCD	IALLPEN	RGN	RYNN	ILPYD	ATRV	KL	SNVDDD	-----	PCSDYINASYIPGN	-----NFRREZIAAQGP																																																																									
hSAP1	EDFADHVRKNERDS	CGFADEYQQL	SLVGH	SQ	-----	SQMVAS	ASENN	AKN	RYRN	VL	PDWSRV	PL	KPIHEE	-----	PGSDYINASFMPGL	-----WSPQEZIAAQGP																																																																									
hSTEP	SRVLQAEELHDEKALDP	FLLQAEFFFE	PMNFVD	-----	PKEYDI	PGLVR	KNR	RYKT	ILPN	HSRV	CL	TS	PPDD	-----	PLSSYINASYIRGYG	-----GEEKYIAAQGP																																																																									
hPCPTP1	SRLLTRSQLRDRVASS	HLLQSEFMEI	PMNFVD	-----	PKEYDI	PRHGT	KNR	RYKT	ILPN	PLSR	VCL	LR	PKVD	-----	SLSTYINASYIRGS	-----GKEKAFIAAQGP																																																																									
hHePTP	GHPLTRWALQRQPPSP	KLLEEF	FLK	PSNFVS	-----	PEDLD	IPGH	ASK	RYKT	ILPN	QSRV	CL	GRA	QSQE	-----	DGDYINASYIRGYD	-----GKEKYZIAAQGP																																																																								
hSHP1	ADINRVLELNKKQES	EDTAKAG	FWEFESL	Q	QKQEV	KNLH	-----	QRLEG	QR	PN	KGK	RYKN	IL	PF	DSRV	IL	QGR	DSN	-----	PGSDYINASYIKN	-----QLLGP	ENAKTYIASQGP																																																																			
hSHP2	AEIESRVRELSKLAETT	DKVKQGF	WEEFETL	Q	QKQEC	LLY	-----	SRKEG	QR	EN	KN	RYKN	IL	PF	DHTR	VL	HD	GP	NE	-----	PVSDYINAN	IMPEFETK	CNNSKPKKSYIAAQGP																																																																		
hPEST	EILRKFIQRVQAMKSP	PDHNGED	FARDFMR	RL	ST	KYRTE	KI	YPT	AT	GE	KE	EN	V	K	RYKD	IL	PF	DHTR	SV	KL	L	KT	PS	-----	QDSDYINAN	FI	KG	-----	YGP	KAYIAAQGP																																																											
hLyPTP	EILQKFLDEAKKGI	TK	-----	EEFLAN	FLKL	QR	ST	KYKAD	KYPT	VA	E	KPK	N	RYKN	RYKD	IL	PF	DHTR	SV	KL	L	KT	PS	-----	EDSSYINAN	FI	KG	-----	YGP	KAYIAAQGP																																																											
hBDP1	DSARSFLERLEARGGREG	AVLAG	FSDI	Q	ACS	AAWK	AD	GV	ST	V	AG	SR	PN	RYKN	RYKD	IL	PF	DHTR	SV	KL	L	KT	PS	-----	GHSDYING	N	F	IR	GV	-----	DGSL	YIAAQGP																																																									
hTPD1	ATNDRCKIL	LEQRLEQG	-----	MVFT	EYER	IL	KKRL	VDG	-----	ECSTAR	L	PN	AER	NR	RYFD	VL	PD	Y	DSRV	EL	VP	T	KE	-----	NTGYINASH	I	K	VS	-----	SGI	EWYIAAQGP																																																										
hTPD2	VTMDERFRT	LKKLEEG	-----	MVFT	EYEQ	IL	PKK	KANG	-----	IF	ST	AAL	PN	AER	NR	RYFD	VL	PD	Y	DSRV	EL	VP	T	KE	-----	NTGYINASH	I	K	V	V	-----	GA	WHYIAAQGP																																																								
hMEG1	HSLE	RESMIQLA	EGLITG	-----	TVLT	Q	DFD	QLY	-----	TM	SC	AK	LP	Q	N	SKN	RYRD	IL	SP	Y	DSRV	EL	VP	T	KE	-----	NEDYINAN	Y	N	M	E	IP	-----	SSS	I	NY	IAAQGP																																																				
hTPPH1	DTLEG	SMAL	KKGL	ESG	-----	TVL	IQ	FEQLY	-----	AI	T	FA	KL	PN	L	D	KNR	RYKD	IL	PF	DHTR	VL	HD	GP	NE	-----	NEDYINAN	Y	N	M	E	IP	-----	AAN	LV	NY	IAAQGP																																																				
hPTPBAS	KSVIRVLRGLDQGI	-----	PSKE	LEN	QL	EL	KPLD	-----	QCL	I	GT	K	PN	RR	KNR	RYKD	IL	PF	DHTR	VL	HD	GP	NE	-----	EGGYINAS	F	I	K	IP	V	-----	KEE	F	Y	IAAQGP																																																						
hPTP1B	MEMEKFEFGLDKSGS	-----	WAAI	YQDI	RL	HE	ASDF	-----	PCRV	A	KL	PN	KNR	RYKN	RYDN	VS	PF	DHTR	SV	KL	L	Q	NE	-----	DNDYINAS	L	K	M	E	-----	E	A	Q	R	S	YIAAQGP																																																					
hTCPTP	TTIEREFEE	LDTQRR	-----	WQ	PL	Y	LEI	RNESH	DY	-----	PHR	V	A	K	F	PN	RR	NR	RYRD	VS	PF	DHTR	SV	KL	L	Q	NA	-----	ENDYINAS	L	V	D	I	E	-----	E	A	Q	R	S	YIAAQGP																																																
hMEG2	MTIQELVDYV	NARQKQ	-----	GI	YEE	EDI	REN	PV	-----	T	F	H	C	S	M	P	GN	LE	KN	RYGD	V	PC	L	D	Q	T	RV	KL	K	R	S	G	H	T	-----	Q	T	D	Y	IN	AS	F	M	D	G	Y	-----	K	K	N	A	Y	I	G	T	Q	GP																																
hIA2	HMIL	LAYMED	HLLRNRDR	-----	LAK	EW	QAL	C	AY	Q	A	E	P	N	-----	T	C	A	T	A	Q	G	E	G	N	I	K	K	N	R	H	P	D	F	L	P	D	H	A	R	I	K	L	K	V	E	S	S	P	-----	R	S	D	Y	IN	AS	P	I	E	H	D	-----	P	R	M	A	Y	I	G	T	Q	GP																	
hIA2beta	HMIL	SYMED	HLLKKNR	-----	L	E	K	E	W	Q	A	E	P	N	-----	S	S	F	A	Q	R	E	N	V	P	K	N	R	S	L	A	V	L	T	Y	D	H	S	R	V	L	L	K	A	E	N	S	H	S	-----	H	S	D	Y	IN	AS	P	I	M	D	H	-----	P	R	N	P	A	Y	I	G	T	Q	GP																
hPTPTyp	TAIKD	CL	L	LE	E	K	T	A	-----	Y	D	I	M	Q	E	F	M	A	L	E	L	K	L	P	G	-----	E	F	Y	S	G	N	Q	P	S	N	R	E	K	N	R	T	S	S	I	-----	S	D	Y	IN	AS	Y	I	R	I	V	N	-----	C	G	E	E	F	Y	I	G	T	Q	GP																				
hHDPTP	ERL	R	L	Q	Q	E	L	E	A	F	R	G	L	G	D	V	-----	G	A	L	D	T	V	W	R	E	L	Q	A	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	IN	AS	C	V	E	G	L	S	-----	P	Y	C	P	L	V	A	T	Q	GP

Consensus - (amino acid identity 100%, 90%, 80%): E N KNR Y D R V 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	GP		
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	Q	I	P	Y	D	F	N	R	V	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	GP			
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	Y	R	S	R	W	-----	T	Q	H	I	G	N	Q	E	E	N	K	S	R	N	S	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	GP					
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	N	R	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	P
hPTPzeta	S	H	I	H	A	Y	V	N	A	L	I	P	G	P	A	-----	G	K	T	K	L	E	K	Q	F	L	V	S	Q	N	I	Q	Q	-----	S	D	Y	S	A	A	L	K	Q	C	N	R	E	K	N	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	Q	S	N	E	F	I	T	Q	H	P				
hPTPsigma	R	S	L	Y	A	I	Q	K	L	A	Q	V	E	T	-----	E	H	V	T	G	M	E	L	F	K	R	L	A	N	S	K	A	H	T	-----	S	R	F	I	S	A	N	L	P	C	N	K	F	K	N	R	L	V	N	I	M	P	Y	E	S	T	R	V	C	L	Q	P	I	R	G	V	-----	E	G	S	D	Y	V	N	A	S	F	I	D	G	Y	-----	R	Q	K	A	Y	I	A	Q			

PTP domains (excluding domains D2)

Amino acid	α2				β4	β5	β6	β7	β8	β9	β10	β11	#180
	#90	#100	#110	#120	#130	#140	#150	#160	#170	#180			
hPTPalpha	K E E T V N D F W R M I W E Q N T A T I V M V T N L K E R K - E C K C A Q Y W P D - - - Q G C W T Y G N I R V S V E D V T V L V D Y T V R K F C I Q Q V G D M T N - - - - - R K P Q R L I T Q F H F T S W P D F G V P F T												
hPTPepsilon	K Q E T V N D F W R M I W E Q K S A T I V M L T N L K E R K - E E K C H Q Y W P D - - - Q G C W T Y G N I R V C V E D C V L V D Y T I R K F C I Q P Q L P D G - - - - - C K A P R L V S Q L H F T S W P D F G V P F T												
hPTPkappa	V H E T V Y D F W R M I W E Q E S A C I V M V T N L V E V G - R V K C Y K Y W P - - - - - D D T E V Y G D F K V T C V E M E P L A E Y V V R T F T L E R R G - - - - - Y N E I R E V K Q F H F T G W P D H G V P Y H												
hPTPmu	M Q E T I Y D F W R M I W H E N T A S I I M V T N L V E V G - R V K C C K Y W P - - - - - D D T E I Y K D I K V T L I E T E L L A E Y V I R T F A V E K R G - - - - - V H E I R E I R Q F H F T G W P D H G V P Y H												
hPTPrho	M Q E T V K D F W R M I W Q E N S A S I V M V T N L V E V G - R V K C V R Y W P - - - - - D D T E V Y G D I K V T L I E T E P L A E Y V I R T F T V Q K K G - - - - - Y H E I R E L R L F H F T S W P D H G V P C Y												
hPTPlamda	K P E M Y D F W R M I W Q E H C S S I V M I T K L V E V G - R V K C S R Y W P - - - - - E D S D T Y G D I K I M L V K T E T L A E Y V V R T F A L E R R G - - - - - Y S A R H E V R Q F H F T A W P D H G V P Y H												
hPTPdelta	L P E T F G D F W R M I W E Q R S A T V V M M T K L E E R S - R V K C D Q Y W P S - - - - - R G T E T H G L V Q V T L L D T V E L A T Y C V R T F A L Y K N G - - - - - S S E K R E V R Q F O F T A W P D H G V P E H												
hPTPsigma	L P E T F G D F W R M I W E Q R S A T I V M M T R L E E K S - R I K C D Q Y W P N - - - - - R G T E T Y G F I Q V T L L D T I E L A T F C V R T F S L H K N G - - - - - S S E K R E V R Q F O F T A W P D H G V P E Y												
hPTPgamma	L K S T F E D F W R M I W E Q N T G I I V M I T N L V E K G - R R K C D Q Y W P T - - - - - E N S E E Y G N I I V T L K S T K I H A C Y T V R R F S I R N T K V K K G Q K G N P K G R Q N E R V I Q Y H Y T Q W P D M G V P E Y												
hPTPzeta	L K S T A E D F W R M I W E H N V E V I V M I T N L V E K G - R R K C D Q Y W P A - - - - - D G S E E Y G N F L V T Q K S V Q V L A Y Y T V R N F T L R N T K I K K G S Q - - - - - K G R P S G R V T Q Y H Y T Q W P D M G V P E Y												
hLAR	L P E T M G D F W R M I W E Q R T A T V V M M T R L E E K S - R V K C D Q Y W P A - - - - - R G T E T C G L I Q V T L L D T V E L A T Y T V R T F A L H K S G - - - - - S S E K R E L R Q F O F T A W P D H G V P E Y												
hCD45	R D E T V D F W R M I W E Q K A T I V M V T R C E E G N - R N K C A E Y W P S M - - - - - E E G T R A F G D V V V R N V N H K R C P D Y I I Q K L N I V N K K E - - - - - K A T G R E V T H I Q F T S W P D H G V P E D												
hGLEPP1	L P E T R N D F W K M V L Q Q K S Q I I V M L T Q C N E K R - R V K C D H Y W P F T - - - - - E E P I A Y G D I T V E M I S E E E Q D D W A C R H F R I N Y A D - - - - - E M Q D V M H F N Y T A W P D H G V P T A												
hPTPS31	L P G T V G D F W R M I W E T R A K T L V M L T Q C F E K G - R I R C H Q Y W P E D - - - - - N K P V T V F G D I V I T K L M E D V Q I D W T I R D L K I E R H G - - - - - D C M T V R Q C N F T A W P D H G V P E N												
hDEP1	L P N T L K D F W R M I W E K N V Y A I I M L T K C V E K G - R R K C D Q Y W P S - - - - - K Q A Q D Y G D I T V A M T S I V L V P E W T I R D T L K V I Q T - - - - - S E S H L R Q F H F T S W P D H G V P D T												
hPTPbeta	L P G T K D D F W K M I W E Q N V H N I V M V T Q C V E K G - R V K C D H Y W P A D - - - - - Q D S L Y G D L I L Q M L S E S V L P E W T I R E F K I C G E E Q - - - - - L D A H R L I R H F H Y T W P D H G V P E T												
hSAP1	L P Q T V G D F W R M I W E Q S H T L V M L T N C M E A G - R N K C H Y W P L D - - - - - S Q P C T H G L R V T L V G E E V M E N W T V R E L L L Q V E E - - - - - S K T L S V R Q F H Y Q A W P D H G V P S S												
hSTEP	I V S T V A D F W R M I W E Q E H T P I I V M I T N I E E M N - - E K C T E Y W P - - - - - E E Q V A Y D G V E I T V Q K V I H T E D Y R L R L I S L K S G T - - - - - E E R G L K H Y W F T S W P D Q K T P D R												
hPCPTP1	M I N T V D D F W Q M I W E Q E D S P V I V M I T K L E K N - E K C V L Y W P - - - - - E K R G I Y G K V E V L V I S V N E C D N Y T I R N L V L K Q G S - - - - - H T Q H V K H Y W T S W P D H K T P D S												
hHePTP	M P N T V S D F W E M I W E Q E V S L I V M L T Q L V E K G - R K C V H Y W P - - - - - T E E E T Y G P F Q I R I Q D M K E C P N Y T V R Q L T I Q Y Q E - - - - - E R R S V K H I L F S A W P D H G V P E S												
hSHP1	L E A T V N D F W Q M A W Q E N S R V I V M T T R E V E K G - R N K C V P Y W P E - - - - - V G M Q R A Y G P Y S V T N C G E H D T E Y K L R T L Q V S P L D N - - - - - G D L I R E I W H Y Q L S W P D H G V P S E												
hSHP2	L Q N T V D F W R M I W E Q N S R V I V M T T K E V E R G - R K C H R Y W P D - - - - - E Y A L K E Y G V M R V R N V N K S A A H D Y T L R E L K L S K V G Q - - - - - G N T E R T V Q Y H F R T W P D H G V P S D												
hPEST	L A N T V I D F W R M I W E Y N V V I I V M A C R E F E M G - R K C E R Y W P L Y - - - - - G E D P I T F A P F K I S C E D E Q A R T D Y F I R T L L E F Q N - - - - - E S R R L Y Q F H Y V N W P D H D V P S S												
hLyPTP	L S T L L D F W R M I W E Y S V L I I G M A C M E Y E M G - K K C E R Y W A E P - - - - - V E M Q L E F G P F S V S C E A E K R K S D Y I I R T L K V K F N S - - - - - E T R T I Y Q F H Y K N W P D H D V P S S												
hBDP1	L P H T L L D F W R L V W E F G V K V I L M A C R E I E N G - R K R C E R Y W A Q E - - - - - Q E L Q T G L F C I T L I K E K W L N E I M L R L T K V T F Q K - - - - - E S R S V Q L Q Y M S W P D H G V P S S												
hPTPD1	L Q N T C O D F W Q M I W E Q G I A I I A M V T A E E G G - R E K S F R Y W P R L G S R H N T V Y G R F K I T T R F R T D S G C Y A T T G L K M K H L L T - - - - - G Q E R T V W H L Q Y T D W P D H G C P E D												
hPTPD2	L P H T C H D F W Q M I W E Q G V N V I A M V T A E E G G - R T K S H R Y W P K L G S K H S S A T Y G K F K V T T K F R T D S V C Y A T T G L K V K H L L S - - - - - G Q E R T V W H L Q Y T D W P D H G C P E D												
hMEG1	L P H T C T D F W Q M I W E Q G S S M V V M L T T Q V E R G - R V K C H Q Y W P E P - - - - - T G S S Y G C Y Q V T C H S E E G N T A Y I F R K M T L F N Q E K - - - - - N E S R P L T Q I Q Y I A W P D H G V P D D												
hPTPH1	L P H T C A Q F W Q V I W E Q K L S L I V M L T T L E R G - R T K C H Q Y W P D P - - - - - P D V M N H G G F H I Q C Q S E D C T I A Y V S R E M L V T N T Q T - - - - - G E E H T V T H L Q Y V A W P D H G V P D D												
hPTPBAS	L P T T V G D F W Q M I W E Q K S T V I A M M T Q E V E G E - K I K C Q R Y W P N I L G - K T T M V S N R L R L A L V R M Q L K G F V V R A M T L E D I Q T - - - - - R E V R H I S H L N F T A W P D H D T P S Q												
hPTP1B	L P N T C G H F W E M I W E Q K S R G V V M L N R V M E K G - S L K C A Q Y W P Q K E E K E M I F E D T N L K L T L I S E D I K S Y T V R Q L E N L T T - - - - - Q E T R E I L H F H Y T T W P D F G V P E S												
hTCPTP	L P N T C C H F W L M I W E Q K T K A V V M L N R I V E K E - S V K C A Q Y W P T D D - Q E M L F K E T G F S V K L L S E D V K S Y T V H L L Q L E N I N S - - - - - G E T R T I S H F H Y T T W P D F G V P E S												
hMEG2	L E N T Y R D F W L M I W E Q K V L V I V M T T R F E E G G - R R K C G Q Y W P L E K - - - - - D S R I R F G F L T V T N L G V E N M N H Y K K T T L E I H N T E E - - - - - R Q K R Q V T H F O F L S W P D Y G V P S S												
hiA2	L S H T I A D F W Q M I W E S G C T V I V M L T P L V E D G - V K Q C D R Y W P D E - - - - - G A S L Y H Y V E V N L V S E H I W C E D F L V R S F Y L K N V Q T - - - - - Q E T R T L T Q F H F L S W P A E G T P A S												
hiA2beta	L P A T V A D F W Q M I W D H N A Q I V M L T P L A E N G - V R Q C Y H Y W P D E - - - - - G S N L Y H I Y E V N L V S E H I W C E D F L V R S F Y L K N L Q T - - - - - N E T R T V T Q F H F L S W Y D R G V P S S												
hPTPTyp	L L S T I A D F W Q M I W E L N S N V I A M I T R E M E G G - I I K C Y H Y W P I S - - - - - L K K P L E L K H F R V F L E N Y Q I L Q Y F I I R M F Q V E K S T G - - - - - T S H S V K Q L Q F T K W P D H G T P A S												
hHDPTP	L P G T I D D F W L M I W H E Q K V S I V M L V S E A E M E - K Q K V A R Y F P T E - - - - - R G Q P M V H G A L S L A L S S V R S T E T H V E R V L S L Q F R D Q - - - - - S L K R S L V H L H F T W P E L G L P D S												
Consensus	T	D F W M W	I V M T	E	K C	Y W P		R		R		W P D G P	
	Motif 5		Motif 6		Motif 7						Motif 8		

PTP domains D2

hPTPalpha	L L H T I E D F W R M I W E W K S C S I V M L T E L E E R G - Q E K C A Q Y W P S - - - - - D G L V S Y G D I T V E L K K E E E C E S Y T V R D L L V T N T R - - - - - E N K S R Q I R Q F H F H G W P E V G I P S D
hPTPepsilon	L A H T V E D F W R M I W E W K S H T I V M L T E V Q E R E - Q D K C Y Q Y W P T - - - - - E G S Y T H G E I T I E I K N D T L S E A I S I R D F L V T L N Q P Q A R Q - - - - - E E Q V R V V R Q F H F H G W P E I G I P A E
hCD45	L K E T I G D F W Q M I F Q R K V K V I V M L T E L K H G D - Q E I C A Q Y W S - - - - - E G K O T Y G D I E V D L K D T D K S S T Y T L R F E L R H S K - - - - - R K D S R T V Y Q Y Q T N W S V E Q L P A E
hPTPgamma	L P H T K D F W R M I W D H N A Q I I V M L P D N K S L A - E D E F V - Y W P S R - - - - - E E S M N C E A F T V L I S K D R L C L S N E E Q I I H D F I L E A T Q - - - - - D D Y V L E V R H F Q C P K W S N P D A P I S
hPTPzeta	L L H T I K D F W R M I W D H N A Q L V M I P D G Q N M A - E D E F V - Y W P N K - - - - - D E P I N C E S F K V T L M A E H K C L S N E E K L I I Q D F I L E A T Q - - - - - D D Y V L E V R H F Q C P K W S N P D S P I S
hPTPsigma	L A E T T E D F W R M L W E H N S T I V M L T K L R E M G - R E K C H Q Y W P A - - - - - E R S A R Y Q Y F V D P M A E Y N M P Q Y I L R E F K V T D A R - - - - - D G Q S R T V R Q F O F T D W P E Q G V P K S
hPTPdelta	L A E T T E D F W R M L W E H N S T I V M L T K L R E M G - R E K C H Q Y W P A - - - - - E R S A R Y Q Y F V D P M A E Y N M P Q Y I L R E F K V T D A R - - - - - D G Q S R T V R Q F O F T D W P E Q G V P K S
hLAR	L A E S T E D F W R M L W E H N S T I V M L T K L R E M G - R E K C H Q Y W P A - - - - - E R S A R Y Q Y F V D P M A E Y N M P Q Y I L R E F K V T D A R - - - - - D G Q S R T I R Q F O F T D W P E Q G V P K T
hPTPrho	L P N T V A D F W R M I W D H N C S S V M L N E M D T - - - - - A Q F C M Q Y W P E - - - - - K T S G C Y G P I Q V E F V S A D I D E D I H R I F R I C N M A R P - - - - - Q D G Y R I V Q H L Q Y I G W P A Y R D T P P
hPTPmu	L P N T V K D F W R L L V D Y H C T S V M L N D V D P - - - - - A Q L C P Q Y W P E - - - - - N G V H R H G P I Q V E F V S A D L E E D I S R I F R I Y N A A R P - - - - - Q D G Y R M V Q Q F O F L G W P M Y R D T P V
hPTPkappa	L P N T V K D F W R L V Y D Y G C T S I V M L N E V D L S - - - - - Q G C Q Y W P E - - - - - E G M L R Y G P I Q V E C M S C M S D C D V I N R I F R I C N L T R P - - - - - Q E G Y L M V Q Q F Q Y L G W A S H R E P G
hPTPlamda	L Q S T P D F W R L V Y D Y G C T S I V M L N Q L N Q S N A W P C L Q Y W P E - - - - - P G R Q Q Y G L M E V E F M S G T A D E D L V A R V F R V Q N I S R L - - - - - Q E G H L L V R H F Q F L R W A S H R E P D

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

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	-----	GPVVHCSAGVGRGTGTFVIDAMMAMMHA	EQK	---	VDVFEFVSRIRNR	QPMV	QTD	MQYTF	IYQAL	LEYLY	GDTEL				
hPTPkappa	--ATGLLSFIRRVKLSNPSSA	-----	GPVVHCSAGAGRTGCFVIDIMLDMAEREGV	---	VDIYNCVKALRSR	RINMV	QTE	EQYIF	IHDAI	LEACLG	GETAI					
hPTPmu	--ATGLLGfVRQVKSKSPSSA	-----	GPLVVHCSAGAGRTGCFVIDIMLDMAEREGV	---	VDIYNCVRELRSR	VNMV	QTE	EQYVF	IHDAI	LEACLG	GDTSV					
hPTPrho	--ATGLLGfVRQVKFLNPPEA	-----	GPVVHCSAGAGRTGCFVIDIMLDMAEREGV	---	VDIFNCVRELRAQR	VNLV	QTE	EQYVF	VHDAI	LEACLG	GNATAI					
hPTPlamda	--ATGLLAFIRRVKASTPPDA	-----	GPVVHCSAGAGRTGCFVIDIMLDMAEREGV	---	VDIYNCVRELRSR	VNMV	QTE	EQYVF	IHDAI	LEACLG	GETTI					
hPTPdelta	--PTPFLAFRLRRVKTCPNPPDA	-----	GPMVVHCSAGVGRGTGCFVIDAMLERIKHEKT	---	LDIYGHVTLMR	RAQR	NYMV	QTE	EQYIF	IHDAI	LEAVT	QGNTEV				
hPTPsigma	--PTPFLAFRLRRVKTCPNPPDA	-----	GPVVHCSAGVGRGTGCFVIDAMLERIKHEKT	---	VDVYGHVTLMR	SQR	NYMV	QTE	EQYSF	IHEAL	LEAVG	QGNTEV				
hPTPgamma	--ALPVLTFVRRSSAARMPET	-----	GPVLVHCSAGVGRGTGTYVIDSMLQKIKDKST	---	VNVLGFLKHIRT	QR	NYL	QTE	EQYIF	IHDAI	LEA	ILGKETEV				
hPTPzeta	--SLPVLTFVRKAAYAKRHAV	-----	GPVVHCSAGVGRGTGTYVIDSMLQKIQHEGT	---	VNIFGFLKHISQR	NYL	QTE	EQYVF	IHDTL	VEA	ILSKETEV					
hLAR	--PTPILAFRLRRVKAACNPLDA	-----	GPMVVHCSAGVGRGTGCFVIDAMLERMKHEKT	---	VDIYGHVTCMR	SQR	NYMV	QTE	EQYVF	IHEAL	LEAAT	CGHTEV				
hCD45	--PHLLKFLRRVNAFSNFFS	-----	GPVVHCSAGVGRGTGTYVIDAMLEGLEAENK	---	VDVYGVVVKLR	RQR	CLMV	QTE	EAQYIL	IHQAL	VEYNQF	GETEV				
hGLEPP1	NAAESILQFVHMVRQATKSK	-----	GPMIIVHCSAGVGRGTGTFIALDRLQLQHIRDHEF	---	VDILGLVSEMR	SR	MSMV	QTE	EQYIF	IHQCV	QLMWM	KKKQF				
hTPS31	--SAPLIHFVKLVRASRAHDT	-----	TPMIVHCSAGVGRGTGTFIALDHLTQHIINDHF	---	VDIYGLVAELR	SE	RMCMV	QNL	LAQYIF	ILHQCI	L	DL	LSNKG	SNQ		
hDEP1	TDLLINFRYLVRDYMKQSPPE	-----	SPVVHCSAGVGRGTGTFIALDRLIYQIENENT	---	VDVYGVVYDLR	MHR	PLMV	QTE	EQYVF	LNQC	VDL	VR	SQ	KDSK		
hPTPbeta	--TQSLIQFVRTVDYINRSPGA	-----	GPTVVHCSAGVGRGTGTFIALDRLIQLQLSDKDS	---	VDIYGAHDL	L	R	VHMV	QTE	CQYV	L	HQC	VR	DR	LR	
hSAP1	PDTLAFWRMLRQWLDQTMEG	-----	GPMIVHCSAGVGRGTGTFIALDVLRLRQLQSEGL	---	LDIYGHVTCMR	SQR	NYMV	QTE	EAQYIF	IHQAL	VEYNQF	GETEV				
hSTEP	--APPILLHLVREVEEAQQEGPHC	-----	APIIVHCSAGIGRTGCFIATSICCCQLRQEGV	---	VDILKTTCCQL	RQD	R	GGMI	QTE	CQYQ	F	VH	V	M	S	
hPCPTP1	--AQLPLQLMLDVEEDRLASQGR	-----	GPVVHCSAGIGRTGCFIATSIGCQQLKEEGV	---	VDALSI	V	C	QLR	M	R	GGMI	QTE	S	E	Q	Y
hHePTP	--AGPLLRLVAEVEESPETAHP	-----	GPVVHCSAGIGRTGCFIATRIGCQQLKARGE	---	VDILGIV	C	QLR	L	D	R	GGMI	QTE	A	Q	Y	F
hSHP1	--PGGVLDFLQVIRNRQESLPH	-----	GPVVHCSAGIGRTGTFIADMLMENISTKGLDCD	I	QKT	I	Q	M	V	R	AQ	R	S	G	M	V
hSHP2	--PGGVLDFLQVIRNRQESLPH	-----	GPVVHCSAGIGRTGTFIADMLMENISTKGLDCD	I	QKT	I	Q	M	V	R	AQ	R	S	G	M	V
hPEST	--FDSILDMISLMRKYQEHED	-----	VPICIHCSAGCGRTGAICADYTWMLLKAGI	PEEF	N	V	F	N	L	I	Q	E	M	R	T	Q
hLyPTP	--IDPILLELIDWVRCYQEDDS	-----	VPICIHCSAGCGRTGAICADYTWMLLKAGI	PEEF	N	V	F	N	L	I	Q	E	M	R	T	Q
hBDP1	--PDHMLAMVEEAARRLQSGP	-----	EPLCVHCSAGCGRTGVLCTVDYVRRQLLLTQMI	PPDF	S	L	F	D	V	L	K	M	R	K	Q	R
hTPD1	--LKGFLSYLEEIQSVRRHTNSTSDPQSPN	-----	PPLLHCSAGVGRGTGVLISELMIACLEHNEV	---	LDIPRVL	D	M	L	R	Q	R	M	M	L	Q	T
hTPD2	--VQGFLSYLEEIQSVRRHTNSMLEGTKNRH	-----	PVVHCSAGVGRGTGVLISELMIACLEHNEV	---	LDIPRVL	D	M	L	R	Q	R	M	M	L	Q	T
hMEG1	--SSDFLDFVCHVRNKRAGKE	-----	EPVVHCSAGIGRTGVLIMETAMCLIECNQP	---	VYPLDI	V	R	T	M	R	D	Q	R	A	M	I
hTPPH1	--SSDFLEFVNYVRSLRVDS	-----	EPLLHCSAGIGRTGVLIMETAMCLIECNQP	---	VYPLDI	V	R	T	M	R	D	Q	R	A	M	I
hTPBAS	--PDDLTFISYMRH IHR	-----	GPITVHCSAGIGRSGLICIDVVLGLISQDL	---	FDISDL	V	R	C	M	R	L	R	H	G	M	V
hTP1B	--PASFLNLFKVRRESGSLSPEH	-----	GPVVHCSAGIGRSGLICIDVVLGLISQDL	---	FDISDL	V	R	C	M	R	L	R	H	G	M	V
hTCPTP	--PASFLNLFKVRRESGSLNPDH	-----	GPAVHCSAGIGRSGLICIDVVLGLISQDL	---	FDISDL	V	R	C	M	R	L	R	H	G	M	V
hMEG2	--AASLIDFLRVVRNQSLAVSNMGARSKQCPEP	-----	PVVHCSAGIGRTGTFCSLDICLAQLEELGT	---	LNVFQT	V	S	R	M	R	T	Q	R	A	F	S
hIA2	--TRPLDFRRKVNKCYGRS	-----	CPVVHCSAGIGRTGTYVIDIMVLRMAKGVK	---	EIDIAAT	L	E	H	V	R	D	Q	R	P	G	L
hIA2beta	--SRSLDFRRKVNKCYGRS	-----	CPVVHCSAGIGRTGTYVIDIMVLRMAKGVK	---	EIDIAAT	L	E	H	V	R	D	Q	R	P	G	L
hPTPTyp	--ADSFIKYIRYARKSHLT	-----	GPMVVHCSAGIGRTGTFIADMLMENISTKGLDCD	I	QKT	I	Q	M	V	R	AQ	R	S	G	M	V
hHDPTP	--PSNLLRFIQEVHAHYLHQRPLH	-----	TPVVHCSAGVGRGTGAFALLYAAVQVEVEAGNG	---	IPELP	Q	L	V	R	R	M	Q	R	K	H	M

PTP domains D2

hPTPalpha	--GKGMISIIAAVQKQKQSGN	-----	HPITVHCSAGAGRTGTFICALSTVLERVKAEGI	---	LDVFQTVKSLRL	QRPHMV	QTE	EQYEF	FCYKVVQ	EYIDA	FS	SDYA
hPTPepsilon	--GKGMIDLIAAVQKQKQQTGN	-----	HPITVHCSAGAGRTGTFICALSNILERVKAEG	---	LDVFQAVKSLRL	QRPHMV	QTE	EQYEF	FCYKVVQ	DFIDI	FS	SDYA
hCD45	--PKELISMIQVVKQLPKQNSSEGNKHHKS	-----	TPLLHCRDGSQQTGIFCALLNLLESAAETEEV	---	VDIFQVVKALR	KARPGM	VST	F	EQYQ	FLYDV	I	ASTYPA
hPTPgamma	--STFELINVIKEEALTRD	-----	GPVVHCSAGVGRGTGTFICALNLSQALENEA	---	VDIFQVVKALR	KARPGM	VST	F	EQYQ	FLYDV	I	ASTYPA
hPTPzeta	--KTFELISVIEEAAARD	-----	GPMIVHDEHGGVTAGTFICALTLMHQLEKENS	---	VDVYQVAKMI	NLMRPG	V	F	ADIE	EQYQ	F	LYKVI
hPTPsigma	--GEGFIDFIGVHKTKEQFGQD	-----	GPISVHCSAGVGRGTGTFITLSIVLERMRYEGV	---	VDIFQTVKMLRT	QRPAMV	QTE	EQYQ	FCYQA	ALEYL	GS	FDHYA
hPTPdelta	--GEGFIDFIGVHKTKEQFGQD	-----	GPISVHCSAGVGRGTGTFITLSIVLERMRYEGV	---	VDIFQTVKMLRT	QRPAMV	QTE	EQYQ	FCYQA	ALEYL	GS	FDHYA
hLAR	--GEGFIDFIGVHKTKEQFGQD	-----	GPISVHCSAGVGRGTGTFITLSIVLERMRYEGV	---	VDIFQTVKMLRT	QRPAMV	QTE	EQYQ	FCYQA	ALEYL	GS	FDHYA
hPTPrho	--SKRSLKVVRRLEKQEQYDGRE	-----	GRTVVHCLNGGGRSGTFCALISVCEMLIQQNI	---	IDVFHIVKTL	LRNKN	S	M	V	E	T	LEQYQ
hPTPmu	--SKRSLKLVIRQVQKQEEYNGGE	-----	GPTVVHCLNGGGRSGTFCALISVCEMLIQQNI	---	IDVFHIVKTL	LRNKN	S	M	V	E	T	LEQYQ
hPTPkappa	--SKRSLKLVIRQVQKQEEYNGGE	-----	GRTIIVHCLNGGGRSGTFCALISVCEMLIQQNI	---	IDVFHIVKTL	LRNKN	S	M	V	E	T	LEQYQ
hPTPlamda	--SKKAFLLLAEDVQWQAESGD	-----	GRTIIVHCLNGGGRSGTFCACATVLEMI	R	CHNL	---	VDVF	F	AAKTL	LRN	K	PNM

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) Ptdrn	(1) HMLAYMEDHLNRND-----RLAKBQALCAY----QAEPNTCATAQEGEIKKK--NRSLPDFPYDHAHAKIKVVESSP-----SRSDYINAFPTIEHDPDR
hIA2beta D1 (NP 002838) PTPRN2	(1) HMLSYMEDHLNKNK-----RLKKEWEALCAY----QAEPNSFVYQREEVVPK--NRSLAVITVDHSSVLLKAENSH-----SHSDYINAFPTIMHDPDR
macnelA2beta D1 (O02695)	(1) HMLSYMEDHLNKNK-----RLKKEWEALCAY----QAEPNSSLVAQREENVPK--NRSLAVITVDHSSVLLKAENSH-----SHSDYINAFPTIMHDPDR
mPTPNP D1 (P80560) Ptdrn2	(1) HMLAYMEDHLNKNK-----RLKKEWEALCAY----QAEPNSSLVAQREENAPK--NRSLAVITVDHSSVLLKXSNH-----SSSDYINAFPTIMHDPDR
rPTNE6 D1 (NP 113788) Ptdrn2	(1) HMLAYMEDHLNKNK-----RLKKEWEALCAY----QAEPNSSLVAQREENAPK--NRSLAVITVDHSSVLLKXSNH-----SNSDYINAFPTIMHDPDR
hCD45 D2 (NP 002829) PTPRC	(1) SEHPYIHNKKRRDPP--SEPSPEAEQRPL----SYRSWRQTQHIQNGEENKSK--NRNSNVIPYDFNRPVKHELEMS--KESEHDSDESSDDSDSEEPKVINASFTMSYWKPF
mCD45 D2 (NP 035340) Ptdrc	(1) SEHSCILHNKKRRDPP--SDPSPEAEQRPL----SYRSWRQTQHIQNGEENKSK--NRNSNVIPYDFNRPVKHELEMS--KESEPEDESDESSDDSDSEETKVINASFTMSYWKPF
rCD45_D2 (XP 213985) Ptdrc	(1) SEHSHYLNKKRRDPP--SEPSLEAEQRPL----SYKGRWTQNTQNGEENKSK--NRNSNVIPYDFNRPVKHELEMS--KESEHDSDESSDDSDSEEXKVINASFTMSYWKPF
ccCD45 D2 (A54080)	(1) QELHSTLNTLQQRSSD--NEPTLLEDFERLP----NFKNWRFTNTGVTENKMKK--NRSSVVPYDFNRPVKHELEMS--KESEHDSDESSDDSDSEEXKVINASFTMSYWKPF
fuCD45 D2 (CAB96211)	(1) SEFHVSVNTLQKNG--SDPSLEAEQRPL----KFKKWRMTMTGSSDEDKSK--NRDSAVIPYDFNRPVKHELEMS--KESEHDSDESSDDSDSEEXKVINASFTMSYWKPF
cypcaCD45 D2 (BAA92179)	(1) -----NKKRRDPP--SEPSPEAEQRPL----SYRSWRQTQHIQNGEENKSK--NRNSNVIPYDFNRPVKHELEMS--KESEHDSDESSDDSDSEEXKVINASFTMSYWKPF
aotvoCD45 D2 (AAM48512) (3')	(1) SELPKHINFKKNDPP--SEPSMREGFORLP----PYTDWRQTQTRRGEQSK--NRSLVVPYDFNRPVKHELEMS--KDSHSDSDSDDSDSEEXKVINASFTMSYWKPF
sharkCD45 D2 (T43148)	(1) TSEIHLQKLYNKVP--GTSSNGEEFKKLT-----IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRPVKRGE-----ENSDYINAFPTIDYRRR
cPTPaloha D2 (AAB04150)	(1) TSETHLQKLYNKIP--GTSNNGEEFKKLT-----IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRPVKRGE-----ENSDYINAFPTIDYRQK
hPTPaloha D2 (NP 002827) PTPRA	(1) TSETHLQKLYNKIP--GTSNNGEEFKKLT-----IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRPVKRGE-----ENSDYINAFPTIDYRQK
mPTPaloha D2 (NP 033006) Ptdra	(1) TSETHLQKLYNKIP--GTSNNGEEFKKLT-----IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRPVKRGE-----ENSDYINAFPTIDYRQK
rPTPaloha D2 (NP 036895) Ptdra	(1) TSETHLQKLYNKIP--GTSNNGEEFKKLT-----IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRPVKRGE-----ENSDYINAFPTIDYRQK
xPTPaloha D2 (AAA17990)	(1) TSETHLQKLYSKFP--GTNSTGEEFKKLT-----IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRPVKRGE-----ENSDYINAFPTIDYRQK
zPTPaloha D2 (NP 571963) ptdra	(1) TSETHMNLKLYAPLP--GAGCGGLEAEKRLTS-----IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRPVKRGE-----ENSDYINAFPTIDYRQK
rVTPR4b D2 (BAA95196)	(1) TSESHLQKLYNRVS--GSGCGNGEEFKKLT-----IKIQNDKMRTNLPAANMKK--NRVLOLIPYDFNRPVKRGE-----ENSDYINAFPTIDYRQK
hPTPepsilon D2 (NP 006495) PTPRE	(1) SSELKHLQTLHGTTT--HFDKIGLEEFKRLTN--VRIMKENMRTGNLPAANMKK--ARVIOIIPYDFNRPVKRGE-----EYSDYINAFPTIDYRQK
mPTPepsilon D2 (NP 035342) Ptdre	(1) SSELERHLQTLHSTAT--HFDKIGLEEFKRLTN--VRIMKENMRTGNLPAANMKK--ARVIOIIPYDFNRPVKRGE-----EYSDYINAFPTIDYRQK
rPTPepsilon D2 (XP 215102) Ptdre	(1) SSELERHLQTLHGTAT--HFDKIGLEEFKRLTN--VRIMKENMRTGNLPAANMKK--ARVIOIIPYDFNRPVKRGE-----EYSDYINAFPTIDYRQK
orylaPTPepsilon D2 (BAC06424)	(1) CSELGHLHRLHNTRG--PNDRILGEEFKRLTN--VRIMKENMRTGNLPAANMKK--ARVIOIIPYDFNRPVKRGE-----EYSDYINAFPTIDYRQK
rVTPR4a D2 (BAA95190)	(1) SSELKHLQKLRNKTG--HFDITGEEFKRLTT--VRIRKDNMRTGNLPAANMKK--ARVLOIIPYDFNRPVKRGE-----EYSDYINAFPTIDYRQK
hPTPkappa D2 (NP 002835) PTPRK	(1) KAAYPDMIRHDSQTN-----SSHKDEPQTLNS--VTPRLQAEDCSIALCLRNHDK--NRSMMDLPPRCLPFLITDGD-----ESNINAFPTIDYRQP
mPTPkappa D2 (NP 033009) Ptdrk	(1) KAAYPDMIRHDSQTN-----SSHKDEPQTLNS--VTPRLQAEDCSIALCLRNHDK--NRSMMDLPPRCLPFLITDGD-----ESNINAFPTIDYRQP
rVTPR2B D2 (BAA95194)	(1) KQAYYEMIRHDSQSN-----SSQLKDEPQTLNS--VSSQLQPEDCSIALCLRNHEK--NRVMDLPPRCLPFLITDGD-----ESNINAFPTIDYRQP
hPTPlamda D2 (NP 005695) PTPRU	(1) KATYEMIRHDSQSN-----SSQLREBPQTLNS--VTPPLDVEECSIALCLRNHDK--NRSMMDLPPRCLPFLITDGD-----DSNINAFPTIDYRQP
mPTPlamda D2 (NP 035344) Ptdrl	(1) RATYEMIRHDSQSN-----SSQLREBPQTLNS--VTPPLDVEECSIALCLRNHDK--NRSMMDLPPRCLPFLITDGD-----DNINAFPTIDYRQP
hPTPmu D2 (NP 002836) PTPRM	(1) RSLYDMNKLDPQTN-----SSQKEPRTLNM--VTPTLRVEDCSIALCLRNHEK--NRCDMLPPRCLPFLITDGD-----ESNINAFPTIDYRQP
mPTPmu D2 (NP 033010) Ptdrm	(1) RSLYDMNKLDPQTN-----SSQKEPRTLNM--VTPTLRVEDCSIALCLRNHEK--NRCDMLPPRCLPFLITDGD-----ESNINAFPTIDYRQP
rPTPmu D2 (XP 237546 (revised))	(1) RSLYDMNKLDPQTN-----SSQKEPRTLNM--VTPTLRVEDCSIALCLRNHEK--NRCDMLPPRCLPFLITDGD-----ESNINAFPTIDYRQP
hPTPrho D2 (NP 573400) PTPRT	(1) RSLYDNISRLDPQTN-----SSQKDEPQTLNI--VTPVRPVEDCSIALCLRNHDK--NRSMMDLPPRCLPFLITDGD-----ESNINAFPTIDYRQP
mPTPrho D2 (NP 067439) Ptdrt	(1) RSLYDNISRLDPQTN-----SSQKDEPQTLNI--VTPVRPVEDCSIALCLRNHDK--NRSMMDLPPRCLPFLITDGD-----ESNINAFPTIDYRQP
cPTPsiama D2 (I50212)	(1) RNLYTYIQKLAQIEVGG--EHVTGMLEFKRLAN--SKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
hLAR D2 (NP 002831) PTPRF	(1) RNLYAHYIQLGQVPPG--ESVTAMELEFKRLAN--SKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
mLAR D2 (NP 035343) Ptdrf	(1) RNLYAHYIQLGQVPPG--ESVTAMELEFKRLAN--SKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
rLAR_D2 (NP 062122) Ptdrf	(1) RNLYAHYIQLGQVPPG--ESVTAMELEFKRLAG--SKARASRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
xLAR D2 (AAF43606)	(1) RSLYAHYIQLGQVPPG--ESVTSMLEFKRLAN--SKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
rLAR D2 (CAC44758)	(1) RSLYTHYIQLGQAPPG--DVTAMELEFKRLAN--SKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
rVTPR2Aa D2 (BAA95188)	(1) RSLFAHYIQLGQVPPA--ETVTAMELEFKRLAN--SKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
hPTPdelta D2 (NP 002830) PTPRD	(1) RNLYAYIQKLTQIETG--ENVTGMLEFKRLAS--SKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
mPTPdelta D2 (D54689)	(1) RNLYAYIQKLTQIETG--ENVTGMLEFKRLAS--SKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
xPTPdelta D2 (AAF43605)	(1) RNLYAYIQKLTQIEPG--ENVTGMLEFKRLAS--FKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
rVTPR2Ab D2 (BAA95191)	(1) RNLYAYIQKLTQVEPG--ENVTGMLEFKRLAN--TKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
hPTPsiama D2 (NP 002841) PTPRS	(1) RSNLYAYIQKLAQVEPG--EHVTGMLEFKRLAN--SKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
mPTPsiama D2 (NP 035348) Ptdrs	(1) RSNLYTYIQKLAQVEPG--EHVTGMLEFKRLAS--SKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
xPTPsiama D2 (AAF43607)	(1) RNLYTYIQKLAQIDVG--EHVIGMLEFKRLAN--SKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
rPTPsiama D2 (CAC44759)	(1) RSLFSYIQLKLAQVEAG--EHVSGMLEFKRLAN--SKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----LEGSDYINAFPTIDYRQK
rPTPsiama D2 (NP 062013) Ptdrd	(1) RSLYTYIQKLAQVEPG--EHVTGMLEFKRLAS--SKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
rVTPR2Ac D2 (BAA95193)	(1) RNLYSYIQLKLTQVETG--EHVTGMLEFKRLAN--SKAHTSRFISANLCLNFKF--NRVNIIPYESTRVCQPGRG-----VEGSDYINAFPTIDYRQK
hPTPgamma D2 (NP 002832) PTPRG	(1) NQLHSYVNSLIPGVG--GKTRLEKQKFLVQ--CNAKYVECFSAQKECNKSK--NRNSVVPARARVGLAPPG-----MKGSDYINAFPTIDYRQK
mPTPgamma D2 (NP 033007) Ptdrg	(1) NQLHSYVNSLIPGVG--GKTRLEKQKFLVQ--CNAKYVECFSAQKECNKSK--NRNSVVPARARVGLAPPG-----MKGSDYINAFPTIDYRQK
rPTPgamma D2 (NP 599183) Ptdrg	(1) NQLHSYVNSLIPGVG--GKTRLEKQKFLVQ--CNAKYVECFSAQKECNKSK--NRNSVVPARARVGLAPPG-----MKGSDYINAFPTIDYRQK
rVTPR5b D2 (BAA95197)	(1) NQLHSYVNSLIPGLS--GKMRLEKQKFLVQ--CNAKFIECFSAQKECNKSK--NRNSVVPARARVGLAPPG-----TKGSDYINAFPTIDYRQK
cPTPgamma D2 (Q98936)	(1) NQLHSYVNSLIPGGI--GKTRLEKQKFLVQ--CNAKYVECFSAQKDCNKSK--NRNSVVPARARVGLAPPG-----MKGSDYINAFPTIDYRQK
hPTPzeta D2 (NP 002842) PTPRZ1	(1) SHHAYYNALLIPGPA--GKTKLEKQQLSQ--SNIQSDYSYALKQCNRK--NRSSVLPVRSRVGLAPSG-----EGSDYINAFPTIDYRQK
cPTPzeta D2 (AAA49015)	(1) THHAYYNALLIPGPT--GKTRLEKQKFLSQ--SNTQCDYSTALKQCNRK--NRSSVLPVRSRVGLAPSG-----EGSDYINAFPTIDYRQK
mPTPzeta D2 (XP 133009) Ptdrz1	(1) SHHSHYVNTLIPGPT--GKTKLEKQQLSQ--SNILQSDYSTALKQCNRK--NRSSVLPVRSRVGLAPSG-----EGSDYINAFPTIDYRQK
rPTPzeta D2 (NP 037212) Ptdrz1	(1) SHHSHYVNTLIPGFS--GKTKLEKQQLSQ--SNILQSDYSTALKQCNRK--NRSSVLPVRSRVGLAPSG-----EGSDYINAFPTIDYRQK
xPTPzeta D2 (BAA97445)	(1) THHSHYVNTLTMGFS--GKSRLEKQKFLSE--PNILQCDYSTALKQCNRK--NRSSVLPVRSRVGLAPSG-----EGSDYINAFPTIDYRQK
rVTPR5a D2 (BAA95195)	(1) NHHTYVNTLTPGFS--GKTKLEKQKFLSQ--PHAKQCDYSYALKQCNRK--NRSSVLPVRSRVGLAPSG-----EGSDYINAFPTIDYRQK
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) Ptprr	(84)	N	---	A	Y	I	A	T	G	G	P	E	T	---
rLAR_D1 (NP 062122) Ptprr	(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) Ptprr	(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)) Ptprr	(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	(80)	N	---	H	Y	I	A	T	G	G	P	E	T	---
cPTPaloha D1 (NP04150)	(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) Ptprr	(85)	N	---	K	F	I	A	A	G	G	P	E	T	---
rPTPpsilon_D1 (XP 215102) Ptprr	(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) Ptprr	(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) Ptprr	(85)	R	---	K	Y	I	A	A	G	G	P	E	T	---
rCD45_D1 (XP 213985) Ptprr	(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---	EKTVDVYGHV	VTLMRS	SQRNY	MQVTE	QVYSFI	HEADLEAMG	
mPTPsiama D1 (NP 035348(revised)) Ptprs (176)	QPTAWP	DHGVPEY	-PTPFLA	LRRVKTCN				PPDA	GPIV	VHCSAGV	GRGTCF	IVDAMLER	KT---	EKTVDVYGHV	VTLMRS	SQRNY	MQVTE	QVYSFI	HEADLEAMG	
rPTPsiama D1 (NP 062013) Ptpord (176)	QPTAWP	DHGVPEY	-PTPFLA	LRRVKTCN				PPDA	GPIV	VHCSAGV	GRGTCF	IVDAMLER	RT---	EKTVDVYGHV	VTLMRS	SQRNY	MQVTE	QVYSFI	HEADLEAMG	
cPTPsiama D1 (I50212) (176)	QPTAWP	DHGVPEY	-PTPFLA	LRRVKTCN				PPDA	GPIV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDVYGHV	VTLMRS	SQRNY	MQVTE	QVYSFI	HEADLEAMG	
xPTPsiama D1 (AAF43607) (176)	QPTAWP	DHGVPEY	-PTPFLA	LRRVKTCN				PPDA	GPIV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDVYGHV	VTLMRS	SQRNY	MQVTE	QVYSFI	HEADLEAMG	
zPTPsiama D1 (CAC44759) (176)	QPTAWP	DHGVPEY	-PTPFLA	LRRVKTCN				PPDA	GPIV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDVYGHV	VTLMRS	SQRNY	MQVTE	QVYSFI	HEADLEAMG	
hLAR D1 (NP 002831) PTPRF (176)	QPMWPD	HGVPEY	-PTPFLA	LRRVKACN				PLDA	GPMV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDVYGHV	VTLMRS	SQRNY	MQVTE	QVYSFI	HEADLEAMG	
mLAR D1 (NP 035343) Ptprf (176)	QPMWPD	HGVPEY	-PTPFLA	LRRVKACN				PLDA	GPMV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDVYGHV	VTLMRS	SQRNY	MQVTE	QVYSFI	HEADLEAMG	
rLAR_D1 (NP 062122) Ptorf (176)	QPMWPD	HGVPEY	-PTPFLA	LRRVKACN				PLDA	GPMV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDVYGHV	VTLMRS	SQRNY	MQVTE	QVYSFI	HEADLEAMG	
xLAR D1 (AAF43606) (176)	QPMWPD	HGVPEY	-PTPFLA	LRRVKACN				PPDA	GPMF	VHCSAGV	GRGTCF	IVDAMLER	KL---	EKTVDVYGHV	VTLMRS	SQRNY	MQVTE	QVYSFI	HEADLEAMG	
hPTPdelta_D1 (NP 002830) PTPRD (176)	QPTAWP	DHGVPEH	-PTPFLA	LRRVKTCN				PPDA	GPMV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDVYGHV	VTLMRA	QRNY	MQVTE	QVYSFI	HEADLEAMT	
mPTPdelta D1 (D54689) (174)	QPTAWP	DHGVPEH	-PTPFLA	LRRVKTCN				PPDA	GPMV	VHCSAGV	GRGTCF	IVDAMLER	KH---	EKTVDVYGHV	VTLMRA	QRNY	MQVTE	QVYSFI	HEADLEAMT	
xPTPdelta D1 (AAF43605) (176)	QPTAWP	DHGVPEH	-PTPFLA	LRRVKTCN				PPDA	GPMV	VHCSAGV	GRGTCF	NVIDAMLER	RH---	EKTVDVYGHV	VTLMRA	QRNY	MQVTE	QVYSFI	HEADLEAMT	
hPTPrho D1 (NP 573400) PTPRT (175)	HFTSWPD	HGVPCY	-ATGLG	VRQVKKFLN				PEEA	GPIV	VHCSAGV	GRGTCF	IAIDTMLDMAEN		EGVVDI	FNCFV	ELRAQRV	NLVQTE	QVYVFD	ADLEACL	
mPTPrho D1 (NP 067439) Ptprt (175)	HFTSWPD	HGVPCY	-ATGLG	VRQVKKFLN				PEEA	GPIV	VHCSAGV	GRGTCF	IAIDTMLDMAEN		EGVVDI	FNCFV	ELRAQRV	NLVQTE	QVYVFD	ADLEACL	
xPTPrho D1 (AAD50295) (175)	HFTSWPD	HGVPCY	-ATGLG	VRQVKKFLN				PPDA	GPIV	VHCSAGV	GRGTCF	IAIDTMLDMAEN		EGVVDI	FNCFV	ELRAQRV	NLVQTE	QVYVFD	ADLEACL	
hPTPmu D1 (NP 002836) PTPRM (175)	HFTGWP	DHGVYH	-ATGLG	VRQVKKSKS				PPSAG	PLV	VHCSAGV	GRGTCF	IVDMLDMAER		EGVVDI	FNCFV	ELRAQRV	NLVQTE	QVYVFD	ADLEACL	
mPTPmu D1 (NP 033010) Pterm (175)	HFTGWP	DHGVYH	-ATGLG	VRQVKKSKS				PPNAG	PLV	VHCSAGV	GRGTCF	IVDMLDMAER		EGVVDI	FNCFV	ELRAQRV	NLVQTE	QVYVFD	ADLEACL	
hPTPkappa D1 (NP 002835) PTPRK (175)	HFTGWP	DHGVYH	-ATGLS	VRRVKKLSN				PPSAG	GPIV	VHCSAGV	GRGTCF	IVDMLDMAER		EGVVDI	FNCFV	ELRAQRV	NLVQTE	QVYVFD	ADLEACL	
mPTPkappa D1 (NP 033009 (revised)) Ptok (175)	HFTGWP	DHGVYH	-ATGLS	VRRVKKLSN				PPSAG	GPIV	VHCSAGV	GRGTCF	IVDMLDMAER		EGVVDI	FNCFV	ELRAQRV	NLVQTE	QVYVFD	ADLEACL	
hPTPlamda D1 (NP 005695) PTPRU (171)	HFTAWP	HGVYH	-ATGLA	LRRVKAST				PPDA	GPIV	VHCSAGV	GRGTCF	IVDMLDMAEC		EGVVDI	FNCFV	ELRAQRV	NLVQTE	QVYVFD	ADLEACL	
mPTPlamda D1 (NP 035344) Ptprl (171)	HFTAWP	HGVYH	-ATGLA	LRRVKAST				PPDA	GPIV	VHCSAGV	GRGTCF	IVDMLDMAEC		EGVVDI	FNCFV	ELRAQRV	NLVQTE	QVYVFD	ADLEACL	
rPTPpsi_D1 (AAB42210) Ptprr Fraam (171)	HFTAWP	HGVYH	-ATGLA	LRRVKAST				PPDA	GPIV	VHCSAGV	GRGTCF	IVDMLDMAEC		EGVVDI	FNCFV	ELRAQRV	NLVQTE	QVYVFD	ADLEACL	
cPTPaloha D1 (AAB04150) (181)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				POYA	GAIV	VHCSAGV	GRGTCF	IVDMLDMAHA		ERKVDVY	GFVSR	ELRAQRV	CMQVTD	MQVYFI	QADLEHYL	
hPTPaloha D1 (NP 002827) PTPRA (181)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				POYA	GAIV	VHCSAGV	GRGTCF	IVDMLDMAHT		ERKVDVY	GFVSR	ELRAQRV	CMQVTD	MQVYFI	QADLEHYL	
mPTPaloha D1 (AAK56109) Ptora (181)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				POYA	GAIV	VHCSAGV	GRGTCF	IVDMLDMAHS		ERKVDVY	GFVSR	ELRAQRV	CMQVTD	MQVYFI	QADLEHYL	
rPTPaloha D1 (NP 036895) Ptora (181)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				POYA	GAIV	VHCSAGV	GRGTCF	IVDMLDMAHS		ERKVDVY	GFVSR	ELRAQRV	CMQVTD	MQVYFI	QADLEHYL	
zPTPaloha D1 (NP 571963) pthora (181)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				POYA	GAIV	VHCSAGV	GRGTCF	IVDMLDMAHA		ERKVDVY	GFVSR	ELRAQRV	CMQVTD	MQVYFI	QADLEHYL	
xPTPaloha D1 (AAA17990) (181)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				POYA	GAIV	VHCSAGV	GRGTCF	IVDMLDMAHT		ERKVDVY	GFVSR	ELRAQRV	CMQVTD	MQVYFI	QADLEHYL	
hPTPension D1 (NP 006495) PTPRE (180)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				POYA	GAIV	VHCSAGV	GRGTCF	IVDMLDMAHT		ERKVDVY	GFVSR	ELRAQRV	CMQVTD	MQVYFI	QADLEHYL	
mPTPension D1 (NP 035342) Ptpre (180)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				PSHA	GPIV	VHCSAGV	GRGTCF	IVDMLDMAHS		ERKVDVY	GFVSR	ELRAQRV	CMQVTD	MQVYFI	QADLEHYL	
rPTPension D1 (XP 215102) Ptpore (180)	HFTSWPD	FVGPFT	-PIGLK	LKKVKACN				PSHA	GPIV	VHCSAGV	GRGTCF	IVDMLDMAHS		ERKVDVY	GFVSR	ELRAQRV	CMQVTD	MQVYFI	QADLEHYL	
hPTPqamma D1 (NP 002832) PTPRG (192)	HNTQWPD	MGVPEY	-ALPVL	TVRRSSAAR				MPET	GPVL	VHCSAGV	GRGTCF	IVDMSLQQ	KD---	KSTVNV	LGLF	KHRTORNY	LVQTE	QVYFI	HDLEAAL	
mPTPqamma D1 (NP 033007) Ptporq (192)	HNTQWPD	MGVPEY	-ALPVL	TVRRSSAAR				MPDM	GPVL	VHCSAGV	GRGTCF	IVDMSLQQ	KD---	KSTVNV	LGLF	KHRTORNY	LVQTE	QVYFI	HDLEAAL	
rPTPqamma D1 (NP 599183) Ptpor (196)	HNTQWPD	MGVPEY	-ALPVL	TVRRSSAAR				MPDM	GPVL	VHCSAGV	GRGTCF	IVDMSLQQ	KD---	KSTVNV	LGLF	KHRTORNY	LVQTE	QVYFI	HDLEAAL	
cPTPqamma D1 (Q98936) (192)	HNTQWPD	MGVPEY	-ALPVL	TVRRSSAAR				TPHM	GPVL	VHCSAGV	GRGTCF	IVDMSLQQ	KD---	KSTVNV	LGLF	KHRTORNY	LVQTE	QVYFI	HDLEAAL	
hPTPzeta D1 (NP 002842) PTPRZ1 (194)	HNTQWPD	MGVPEY	-SLPVL	TVRRKAAAYAK				RHAV	GPVV	VHCSAGV	GRGTCF	IVDMSLQQ	QH---	EGTVN	LFGFL	KHRSQRNY	LVQTE	QVYFI	HDLEAAL	
rPTPzeta D1 (NP 037212) Ptporz1 (194)	HNTQWPD	MGVPEY	-SLPVL	TVRRKAAAYAK				RHAV	GPVV	VHCSAGV	GRGTCF	IVDMSLQQ	QH---	EGTVN	LFGFL	KHRSQRNY	LVQTE	QVYFI	HDLEAAL	
cPTPzeta D1 (AAA49015) (187)	HNTQWPD	MGVPEY	-TLPVL	TVRRKASHAK				RHAV	GPVV	VHCSAGV	GRGTCF	IVDMSLQQ	QH---	EGTVN	LFGFL	KHRTORNY	LVQTE	QVYFI	HDLEAAL	
xPTPzeta D1 (BAA97445) (187)	HNTQWPD	MGVPEY	-TLPVL	TVRRKASHAK				KLN	GPVV	VHCSAGV	GRGTCF	IVDMSLQQ	QH---	EGTVN	LFGFL	KHRSQRNY	LVQTE	QVYFI	HDLEAAL	
hCD45 D1 (NP 002829) PTPRC (180)	QFTSWPD	HGVPEE	-PHLLK	LRRVNAFNS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLEGEA		EGKVDVY	GYVVK	LRRQRCL	MQVTE	QVYIIL	IQALVEYNQ	
mCD45 D1 (NP 035340) Ptprc (180)	QFTSWPD	HGVPEE	-PHLLK	LRRVNAFNS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLEGEA		EGKVDVY	GYVVK	LRRQRCL	MQVTE	QVYIIL	IQALVEYNQ	
rCD45_D1 (XP 213985) Ptporc (180)	QFTSWPD	HGVPEE	-PHLLK	LRRVNAFNS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLEGEA		EGKVDVY	GYVVK	LRRQRCL	MQVTE	QVYIIL	IQALVEYNQ	
cCD45 D1 (A54080) (180)	QFTSWPD	HGVPEE	-PHLLK	LRRVNAFNS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLEGEA		EGKVDVY	GYVVK	LRRQRCL	MQVTE	QVYIIL	IQALVEYNQ	
cypcaCD45 D1 (BAA92179) (177)	QFTSWPD	HGVPEE	-PHLLK	LRRVNAFNS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLEGEA		EGKVDVY	GYVVK	LRRQRCL	MQVTE	QVYIIL	IQALVEYNQ	
fuCD45 D1 (CAB96211) (180)	QFTSWPD	HGVPEE	-PHLLK	LRRVNAFNS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLEGEA		EGKVDVY	GYVVK	LRRQRCL	MQVTE	QVYIIL	IQALVEYNQ	
sharkCD45 D1 (T43148) (180)	QFTSWPD	HGVPEE	-PHLLK	LRRVNAFNS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLEGEA		EGKVDVY	GYVVK	LRRQRCL	MQVTE	QVYIIL	IQALVEYNQ	
hDEP1 D1 (NP 002834) PTPRJ (176)	HFTSWPD	HGVPEE	-PHLLK	LRRVNAFNS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLEGEA		EGKVDVY	GYVVK	LRRQRCL	MQVTE	QVYIIL	IQALVEYNQ	
rDEP1 D1 (NP 058965) Ptpri (176)	HFTSWPD	HGVPEE	-PHLLK	LRRVNAFNS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLEGEA		EGKVDVY	GYVVK	LRRQRCL	MQVTE	QVYIIL	IQALVEYNQ	
mDEP1 D1 (NP 033008) Ptpri (176)	HFTSWPD	HGVPEE	-PHLLK	LRRVNAFNS				NFFS	GPIV	VHCSAGV	GRGTCF	IGIDAMLEGEA		EGKVDVY	GYVVK	LRRQRCL	MQVTE	QVYIIL	IQALVEYNQ	
hGLEPP1_D1 (NP 109592) PTPRO (176)	NVTAWP	DHGVPEE	-PQLV	VMRQQAT				KSK	GPMI	VHCSAGV	GRGTCF	IADRLHQH	RD---	HEFVDI	LGLV	SEMS	SYRMS	MQVTE	QVYFI	HCCQLMWW
rGLEPP1_D1 (NP 059032) Ptpro (176)	NVTAWP	DHGVPEE	-PQLV	VMRQQAT				KSK	GPMI	VHCSAGV	GRGTCF	IADRLHQH	RD---	HEFVDI	LGLV	SEMS	SYRMS	MQVTE	QVYFI	HCCQLMWW
mPTPphi D1 (NP 035346) Ptpro (176)	NVTAWP	DHGVPEE	-PQLV	VMRQQAT				KSK	GPMI	VHCSAGV	GRGTCF	IADRLHQH	RD---	HEFVDI	LGLV	SEMS	SYRMS	MQVTE	QVYFI	HCCQLMWW
rabPTPoc D1 (AAB16824) (176)	NVTAWP	DHGVPEE	-PQLV	VMRQQAT				KSK	GPMI	VHCSAGV	GRGTCF	IADRLHQH	RD---	HEFVDI	LGLV	SEMS	SYRMS	MQVTE	QVYFI	HCCQLMWW
hPTPbeta D1 (NP 002828) PTPRB (179)	HNTVWPD	HGVPEE	-TQSL	IQVRRVRYDINR				SPGA	GTVV	VHCSAGV	GRGTCF	IADRLHQH	DS---	KDSVDI	YGAH	DLRHRVH	MQVTE	QVYVLL	HCCQVDRVIR	
mPTPbeta D1 (NP 084204) Ptprb (179)	HNTVWPD	HGVPEE	-TQSL	IQVRRVRYDINR				SPGA	GTVV	VHCSAGV	GRGTCF	IADRLHQH	DS---	KDSVDI	YGAH	DLRHRVH	MQVTE	QVYVLL	HCCQVDRVIR	
rPTPbeta D1 (XP 235156 (revised)) (179)	HNTVWPD	HGVPEE	-TQSL	IQVRRVRYDINR				SPGA	GTVV	VHCSAGV	GRGTCF	IADRLHQH	DS---	KDSVDI	YGAH	DLRHRVH	MQVTE	QVYVLL	HCCQVDRVIR	
hPTSP31 D1 (AR073855) PTPGMC1 (177)	NFTAWP	DHGVPEE	-SAPL	IHKVLRASR				AHDTT	PMV	VHCSAGV	GRGTCF	IADRLHQH	ND---	HDVVDI	YGLV	ELSER	CMCMLAQY	IFLHCCQLDLS		
rPTPGMC1 D1 (NP 075214) Ptporq (177)	NFTAWP	DHGVPEE	-SAPL	IHKVLRASR				AHDTT	PMV	VHCSAGV	GRGTCF	IADRLHQH	ND---	HDVVDI	YGLV	ELSER	CMCMLAQY	IFLHCCQLDLS		
hSAP1_D1 (NP 002833) PTPRH (178)	HNTAWP	DHGVPEE	-PDTL	LAWRKQWLDO				TMEG	GPIV	VHCSAGV	GRGTCF	IADRLHQH	QS---	EGLV	GFESFV	KRRSRPL	MQVTE	QVYVFL	HCCQSSN	
mSAP1 D1 (BAC37443) (178)	HNTAWP	DHGVPEE	-PDTL	LAWRKQWLDO				TMEG	GPIV	VHCSAGV</										

VectorNTI Screen View - Alignment\_195\_Vert\_PTP\_Domains\_D1\_and\_D2 (VNTI 8.0).apr

rOSTPTP D1 (NP 149090) Eso (178)	QPTWDFDSVPEA--PSSLLAVELVQEQVQA-----TQGKGLIIVHCSAGVGRGTGFVALLRLLRQEE---EKVADVNTVYILRLHRPLMOTLSQYIFLHSCILNKIL
hPCPTP1 D1 (NP 002840) PTPRR (174)	WVTSWDFDKTDS--AQPQLQLMLDVEDRDLA-----SQGRGPIVVHCSAGVGRGTGCFIATISIGCQQKE---GVDVDSALVLCOLRMDRGGMVQTSQYEFVHHAALCLYES
rPCPTP1 D1 (NP 446046) Ptprr (174)	WVTSWDFDKTDS--AQPQLQLMLDVEDRDLA-----SEGRGPIVVHCSAGVGRGTGCFIATISIGCQQKE---GVDVDSALVLCOLRMDRGGMVQTSQYEFVHHAALCLYES
mPTPSL D1 (NP 035347) Ptprr (174)	WVTSWDFDKTDS--AQPQLQLMLDVEDRDLA-----SEGRGPIVVHCSAGVGRGTGCFIATISIGCQQKE---GVDVDSALVLCOLRMDRGGMVQTSQYEFVHHAALCLYES
hSTEP D1 (NP 116710) PTPN5 (174)	WFTSWFDQKTD--APPPLHLHLMREVEEAAQQE-----GPHCPGLIIVHCSAGVGRGTGCFIATISIGCQQKE---GVDVLLKTTCCQLRQDRGGMIOCTCQYQFVHHAALCLYES
mSTEP D1 (NP 038671) Pton5 (174)	WFTSWFDQKTD--APPPLHLHLMREVEEAAQQE-----GPHCPGLIIVHCSAGVGRGTGCFIATISIGCQQKE---GVDVLLKTTCCQLRQDRGGMIOCTCQYQFVHHAALCLYES
rSTEP D1 (NP 062126) Pton5 (174)	WFTSWFDQKTD--APPPLHLHLMREVEEAAQQE-----GPHCPGLIIVHCSAGVGRGTGCFIATISIGCQQKE---GVDVLLKTTCCQLRQDRGGMIOCTCQYQFVHHAALCLYES
hHePTP D1 (NP 002823) PTPN7 (172)	LPSAWDFDQTES--AGPPLRLVAEVEETP-ET-----AAHPGPIVVHCSAGVGRGTGCFIATISIGCQQKA---RGEVDLGLVLCOLRDRGGMIOCTAQQYQFHLHTALYAG
mHePTP D1 (NP 796055) Pton7 (172)	LPSAWDFDQTES--AGPPLRLVAEVEETP-ET-----AAHPGPIVVHCSAGVGRGTGCFIATISIGCQQKA---RGEVDLGLVLCOLRDRGGMIOCTAQQYQFHLHTALYAG
rLCPTP D1 (P49445) Pton7 (172)	LPSAWDFDQTES--AGPPLRLVAEVEETP-ET-----AAHPGPIVVHCSAGVGRGTGCFIATISIGCQQKA---RGEVDLGLVLCOLRDRGGMIOCTAQQYQFHLHTALYAG
hLyPTP D1 (NP 057051) PTPN22 (185)	HVKNWDFDQVSS---DPILLQLVDMVRCYQ-----EDDSVVICVHCSAGVGRGTGCFIATISIGCQQKDGIIIPENFVSFSLIEEMRTORPSLVQTSQYELVAVLLELFK
mPEP D1 (NP 033005) Pton8 (185)	HVKNWDFDQVSS---DPILLQLVDMVRCYQ-----EDDSVVICVHCSAGVGRGTGCFIATISIGCQQKDGIIIPENFVSFSLIEEMRTORPSLVQTSQYELVAVLLELFK
hPEST D1 (NP 002826) PTPN12 (189)	HVVNWDFDQVSS---FDSLIDMLSLMRKYY-----EHEDVICVHCSAGVGRGTGCFIATISIGCQQKAGKIPPEEFNVNLIQEMRTORHSVQTKQYELVHRAALQLF
rRKPTP D1 (NP 476456) Pton12 (189)	HVVNWDFDQVSS---FDSLIDMLSLMRKYY-----EHEDVICVHCSAGVGRGTGCFIATISIGCQQKAGKIPPEEFNVNLIQEMRTORHSVQTKQYELVHRAALQLF
mPEST D1 (NP 035333) Pton12 (189)	HVVNWDFDQVSS---FDSLIDMLSLMRKYY-----EHEDVICVHCSAGVGRGTGCFIATISIGCQQKAGKIPPEEFNVNLIQEMRTORHSVQTKQYELVHRAALQLF
hBDP1 D1 (NP 055184) PTPN18 (186)	QVMSWDFDQVSS---PDHLLDMVEEARLQGG-----SGPPEVICVHCSAGVGRGTGCFIATISIGCQQKLTQMIPPDPFSLFVDLTKMKRQORPAAVQTEQYRFLVHTVAQMFC
mPTPK1_D1 (NP 035336) Pton18 (186)	QVMSWDFDQVSS---SDHLLTMVEEARCLQG-----LGPPEVICVHCSAGVGRGTGCFIATISIGCQQKLTQTIPPDPFSLFQVLEMKRQORPAAVQTEQYRFLVHTVAQMFC
rPTP20 D1 (AAC52896) (186)	QVMSWDFDQVSS---SDHLLTMVEEARCLQG-----LGPPEVICVHCSAGVGRGTGCFIATISIGCQQKLTQTIPPDPFSLFQVLEMKRQORPAAVQTEQYRFLVHTVAQMFC
hSHP1 D1 (NP 002822) PTPN6 (193)	QVLSWDFDQVSE--PGGGLSLDQINQRQES-----LPHAGPIIVHCSAGVGRGTGFIIVIDLMLMESTKGLGCDLIDQKTIQVMVRAORSGMVQTEAQYKFIIVAAQFPE
mSHP1 D1 (NP 038573) Hcph (193)	QVLSWDFDQVSE--PGGGLSLDQINQRQES-----LPHAGPIIVHCSAGVGRGTGFIIVIDLMLMESTKGLGCDLIDQKTIQVMVRAORSGMVQTEAQYKFIIVAAQFPE
rSHP1_D1 (NP 446360) Ptoh6 (193)	QVLSWDFDQVSE--PGGGLSLDQINQRQES-----LPHAGPIIVHCSAGVGRGTGFIIVIDLMLMESTKGLGCDLIDQKTIQVMVRAORSGMVQTEAQYKFIIVAAQFPE
zSHP1 D1 (AAH44414) (193)	QVLSWDFDQVQE--PGGGLSLDQINQRQEE-----LRSSGPIIVHCSAGVGRGTGFIIVIDLMLMESTDAKGLGCDLIDQKCIIMMVRDORSGMVQTEAQYKFIIVAAQFPE
rVPTPN6c D1 (BAA95199) (162)	QVLSWDFDQVNE--PGGGLSLDQVNRKQES-----IPDTPGPIIVHCSAGVGRGTGFIIVIDLMLSDI SRQGLGCDLIDPKTIQIVRQORSGMVQTEAQYKFIIVAAQFPE
hSHP2 D1 (NP 002825) PTPN11 (196)	HFRWDFDQVSD--PGGGLDLEEVHHKQES-----IMDAGPIVVHCSAGVGRGTGFIIVIDLMLDI REKGVDCDIDVPKTIQMVRSORSGMVQTEAQYRFIIVAAQHYE
mSHP2 D1 (NP 035332) Pton11 (200)	HFRWDFDQVSD--PGGGLDLEEVHHKQES-----IVDAGPIVVHCSAGVGRGTGFIIVIDLMLDI REKGVDCDIDVPKTIQMVRSORSGMVQTEAQYRFIIVAAQHYE
rSHP2_D1 (NP 037220) Pton11 (196)	HFRWDFDQVSD--PGGGLDLEEVHHKQES-----IVDAGPIVVHCSAGVGRGTGFIIVIDLMLDI REKGVDCDIDVPKTIQMVRSORSGMVQTEAQYRFIIVAAQHYE
cSHP2 D1 (JCS167) (196)	HFRWDFDQVSD--PGGGLDLEEVHHKQES-----ISDAGPIVVHCSAGVGRGTGFIIVIDLMLDI REKGVDCDIDVPKTIQMVRSORSGMVQTEAQYRFIIVAAQHYE
zSHP2 D1 (AAH45328) (196)	HFRWDFDQVGD--PGGGLDLEEVKPKQEG-----ITGAGPIVVHCSAGVGRGTGFIIVIDLMLDI REKGVDCDIDVPKTIQMVRSORSGMVQTEAQYRFIIVAAQHYE
xSHP2 D1 (A56561) (196)	HFRWDFDQVAD--PGGGLDLEEVHHKQEQ-----ITDAGPIVVHCSAGVGRGTGFIIVIDLMLDI REKGVDCDIDVPKTIQMVRSORSGMVQTEAQYRFIIVAAQHYE
hFKTWPFDQVSD--PGGGLDLEEVNKKQDN-----IPEAGPIVVHCSAGVGRGTGFIIVIDLMLDI REKGVDCDIDVPKSIQMVRSORSGMVQTEAQYRFIIVAAQHYE	
rVPTPN6b D1 (BAA95198) (167)	QVTDWDFEHCED--LKGFLSLLEEIQSVRRHTNSTS--D-PQSPNPLVHCSAGVGRGTGFIIVLSIMVAC EHN---EVLDPRLVLELQORRMVLTGLCOYTFVVRVLLIQFQK
hPTPD1 D1 (NP 008970) PTPN21 (184)	QVTDWDFEHCED--LKGFLSLLEEIQSVRRHTNSTS--D-PQSPNPLVHCSAGVGRGTGFIIVLSIMVAC EHN---EVLDPRLVLELQORRMVLTGLCOYTFVVRVLLIQFQK
mPTPRL1 D1 (NP 036007) Pton21 (184)	QVTDWDFEHCED--LKGFLSLLEEIQSVRRHTNSTS--D-PQSPNPLVHCSAGVGRGTGFIIVLSIMVAC EHN---EVLDPRLVLELQORRMVLTGLCOYTFVVRVLLIQFQK
rPTP2E D1 (NP 598229) Pto2E (184)	QVTDWDFEHCED--LKGFLSLLEEIQSVRRHTNSTS--D-PQSPNPLVHCSAGVGRGTGFIIVLSIMVAC EHN---EVLDPRLVLELQORRMVLTGLCOYTFVVRVLLIQFQK
hPTPD2 D1 (NP 005392) PTPN14 (183)	QVTDWDFEHCED--VQGFSLSLLEEIQSVRRHTNSML--EGTKNRHPIVHCSAGVGRGTGFIIVLSIMVAC EHN---EKVPEMMLLELRLRQRMFMTIAAQYKFIIVAAQFQK
mPTP36 D1 (NP 033002) Pton14 (183)	QVTDWDFEHCED--VQGFSLSLLEEIQSVRRHTNSML--EGTKNRHPIVHCSAGVGRGTGFIIVLSIMVAC EHN---EKVPEMMLLELRLRQRMFMTIAAQYKFIIVAAQFQK
rPTPD2 D1 (XP 223062 (revised)) (183)	QVTDWDFEHCED--VQGFSLSLLEEIQSVRRHTNSVL---EGVKTRHPIVHCSAGVGRGTGFIIVLSIMVAC EHN---EKVPEMMLLELRLRQRMFMTIAAQYKFIIVAAQFQK
hMEG1 D1 (NP 002821) PTPN4 (178)	QVLAWDFDQVDD--SSDFLDVFNCHRNKR-----ACKKEPIVVHCSAGVGRGTGFIIVLMTACL ECN---QPVYPLDIDVTRDORAMMIOQTSQYRFFVCEALIKVYE
mMEG1 D1 (NP 064317) Pton4 (178)	QVLAWDFDQVDD--SSDFLDVFNCHRNKR-----ACKKEPIVVHCSAGVGRGTGFIIVLMTACL ECN---QPVYPLDIDVTRDORAMMIOQTSQYRFFVCEALIKVYE
zMEG1 D1 (CAD43435) (173)	QVLAWDFDQVDD--STDFLDVFNCHRNKR-----AGKDEPIVVHCSAGVGRGTGFIIVLMTACL ECLS---QVFPLEIVVTRDORAMMIOQTSQYRFFVCEALIKVYE
hPTPH1 D1 (NP 002820) PTPN3 (178)	QVVAWDFDQVDD--SSDFLEFVNYRSLR-----VDSPELVHCSAGVGRGTGFIIVLMTACL ETERN---LPVYPLDIDVTRDORAMMIOQTSQYRFFVCEALIKVYE
mPTPH1 D1 (XP 143789) Pton3 (178)	QVVAWDFDQVDD--SSDFLEFVNYRSLR-----VDSPELVHCSAGVGRGTGFIIVLMTACL ETERN---LPVYPLDIDVTRDORAMMIOQTSQYRFFVCEALIKVYE
hPTPBAS D1 (NP 006255) PTPN13 (178)	NFTAWDFDHTSQ--PDDLFTFSYRHI-----HRSGPITVHCSAGVGRGTGFIIVLMTACL ECLSQD---LDFDLESDLVRCMLRQRHGMVQTEQYRFFVCEALIKVYE
mPTPBAS D1 (NP 035334) Pton13 (178)	NFTAWDFDHTSQ--PDDLFTFSYRHI-----RRSGPITVHCSAGVGRGTGFIIVLMTACL ECLSQD---LEFDLESDLVRCMLRQRHGMVQTEQYRFFVCEALIKVYE
bPTPA14 D1 (NP 777015) PTPN13 (178)	NFTAWDFDHTSQ--PDDLFTFSYRHHV-----HRSGPITVHCSAGVGRGTGFIIVLMTACL ECLSQD---LEFDLESDLVRCMLRQRHGMVQTEQYRFFVCEALIKVYE
hPTP1A D1 (AL050040) PTPN20 (177)	CFTKWDFDGTAS--ADSFLLKRYRKS-----HITGPIVVHCSAGVGRGTGFIIVLMTACL EKN---YSDFMNIVLQORRQORGMIOQTSQYRFFVCEALIKVYE
mPTP1Typ_D1 (NP 033004) Pton20 (176)	CFTKWDFDGTAS--ADSFLLKRYRKS-----HITGPIVVHCSAGVGRGTGFIIVLMTACL EKN---YSDFMNIVLQORRQORGMIOQTSQYRFFVCEALIKVYE
cPTP1B D1 (O13016) (175)	HVTTWDFDQVSES--PASFLLFKVRESGS-----LNPEYGPVVHCSAGVGRGTGFIIVLMTACL EKN---YSDFMNIVLQORRQORGMIOQTSQYRFFVCEALIKVYE
hPTP1B D1 (NP 002818) PTPN1 (175)	HVTTWDFDQVSES--PASFLLFKVRESGS-----LSPHEGPIVVHCSAGVGRGTGFIIVLMTACL ECLL---DKRKPDPSSVDKVVLEMLRFRMGLIQTALQRLRSLVLAIEGAK
mPTP1B D1 (NP 035331) Pton1 (175)	HVTTWDFDQVSES--PASFLLFKVRESGS-----LSPHEGPIVVHCSAGVGRGTGFIIVLMTACL ECLL---DKRKPDPSSVDKVVLEMLRFRMGLIQTALQRLRSLVLAIEGAK
rPTP1B D1 (NP 036769) Pton1 (175)	HVTTWDFDQVSES--PASFLLFKVRESGS-----LSPHEGPIVVHCSAGVGRGTGFIIVLMTACL ECLL---DKRKPDPSSVDKVVLEMLRFRMGLIQTALQRLRSLVLAIEGAK
zPTP1B D1 (NP 570999) pto1b (173)	HVTTWDFDQVSES--PASFLLFKVRESGS-----LSPHEGPIVVHCSAGVGRGTGFIIVLMTACL ECLL---DKRKPDPSSVDKVVLEMLRFRMGLIQTALQRLRSLVLAIEGAK
hTCTPT D1 (NP 002819) PTPN2 (174)	HVTTWDFDQVSES--PASFLLFKVRESGS-----LNPDPHGPVHCSAGVGRGTGFIIVLMTACL EKEG---DDVNVKQVLLNMRKYRMLIQTALQRLRSLVLAIEGAK
mTCTPT D1 (NP 033003) Pton2 (174)	HVTTWDFDQVSES--PASFLLFKVRESGS-----LNPDPHGPVHCSAGVGRGTGFIIVLMTACL EKEG---EDVNVKQVLLNMRKYRMLIQTALQRLRSLVLAIEGAK
rTCTPT D1 (NP 446442) Pton2 (174)	HVTTWDFDQVSES--PASFLLFKVRESGS-----LNPDPHGPVHCSAGVGRGTGFIIVLMTACL EKEG---EDVNVKQVLLNMRKYRMLIQTALQRLRSLVLAIEGAK
zTCTPT D1 (AAH44373) (173)	HVTTWDFDQVSES--PASFLLFKVRESGS-----LGMGEQGPVHCSAGVGRGTGFIIVLMTACL EKEEL---GTNVVQTVSRMRTORAFSIOQTSQYRFFVCEALIKVYE
hMEG2 D1 (NP 002824) PTPN9 (179)	QVLSWDFDQVSS--AASLIDLRVNRNQSLAVSNMGRSCKGCPPEPIVHCSAGVGRGTGFIIVLMTACL EEL---GTNVVQTVSRMRTORAFSIOQTSQYRFFVCEALIKVYE
mMEG2_D1 (NP 062625) Pton9 (179)	QVLSWDFDQVSS--AASLIDLRVNRNQSLAVSNMGRSCKGCPPEPIVHCSAGVGRGTGFIIVLMTACL EEL---GTNVVQTVSRMRTORAFSIOQTSQYRFFVCEALIKVYE
xPTPX10 D1 (B53978) (179)	QVMSWDFDQVSKS--ASALIDRSQKHQAVAVQNLGMEWTKGCPPEPIVHCSAGVGRGTGFIIVLMTACL EEL---GTNVVQTVSRMRTORAFSIOQTSQYRFFVCEALIKVYE
xPTPX1 D1 (AAH43621) (179)	QVMSWDFDQVSKS--ASALIDRSQKHQAVAVQNLGMAWTGHPAGPPIVHCSAGVGRGTGFIIVLMTACL EEL---GTNVVQTVSRMRTORAFSIOQTSQYRFFVCEALIKVYE
hHDPTP D1 (NP 056281) PTPN23 (183)	HFFTWFELGLDS--PSNLLRTOEHAHYLHQR-----PLHTFIVHCSAGVGRGTGFIIVLMTACL EAG---NGIPELQVLRMRQRKHMDEKHLHRLRCEAVVRRHBE
mHDPTP D1 (AAH22721) (183)	HFFTWFELGLDS--PSNLLRTOEHAHYLHQR-----PLHTFIVHCSAGVGRGTGFIIVLMTACL EAG---NGIPELQVLRMRQRKHMDEKHLHRLRCEAVVRRHBE
rPTPTD14 D1 (T14355) (183)	HFFTWFELGLDS--PSNLLRTOEHAHYLHQR-----PLHTFIVHCSAGVGRGTGFIIVLMTACL EAG---NGIPELQVLRMRQRKHMDEKHLHRLRCEAVVRRHBE
hIA2 D1 (NP 002837) PTPRN (179)	HFLSWFACETAS--TRPFLDRRKNKCYR-----GRSCIVHCSAGVGRGTGFIIVLMTACL EAG---VKEIDVLAATLHVDRDORPGLVRSKDOEFALTAVAEEN
mIA2 D1 (NP 033011) Ptprr (179)	HFLSWFACETAS--TRPFLDRRKNKCYR-----GRSCIVHCSAGVGRGTGFIIVLMTACL EAG---VKEIDVLAATLHVDRDORPGLVRSKDOEFALTAVAEEN
rIA2_D1 (NP 446333) Ptprr (179)	HFLSWFACETAS--TRPFLDRRKNKCYR-----GRSCIVHCSAGVGRGTGFIIVLMTACL EAG---VKEIDVLAATLHVDRDORPGLVRSKDOEFALTAVAEEN

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	FALTAVAEEN				
hIA2beta D1 (NP 002838) PTPRN2 (179)	HFLSNYDRGVSS--SRSL	LDLRRKVNKCYR-----	GRSC	ILVHCS	DGAGRTGTYV	LDLDMVNNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQDFE	FALTAVAEEN				
macnelA2beta D1 (O02695) (179)	HFLSNYDRGVSS--SRSL	LDLRRKVNKCYR-----	GRSC	ILVHCS	DGAGRTGTYV	LDLDMVNNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQDFE	FALTAVAEEN				
mPTPNP D1 (P80560) Ptdrn2 (179)	HFLSNYDRGVSS--TRSL	LDLRRKVNKCYR-----	GRSC	ILVHCS	DGAGRTGTYV	LDLDMVNNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQDFE	FALTAVAEEN				
rPTPNE6 D1 (NP 113788) Ptdrn2 (179)	HFLSNYDRGVSS--TRSL	LDLRRKVNKCYR-----	GRSC	ILVHCS	DGAGRTGTYV	LDLDMVNNR	AKG--AKE	LDIAATLEHVRDORPGLVRSKQDFE	FALTAVAEEN				
hCD45 D2 (NP 002829) PTPRC (199)	QNTNNSVEQFAE--PKEL	ISMVQVKKQLPKQNSSEG	---	KYHKS	SLVHR	RDSSQQTGL	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP				
mCD45 D2 (NP 035340) Ptdrc (199)	QCTTWKGEFAE--PKDL	VTLQNKQKLPKSGSEG	---	KYHKS	SLVHR	RDSSQQTGL	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP				
rCD45 D2 (XP 213985) Ptdrc (199)	QCTTWKGEFAE--PKDL	VTLQNKQKLPKSGSEG	---	KYHKS	SLVHR	RDSSQQTGL	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP				
cCD45 D2 (A54080) (199)	QYHKNGLDVPE--PKDL	VDMVLSKQKVPSPASEDS	---	RNSRS	YFVH	CDSSQQTGL	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP				
fuCD45 D2 (CAB96211) (199)	QFLKMGKVEPE--PKDL	ADLKEKHKRCGY	---	TWPR	STV	IVH	CN	SGSRGAF	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
cypcaCD45 D2 (BAA92179) (197)	QFLKMGKVEPE--PKDL	VDMVLSKQKVPSPASEDS	---	RNSRS	YFVH	CDSSQQTGL	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP				
aotvoCD45 D2 (AAM48512) (3') (191)	QYTNNSVXXLAX--PKEL	ISMVQVKKQLPKQNSSEG	---	KXHK	SLV	HRDSSQQTGL	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP				
sharkCD45 D2 (T43148) (198)	HFHDWASELED--PSNF	TKMLRSKELKSLTQPEE	---	SSL	SPSL	VH	CS	DGAKTGV	YAWILL	DNADT--	ENVLDVLTQVVKALRKARPGMVSTFQYQFLVDVASTYP		
cPTPaloha D2 (AAB04150) (181)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGNH	PIVH	CS	AG	AGRTGTF	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
hPTPaloha D2 (NP 002827) PTPRA (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGNH	PIVH	CS	AG	AGRTGTF	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
mPTPaloha D2 (NP 033006) Ptdra (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGNH	PIVH	CS	AG	AGRTGTF	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
rPTPaloha D2 (NP 036895) Ptdra (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGNH	PIVH	CS	AG	AGRTGTF	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
xPTPaloha D2 (AAA17990) (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGNH	PIVH	CS	AG	AGRTGTF	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
zPTPaloha D2 (NP 571963) ptdra (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGNH	PIVH	CS	AG	AGRTGTF	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
rvPTPR4b D2 (BAA95196) (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGNH	PIVH	CS	AG	AGRTGTF	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
hPTPepsilon D2 (NP 006495) PTPRE (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGNH	PIVH	CS	AG	AGRTGTF	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
mPTPepsilon D2 (NP 035342) Ptdre (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGNH	PIVH	CS	AG	AGRTGTF	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
rPTPepsilon D2 (XP 215102) Ptdre (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGNH	PIVH	CS	AG	AGRTGTF	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
orylaPTPepsilon D2 (BAC06424) (187)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGNH	PIVH	CS	AG	AGRTGTF	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
rvPTPR4a D2 (BAA95190) (182)	HFHGWFEVGLSD--GKGN	INLIAAQKQQQ	---	QSGNH	PIVH	CS	AG	AGRTGTF	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
hPTPkappa D2 (NP 002835) PTPRK (180)	QNLGASREVPGS--KRSF	LKLLQLEKQWEEC	---	EEGE	RTLH	CLNG	GG	RGMP	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
mPTPkappa D2 (NP 033009) Ptdrk (180)	QNLGASREVPGS--KRSF	LKLLQLEKQWEEC	---	EEGE	RTLH	CLNG	GG	RGMP	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
rvPTPR2B D2 (BAA95194) (180)	QNLGASREVPGS--KRSF	LKLLQLEKQWEEC	---	EEGE	RTLH	CLNG	GG	RGMP	CAFLNLL	LSAET--	EVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP		
hPTPlamda D2 (NP 005695) PTPRU (183)	QFLRNSARDTPDS--KRAF	LHLILAEKQWAE	---	GDERT	VH	CLNG	GG	RGMT	CACATV	LEMRC--	HNLVDVFFAAKTLRNYKSNMVEITMDFHFCVDVALEYE		
mPTPlamda D2 (NP 035344) Ptdrl (183)	QFLRNSARDTPDS--KRAF	LHLILAEKQWAE	---	GDERT	VH	CLNG	GG	RGMT	CACATV	LEMRC--	HNLVDVFFAAKTLRNYKSNMVEITMDFHFCVDVALEYE		
mPTPmu D2 (NP 002836) PTPRM (180)	QFLGWMRDTPVPS--KRSF	LKLLQLEKQWEEYN	---	GGEG	PTVH	CLNG	GG	RRGTF	CALISV	ICMRRH--	QRTVDVFFHAVKTLRNNKSNMVDLLDQYKFCVEVALEYEN		
mPTPmu D2 (NP 033010) Ptdrm (180)	QFLGWMRDTPVPS--KRSF	LKLLQLEKQWEEYN	---	GGEG	PTVH	CLNG	GG	RRGTF	CALISV	ICMRRH--	QRTVDVFFHAVKTLRNNKSNMVDLLDQYKFCVEVALEYEN		
rPTPmu D2 (XP 237546 (revised)) (180)	QFLGWMRDTPVPS--KRSF	LKLLQLEKQWEEYN	---	GGEG	PTVH	CLNG	GG	RRGTF	CALISV	ICMRRH--	QRTVDVFFHAVKTLRNNKSNMVDLLDQYKFCVEVALEYEN		
hPTPrho D2 (NP 573400) PTPRT (180)	QILGWARDTPPS--KRSF	LKVVRREKQWEEQYD	---	GREGR	TVH	CLNG	GG	RRGTF	CALISV	ICMRRH--	QNTVDVFFHIVKTLRNNKSNMVEITLQYKFCVEVALEYES		
mPTPrho D2 (NP 067439) Ptdrr (180)	QILGWARDTPPS--KRSF	LKVVRREKQWEEQYD	---	GREGR	TVH	CLNG	GG	RRGTF	CALISV	ICMRRH--	QNTVDVFFHIVKTLRNNKSNMVEITLQYKFCVEVALEYES		
cPTPsiama D2 (I50212) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
hLAR D2 (NP 002831) PTPRF (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
mLAR D2 (NP 035343) Ptdrf (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
rLAR D2 (NP 062122) Ptdrf (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
xLAR D2 (AAF43606) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
zLAR D2 (CAC44758) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
rvPTPR2Aa D2 (BAA95188) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
hPTPdelta D2 (NP 002830) PTPRD (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
mPTPdelta D2 (D54689) (181)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
xPTPdelta D2 (AAF43605) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
rvPTPR2Ab D2 (BAA95191) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
hPTPsiama D2 (NP 002841) PTPRS (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
mPTPsiama D2 (NP 035348) Ptdrs (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
xPTPsiama D2 (AAF43607) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
zPTPsiama D2 (CAC44759) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
rPTPsiama D2 (NP 062013) Ptdrd (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
rvPTPR2Ac D2 (BAA95193) (182)	QFTDWEQGVVFKS--GEGF	LDLGOVHKTKEQFG	---	QDGP	ITVH	CS	AG	AGRTGTF	VITLS	SIVL	ERNRY--	EGVVDVVFQVVKALRKARPGMVSTFQYQFLVDVASTYP	
hPTPaamma D2 (NP 002832) PTPRG (186)	QCPKWFNPDAFIS--STFEL	LVNFKKEALT	---	RDGP	ITVH	DE	HG	GV	TSAGT	LCAL	TTL	HHQEK--	ENSVDVYQVAKMNLNMRPGVFTFDI
mPTPaamma D2 (NP 033007) Ptdra (186)	QCPKWFNPDAFIS--STFEL	LVNFKKEALT	---	RDGP	ITVH	DE	HG	GV	TSAGT	LCAL	TTL	HHQEK--	ENSVDVYQVAKMNLNMRPGVFTFDI
rPTPaamma D2 (NP 599183) Ptdra (178)	YVLEVRHGFAPIS--STFEL	LVNFKKEALA	---	RDGP	ITVH	DE	HG	GV	TSAGT	LCAL	TTL	HHQEK--	ENSVDVYQVAKMNLNMRPGVFTFDI
rvPTPR5b D2 (BAA95197) (186)	QCPKWFNPDAFIS--STFEL	LVNFKKEAST	---	RDGP	ITVH	DE	HG	GV	TSAGT	LCAL	TTL	HHQEK--	ENSVDVYQVAKMNLNMRPGVFTFDI
cPTPaamma D2 (Q98936) (186)	QCPKWFNPDAFIS--STFEL	LVNFKKEALT	---	RDGP	ITVH	DE	HG	GV	TSAGT	LCAL	TTL	HHQEK--	ENSVDVYQVAKMNLNMRPGVFTFDI
hPTPzeta D2 (NP 002842) PTPRZ1 (185)	QCPKWFNPDSFIS--KTFEL	LVNFKKEAAN	---	RDGP	ITVH	DE	HG	GV	TSAGT	LCAL	TTL	HHQEK--	ENSVDVYQVAKMNLNMRPGVFTFDI
cPTPzeta D2 (AAA49015) (185)	QCPKWFNPDSFIS--KTFEL	LVNFKKEAAN	---	RDGP	ITVH	DE	HG	GV	TSAGT	LCAL	TTL	HHQEK--	ENSVDVYQVAKMNLNMRPGVFTFDI
mPTPzeta D2 (XP 133090) Ptdrz1 (185)	QCPKWFNPDSFIS--KTFEL	LVNFKKEAAN	---	RDGP	ITVH	DE	HG	GV	TSAGT	LCAL	TTL	HHQEK--	ENSVDVYQVAKMNLNMRPGVFTFDI
rPTPzeta D2 (NP 037212) Ptdrz1 (185)	QCPKWFNPDSFIS--KTFEL	LVNFKKEAAN	---	RDGP	ITVH	DE	HG	GV	TSAGT	LCAL	TTL	HHQEK--	ENSVDVYQVAKMNLNMRPGVFTFDI
xPTPzeta D2 (BAA97445) (185)	QCPKWFNPDSFIS--KTFEL	LVNFKKEAAN	---	RDGP	ITVH	DE	HG	GV	TSAGT	LCAL	TTL	HHQEK--	ENSVDVYQVAKMNLNMRPGVFTFDI
rvPTPR5a D2 (BAA95195) (181)	QSPRWFNPDSFIS--KTFEL	LVNFKKEAAN	---	RDGP	ITVH	DE	HG	GV	TSAGT	LCAL	TTL	HHQEK--	ENSVDVYQVAKMNLNMRPGVFTFDI
Consensus (237)	QFTWPDHGVV	LLFI	V										