

# Alignment of 37 Human PTP 'catalytic' domains (excluding domain D2 sequences)

Amino acid	#10	#20	#30	#40	#50	#60	#70	#80		
hPTPalpha	DKLEEEIINRRMADDN	---KLFREEFNAL	ACPIQA	---TCEAASKEENKRN	VYVNI	LDYDHSRRLT	VEGV	---PDSY	YNAFNGV	---DEKNKFA
hPTPepsilon	DLIETIRASDDC	---FRREIRAS	ACPIQA	---TCEAASKEENKRN	VYVNI	LDYDHSRRLT	VEGV	---PDSY	YNAFNGV	---DEKNKFA
hPTPKappa	ADLLQHIINLMKTS	---YGFKEEYEF	FEQOSA	---SWDAKADQNRN	GNVNI	IAYDHSRRLT	LOPVEDD	---PSSDY	YNAFNGV	---QRSHY
hPTPmu	ADLLQHIINOMKCAEG	---YGFKEEYEF	FEQOSA	---SWDAKADQNRN	GNVNI	IAYDHSRRLT	LOPVEDD	---PSSDY	YNAFNGV	---QRSHY
hPTPrho	ADLLQHIINOMKCAEG	---YGFKEEYEF	FEQOSA	---SWDAKADQNRN	GNVNI	IAYDHSRRLT	LOPVEDD	---PSSDY	YNAFNGV	---QRSHY
hPTPlamda	ADLLQHIINOMKCAEG	---YGFKEEYEF	FEQOSA	---SWDAKADQNRN	GNVNI	IAYDHSRRLT	LOPVEDD	---PSSDY	YNAFNGV	---QRSHY
hPTPdelta	LELADLHIERLKANDN	---LKFSEYEF	DPGQGF	---TWEHNSLEVNPKN	RYANV	IAYDHSRRLT	LOPVEDD	---PSSDY	YNAFNGV	---RKNAY
hPTPsigma	ADMAEHTERLKANDS	---LKLSEYEF	DPGQGF	---TWEHNSLEVNPKN	RYANV	IAYDHSRRLT	LOPVEDD	---PSSDY	YNAFNGV	---RKNAY
hPTPgammagamma	QVVKHIGELYSNNQ	---HGFSEDFE	QRCTADMN	---TAEHSNHPENKHK	RYINL	IAYDHSRRLT	LOPVEDD	---PSSDY	YNAFNGV	---RKNAY
hPTPzeta	KHFPHKAVDLHASSGF	---TEEFETLKE	FYQSDVLDGI	---TADSSNHDPNKHK	RYINL	IAYDHSRRLT	LOPVEDD	---PSSDY	YNAFNGV	---RKNAY
hLAR	TDLADNLERLKANDG	---LKFSEYEF	DPGQGF	---TWEHNSLEVNPKN	RYANV	IAYDHSRRLT	LOPVEDD	---PSSDY	YNAFNGV	---RKNAY
hCD45	DILLETYKRRKIADEG	---RFLAEFQSI	PRVFSKF	---PIKEARKFPNOKN	RYVDI	LDYDHSRRLT	VEGV	---GASNY	YNAFNGV	---DEKNKFA
hGLEPP1	DDFDAYIKDMKADS	---YKFLQFEE	KLIGLDI	---PFAADLPNRCKN	RYVNI	LDYDHSRRLT	VEGV	---EGADY	YNAFNGV	---NSPQEI
hTPSP31	KPFLQVHFRCTNNN	---LKFSEYEF	RFQDL	---SSTADLPWRNR	RYVNI	LDYDHSRRLT	VEGV	---PSSDY	YNAFNGV	---RKNAY
hDEP1	KSFAYVFKKQADS	---CFAEYEDL	KLVLGSD	---PKYAELEENRKN	RYNVL	LDYDHSRRLT	VEGV	---TDDY	YNAFNGV	---NSPQEI
hPTPbeta	NEQFEGHFMKQADSN	---YLLSKEYE	KDVGRRN	---SCDIALLENRKN	RYNVL	LDYDHSRRLT	VEGV	---PCSDY	YNAFNGV	---RKNAY
hSAP1	EDFADHVRNDRNSN	---CGFADEYQ	SLVGHSSQ	---SOMVASSENARK	RYNVL	LDYDHSRRLT	VEGV	---PGSDY	YNAFNGV	---RKNAY
hSTEP	SRVLQALRLEHKALDP	---FLLQAEF	PMNFVD	---PKEYDIPGLVRK	RYNVL	LDYDHSRRLT	VEGV	---PLSSY	YNAFNGV	---RKNAY
hPCPTP1	SRILTRSQLDRVASS	---HLLQSEFM	PMNFVD	---PKEYDIPGLVRK	RYNVL	LDYDHSRRLT	VEGV	---PLSSY	YNAFNGV	---RKNAY
hHePTP	GHPLTRWALQRPPSP	---KQLSEEF	KLIFNFVS	---PEDLDIPGHASK	RYNVL	LDYDHSRRLT	VEGV	---DGDY	YNAFNGV	---RKNAY
hSHP1	ADIENTRVLNKKQSEDTAKAG	WEEFESL	LKQEVKNLH	---ORLEQRPNENK	RYNVL	LDYDHSRRLT	VEGV	---PGSDY	YNAFNGV	---RKNAY
hSHP2	AEIESRVRLELQKLAETDPKQGG	WEEFETL	QQECKLYL	---SRKEGQRPNENK	RYNVL	LDYDHSRRLT	VEGV	---PVSDY	YNAFNGV	---RKNAY
hPEST	EILKQFIRQVQKMSDHNEDFN	FARDFMRL	RRLSTKYRTEKIYPT	TAEGEENVKK	RYNVL	LDYDHSRRLT	VEGV	---QDSDY	YNAFNGV	---RKNAY
hLYPTP	EILKQFIRQVQKMSDHNEDFN	FARDFMRL	RRLSTKYRTEKIYPT	TAEGEENVKK	RYNVL	LDYDHSRRLT	VEGV	---QDSDY	YNAFNGV	---RKNAY
hBDP1	DSARSFLERLEARGRGITK	---EFAVLEF	SDIACSA	AAWKAADGVCST	VAGSRPNVRK	RYNVL	LDYDHSRRLT	VEGV	---GSDY	YNAFNGV
hPTPD1	ATNDRCKLLEQRLEGG	---MVFTEER	LKRRLVGD	---EGSTARLPENR	RYNVL	LDYDHSRRLT	VEGV	---NTG	YNAFNGV	---RKNAY
hPTPD2	VQELRFRTRKMLLE	---MVFTEER	LKRRLVGD	---EGSTARLPENR	RYNVL	LDYDHSRRLT	VEGV	---NTG	YNAFNGV	---RKNAY
hMEG1	HLRESLMIQLEAGLITG	---VTLTDFQ	LRKPKGM	---TMSCAKLPQNI	ISKRYD	LDYDHSRRLT	VEGV	---NEDY	YNAFNGV	---RKNAY
hPTPH1	DTLEGSMAQLKKGLESG	---TVLQFEL	YRKKPGL	---AIFTAKLPQNLK	RYNVL	LDYDHSRRLT	VEGV	---NEDY	YNAFNGV	---RKNAY
hPTPBA5	KSVIRVRLGLDQGI	---PSKELN	QELKPLD	---OCLIGQTKENR	RYNVL	LDYDHSRRLT	VEGV	---EGGY	YNAFNGV	---RKNAY
hPTP1B	MEMEKEFEQDKSGS	---WAAIYQD	REASDF	---PCHRYAKLPKNR	RYNVL	LDYDHSRRLT	VEGV	---DNDY	YNAFNGV	---RKNAY
hTCPTP	TTIEREFEEQLDQRR	---WQPLYLE	RNESHDY	---PHRYAKFENRNR	RYNVL	LDYDHSRRLT	VEGV	---ENDY	YNAFNGV	---RKNAY
hMEG2	MTIQELVDYVNRQKQ	---GIYEEY	QRENPGV	---TFCHSCMSPG	LNKRYD	LDYDHSRRLT	VEGV	---QTDY	YNAFNGV	---RKNAY
hIA2	HMILAYMEDHLNRDR	---LAKWEAL	CAYAEPN	---TCATAGEGN	IKKRNHP	LDYDHSRRLT	VEGV	---RSDY	YNAFNGV	---RKNAY
hIA2beta	HMILAYMEDHLNRDR	---LAKWEAL	CAYAEPN	---TCATAGEGN	IKKRNHP	LDYDHSRRLT	VEGV	---RSDY	YNAFNGV	---RKNAY
hPTPTyp	TAIKDCLKLIEEKATA	---YDIHQEF	MALILK	NPLG	---SFYSGNQR	SNRKNR	LDYDHSRRLT	VEGV	---SKDY	YNAFNGV
hHDPTP	ERLRQLQDELEAFRGLQGD	VALDTVYWR	LEDAEQHDAR	---GRSIA	ARCYSY	LNKRYD	LDYDHSRRLT	VEGV	---KDDY	YNAFNGV
Consensus	(amino acid identity 100%, 90%, 80%)	E								

Amino acid	#90	#100	#110	#120	#130	#140	#150	#160	#170	#180												
hPTPalpha	KEEIVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTPepsilon	KQETVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTPKappa	VHETIYD	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTPmu	MOEITIYD	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTPrho	MOEITIYD	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTPlamda	KPEMIVD	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTPdelta	LEPITGDF	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTPsigma	LEPITGDF	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTPgammagamma	KSTFEDF	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTPzeta	LKSTEDF	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hLAR	LEPITGDF	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hCD45	RDETVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hGLEPP1	LEPITGDF	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hTPSP31	LPQTVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hDEP1	LPQTVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTPbeta	LPQTVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hSAP1	LPQTVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hSTEP	LPQTVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPCPTP1	LPQTVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hHePTP	LPQTVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hSHP1	LEATVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hSHP2	LQNTVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPEST	LANTVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hLYPTP	LSTVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hBDP1	LSTVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTPD1	LQNTVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTPD2	LQNTVND	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hMEG1	LPHTCHD	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTPH1	LPHTCAQ	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTPBA5	LPHTCAQ	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hPTP1B	LPHTCAQ	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hICP1P	LPNTCCH	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hMEG2	LENTYAD	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hIA2	LSHITAD	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DFG	VFFT
hIA2beta	LSHITAD	FWRMI	IWEQNTAI	IVMVNTL	KEK	ERK	ECK	CAQYWP	---GGQWTY	GNIRVSV	VEDVT	LDVDT	VKRF	CIQQV	GDMTN	---RK	PQL	ITOF	HFTS	WDF	DF	

	(1)	10	20	30	40	50	60	70	80	90	100	111																																					
hCD45 D1 (NP_002829) PTPRC	(1)	DILETYKRKIAD	EG-----RL	LAEFQST	PRVFSKF--	PIKEARKF	FNQNKNRYVD	ILPYDYNRV	ELSEINGDAG--	SNYINASYIDGF	-----	KEPRKYIAAQG																																					
hPTPalph D1 (NP_002827) PTPRA	(1)	DKLEEEENRRM	ADDN-----	KLREEFN	ALPACPIQA--	TCEAASKE	ENKEKNRYVN	ILPYDHSRV	VHLLTPVEGVPD--	SDYINASFINGM	-----	QEKNKFIAAQG																																					
hPTPepsilon D1 (NP_006495) PTPRE	(1)	EHLLEEEERIR	SADD-----	KQFRE	EFNSLPSGHIQ	Q--TFELANKE	ENREKNRYPN	ILENDHSRV	ILSQLDGI	PC--SDYINASYIDGY	-----	KEKNKFIAAQG																																					
hPTPlamda D1 (NP_005695) PTPRU	(1)	ADLLQHNQMK	TAEG-----	YGFQ	EYESFFEG	-----	WDATKKK	KVKGSRQEP	MPAYDRHRV	KLHPMLGDPN--	ADYINANYIDGY	-----	HRSNHFIATQG																																				
hPTPkappa D1 (NP_002835) PTPRK	(1)	ADLLQHNLM	MKTSDS-----	YGFKE	EYESFFEG	QSA--	SWDVAKK	DNRAKNRYGN	LAYDHSRV	ILQVPVEDDPS--	SDYINANYIDGY	-----	QRP SHYIATQG																																				
hPTPmu D1 (NP_002836) PTPRM	(1)	ADLLQHTQM	KCAEG-----	YGFKE	EYESFFEG	QSA--	PWDSAKK	DNRMKNRYGN	LAYDHSRV	LQTI	EGDTN--	SDYINANYIDGY	-----	HRPNHYIATQG																																			
hPTPrho D1 (NP_573400) PTPRT	(1)	ADLLQHTQM	KRGQG-----	YGFKE	EYESFFEG	QTA--	SWDTAKED	ENRNKNRYGN	LSYDHSRV	LLVLDGDPH--	ADYINANYIDGY	-----	HRPRHYIATQG																																				
hPTPsiama D1 (NP_002841) PTPRS	(1)	ADMAEHTER	LKANDS-----	LKLSQ	EYESIDDPG	QF--	TWEHSN	LEVNKPKNRYANV	LAYDHSRV	ILQPIEGIMG--	SDYINANYIDGY	-----	RRQNAHYIATQG																																				
hPTPdelta D1 (NP_002830) PTPRD	(1)	LELADHTE	RKANDN-----	LKFSQ	EYESIDDPG	QF--	TWEHSN	LEVNKPKNRYANV	LAYDHSRV	LLSAIEGIPG--	SDYINANYIDGY	-----	RKQNAHYIATQG																																				
hLAR D1 (NP_002831) PTPRF	(1)	TDLADNTE	RKANDG-----	LKFSQ	EYESIDDPG	QF--	TWENS	NLEVNKPKNRYANV	LAYDHSRV	ILTSIDGVPG--	SDYINANYIDGY	-----	RKQNAHYIATQG																																				
hPTPaamma D1 (NP_002832) PTPRG	(1)	KQFVKHTE	GELYSNQ-----	HGFSE	DFEIVQ	RCTADMN	ITAEHSNH	PKNKKNRYIN	LAYDHSRV	KLRPLPGKDSKH	SDYINANYIDGY	-----	NKAKAYIATQG																																				
hPTPzeta D1 (NP_002842) PTPRZ1	(1)	KHFFKHVAD	LHASSG--	FTEEF	ETLKEFYQ	EQVQ	SCTVDL	LGITADS	SNHDPN	KKKNRYINL	WAYDHSRV	KLAQLAEKDGKLT	SDYINANYIDGY	-----	NRPKAYIAAQG																																		
hSAP1 D1 (NP_002833) PTPRH	(1)	EDFADHTE	RKNERDSN-----	CGFAD	EYQQL	SLVGH	SQ--	SQMVAS	ASENNAKNRYRN	VL	PYDWSRV	LKPIHEEPG--	SDYINASFMPGL	-----	WSPQEFIATQG																																		
hDEP1 D1 (NP_002834) PTPRJ	(1)	ENFEAYFK	KQADSN-----	CGFAE	EYEDL	KLVG	ISQ--	PKYAAEL	ENRGKNRYNN	VL	PYDIRV	KLSVQTHST--	DDYINANYMPGN	-----	HSK KDFIATQG																																		
hPTPbeta D1 (NP_002828) PTPRB	(1)	NQFEGHF	MKLQADSN-----	YLLSK	EYEEK	KDVGR	NQ--	SCDIAL	LLFENRGKNRYNN	IL	PYDA	TRV	KLSNVDDDP	SDYINASYIPGN	-----	NFRREYIVTQG																																	
hGLEPP1 D1 (NP_109592) PTPRO	(1)	DDFDAYTK	DMAKDS-----	YKSLQ	PEEL	KLIG	LDI--	PHFADL	FLNRCNRYTN	IL	PYDF	SRV	LVS MNEEG	ADYINANYIPGN	-----	NSPQEFIATQG																																	
hPTPS31 D1 (AR073855) PTPGMC1	(1)	KSFLLQHV	EELCTNN-----	LKQ	EEFSEL	PKFL	QDL--	SSTADL	PWNRANKRFPN	L	FPYNNNRV	KLIADASVPG--	SDYINASYISGY	-----	LCPNEFIATQG																																		
hHePTP D1 (NP_002823) PTPN7	(1)	HPITRWAL	LQRPPSP-----	KQLEE	EFLLK	PSNF	VS--	PEDLDI	PGHASKDRYKT	IL	ENPQ	SRV	CLGRAQSQED--	GDYINANYIRGYD	-----	GKEKVIATQG																																	
hPCPTP1 D1 (NP_002840) PTPRR	(1)	SRLTRS	QLRDVASS-----	HLLQ	SFEME	PMNF	VDD--	PKEIDI	PRHGTKNRYKT	IL	ENPL	SRV	CLRPKNVTDS--	L	STYINANYIRGYS	-----	GKEKVIATQG																																
hSTEP D1 (NP_116170) PTPN5	(1)	SRVLQAEEL	LHEKALDP-----	FLLQA	EFPEI	PMNF	VDD--	PKEYDI	PLGVRKNRYKT	IL	ENPH	SRV	CLTSPDPDDP--	L	SSYINANYIRGYS	-----	GEEKVIATQG																																
hSHP1 D1 (NP_002822) PTPN6	(1)	ADLENR	LELNKKQES-EDTAKAG	WEFE	ESL	QKQEV	KNLHQRLE	EGQR	ENKGNRYKN	IL	FDHSRV	ILQGRDSNIPG--	SDYINANYIKNQLL	GPD--	ENAKTYIASQG																																		
hSHP2 D1 (NP_002825) PTPN11	(1)	AELSR	RELKSLAET-TDKVKQG	WEFE	ETL	QQECK	LLYSRKE	GQRQ	ENKKNRYKN	IL	FDHT	TRV	VLHDGDPNEPV--	SDYINANIIMPEFETKCNNSKPKKS	YIATQG																																		
hTPD1 D1 (NP_008970) PTPN21	(1)	ATNDR	CKILEQRLEGG-----	MVF	TEYER	LKKRL	VDG--	ECSTAR	LPENAE	RNR	FD	VL	PYDD	ARV	ELVPTKENN--	TGYINASHIKVSVS	-----	GIEWDYIATQG																															
hTPD2 D1 (NP_005392) PTPN14	(1)	VPNDR	FRTLKKKLEEG-----	MVF	TEYEQ	PKKK	ANG--	IFSTAAL	PENAE	SR	IRE	VV	PYE	ENR	VELIPTKENN--	TGYINASHIKVVVG	-----	GAEWHYIATQG																															
hMEG1 D1 (NP_002821) PTPN4	(1)	HSIRES	IQLAEG	LITG-----	TVLTQ	FDQ	YRKK	PGM--	TMSCAK	L	PNIS	KNRYRD	SPYDA	TRV	LLKGN--	EDYINANYINMEIPSS	-----	SIINQYIACQG																															
hTPH1 D1 (NP_002820) PTPN3	(1)	DTLEGS	MAQLKKGLESG-----	TVLIQ	PEQ	YRKK	PGL--	AITFAK	L	QNL	KNRYKD	VL	PYDT	TRV	LLQGN--	EDYINASYNMEIPAA	-----	NLVNKYIATQG																															
hMEG2 D1 (NP_002824) PTPN9	(1)	MTIQEL	VDYVNRQK-----	QGIYE	EYEDI	RR	NPV	G--	TFHCS	MS	PN	LE	KNRYGD	VPCLDQ	TRV	KLTKRSGHTQ--	TDYINASFMDGY	-----	KQKNAYIGTQG																														
hPTP1B D1 (NP_002818) PTPN1	(1)	MEMEKE	FEQIDKSGS-----	WAAIY	QD	RHEA	SDF--	PCRVAK	L	PKNKNRYRD	VS	FDHSRV	IKLHQED--	NDYINASLTKME	-----	EAQRSYILTQG																																	
hTCPTP D1 (NP_002819) PTPN2	(1)	TTIERE	FEELDTQRR-----	WOPLY	LE	RNE	SHDY--	PHRVAK	F	ENRNRNRYRD	SPYD	HSRV	KLQNAE--	NDYINASLV	DI	E	EAQRSYILTQG																																
hPTPBAS D1 (NP_006255) PTPN13	(1)	ANLKS	VTRVLRGLLDQ-----	GIPSK	EL	ENL	QELK	PLD--	QCLI	GQTR	ENRR	KNRYKN	ILPYDA	TRV	PLGDE--	GGYINASFIKIPVG	-----	KEEFVYIACQG																															
hPTPTyp D1 (AL050040) PTPN20	(1)	TAL	KDCKILEEK	TAA-----	YD	MQ	EF	MA	EL	KNL	LP	G--	EFYS	GNQ	SNRE	KNRYRD	ILPYDS	TRV	PLGKS--	KDYINASYIRIVNC	-----	GEEYFYIATQG																											
hBDP1 D1 (NP_055184) PTPN18	(1)	DSAR	SFERLEARGGREGAV	LAGE--	SDI	QACSA	AAWKADGVC	STVA	GSR	P	NVR	KNRYKD	VL	PYDQ	TRV	LLSLLQ	QEGH--	SDYINGNFIR	GV	-----	DGSLAYIATQG																												
hLvPTP D1 (NP_057051) PTPN22	(1)	EITL	QKFDDEAQS	SKKIT-KEEFANE	LKLKR	QST	TKYKADKTY	PTTV	A	E	K	KNRYKD	ILPYDY	SRV	ELSL	ITSD	ED--	SSYINANFIK	GV	-----	YGPKAYIATQG																												
hPEST D1 (NP_002826) PTPN12	(1)	RKFI	QRVQAMKSPDHNGED	NFARD	MRLRRL	SL	TKYRTEKI	YPTAT	GEKE	EN	VK	KNRYKD	IL	FDHSRV	KL	TLK	TPSQD--	SDYINANFIK	GV	-----	YGPKAYIATQG																												
hHDPTP D1 (NP_056281) PTPN23	(1)	ERLR	QQLLEAFRQGL	GDV--	GALD	T	VRE	QDAQ	EHD	ARG	SI	AI	ARC	YSL	KNRH	QD	VM	FD	SNRV	LLRS	GK--	DDYINASCVE	GLS	-----	PYCPFLYATQA																								
hIA2 D1 (NP_002837) PTPRN	(1)	HMIL	LAYEDHLRNRDR-----	LAK	EWQ	AL	CAYQAE	PN-TCAT	AQ	EG	EN	IK	KNRH	PD	FL	PYD	H	RI	KL	VE	SS	PSR--	SDYINASPI	IE	HD	-----	PRMPAYIATQG																						
hIA2beta_D1 (NP_002838) PTPRN2	(1)	HMIL	LSYEDHLK	KNR-----	LAK	EWQ	AL	CAYQAE	PN-SSFV	AQ	EG	EN	V	KNR	SLA	LT	YD	HSRV	LL	KA	EN	SSH--	SDYINASPI	IE	HD	-----	PRMPAYIATQG																						
Consensus	(1)	L	I	L		F	E	Y	E	L		A	P	E	N	R	K	N	R	Y	I	L	P	Y	D	H	S	R	V	L		S	D	Y	I	N	A	N	Y	I	G	Y		Y	I	A	T	Q	G

	(112)	112	120	130	140	150	160	170	180	190	200	210	222																																																																											
hCD45 D1 (NP_002829) PTPRC (93)	PRDE	TVDD	FWRM	WEQKAT	VIVM	TRCE	EGNR	NKCAE	YWP	--SM	EETRA	GDVV	KINQHKRCP	DYI	LQK	NI	VNKK	E-----	KATG	RE	THIQ	FTS	WPDH	GVPE																																																																
hPTPalph D1 (NP_002827) PTPRA (93)	PKEE	TVND	FWRM	WEQN	ATIVM	VTLN	KERKE	CKCAQ	YWP	---D	QCW	TYGN	IRV	SV	ED	TVL	VDY	TV	RKFC	Q	QV	GDM	TN-----	RKPQ	RL	TF	QH	F	T	S	W	P	D	H	G	V	P	E																																																		
hPTPepsilon D1 (NP_006495) PTPRE (93)	PKQE	TVND	FWRM	VWEQK	SATIVM	LTLN	KERKE	EKCHQ	YWP	---D	QCW	TYGN	IRV	CV	ED	CV	VLV	DY	TI	RKFC	Q	Q	PL	PDG	---	CKAP	RL	VS	QL	H	F	T	S	W	P	D	H	G	V	P	E																																															
hPTPlamda D1 (NP_005695) PTPRU (88)	PKPE	MYD	FWRM	WEHCSS	IIVM	IKLV	EVGR	VKCSR	YWP	---	EDS	TYGD	IR	ML	V	K	T	E	T	L	A	E	V	V	R	T	F	A	L	E	R	R	G	---	YSAR	HE	V	R	Q	F	H	T	S	W	P	D	H	G	V	P	E																																					
hPTPkappa D1 (NP_002835) PTPRK (92)	PVHE	TVYD	FWRM	WEQES	ACIVM	VTLN	VEVGR	VKCYK	YWP	---	DD	TEV	YGD	F	V	T	CV	EM	E	P	L	A	E	V	V	R	T	F	L	E	R	R	G	---	YNE	I	R	E	V	K	Q	F	H	T	S	W	P	D	H	G	V	P	E																																			
hPTPmu D1 (NP_002836) PTPRM (92)	PMQE	TIYD	FWRM	VWHE	TASIVM	VTLN	VEVGR	VKCKQ	YWP	---	DD	TEV	YGD	F	V	T	CV	EM	E	P	L	A	E	V	V	R	T	F	L	E	R	R	G	---	VHE	I	R	E	V	K	Q	F	H	T	S	W	P	D	H	G	V	P	E																																			
hPTPrho D1 (NP_573400) PTPRT (92)	PMQE	TIYD	FWRM	VWHE	TASIVM	VTLN	VEVGR	VKCKQ	YWP	---	DD	TEV	YGD	F	V	T	CV	EM	E	P	L	A	E	V	V	R	T	F	L	E	R	R	G	---	YHE	I	R	E	V	K	Q	F	H	T	S	W	P	D	H	G	V	P	E																																			
hPTPsiama D1 (NP_002841) PTPRS (92)	PLPE	TFGD	FWRM	VWQES	SATIVM	TRLN	EESK	IKCDQ	YWP	---	NR	GET	YGF	I	Q	V	L	L	D	T	E	L	A	E	V	V	R	T	F	L	E	R	R	G	---	SSE	K	R	E	V	R	Q	F	H	T	S	W	P	D	H	G	V	P	E																																		
hPTPdelta D1 (NP_002830) PTPRD (92)	SLPE	TFGD	FWRM	VWQES	SATIVM	TRLN	EESK	IKCDQ	YWP	---	SR	GET	YGF	I	Q	V	L	L	D	T	E	L	A	E	V	V	R	T	F	L	E	R	R	G	---	SSE	K	R	E	V	R	Q	F	H	T	S	W	P	D	H	G	V	P	E																																		
hPTPdelta D1 (NP_002830) PTPRD (92)	PLPE	TFGD	FWRM	VWQES	SATIVM	TRLN	EESK	IKCDQ	YWP	---	AR	GET	YGF	I	Q	V	L	L	D	T	E	L	A	E	V	V	R	T	F	L	E	R	R	G	---	SSE	K	R	E	V	R	Q	F	H	T	S	W	P	D	H	G	V	P	E																																		
hLAR D1 (NP_002831) PTPRF (92)	PLPE	TFGD	FWRM	VWQES	SATIVM	TRLN	EESK	IKCDQ	YWP	---	AR	GET	YGF	I	Q	V	L	L	D	T	E	L	A	E	V	V	R	T	F	L	E	R	R	G	---	SSE	K	R	E	V	R	Q	F	H	T	S	W	P	D	H	G	V	P	E																																		
hPTPaamma D1 (NP_002832) PTPRG (97)	PLKS	TFED	FWRM	WEQN	TGIVM	IKLV	EVGR	VKCDQ	YWP	---	TEN	SE	YGN	I	V	T	L	K	S	T	I	H	A	C	T	V	R	R	F	S	I	R	N	T	K	V	K	K	G	Q	K	N	P	K	R	Q	N	E	R	V	I	Q	Y	H	T	S	W	P	D	H	G	V	P	E																								
hPTPzeta D1 (NP_002842) PTPRZ1 (102)	PLKS	TAED	FWRM	WEHNV	EIVM	IKLV	EVGR	VKCDQ	YWP	---	AD	G	SE	YGN	F	L	V	T	Q	S	V	Q	V	L	A	E	V	V	R	T	F	L	E	R	R	G	---	KGR	P	S	G	R	V	T	Q	Y	H	T	S	W	P	D	H	G	V	P	E																															
hSAP1 D1 (NP_002833) PTPRH (93)	PLPQ	TVGD	FWR	VWEQQ	SHTV	MLT	NCME	AGR	VKCE	YWP	---	LDS	Q	P	C	T	H	G	R	V	L	V	G	E	E	V	M	N	T	V	R	E	L	L	L	Q	V	E	E	---	Q	K	T	L	S	V	R	Q	F	H	T	S	W	P	D	H	G	V	P	E																												
hDEP1 D1 (NP_002834) PTPRJ (92)	PLPNT	KDF	FWRM	VWEK	NVYAI	MLT	KCV	EQGR	T	K	C	E	Y	W	P	---	SK	A	Q	D	Y	G	D	I	V	A	M	T	S	E	I	V	L	P	E	T	I	R	D	F	T	V	K	N	I	Q	T	---	S	S	H	P	R	Q	F	H	T	S	W	P	D	H	G	V	P	E																						
hPTPbeta D1 (NP_002828) PTPRB (93)	PLPG	TKDD	FWK	MYWEQ	NVHNI	VMT	QCV	E	K	R	V	K	D	H	Y	W	P	---	AD	Q	S	L	Y	G	D	L	I	Q	M	L	S	E	S	V	L	P	E	T	I	R	E	F	K	I	C	G	E	E	Q	---	L	D	A	H	R	L	R	F	H	T	S	W	P	D	H	G	V	P	E																			
hGLEPP1 D1 (NP_109592) PTPRO (93)	PLPET	RND	FWK	MYLQ	QK	QIV	M	L	T	Q	C	N	E	K	R	V	K	D	H	Y	W	P	---	F	T	E	E	P	I	A	Y	G	D	I	V	E	M	I	S	E	E	E	Q	D	W	A	C	H	R	F	R	I	N	Y	A	D	---	E	M	Q	D	V	M	H	E	N	Y	T	A	W	P	D	H	G	V	P	E											
hPTPS31 D1 (AR073855) PTPGMC1 (93)	PLPG	TVGD	FWRM	VWET	RAKT	IVM	L	T	Q	C	F	E	K	G	R	I	R	C	H	Q	Y	W	P	---	ED	N	K	P	V	T	V	G	D	I	V	I	T	K	L	M	E	D	V	Q	I	D	W	T	I	R	D	K	I	E	R	H	G	---	L	C	M	T	V	R	Q	C	N	F	T	A	W	P	D	H	G	V	P	E										
hHePTP D1 (NP_002823) PTPN7 (92)	PMEN	TVSD	FWE	MYV	QEEV	SIVM	L	T	Q	L	R	E	-	G	E	K	C	V	H	Y	W	P	---	T	E	E	T	Y	G	P	F	Q	I	R	I	Q	D	M	K	E	C	P	T	V	R	Q	L	I	Q	Y	Q	E	---	E	R	S	V	K	H	I	L	S	A	W	P	D	H	G	V	P	E																	
hPCPTP1 D1 (NP_002840) PTPRR (94)	PMIN	TVDD	FQW	MYV	QEDS	PVIM	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	L	V	I	S	V	N	E	C	D	N	V	T	I	R	N	V	L	K	Q	G	S	---	H	T	Q	H	V	K	H	I	W	Y	T	S	W	P	D	H	K	T	P	E													
hSTEP D1 (NP_116170) PTPN5 (94)	PLVST	VAD	FWRM	VWQEH	PIV	M	T	N	E	E	-	M	N	E	K	C	T	E	Y	W	P	---	E	E	Q	V	A	D	G	E	T	V	Q	K	V	I	H	T	E	V	R	L	R	L	S	L	K	S	G	T	---	E	R	G	K	H	Y	F	T	S	W	P	D	Q	K	T	P	E																				
hSHP1 D1 (NP_002822) PTPN6 (107)	CLEAT	VND	FQW	MYV	QENSR	VIM	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	T	E	K	L	R	T	L	Q	V	S	P	L	D	N	---	G	D	L	I	R	E	W	H	Y	Q	L	S	W	P	D	H	G	V	P	E									
hSHP2 D1 (NP_002825) PTPN11 (110)	CLQNT	VND	FWRM	VWQEN	SRVIM	T	T	K	E	V	E	R	G	S	K	C	V	K	Y	W	P	---	D	E	Y	A	L	K	E	Y	G	V	M	R	V	R	N	V	K	E	S	A	A	H	D	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	S	W	P	D	H	G	V	P	E								
hPTPD1 D1 (NP_008970) PTPN21 (96)	PLQNT	TCQD	FQW	MYV	EQG	I	A	I	A	M	V	T	A	B	E	E	G	G	R	E	K	S	F	R	Y	W	P	R	L	G	S	R	H	N	T	V	T	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
hPTPD2 D1 (NP_005392) PTPN14 (95)	PLPHT	CHDF	FQW	MYV	EQG	V	N	V	I	A	M	V	T	A	B	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	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
hMEG1 D1 (NP_002821) PTPN4 (93)	PLPHT	CTD	FQW	MYV	EQG	S	M	V	V	M	L	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	I	F	R	K	W	T	F	N	Q	E	K	N	---	E	S	R	P	T	Q	I	Q	Y	I	A	W	P	D	H	G	V	P	E							
hPTPH1 D1 (NP_002820) PTPN3 (93)	PLPHT	CAQ	FQW	MYV	EQK	L	S	L	V	M	L	T	T	L	T	E	R	G	R	V	K	C	H	Q	Y	W	P	---	D	P	P	D	V	M	N	H	G	G	F	H	I	Q	C	S	E	D	C	T	I	A	V	S	R	E	L	V	T	N	T	Q	T	G	---	E	H	T	V	H	L	Q	Y	V	A	W	P	D	H	G	V	P	E							
hMEG2 D1 (NP_002824) PTPN9 (93)	PLENT	TYRD	FWL	MYV	EQK	V	L	V	I	M	T	R	F	E																																																																										

	(223)	223	230	240	250	260	270	280	290	300	310	326																																																															
hCD45 D1 (NP 002829) PTPRC (192)	D	---	PHL	LKLR	RVNA	FSNFFS	-----	GPIV	VHCS	AGV	GRT	GTY	I	GID	AM	LEG	EA	ENK	---	V	D	V	G	Y	V	V	K	L	R	Q	R	C	L	M	V	Q	V	E	A	Q	Y	I	L	H	Q	A	L	V	E	Y	N	Q																							
hPTPalph D1 (NP 002827) PTPRA (193)	T	---	PIG	MLK	FLK	VK	KACN	PQYA	-----	GAI	VVHCS	AGV	GRT	GTF	V	V	I	D	A	M	L	D	M	H	T	E	R	K	---	V	D	V	G	F	V	S	R	I	A	Q	R	C	Q	M	V	Q	T	D	M	Q	Y	V	F	I	Y	Q	A	L	L	E	H	Y	L												
hPTPepsilon D1 (NP 006495) PTPRE (192)	T	---	PIG	MLK	FLK	VK	T	LN	PVHA	-----	GPIV	VHCS	AGV	GRT	GTF	V	I	D	A	M	A	M	H	A	E	Q	K	---	V	D	V	F	E	F	V	S	R	I	N	Q	R	P	Q	M	V	Q	T	D	M	Q	Y	T	F	I	Y	Q	A	L	L	E	Y	L													
hPTPlamda D1 (NP 005695) PTPRU (183)	H	---	ATG	L	L	A	F	I	R	V	K	A	S	T	P	P	D	A	-----	GPIV	VHCS	AGT	GRT	G	C	F	I	V	L	D	V	M	L	D	M	A	C	E	G	V	---	V	D	I	N	C	V	K	T	C	S	R	R	V	N	M	I	Q	T	E	E	Q	I	F	I	H	D	A	I	L	E	A	C	L	
hPTPkappa D1 (NP 002835) PTPRK (187)	H	---	ATG	L	L	S	F	I	R	V	K	L	S	N	P	P	S	A	-----	GPIV	VHCS	AGAG	GRT	G	C	F	I	V	I	D	I	M	L	D	M	A	E	R	E	G	V	---	V	D	I	N	C	V	K	L	S	R	R	I	N	M	V	Q	T	E	E	Q	I	F	I	H	D	A	I	L	E	A	C	L	
hPTPmu D1 (NP 002836) PTPRM (187)	H	---	ATG	L	L	G	F	V	R	Q	V	K	S	K	S	P	P	S	A	-----	GPIV	VHCS	AGAG	GRT	G	C	F	I	V	I	D	I	M	L	D	M	A	E	R	E	G	V	---	V	D	I	N	C	V	R	L	S	R	R	V	N	M	V	Q	T	E	E	Q	I	F	I	H	D	A	I	L	E	A	C	L
hPTPrho D1 (NP 573400) PTPRT (187)	Y	---	ATG	L	L	G	F	V	R	Q	V	K	F	L	N	P	P	E	A	-----	GPIV	VHCS	AGAG	GRT	G	C	F	I	A	I	D	T	M	L	D	M	A	E	N	E	G	V	---	V	D	I	N	C	V	R	L	A	Q	R	V	N	M	I	Q	T															

Consensus (223) LL FVR VR GPIVVHCSAGVGRTG FIVID ML I VDIY V MR QR MVQTEEQY FIIH AILE