

Database of vertebrate PTPs and assignment of ortholog sequences

A non-redundant set of PTP domain sequences - mRNA and protein entries

Name	Sub-type	Human ortholog	Full length name	Synonyms	Swiss Prot	Reference Entry	Additional Genbank™ accession number													
						Protein	mRNA													
Nontransmembrane PTP subtypes (nonreceptor-like PTPs)																				
hPTP1B	NT1	-	PTP1B	PTP-1, PTP-1B	P18031	NP_002818	NM_002827	M31724	M33689	BC016660	BC018164									
mPTP1B	NT1	PTP1B	PTP1B	PTP-1, HA2, PTP-HA2	P35521	NP_035531	NM_011201	U24700	Z23057	M97590	L40595		BC005723	BC010191						
rPTP1B	NT1	PTP1B	PTP1B	PTP-1	P20417	NP_026189	NM_012637	M3992												
cPTP1B	NT1	PTP1B	PTP1B		Q13016	AAA91188	U48662	U88410	L20630											
zPTP1B	NT1	PTP1B	PTP1B			NP_570999	NM_130924	AF097481	AF097482	AF097483	Y14427									
hTCP1P	NT1	-	TC-PTP (T-Cell phosphatase)	PTP-2	P17706	NP_002819	NM_002828	M25393	M81478	M80737	BC016727	BC008244								
mTCP1P	NT1	TCPTP	TC-PTP (T-Cell phosphatase)	PTP-2	Q06180	NP_033003	NM_008977	S52655	M81477	M80739	AK014528	BC008269								
rTCP1P	NT1	TCPTP	TC-PTP (T-Cell phosphatase)	PTP-2, PTP-S	P35233	NP_446442	NM_053990	X58828												
ryPTPN3	NT1	TCPTP	TC-PTP (T-Cell phosphatase)	PTP-2		BAA95189	AB033582													
zTCP1P	NT1	TCPTP	TC-PTP (T-Cell phosphatase)	PTP-2		AAH44373	BC044373													
hSHP1	NT2	-	Src homology domain 2 containing PTP1	SH-PTP1, SHP, HCP, PTP1C me, motheaten	P29350	NP_002822	NM_002831	M74903	X62055	M77273	M90388	X82817	X82818	AF178946	BC002523	BC007667				
mSHP1	NT2	SHP1	Src homology domain 2 containing PTP1		P29351	NP_038573	NM_013545	M68902	M90389	U65953	U65954	U65955	BC01266	S63763	S63764	S63803				
rSHP1	NT2	SHP1	Src homology domain 2 containing PTP1			NP_446360	NM_053908	U77038	AF468653											
ryPTPN6a	NT2	SHP1	Src homology domain 2 containing PTP1			BAA95187	AB033580													
ryPTPN6c	NT2	SHP1	Src homology domain 2 containing PTP1			BAA95199	AB033592													
zSHP1	NT2	SHP1	Src homology domain 2 containing PTP1			AAH44414	BC044414													
hSHP2	NT2	-	Src homology domain 2 containing PTP2	SH-PTP2, SH-PTP3, Syp, PTP-2C, PTP1D, BP	Q06174	NP_039323	NM_002834	D13540	L03535	L07527	X70766	L08807	S78088	S39383	BC008692					
mSHP2	NT2	SHP2	Src homology domain 2 containing PTP2	SH-PTP2, Syp	P35235	NP_035332	NM_011202	L08663	D84372											
rSHP2	NT2	SHP2	Src homology domain 2 containing PTP2	PTP-1D	P41499	NP_037220	NM_013088	U09307	U05963	D83016										
cSHP2	NT2	SHP2	Src homology domain 2 containing PTP2	SH-PTP2, Syp	JC5167	AAAC60049	U38620													
ryPTPN6b	NT2	SHP2	Src homology domain 2 containing PTP2			BAA95198	AB033591													
zSHP2	NT2	SHP2	Src homology domain 2 containing PTP2			AAH45328	BC045328													
xSHP2	NT2	SHP2	Src homology domain 2 containing PTP2			AAAG5731	U15287													
hMEG2	NT3	-	Megakaryocyte-PTP2		P43378	NP_002824	NM_002833	M83738	BC010863											
mMEG2	NT3	MEG2	Megakaryocyte-PTP2			NP_062825	NM_019651	AF013490												
rMEG2	NT3	MEG2	Megakaryocyte-PTP2			XP_217150	XM_217150													
xPTPX1	NT3	a)				AAH43621	BC043621													
xPTPX10	NT3	a)				AAA21728	L33099													
hPEST	NT4	-	Pro, Glu, Ser, Thr-rich PTP	PTP-PEST, PTPG1	Q05209	NP_002826	NM_002835	D13380	M93425	S69184	S69182	S69183								
mPEST	NT4	PEST	Pro, Glu, Ser, Thr-rich PTP	PTP1P9, P19-PTP	P35831	NP_035333	NM_011203	X86781	X63440	S36169										
rRKPTP	NT4	PEST	Rat kidney PTP			NP_476456	NM_057115	D38072												
hLyPTP	NT4	-	Lymphoid phosphatase	LyP1, LyP2		NP_057051	NM_015967	AF001846	AF001847	AF077031	AF150732	BC011778								
mPEP	NT4	LyPTP	Hematopoietic cell PTP		P29352	NP_033005	NM_008979	M90388												
hBDP1	NT4	-	Brain derived phosphatase 1			NP_055184	NM_014369	X79568	BC024280											
rPTP20	NT4	BDP1				AAAC52896	U96973													
mPTPK1	NT4	BDP1		PTPFLP1 (Fetal liver phosphatase 1)		NP_035336	NM_011206	U35124	U52523	U49853	BC008512									
hMEG1	NT5	-	Megakaryocyte-PTP1	PTPG1, PTPF36-15	P29074	NP_002821	NM_002830	M68941	AAB28477	BC010674										
mMEG1	NT5	MEG1	Megakaryocyte-PTP1	PTP1Ep (Testis-enriched phosphatase)		NP_064317	NM_019933	AF106702												
zMEG1	NT5	MEG1	Megakaryocyte-PTP1			CAD43435	AL072057													
hPTPH1	NT5	-			P28045	NP_002920	NM_002929	M64572	S39392											
mPTPH1	NT5	PTPH1				XP_143789	XM_143789													
zPTPH1	NT5	PTPH1		MEG1		AAAC97938	AF097477	AF097478	AF097479	AF097480										
hPTPD1	NT6	-	PTPD1		Q16825	NP_008970	NM_007039	X79510												
mPTPRL10	NT6	PTPD1	PTPD1			NP_036907	NM_011137	Q37891	D83072	AK013777										
rPTP2E	NT6	PTPD1	PTPD1			Q62128	NP_598229	NM_133545	U11971	U18293										
hPTPD2	NT6	-	PTPD2	PEZ (Phosphatase ezrin-like)		Q15678	NP_005392	NM_005401	X82676											
mPTP36	NT6	PTPD2	PTPD2			Q62130	NP_033002	NM_008976	D31842	AF17092	AF17093	AF17094	AF17095							
rPTPD2	NT6	PTPD2	PTPD2			XP_223062	XM_223062													
hPTPBAS	NT7	-	FAS-associated PTP1	BAS, PTP1E, PTP1F, FAP-1, PTP1L, CD95	Q12923	NP_006265	NM_006264	X80289	U12128	D21209	D21210	D21211	U81561	X79676						
mPTPBL	NT7	PTPBAS		DPZ2PTP, PTPRIP		NP_035334	NM_011204	D28529	Z27440	D83966	AK014577									
rPTPBAS	NT7	PTPBAS				CAA69166	Y07832													
bPTPBA14	NT7	PTPBAS				NP_777015	NM_147590	U20807												
hPTPTyp	NT8	-	Testis-specific tyrosine phosphatase	Typ		NP_056420	NM_015605	AL050040	B1547503											
mPTPTyp	NT8	PTPTyp	Testis-specific tyrosine phosphatase	Typ		NP_033004	NM_008978	D64141	AK017003											
rPTPTyp	NT8	PTPTyp	Testis-specific tyrosine phosphatase	Typ		XP_224639	XM_224639													
hHDPTP	NT9	-	His-domain containing PTP	HD-PTP, PTPD14	T14756	NP_056281	NM_015466	AB025194	AB040904	AL110210	AF169350	AB025194	AF290614	BC027711	BC004481	AK055157				
mHDPTP	NT9	HDPTP	His-domain containing PTP	HD-PTP, PTPD14		AAH22721	BC022721	XM_135197												
rPTPD14	NT9	HDPTP	His-domain containing PTP	HD-PTP	T14355	AAAC62959	AF077000	AF175208												
Receptor-like PTP subtypes																				
hCD45	R1/R6	-	Cluster of differentiation 45	Leukocyte common antigen (LCA), T200, PTPRC	P08575	NP_002829	NM_002838	Y00638	Y00062											
mCD45	R1/R6	CD45	Cluster of differentiation 45	LCA, T200, Ly5	P06800	NP_035340	NM_011210	M14342	M92933	M33482	M15174									
rCD45	R1/R6	CD45	Cluster of differentiation 45	Leukocyte common antigen	P04157	XP_213985	XM_213985	M10072	Y00065	M25820	M25821	M25822	M25823	K03039						
cCD45	R1/R6	CD45	Cluster of differentiation 45	chicken PTPdelta		AA0480	L12935	Z21960												
hCD45	R1/R6	CD45	Cluster of differentiation 45			CAAC6211	AJ342429													
adovCD45	R1/R6	CD45	Cluster of differentiation 45			AAAM48511.A	AF364095	AF364096												
sharkCD45	R1/R6	CD45	Cluster of differentiation 45			I43148	U34760													
cypcaCD45	R1/R6	CD45	Cluster of differentiation 45			BAA92179	AB031424													
xCD45	R1/R6	CD45	Cluster of differentiation 45			AAB81279	AF024438													
hLAR	R2A	-	Leukocyte common antigen-related PTP	PTP-LAR	P10586	NP_002831	NM_002840	Y00815												
mLAR	R2A	LAR	Leukocyte common antigen-related PTP	PTP-LAR		NP_035343	NM_011213	Z37988	Z23049	Z23061	AF300943	AA591035								
rLAR	R2A	LAR	Leukocyte common antigen-related PTP	PTP-LAR		NP_062122	NM_019249	L11586	U00477	X83546	X83505	MG0103								
xLAR	R2A	LAR	Leukocyte common antigen-related PTP	PTP-LAR		AAF43606	AF197945													

Abbreviations used for vertebrate sequences

Abbreviation (PTP prefix)	Species (Common Name)	Species
aotusPTP	Monkey (noisy night)	<i>Aotus vociferans</i>
bPTP	Cow	<i>Bos taurus</i>
cypcaPTP	Common Carp	<i>Cyprinus carpio</i>
zPTP	Zebrafish	<i>Danio rerio</i>
cPTP	Chicken	<i>Gallus gallus</i>
sharkPTP	Horn Shark	<i>Heterodontus francisci</i>
hPTP	Human	<i>Homo sapiens</i>
macfaPTP	Monkey (Crab-eating)	<i>Macaca fascicularis</i>
macmuPTP	Monkey (rhesus)	<i>Macaca mulatta</i>
macnePTP	Monkey (Pig-tailed macaque)	<i>Macaca nemestrina</i>
mPTP	Mouse	<i>Mus musculus</i>
rabPTP	Rabbit	<i>Oryctolagus cuniculus</i>
orylaPTP	Japanese ricefish	<i>Oryzias latipes</i>
ryPTP	Stingray	<i>Potamotrygon motoro</i>
rPTP	Rat	<i>Rattus norvegicus</i>
pigPTP	Pig	<i>Sus scrofa</i>
fuPTP	Fugu	<i>Takifugu rubripes</i>
xPTP	African clawed frog	<i>Xenopus laevis</i>

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Invertebrates - PSI BLAST Result

Seq No	Accession nr	SourceID	NR	Subtype	Species	Species	Name	Human Ortholog	Synonyms	Gene ID	AA	Comments
135	gi 1079024	pir	S53089	Ref	R2A	<i>Anopheles gambiae</i>	African malaria	anLAR	LAR			1231
384	gi 11358730	pir	T51846	Ref	?	<i>Arabidopsis thaliana</i>	<i>Arabidopsis thaliana</i>	larath	PTP1			340
380	gi 3413425	emb	CAA06978	?	?	<i>Arabidopsis thaliana</i>	<i>Arabidopsis thaliana</i>	larath	PTP1	locus ATH6309		340
507	gi 12324541	gb	AAG52227	?	?	<i>Arabidopsis thaliana</i>	<i>Arabidopsis thaliana</i>					169
259	gi 7684260	dbj	BAA9	?	?	<i>Arabidopsis thaliana</i>	<i>Arabidopsis thaliana</i>					469
275	gi 7684254	dbj	BAA9	?	?							469
281	gi 7684252	dbj	BAA9	?	?							470
383	gi 7684256	dbj	BAA9	?	?							
429	gi 7684305	dbj	BAA9	?	?							
433	gi 7684250	dbj	BAA9	?	?							480
440	gi 7684258	dbj	BAA9	?	?							
454	gi 7684248	dbj	BAA9	?	?							
473	gi 7684307	dbj	BAA9	?	?							
86	gi 12698664	gb	AAK0	?	?							2200
99	gi 6226890	sp	P2811	?	?							1026
84	gi 7511581	pir	T1911	?	?							1585
85	gi 12698666	gb	AAK0	?	?							1487
97	gi 7497608	pir	T1963	?	?							624
212	gi 7505278	pir	T2330	?	?							1156
266	gi 7503426	pir	T2191	?	?							1367
286	gi 7504815	pir	T3433	?	?							668
378	gi 7503637	pir	T2911	?	?							374
400	gi 7508204	pir	T2511	?	?							591
402	gi 11275230	pir	T4251	?	?							
403	gi 7504323	pir	T2951	?	?							
405	gi 7499844	pir	T2134	?	?							
409	gi 7332259	gb	AAF6	?	?							
410	gi 7506013	pir		?	?							
415	gi 14574315	gb	AAK6	?	?							
423	gi 7508547	pir	T25917	?	?	<i>Caenorhabditis elegans</i>	C.elegans			T27A3.5		
424	gi 7504409	pir	T30111	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F56D1.4		
430	gi 2854164	gb	AAC02582	?	?	<i>Caenorhabditis elegans</i>	C.elegans			C17H12.3		
431	gi 7105608	gb	AAF36005	?	?	<i>Caenorhabditis elegans</i>	C.elegans			Y71F9AL.4		
432	gi 4966291	gb	AAD34661	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F20H11.4		
434	gi 7508697	pir	T25430	?	?	<i>Caenorhabditis elegans</i>	C.elegans			T28F4.3	490	
437	gi 7500661	pir	T33446	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F36H12.10		
438	gi 14574622	gb	AAK68680	?	?	<i>Caenorhabditis elegans</i>	C.elegans			C02B10.6		
439	gi 13559717	gb	AAK29923	?	?	<i>Caenorhabditis elegans</i>	C.elegans			Y48G9A.9		
442	gi 7500656	pir	T21883	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F36H1.3		
444	gi 7511101	pir	T25992	?	?	<i>Caenorhabditis elegans</i>	C.elegans			ZK354.8		
445	gi 1943802	gb	AAB52456	?	?	<i>Caenorhabditis elegans</i>	C.elegans			B0207.1		
447	gi 7505473	pir	T23421	?	?	<i>Caenorhabditis elegans</i>	C.elegans			K07F5.8	284	
451	gi 7507803	pir	T23738	?	?	<i>Caenorhabditis elegans</i>	C.elegans			T13H5.1		
453	gi 14573993	gb	AAK68274	?	?	<i>Caenorhabditis elegans</i>	C.elegans			C55B7.3		
456	gi 7506519	pir	T24090	?	?	<i>Caenorhabditis elegans</i>	C.elegans					
462	gi 7503631	pir	T29156	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F47B3.1		
463	gi 7503636	pir	T29153	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F47B3.6		
465	gi 7498856	pir	T20729	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F10G8.1		
476	gi 5701822	emb	CAB52188	?	?	<i>Caenorhabditis elegans</i>	C.elegans	wIDA-1				
480	gi 7511170	pir	T32869	?	?	<i>Caenorhabditis elegans</i>	C.elegans			ZK484.7		
481	gi 7503761	pir	T22382	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F48F5.1		
491	gi 3342257	gb	AAC27552	?	?	<i>Caenorhabditis elegans</i>	C.elegans	wCLR-1			942	Truncated
494	gi 7509339	pir	T26452	?	?	<i>Caenorhabditis elegans</i>	C.elegans			Y113G7C.1		
496	gi 7496955	pir	T34151	?	?	<i>Caenorhabditis elegans</i>	C.elegans			C33H5.16		
499	gi 7498859	pir	T20724	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F10G8.4		
500	gi 7504215	pir	T22872	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F54F12.1		
502	gi 7500825	pir	T21973	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F38H4.4		
503	gi 7508902	pir	T29019	?	?	<i>Caenorhabditis elegans</i>	C.elegans			W03F11.4		
504	gi 14550387	gb	AAK18987	?	?	<i>Caenorhabditis elegans</i>	C.elegans			W03F11.4		
508	gi 11359780	pir	T45039	?	?	<i>Caenorhabditis elegans</i>	C.elegans			Y39B6B.m		Imported
511	gi 7506672	pir	T33093	?	?	<i>Caenorhabditis elegans</i>	C.elegans			R12E2.10		
512	gi 7508144	pir	T29763	?	?	<i>Caenorhabditis elegans</i>	C.elegans			T21E3.1		
513	gi 7506015	pir	T23725	?	?	<i>Caenorhabditis elegans</i>	C.elegans			M05B5.1		
518	gi 6425532	emb	CAB60442	?	?	<i>Caenorhabditis elegans</i>	C.elegans			Y80D3A.8		
525	gi 7497483	pir	T29814	?	?	<i>Caenorhabditis elegans</i>	C.elegans			C46A5.1		
526	gi 7508034	pir	T15125	?	?	<i>Caenorhabditis elegans</i>	C.elegans			T20B6.1		
527	gi 7496931	pir	T15749	?	?	<i>Caenorhabditis elegans</i>	C.elegans			C33F10.8		
530	gi 7510958	pir	T27722	?	?	<i>Caenorhabditis elegans</i>	C.elegans			ZK1251.5		
531	gi 156407	gb	AAA28127	?	?	<i>Caenorhabditis elegans</i>	C.elegans	wPTPA			107	Locus CELPTPAA
532	gi 7331823	gb	AAF60511	?	?	<i>Caenorhabditis elegans</i>	C.elegans			Y39A3A.4		
535	gi 11359772	pir	T45031	?	?	<i>Caenorhabditis elegans</i>	C.elegans			Y39B6B.e		Imported
541	gi 7503632	pir	T29155	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F47B3.2		
546	gi 7507098	pir	T24462	?	?	<i>Caenorhabditis elegans</i>	C.elegans			T04F3.3		
549	gi 131558	sp	P28192	?	?	<i>Caenorhabditis elegans</i>	C.elegans	wPTP2		PTP2	108	
552	gi 14578260	gb	AAK68894	?	?	<i>Caenorhabditis elegans</i>	C.elegans			Y54F10BM.3		
562	gi 7505471	pir	T23412	?	?	<i>Caenorhabditis elegans</i>	C.elegans			K07F5.6		
563	gi 7499471	pir	T34229	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F20B6.1		
573	gi 7509842	pir	T26897	?	?	<i>Caenorhabditis elegans</i>	C.elegans			Y44A6D.4		
583	gi 7505672	pir	T32088	?	?	<i>Caenorhabditis elegans</i>	C.elegans			K09F6.3		
584	gi 7503402	pir	T22184	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F44F4.2		
585	gi 7506753	pir	T15279	?	?	<i>Caenorhabditis elegans</i>	C.elegans			R155.3		
593	gi 7508757	pir	T26040	?	?	<i>Caenorhabditis elegans</i>	C.elegans			W01B6.6		
604	gi 13559665	gb	AAK29874	?	?	<i>Caenorhabditis elegans</i>	C.elegans			Y22D7AR.		
606	gi 7506022	pir	T23733	?	?	<i>Caenorhabditis elegans</i>	C.elegans			M05D6.3		
609	gi 7500460	pir	T21741	?	?	<i>Caenorhabditis elegans</i>	C.elegans			F35C11.2		
New	gi 24418239	gb	AAK29895	?	?	<i>Caenorhabditis elegans</i>	C.elegans			Y48G1C.5		
New	gi 23820863	gb	AAD31046	R8		<i>Caenorhabditis elegans</i>	C.elegans		IA2 subtype		767	
New	gi 16604217	gb	AAK68563	R8		<i>Caenorhabditis elegans</i>	C.elegans		IA2 subtype	Y69A2AR.19		Hypothetical protein
261	gi 9229928	dbj	BAB00633	NT5		<i>Ciona intestinalis</i>	Ciona intest	Ci-PTP	PTPH1/MEG1		987	
162	gi 464500	sp	P34138	NT1		<i>Dictyostelium discoideum</i>	Dictyostelium	PTPA	PTP1B Subtype	PTP2_DICDI	377	
330	gi 1709903	sp	P54637	?		<i>Dictyostelium discoideum</i>	Dictyostelium	PTP3		PTP3_DICDI		
407	gi 348540	pir	A44267	?		<i>Dictyostelium discoideum</i>	Dictyostelium	PTP1		PTP1_DICDI	521	Nonreceptor type1
408	gi 464498	sp	P34137	?		<i>Dictyostelium discoideum</i>	Dictyostelium	PTP1		PTP1_DICDI	521	
140	gi 1079130	pir	A46101	Ref	NT1	<i>Drosophila melanogaster</i>	Drosophila	dPTP6F	PTP1B/TCPTP		535	Short spliceform
153	gi 125977	sp	P16621	Ref	R2A	<i>Drosophila melanogaster</i>	Drosophila	dLAR	LAR		2029	

Under construction !!!

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Seq No	Accession nr	SourceID	NR	Subtype	Species	Species	Name	Human Ortholog	Synonyms	Gene ID	AA	Comments
288	gi 1362625	pir	A49502	Ref	R3	<i>Drosophila melanoga</i>	Drosophila	dPTP4E	PTPbeta subtype		1767	Spliceform A
361	gi 118913	sssp	P16620	Ref	?	<i>Drosophila melanoga</i>	Drosophila	dPTP69D				
368	gi 1428610	sp	P29349	Ref	NT2	<i>Drosophila melanoga</i>	Drosophila	CSW	SHP2	Cockscrew		
421	gi 1318272	gb	AAK14909	Ref	R8	<i>Drosophila melanoga</i>	Drosophila	IA2	IA2			
580	gi 5052738	gb	AAA38688	Ref	?	<i>Drosophila melanoga</i>	Drosophila	dPTP-ER				
137	gi 347081	gb	AAA28748		NT1	<i>Drosophila melanoga</i>	Drosophila	dPTP61F	PTP1B/TCPTP		548	
139	gi 1079129	pir	B46101		NT1	<i>Drosophila melanoga</i>	Drosophila	dPTP61F	PTP1B/TCPTP		548	Long spliceform
New	gi 20455509	sp	P35992	Ref	R3	<i>Drosophila melanoga</i>	Drosophila	dPTP10D	Beta Subtype		1631	Long Spliceform
141	gi 7292073	gb	AAF47486		NT1	<i>Drosophila melanoga</i>	Drosophila	dPTP61F	PTP1B/TCPTP	CG9181-PB	535	
142	gi 7292074	gb	AAF47487		NT1	<i>Drosophila melanoga</i>	Drosophila	dPTP61F	PTP1B/TCPTP	CG9181-PB	548	
New	gi 22833100	gb	AAF48072	Ref	R3	<i>Drosophila melanoga</i>	Drosophila	DROTP10	GLEPP/S31	CG1817-PB	1962	
New	gi 24651039	ref	NP_733288	Ref	R5	<i>Drosophila melanoga</i>	Drosophila	PTP99A		CG2005-PA	1226	
222	gi 157298	gb	AAA28485		R5	<i>Drosophila melanoga</i>	Drosophila	dPTP99A				
223	gi 157300	gb	AAA28486		R5	<i>Drosophila melanoga</i>	Drosophila	dPTP99B			1231	
226	gi 548625	sssp	P35832		R5	<i>Drosophila melanoga</i>	Drosophila	dPTP99A			1301	
245	gi 103342	pir	D41214		R3	<i>Drosophila melanoga</i>	Drosophila	dPTP10D	Beta Subtype		1557	Short Spliceform
250	gi 157296	gb	AAA28484		R3	<i>Drosophila melanoga</i>	Drosophila	DROTP10	GLEPP/S31	CG1817-PB	1631	
251	gi 158645	gb	AAA28952		R3	<i>Drosophila melanoga</i>	Drosophila	DROTP10	GLEPP/S31	DROTP10D	1558	
272	gi 7290546	gb	AAF45998		R3	<i>Drosophila melanoga</i>	Drosophila	dPTP4E	Beta Subtype	CG6899-PA	1767	
287	gi 433182	gb	AAAY6834		R3	<i>Drosophila melanoga</i>	Drosophila	dPTP4E	PTPbeta subtype	DRORPTP4E	1767	
289	gi 1362626	pir	B49502		R3	<i>Drosophila melanoga</i>	Drosophila	dPTP4E	PTPbeta subtype	DRORPTP4E		Spliceform B
316	gi 10727513	gb	AAF58051		?	<i>Drosophila melanoga</i>	Drosophila	dPt52F		CG18243-PA	1419	
352	gi 7294551	gb	AAF49892		?	<i>Drosophila melanoga</i>	Drosophila			CG10975-PA	1462	
363	gi 1375482	gb	AAB02545		NT2	<i>Drosophila melanoga</i>	Drosophila		SHP1 subtype	Cockscrew		
369	gi 283728	pir	A43254		NT2	<i>Drosophila melanoga</i>	Drosophila	CSW	SHP2	Cockscrew	841	
370	gi 6706168	emb	CAB65871		NT2	<i>Drosophila melanoga</i>	Drosophila	CSW	SHP2	Cockscrew	945	Poor sequence quality
371	gi 1375479	gb	AAB02543		NT2	<i>Drosophila melanoga</i>	Drosophila	CSW	SHP2	Cockscrew	841	
372	gi 1375480	gb	AAB02544		NT2	<i>Drosophila melanoga</i>	Drosophila	CSW	SHP2	cockscrew protein 4A	945	
412	gi 7296137	gb	AAF51431		R8?	<i>Drosophila melanoga</i>	Drosophila		IA2 subtype	CG31795-PB	1180	
435	gi 7263020	gb	AAF44063		NT5	<i>Drosophila melanoga</i>	Drosophila	Ptpmeg	MEG1 Subtype		517	
436	gi 23092701	gb	AAF47380		NT5	<i>Drosophila melanoga</i>	Drosophila	Ptpmeg	MEG1 Subtype	CG1228-PA	952	
470	gi 6652822	gb	AAF22489		NT6	<i>Drosophila melanoga</i>	Drosophila	PTPpez			1295	
472	gi 7263018	gb	AAF44062		NT6	<i>Drosophila melanoga</i>	Drosophila	PTPpez			1252	
501	gi 7299485	gb	AAF54673		?	<i>Drosophila melanoga</i>	Drosophila	CG14714-PA				
New	gi 22946736	gb	AAF53658		?	<i>Drosophila melanoga</i>	Drosophila			CG7180-PA	682	
New	gi 23093475	gb	AAF49705		?	<i>Drosophila melanoga</i>	Drosophila			CG9311-PA	1833	
New	gi 21645298	gb	AAF46739		?	<i>Drosophila melanoga</i>	Drosophila			CG9856-PA	1377	
New	gi 22946866	gb	AAF53837		R2A	<i>Drosophila melanoga</i>	Drosophila	dLAR	LAR	CG10443-PA	2029	
211	gi 5572699	dbj	BAA82558	Ref	R4	<i>Ephydatia fluviatilis</i>	Sponge	sPTR4			471	
441	gi 5572713	dbj	BAA82565	Ref	NT2	<i>Ephydatia fluviatilis</i>	Sponge	sPTPN6				
443	gi 5572715	dbj	BAA82566	Ref	NT6?	<i>Ephydatia fluviatilis</i>	Sponge	sPTPN8				
449	gi 5572703	dbj	BAA82560	Ref	R5	<i>Ephydatia fluviatilis</i>	Sponge	sPTR5				
452	gi 5572709	dbj	BAA82563	Ref	?	<i>Ephydatia fluviatilis</i>	Sponge	sPTPN2				
455	gi 5572705	dbj	BAA82561	Ref	R3	<i>Ephydatia fluviatilis</i>	Sponge	sPTR3				
471	gi 5572707	dbj	BAA82562	Ref	NT1?	<i>Ephydatia fluviatilis</i>	Sponge	sPTPN1				
489	gi 5572711	dbj	BAA82564	Ref	R7	<i>Ephydatia fluviatilis</i>	Sponge	sPTR7				
382	gi 5572701	dbj	BAA82559	Ref	R2B	<i>Ephydatia fluviatilis</i>	Sponge	sPTR2B				
274	gi 7684309	dbj	BAA95176	Ref	R2A	<i>Epatretus burgeri</i>	Hagfish	hgPTPR2A	LAR subtype		469	
468	gi 7684311	dbj	BAA95177	Ref	R5	<i>Epatretus burgeri</i>	Hagfish	hgPTPR5a				
267	gi 7684313	dbj	BAA95178	Ref	R2A	<i>Epatretus burgeri</i>	Hagfish	hgPTPR2A	LAR Subtype		468	
366	gi 7684315	dbj	BAA95179	Ref	R4	<i>Epatretus burgeri</i>	Hagfish	hgPTPR4	PTPalpha			
466	gi 7684317	dbj	BAA95180	Ref	R3	<i>Epatretus burgeri</i>	Hagfish	hgPTPR3				
420	gi 7684319	dbj	BAA95181	Ref	R2B	<i>Epatretus burgeri</i>	Hagfish	hgPTPR2B	PTPmu			
312	gi 7684321	dbj	BAA95182	Ref	R2A	<i>Epatretus burgeri</i>	Hagfish	hgPTPR2A	LAR Subtype			
413	gi 7684323	dbj	BAA95183	Ref	NT2	<i>Epatretus burgeri</i>	Hagfish	hgPTPN6a				
495	gi 7684325	dbj	BAA95184	Ref		<i>Epatretus burgeri</i>	hagfish	hgPTPR5b				
425	gi 7684327	dbj	BAA95185	Ref	NT2	<i>Epatretus burgeri</i>	Hagfish	hgPTPN6b				
450	gi 7684329	dbj	BAA95186	Ref	?	<i>Epatretus burgeri</i>	Hagfish	hgPTPN3				
256	gi 13276131	emb	CAC33882	Ref	R3	<i>Geodia cydonium</i>	Geodia cydonium	GLEPP1			999	similar to PTPlama; Ig and F
381	gi 3413473	emb	CAA06975		?	<i>Glycine max</i>	Soybean	glymaPTP1		locus GMA6308		
96	gi 7511703	pir	T31093	Ref	R2A	<i>Hirudo medicinalis</i>	Medical leach	hmLAR1	LAR Subtype	LAR1	1437	
189	gi 7511704	pir	T30938	Ref	R2A	<i>Hirudo medicinalis</i>	Medical leach	hmLAR2	LAR subtype		2051	
492	gi 11359667	pir	T49403		NT4?	<i>Neurospora crassa</i>	Neurospora crassa				1132	
493	gi 11544694	emb	CAB91306		?	<i>Neurospora crassa</i>	Neurospora crassa				1104	
396	gi 7488838	pir	T06536	Ref	?	<i>Pisum sativum</i>	garden pea	pissaPTP1				
418	gi 6319971	ref	NP_010051	Ref	?	<i>Saccharomyces cere</i>	Baker's yeast	SaccePTP1P		PTP1P		
553	gi 6324782	ref	NP_014851	Ref	?	<i>Saccharomyces cere</i>	Baker's yeast	SaccePTP2P			750	
566	gi 6320919	ref	NP_010998	Ref	?	<i>Saccharomyces cere</i>	Baker's yeast	SaccePTP3P			928	
554	gi 172382	gb	AA859323		?	<i>Saccharomyces cere</i>	Baker's yeast	SaccePTP2P			750	
404	gi 11263050	pir	T45160		?	<i>Schizosaccharomyce</i>	fission yeast	SchpoPTP				
393	gi 131684	sssp	P27574	Ref	?	<i>Schizosaccharomyce</i>	fission yeast	SchpoPYP1				
394	gi 417567	sssp	P32586	Ref	?	<i>Schizosaccharomyce</i>	fission yeast	SchpoPYP2				
397	gi 417568	sssp	P32587	Ref	?	<i>Schizosaccharomyce</i>	fission yeast	SchpoPYP3				
498	gi 131455	sssp	P28201		?	<i>Styela plicata</i>	Styela plicata					
515	gi 131457	sssp	P28203		?	<i>Styela plicata</i>	Styela plicat	PT11				
521	gi 131463	sssp	P28208		?	<i>Styela plicata</i>	Styela plicat	PT16				PTPmu-like?
528	gi 131456	sssp	P28202		?	<i>Styela plicata</i>	Styela plicat	PT10				
544	gi 131464	sssp	P28209	Ref	?	<i>Styela plicata</i>	Styela plicat	PT17				
545	gi 131478	sssp	P28213	Ref	?	<i>Styela plicata</i>	Styela plicat	PT21				
550	gi 131479	sssp	P28214	Ref	?	<i>Styela plicata</i>	Styela plicat	PT22				
555	gi 131460	sssp	P28205	Ref	?	<i>Styela plicata</i>	Styela plicat	PT13				
557	gi 131461	sssp	P28206	Ref	?	<i>Styela plicata</i>	Styela plicat	PT14				
558	gi 131465	sssp	P28210	Ref	?	<i>Styela plicata</i>	Styela plicat	PT18				
560	gi 131452	sssp	P28198	Ref	?	<i>Styela plicata</i>	Styela plicat	PT06				
565	gi 131466	sssp	P28211	Ref	?	<i>Styela plicata</i>	Styela plicat	PT19				
569	gi 131480	sssp	P28215	Ref	?	<i>Styela plicata</i>	Styela plicat	PT23				
570	gi 131477	sssp	P28212	Ref	?	<i>Styela plicata</i>	Styela plicat	PT20				
575	gi 131481	sssp	P28216	Ref	?	<i>Styela plicata</i>	Styela plicat	PT24				
579	gi 131482	sssp	P28217	Ref	?	<i>Styela plicata</i>	Styela plicat	PT25				
582	gi 131483	sssp	P28218	Ref	?	<i>Styela plicata</i>	Styela plicat	PT26				
591	gi 131449	sssp	P28195	Ref	?	<i>Styela plicata</i>	Styela plicat	PT03				
594	gi 131484	sssp	P28219	Ref	?	<i>Styela plicata</i>	Styela plicat	PT27				
595	gi 131458	sssp	P28204	Ref	?	<i>Styela plicata</i>	Styela plicat	PT12				
597	gi 6226682	sssp	P28199	Ref	?	<i>Styela plicata</i>	Styela plicat	PT07				fragment
598	gi 131451	sssp	P28197	Ref	?	<i>Styela plicata</i>	Styela plicat	PT05				fragment
605	gi 131447	sssp	P28193	Ref	?	<i>Styela plicata</i>	Styela plicat	PT01				
610	gi 131454	sssp	P28200	Ref	?	<i>Styela plicata</i>	Styela plicat	PT08				

Abbreviations used for non-vertebrate sequences

Abbreviation (PTP prefix)	Species (Common Name)	Species
amPTP	Amphioxus	<i>Branchiostoma belcheri</i>
ciPTP	Ciona intestinalis	<i>Ciona intestinalis</i>
hmPTP	Leach	<i>Hirudo medicinalis</i>
anPTP	Mosquito (African malaria)	<i>Anopheles gambiae</i>
dmPTP	Fruitfly	<i>Drosophila melanogaster</i>
psPTP	Garden Pea	<i>Pisum sativum</i>
hgPTP	Hagfish	<i>Eptatretus burgeri</i>
ddPTP	Slime mold	<i>Dictyostelium discoideum</i>
gmPTP	Soybean	<i>Glycine max</i>
gcPTP	Sponge	<i>Geodia cydonium</i>
efPTP	Sponge	<i>Ephydatia fluviatilis</i>
spPTP	Styela plicata	<i>Styela plicata</i>
arPTP	Thale cress	<i>Arabidopsis thaliana</i>
cerivPTP	Yeast	<i>Saccharomyces cerevisiae</i>
pombePTP	Yeast	<i>Saccharomyces pombe</i>
cePTP	Worm	<i>Caenorhabditis elegans</i>
ncPTP	Neurospora crassa	<i>Neurospora crassa</i>

Annotation of non-vertebrate PTP sequences coming soon

PTP-related structures including auxillary domains

PTP	Species	Ligand	Mutation	PDB ID
N-terminal SH2 do	Mouse	Peptide from PDGFR (site 1009): VLpYTAVQP		1AYA
N-terminal SH2 do	Mouse	Peptide from IRS-1 (site 895): GEpYVNIEF		1AYB
N-terminal SH2 do	Mouse	Peptide from the PDGFR (site 740): GpYMDMS		1AYC
N-terminal SH2 do	Mouse	No ligand	None	1AYD
N-Terminal domain	Yersinia pestis	No ligand	None	1HUF
N-Terminal domain	pseudotuberculosis	No ligand	None	1K46
N-Terminal domain	pseudotuberculosis	No ligand	None	1MOV
Energy-coupling p	Escherichia coli	An energy-coupling protein from bacteria, IIBce	None	1IIB
LMW-PTP	Bos taurus	Solution structure of a low molecular weight pro	None	1BVH
PDZ domain of PT	Mouse	Structure, Dynamics and Binding Characteristic	None	1GM1
PDZ Domain from	Human	C-Terminal Peptide from the Fas Receptor		3PDZ
SH3 domain of CS	Mouse	25-residue peptide from the PEST-domain of P	None	1JEG
Arsenate reductas	Bacillus Subtilis	Similar to Low Molecular Weight Protein Tyrosine Phosphatase		1JL3
Mkp-3 Erk3 bindin	Human			1HZM
Pac-1	Human		Active site mutation	1KZ

Table S1 (Supplement to Table 1 in manuscript)

Genomic PTP sequence database (draft-quality and finished clones)

Summary of accession numbers identified by mining the human genome for PTP-like sequences

PTP			Chromosomal location				Accession numbers				
Name	Gene Symbol	Locus ID LocusLink	Chr.	Assembly Build 33	Experimental cytogenetic mapping PubMed		Genomic clones ID GenBank				
PTP-encoding genes											
LyPPT	PTPN22	26191	1	1p13.2	1p13	Cohen et al	AL137856	AL365321			NT_019273
LAR	PTPRF	5792	1	1p34.2	1p32	Jirik et al	AC092815	AL158083			NT_032971
PTPlamda	PTPRU	10076	1	1p35.3	1p35	Avraham et al	AL049570				NT_004538
CD45	PTPRC	5788	1	1q31.3	1q31-q32	Goff et al	AC117946	AL157402	AL355988		NT_029862
HePTP	PTPN7	5778	1	1q32.1	1q32.1	Zanke et al, Adachi et al	AL592300				NT_034408
PTP-OST	N.A.	N.A.	1	1q32.1	N.D.		AL356953	AL592300	AL354751		NT_034408
PTPD2	PTPN14	5784	1	1q32.3	1q32.2-q41	Smith et al	AL603838	AL592216	AC026065	AC068586	AL590137
MEG1	PTPN4	5775	2	2q14.2	N.D.		AC016691	AC104668	AC041008	AC015719	AC092455
BDP1	PTPN18	26469	2	2q21.2	N.D.		AC068137				NT_032991
IA2	PTPRN	5798	2	2q35	2q35	Lan et al, Morahan et al	AC114803	AC060820	AF042285		NT_005403
PTPgamma	PTPRG	5793	3	3p14.2	3p21	Laforgia et al	AC092502	AC024885			NT_005999
HDPTP	PTPN23	25930	3	3p21.31	3p21.3	Toyooka et al	AC099778	AC023230			NT_022567
PTPBAS	PTPN13	5783	4	4q21.3	4q21.3	Inazawa et al, Maaqdenberg et al	AC105413	AC007525	AC079237		NT_006204
PTPkappa	PTPRK	5796	6	6q22.33	Chr 6	Yang et al	AL035470	AL035465			NT_025741
PEST	PTPN12	5782	7	7q11.23	7q11.23	Takekawa et al, Charest et al	AC006451	AC090421			NT_007933
PTPzeta	PTPRZ1	5803	7	7q31.31	7q31.3	Ariyama et al, Morton et al	AC006020	AC073471			NT_007933
IA2beta	PTPRN2	5799	7	7q36.3	7q36 (7q22-qtter)	Morahan et al, (Jiang et al)	AC093856	AC005481	AC006372	AC006321	AC079590
PTPdelta	PTPRD	5789	9	9p24.1	9p24	Hasegawa et al	AL445926	AC026466	AI590397	AL391275	NT_008413
PTPH1	PTPN3	5774	9	9q31.3	9q31	Itoh et al	AL359963	AL450025	AC013568	AC026568	NT_017568
PTP1yp	PTPN20*	26095	10	10q11.22	N.D.		AL672108	AL450334	AC026739	AL358791	NT_031847
PTPepsilon	PTPRE	5791	10	10q26.2	10q26	Helson et al, Melhado et al	AL390236				NT_008818
DEP1	PTPRJ	5795	11	11p11.2	11p11.2	Honda et al, Borges et al	AC026975				NT_008978
STEP	PTPN5	5776	11	11p15.1	11p15.2-p15.1	Li et al	AC103974	AC016750			NT_009307
GLEPP1	PTPRO	5800	12	12p12.3	12p12-p13	Wiggins et al	AC007542				NT_009714
SHP1	PTPN6	5777	12	12p13.31	12p13	Plutzky et al	U47924	AC006512	M86525		NT_035206
PCPTP1	PTPRR	5801	12	12q15	12q15	Bektas et al	AC083809	AC090676	AC015544	AC090670	AC055123
PTPbeta	PTPRB	5787	12	12q15	12q15-q21	Harder et al	AC025569	AC083809	AC011053	AC015544	NT_009540
PTPS31	PTPGMC1*	8680	12	12q21.13	12q15	Wright et al	AC074031	AC025568	AC078825		NT_019546
SHP2	PTPN11	5781	12	12q24.13	12q24.1-q24.3	Dechert et al, Isobe et al	AC004216	AC004086			NT_009770
PTPD1	PTPN21	11099	14	14q31.3-q32.11	N.D.		AL162171	AL049834	AL353786		NT_026437
MEG2	PTPN9	5780	15	15q24.2	N.D.		AC105036	AC016402	AC009712	AC012527	NT_024654
TCPTP	PTPN2	5771	18	18p11.21	Chr 18	Sakaguchi et al	AP001077	AC007734	AP002449	AC067860	AC069433
PTPmu	PTPRM	5797	18	18p11.23	18p11.2	Suijkerbuijk et al, Gebbink et al	AP001094	AC021310	AC006566	AC069097	AC023663
PTPsiigma	PTPRS	5802	19	19p13.3	19p13.3	Wagner et al	AC118535	AC005788			NT_011255
SAP1	PTPRH	5794	19	19q13.42	19q13.4	Matozaki et al, Marnaros et al	AC010819	AC010327			NT_011225
PTPalpha	PTPRA	5786	20	20p13	20p12-pter	Rao et al	AL121905	AL138803			NT_011387
PTPrho	PTPRT	11122	20	20q12-q13.11	Chr 20	McAndrew et al	AL024473	AL049812			NT_011362
PTPIB	PTPN1	5770	20	20q13.13	20q13.1-q13.2	Brown-Shimer et al, Forsell et al	AL133230				NT_011362
PTP pseudogenes with exon-like structure											
SHP3-P1	N.A.	N.A.	1	1p36.33	N.D.		AL390719				NT_004350
PTPdelta-P5	N.A.	N.A.	5	5q23.1	N.D.		AC073538	AC114322			NT_030685
PTP pseudogenes (retrotransposed intronless genes)											
TCPTP-P1	N.A.	N.A.	1	1q25.2	1q22-q24	Johnson et al	AL162255				NT_004487
TCPTP-P13	N.A.	N.A.	13	13q12.3	13q12-q13	Johnson et al	AL353648	AL138681			NT_009799
SHP2-P3	N.A.	N.A.	3	3q13.12	3q13.1-q13.2	Dechert et al	AC074043				NT_019350
SHP2-P4	N.A.	N.A.	4	4q21.22	4q21	Dechert et al	AC067942	AC027573			NT_006328
SHP2-P5	N.A.	N.A.	5	5p14.2	5p14	Dechert et al	AC104460				NT_006547
SHP2-P6	N.A.	N.A.	6	6q23.3	6q23-6q24	Dechert et al	AL356234	AC058810	AC068118		NT_025741
SHP2-P8	N.A.	N.A.	8	8q12.1	8q12	Dechert et al	AC009927	AC020782			NT_008183
Meg1-P8	N.A.	N.A.	8	8p23.1	N.D.		AF287957	AC009632	AC091099		NT_023736
PTPalpha-P9	N.A.	N.A.	9	9q21.33	N.D.		AL137849	AL450106			NT_023935
Other PTP-like sequences not present in assembly (Build 33)											
PTP-like	N.A.	N.A.	4	N.A.	N.D.		AC040993				N.A.

*Interim gene symbols. Not officially approved by the HUGO gene nomenclature

Accession numbers in yellow are draft-quality sequences not used in the current genome assembly (Build 33)
See manuscript for discussion of accession numbers for PTPPOST

Summary of accession numbers retrieved by our genome-wide search which were not classical PTPs

PTP			Chromosomal location & PubMed				Accession numbers			Other links	
Name	Gene Symbol	Locus ID LocusLink	Chr.	Assembly Build 31	PubMed PubMed	Genomic clones ID GenBank			Unigene Unigene	GDB GDB	
PTP gene annotation without sequence information											
PTPRZ2	PTPRZ2	5804			Onyango et al					6763972	
PTPN8	PTPN8	5779									
PTPRQ	PTPRQ	23628									
PTPN17	PTPN17	5785									
PTP gene symbols assigned to non-classical PTP sequences											
PTPLA	PTPLA	9200	10	10p12.33	Uwanogho et al, Li et al	AF114494				Hs.114062	9955456
PTPLB	PTPLB	9199	3q21	3q21.1	Uwanogho et al	AC023165	AC020631	AC084039	AC025571		9955218
PTPLC	PTPLC	9198		Not present	Uwanogho et al	Not known					9955217
False positive hits from our genome-wide PTP homology search including hits to dual-specificity phosphatases (DSPs)											
Weak PTP motif			8	8p22		AC090420	AC087821	AC024929	AC024037		
Weak PTP motif			12	12q21.33		AC025034					
Weak PTP motif			?	Not present		AC013659					
Not a PTP			1	1p32.3		AL354778					
Not a PTP			1	Not present		AL359084					
Not a PTP			3	3q28		AC063939					
Not a PTP			4	4q32.3		AC021151					
Not a PTP			10	10q23.31		AL356073	AP001849				
Not a PTP			11	11q11		AC027239	AP001998				
Not a PTP			18	Not present		AC090410					
DSP	DUSP2	1844	2	2q11.2		AC012307					
DSP			7	7p12.3		AC006024	AC004899				
DSP	DUSP4	1846	8	8p12		AC055851	AC024678	AC084262	AC020588		
DSP			8p12	Not present		AC090140					
DSP			9	9p13.3		AL356489					
DSP	DUSP14	11072	17	17q12		AC004099					

Accession numbers in yellow are draft-quality sequences not used in the current genome assembly (Build 31)

Table S2 (Supplement to Table 2 in manuscript)

Genomic annotation of PTP genes - Hyperlinked database

Name	Ref Sequences		Annotated Gene Information							Mouse Ortholog	
	PTP	mRNA Genbank	Protein Genbank	GeneSymbol Home	Locus ID Home	Unigene Home	euGene Home	Ensembl gene ID Home	GDB Home	OMIM Home	GeneSymbol Home
hLyPTP	NM_015967	NP_057051	PTPN22	26191	Hs.87860	26191	ENSG00000134242	11507553	606986	Ptpn8	19260
hLAR	NM_002840	NP_002831	PTPRF	5792	Hs.75216	5792	ENSG00000142949	120138	179590	Ptpfr	19268
hPTPlamda	NM_005704	NP_005695	PTPRU	10076	Hs.19718	10076	ENSG00000060656	9954970	602454	Ptpri	19273
hCD45	NM_002838	NP_002829	PTPRC	5788	Hs.170121	5788	ENSG00000081237	119768	151460	Ptprc	19264
hHePTP	NM_002832	NP_002823	PTPN7	5778	Hs.35	5778	ENSG00000143851	135507	176889	Ptpn7	170476
hPTP-OST	N.A.	N.A.	N.A.	N.A.	N.A.	N.A.	N.A.	N.A.	N.A.	Ptprv	13924
hPTPD2	NM_005401	NP_005392	PTPN14	5784	Hs.159238	5784	ENSG00000065995	454485	603155	Ptpn14	19250
hBDP1	NM_014369	NP_055184	PTPN18	26469	Hs.278597	26469	ENSG00000072135	10795928	606587	Ptpn18	19253
hMEG1	NM_002830	NP_002821	PTPN4	5775	Hs.73826	5775	ENSG00000088179	131387	176878	Ptpn4	19258
hIA2	NM_002846	NP_002837	PTPRN	5798	Hs.89655	5798	ENSG00000054356	454048	601773	Ptpn	19275
hHDPTP	NM_015466	NP_056281	PTPN23	25930	Hs.25524	25930	ENSG00000076201	11507555	606584	N.A.	N.A.
hPTPgamma	NM_002841	NP_002832	PTPRG	5793	Hs.89627	5793	ENSG00000144724	127351	176886	Ptprg	19270
hPTPBAS	NM_006264	NP_006255	PTPN13	5783	Hs.211595	5783	N.A.	306348	600267	Ptpn13	19249
hPTPkappa	NM_002844	NP_002835	PTPRK	5796	Hs.79005	5796	ENSG00000152894	9834527	602545	Ptprk	19272
hPEST	NM_002835	NP_002826	PTPN12	5782	Hs.62	5782	ENSG00000127947	136846	600079	Ptpn12	19248
hPTPzeta	NM_002851	NP_002842	PTPRZ1	5803	Hs.78867	5803	ENSG00000106278	127353	176891	Ptprz1	19283
hIA2beta	NM_002847	NP_002838	PTPRN2	5799	Hs.74624	5799	ENSG00000002748	9785772	601698	Ptpn2	19276
hPTPdelta	NM_002839	NP_002830	PTPRD	5789	Hs.158112	5789	ENSG00000099228	131384	601598	Ptprd	19266
hPTPH1	NM_002829	NP_002820	PTPN3	5774	Hs.153932	5774	ENSG00000070159	131386	176877	Ptpn3	19257
hPTPTyp	NM_015605	NP_056420	PTPN20*	26095	N.A.	N.A.	ENSG00000126542	N.A.	N.A.	Ptpn20	19256
hPTPepsilon	NM_006504	NP_006495	PTPRE	5791	Hs.31137	5791	ENSG00000132334	131385	600926	Ptpre	19267
hDEP1	NM_002843	NP_002834	PTPRJ	5795	Hs.171992	5795	ENSG00000149177	385040	600925	Ptpri	19271
hSTEP	NM_032781	NP_116170	PTPN5	5776	Hs.248318	5776	ENSG00000110786	131388	176879	Ptpn5	19259
hSHP1	NM_002831	NP_002822	PTPN6	5777	Hs.63489	5777	ENSG00000111679	131389	176883	Hcph	15170
hGLEPP1	NM_030667	NP_109592	PTPRO	5800	Hs.258609	5800	ENSG00000084474	454477	600579	Ptpro	19277
hPCPTP1	NM_002849	NP_002840	PTPRR	5801	Hs.198288	5801	ENSG00000111585	9835737	602853	Ptprr	19279
hPTPbeta	NM_002837	NP_002828	PTPRB	5787	Hs.123641	5787	ENSG00000127329	127352	176882	Ptprb	12263
hPTPS31	AF169351	AAD50277	PTPGMC1*	8680	N.A.	8680	ENSG00000091041	9956257	603317	N.A.	N.A.
hSHP2	NM_002834	NP_002825	PTPN11	5781	Hs.22868	5781	ENSG00000089131	137093	176876	Ptpn11	19247
hPTPD1	NM_007039	NP_008970	PTPN21	11099	Hs.155693	11099	ENSG00000070778	9956481	603271	Ptpn21	24000
hMEG2	NM_002833	NP_002824	PTPN9	5780	Hs.147663	5780	ENSG00000169410	132399	600768	Ptpn9	56294
hPTPmu	NM_002845	NP_002836	PTPRM	5797	Hs.154151	5797	ENSG00000069927	128093	176888	Ptpm	19274
hTCGTP	NM_002828	NP_002819	PTPN2	5771	Hs.82829	5771	ENSG00000128772	128098	176887	Ptpn2	19255
hPTPsigma	NM_002850	NP_002841	PTPRS	5802	Hs.159534	5802	ENSG00000105426	555925	601576	Ptprs	19280
hSAP1	NM_002842	NP_002833	PTPRH	5794	Hs.179770	5794	ENSG00000080031	305504	602510	N.A.	N.A.
hPTPalpha	NM_002836	NP_002827	PTPRA	5786	Hs.26045	5786	ENSG00000037980	126732	176884	Ptpra	19262
hPTPrho	NM_007050	NP_008981	PTPRT	11122	Hs.225952	11122	ENSG00000087530	9785461	N.A.	Ptprt	19281
hPTP1B	NM_002827	NP_002818	PTPN1	5770	Hs.155894	5770	ENSG00000063920	126728	176885	Ptpn1	10246

*Interim gene symbols. Not officially approved by the HUGO gene nomenclature

RefSeq sequences in yellow are predicted sequences supported by partial mRNA and ESTs

Note, there is no RefSeq sequences available for human PTPS31 and human PTP-OST

Table S3 (Website database)

PTP isoforms - Alternative splicing enhances the diversity of PTP proteins

PTP	Isoform	Variants	Ref Sequences	Accession numbers	Comments and Analysis (Revised RefSeq Annotation)	
hLypTP	Lyp1	Variant (1)	NP_057051	NM_015967	AF001846 , AF077031 , U69700	This variant (1) encodes the longer isoform (1) which is 116 aa longer than isoform 2 and has a distinct C-terminus.
		Variant (2)	NP_036543	NM_012411	AF001847	This variant (2) uses an alternative splice site within the coding region, resulting in a frameshift and use of an upstream stop codon, as compared to
	Lyp2	Variant (3)	N.A.	N.A.	AF150732	No genomic evidence for this variant - the unique part of this mRNA does not align to genomic sequence
		Variant (4)	N.A.	N.A.	BC017785	Predicted protein for this mRNA is nonsense
hLAR	Variant (1)	NP_002831	NM_002840	Y00815 , BI711143 , BC012102 , BC029486	This variant (1) contains an extra exon when compared to variant 2. It thus encodes a protein that has an extra 9 aa (WRPEESEDY) in the extracell	
	Variant (2)	NP_569707	NM_130440	BQ920757 , BQ894845	This variant (2) lacks an exon within the coding region when compared to variant 1. It thus encodes a protein that lacks a 9 aa present in isoform 1.	
hPTPlamda	Variant (1)	NP_573439	NM_133178	X97198 , AK094849 , BC033131 , U73727	This variant (1) lacks an exon within the coding region when compared to variant 3. The translation remains in-frame, and thus results in a protein t	
	Variant (2)	NP_573438	NM_133177	U71075	This variant (2) lacks two internal fragments, and contains an extra fragment within the coding region when compared to variant 3. The translation r	
	Variant (3)	NP_005695	NM_005704	X95712	This variant (3) encodes the longest isoform (3).	
hCD45	CD45RABC	Variant (1)	NP_002829	NM_002838	Y00062 , Y00638	This variant (1) encodes the longest isoform (1) (includes exon 4, 5 & 6 which are called exon A, B & C in the literature).
		Variant (2)	NP_563578	NM_080921	Y00062	This variant (2) lacks exon 4, 5 & 6 within the coding region when compared to variant 1. It thus encodes a protein that lacks a 161 aa internal fragm
	CD45RAB	Variant (3)	NP_563579	NM_080922	BC014239 , Y00062	This variant (3) lacks exon 6 within the coding region when compared to variant 1. It thus encodes a protein that lacks a 48 aa internal fragment, as
		Variant (4)	NP_563580	NM_080923	BC017863 , Y00062	This variant (4) has a unique 3' sequence when compared to variant 1. The first 31 aa of isoform 4 are identical to isoform 1, and the 3 aa at the C-t
CD45RA	Variant (5)	N.A.	N.A.		Yu et al (2002)	
	Variant (6)	N.A.	N.A.		Fukuhara K et al (2002)	
	Variant (7)	N.A.	N.A.		Fukuhara K et al (2002)	
	Other Variat	N.A.	N.A.		Hermiston ML, Xu Z, Weiss A (Variants of exon 7, 8 and 10)	
hHePTP	Variant (1)	NP_002823	NM_002832	BC001746 , BG340453 , D11327 , M64322 , S78090	This variant (1) contains a different 5' region, which includes a part of the coding sequence when compared to variant 2. It thus encodes a protein th	
	Variant (2)	NP_542155	NM_080588	BC001746	This variant (2) contains an alternate 5' region, which includes an additional in-frame translation start codon, as compared to variant 1. It thus encod	
	Variant (3)	NP_542156	NM_080589	D11327	This variant (3) lacks an internal 3' UTR region, and encodes an identical protein, as compared to variant 1	
	Variant (4)	N.A.	N.A.	AF394064	This variant (4) contains an alternate 5' region which includes part of the coding sequence when compared to variant 1. It thus encodes a protein th	
hOST-PTP	-	N.A.	N.A.		Morrison et al, Lee et al, Mauro et al, Lathrop et al	
hPTPD2	-	NP_005392	NM_005401	BC017300 , X82676	Supported by alignment with both mRNA and ESTs	
hBDP1	-	NP_055184	NM_014369	BI261717 , X79568 , BC024280	Supported by alignment with both mRNA and ESTs	
hMEG1	-	NP_002821	NM_002830	BC010674 , M68941	Supported by alignment with both mRNA and ESTs	
hPTPIA2	-	NP_002837	NM_002846	BC007713 , L18983 , X62899	Supported by alignment with both mRNA and ESTs	
hHDPTP	-	NP_056281	NM_015466	AB025194 , AB040904 , AK05515 , AL110210 , AF2906	Supported by alignment with both mRNA and ESTs	
hPTPgamm	-	NP_002832	NM_002841	AI872451 , L09247 , AI872451 , X54132	Supported by alignment with both mRNA and ESTs	
hPTPBAS	Variant (1)	NP_542414	NM_080683	D21209	This variant (1) lacks an internal fragment within the coding region when compared to variant 4. The translation remains in frame, and the encoded	
	Variant (2)	NP_006255	NM_006264	D21210	This variant (2) lacks an internal exon (GMTMHSSGNSSSQVPLKEN) within the coding region when compared to variant 4. The translation remains	
	Variant (3)	NP_542415	NM_080684	D21211	This variant (3) lacks an internal fragment (2 consecutive exons) within the coding region when compared to variant 4. The translation remains in fra	
	Variant (4)	NP_542416	NM_080685	D21209 , U12128	This variant (4) encodes the longest isoform (4).	
hPTPkappa	-	NP_002835	NM_002844	BI755683 , L77886 , Z70660	Supported by alignment with both mRNA and ESTs	
hPEST	Variant (1)	NP_002826	NM_002835	M93425 , D13380	Supported by alignment with both mRNA and ESTs	
	Variant (2)	N.A.	N.A.	S69182 , B6829296	Supported by alignment with both mRNA and ESTs	
hPTPzeta	-	NP_002842	NM_002851	M93426 , U88967	Supported by alignment with mRNA	
hPTPIA2beta	Variant (1)	NP_002838	NM_002847	U66702 , AB002385 , AF007555 , BC030400	This variant (1) encodes the longest isoform (1).	
	Variant (2)	NP_570857	NM_130842	U81561	This variant (2) lacks an internal fragment within the coding region when compared to variant 1. The translation remains in-frame, and thus results ir	
	Variant (3)	NP_570858	NM_130843	U65065 , U81561	This variant (3) lacks an internal fragment within the coding region when compared to variant 1. The translation remains in-frame, and thus results ir	
hPTPdelta	Variant (1)	NP_002830	NM_002839	L38929 , X54133	This variant (1) encodes the longest isoform (1).	
	Variant (2)	NP_569075	NM_130391	L38929	Pulido et al This variant (2) lacks two separate internal segments within the coding region. It thus encodes a protein that lacks a 9 aa, and a 4 aa int	
	Variant (3)	NP_569076	NM_130392	L38929	This variant (3) lacks an internal segment within the coding region. It thus encodes a protein that lack a 9 aa internal fragment, as compared to isofo	
	Variant (4)	NP_569077	NM_130393	L38929	This variant (4) lacks an internal segment within the coding region. It thus encodes a protein that lacks a 411 aa internal fragment, and has one ami	
hPTPH1	-	NP_002820	NM_002829	M64572 , W15441 , S39392 , S76309	Supported by alignment with both mRNA and ESTs	
hPTPTyp	-	NP_056420	NM_015605	BC036539 , CAB43248 , AL050040	Supported by alignment with both mRNA and ESTs	
hPTPepsilon	RPTP _ε	Variant (1)	NP_006495	NM_006504	BI559814 , X54134	This variant (1) contains a different 5' end region that includes a part of the coding region, when compared to variant 2. It thus encodes a protein the
	cytPTP _ε	Variant (2)	NP_569119	NM_130435	AJ315969 , BI910569	This variant (1) contains a different 5' end region that includes a part of the coding region, when compared to variant 2. It thus encodes a protein the
	cytPTP _ε -PD1	Variant (3)	N.A.	N.A.	AJ430580	Wabakken et al (2002)
hDEP1	-	NP_002834	NM_002843	U10886 , D37781 , AL359057	supported by alignment with both mRNA and ESTs	
hSTEP	-	NP_116170	NM_032781	U27831 , AK090923 , BC039897 , AL832541	supported by alignment with both mRNA and ESTs	
hSHP1	Variant (1)	NP_002822	NM_002831	AH003242 , BC002523 , M77273 , U15536	This variant (1) lacks an internal fragment within the coding region, which leads to a translation frame change when compared to variant 3. It encod	
	Variant (2)	NP_536858	NM_080548	BC002523 , U15537	This variant (2) contains a different 5' end region including 5' UTR and a small portion of the coding region, and lacks an internal fragment within the	
	Variant (3)	NP_536859	NM_080549	AF178946 , AH003242 , BC002523 , U15536	This variant (3) encodes the longest isoform (3).	
	Variant (1)	NP_109592	NM_030667	U20489 , Z48541 , BC035960	This variant (1) encodes the longest isoform (a) known to date. The encoded protein has a large extracellular domain containing 8 repeats of a fibro	
	Variant (2)	NP_002839	NM_002848	U20489 , Z48541	This variant (2) lacks an internal 84 nt exon compared to variant 1, resulting in an isoform (b) that is missing a cytoplasmic juxtamembrane region co	
	Variant (3)	NP_109594	NM_030669	AF187043 , Z48541	This variant (3) has a different 5' UTR and a downstream in-frame start codon compared to variant 1. Compared to isoform a, the encoded isoform (
Variant (4)	NP_109593	NM_030668	AF187044 , Z48541	This variant (4), compared to variant 1, has a different 5' UTR, has a downstream in-frame start codon, and lacks an internal 84 nt exon. Compared		
Variant (5)	NP_109596	NM_030671	AF152378 , Z48541	This variant (5), compared to variant 1, has a different 5' UTR, has a downstream in-frame start codon, and includes an additional sequence within t		
Variant (6)	NP_109595	NM_030670	AF187042 , Z48541	This variant (6), compared to variant 1, has a different 5' UTR, has a downstream in-frame start codon, lacks an internal 84 nt exon, and includes an		
hPCPTP1	Variant (1)	NP_002840	NM_002849	D64053	This variant (1) contains a different 5' end region when compared to variant 2. It thus encodes a protein that has a longer N-terminus, as compared i	
Variant (2)	NP_570897	NM_130846	U77917	This variant (2) contains a different 5' end region, and uses a downstream in-frame start codon, when compared to variant 1. The resulting protein is		
hPTPbeta	-	NP_002828	NM_002837	BE042873 , X54131	supported by alignment with both mRNA and ESTs	
hPTPS31	S31F_Var1	Variant (1)	N.A.	N.A.	AR073855 , I32039 , AF169351	Andersen et al (2003)
	S31F_Var2	Variant (2)	N.A.	N.A.		Andersen et al (2003)
	S31F_Var3	Variant (3)	N.A.	N.A.		Andersen et al (2003)
	S31C	Variant (4)	N.A.	N.A.	I32037	Andersen et al (2003)
	S31D	Variant (5)	N.A.	N.A.	I32035	Andersen et al (2003)
hSHP2	Variant (1)	NP_002825	NM_002834	BE042873 , X54131	This variant (1) contains a different 3' end region, and encodes a longer isoform (1), as compared to variant 2.	
	Variant (2)	NP_542168	NM_080601	BC008692 , BF515187	This variant (2) contains an alternate 3' end region, which includes a part of the coding region when compared to variant 1. It thus encodes a protein	
hPTPD1	-	NP_008970	NM_007039	AI800682 , X79510	supported by alignment with both mRNA and ESTs	
hMEG2	-	NP_002824	NM_002833	M83738 , BC010863	supported by alignment with both mRNA and ESTs	
hPTPmu	Variant (1)	NP_002836	NM_002845	AA281524 , X58288	supported by alignment with both mRNA and ESTs	
	Variant (2)	N.A.	N.A.	BE439911	Supported by human and bovine ESTs - insertion of GGAGGAGCNSPSPRESVQ within the PTP domain	
hTCPTP	TC48	Variant (1)	NP_002819	NM_002828	AW592324 , BG699440 , M25393	This variant (1) contains a different 3' region, and encodes the longest isoform (1), as compared to variant 2 and
		Variant (2)	NP_536347	NM_080422	BC008244 , BG699440	This variant (2) contains an alternate 3' region, which includes a part of the C-terminal coding region, when compared to variant 1. The resulting pro
	Variant (3)	NP_536348	NM_080423	BC016727 , BG699440	This variant (3) contains an alternate 3' region, which includes a part of the C-terminal coding region, when compared to variant 1. The resulting pro	
hPTPsigma	Variant (1)	NP_002841	NM_002850	U35234 , BI461316 , S78080 , S78086	This variant (1) encodes the longest isoform (1).	
	Variant (2)	NP_570924	NM_130854	BI461316 , U35234	This variant (2) lacks four internal fragments within the coding region when compared to variant 1. The translation remains in-frame, and thus result	
	Variant (3)	NP_570923	NM_130853	U41727	This variant (3) lacks four internal fragments within the coding region when compared to variant 1. The translation remains in-frame, and thus result	
	Variant (4)	NP_570925	NM_130855	U403125	This variant (4) lacks three internal fragments within the coding region when compared to variant 1. The translation remains in-frame, and thus result	
hSAP1	-	NP_002833	NM_002842	D15049	supported by alignment with both mRNA and ESTs	
hPTPalpha	Variant (1)	NP_002827	NM_002836	M34668 , AI284972	This variant (1) contains a unique 5' UTR region when compared to other variants. The genomic exons forming the 5' end region of this transcript ar	
	Variant (2)	NP_543030	NM_080840	BI597187 , X54890	This variant (2) contains a different 5' UTR region, and lacks an internal segment within the coding region, when compared to variant 1. The resultin	
	Variant (3)	NP_543031	NM_080841	M34668 , X53364	This variant (3) contains an extra internal segment in the 5' UTR region, and lacks an internal segment within the coding region, when compared to	
hPTPrho	Variant (1)	NP_573400	NM_133170	AF043644 , R50970	This variant (1) contains an additional fragment within the coding region when compared to variant 2, and thus encodes a protein that contains an e	
	Variant (2)	NP_008981	NM_007050	AF043644 , R50970	This variant (2) lacks a fragment within the coding region when compared to variant 1. The translation remains in-frame, and thus encodes a protein	
hPTP1B	Variant (1)	NP_002818	NM_002827	AU117677 , M33689	This variant (1) is 435 aa long and is encoded by 10 exons. It differ in its exon 10 encoded C-terminal sequence (FLFNSNT*) from variant (2). Its m	
	Variant (2)	N.A.	N.A.	BU430170	This variant (2) is 432 aa long and has an alternative termination codon in exon 9. It differ in its C-terminal	

Ref Sequences in yellow are predicted sequences supported by partial mRNA and ESTs

Table S4 (Website database)

Genetic variation and disease annotation of PTP loci

Name		Chr Location	OMIM	LocusLink	Mitelman	Morbid	SNPs	Chr aberrations in cancers		PubMed and OMIM Search	References
PTP	Gene	UCSC View	Home	Home	Home	Home	Home	deletions	uplications		
hLyPTP	PTPN22	1p13.2	606986	26191	Map	Map	Map	Yes	-	Region associated with rearrangements in solid and hemopoietic tumors	Cohen et al, Hill et al
hLAR	PTPRE	1p34.2	179590	5792	Map	Map	Map	Yes	-	Frequently deleted in human neuroblastoma. Small cell lung cancer (Co	Link et al, Harder et al, Zabolotny et al
hPTPlamda	PTPRU	1p35.2	602454	10076	Map	Map	Map	Yes	-	Parkinson, onset	
hCD45	PTPRC	1q31.3	151460	5788	Map	Map	Map	-	-	Autoimmunity (SCID). Multiple sclerosis.Susceptibility to HIV-1 infection	Jacobsen et al, Vorechovsky et al, Barcellos et al, Kung et al, Tchilian et al
hHePTP	PTPN7	1q32.1	176889	5778	Map	Map	Map	Yes	Yes	Non-Hodgkin lymphomas	
hPTPD2	PTPN14	1q32.3	603155	5784	Map	Map	Map	Yes	Yes		
hBDP1	PTPN18	2q21.1	N.A.	26469	Map	Map	Map	-	-		
hMEG1	PTPN4	2q14.2	176878	5775	Map	Map	Map	-	-		
hPTPIA2	PTPRN	2q35	601773	5798	Map	Map	Map	-	-	Autoantigens in type I insulin-dependent diabetes mellitus (IDDM),	Cui et al
hHDPTP	PTPN23	3p21.31	N.A.	25930	Map	Map	Map	Yes	-		
hPTPgamma	PTPRG	3p14.2	176886	5793	Map	Map	Map	Yes	-	3p14.2 hot spot for alterations in lung cancer	LaForgia et al, Pitterle et al, Panagopoulos et al
hPTPBAS	PTPN13	4q21.3	600267	5783	Map	Map	Map	Yes	-	4q21.3 frequently deleted in liver and ovarian cancers	Inazawa
hPTPkappa	PTPRK	6q22.33	602545	5796	Map	Map	Map	Yes	-	Tumor supressor, frequently deleted in primary CNS lymphomas	Zhang et al, Nakamura et al
hPEST	PTPN12	7q11.23	600079	5782	Map	Map	Map	Yes	-	Aberrant transcripts in Colon cancer. Tumorigenesis ?	Takekawa et al
hPTPzeta	PTPRZ1	7q31.31	176891	5803	Map	Map	Map	Yes	-		
hPTPIA2beta	PTPRN2	7q36.3	601698	5799	Map	Map	Map	Yes	-	Autoantigens in type I insulin-dependent diabetes mellitus (IDDM),	Cui et al
hPTPdelta	PTPRD	9p24.1	601598	5789	Map	Map	Map	-	-		
hPTPH1	PTPN3	9q31.3	176877	5774	Map	Map	Map	Yes	-		
hPTPtyp	PTPN20	10q11.21-q11.22	N.A.	N.A.	Map	Map	Map	-	-		
hPTPepsilon	PTPRE	10q26.2	600926	5791	Map	Map	Map	-	-		
hDEP1	PTPRJ	11p11.2	600925	5795	Map	Map	Map	Yes	-	Colon cancer somatic mutations, Susceptibility to colon cancer-1	Ruivenkamp et al, Watanabe et al
hSTEP	PTPN5	11p15.1	176879	5776	Map	Map	Map	-	-		
hSHP1	PTPN6	12p13.31	176883	5777	Map	Map	Map	Yes	-	Sezary syndrome. Leukemogenesis.Experimental autoimmune enceph	Beghini et al, Leon et al, Deng et al, Tidow et al, Oka T
hGLEPP1	PTPRO	12p12.3	600579	5800	Map	Map	Map	Yes	-		
hPCPTP1	PTPRR	12q15	602853	5801	Map	Map	Map	-	-	Diabetes ?	Bektas et al
hPTPbeta	PTPRB	12q15	176882	5787	Map	Map	Map	-	-		
hPTPS31	PTPGMC1	12q21.31	603317	8680	Map	-	Map	-	-		
hSHP2	PTPN11	12q24.13	176876	5781	Map	Map	Map	-	-	Noonan syndrome 1, Cardiofaciocutaneous syndrome, AML	Tartaglia et al, Kavamura et al
hPTPD1	PTPN21	14q31.3-q32.11	603271	11099	Map	Map	Map	Yes	Yes		
hMEG2	PTPN9	15q24.2	600768	5780	Map	Map	Map	-	-		
hPTPmu	PTPRM	18p11.23	176888	5797	Map	Map	Map	-	-		
hTCPTP	PTPN2	18p11.21	176887	5771	Map	Map	Map	-	-		
hPTPsigma	PTPRS	19p13.3	601576	5802	Map	Map	Map	Yes	-		
hSAP1	PTPRH	19q13.42	602510	5794	Map	Map	Map	-	-	Overexpressed in colorectal cancer. Not a Peutz-Jeghers synd. candida	Seo et al, Marmaros et al
hPTPalpha	PTPRA	20p13	176884	5786	Map	Map	Map	-	-		
hPTPrho	PTPRT	20q12-q13.11	N.A.	11122	Map	Map	Map	Yes	-	Myeloproliferative disorders	
hPTP1B	PTPN1	20q13.13	176885	5770	Map	Map	Map	-	-	Insulin resistance, Obesity QTL, Breast Carcinomas, Ovarian cancer	Echwald, Dipaola, Gu, Lembertas, Lee, Hunt, Zoderivan, Tanner, Kon

Table S5 (Supplement to Table 4 in manuscript)

Disease markers in diabetes in relation to PTP loci - Hyperlinked references

Chromosome	Reference	Population	Method	Confirmed in Population	References (PubMed)
1p36.3-1p36.23	Lou et al.	Northern China Han Families	ASP	Extended sample of Northern China Han families	Du et al.
1q24-25	Hanson et al.	Utah Caucasians	ASP	French and UK Caucasians, Amish	Wiltshire et al. , Vionnet et al. , Elbein et al.
2q37.3	Hanis et al.	Mexican Americans	ASP	French and UK Caucasians	Elbein et al. , Hani et al.
3q27-qter	Vionnet et al.	French Caucasians		Native Americans	Hegele et al.
5q13	Wiltshire et al.	UK Caucasians	ASP	French Caucasians, Native Americans	Wiltshire et al.
8p21-22	Wiltshire et al.	UK Caucasians	ASP		
9p13-q21	Duggirala et al.	Mexican Americans	ASP	Finnish Caucasians, American Caucasians	Lindgren et al. , Ehm et al.
10q23.3	Duggirala et al.	Mexican Americans	QTL (age at onset)	Finnish and UK Caucasians,	Wiltshire et al. , Vionnet et al. , Ghosh et al.
11q23-24	Hanson et al.	Pima Indians	ASP	UK Caucasians	Elbein et al.
12q24	Mahtani et al.	Finnish Caucasians	QTL (low insulin level)	African Americans, American & Swedish Caucasians	Ehm et al. , Bowden et al. , Lindgren et al.
20q13.1-q13.2	Ghosh et al.	Finnish Caucasians	ASP	French & Americans Caucasians, Ashkenazi Jews, Japanese	Permutt et al. , Bowden et al. , Mori et al. , Zouali et al.

QTL: Quantitative Trait Locus

ASP: Affected Sibling Pair