

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
		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, B1711143, 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 extrac
		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.
		Variant (3)	NP_573439	NM_133178	X97198, AK094849, BC033131, U73727	This variant (3) lacks an exon within the coding region when compared to variant 3. The translation remains in-frame, and thus results in a protein t
hPTPlamda		Variant(1)	NP_573438	NM_133177	U71075	This variant (1) encodes the longest isoform (1).
		Variant(2)	NP_005698	NM_005704	X95712	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_005698	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
		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
		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)
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
		-	NP_005392	NM_005401	BC017300, X82676	Supported by alignment with both mRNA and ESTs
hBPD1		-	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	AB025154, AB049004, 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 (GMTMHSSGNSSQVLPKEN) 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, BC034040	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
		Variant (4)	NP_002830	NM_002839	L38929, X54133	This variant (4) encodes the longest isoform (1).
hPTPdelta		Variant (1)	NP_569075	NM_130391	L38929	Putlido 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
		Variant (5)	NP_002820	NM_002829	M64572, W15441, S39392, S76309	Supported by alignment with both mRNA and ESTs
hPTPH1		-	NP_056420	NM_015605	BC036539, CAB43248, AL050040	Supported by alignment with both mRNA and ESTs
hPTPtyl	RPTP α	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
		Variant (2)	NP_569119	NM_130435	AJ315969, BI910569	This variant (2) 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
		Variant (3)	N.A	N.A	AJ430580	Wabakken et al (2002)
hDEP1		-	NP_002834	NM_002843	UI0886, D37781, AL359057	supported by alignment with both mRNA and ESTs
hSTEP		-	NP_116170	NM_032781	UJ27831, 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	UJ20489, 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_109593	NM_030668	AF187043, 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 (
hGLEPP1		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
		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
		Variant (3)	NP_002828	NM_002837	BE042873, X54131	supported by alignment with both mRNA and ESTs
hPTP531	S31F	Var1	N.A	N.A	AR073855, I32039, AF169351	Andersen et al (2003)
		Var2	N.A	N.A		Andersen et al (2003)
		Var3	N.A	N.A		Andersen et al (2003)
		Var4	N.A	N.A	I32037	Andersen et al (2003)
		Var5	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 GGAGGEEANCSPPRESVSQ 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	U40317	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, A1284972	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	B430170	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