

GeneDoc Screen View - Alignment\_234\_Vert\_PTP\_Domains\_D1\_and\_D2 (GeneDoc).msb

Table with 3 columns: Protein Name, Amino Acid Sequence (with alignment markers), and Residue Number. The table lists numerous protein variants such as hPTPsi, rPTPsi, and mPTPsi, showing their alignment to a reference sequence with asterisks indicating conserved residues. The residue numbers are listed at the end of each line, ranging from 100 to 95.

GeneDoc Screen View - Alignment 234 Vert PTP Domains D1 and D2 (GeneDoc).msb

Table with 4 columns: Protein Name, Amino Acid Sequence, Protein Name, and Residue Number. The table shows a multiple sequence alignment of 234 PTP domains, with amino acid sequences and residue numbers listed for each. Some residues are highlighted in blue or red in the original image.





	*	300	*	320	*	340	*	
hPTPsigma	:	VVHCSA	VGRTR	CFIVDAMDAMLERIKP	---EKTVDVYGHVTL	RSQ	NYMVQTED	YSFIHEALLEAVG : 275
mPTPsigma	:	VVHCSA	VGRTR	CFIVDAMDAMLERIKT	---EKTVDVYGHVTL	RSQ	NYMVQTED	YCFIHEALLEAVG : 275
rPTPsigma	:	VVHCSA	VGRTR	CFIVDAMDAMLERIRT	---EKTVDVYGHVTL	RSQ	NYMVQTED	YSFIHEALLEAVG : 275
cPTPsigma	:	VVHCSA	VGRTR	CFIVDAMDAMLERIKH	---EKTVDVYGHVTL	RSQ	NYMVQTED	YSFIHDALLEAVA : 275
xPTPsigma	:	VVHCSA	VGRTR	CFIVDAMDAMLERIKH	---EKTVDVYGHVTL	RSQ	NYMVQTED	YSFIHDALLEAVA : 275
zPTPsigma	:	LAHCSA	VGRTR	CFIVDAMDAMLERIKH	---EKTVDVYGHVTL	RSQ	NYMVQTED	YSFIHDALLEAVA : 275
hLAR_D1 (N	:	VVHCSA	VGRTR	CFIVDAMDAMLERMKH	---EKTVDVYGHVTC	RSQ	NYMVQTED	YVFIHEALLEAAT : 275
mLAR_D1 (N	:	VVHCSA	VGRTR	CFIVDAMDAMLERMKH	---EKTVDVYGHVTC	RSQ	NYMVQTED	YVFIHEALLEAAM : 275
rLAR_D1 (N	:	VVHCSA	VGRTR	CFIVDAMDAMLERMKH	---EKTVDVYGHVTC	RSQ	NYMVQTED	YVFIHEALLEAAM : 275
xLAR_D1 (A	:	FVHCSA	VGRTR	CFIVDAMDAMLERVKL	---EKTVDVYGHVTC	RSQ	NYMVQTED	YIFIHEALLEAVM : 275
hPTPdelta	:	VVHCSA	VGRTR	CFIVDAMDAMLERIKH	---EKTVDVYGHVTL	RAQ	NYMVQTED	YIFIHDALEAVT : 275
mPTPdelta	:	VVHCSA	VGRTR	CFIVDAMDAMLERIKH	---EKTVDVYGHVTL	RAQ	NYMVQTED	YIFIHDALEAVT : 273
xPTPdelta	:	VVHCSA	VGRTR	CFIVDAMDAMLERIKH	---EKTVDVYGHVTL	RAQ	NYMVQTED	YIFIHDALEAVT : 275
hPTPrho D1	:	VVHCSA	VGRTR	CFIADTMDLMAEN	---EGVVDIFNCVRE	RAQ	VNMLVQTEE	YVVFHDALEACL : 274
mPTPrho D1	:	VVHCSA	VGRTR	CFIADTMDLMAEN	---EGVVDIFNCVRE	RAQ	VNMLVQTEE	YVVFHDALEACL : 274
xPTPrho D1	:	VVHCSA	VGRTR	CFIADTMDLMAEN	---EGVVDIFNCVRE	RAQ	VNMLVQTEE	YVVFHDALEACL : 274
hPTPmu D1	:	VVHCSA	VGRTR	CFIVDIDMLDMAER	---EGVVDIYNCVRE	RSR	VNMLVQTEE	YVFIHDALLEACL : 274
mPTPmu D1	:	VVHCSA	VGRTR	CFIVDIDMLDMAER	---EGVVDIYNCVRE	RSR	VNMLVQTEE	YVFIHDALLEACL : 274
hPTPkappa	:	VVHCSA	VGRTR	CFIVDIDMLDMAER	---EGVVDIYNCVKA	RSR	INMLVQTEE	YIFIHDALEACL : 274
mPTPkappa	:	VVHCSA	VGRTR	CFIVDIDMLDMAER	---EGVVDIYNCVKA	RSR	INMLVQTEE	YIFIHDALEACL : 274
hPTPlamda	:	VVHCSA	TGRTR	CFIVLDMMLDMAEC	---EGVVDIYNCVKT	CSR	VNMIQTEE	YIFIHDALEACL : 270
mPTPlamda	:	VVHCSA	TGRTR	CFIVLDMMLDMAEC	---EGVVDIYNCVKT	CSR	VNMIQTEE	YIFIHDALEACL : 270
rPTPpsi D1	:	VVHCSA	TGRTR	CFIVLDMMLDMAEC	---EGVVDIYNCVKT	CSR	VNMIQTEE	YIFIHDALEACL : 270
hSHP1 D1 (	:	LVHCSA	IGRTR	TFIIVDMLMENISTKGLDCCDIDIQKTIQM	RAQ	SGMVQTEA	YKFIYVAIAQFIE	: 267
mSHP1 D1 (	:	LVHCSA	IGRTR	TFIIVDMLMESISTKGLDCCDIDIQKTIQM	RAQ	SGMVQTEA	YKFIYVAIAQFIE	: 297
rSHP1 D1 (	:	LVHCSA	IGRTR	TFIIVDMLMESVSTKGLDCCDIDIQKTIQM	RAQ	SGMVQTEA	YKFIYVAIAQFIE	: 297
zSHP1 D1 (	:	LVHCSA	IGRTR	TFIIVDMLLDSIDAKGLDCCDIDIQKTIQM	RDQ	SGMVQTEA	YKFIYLAVALQYVE	: 267
ryPTPN6c D	:	LVHCSA	IGRTR	TFIIVDMLISDISRQGLDCCDIDPKTIQI	RKQ	SGMVQTEA	YKFIYMAVQYIE	: 296
hSHP2 D1 (	:	VVHCSA	IGRTR	TFIIVDMLISDISRQGLDCCDIDPKTIQM	RSQ	SGMVQTEA	YKFIYMAVQYIE	: 300
mSHP2 D1 (	:	VVHCSA	IGRTR	TFIIVDMLISDISRQGLDCCDIDPKTIQM	RSQ	SGMVQTEA	YKFIYMAVQYIE	: 304
rSHP2 D1 (	:	VVHCSA	IGRTR	TFIIVDMLISDISRQGLDCCDIDPKTIQM	RSQ	SGMVQTEA	YKFIYMAVQYIE	: 300
zSHP2 D1 (	:	VVHCSA	IGRTR	TFIIVDMLISDISRQGLDCCDIDPKTIQM	RSQ	SGMVQTEA	YKFIYMAVQYIE	: 300
CSHP2 D1 (	:	VVHCSA	IGRTR	TFIIVDMLISDISRQGLDCCDIDPKTIQM	RSQ	SGMVQTEA	YKFIYMAVQYIE	: 300
zSHP2 D1 (	:	VVHCSA	IGRTR	TFIIVDMLISDISRQGLDCCDIDPKTIQM	RSQ	SGMVQTEA	YKFIYMAVQYIE	: 300
xSHP2 D1 (	:	VVHCSA	IGRTR	TFIIVDMLISDISRQGLDCCDIDPKTIQM	RSQ	SGMVQTEA	YKFIYMAVQYIE	: 300
ryPTPN6b D	:	VVHCSA	IGRTR	TFIIVDMLISDISRQGLDCCDIDPKTIQM	RSQ	SGMVQTEA	YKFIYMAVQYIE	: 271
cPTPalpha	:	VVHCSA	VGRTR	TFIVDAMDMLMHA	---ERKVDVYGFVSR	RAQ	CQMVDQDM	YVFIYQALLEHYL : 280
hPTPalpha	:	VVHCSA	VGRTR	TFIVDAMDMLMHT	---ERKVDVYGFVSR	RAQ	CQMVDQDM	YVFIYQALLEHYL : 280
mPTPalpha	:	VVHCSA	VGRTR	TFIVDAMDMLMHS	---ERKVDVYGFVSR	RAQ	CQMVDQDM	YVFIYQALLEHYL : 280
rPTPalpha	:	VVHCSA	VGRTR	TFIVDAMDMLMHS	---ERKVDVYGFVSR	RAQ	CQMVDQDM	YVFIYQALLEHYL : 280
zPTPalpha	:	VVHCSA	VGRTR	TFIVDAMDMLMGA	---ERKVDVYGFVTR	RAQ	CQMVDQDM	YVFIYQALLEHYL : 280
xPTPalpha	:	VVHCSA	VGRTR	TFIVDAMDMLMNT	---ERKVDVYGFVTR	RAQ	CQMVDQDM	YVFIYQALLEHFL : 280
hPTPepsilo	:	VVHCSA	VGRTR	TFIVDAMDMMHA	---EQKVDVFEFVSR	RNQ	PQMVDQDM	YTFIYQALLEEYL : 279
mPTPepsilo	:	VVHCSA	VGRTR	TFIVDAMDMMHS	---EQKVDVFEFVSR	RNQ	PQMVDQDM	YTFIYQALLEEYL : 279
rPTPepsilo	:	VVHCSA	VGRTR	TFIVDAMDMMHS	---EQKVDVFEFVSR	RNQ	PQMVDQDM	YTFIYQALLEEYL : 279
hPTPgammma	:	LHCSA	VGRTR	TFIVDMSLQIQK	---KSTVNLGFLKH	RTQ	NYLVQTEE	YIFIHDALEAIL : 291
mPTPgammma	:	LHCSA	VGRTR	TFIVDMSLQIQK	---KSTVNLGFLKH	RTQ	NYLVQTEE	YIFIHDALEAIL : 291
rPTPgammma	:	LHCSA	VGRTR	TFIVDMSLQIQK	---KSTVNLGFLKH	RTQ	NYLVQTEE	YIFIHDALEAIL : 295
cPTPgammma	:	VVHCSA	VGRTR	TFIVDMSLQIQK	---KSTVNLGFLKH	RTQ	NYLVQTEE	YIFIHDALEAIL : 291
hPTPzeta D	:	VVHCSA	VGRTR	TFIVDMSLQIQH	---EGTVNIFGFLKH	RSQ	NYLVQTEE	YVFIHDTLVEAIL : 293
rPTPzeta D	:	VVHCSA	VGRTR	TFIVDMSLQIQH	---EGTVNIFGFLKH	RSQ	NYLVQTEE	YVFIHDTLVEAIL : 293
cPTPzeta D	:	VVHCSA	VGRTR	TFIVDMSLQIQH	---EGTVNIFGFLKH	RTQ	NYLVQTEE	YIFIHDALEAIL : 286
xPTPzeta D	:	VVHCSA	VGRTR	TFIVDMSLQIQH	---EGTVNIFGFLKH	RSQ	NYLVQTEE	YIFIHDALEAIL : 284
hCD45 D1 (	:	VVHCSA	VGRTR	TYIGDAMLEGLEA	---ENKVDVYGVVVK	RRQ	CLMVQVEA	YILLHQALVEYHQ : 279
mCD45 D1 (	:	VVHCSA	VGRTR	TYIGDAMLEGLEA	---EGKVDVYGVVVK	RRQ	CLMVQVEA	YILLHQALVEYHQ : 279
rCD45 D1 (	:	VVHCSA	VGRTR	TYIGDAMLEGLEA	---EGKVDVYGVVVK	RRQ	CLMVQVEA	YILLHQALVEYHQ : 279
zCD45 D1 (	:	VVHCSA	VGRTR	TYIGDAMLEGLDA	---EGKVDVYGVVVK	RRQ	CLMVQVES	YILLHQALVEYHQ : 279
cypcaCD45	:	VVHCSA	VGRTR	TYMSIDAMLESLEA	---EGRVDVYGFVAK	RRQ	CLMVQVEA	YILLHTALVEYHQ : 276
fuCD45 D1	:	VVHCSA	VGRTR	TYIGDAMLESLEA	---EGRVDVYGVVVM	RRQ	CLMVQVEA	YILLHQALLEHTQ : 279
sharkCD45	:	VVHCSA	VGRTR	SYIGDAMMOGLEA	---EGRVDVYGVIVQ	RRQ	CLMVQVEA	YILLHQALLEYVL : 279
hDEP1 D1 (	:	LHCSA	VGRTR	TFIADRLIYQIEN	---ENTVDVYGIYVD	RMH	PLMVQTEE	YVFLNQCVLDIIR : 277
rDEP1 D1 (	:	LHCSA	VGRTR	TFIADRLIYQIEN	---ENTVDVYGIYVD	RMH	PLMVQTEE	YVFLNQCVLDIIR : 277
mDEP1 D1 (	:	LHCSA	VGRTR	TFIADRLIYQIEN	---ENTVDVYGIYVD	RMH	PLMVQTEE	YVFLNQCVLDIIR : 277
hGLEP1 D1	:	LHCSA	VGRTR	TFIADRLIYQIRD	---HEFVDILGLVSE	RSY	MSMVQTEE	YIFIHQCQLMWM : 277
rGLEP1 D1	:	LHCSA	VGRTR	TFIADRLIYQIRD	---HEFVDILGLVSE	RSY	MSMVQTEE	YIFIHQCQLMWM : 277
mPTPphi D1	:	LHCSA	VGRTR	TFIADRLIYQIRD	---HEFVDILGLVSE	RSY	MSMVQTEE	YIFIHQCQLMWM : 277
rabPTPoc D	:	LHCSA	VGRTR	TFIADRLIYQIRD	---HEFVDILGLVSE	RSY	MSMVQTEE	YIFIHQCQLMWM : 277
hPTPbeta D	:	VVHCSA	VGRTR	TFIADRLIYQILDS	---KDSVDIYGAHVD	RLH	VHVMQTEC	YVYLHQCVRDVLR : 280
mPTPbeta D	:	VVHCSA	VGRTR	TFIADRLIYQILDS	---KDSVDIYGAHVD	RLH	VHVMQTEC	YVYLHQCVRDVLR : 280
rPTPbeta D	:	VVHCSA	VGRTR	TFIADRLIYQILDS	---KDSVDIYGAHVD	RLH	VHVMQTEC	YVYLHQCVRDVLR : 280
hPTP31 D1	:	VVHCSA	VGRTR	TFIADRLIYQHIND	---HDFVDIYGLVAE	RSE	MCMVQNL	YIFLHQCILDLLS : 276
rPTP31 D1	:	VVHCSA	VGRTR	TFIADRLIYQHIND	---HDFVDIYGLVAE	RSE	MCMVQNL	YIFLHQCILDLLS : 276
hSAP1 D1 (	:	VVHCSA	VGRTR	TFIADRLIYQLS	---EGLLGFPSFVKK	RES	PLMVQTEA	YVFLHQICGSSN : 279
mSAP1 D1 (	:	VVHCSA	VGRTR	TFIADRLIYQLS	---EGLLGFPSFVKK	RES	PLMVQTEA	YVFLHQICGSSN : 279
rPTPBEM2 D	:	VVHCSA	VGRTR	TFIADRLIYQLS	---EGLLGFPSFVKK	RES	PLMVQTEA	YVFLHQICGSSN : 279
mPTPEP D1	:	LHCSA	VGRTR	TFIADRLIYQLS	---EGLLGFPSFVKK	RES	PLMVQTEA	YVFLHQICGSSN : 279
rOSTPTP D1	:	LHCSA	VGRTR	TFIADRLIYQLS	---EGLLGFPSFVKK	RES	PLMVQTEA	YVFLHQICGSSN : 279
hCPTP1 D1	:	VVHCSA	VGRTR	CFIATSICCOQLKE	---EGVVDALSIVCQ	RVD	GGMVQTEA	YEFVHHALCLFES : 275
rCPTP1 D1	:	VVHCSA	VGRTR	CFIATSICCOQLKE	---EGVVDALSIVCQ	RVD	GGMVQTEA	YEFVHHALCLFES : 275
mPTP8L D1	:	VVHCSA	VGRTR	CFIATSICCOQLKE	---EGVVDALSIVCQ	RVD	GGMVQTEA	YEFVHHALCLFES : 275
hSTEP D1 (	:	LHCSA	IGRTR	CFIATSICCOQLRQ	---EGVVDLKTTCQ	RQD	GGMIQTEC	YQFVHHVMSLYEK : 276
mSTEP D1 (	:	LHCSA	IGRTR	CFIATSICCOQLRQ	---EGVVDLKTTCQ	RQD	GGMIQTEC	YQFVHHVMSLYEK : 276
rSTEP D1 (	:	LHCSA	IGRTR	CFIATSICCOQLRQ	---EGVVDLKTTCQ	RQD	GGMIQTEC	YQFVHHVMSLYEK : 276
hHePTP D1	:	VVHCSA	VGRTR	CFIATRIGCOQLKA	---RGEVDILGIVCQ	RLD	GGMIQTEA	YQFLHHTLALYAG : 273
mHePTP D1	:	VVHCSA	VGRTR	CFIATRIGCOQLKA	---RGEVDILGIVCQ	RLD	GGMIQTEA	YQFLHHTLALYAG : 273
rLCPTP D1	:	VVHCSA	VGRTR	CFIATRIGCOQLKA	---RGEVDILGIVCQ	RLD	GGMIQTEA	YQFLHHTLALYAG : 273
hLYPTP D1	:	CHCSA	CGRTR	IVICADYTWMLLKDGIPENFVFNLIQEQ	RTQ	PSLVQTEE	YELVYSAVLELFFK : 287	
mPEP D1 (N	:	CHCSA	CGRTR	IVICADYTWMLLKDGIPENFVFNLIQEQ	RTQ	PSLVQTEE	YELVYSAVLELFFK : 287	
hPEST D1 (	:	CHCSA	CGRTR	IVICADYTWMLLKDGIPENFVFNLIQEQ	RTQ	PSLVQTEE	YELVYSAVLELFFK : 287	
rRKPTP D1	:	CHCSA	CGRTR	IVICADYTWMLLKDGIPENFVFNLIQEQ	RTQ	PSLVQTEE	YELVYSAVLELFFK : 287	
mPEST D1 (	:	CHCSA	CGRTR	IVICADYTWMLLKDGIPENFVFNLIQEQ	RTQ	PSLVQTEE	YELVYSAVLELFFK : 287	
hBDP1 D1 (	:	CVHCSA	CGRTR	IVICADYTWMLLKDGIPENFVFNLIQEQ	RTQ	PSLVQTEE	YELVYSAVLELFFK : 287	
rPTP20 D1	:	CVHCSA	CGRTR	IVICADYTWMLLKDGIPENFVFNLIQEQ	RTQ	PSLVQTEE	YELVYSAVLELFFK : 287	
hPTP21 D1	:	LHCSA	VGRTR	VFVLSMIMACLEHN	---EVLDPVRLDM	RQD	MMLVQTEA	YTFVYRVLIQFLK : 292
mPTPRL10 D	:	LHCSA	VGRTR	VFVLSMIMACLEHN	---EVLDPVRLDM	RQD	MMLVQTEA	YTFVYRVLIQFLK : 292
rPTP22 D1	:	LHCSA	VGRTR	VFVLSMIMACLEHN	---EVLDPVRLDM	RQD	MMLVQTEA	YTFVYRVLIQFLK : 292
hPTP22 D1	:	LHCSA	VGRTR	VFVLSMIMACLEHN	---EVLDPVRLDM	RQD	MMLVQTEA	YTFVYRVLIQFLK : 292
mPTP36 D1	:	VVHCSA	VGRTR	VFVLSMIMACLEHN	---EVLDPVRLDM	RQD	MMLVQTEA	YTFVYRVLIQFLK : 292
rPTP22 D1	:	VVHCSA	VGRTR	VFVLSMIMACLEHN	---EVLDPVRLDM	RQD	MMLVQTEA	YTFVYRVLIQFLK : 292
hMEG1 D1 (	:	VVHCSA	VGRTR	VFVLSMIMACLEHN	---EVLDPVRLDM	RQD	MMLVQTEA	YTFVYRVLIQFLK : 292
mMEG1 D1 (	:	VVHCSA	VGRTR	VFVLSMIMACLEHN	---EVLDPVRLDM	RQD	MMLVQTEA	YTFVYRVLIQFLK : 292
zMEG1 D1 (	:	VVHCSA	VGRTR	VFVLSMIMACLEHN	---EVLDPVRLDM	RQD	MMLVQTEA	YTFVYRVLIQFLK : 292
hPTPH1 D1	:	LHCSA	IGRTR	VLTMETAMCLTECN	---QPVPFLDIVRT	RDQ	AMMIQTPS	YRFVCEAILKVYE : 277
mPTPH1 D1	:	LHCSA	IGRTR	VLTMETAMCLTECN	---QPVPFLDIVRT	RDQ	AMMIQTPS	YRFVCEAILKVYE : 277
rPTPH1 D1	:	LHCSA	IGRTR	VLTMETAMCLTECN	---QPVPFLDIVRT	RDQ	AMMIQTPS	YRFVCEAILKVYE : 277
hPTPBAS D1	:	LHCSA	IGRTR	VLTMETAMCLTECN	---QPVPFLDIVRT	RDQ	AMMIQTPS	YRFVCEAILKVYE : 277
mPTPB1 D1	:	LHCSA	IGRTR	VLTMETAMCLTECN	---QPVPFLDIVRT	RDQ	AMMIQTPS	YRFVCEAILKVYE : 277
hPTPB1 D1	:	LHCSA	IGRTR	VLTMETAMCLTECN	---QPVPFLDIVRT	RDQ	AMMIQTPS	YRFVCEAILKVYE : 277
zPTPB1 D1	:	LHCSA	IGRTR	VLTMETAMCLTECN	---QPVPFLDIVRT	RDQ	AMMIQTPS	YRFVCEAILKVYE : 277
hTPPBA14 D	:	LHCSA	IGRTR	VLTMETAMCLTECN	---QPVPFLDIVRT	RDQ	AMMIQTPS	YRFVCEAILKVYE : 277
hPTPTyp D1	:	VVHCSA	VGRTR	VFLCVDVVFCAIVKD	---CSFNIMDIVAQ	REQ	SGMVQTEA	YHFCYDIVLEVLIR : 274
mPTPTyp D1	:	VVHCSA	VGRTR	VFLCVDVVFCAIVKD	---CSFNIMDIVAQ	REQ	SGMVQTEA	YHFCYDIVLEVLIR : 274
cPTP1B D1	:	VVHCSA	IGRTR	TFCLVDTCLLLMDKRKDPSSVDVQVLE	RRY	MGLIQTAD	LRFSLAVIEGAK : 279	
hPTP1B D1	:	VVHCSA	IGRTR	TFCLVDTCLLLMDKRKDPSSVDVQVLE	RRY	MGLIQTAD	LRFSLAVIEGAK : 279	
mPTP1B D1	:	VVHCSA	IGRTR	TFCLVDTCLLLMDKRKDPSSVDVQVLE	RRY	MGLIQTAD	LRFSLAVIEGAK : 279	
rPTP1B D1	:	VVHCSA	IGRTR	TFCLVDTCLLLMDKRKDPSSVDVQVLE	RRY	MGLIQTAD	LRFSLAVIEGAK : 279	
zPTP1B D1	:	VVHCSA	IGRTR	TFCLVDTCLLLMDKRKDPSSVDVQVLE	RRY	MGLIQTAD	LRFSLAVIEGAK : 279	
hTCTP D1	:	VVHCSA	IGRTR	TFCLVDTCLLLMDKRKDPSSVDVQVLE	RRY	MGLIQTAD	LRFSLAVIEGAK : 275	

GeneDoc Screen View - Alignment\_234\_Vert\_PTP\_Domains\_D1\_and\_D2 (GeneDoc).msb

Table with 2 columns: Protein Name and Sequence/Position. The table lists various protein domains and their alignments, including mTCPD1, hMEG2, xPTP, hHDPTF, rPTPD14, hIA2, rIA2, bIA2, hIA2beta, macneIA2, mPTPNP, rPTPNE6, hCD45, mCD45, rCD45, cCD45, fuCD45, cypcaCD45, actvoCD45, sharKCD45, cPTPalph, hPTPalph, mPTPalph, rPTPalph, xPTPalph, zPTPalph, ryPTPR4b, hPTPepsilo, mPTPepsilo, orylaPTPep, ryPTPR4a, hPTPkappa, mPTPkappa, ryPTPR2B, hPTPlamda, mPTPlamda, hPTPmu, mPTPmu, rPTPmu, hPTPrho, mPTPrho, cPTPsi, hLAR, mLAR, rLAR, xLAR, zLAR, ryPTPR2Aa, hPTPdelta, mPTPdelta, xPTPdelta, ryPTPR2Ab, hPTPsi, mPTPsi, xPTPsi, zPTPsi, rPTPsi, ryPTPR2Ac, hPTPgamma, mPTPgamma, rPTPgamma, ryPTPR5b, cPTPgamma, hPTPzeta, cPTPzeta, mPTPzeta, rPTPzeta, xPTPzeta, ryPTPR5a, actvoCD45, CMG-PTP1, CMG-PTP2, cPTP-NT1su, cPTP-R2Asu, cPTP-R2Bsu, macfaSTEP, macmuPTPfal, macmuPTPze, mPTPzeta, orylaPTPal, orylaPTPep, piqPTP-R5s, rMEG2, rPTPBAS, rPTPdelta, rPTPmu, rPTPtyp, ryPTPN3, ryPTPN6a, ryPTPR2Aa, ryPTPR2Ab, ryPTPR2Ac, ryPTPR2B, ryPTPR4a, ryPTPR4b, ryPTPR5a, ryPTPR5b, ryPTPR8, xCD45, xCD45, zIA2, zIA2beta, zLAR, zPTP-NT1su, zPTP-NT5su, zPTPH1.