PTP domains (excluding domains D2)

```
                    α1'                α2'                α1                β1                β2                β3
Amino acid in hPTP1B  #10                #20                #30                #40                #50                #60                #70                #80
hPTPalpha   DKLEEEINRRMADDN------KLFREEFNALPACPIQA------TCEAASKEENKEKNRYVNILPYDHSRVHLTPVEGV--PDSDYINASFINGY--------QEKNKFIAAQGP
hPTPepsilon EHLEEEIRIRSADDC------KQFREEFNSLPSGHIQG------TFELANKEENREKNRYPNILPNDHSRVILSQLDGI--PCSDYINASYIDGY--------KEKNKFIAAQGP
hPTPkappa   ADLLQHINLMKTSDS------YGFKEEYESFFEGQSA-------SWDVAKKDQNRAKNRYGNIIAYDHSRVILQPVEDD--PSSDYINANYIDGY--------QRPSHYIATQGP
hPTPmu      ADLLQHITQMKCAEG------YGFKEEYESFFEGQSA-------PWDSAKKDENRMKNRYGNIIAYDHSRVRLQTIEGD--TNSDYINGNYIDGY--------HRPNHYIATQGP
hPTPrho     ADLLQHITQMKRGQG------YGFKEEYEALPEGQTA-------SWDTAKEDENRNKNRYGNIISYDHSRVRLLVLDGD--PHSDYINANYIDGY--------HRPRHYIATQGP
hPTPlamda   ADLLQHINQMKTAEG------YGFKQEYESFFEGWDA-------T----KKKDKVKGSRQEPMPAYDRHRVKLHPMLGD--PNADYINANYIDGY--------HRSNHFIATQGP
hPTPdelta   LELADHIERLKANDN------LKFSQEYESIDPGQQF-------TWEHSNLEVNKPKNRYANVIAYDHSRVLLSAIEGI--PGSDYVNANYIDGY--------RKQNAYIATQGS
hPTPsigma   ADMAEHTERLKANDS------LKLSQEYESIDPGQQF-------TWEHSNLEVNKPKNRYANVIAYDHSRVILQPIEGI--MGSDYINANYVDGY--------RRQNAYIATQGP
hPTPgamma   KQFVKHIGELYSNNQ------HGFSEDFEEVQRCTADMN-I---TAEHSNHPENKHKNRYINILAYDHSRVKLRPLPGKDSKHSDYINANYVDGY--------NKAKAYIATQGP
hPTPzeta    KHFPKHVADLHASSGF--TEEFETLKEFYQEVQSCTVDLGI---TADSSNHPDNKHKNRYINIVAYDHSRVKLAQLAEKDGKLTDYINANYVDGY--------NRPKAYIAAQGP
hLAR        TDLADNIERLKANDG------LKFSQEYESIDPGQQF-------TWENSNLEVNKPKNRYANVIAYDHSRVILTSIDGV--PGSDYINANYIDGY--------RKQNAYIATQGP
hCD45       DILLETYKRKIADEG------RLFLAEFQSIPRVFSKF------PIKEARKPFNQNKNRYVDILPYDYNRVELSEINGD--AGSNYINASYIDGF--------KEPRKYIAAQGP
hGLEPP1     DDFDAYIKDMAKDSD------YKFSLQFEELKLIGLDI------PHFAADLPLNRCKNRYTNILPYDFSRVRLVSMNEE--EGADYINANYIPGY--------NSPQEYIATQGP
hPTPS31     KSFLQHVEELCTNNN------LKFQEEFSELPKFLQDL------SSTDADLPWNRAKNRFPNIKPYNNNRVKLIADASV--PGSDYINASYISGY--------LCPNEFIATQGP
hDEP1       ENFEAYFKKQQADSN------CGFAEEYEDLKLVGISQ------PKYAAELAENRGKNRYNNVLPYDISRVKLSVQTHS---TDDYINANYMPGY--------HSKKDFIATQGP
hPTPbeta    NQFEGHFMKLQADSN------YLLSKEYEELKDVGRNQ------SCDIALLPENRGKNRYNNILPYDATRVKLSNVDDD--PCSDYINASYIPGN--------NFRREYIVTQGP
hSAP1       EDFADHVRKNERDSN------CGFADEYQQLSLVGHSQ------SQMVASASENNAKNRYRNVLPYDWSRVPLKPIHEE--PGSDYINASFMPGL--------WSPQEFIATQGP
hSTEP       SRVLQAEELHEKALDP-----FLLQAEFFEIPMNFVD--------PKEYDIPGLVRKNRYKTILPNPHSRVCLTSPDPDD-PLSSYINANYIRGYG-------GEEKVYIATQGP
hPCPTP1     SRILTRSQLRDVVASS-----HLLQSEFMEIPMNFVD--------PKEIDIPRHGTKNRYKTILPNPLSRVCLRPKNVTD-SLSTYINANYIRGYS-------GKEKAFIATQGP
hHePTP      GHPLTRWALQRQPPSP-----KQLEEEFLKIPSNFVS--------PEDLDIPGHASKDRYKTILPNPQSRVCLGRAQSQE--DGDYINANYIRGYD-------GKEKVYIATQGP
hSHP1       ADIENRVLELNKKQESEDTAKAGFWEEFESLQKQEVKNLH----QRLEGQRPENKGKNRYKNILPFDHSRVILQGRDSNI-PGSDYINANYIKN--QLLGPD-ENAKTYIASQGC
hSHP2       AEIESRVRELSKLAETTDKVKQGFWEEFETLQQQECKLLY----SRKEGQRQENKNKNRYKNILPFDHTRVVLHDGDPNE-PVSDYINANIIMPEFETKCNNSKPKKSYIATQGC
hPEST       EILRKFIQRVQAMKSPDHNGEDNFARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYKDILPFDHSRVKLTLKTPS--QDSDYINANFIKGV--------YGPKAYVATQGP
hLyPTP      EILQKFLDEAQSKKITK----EEFANEFLKLKRQSTKYKADKTYPTTVAEKPKNIKKNRYKDILPYDYSRVELSLITSD--EDSSYINANFIKGV--------YGPKAYIATQGP
hBDP1       DSARSFLERLEARGGREG---AVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEE--GHSDYINGNFIRGV--------DGSLAYIATQGP
hPTPD1      ATNDERCKILEQRLEQG-----MVFTEYERILKKRLVDG-----ECSTARLPENAERNRFQDVLPYDDARVELVPTKEN---NTGYINASHIKVSV------SGIEWDYIATQGP
hPTPD2      VPMDERFRTLKKKLEEG-----MVFTEYEQIPKKKANG------IFSTAALPENAERSRIREVVPYEENRVELIPTKEN---NTGYINASHIKVVVG------GAEWHYIATQGP
hMEG1       HSLRESMIQLAEGLITG-----TVLTQFDQLYRKKPGM------TMSCAKLPQNISKNRYRDISPYDATRVILKG-------NEDYINANYINMEIP----SSSIINQYIACQGP
hPTPH1      DTLEGSMAQLKKGLESG-----TVLIQFEQLYRKKPGL------AITFAKLPQNLDKNRYKDVLPYDTTRVLLQG-------NEDYINASYVNMEIP----AANLVNKYIATQGP
hPTPBAS     KSVIRVLRGLLDQGI--------PSKELENLQELKPLD------QCLIGQTKENRRKNRYKNILPYDATRVPLGD-------EGGYINASFIKIPVG------KEEFVYIACQGP
hPTP1B      MEMEKEFEQIDKSGS--------WAAIYQDIRHEASDF------PCRVAKLPKNKNRNRYRDVSPFDHSRIKLHQE------DNDYINASLIKME--------EAQRSYILTQGP
hTCPTP      TTIEREFEELDTQRR--------WQPLYLEIRNESHDY------PHRVAKFPENRNRNRYRDVSPYDHSRVKLQNA------ENDYINASLVDIE--------EAQRSYILTQGP
hMEG2       MTIQELVDYVNARQKQ------GIYEEYEDIRRENPVG------TFHCSMSPGNLEKNRYGDVPCLDQTRVKLTKRSGHT--QTDYINASFMDGY--------KQKNAYIGTQGP
hIA2        HMILAYMEDHLRNRDR-------LAKEWQALCAYQAEPN-----TCATAQGEGNIKKNRHPDFLPYDHARIKLKVESSPS--RSDYINASPIIEHD-------PRMPAYIATQGP
hIA2beta    HMILSYMEDHLKNKNR--------LEKEWEALCAYQAEPN-----SSFVAQREENVPKNRSLAVLTYDHSRVLLKAENSHS--HSDYINASPIMDHD-------PRNPAYIATQGP
hPTPTyp     TAIKDCLKILEEKTAA.....YDIMQEFMALELKNLPG......EFYSGNQPSNREKNRYRDILPYDSTRVPLGK.......SKDYINASYIRIVN......CGEEYFYIATQGP
hHDPTP      ERLRQLQQELEAFRGQLGDV.GALDTVWRELQDAQEHDAR....GRSIAIARCYSLKNRHQDVMPYDSNRVVLRSG......KDDYINASCVEGLS......PYCPPLVATQAP
Consensus - (amino acid identity 100%, 90%, 80%):   E                          N   KNRY          D   RV  L          DYINA                                  YIATQGP
                                                                               Motif 1           Motif 2           Motif 3                                  Motif 4
```

PTP domains D2

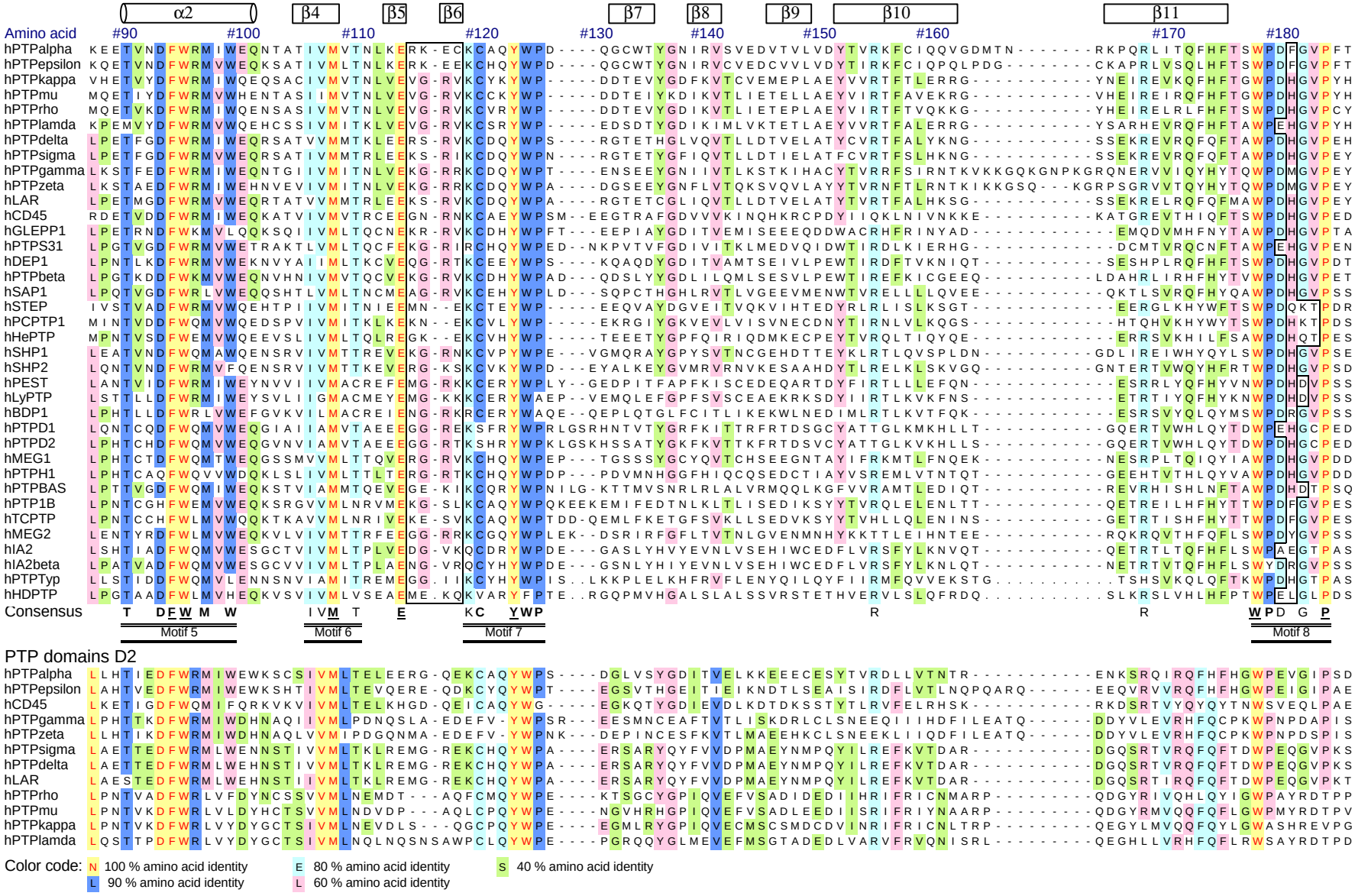
```
hPTPalpha   TSLETHLQKIYNKIPG--TSNNGLEEEFKKLTSIKIQN-----DKMRTGNLPANMKKNRVLQIIPYEFNRVIIPVKRGE--ENTDYVNASFIDGY--------RQKDSYIASQGP
hPTPepsilon SSLEKHLQTMHGTTTH--FDKIGLEEEFRKLTNVRIMK-----ENMRTGNLPANMKKARVIQIIPYDFNRVILSMKRGQ--EYTDYINASFIDGY--------RQKDYFIATQGP
hCD45       SELHPYLHNMKKRDPP--SEPSPLEAEFQRLPSYRSWR------TQHIGNQEENKSKNRNSNVIPYDYNRVPLKHELEM(19)EPSKYINASFIMSY--------WKPEVMIAAQGP
hPTPgamma   NQLHSYVNSILIPGVG---GKTRLEKQFKLVTQCNAKY-----VECFSAQKECNKEKNRNSSVVPSERARVGLAPLPGM--KGTDYINASYIMGY--------YRSNEFIITQHP
hPTPzeta    SHIHAYVNALLIPGPA---GKTKLEKQFQLLSQSNIQQ-----SDYSAALKQCNREKNRTSSIIPVERSRVGISSLSG---EGTDYINASYIMGY--------YQSNEFIITQHP
hPTPsigma   RSLYAYIQKLAQVEPG--EHVTGMELEFKRLANSKAHT-----SRFISANLPCNKFKNRLVNIMPYESTRVCLQPIRGV--EGSDYINASFIDGY--------RQQKAYIATQGP
hPTPdelta   RNLYAYIQKLTQIETG--ENVTGMELEFKRLASSKAHT-----SRFISANLPCNKFKNRLVNIMPYESTRVCLQPIRGV--EGSDYINASFIDGY--------RQQKAYIATQGP
hLAR        RNLYAHIQKLGQVPPG--ESVTAMELEFKLLASSKAHT-----SRFISANLPCNKFKNRLVNIMPYELTRVCLQPIRGV--EGSDYINASFLDGY--------RQQKAYIATQGP
hPTPrho     CEFRSLYYNISRLDPQ--TNSSQIKDEFQTLNIVTPRVRP---EDCSIGLLPRNHDKNRSMDVLPLDRCLPFLISVDG---ESSNYINAALMDSH--------KQPAAFVVTQHP
hPTPmu      SQVRSLYYDMNKLDPQ--TNSSQIKEEFRTLNMVTPTLRV---EDCSIALLPRNHEKNRCMDILPPDRCLPFLITIDG---ESSNYINAALMDSY--------KQPSAFIVTQHP
hPTPkappa   CEFKAAYFDMIRIDSQ--TNSSHLKDEFQTLNSVTPRLQA---EDCSIACLPRNHDKNRFMDMLPPDRCLPFLITIDG---ESSNYINAALMDSY--------RQPAAFIVTQYP
hPTPlamda   SEFKATYKEMIRIDPQ--SNSSQLREEFQTLNSVTPPLDV---EECSIALLPRNRDKNRSMDVLPPDRCLPFLISTDG---DSNNYINAALTDSY--------TRSAAFIVTLHP
```

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

(19) amino acid insert - conserved among vertebrate CD45 orthologs
SKESEHDSDESSDDDSDSE

Andersen et al. Mol. Cell. Biol. 2001
Andersen et al. FASEB J. 2004

PTP domains (excluding domains D2)



PTP domains D2

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

Andersen et al. Mol. Cell. Biol. 2001
Andersen et al. FASEB J. 2004

PTP domains (excluding domains D2)

```
              α3                                      β12        α4                    α5               α6
Amino acid    #190      #200                          #210       #220      #230      #240      #250      #260      #270      #280
hPTPalpha     --PIGMLKFLKKVKACNPQYA-------------GAIVVHCSAGVGRTGTFVVIDAMLDMMHTERK---VDVYGFVSRIRAQRCQMVQTDMQYVFIYQALLEHYLYGDTEL
hPTPepsilon   --PIGMLKFLKKVKTLNPVHA-------------GPIVVHCSAGVGRTGTFIVIDAMMAMMHAEQK---VDVFEFVSRIRNQRPQMVQTDMQYTFIYQALLEYYLYGDTEL
hPTPkappa     --ATGLLSFIRRVKLSNPPSA-------------GPIVVHCSAGAGRTGCYIVIDIMLDMAEREGV---VDIYNCVKALRSRRINMVQTEEQYIFIHDAILEACLCGETAI
hPTPmu        --ATGLLGFVRQVKSKSPPSA-------------GPLVVHCSAGAGRTGCFIVIDIMLDMAEREGV---VDIYNCVRELRSRRVNMVQTEEQYVFIHDAILEACLCGDTSV
hPTPrho       --ATGLLGFVRQVKFLNPPEA-------------GPIVVHCSAGAGRTGCFIAIDTMLDMAENEGV---VDIFNCVRELRAQRVNLVQTEEQYVFVHDAILEACLCGNTAI
hPTPlamda     --ATGLLAFIRRVKASTPPDA-------------GPIVIHCSAGTGRTGCYIVLDVMLDMAECEGV---VDIYNCVKTLCSRRVNMIQTEEQYIFIHDAILEACLCGETTI
hPTPdelta     --PTPFLAFLRRVKTCNPPDA-------------GPMVVHCSAGVGRTGCFIVIDAMLERIKHEKT---VDIYGHVTLMRAQRNYMVQTEDQYIFIHDALLEAVTCGNTEV
hPTPsigma     --PTPFLAFLRRVKTCNPPDA-------------GPIVVHCSAGVGRTGCFIVIDAMLERIKPEKT---VDVYGHVTLMRSQRNYMVQTEDQYSFIHEALLEAVGCGNTEV
hPTPgamma     --ALPVLTFVRRSSAARMPET-------------GPVLVHCSAGVGRTGTYIVIDSMLQQIKDKST---VNVLGFLKHIRTQRNYLVQTEEQYIFIHDALLEAILGKETEV
hPTPzeta      --SLPVLTFVRKAAYAKRHAV-------------GPVVVHCSAGVGRTGTYIVLDSMLQQIQHEGT---VNIFGFLKHIRSQRNYLVQTEEQYVFIHDTLVEAILSKETEV
hLAR          --PTPILAFLRRVKACNPLDA-------------GPMVVHCSAGVGRTGCFIVIDAMLERMKHEKT---VDIYGHVTCMRSQRNYMVQTEDQYVFIHEALLEAATCGHTEV
hCD45         --PHLLLKLRRRVNAFSNFFS-------------GPIVVHCSAGVGRTGTYIGIDAMLEGLEAENK---VDVYGYVVKLRRQRCLMVQVEAQYILIHQALVEYNQFGETEV
hGLEPP1       NAAESILQFVHMVRQQATKSK-------------GPMIIHCSAGVGRTGTFIALDRLLQHIRDHEF---VDILGLVSEMRSYRMSMVQTEEQYIFIHQCVQLMWMKKKQQF
hPTPS31       --SAPLIHFVKLVRASRAHDT-------------TPMIVHCSAGVGRTGVFIALDHLTQHINDHDF---VDIYGLVAELRSERMCMVQNLAQYIFLHQCILDLLSNKGSNQ
hDEP1         TDLLINFRYLVRDYMKQSPPE-------------SPILVHCSAGVGRTGTFIAIDRLIYQIENENT---VDVYGIVYDLRMHRPLMVQTEDQYVFLNQCVLDIVRSQKDSK
hPTPbeta      --TQSLIQFVRTVRDYINRSPGA-----------GPTVVHCSAGVGRTGTFIALDRILQQLDSKDS---VDIYGAVHDLRLHRVHMVQTECQYVYLHQCVRDVLRARKLRS
hSAP1         PDTLLAFWRMLRQWLDQTMEG-------------GPPIVHCSAGVGRTGTLIALDVLLRQLQSEGL---LGPFSFVRKMRESRPLMVQTEAQYVFLHQCICGSSNSQPRPQ
hSTEP         --APPLLHLVREVEEAAQQEGPHC----------APIIVHCSAGIGRTGCFIATSICCQQLRQEGV---VDILKTTCQLRQDRGGMIQTCEQYQFVHHVMSLYEKQLSHQS
hPCPTP1       --AQPLLQLMLDVEEDRLASQGR-----------GPVVVHCSAGIGRTGCFIATSIGCQQLKEEGV---VDALSIVCQLRMDRGGMVQTSEQYEFVHHALCLYESRLSAET
hHePTP        --AGPLLRLVAEVEESPETAAHP-----------GPIVVHCSAGIGRTGCFIATRIGCQQLKARGE---VDILGIVCQLRLDRGGMIQTAEQYQFLHHTLALYAGQLPEEP
hSHP1         --PGGVLSFLDQINQRQESLPHA-----------GPIIVHCSAGIGRTGTIIVIDMLMENISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIETTKKKL
hSHP2         --PGGVLDFLEEVHHKQESIMDA-----------GPVVVHCSAGIGRTGTFIVIDILIDIIREKGVDCDIDVPKTIQMVRSQRSGMVQTEAQYRFIYMAVQHYIETLQRRI
hPEST         --FDSILDMISLMRKYQEHED-------------VPICIHCSAGCGRTGAICAIDYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQLY
hLyPTP        --IDPILELIWDVRCYQEDDS-------------VPICIHCSAGCGRTGVICAIDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVI
hBDP1         --PDHMLAMVEEARRLQGSGP-------------EPLCVHCSAGCGRTGVLCTVDYYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNA
hPTPD1        --LKGFLSYLEEIQSVRRHTNSTSDPQSPN----PPLLVHCSAGVGRTGVVILSEIMIACLEHNEV---LDIPRVLDMLRQQRMMLVQTLCQYTFVYRVLIQFLKSSRLI*
hPTPD2        --VQGFLSYLEEIQSVRRHTNSMLEGTKNRH---PPIVVHCSAGVGRTGVLILSELMIYCLEHNEK---VEVPMMLRLLREQRMFMIQTIAQYKFVYQVLIQFLQNSRLI*
hMEG1         --SSDFLDFVCHVRNKRAGKE-------------EPVVVHCSAGIGRTGVLITMETAMCLIECNQP---VYPLDIVRTMRDQRAMMIQTPSQYRFVCEAILKVYEEGFVKP
hPTPH1        --SSDFLEFVNYVRSLRVDS--------------EPLLVHCSAGIGRTGVLVTMETAMCLTERNLP---IYPLDIVRKMRDQRAMMVQTSSQYKFVCEAILRVYEEGLVQM
hPTPBAS       --PDDLLTFISYMRHIHRS---------------GPIITHCSAGIGRSGTLICIDVVLGLISQDLD---FDISDLVRCMRLQRHGMVQTEDQYIFCYQVILYVLTRLQAEE
hPTP1B        --PASFLNFLFKVRESGSLSPEH-----------GPVVVHCSAGIGRSGTFCLADTCLLLMDKRKDPSSVDIKKVLLEMRKFRMGLIQTADQLRFSYLAVIEGAKFIMGDS
hTCPTP        --PASFLNFLFKVRESGSLNPDH-----------GPAVIHCSAGIGRSGTFSLVDTCLVLMEKGDD---INIKQVLLNMRKYRMGLIQTPDQLRFSYMAIIEGAKCIKGDS
hMEG2         --AASLIDFLRVVRNQQSLAVSNMGARSKGQCPEPPIVVHCSAGIGRTGTFCSLDICLAQLEELGT---LNVFQTVSRMRTQRAFSIQTPEQYYFCYKAILEFAEKEGMVS
hIA2          --TRPLLDFRRKVNKCYRGRS-------------CPIIVHCSDGAGRTGTYILIDMVLNRMAKGVK--EIDIAATLEHVRDQRPGLVRSKDQFEFALTAVAEEVNAILKAL
hIA2beta      --SRSLLDFRRKVNKCYRGRS-------------CPIIVHCSDGAGRSGTYVLIDMVLNKMAKGAK--EIDIAATLEHLRDQRPGMVQTKEQFEFALTAVAEEVNAILKAL
hPTPTyp       ..ADSFIKYIRYARKSHLT...............GPMVVHCSAGIGRTGVFLCVDVVFCAIVKDCS...FNIMDIVAQMREQRSGMVQTKEQYHFCYDIVLEVLRKLLTLD
hHDPTP        ..PSNLLRFIQEVHAHYLHQRPLH..........TPIIVHCSSGVGRTGAFALLYAAVQEVEAGNG..IPELPQLVRRMRQQRKHMLQEKLHLRFCYEAVVRHVEQVLQRH
Consensus           L                            P  VHCSAG GRTG                              R  R    QT  QY F
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Motif 9

Motif 10

PTP domains D2

```
hPTPalpha     --GKGMISIIAAVQKQQQSGN-------------HPITVHCSAGAGRTGTFCALSTVLERVKAEGI---LDVFQTVKSLRLQRPHMVQTLEQYEFCYKVVQEYIDAFSDYA
hPTPepsilon   --GKGMIDLIAAVQKQQQTGN-------------HPITVHCSAGAGRTGTFIALSNILERVKAEGL---LDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQDFIDIFSDYA
hCD45         --PKELISMIQVVKQKLPQKNSSEGNKHHKS---TPLLIHCRDGSQQTGIFCALLNLLESAETEEV---VDIFQVVKALRKARPGMVSTFEQYQFLYDVIASTYPAQNGQV
hPTPgamma     ----STFELINVIKEEALTRD-------------GPTIVHDEYGAVSAGMLCALTTLSQQLENENA---VDVFQVAKMINLMRPGVFTDIEQYQFIYKARLSLVSTKENGN
hPTPzeta      ----KTFELISVIKEEAANRD-------------GPMIVHDEHGGVTAGTFCALTTLMHQLEKENS---VDVYQVAKMINLMRPGVFADIEQYQFLYKVILSLVSTRQEEN
hPTPsigma     --GEGFIDFIGQVHKTKEQFGQD-----------GPISVHCSAGVGRTGVFITLSIVLERMRYEGV---VDIFQTVKMLRTQRPAMVQTEDEYQFCYQAALEYLGSFDHYA
hPTPdelta     --GEGFIDFIGQVHKTKEQFGQD-----------GPISVHCSAGVGRTGVFITLSIVLERMRYEGV---VDIFQTVKMLRTQRPAMVQTEDQYQFSYRAALEYLGSFDHYA
hLAR          --GEGFIDFIGQVHKTKEQFGQD-----------GPITVHCSAGVGRTGVFITLSIVLERMRYEGV---VDMFQTVKTLRTQRPAMVQTEDQYQLCYRAALEYLGSFDHYA
hPTPrho       -SKRSLLKVVRRLEKWQEQYDGRE----------GRTVVHCLNGGGRSGTFCAICSVCEMIQQQNI---IDVFHIVKTLRNNKSNMVETLEQYKFVYEVALEYLSSF*
hPTPmu        -SKRSFLKLIRQVDKWQEEYNGGE----------GPTVVHCLNGGGRSGTFCAISIVCEMLRHQRT---VDVFHAVKTLRNNKPNMVDLLDQYKFCYEVALEYLNSG*
hPTPkappa     -SKRSFLKLILQVEKWQEECEEGE----------GRTIIHCLNGGGRSGMFCAIGIVVEMVKRQNV---VDVFHAVKTLRNSKPNMVEAPEQYRFCYDVALEYLESS*
hPTPlamda     -SKKAFLHLLAEVDKWQAESGD------------GRTIVHCLNGGGRSGTFCACATVLEMIRCHNL---VDVFFAAKTLRNYKPNMVETMDQYHFCYDVALEYLEGLESR*
```

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

Andersen et al. Mol. Cell. Biol. 2001
Andersen et al. FASEB J. 2004