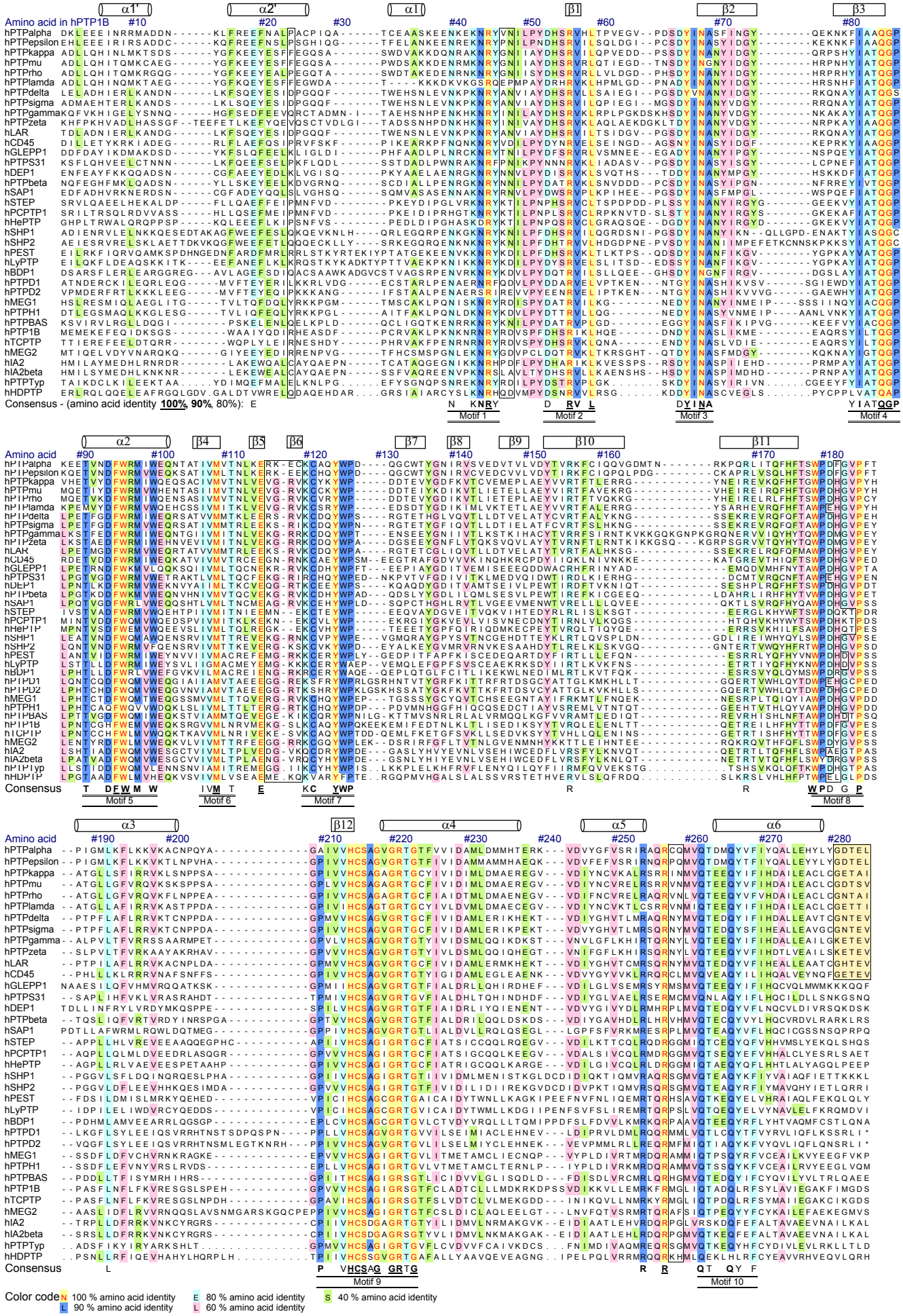
Alignment of 37 Human PTP 'catalytic' domains (excluding domain D2 sequences)



Andersen et al. Mol. Cell. Biol. 2001
Andersen et al. FASEB J. 2003

Section 1

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                                  (1) 1         10        20        30        40        50        60        70        80        90        100       111
hCD45  D1 (NP  002829) PTPRC      (1) DILLETYKRKIADEG-------RLFLAEFQSIPRVFSKF--PIKEARKPFNQNKNRYVDILPYDYNRVELSEINGDAG--SNYINASYIDGF--------KEPRKYIAAQG
hPTPalpha  D1 (NP  002827) PTPRA  (1) DKLEEEINRRMADDN-------KLFREEFNALPACPIQA--TCEAASKEENKEKNRYVNILPYDHSRVHLTPVEGVPD--SDYINASFINGY--------QEKNKFIAAQG
hPTPepsilon  D1 (NP  006495) PTPRE (1) EHLEEEIRIRSADDC-------KQFREEFNSLPSGHIQG--TFELANKEENREKNRYPNILPNDHSRVILSQLDGIPC--SDYINASYIDGY--------KEKNKFIAAQG
hPTPlamda  D1 (NP  005695) PTPRU  (1) ADLLQHINQMKTAEG-------YGFKQEYESFFEG-------WDATKKKDKVKGSRQEPMPAYDRHRVKLHPMLGDPN--ADYINANYIDGY--------HRSNHFIATQG
hPTPkappa  D1 (NP  002835) PTPRK  (1) ADLLQHINLMKTSDS-------YGFKEEYESFFEGQSA---SWDVAKKDQNRAKNRYGNIIAYDHSRVILQPVEDDPS--SDYINANYIDGY--------QRPSHYIATQG
hPTPmu  D1 (NP  002836) PTPRM     (1) ADLLQHITQMKCAEG-------YGFKEEYESFFEGQSA---PWDSAKKDENRMKNRYGNIIAYDHSRVRLQTIEGDTN--SDYINGNYIDGY--------HRPNHYIATQG
hPTPrho  D1 (NP  573400) PTPRT    (1) ADLLQHITQMKRGQG-------YGFKEEYEALPEGQTA---SWDTAKEDENRNKNRYGNIISYDHSRVRLLVLDGDPH--SDYINANYIDGY--------HRPRHYIATQG
hPTPsigma  D1 (NP  002841) PTPRS  (1) ADMAEHTERLKANDS-------LKLSQEYESIDPGQQF---TWEHSNLEVNKPKNRYANVIAYDHSRVILQPIEGIMG--SDYINANYVDGY--------RRQNAYIATQG
hPTPdelta  D1 (NP  002830) PTPRD  (1) LELADHIERLKANDN-------LKFSQEYESIDPGQQF---TWEHSNLEVNKPKNRYANVIAYDHSRVLLSAIEGIPG--SDYVNANYIDGY--------RKQNAYIATQG
hLAR  D1 (NP  002831) PTPRF       (1) TDLADNIERLKANDG-------LKFSQEYESIDPGQQF---TWENSNLEVNKPKNRYANVIAYDHSRVILTSIDGVPG--SDYINANYIDGY--------RKQNAYIATQG
hPTPgamma  D1 (NP  002832) PTPRG  (1) KQFVKHIGELYSNNQ-------HGFSEDFEEVQRCTADMNITAEHSNHPENKHKNRYINILAYDHSRVKLRPLPGKDSKHSDYINANYVDGY--------NKAKAYIATQG
hPTPzeta  D1 (NP  002842) PTPRZ1  (1) KHFPKHVADLHASSG--FTEEFETLKEFYQEVQSCTVDLGITADSSNHPDNKHKNRYINIVAYDHSRVKLAQLAEKDGKLTDYINANYVDGY--------NRPKAYIAAQG
hSAP1  D1 (NP  002833) PTPRH      (1) EDFADHVRKNERDSN-------CGFADEYQQLSLVGHSQ--SQMVASASENNAKNRYRNVLPYDWSRVPLKPIHEEPG--SDYINASFMPGL--------WSPQEFIATQG
hDEP1  D1 (NP  002834) PTPRJ      (1) ENFEAYFKKQQADSN-------CGFAEEYEDLKLVGISQ--PKYAAELAENRGKNRYNNVLPYDISRVKLSVQTHST---DDYINANYMPGY--------HSKKDFIATQG
hPTPbeta  D1 (NP  002828) PTPRB   (1) NQFEGHFMKLQADSN-------YLLSKEYEELKDVGRNQ--SCDIALLPENRGKNRYNNILPYDATRVKLSNVDDDPC--SDYINASYIPGN--------NFRREYIVTQG
hGLEPP1  D1 (NP  109592) PTPRO    (1) DDFDAYIKDMAKDSD-------YKFSLQFEELKLIGLDI--PHFAADLPLNRCKNRYTNILPYDFSRVRLVSMNEEEG--ADYINANYIPGY--------NSPQEYIATQG
hPTPS31  D1 (AR073855) PTPGMC1    (1) KSFLQHVEELCTNNN-------LKFQEEFSELPKFLQDL--SSTDADLPWNRAKNRFPNIKPYNNNRVKLIADASVPG--SDYINASYISGY--------LCPNEFIATQG
hHePTP  D1 (NP  002823) PTPN7     (1) HPLTRWALQRQPPSP-------KQLEEEFLKIPSNFVS----PEDLDIPGHASKDRYKTILPNPQSRVCLGRAQSQED--GDYINANYIRGYD-------GKEKVYIATQG
hPCPTP1  D1 (NP  002840) PTPRR    (1) SRILTRSQLRDVVASS------HLLQSEFMEIPMNFVD----PKEIDIPRHGTKNRYKTILPNPLSRVCLRPKNVTDS-LSTYINANYIRGYS-------GKEKAFIATQG
hSTEP  D1 (NP  116170) PTPN5      (1) SRVLQAEELHEKALDP------FLLQAEFFEIPMNFVD----PKEYDIPGLVRKNRYKTILPNPHSRVCLTSPDPDDP-LSSYINANYIRGYG-------GEEKVYIATQG
hSHP1  D1 (NP  002822) PTPN6      (1) ADIENRVLELNKKQES-EDTAKAGFWEEFESLQKQEVKNLHQRLEGQRPENKGKNRYKNILPFDHSRVILQGRDSNIPG-SDYINANYIKNQLLGPD---ENAKTYIASQG
hSHP2  D1 (NP  002825) PTPN11     (1) AEIESRVRELSKLAET-TDKVKQGFWEEFETLQQQECKLLYSRKEGQRQENKNKNRYKNILPFDHTRVVLHDGDPNEPV-SDYINANIIMPEFETKCNNSKPKKSYIATQG
hPTPD1  D1 (NP  008970) PTPN21    (1) ATNDERCKILEQRLEQG-----MVF-TEYERILKKRLVDG-ECSTARLPENAERNRFQDVLPYDDARVELVPTKENN---TGYINASHIKVSVS------GIEWDYIATQG
hPTPD2  D1 (NP  005392) PTPN14    (1) VPMDERFRTLKKKLEEG-----MVF-TEYEQIPKKKANG--IFSTAALPENAERSRIREVVPYEENRVELIPTKENN---TGYINASHIKVVVG------GAEWHYIATQG
hMEG1  D1 (NP  002821) PTPN4      (1) HSLRESMIQLAEGLITG------TVLTQFDQLYRKKPGM--TMSCAKLPQNISKNRYRDISPYDATRVILKGN-------EDYINANYINMEIPSS----SIINQYIACQG
hPTPH1  D1 (NP  002820) PTPN3     (1) DTLEGSMAQLKKGLESG------TVLIQFEQLYRKKPGL--AITFAKLPQNLDKNRYKDVLPYDTTRVLLQGN-------EDYINASYVNMEIPAA----NLVNKYIATQG
hMEG2  D1 (NP  002824) PTPN9      (1) MTIQELVDYVNARQK-------QGIYEEYEDIRRENPVG--TFHCSMSPGNLEKNRYGDVPCLDQTRVKLTKRSGHTQ--TDYINASFMDGY--------KQKNAYIGTQG
hPTP1B  D1 (NP  002818) PTPN1     (1) MEMEKEFEQIDKSGS---------WAAIYQDIRHEASDF--PCRVAKLPKNKNRNRYRDVSPFDHSRIKLHQED------NDYINASLIKME--------EAQRSYILTQG
hTCPTP  D1 (NP  002819) PTPN2     (1) TTIEREFEELDTQRR---------WQPLYLEIRNESHDY--PHRVAKFPENRNRNRYRDVSPYDHSRVKLQNAE------NDYINASLVDIE--------EAQRSYILTQG
hPTPBAS  D1 (NP  006255) PTPN13   (1) ANLKSVIRVLRGLLDQ------GIPSKELENLQELKPLD--QCLIGQTKENRRKNRYKNILPYDATRVPLGDE-------GGYINASFIKIPVG------KEEFVYIACQG
hPTPTyp  D1 (AL050040) PTPN20     (1) TAIKDCLKILEEKTAA------YDIMQEFMALELKNLPG--EFYSGNQPSNREKNRYRDILPYDSTRVPLGKS-------KDYINASYIRIVNC------GEEYFYIATQG
hBDP1  D1 (NP  055184) PTPN18     (1) DSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGH--SDYINGNFIRGV--------DGSLAYIATQG
hLvPTP  D1 (NP  057051) PTPN22    (1) EILQKFLDEAQSKKIT-KEEFANEFLKLKRQSTKYKADKTYPTTVAEKPKNIKKNRYKDILPYDYSRVELSLITSDED--SSYINANFIKGV--------YGPKAYIATQG
hPEST  D1 (NP  002826) PTPN12     (1) RKFIQRVQAMKSPDHNGEDNFARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYKDILPFDHSRVKLTLKTPSQD--SDYINANFIKGV--------YGPKAYVATQG
hHDPTP  D1 (NP  056281) PTPN23    (1) ERLRQLQQELEAFRGQLGDV--GALDTVWRELQDAQEHDARGRSIAIARCYSLKNRHQDVMPYDSNRVVLRSGK------DDYINASCVEGLS-------PYCPPLVATQA
hIA2  D1 (NP  002837) PTPRN       (1) HMILAYMEDHLRNRDR--------LAKEWQALCAYQAEPN-TCATAQGEGNIKKNRHPDFLPYDHARIKLKVESSPSR--SDYINASPIIEHD-------PRMPAYIATQG
hIA2beta_D1 (NP_002838) PTPRN2    (1) HMILSYMEDHLKNKNR--------LEKEWEALCAYQAEPN-SSFVAQREENVPKNRSLAVLTYDHSRVLLKAENSHSH--SDYINASPIMDHD-------PRNPAYIATQG
Consensus                         (1)  L   I  L              F  EYE L             A  PENR KNRY  ILPYDHSRV L          SDYINANYI GY             YIATQG
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Section 2

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                                                  (112) 112       120       130       140       150       160       170       180       190       200       210       222
                hCD45  D1 (NP  002829) PTPRC      (93) PRDETVDDFWRMIWEQKATVIVMVTRCEEGNRNKCAEYWP--SMEEGTRAFGDVVVKINQHKRCPDYIIQKLNIVNKKE----------KATGREVTHIQFTSWPDHGVPE
             hPTPalpha  D1 (NP  002827) PTPRA      (93) PKEETVNDFWRMIWEQNTATIVMVTNLKERKECKCAQYWP----DQGCWTYGNIRVSVEDVTVLVDYTVRKFCIQQVGDMTN-------RKPQRLITQFHFTSWPDFGVPF
           hPTPepsilon  D1 (NP  006495) PTPRE      (93) PKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQYWP----DQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDG--------CKAPRLVSQLHFTSWPDFGVPF
             hPTPlamda  D1 (NP  005695) PTPRU      (88) PKPEMVYDFWRMVWQEHCSSIVMITKLVEVGRVKCSRYWP-----EDSDTYGDIKIMLVKTETLAEYVVRTFALERRG-----------YSARHEVRQFHFTAWPEHGVPY
             hPTPkappa  D1 (NP  002835) PTPRK      (92) PVHETVYDFWRMIWQEQSACIVMVTNLVEVGRVKCYKYWP-----DDTEVYGDFKVTCVEMEPLAEYVVRTFTLERRG-----------YNEIREVKQFHFTGWPDHGVPY
              hPTPmu  D1 (NP  002836) PTPRM      (92) PMQETIYDFWRMVWHENTASIIMVTNLVEVGRVKCCKYWP-----DDTEIYKDIKVTLIETELLAEYVIRTFAVEKRG-----------VHEIREIRQFHFTGWPDHGVPY
             hPTPrho  D1 (NP  573400) PTPRT      (92) PMQETVKDFWRMIWQENSASIVMVTNLVEVGRVKCVRYWP-----DDTEVYGDIKVTLIETEPLAEYVIRTFTVQKKG-----------YHEIRELRLFHFTSWPDHGVPC
            hPTPsigma  D1 (NP  002841) PTPRS      (92) PLPETFGDFWRMVWEQRSATIVMMTRLEEKSRIKCDQYWP----NRGTETYGFIQVTLLDTIELATFCVRTFSLHKNG-----------SSEKREVRQFQFTAWPDHGVPE
             hPTPdelta  D1 (NP  002830) PTPRD      (92) SLPETFGDFWRMIWEQRSATVVMMTKLEERSRVKCDQYWP----SRGTETHGLVQVTLLDTVELATYCVRTFALYKNG-----------SSEKREVRQFQFTAWPDHGVPE
                 hLAR  D1 (NP  002831) PTPRF      (92) PLPETMGDFWRMVWEQRTATVVMMTRLEEKSRVKCDQYWP----ARGTETCGLIQVTLLDTVELATYTVRTFALHKSG-----------SSEKRELRQFQFMAWPDHGVPE
            hPTPgamma  D1 (NP  002832) PTPRG      (97) PLKSTFEDFWRMIWEQNTGIIVMITNLVEKGRRKCDQYWP----TENSEEYGNIIVTLKSTKIHACYTVRRFSIRNTKVKKGQKGNPKGRQNERVVIQYHYTQWPDMGVPE
            hPTPzeta  D1 (NP  002842) PTPRZ1    (102) PLKSTAEDFWRMIWEHNVEVIVMITNLVEKGRRKCDQYWP----ADGSEEYGNFLVTQKSVQVLAYYTVRNFTLRNTKIKKGSQ---KGRPSGRVVTQYHYTQWPDMGVPE
              hSAP1  D1 (NP  002833) PTPRH      (93) PLPQTVGDFWRLVWEQQSHTLVMLTNCMEAGRVKCEHYWP---LDSQPCTHGHLRVTLVGEEVMENWTVRELLLLQVEE-----------QKTLSVRQFHYQAWPDHGVPS
              hDEP1  D1 (NP  002834) PTPRJ      (92) PLPNTLKDFWRMVWEKNVYAIIMLTKCVEQGRTKCEEYWP----SKQAQDYGDITVAMTSEIVLPEWTIRDFTVKNIQT-----------SESHPLRQFHFTSWPDHGVPD
            hPTPbeta  D1 (NP  002828) PTPRB      (93) PLPGTKDDFWKMVWEQNVHNIVMVTQCVEKGRVKCDHYWP---ADQDSLYGDLILQMLSESVLPEWTIREFKICGEEQ----------LDAHRLIRHFHYTVWPDHGVPE
            hGLEPP1  D1 (NP  109592) PTPRO      (93) PLPETRNDFWKMVLQQKSQIIVMLTQCNEKRRVKCDHYWP---FTEEPIAYGDITVEMISEEEQDDWACRHFRINYAD-------------EMQDVMHFNYTAWPDHGVPT
           hPTPS31  D1 (AR073855) PTPGMC1       (93) PLPGTVGDFWRMVWETRAKTLVMLTQCFEKGRIRCHQYWP--EDNKPVTVFGDIVITKLMEDVQIDWTIRDLKIERHG-------------DCMTVRQCNFTAWPEHGVPE
             hHePTP  D1 (NP  002823) PTPN7      (92) PMPNTVSDFWEMVWQEEVSLIVMLTQLRE-GKEKCVHYWP-----TEEETYGPFQIRIQDMKECPEYTVRQLTIQYQE-------------ERRSVKHILFSAWPDHQTPE
            hPCPTP1  D1 (NP  002840) PTPRR      (94) PMINTVDDFWQMVWQEDSPVIVMITKLKE-KNEKCVLYWP-----EKRGIYGKVEVLVISVNECDNYTIRNLVLKQGS-------------HTQHVKHYWYTSWPDHKTPD
              hSTEP  D1 (NP  116170) PTPN5      (94) PIVSTVADFWRMVWQEHTPIIVMITNIEE-MNEKCTEYWP-----EEQVAYDGVEITVQKVIHTEDYRLRLISLKSGT-------------EERGLKHYWFTSWPDQKTPD
              hSHP1  D1 (NP  002822) PTPN6    (107) CLEATVNDFWQMAWQENSRVIVMTTREVEKGRNKCVPYWP---EVGMQRAYGPYSVTNCGEHDTTEYKLRTLQVSPLDN----------GDLIREIWHYQYLSWPDHGVPS
              hSHP2  D1 (NP  002825) PTPN11   (110) CLQNTVNDFWRMVFQENSRVIVMTTKEVERGKSKCVKYWP---DEYALKEYGVMRVRNVKESAAHDYTLRELKLSKVGQ----------GNTERTVWQYHFRTWPDHGVPS
             hPTPD1  D1 (NP  008970) PTPN21     (96) PLQNTCQDFWQMVWEQGIAIIAMVTAEEEGGREKSFRYWPRLGSRHNTVTYGRFKITTRFRTDSGCYATTGLKMKHLLTG-----------QERTVWHLQYTDWPEHGCPE
             hPTPD2  D1 (NP  005392) PTPN14     (95) PLPHTCHDFWQMVWEQGVNVIAMVTAEEEGGRTKSHRYWPKLGSKHSSATYGKFKVTTKFRTDSVCYATTGLKVKHLLSG-----------QERTVWHLQYTDWPDHGCPE
              hMEG1  D1 (NP  002821) PTPN4      (93) PLPHTCTDFWQMTWEQGSSMVVMLTTQVERGRVKCHQYWP---EPTGSSSYGCYQVTCHSEEGNTAYIFRKMTLFNQEKN-----------ESRPLTQIQYIAWPDHGVPD
             hPTPH1  D1 (NP  002820) PTPN3      (93) PLPHTCAQFWQVVWDQKLSLIVMLTTLTERGRTKCHQYWP---DPPDVMNHGGFHIQCQSEDCTIAYVSREMLVTNTQTG-----------EEHTVTHLQYVAWPDHGVPD
             hMEG2  D1 (NP  002824) PTPN9      (93) PLENTYRDFWLMVWEQKVLVIVMTTRFEEGGRRKCGQYWP--LEKDSRIRFGFLTVTNLGVENMNHYKKTTLEIHNTEER-----------QKRQVTHFQFLSWPDYGVPS
             hPTP1B  D1 (NP  002818) PTPN1      (87) PLPNTCGHFWEMVWEQKSRGVVMLNRVMEKGSLKCAQYWPQKEEKEMIFEDTNLKLTLISEDIKSYYTVRQLELENLTTQ-----------ETREILHFHYTTWPDFGVPE
             hTCPTP  D1 (NP  002819) PTPN2      (87) PLPNTCCHFWLMVWQQKTKAVVMLNRIVEKESVKCAQYWP-TDDQEMLFKETGFSVKLLSEDVKSYYTVHLLQLENINSG-----------ETRTISHFHYTTWPDFGVPE
            hPTPBAS  D1 (NP  006255) PTPN13     (91) PLPTTVGDFWQMIWEQKSTVIAMMTQEVEGEKIKCQRYWP-NILGKTTMVSNRLRLALVRMQQLKGFVVRAMTLEDIQTR-----------EVRHISHLNFTAWPDHDTPS
            hPTPTyp  D1 (AL050040) PTPN20     (91) PLLSTIDDFWQMVLENNSNVIAMITREMEGGIIKCYHYWP--ISLKKPLELKHFRVFLENYQILQYFIIRMFQVVEKSTG-----------TSHSVKQLQFTKWPDHGTPA
             hBDP1  D1 (NP  055184) PTPN18    (102) PLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA--QEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK-------------ESRSVYQLQYMSWPDRGVPS
             hLvPTP  D1 (NP  057051) PTPN22    (101) PLSTTLLDFWRMIWEYSVLIIGMACMEYEMGKKKCERYWA--EPVEMQLEFGPFSVSCEAEKRKSDYIIRTLKVKFNS-------------ETRTIYQFHYKNWPDHDVPS
              hPEST  D1 (NP  002826) PTPN12    (102) PLANTVIDFWRMIWEYNVVIIVMACREFEMGRKKCERYWP--LYGEDPITFAPFKISCEDEQARTDYFIRTLLLEFQN-------------ESRRLYQFHYVNWPDHDVPS
            hHDPTP  D1 (NP  056281) PTPN23     (97) PLPGTAADFWLMVHEQKVSVIVMLVSEAEMEKQKVARYFP--TERGQPMVHGALSLALSSVRSTETHVERVLSLQFRDQS-----------LKRSLVHLHFPTWPELGLPD
              hIA2  D1 (NP  002837) PTPRN      (94) PLSHTIADFWQMVWESGCTVIVMLTPLVEDGVKQCDRYWP---DEGASLYHVYEVNLVSEHIWCEDFLVRSFYLKNVQTQ-----------ETRTLTQFHFLSWPAEGTPA
           hIA2beta_D1 (NP_002838) PTPRN2       (94) PLPATVADFWQMVWESGCVVIVMLTPLAENGVRQCYHYWP---DEGSNLYHIYEVNLVSEHIWCEDFLVRSFYLKNLQTN-----------ETRTVTQFHFLSWYDRGVPS
                      Consensus (112) PLP TV DFWRMVWEQ S VIVMLT L E GR KC  YWP          YG I VTL        DY VR L L                 E R V QFHFTSWPDHGVPE
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Section 3

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                                                  (223) 223       230         240         250         260         270         280         290         300         310         326
                                                        |         |         |         |         |         |         |         |         |         |         |         |
                 hCD45  D1 (NP  002829) PTPRC (192) D---PHLLLKLRRRVNAFSNFFS----------GPIVVHCSAGVGRTGTYIGIDAMLEGLEAENK---VDVYGYVVKLRRQRCLMVQVEAQYILIHQALVEYNQ
                hPTPalpha  D1 (NP  002827) PTPRA (193) T---PIGMLKFLKKVKACNPQYA----------GAIVVHCSAGVGRTGTFVVIDAMLDMMHTERK---VDVYGFVSRIRAQRCQMVQTDMQYVFIYQALLEHYL
              hPTPepsilon  D1 (NP  006495) PTPRE (192) T---PIGMLKFLKKVKTLNPVHA----------GPIVVHCSAGVGRTGTFIVIDAMMAMMHAEQK---VDVFEFVSRIRNQRPQMVQTDMQYTFIYQALLEYYL
               hPTPlamda  D1 (NP  005695) PTPRU (183) H---ATGLLAFIRRVKASTPPDA----------GPIVIHCSAGTGRTGCYIVLDVMLDMAECEGV---VDIYNCVKTLCSRRVNMIQTEEQYIFIHDAILEACL
               hPTPkappa  D1 (NP  002835) PTPRK (187) H---ATGLLSFIRRVKLSNPPSA----------GPIVVHCSAGAGRTGCYIVIDIMLDMAEREGV---VDIYNCVKALRSRRINMVQTEEQYIFIHDAILEACL
                 hPTPmu  D1 (NP  002836) PTPRM (187) H---ATGLLGFVRQVKSKSPPSA----------GPLVVHCSAGAGRTGCFIVIDIMLDMAEREGV---VDIYNCVRELRSRRVNMVQTEEQYVFIHDAILEACL
                hPTPrho  D1 (NP  573400) PTPRT (187) Y---ATGLLGFVRQVKFLNPPEA----------GPIVVHCSAGAGRTGCFIAIDTMLDMAENEGV---VDIFNCVRELRAQRVNLVQTEEQYVFVHDAILEACL
              hPTPsigma  D1 (NP  002841) PTPRS (188) Y---PTPFLAFLRRVKTCNPPDA----------GPIVVHCSAGVGRTGCFIVIDAMLERIKPEKT---VDVYGHVTLMRSQRNYMVQTEDQYSFIHEALLEAVG
               hPTPdelta  D1 (NP  002830) PTPRD (188) H---PTPFLAFLRRVKTCNPPDA----------GPMVVHCSAGVGRTGCFIVIDAMLERIKHEKT---VDIYGHVTLMRAQRNYMVQTEDQYIFIHDALLEAVT
                   hLAR  D1 (NP  002831) PTPRF (188) Y---PTPILAFLRRVKACNPLDA----------GPMVVHCSAGVGRTGCFIVIDAMLERMKHEKT---VDIYGHVTCMRSQRNYMVQTEDQYVFIHEALLEAAT
              hPTPgamma  D1 (NP  002832) PTPRG (204) Y---ALPVLTFVRRSSAARMPET----------GPVLVHCSAGVGRTGTYIVIDSMLQQIKDKST---VNVLGFLKHIRTQRNYLVQTEEQYIFIHDALLEAIL
               hPTPzeta  D1 (NP  002842) PTPRZ1 (206) Y---SLPVLTFVRKAAYAKRHAV----------GPVVVHCSAGVGRTGTYIVLDSMLQQIQHEGT---VNIFGFLKHIRSQRNYLVQTEEQYVFIHDTLVEAIL
                  hSAP1  D1 (NP  002833) PTPRH (190) S---PDTLLAFWRMLRQWLDQTMEG--------GPPIVHCSAGVGRTGTLIALDVLLRQLQSEGL---LGPFSFVRKMRESRPLMVQTEAQYVFLHQCICGSSN
                  hDEP1  D1 (NP  002834) PTPRJ (188) T---TDLLINFRYLVRDYMKQSPPE--------SPILVHCSAGVGRTGTFIAIDRLIYQIENENT---VDVYGIVYDLRMHRPLMVQTEDQYVFLNQCVLDIVR
               hPTPbeta  D1 (NP  002828) PTPRB (191) T---TQSLIQFVRTVRDYINRSPGA--------GPTVVHCSAGVGRTGTFIALDRILQQLDSKDS---VDIYGAVHDLRLHRVHMVQTECQYVYLHQCVRDVLR
               hGLEPP1  D1 (NP  109592) PTPRO (188) ANA-AESILQFVHMVRQQATKSK----------GPMIIHCSAGVGRTGTFIALDRLLQHIRDHEF---VDILGLVSEMRSYRMSMVQTEEQYIFIHQCVQLMWM
              hPTPS31  D1 (AR073855) PTPGMC1 (189) N---SAPLIHFVKLVRASRAHDT----------TPMIVHCSAGVGRTGVFIALDHLTQHINDHDF---VDIYGLVAELRSERMCMVQNLAQYIFLHQCILDLLS
               hHePTP  D1 (NP  002823) PTPN7 (184) S---AGPLLRLVAEVEESPETAAHP--------GPIVVHCSAGIGRTGCFIATRIGCQQLKARGE---VDILGIVCQLRLDRGGMIQTAEQYQFLHHTLALYAG
              hPCPTP1  D1 (NP  002840) PTPRR (186) S---AQPLLQLMLDVEEDRLASQGR--------GPVVVHCSAGIGRTGCFIATSIGCQQLKEEGV---VDALSIVCQLRMDRGGMVQTSEQYEFVHHALCLYES
                hSTEP  D1 (NP  116170) PTPN5 (186) R---APPLLHLVREVEEAAQQEGPHC-------APIIVHCSAGIGRTGCFIATSICCQQLRQEGV---VDILKTTCQLRQDRGGMIQTCEQYQFVHHVMSLYEK
                hSHP1  D1 (NP  002822) PTPN6 (205) E---PGGVLSFLDQINQRQESLPHA--------GPIIVHCSAGIGRTGTIIVIDMLMENISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIE
                hSHP2  D1 (NP  002825) PTPN11 (208) D---PGGVLDFLEEVHHKQESIMDA--------GPVVVHCSAGIGRTGTFIVIDILIDIIREKGVDCDIDVPKTIQMVRSQRSGMVQTEAQYRFIYMAVQHYIE
               hPTPD1  D1 (NP  008970) PTPN21 (196) DLKGFLSYLEEIQSVRRHTNSTSDPQSPN----PPLLVHCSAGVGRTGVVILSEIMIACLEHNEV---LDIPRVLDMLRQQRMMLVQTLCQYTFVYRVLIQFLK
               hPTPD2  D1 (NP  005392) PTPN14 (195) DVQGFLSYLEEIQSVRRHTNSMLEGTKNRH---PPIVVHCSAGVGRTGVLILSELMIYCLEHNEK---VEVPMMLRLLREQRMFMIQTIAQYKFVYQVLIQFLQ
                 hMEG1  D1 (NP  002821) PTPN4 (190) D---SSDFLDFVCHVRNKRAGKE----------EPVVVHCSAGIGRTGVLITMETAMCLIECNQP---VYPLDIVRTMRDQRAMMIQTPSQYRFVCEAILKVYE
                hPTPH1  D1 (NP  002820) PTPN3 (190) D---SSDFLEFVNYVRSLRVDS----------EPLLVHCSAGIGRTGVLVTMETAMCLTERNLP---IYPLDIVRKMRDQRAMMVQTSSQYKFVCEAILRVYE
                 hMEG2  D1 (NP  002824) PTPN9 (191) SAASLIDFLRVVRNQQSLAVSNMGARSKGQCPEPPIVVHCSAGIGRTGTFCSLDICLAQLEELGT---LNVFQTVSRMRTQRAFSIQTPEQYYFCYKAILEFAE
                hPTP1B  D1 (NP  002818) PTPN1 (187) S---PASFLNFLFKVRESGSLSPEH--------GPVVVHCSAGIGRSGTFCLADTCLLLMDKRKDPSSVDIKKVLLEMRKFRMGLIQTADQLRFSYLAVIEGAK
                hTCPTP  D1 (NP  002819) PTPN2 (186) S---PASFLNFLFKVRESGSLNPDH--------GPAVIHCSAGIGRSGTFSLVDTCLVLMEKGDD---INIKQVLLNMRKYRMGLIQTPDQLRFSYMAIIEGAK
               hPTPBAS  D1 (NP  006255) PTPN13 (190) Q---PDDLLTFISYMRHIHRS-----------GPIITHCSAGIGRSGTLICIDVVLGLISQDLD---FDISDLVRCMRLQRHGMVQTEDQYIFCYQVILYVLT
               hPTPTyp  D1 (AL050040) PTPN20 (189) S---ADSFIKYIRYARKSHLT------------GPMVVHCSAGIGRTGVFLCVDVVFCAIVKDCS---FNIMDIVAQMREQRSGMVQTKEQYHFCYDIVLEVLR
                hBDP1  D1 (NP  055184) PTPN18 (198) S---PDHMLAMVEEARRLQGSGP----------EPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFC
               hLvPTP  D1 (NP  057051) PTPN22 (197) S---IDPILELIWDVRCYQEDDS----------VPICIHCSAGCGRTGVICAIDYTWMLLKDGIIPENFSVFSLIREMRTQRPSLVQTQEQYELVYNAVLELFK
                hPEST  D1 (NP  002826) PTPN12 (198) S---FDSILDMISLMRKYQEHED----------VPICIHCSAGCGRTGAICAIDYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFE
               hHDPTP  D1 (NP  056281) PTPN23 (195) S---PSNLLRFIQEVHAHYLHQRPLH-------TPIIVHCSSGVGRTGAFALLYAAVQEVEAGNG--IPELPQLVRRMRQQRKHMLQEKLHLRFCYEAVVRHVE
                 hIA2  D1 (NP  002837) PTPRN (191) S---TRPLLDFRRKVNKCYRGRS----------CPIIVHCSDGAGRTGTYILIDMVLNRMAKGVK--EIDIAATLEHVRDQRPGLVRSKDQFEFALTAVAEEVN
              hIA2beta_D1 (NP_002838) PTPRN2 (191) S---SRSLLDFRRKVNKCYRGRS----------CPIIVHCSDGAGRSGTYVLIDMVLNKMAKGAK--EIDIAATLEHLRDQRPGMVQTKEQFEFALTAVAEEVN
                      Consensus (223)                LL FVR VR                  GPIVVHCSAGVGRTG FIVID ML  I        VDIY  V  MR QR  MVQTEEQY FIH AILE
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