Human Protein-Tyrosine Phosphatase Catalytic Domain Alignment

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PTP-1B     31  PCRVAKLPKNKNRNRYRDVSPFDHSRIKLH-----QEDNDYINASLIKMEEAQR--------SYIL
TC-PTP     33  PHRVAKFPENRNRNRYRDVSPYDHSRVKLQ-----NAENDYINASLVDIEEAQR--------SYIL
PTP-MEG1  670  TMSCAKLPQNISKNRYRDISPYDATRVILK-----GNE-DYINANYINMEIPSSSI----INQYIA
PTP-β    1718  SCDIALLPENRGKNRYNNILPYDATRVKLSNVDDDP-CSDYINASYIPGNNF--------RREYIV
CD45      666  PIKEARKPFNQNKNRYVDILPYDYNRVELSEINGDA-GSNYINASYIDGFKE--------PRKYIA
SHP-2     264  SRKEGQRQENKNKNRYKNILPFDHTRVVLHDGDPNEPVSDYINANIIMPEFETKCNNSKPKKSYIA
PTP-G1     49  PTATGEKEENVKKNRYKDILPFDHSRVKLTLKTPSQ-DSDYINAANFIKGVYG-------PKAYVA

PTP-1B     84  TQGPLPNTCGHFWEMVWEQKSRGVVMLNRVMEKGSLKCAQYWPQKEEKEMIFEDTNLKLTL
TC-PTP     86  TQGPLPNTCCHFWLMVWQQKTKAVVMLNRIVEKESVKCAQYWP-TDDQEMLFKETGFSVKL
PTP-MEG1  726  CQGPLPHTCTDFWQMTWEQGSSMVVMLTTQVERGRVKCHQYWP---EPTGSSSYGCYQVTC
PTP-β    1775  TQGPLPGTKDDFWKMVWEQNVHNIVMVTQCVEKGRVKCDHYWPA--DQD-SLYYGDLILQM
CD45      723  AQGPRDETVDDFWRMIWEQKATVIVMVTRCEEGNRNKCAEYWPS--MEEGTRAFGDVVVKI
SHP-2     330  TQGCLQNTVNDFWRMVFQENSRVIVMTTKEVERGKSKCVKYWP---DEYALKEYGVMRVRN
PTP-G1    106  TQGPLANTVIDFWRMIWEYNVVIIVMACREFEMGRKKCERYWPL--YGEDPITFAPFKISC

PTP-1B    145  ISEDIKSYYTVRQLELENLTT-QETREILHFHYTTWPDFGVPESPASFLNFLFKVR
TC-PTP    146  LSEDVKSYYTVHLLQLENINS-GETRTISHFHYTTWPDFGVPESPASFLNFLFKVR
PTP-MEG1  784  HSEEGNTAYIFRKMTLFNQEK-NESRPLTQIQYIAWPDHGVPDDSSDFLDFVCHVR
PTP-β    1833  LSESVLPEWTIREFKICGEEQLDAHRLIRHFHYTVWPDHGVPETTQSLIQFVRTVR
CD45      782  NQHKRCPDYIIQKLNIVNKKEKATGREVTHIQFTSWPDHGVPEDPHLLLKLRRRVN
SHP-2     388  VKESAAHDYTLRELKLSKVGQGNTERTVWQYHFRTWPDHGVPSDPGGVLDFLEEVH
PTP-G1    165  EDEQARTDYFIRTLLLEFQ---NESRRLYQFHYVNWPDHDVPSSFDSILDMISLMR

PTP-1B    200  ESGSLSPEHGPVVVHCSAGIGRSGTFCLADTCLLLMDKRKDPSSVDIKK
TC-PTP    201  ESGSLNPDHGPAVIHCSAGIGRSGTFSLVDTCLVLMEKGDD---INIKQ
PTP-MEG1  839  NKRAGKEE--PVVVHCSAGIGRTGVLITMETAMCLIECNQP---VYPLD
PTP-β    1889  DYINRSPGAGPTVVHCSAGVGRTGTFIALDRILQQLDSK---DSVDIYG
CD45      838  AFSN--FFSGPIVVHCSAGVGRTGTYIGIDAMLEGLEAE---NKVDVYG
SHP-2     444  HKQESIMDAGPVVVHCSAGIGRTGTFIVIDILIDIIREKGVDCDIDVPK
PTP-G1    218  KYQE--HEDVPICIHCSAGCGRTGAICAIDYTWNLLKAGKIPEEFNVFL

PTP-1B    249  VLLEMRKFRMGLIQTADQLRFSYLAVIE  276
TC-PTP    247  VLLNMRKYRMGLIQTPDQLRFSYMAIIE  274
PTP-MEG1  883  IVRTMRDQRAMMIQTPSQYRFVCEAILK  910
PTP-β    1933  AVHDLRLHRVHMVQTECQYVYLHQCVRD 1962
CD45      882  YVVKLRRQRCLMVQVEAQYILIHQALVE  909
SHP-2     493  DVQMVRSQRSGMVQTEAQYRFIYMAVQH  520
PTP-G1    266  TIQEMRTQRHSAVQTKEQYELVHRAIAQ  292
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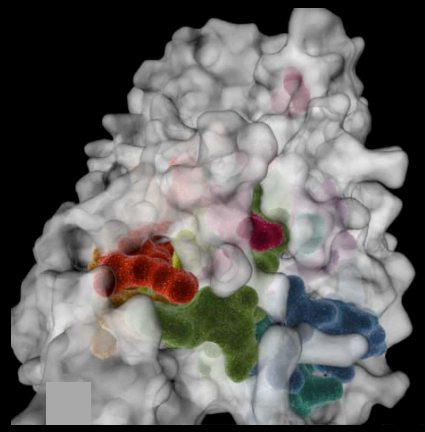
Human Protein-Tyrosine Phosphatase 1B (residues 1-299, white)

ETDYpYRKGGKGLL peptide from Insulin Receptor (dark grey)

PDB: 1G1G