

Supplementary Figure 4. Alignment of protein sequences of TSP2 and sTSP2

Alignment of TSP2 with sTSP2. Similarity : 209/1172 (17.83 %)

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TSP2 1  MWVRLVLLALWVWPSTQAGHQDKDTTFDLFSISINIRKTI GAKQFRGPDPGVPAYRFVRF 60
sTSP2 1  ----- 0

TSP2 61  DYIPPNADDLSKITKIMRQKEGFFLTAQLKQDGKSRGTL LALEGPGLSQRQFEIVSNGP 120
sTSP2 1  ----- 0

TSP2 121 ADTLDLTYWIDGTRHVSVLEEDVGLADSQWKNVTQVAGET YSLHVGCDLIDSFALDEPFY 180
sTSP2 1  ----- 0

TSP2 181 EHLQAEKSRMYVAKGSARESHFRGLLQNVHLVFENSVED ILSKKGCCQQGAEINAI SEN 240
sTSP2 1  ----- 0

TSP2 241 TETLRLGPHVTTEYVGPSSERRPEVCERSCEELGNMVQ ELSGLHVLVNQLSENKRV S ND 300
sTSP2 1  ----- 0

TSP2 301 NQFLWELIGGPPKTRNMSACWQDGRFFAENETWVVDSC TCTCKKFKTICHQITCPP ATC 360
sTSP2 1  ----- 0

TSP2 361 ASPSFVEGECCPSCLHSVDGEGWSPWAEWTQCSVTCGS GTQQRGRSCDVTSNTCLG PSI 420
sTSP2 1  ----- 0

TSP2 421 QTRACSLSKCDTRIRQDGGWSHWSPWSSCVTCGVGNIT RIRLNCSPVPQMGKNC KSGS 480
sTSP2 1  ----- 0

TSP2 481 RETKACQGAPCPIDGRWSPWSPWACTVTCAGGIRERTRV C NSPEPQYGGKACVGDVQ ER 540
sTSP2 1  ----- 0

TSP2 541 QMCNKRSCPVDGCLSNPCFPGAQCSSFPDGSWSCGSCP V GFLNGTHCEDLDECALV PDI 600
sTSP2 1  ----- 0

TSP2 601 CFSTSKVPRCVNTQPGFHCLPCPPRYRGNQFVGVGLEA AKTEKQVCEPENCKDKTHN CH 660
sTSP2 1  ----- 0

TSP2 661 KHAECIYLGHFSDPMYKCECQTYAGDGLICGEDSDL D GWPNLNLVCATNATYHCKDNC 720
sTSP2 1  ----- 0

TSP2 721 PHLPSNGQEDFDKDIGDACDDDDNDGVTDKDNQQLLFN PRQADYDKDEVGDRCDNCP 780
sTSP2 1  ----- 0

TSP2 781 YVHNPAQIDTDNNGEGDACSVIDGDDVFNERDNC PYVYNTDQRD TDG DGVGDHCNCP L 840
sTSP2 1  ----- 0

TSP2 841 VHNPDQTDVDNDLVGDQCDNNEIDDDGHQNNQDNCPY I SNANQADHDRDGGDADCPDD 900
sTSP2 1  ----- 0

TSP2 901 DNDGVPDRDRNCRLVFNPDQEDLDGDRGDICKDDFDND NIPIDDDVCPENNAISETDFR 960
sTSP2 1  ----- 0

TSP2 961 NFMVPLDPKGTQIDPNWVIRHQGKELVQTANSDPGI AVGFDEFGSVDFSGTFYVNTDR 1020
sTSP2 1  ---MVPLDPKGTQIDPNWVIRHQGKELVQTANSDPGI AVGFDEFGSVDFSGTFYVNTDR 57

TSP2 1021 DDDYAGFVFGYQSSSRFYVVMWKQVTQTYWEDQPTRAY GYSGVSLKVVNSTTGTGEHLRN 1080
sTSP2 58 DDDYAGFVFGYQSSSRFYVVMWKQVTQTYWEDQPTRAY GYSGVSLKVVNSTTGTGEHLRN 117

TSP2 1081 ALWHTGNTPGQVRTLWHDPRNIGWKDYTAYRWHLTRPKT GYIRVLVHEGKQVMADSGPI 1140
sTSP2 118 ALWHTGNTPGQVRTLWHDPRNIGWKDYTAYRWHLTRPKT GYIRVLVHEGKQVMADSGPI 177

TSP2 1141 YDQTYAGGRLGLFVFSQEMVYFSDLKYECRDI 1172
sTSP2 178 YDQTYAGGRLGLFVFSQEMVYFSDLKYECRDI 209
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