

Alignment of Commissureless and C. elegans C17G10.7

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Comm  MISTTDYPTVETTTTAEELYAEYISAPASSMSPAAIAEHLQQNQITFEIPSAHDLRHIDALNSFNALLQRIGNAAVSYDPAPP
C17G10 MDHSTRFRVHNWLRSRRLKFQSRMCLLM-LVMI-NFVNSVILTLEICGE-DSNM TLLM-FVNTF---VVFLSMYGL---
                + S      M      I      +T+EI      D      F      Y

Comm  SGWSPDGSISTEQLSKSVVLDLADLRDRSEESGESSWWSQIFGDADMHVIINYLWIGVVSSLVILSLVFLFSCYFYR-KFRTWKK
C17G10 -----YNFRPVFLSPNVLLKIILSSSAL-FYGLQMAETTSNSAIFV-WLTISIVFFILEIHTM-FSTTFDIIKQLNLR-
                + V+L      L      S      ++      +      ++ + W+ +      ++IL + ++ FS++F++ K----+

Comm  CNKDIRAQIHAASDSYSSHLVGCDSARLLLHQMQHPHRSSEAGFYQIESPPCYT----IATGLPSYDEALHH--QPR
C17G10 AYSK-----PPNYNQVMSIDVPPPSYEEALVRLEQNR
                K                        PP Y      I      PSY+EAL      Q R

Comm  HFAYGMKFVYPSLA AVHHHHHCISNWEKQEPLNKLQCKLSAAA AVEEDKADSSSSTSASASPSSSESSNLA
C17G10 ---TAAKNQSS-----
                K

Comm  TATPAICINMPSGRQDEEVDNSDSDAI AVAVAVAQSLQPAAPADDDCASLVVVVAA
C17G10 -----PKPDQPAQLNTCDLAHLVV
                QPA      D      LVV

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Alternative interpretation of C17G10.7 as a four-pass transmembrane protein
 Transmembrane domains are highlighted in blue.

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C17G10.7 MDHSTRFRVHNWLRSRRLKFQSRMCLLMLVMINFNVSILTLEICGEDSNMTLLMFFVNTFVFLSMYGL
C17G10.7 YNFRPVFLSPNVLLKIILSSSALFYGLQMAETTSNSAIFVWLTISIVFFILEIHTMFSTTFDIIKQLNLR
C17G10.7 AYSKPPNYNQVMSIDVPPPSYEEALVRLEQNR TAAKNQSSPKPDQPAQLNTCDLAHLVV

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