

Conceptual Translation of Human TMEM169 NP_001135782.1

gggcgggtgctcgagcccacgtgaccaccagaacccccgcaccctccccggccccggccccgccccgc 0
 cgccccggccggcgaagccgcgcatcctccccggagc 0 5' upstream

agaaccgctccccgccggctgtccgcaacctccgccagcgtcggtcacctgggcaggtgtg 60
 gtgcagctggaaaaagaaaggctgctgctcggcgccctcgtgccccgctgccgggggt 120 [exn1/exn2](#)
 cggacgtcggcgatgctgtggctccaagggtggaatgcatccttgggacatctttgcatagc 180 [exn2/exn3](#)
 M L W L Q V E C I L G T S L H S

cccatctaggaagaagttctgtgatgtgtgaactgtgagtttactcaacaagtccaact 240
 P I *

ctttataagacataggtagacgtcaggtctggaatggaagagccaacagcagtagaaggc 300 [Kozak sequence](#)
 M E E P T A V E G 9 [CK2 phospho. site](#)

caggtccagcttccaagccccaccagggctctctcaggaaggctgtggctgctgcctg 360
 Q V Q L P S P H Q G S L R K A V A A A L 29

gcgctggatggggaatccacaatggggcacaggaaaaagaagaggaaagagtcacgcca 420
 A L D G E S T M G H R K K K R K E S R P 49

gaatccatcatcatctaccgctcagacaatgagaaaacagatgaggagcccggagaatca 480
 E S I I I Y R S D N E K T D E E P G E S 69 [CK2 phospho. site](#)

gaaggtggagatcagcctaaagaggaggaggagatgatttcctagactatcctgtggat 540
 E G G D Q P K E E E G D D F L D Y P V D 89

gatgatatgtggaacctgcctctggacagccgctacgtcaccttaactgggaccatcaca 600 [exn3/exn4](#)
 D D M W N L P L D S R Y V T L T G T I T 109
 cgaggaagaaaaagggtcagatgggtggacatccatgtcacattgacagagaaagagctg 660
 R G K K K G Q M V D I H V T L T E K E L 129 [CK2 phospho. site](#)

caggaactgaccaaacctaaagagtcatcaagggaacgacgcctgaaggaagaatggcc 720 [CK2 phospho. site](#)
 Q E L T K P K E S S R E T T P E G R M A 149 [protein family m15052](#)

tgccagatgggagctgaccgtgggccccatgtggctcctctggacgctgatctgcctgcct 780
 C Q M G A D R G P H V V L W T L I C L P 169 [transmembrane region](#)

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 V V F I L S F V V S F Y Y G T I T W Y N 189

atcttctcgtgtataatgaggaaaggaccttctggcacaagatctcgtattgcccttgc 900
 I F L V Y N E E R T F W H K I S Y C P C 209 [exp.sumoylation site](#)

ctcgttctcttctatccagtgctcatcatggccatggcttcttccctcggcctctacgct 960
 L V L F Y P V L I M A M A S S L G L Y A 229 [transmembrane region](#)

gctgtgggtccagctctcgtggctcctgggaagcatggtggcaagctgccccgggacatggag 1020 [N-myristoylation site](#)
 A V V Q L S W S W E A W W Q A A R D M E 249

aaaggcttctgtggctggctctgcagcaagctgggtctggaggactgttctcctacagc 1080

K G F C G W L C S K L G L E D C S P Y S 269 N-myristoylation site
 attgtggagttgcttgaatccgacaatatctcaagcactctctccaacaaggaccccatc 1140
I V E L L E S D N I S S T L S N K D P I 289 CK2 phospho. site (2)
 caagaagtagaaacctccacggctc**taa**actcccaacaacttactccctcctctggcccca 1200
 Q E V E T S T V * 297
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 aatgaagacaaagaa**ataaaaaataa**agtctgatta**a**cttttgc**a** 3408 major poly A site(2)