

CCDC184 Conceptual Translation:

acccagctgctgctgccacactcgcgggcgctgcccggaatggcctgggggagtcccg 60
agtccgacgcgcccgtggcctcagcctggacgcggaccctccgcgagcgcgtctgtgac 120 upstream in-frame stop
ccacggaaccggcaggcgctctctgcttgtggcgcccagagggcgggcgctgacacgggcg 180
cgatccggggaggcgaggcaggcgaggcactttcgtcccggggcgatcccaagagacgcc 240
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caccocggaggccgggctggacgcgaccagagcctccgccaccocgcttctgccactca 480
I *M 1 [DoUF] highly Conserved

tgaggagcggctgctgaggatcatgaccaaggacgcggcgacatgccggcgcccctgg 540
E D G L L E I M T K D G G D M P A P L E 21 Helix

agggtgccaccgtgccggcagtgggggacgtgatctccggggagtacaacggcgcatga 600
V S T V P A V G D V I S G E Y N G G M K 41 [coiled-coil]

aggaactgatggagcacctgaaagcccagctgcaagccctgtttgaggacgtgagggcc 660
E L M E H L K A Q L Q A L F E D V R A M 61

tgagggggggccctggacgagcaggcctcgcacatccaggtgctctcggacgacgtgtgcg 720
R* G A L D E Q A S H I Q V L S D D V C A 81 *Glutaredoxin domain*

ccaaccagcgagccatcgtctccatgtgccagattatgaccactgcgccccgccaggcg 780
N Q R A I V S M C Q I M T T A P R Q G G 101 Phosphorylation

gcttgggctgggtcggcggaaggggagcttccagagcgaccccccaagagccggagactc 840
L "G V V G G K G S F Q S D" P Q E P E T P 121 disordered|SUMOylation

cttcgcctgggatcggggacagcggttctgctgggtcgcgatcccaggagcaggaggaag 900
S P "G I G D S G" L L G R D P E D E E E E 141 Glutamic acid-rich

aggaagaagagaaggagatgccagccccgccacaccctccagtcactgtgagcggccccg 960
E E E K E M P S P A T P S S H C E R P E 161 Lysine acetylation

aaagcccctgtgctgggtctccttgggggggacgggccacttgtggagcccctcgacatgc 1020
S P C A "G L L G G D G" P L V E P L D M P 181 "N-Myristoylation site"

ccgacattaccctgctgcaactggagggcgaggcctccctgtgaggggactccgtggggc 1080
D I T L L O L E G E A S] L I 194 DoUF] highly Conserved

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tgtgtattccttctcaatgctttccttgggtgttaacctt**aat**aaaaaggcgtcatctccc 2280 **reg polyA**
ctc 2283**poly-A**