

Conceptual Translation of Human FAM131A¹

gcttttggttctctgcatcaacacagccagcatgcctatgatttctgtgctgggcaaa 58
[M P M I S V L G K 9 [excluded in isoform 2]

atgtttctgtggcagcgtgaaggcctggaggacgatggacttgtcagacaagtgcgaga 118
M F L W Q R E G P G G R W T C Q T S R R 29

gtgtcctcggacccccgcttgggctgtggagtggatcgaacttctcggggctctctctcta 178 ex1|ex2
V S S D P A W A V E W I E L P R G L S L 49

tcctctttgggatctgctcgaaccctccgaggctggagcaggtcctcccgccttctctcg 238
S S L G S A R T L R G W S R S S R P S S 69

gtggacagtcaggacttgcagagggtgaatggttgagacacagtcgcgatgctgcccaag 298 ex2|ex3
V D S Q D L P E V N V G D T V A] M L P K 89 excluded in isoform 2]

tcccgcgagccctaactatccaggagatcgctgcgctggccaggtcctccctgcatgggt 358 ex3|ex4
S R R A L T I Q E I A **A L A R S S L H G** 109

atttcccagggtggtgaaggaccacgtgaccaagcctaccgccatggcccagggccgagtg 418
I **S Q V V K D H V T K P T A M A Q G R V** 129

gctcacctcattgagtggaagggctggagcaagccgagtgactcacctgctgccctggaa 478
A H L I E W K G W S K P S D S P A A L E 149

tcagccttttctcctattcagacctcagcagggggaacaagaggctcgtcttgcagca 538
S A F S S Y S D L S E **G E Q E A R F A A** 169

ggagtggtgagcagtttgccatcgcggaagccaagctccgagcatggtcttcggtggat 598 ex4|ex5
G V A E Q F A I A E A K L R A W S S V D 189

ggcgaggactccactgatgactcctatgatgaggactttgctgggggaatggacacagac 658 ex5|ex6
G E D S T D D S Y D E D F A G G M D T D 209

atggctgggcagctgccccctggggccgcacctccaggacctgttcaccggccaccggttc 718
M A G Q L P L G P H L Q D L F T G H R F 229

tcccgccctgtgcccagggctccgtggagcctgagagcgactgctcacagaccgtgtcc 778
S R P V R Q G S V E P E S D C S Q T V S 249

ccagacaccctgtgctctagtctgtgcagcctggaggatgggttgttgggctccccggcc 838
P D T L **C S S L C S L E D G L L G S P A** 269

cggctggcctcccagctgctgggcgatgagctgcttctcgccaaactgccccccagccgg 898
R L A S Q L L G D E L L L A K L P P S R 289

¹ Translated NM_144635 mRNA sequence using Six-Frame_Translation tool at Bioline
<https://www.bioline.com/media/calculator/01_13.html>

gaaagtgccttccgcagcctgggcccactggaggcccaggactcactctacaactcgccc 958
E S A F R S L G P L E A Q D S L Y N S P 309

ctcacagagtcctgcctttccccgcggaggaggagccagccccctgcaaggactgccag 1018
L T E S C L S P A E E E P A P C K D C Q 329

ccactctgcccaccactaacgggcagctgggaacggcagcggcaagcctctgacctggcc 1078
P L C P P L T G S W E R Q R Q A S D L A 349 *disordered*

tcttctgggggtggtgtccttagatgaggatgaggcagagccagaggaacagtgaaccaca 1138
S S G V V S L D E D E A E P E E Q * 366

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cacaagcattctatatataagtggctcattaggtgtttattttgttctatthaagaatt 2398
gttttattaaattaaataaaatctttgtaaattctcta 2437 *Poly-A Sig|Sig|Site|Site*