

Human MIPOL1 isoform 1 (NM_001195297.1) annotated conceptual translation

aaaccagagacattgccagagcaaacaagaacagaaata **caa**atggagaactgggtcaaaa 660 **CDS start**|**caa**atgg:ribosome binding site
| M E N W S K 6 |absent in isoform 2
gacataaccacagttatcttgaacaagaaactacggggataaataaaaagtacgcagcca 720 **ex5|ex6**
D I T H S Y L E Q E T T G I N K S T Q P 26
gatgagcaactgactatgaattctgagaaaagtatgcatcggaaatccactgaattagtt 780
D E Q L T M N S E K S M H R K S T E L V 46
aatgaaataacatgtgagaacacagaatggccagggcagagatcaacgaattttcagatc 840
N E I T C E N T E W P G Q R S T N F Q I 66
atcagttcttatccagatgatgagtctgtttactgcactactgaaaaataca **ac**gttatg 900 **ex6|ex7**
I S S Y P D D E S V Y C T T E K Y N V M 86
gaacatagacataatgatatgcattatgaatgtatgactccttgtcaagttacttcagac 960
E H R H N D M H Y E C M T P C Q V T <S D 106 <106-340> COG1196 region¹
tcagataaagagaagacaatagcattttcttctaaaagaattggatattctcagaacaagc 1020
(S D K E K T I A F L L K **E L** D I L R T S 126 (coiled-coil domain 1)
aataaaaa**gc**ttcagcagaaattggctaaagaagataaagaacagagaaaactaaagttt 1080 **ex7|ex8**
N K K L Q Q K L A K E D K E Q R K L K F 146 **Bipartite NLS**
aagctggaactccaagagaaagaacagaagctaaaattgctgaaaagacagcagc**gc**tctg 1140 **ex8|ex9**
K L E L Q E K E T **E A K I A E K T A A L** 166 165-169 ALVEE → ERRGV in iso3
gttgaagaagtgtatTTTTGCGCAGAAGGAACGTGATGAAGCTGTTATGTCTAGACTGCAA 1200
V E E [V Y F A Q K E R D E A V | M S R L Q 186
ttagccattgaggagagagatgaagcaattgcacgagccaagcatatggaaatgtctcta 1260
L **A I E E R D E A I A R A K H M E M S L** 206
aaag**tg**ctagaaaatattaaccctgaagaaaatgacat**ga**cattacaggaattactgaac 1320 **ex9|ex10; ex10|ex11**
K V L E N I) N P E E N D M T L Q E **L L N** 226 **Conserved in all orthologs**
agaataaacaatgcagacacagggatagctattcagaagaatggagctataattgtggat 1380
R I N N A D T **G I A I Q K N G A I I V D** 246
agaatctacaagaccaaggaatgtaaaatgagaataactgcagaagaaatgagtgcacta 1440 {259-431} COG4372 region¹
R I Y K T K (E C K M R I {T A E **E M S A L** 266 (coiled-coil domain 2)
atagaagaacgggatgctgccttgtctaa**gt**gcaaacggttagagcaggagcttcatcat 1500 **ex11|ex12**
I E **E R D A A L S K C K R L E Q E L H H** 286
gtgaaagagcagaaccagacttcagcaacaacatgagacatctgactgctgaaaacaat 1560
V K E Q N Q T S A N N M R H L T A E N N 306
caagaacgtgctctga**gg**caaagttgttatctatgcaacaagccagagaaaactgcagtt 1620 **absent in isoform 2 |**
Q E R A L K A K L L S M Q Q A **R E T A V** 326 [absent in isoform 3
caacagtacaaaaaactggaagaggaaatccagacccttcgagtttactac**ag**ttttacac 1680 **ex13|ex14**
Q Q Y K K L E E E I Q T L R> V Y Y S L H 346
aaatctttatctcaagaagaaaatctgaaggatcagtttaactatacccttagtacatat 1740
K S L S Q E E N L K D Q F N Y T L S T Y 366
gaagaagcttttaaaaaacagagagaacattgtttccatcactcaacaacaaaatgaggaa 1800
E E A L K N R E N I V S I T Q Q Q N E E 386
ctggctactcaactgcaacaagctctgacagagcagcaaatatggaattacaacttcaa 1860
L A T Q **L Q Q A L T E R A N M E L Q L Q** 406
catgccagagaggcctccaagtggccaatgaaaaagttcaaa**ag**tttgaaaggctggtg 1920 **ex14|ex15**
H A R E A S Q V A N E K V Q K L E **R L V** 426
gatgtactgaggaagaaggttggaaaccgggaccatgaggacagtgatc**tg**attgaaaaaa 1980 **CDS stop**
D **V L R K} K V G T) G T M R T V I] *** 442 absent in isoform 3]

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