

1 ATGGGCTCACGCCTCTCATGTTCTTGCTCACAAGCCGAATGCTGGACGAATGATGAATCT
 1 M G S R L S C S C S Q A E C W T N D E S
 Myr?
 61 ACATTGAGAATTGACGCGGAGTTGTTTGAGTTATCACAGGACGGACAAAAGTGGGATAAG
 21 T L R I D A E L F E L S Q D G Q K W D K
 121 CTTGACGGAAGGCTGGCCAACGTACGTGTATTCAACGCATTTCGACGACTCTTCCCCACGT
 41 L D G R L A N V R V F N A F D D S S P R
 181 CTTCTTGCCACATCATCATCCGGTCAAGTTCTTCTGGACACTCTAATTCCAATGGGAGAA
 61 L L A T S S S G Q V L L D T L I P M G E
 241 AAGGTTTCATAAAGTCAGCGACTTTTTTGTGTATTTGAAGACGGAAGGAAGAACAATTGGA
 81 K V H K V S D F F V Y L K T E G R T I G
 301 TTCAATACGTTAAGCTCGAGGGACACTTCTTACTCATTTCTCAGGCGACAAATACAAC
 101 F N T L S S R D T S L L I S Q A T N T T
 361 GCCTTCAATATGTTTCAACATTCACTCTCAGTTTCCGTATCCAGAATTGCTACATTTGAA
 121 A F N M F Q H S F S V S V S R I A T F E
 421 GGTGATTCTATTCAACCTTGTGATGAGCAGCCAGAAACGTCAAATGTCTCACTAAATCCG
 141 G D S I Q P C D E Q P E T S N V S L N P
 481 TTAAATATGGTTTTCAACTACAAAGGATCACCTGTTGAGATTGATTTGCTGGAATGTTTC
 161 L N M V F N Y K G S P V E I D L L E C F
 541 GCGTGCTCATCAGAAGCTGAAAACGTGTGTCGACATAGCACATGCCAACACATATTTTCGT
 181 A C S S E A E N C V D I A H A N N I F R
 601 GTAATTGTGTCAGCACATGCTCATCTTTTTCTTATTCAAGCTCTGAATGTATCATCACTT
 201 V I V S A H A H L F L I Q A L N V S S L
 661 CTTCTTGCTCGAACCACCTCGAATCTAGTTGCCATCAATTATTTGGCTCGGCAAAATGAT
 221 L L A R T T S N L V A I N Y L A R Q N D
 721 AAAATTCAACAAAAATTGATTGCTCTGTTGGAAACATCAGAATCAAGTGAGAATGCGTGC
 241 K I Q Q K L I A L L E T S E S S E N A S
 781 AAGGAAGATATTCGACAAATGCTTCTTCTGAAGAATGTAGTAGTGACACAGAGATTGAAC
 261 K E D I R Q M L L L K N V V V T Q R L N
 841 TCACTTCAACAGAGAGCACTACCGGGAATTGAGCTTATCCAACACGATATCTCACCTCAA
 281 S L Q Q R A L P G I E L I Q H D I S P Q
 901 ATTGATCAGAAGCTACTCGAAAAGTGTGACTTCCATCACTGTTTTTATATCATTTTAAT
 301 I D Q K L L E K C R L P S L F L Y H F N
 961 ATGAATTCGTTTTCGAATATGGCGAAAACCAATGGAAACACGTGACATGAACACAATGGGA
 321 M N S F R I W R K P M E T R D M N T M G
 1021 TCATCAATGGCATCCACCAATCATGTGACAACCTATAATGGTACAACACTACGTTTCATACT
 341 S S M A S T N H V T T H N G T T T F H T
 1081 ACGAATCCCACAAAACCAAGACTTTTGTGAAGGATCGTTGGCTCCTGGATGCTCATTGGCC
 361 T N P T K P R L C E G S L A P G C S L A
 1141 GAGGCATCCGAACAGAGAAAACGAGAGATGGCGGAGCAGAAAAAAGAGTTGGCAGGCCCA
 381 E A S E Q R K R E M A E Q K K E L A G P
 1201 TCTTCCGAGAGGATTACTTTCGTGAGAAAGACAAATGGACGTCTTGGACTCACTATATAC
 401 S S A E D Y F V R K T N G R L G L T I Y
 1261 GCGCATAACGATGATGGGGTCATCAGGGCTGAG**GTTTCGTGGAGTGACGTCAATTTGCTCCG**
 421 A H N D D G V I R A E V R G V T S F A P

EVH1-like domain

1321 **AGATGTGCTCAAGTTGGAGATTCGGTTGTAGCGGTAGACAGTGAACATCATATCATCAGTT**
441 R C A Q V G D S V V A V D S E L I S S V **PDZ-like domain**

1381 **AGAAACGCTTCGGATGTTGAGAACTTTTGAGAATCGGAAAAGTAATACATTTACGAAGA**
461 R N A S D V E K L L R I G K V I H L R R

1441 **AAGACTCCTCTAACTCCAAGAGCACCGTCTCAACTCGACGCAACTAATGTCAATAAGAAA**
481 K T P L T P R A P S Q L D A T N V N K K **removed by tm1556**

1501 **ACGGGCTGTGCAAAGTTGGCGATGGCTCTGCAAGAATTGTTGGTCACTGAGAAGAAATAT**
501 T G C A K L A M A L Q E L L V T E K K Y

1561 **GTCAGCGATCTTCGAGAGATGAATGAAGTTTTTCTGTGTATGAGACAAGTCCGAGATATT**
521 V S D L R E M N E V F L C M R Q V R D I

1621 **ATGAATGCAGCAATACGGTTGTATAAAATGCAAACATCGTTTGTGGACAGTATTGAGGAA**
541 M N A A I R L Y K M Q T S F V D S I E E

1681 **GCCATTGGAGACATGAGTAGACAGGATATTTCTGTTGCTCAGATTAGGGATTCTGTAATG**
561 A I G D M S R Q D I S V A Q I R D S V M

1741 **CGAGTGTGTGCAGTATTCATCAACAAATGTTCTGATTTCAAATCTATGCAGAATATGCA**
581 R V C A V F I N K C S D F K I Y A E Y A **DH domain**

1801 **CCCGGTTACCATCTCCTCCAACATGAGATCAAAAACAAAAAGAGCTTCTATCAAAATTG**
601 A G Y H L L Q H E I K N K K E L L S K L

1861 **GAAGCTGTAAACAGTACAAGAGAGCAACATTGTTCTTGGGAATCTCGGATGATTAAACCA**
621 E A V N S T R E Q H C S W E S R M I K P **removed by ok772**

1921 **GTCCAGAGAATTGTACAATATCCACTTTTACTGAAAAACATTGCCGATGCACTTCCGAAG**
641 V Q R I V Q Y P L L L K N I A D A L P K

1981 **GATGCACGAGAGAGGGTTCAAGTGGAGGCAGCATTGCAAAAAATGCAGACGTCTGCAGAA**
661 D A R E R V Q V E A A L Q K M Q T S A E

2041 **TATGTGAATGAAATGCAAAGGCTTCATGAAGATTATGCACAATATATGGAGACTGTTAGG**
681 Y V N E M Q R L H E D Y A Q Y M E T V R

2101 **AAAGCTAATGAGCCAATGTTGGCTGAAAAGAGTCTTCGCCTCGACACTCGAGAGCTTCTA**
701 K A N E P M L A E K S L R L D T R E L L

2161 **GTTTTTGCACACATAAAATGGAGAGATGCTCCAGCGGAGCACTACGTTGTGTTCTGTTT**
721 V F A H I K W R D A P A E H Y V V F V F

2221 **CACTCTTTAATACTGCTCCTTCCATCGTATGCTAGGAAAGAGATTAAGATGAAATGGACT**
741 H S L I L L L P S Y A R K E I K M K W T **PH domain**

2281 **CGTGTCTCCCAATAAATGAAGTTGATATCAACGAAATGCCAAATGATGCATTAATCTA**
761 R V L P I N E V D I N E M P N D A L N L

2341 **AAACTTTATCATGCTGCTTTTTGAAGGACCAAATGGACAATTAAGTCATTCCAATCCAAT**
781 K L Y H A A F E G P N G Q L S H S N P N

2401 **ACAGTCTACAATATTGAATGTTGTCAATCTCAACTGAAACAGCATCTTATCAAAAATATC**
801 T V Y N I E C C Q S Q L K Q H L I K N I

2461 **AAAAAAGCTCGAACTTTATTCTCTCGAGAATCACATCGTCCATTAAGTGATCTAGTCAA**
821 K K A R T L F S R E S H R P L S G S S Q

2521 **TCGGATGGTGGTTATGTGTGAGAAGTCTCTAAGGAACATCGAAATTCAAAATAG**
841 S D G G Y V S E V S K E H R N S K *