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tgcgctttaggctcaccgcgggcgaagcgggagaagccaggtgcctcaataaacatggccgcca
gcgtcaaccggctcgggagggcgcgctgcccgttgggaatgcaggtttggcgt

H P A R N H V M Q E V P E A A G L A R V
3 caccggcccggaaccacgtgatgcaggaggtgcccgaggcgggggctcgcgagggtg 62
E P P R R S. S. G V G A A R L R F P G G S

63 gagccgctcggcgttcgagcgggtgggggctgccggttgagatttcccgggggtcc 122
R P L R A R A C V L A L A V L A L P E R

123 cggcctctgcgtgcacggcctgcgtgctcgcgctcgcgggttctggcgctgccggaaagg 182
N N A D S. M S A H S. M L C E R I A I A K

183 aataatgctgacagcatgtctgcacattccatgctctgtgaacgaatcgccatagccaag 242
E L I K R A E S. L S. R S. R K G G I E G G

243 gaactgatcaagagagcagaaatcactttctagatcaagaaaaggctggcatagaagggtgt 302
A K L C S K L K A E L K F L Q K V E A G

303 gcaaagctgtgcagcaaattgaaggcagaattaaaattcttgcagaaagtagaagctggg 362
K V A I K E S H L Q S T N L T H L R A I

363 aaagtagctattaagagtctcatttacagagcactaacctaacacacctgagagccatt 422
V E S. A E N L E E V V S V L H V E G Y T

423 gtggaatcagcagaaaacctggaagaagttgttagtgcttctcatgtctttggttataca 482
D T. L G E K Q T. L V V D V V A N G G H T

483 gataccttaggagaaaagcaaacccttgtggtagatgtagttgcaaatgggtggtcatact 542
W V K A I G R K A E A L H N I W L G R G

543 tgggtgaaagccattggcgggaaggctgaagctcttcataacatctggctgggcaggggc 602
Q Y G D K S. I I E Q A E D F L Q A S H Q

603 caatatggtgacaaaagcatcattgagcaggctgaagacttctccaggccagtcaccag 662
Q P V Q Y S N P H I I F A F Y N S V S S.

663 cagccagtgcagtatagcaaccctcacatcatctttgcattttacaacagtgctctccagc 722
P M A E K L K E M G I S. V R G D I V A V

723 cccatggcagagaagctgaaagaaatgggcatactctgtgagaggagacatagtagcagtc 782
N A L L D H P E E L Q P S. E S. E S. D D E

783 aacgctctgttagatcaccctgaagagcttcaaccaagtgagagtgaatcagatgatgag 842
G P E L L Q V T/TR V D R E N I L A S V A

843 ggcctgaacttttgcaggtgatgcagagttgaccgagaaaatatactagcaagtggttgcg 902
F P T E I K V D V C K R V N L D I T T L

903 tttccaacagaaattaaggtcgatgtgtgcaaaagagtaaatctggacattactacttta 962

I T Y **V S** A L S. Y G **G** C H F I **F K E** K V
 963 **atcacatatgtatctgcctcagctatggaggctgccactttatatttcaagagaaagtg** 1022
 L T E Q A E Q **E R** K E Q V L P Q L E A F
 1023 **ctcacagaacaagcagagcaagagaggaaagagcaggttctacctcagctggaggccttt** 1082
 M K D K E **L** F A **C** E S **A** V K D F Q S **L** L
 1083 **atgaaggacaaggagttgtttgcttgtgaatctgctgtcaaggactttcagtctatttta** 1142
D T L **G G** P G **E R E R** A T V **L** I K R I N
 1143 **gataccttaggaggacctggggagagagagagggccactgtgttaattaagcgaattaat** 1202
V V P D Q P S. E R A L R **L** V A S S. K I N
 1203 **gtggtaccagaccagccttctgagcgtgccttgagactagtggccagttcaaaaattaat** 1262
 S. R S L T. I **F** G T G D T. L K A I **T M T A**
 1263 **agccgctcattaacaatttttgggacgggagacaccctaaaagccatcacaatgactgct** 1322
N S G **F** V R A A N N Q G V K F S V F I H
 1323 **aatagtggttttgtcagagctgcaaacaccagggtgttaatttagtggtttatccat** 1382
 Q P R A L T. E S. K E A L A T P L P K D Y
 1383 **cagcccagagcacttactgagagtaaagaggctctagccacccttaccaaaagactac** 1442
 T T D S E H * R Y P L N I F V E V S Y L
 1443 **acaactgacagtgaacact**aaagataccctttaaatatttttgtggaagtaagttattta 1502
 1503 taccaaaggctgggtcttcccatctaaactgggtgggaaaaaaggctctatagtaaaagtaa 1562
 1563 aactgagaactcttaaacagtagagtttctttgtctctcatctaaagtatataacctcc 1622
 1623 caaagtagaaaaagcacaagagagaagcttatctatcaaactgtc**tgccattagtgca**att 1682
 1683 aagaaccgaaatacgtctatataaagctttcagctgtattgtaatactttgattcgatag 1742
 1743 ggctacaactcccctactgctaa**ccacatttcatggaatatgg**ctacattgcacattgca 1802
 1803 ttaaatatctggagaaaattcaaaaaaaaaaaaaaaaaaaaaa | 1844

Legend:

- XXX= Linker region between domains
- XXX**= Domain 1
- XXX**= Domain 2
- XXX**=Conserved AA
- XXX=Hydrophobic domains
- XXX= Glycosylation
- X.= Phosphorylation site
- = Alpha helix region
- = Beta strand region
- = Coil region
- XXX** = Possible stem loop formation
- XXX** =Exon X