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<!-- saved from url=(0043)http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi -->
<html><head><meta http-equiv="Content-Type" content="text/html; charset=ISO-8859-1"></head><body><p><!--
QBlastInfoBegin
        Status=READY
QBlastInfoEnd
--></p><p>
</p><pre>BLASTN 2.2.26+
Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and
Webb Miller (2000), "A greedy algorithm for aligning DNA
sequences", J Comput Biol 2000; 7(1-2):203-14.


RID: XCUPTGJ401S


Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
           16,175,421 sequences; 41,344,666,538 total letters
Query=
Length=17476


                                                                 Score        E
Sequences producing significant alignments:                     (Bits)     Value

emb|AM902716.1|  Bordetella petrii strain DSM 12804, complete ...  3.227e+04  0.0
gb|CP000884.1|  Delftia acidovorans SPH-1, complete genome         3.110e+04  0.0
dbj|AP012280.1|  Pseudomonas aeruginosa NCGM2.S1 DNA, complete...  1.658e+04  0.0
gb|CP002738.1|  Methylomonas methanica MC09, complete genome       4486       0.0
gb|CP002475.1|  Streptomyces flavogriseus ATCC 33331, complete...  56.5       0.002

ALIGNMENTS
&gt;emb|AM902716.1| Bordetella petrii strain DSM 12804, complete genome
Length=5287950

 Features in this part of subject sequence:
   hypothetical protein predicted by Glimmer/Critica
   hypothetical protein predicted by Glimmer/Critica

 Score = 3.227e+04 bits (17476),  Expect = 0.0
 Identities = 17476/17476 (100%), Gaps = 0/17476 (0%)
 Strand=Plus/Plus

CDS: Putative 1       1                                V  G  D  N  G  R  Y  T  K  T  D
Query                 1        GGATCGAGACGCAAGGGCGAACCTTTGTGGGCGACAACGGACGCTACACAAAAACAGATT  60
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4495886  GGATCGAGACGCAAGGGCGAACCTTTGTGGGCGACAACGGACGCTACACAAAAACAGATT  4495945
CDS:hypothetical pro  1                                M  G  D  N  G  R  Y  T  K  T  D
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CDS: Putative 1       12       L  I  V  T  D  L  R  V  P  V  I  L  G  R  G  E  G  M  G  A
Query                 61       TGATAGTCACCGACTTGCGGGTTCCGGTCATTCTGGGGCGTGGTGAGGGCATGGGGGCTC  120
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4495946  TGATAGTCACCGACTTGCGGGTTCCGGTCATTCTGGGGCGTGGTGAGGGCATGGGGGCTC  4496005
CDS:hypothetical pro  12       L  I  V  T  D  L  R  V  P  V  I  L  G  R  G  E  G  M  G  A

CDS: Putative 1       32       P  V  G  G  S  M  A  F  E  V  K  C  G  K  A  E  Y  L  Y  S
Query                 121      CGGTGGGCGGCTCGATGGCATTCGAAGTGAAATGCGGCAAGGCGGAATACCTCTATTCGC  180
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496006  CGGTGGGCGGCTCGATGGCATTCGAAGTGAAATGCGGCAAGGCGGAATACCTCTATTCGC  4496065
CDS:hypothetical pro  32       P  V  G  G  S  M  A  F  E  V  K  C  G  K  A  E  Y  L  Y  S

CDS: Putative 1       52       Q  K  D  H  M  I  F  Q  A  E  G  H  K  Q  A  D  A  Q  C  T
Query                 181      AGAAAGATCACATGATTTTTCAGGCTGAAGGGCACAAGCAAGCAGATGCGCAATGCACTC  240
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496066  AGAAAGATCACATGATTTTTCAGGCTGAAGGGCACAAGCAAGCAGATGCGCAATGCACTC  4496125
CDS:hypothetical pro  52       Q  K  D  H  M  I  F  Q  A  E  G  H  K  Q  A  D  A  Q  C  T

CDS: Putative 1       72       L  C  S  R  D  I  H  D  L  P  E  E  K  Q  K  E  L  R  D  A
Query                 241      TTTGCTCGCGAGATATCCACGATTTGCCAGAAGAAAAACAGAAAGAACTGCGCGACGCCT  300
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496126  TTTGCTCGCGAGATATCCACGATTTGCCAGAAGAAAAACAGAAAGAACTGCGCGACGCCT  4496185
CDS:hypothetical pro  72       L  C  S  R  D  I  H  D  L  P  E  E  K  Q  K  E  L  R  D  A

CDS: Putative 1       92       L  R  E  A  G  S  P  M  V  G  M  L  P  R  K  N  E  I  D  Q
Query                 301      TGCGCGAAGCTGGCTCACCAATGGTGGGAATGTTGCCAAGGAAAAATGAAATAGATCAGT  360
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496186  TGCGCGAAGCTGGCTCACCAATGGTGGGAATGTTGCCAAGGAAAAATGAAATAGATCAGT  4496245
CDS:hypothetical pro  92       L  R  E  A  G  S  P  M  V  G  M  L  P  R  K  N  E  I  D  Q

CDS: Putative 1       112      S  C  L  D  F  I  R  Q  N  E  E  E  Q  P  *
CDS: Putative 2       1                                                M  K  I  R  F  A  I
Query                 361      CCTGTCTTGATTTCATCCGCCAAAACGAGGAGGAGCAACCATGAAAATACGTTTCGCAAT  420
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496246  CCTGTCTTGATTTCATCCGCCAAAACGAGGAGGAGCAACCATGAAAATACGTTTCGCAAT  4496305
CDS:hypothetical pro  112      S  C  L  D  F  I  R  Q  N  E  E  E  Q  P
CDS:hypothetical pro  1                                                M  K  I  R  F  A  I

CDS: Putative 2       8          I  S  H  D  L  L  A  Q  V  R  A  E  V  D  V  L  L  H  A  V
Query                 421      TATTAGCCATGACCTTCTCGCACAAGTCCGGGCTGAAGTTGATGTCCTCCTGCATGCAGT  480
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496306  TATTAGCCATGACCTTCTCGCACAAGTCCGGGCTGAAGTTGATGTCCTCCTGCATGCAGT  4496365
CDS:hypothetical pro  8          I  S  H  D  L  L  A  Q  V  R  A  E  V  D  V  L  L  H  A  V

CDS: Putative 2       28         N  V  G  D  M  D  G  V  D  A  S  T  A  R  L  L  E  L  T  V
Query                 481      AAATGTCGGAGATATGGATGGCGTGGATGCGTCCACCGCACGCCTCTTGGAGCTGACAGT  540
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496366  AAATGTCGGAGATATGGATGGCGTGGATGCGTCCACCGCACGCCTCTTGGAGCTGACAGT  4496425
CDS:hypothetical pro  28         N  V  G  D  M  D  G  V  D  A  S  T  A  R  L  L  E  L  T  V
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CDS: Putative 2       48          D  C  R  S  I  E  L  S  E  E  E  W  R  A  F  L  S  E  I  R
Query                 541      TGATTGCAGATCGATTGAGTTGTCCGAGGAAGAGTGGCGCGCATTTCTAAGCGAAATCAG  600
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496426  TGATTGCAGATCGATTGAGTTGTCCGAGGAAGAGTGGCGCGCATTTCTAAGCGAAATCAG  4496485
CDS:hypothetical pro  48          D  C  R  S  I  E  L  S  E  E  E  W  R  A  F  L  S  E  I  R

CDS: Putative 2       68          A  K  N  P  E  F  E  S  S  Y  L  L  P  G  T  I  C  A  P  L
Query                 601      GGCCAAGAACCCTGAGTTCGAATCGAGCTACTTGTTGCCTGGGACTATTTGCGCGCCCCT  660
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496486  GGCCAAGAACCCTGAGTTCGAATCGAGCTACTTGTTGCCTGGGACTATTTGCGCGCCCCT  4496545
CDS:hypothetical pro  68          A  K  N  P  E  F  E  S  S  Y  L  L  P  G  T  I  C  A  P  L

CDS: Putative 2       88          F  P  N  L  S  V  A  D  D  Y  V  L  E  L  P  I  D  G  D  M
Query                 661      GTTTCCAAACCTCTCGGTAGCTGACGACTATGTTCTCGAACTTCCAATCGATGGTGATAT  720
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496546  GTTTCCAAACCTCTCGGTAGCTGACGACTATGTTCTCGAACTTCCAATCGATGGTGATAT  4496605
CDS:hypothetical pro  88          F  P  N  L  S  V  A  D  D  Y  V  L  E  L  P  I  D  G  D  M

CDS: Putative 2       108         E  E  E  E  A  N  V  *
Query                 721      GGAAGAGGAGGAAGCTAATGTTTGATGAGGCCTTTGGAATGGCTGCGATGTGCGCTGGAA  780
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496606  GGAAGAGGAGGAAGCTAATGTTTGATGAGGCCTTTGGAATGGCTGCGATGTGCGCTGGAA  4496665
CDS:hypothetical pro  108         E  E  E  E  A  N  V

Query                 781      AATTTCGCGAGGGAGTGCGTGATACGTTCGGCGCGTCCATTGTTGCTGATGTACTTGATC  840
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496666  AATTTCGCGAGGGAGTGCGTGATACGTTCGGCGCGTCCATTGTTGCTGATGTACTTGATC  4496725

Query                 841      CGATTCTCAAGGAAGTCGATTCACTCCGCATTTTCAATGCGGCTTACCAGCAGCAATCGC  900
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496726  CGATTCTCAAGGAAGTCGATTCACTCCGCATTTTCAATGCGGCTTACCAGCAGCAATCGC  4496785

Query                 901      TCGCCATTGATCGAACTTTGAATGACGTTCGCGAGCTCCAGTTCAAAGACAGTGGGTGGA  960
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496786  TCGCCATTGATCGAACTTTGAATGACGTTCGCGAGCTCCAGTTCAAAGACAGTGGGTGGA  4496845

CDS: Putative 3       1               M  S  E  S  A  K  D  F  Q  S  V  I  F  K  L  H  K  A  I
Query                 961      ATCAATGAGTGAAAGCGCGAAGGATTTTCAGAGCGTAATTTTCAAGCTACACAAGGCAAT  1020
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496846  ATCAATGAGTGAAAGCGCGAAGGATTTTCAGAGCGTAATTTTCAAGCTACACAAGGCAAT  4496905
CDS:hypothetical con  1               M  S  E  S  A  K  D  F  Q  S  V  I  F  K  L  H  K  A  I

CDS: Putative 3       20          A  D  Y  Q  E  G  C  A  R  I  D  R  E  F  N  A  T  K  K  T
Query                 1021     TGCGGACTATCAAGAAGGTTGTGCGCGCATCGACCGCGAATTCAATGCCACTaaaaaaaC  1080
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4496906  TGCGGACTATCAAGAAGGTTGTGCGCGCATCGACCGCGAATTCAATGCCACTAAAAAAAC  4496965
CDS:hypothetical con  20          A  D  Y  Q  E  G  C  A  R  I  D  R  E  F  N  A  T  K  K  T

CDS: Putative 3       40          L  N  E  D  Q  E  R  N  R  S  I  R  K  S  N  W  Q  A  G  F
Query                 1081     ATTGAACGAAGACCAGGAGCGCAATCGGAGCATAAGGAAGTCGAATTGGCAGGCAGGCTT  1140
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4496966   ATTGAACGAAGACCAGGAGCGCAATCGGAGCATAAGGAAGTCGAATTGGCAGGCAGGCTT  4497025
CDS:hypothetical con   40          L  N  E  D  Q  E  R  N  R  S  I  R  K  S  N  W  Q  A  G  F

CDS: Putative 3        60          V  R  E  W  E  S  N  A  T  A  I  A  N  A  S  A  Q  L  R  Q
Query                  1141      TGTCAGAGAGTGGGAAAGTAATGCAACTGCTATAGCGAACGCAAGTGCACAGCTTAGACA  1200
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4497026   TGTCAGAGAGTGGGAAAGTAATGCAACTGCTATAGCGAACGCAAGTGCACAGCTTAGACA  4497085
CDS:hypothetical con   60          V  R  E  W  E  S  N  A  T  A  I  A  N  A  S  A  Q  L  R  Q

CDS: Putative 3        80          H  Q  P  A  F  V  D  F  C  V  D  K  P  L  M  A  S  E  I  P
Query                  1201      ACATCAGCCTGCCTTCGTGGATTTTTGTGTAGACAAGCCATTGATGGCATCGGAAATTCC  1260
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4497086   ACATCAGCCTGCCTTCGTGGATTTTTGTGTAGACAAGCCATTGATGGCATCGGAAATTCC  4497145
CDS:hypothetical con   80          H  Q  P  A  F  V  D  F  C  V  D  K  P  L  M  A  S  E  I  P

CDS: Putative 3        100         A  G  L  V  L  G  S  E  Q  V  S  F  E  K  L  S  C  Q  S  P
Query                  1261      AGCAGGTCTTGTGCTTGGCTCGGAGCAAGTCTCTTTTGAGAAGCTCTCTTGTCAATCCCC  1320
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4497146   AGCAGGTCTTGTGCTTGGCTCGGAGCAAGTCTCTTTTGAGAAGCTCTCTTGTCAATCCCC  4497205
CDS:hypothetical con   100         A  G  L  V  L  G  S  E  Q  V  S  F  E  K  L  S  C  Q  S  P

CDS: Putative 3        120         K  V  I  S  F  P  F  S  S  A  L  V  F  P  Q  G  D  A  E  K
Query                  1321      AAAAGTCATCTCTTTCCCCTTCTCCAGCGCTCTTGTTTTTCCGCAAGGCGATGCGGAGAA  1380
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4497206   AAAAGTCATCTCTTTCCCCTTCTCCAGCGCTCTTGTTTTTCCGCAAGGCGATGCGGAGAA  4497265
CDS:hypothetical con   120         K  V  I  S  F  P  F  S  S  A  L  V  F  P  Q  G  D  A  E  K

CDS: Putative 3        140         K  R  L  A  H  C  L  L  L  R  L  L  S  A  L  P  A  G  Q  V
Query                  1381      GAAAAGACTCGCGCATTGTCTCTTGTTGCGGTTGCTGTCGGCTTTGCCTGCAGGTCAAGT  1440
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4497266   GAAAAGACTCGCGCATTGTCTCTTGTTGCGGTTGCTGTCGGCTTTGCCTGCAGGTCAAGT  4497325
CDS:hypothetical con   140         K  R  L  A  H  C  L  L  L  R  L  L  S  A  L  P  A  G  Q  V

CDS: Putative 3        160         E  L  T  L  I  D  P  L  Q  Q  G  Q  S  V  E  P  F  L  P  L
Query                  1441      AGAGTTGACACTGATTGACCCCCTACAGCAGGGTCAATCGGTCGAGCCGTTCCTACCATT  1500
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4497326   AGAGTTGACACTGATTGACCCCCTACAGCAGGGTCAATCGGTCGAGCCGTTCCTACCATT  4497385
CDS:hypothetical con   160         E  L  T  L  I  D  P  L  Q  Q  G  Q  S  V  E  P  F  L  P  L

CDS: Putative 3        180         L  K  V  E  Q  L  V  P  Q  G  H  V  L  T  R  A  D  E  I  E
Query                  1501      GCTGAAGGTTGAGCAATTGGTGCCGCAAGGTCATGTTCTTACTCGTGCGGACGAAATCGA  1560
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4497386   GCTGAAGGTTGAGCAATTGGTGCCGCAAGGTCATGTTCTTACTCGTGCGGACGAAATCGA  4497445
CDS:hypothetical con   180         L  K  V  E  Q  L  V  P  Q  G  H  V  L  T  R  A  D  E  I  E

CDS: Putative 3        200         A  A  L  G  Q  L  T  D  E  I  E  E  L  I  Q  L  R  F  N  E
Query                  1561      AGCAGCGCTCGGACAACTGACGGACGAAATTGAGGAGCTGATCCAGCTGCGGTTCAATGA  1620
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4497446   AGCAGCGCTCGGACAACTGACGGACGAAATTGAGGAGCTGATCCAGCTGCGGTTCAATGA  4497505
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CDS:hypothetical con  200        A  A  L  G  Q  L  T  D  E  I  E  E  L  I  Q  L  R  F  N  E

CDS: Putative 3       220        K  A  S  N  W  L  K  Y  N  A  V  Q  P  D  A  P  L  P  Y  K
Query                 1621     GAAGGCATCCAACTGGTTGAAATACAACGCAGTTCAACCCGATGCCCCGTTGCCTTACAA  1680
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4497506  GAAGGCATCCAACTGGTTGAAATACAACGCAGTTCAACCCGATGCCCCGTTGCCTTACAA  4497565
CDS:hypothetical con  220        K  A  S  N  W  L  K  Y  N  A  V  Q  P  D  A  P  L  P  Y  K

CDS: Putative 3       240        V  V  L  L  F  D  V  P  E  Q  I  S  E  K  S  L  W  L  L  G
Query                 1681     GGTAGTACTGCTCTTTGATGTGCCAGAGCAGATATCGGAAAAATCTCTTTGGCTCCTTGG  1740
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4497566  GGTAGTACTGCTCTTTGATGTGCCAGAGCAGATATCGGAAAAATCTCTTTGGCTCCTTGG  4497625
CDS:hypothetical con  240        V  V  L  L  F  D  V  P  E  Q  I  S  E  K  S  L  W  L  L  G

CDS: Putative 3       260        R  I  C  E  N  G  P  R  C  G  V  L  P  I  I  A  I  D  E  Q
Query                 1741     ACGCATCTGCGAAAACGGTCCACGCTGCGGCGTGCTGCCCATCATTGCAATTGATGAGCA  1800
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4497626  ACGCATCTGCGAAAACGGTCCACGCTGCGGCGTGCTGCCCATCATTGCAATTGATGAGCA  4497685
CDS:hypothetical con  260        R  I  C  E  N  G  P  R  C  G  V  L  P  I  I  A  I  D  E  Q

CDS: Putative 3       280        R  M  E  D  R  R  Y  E  K  L  N  A  T  L  K  N  S  T  T  Q
Query                 1801     GCGCATGGAAGACCGGCGATATGAAAAGCTCAACGCCACGCTGAAAAACTCAACCACGCA  1860
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4497686  GCGCATGGAAGACCGGCGATATGAAAAGCTCAACGCCACGCTGAAAAACTCAACCACGCA  4497745
CDS:hypothetical con  280        R  M  E  D  R  R  Y  E  K  L  N  A  T  L  K  N  S  T  T  Q

CDS: Putative 3       300        L  N  D  L  L  Q  R  A  G  A  G  G  L  S  F  T  Y  Q  P  E
Query                 1861     ACTGAATGATCTCTTGCAACGCGCTGGGGCTGGTGGGCTGTCATTCACATATCAACCGGA  1920
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4497746  ACTGAATGATCTCTTGCAACGCGCTGGGGCTGGTGGGCTGTCATTCACATATCAACCGGA  4497805
CDS:hypothetical con  300        L  N  D  L  L  Q  R  A  G  A  G  G  L  S  F  T  Y  Q  P  E

CDS: Putative 3       320        Q  W  P  R  Q  D  V  L  D  G  F  I  A  R  L  A  E  D  C  A
Query                 1921     GCAATGGCCGCGACAAGATGTGCTGGATGGCTTTATCGCAAGGCTCGCTGAAGATTGTGC  1980
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4497806  GCAATGGCCGCGACAAGATGTGCTGGATGGCTTTATCGCAAGGCTCGCTGAAGATTGTGC  4497865
CDS:hypothetical con  320        Q  W  P  R  Q  D  V  L  D  G  F  I  A  R  L  A  E  D  C  A

CDS: Putative 3       340        A  R  T  R  F  K  K  T  M  A  D  L  W  T  S  F  G  K  E  E
Query                 1981     TGCTAGGACGCGCTTCAAGAAAACGATGGCTGATCTCTGGACGAGCTTCGGCAAGGAAGA  2040
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4497866  TGCTAGGACGCGCTTCAAGAAAACGATGGCTGATCTCTGGACGAGCTTCGGCAAGGAAGA  4497925
CDS:hypothetical con  340        A  R  T  R  F  K  K  T  M  A  D  L  W  T  S  F  G  K  E  E

CDS: Putative 3       360        T  T  L  G  G  F  D  I  P  I  G  W  T  S  A  G  D  L  A  T
Query                 2041     GACGACTCTTGGTGGCTTTGATATTCCCATCGGCTGGACGAGCGCCGGCGACCTCGCGAC  2100
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4497926  GACGACTCTTGGTGGCTTTGATATTCCCATCGGCTGGACGAGCGCCGGCGACCTCGCGAC  4497985
CDS:hypothetical con  360        T  T  L  G  G  F  D  I  P  I  G  W  T  S  A  G  D  L  A  T
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CDS: Putative 3       380        L  R  L  G  A  T  D  S  E  H  H  V  L  L  A  G  K  T  G  S
Query                 2101     CCTGAGACTGGGCGCGACGGACTCCGAGCATCATGTACTGCTTGCGGGGAAGACAGGCTC  2160
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4497986  CCTGAGACTGGGCGCGACGGACTCCGAGCATCATGTACTGCTTGCGGGGAAGACAGGCTC  4498045
CDS:hypothetical con  380        L  R  L  G  A  T  D  S  E  H  H  V  L  L  A  G  K  T  G  S

CDS: Putative 3       400        G  K  S  N  L  L  H  V  L  I  H  T  L  C  E  K  Y  P  T  E
Query                 2161     GGGAAAATCCAATCTGCTCCATGTTTTGATTCACACGTTATGCGAGAAATATCCGACCGA  2220
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4498046  GGGAAAATCCAATCTGCTCCATGTTTTGATTCACACGTTATGCGAGAAATATCCGACCGA  4498105
CDS:hypothetical con  400        G  K  S  N  L  L  H  V  L  I  H  T  L  C  E  K  Y  P  T  E

CDS: Putative 3       420        E  L  D  L  Y  L  L  D  Y  K  E  S  T  E  F  N  I  Y  A  T
Query                 2221     GGAGCTTGATCTTTATCTACTGGATTACAAGGAATCGACTGAGTTCAATATTTACGCAAC  2280
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4498106  GGAGCTTGATCTTTATCTACTGGATTACAAGGAATCGACTGAGTTCAATATTTACGCAAC  4498165
CDS:hypothetical con  420        E  L  D  L  Y  L  L  D  Y  K  E  S  T  E  F  N  I  Y  A  T

CDS: Putative 3       440        P  P  V  P  Q  A  R  L  V  A  T  E  S  D  P  E  Y  G  V  T
Query                 2281     GCCCCCAGTCCCACAGGCCCGCCTTGTCGCTACGGAAAGTGACCCTGAATATGGCGTCAC  2340
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4498166  GCCCCCAGTCCCACAGGCCCGCCTTGTCGCTACGGAAAGTGACCCTGAATATGGCGTCAC  4498225
CDS:hypothetical con  440        P  P  V  P  Q  A  R  L  V  A  T  E  S  D  P  E  Y  G  V  T

CDS: Putative 3       460        V  L  R  H  L  V  D  E  L  E  T  R  A  R  I  F  K  S  K  N
Query                 2341     TGTATTAAGGCATCTTGTGGATGAACTGGAAACGCGTGCACGCATATTCAAGTCAAAAAA  2400
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4498226  TGTATTAAGGCATCTTGTGGATGAACTGGAAACGCGTGCACGCATATTCAAGTCAAAAAA  4498285
CDS:hypothetical con  460        V  L  R  H  L  V  D  E  L  E  T  R  A  R  I  F  K  S  K  N

CDS: Putative 3       480        V  N  D  F  S  E  Y  R  K  S  S  G  V  R  L  P  R  A  L  L
Query                 2401     TGTCAACGATTTCAGCGAATACCGTAAATCAAGCGGGGTACGGTTGCCCCGCGCTCTGCT  2460
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4498286  TGTCAACGATTTCAGCGAATACCGTAAATCAAGCGGGGTACGGTTGCCCCGCGCTCTGCT  4498345
CDS:hypothetical con  480        V  N  D  F  S  E  Y  R  K  S  S  G  V  R  L  P  R  A  L  L

CDS: Putative 3       500        V  I  D  E  F  Q  I  L  F  S  E  S  R  Q  V  A  E  A  A  E
Query                 2461     AGTCATAGATGAGTTCCAAATTCTGTTCTCAGAAAGTCGCCAGGTGGCAGAAGCTGCTGA  2520
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4498346  AGTCATAGATGAGTTCCAAATTCTGTTCTCAGAAAGTCGCCAGGTGGCAGAAGCTGCTGA  4498405
CDS:hypothetical con  500        V  I  D  E  F  Q  I  L  F  S  E  S  R  Q  V  A  E  A  A  E

CDS: Putative 3       520        Q  L  L  S  K  L  L  K  Q  G  R  S  F  G  I  H  I  L  L  A
Query                 2521     GCAGCTGCTGTCGAAGCTCTTGAAACAGGGGCGCTCGTTCGGTATTCACATCCTCCTGGC  2580
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4498406  GCAGCTGCTGTCGAAGCTCTTGAAACAGGGGCGCTCGTTCGGTATTCACATCCTCCTGGC  4498465
CDS:hypothetical con  520        Q  L  L  S  K  L  L  K  Q  G  R  S  F  G  I  H  I  L  L  A

CDS: Putative 3       540        T  Q  T  L  K  G  I  N  A  Q  S  I  G  S  I  I  T  Q  L  G
Query                 2581     TACTCAGACTTTGAAAGGCATCAACGCGCAGTCAATCGGAAGCATCATCACCCAGTTGGG  2640
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4498466   TACTCAGACTTTGAAAGGCATCAACGCGCAGTCAATCGGAAGCATCATCACCCAGTTGGG  4498525
CDS:hypothetical con   540         T  Q  T  L  K  G  I  N  A  Q  S  I  G  S  I  I  T  Q  L  G

CDS: Putative 3        560         C  R  I  A  L  A  C  G  Q  E  D  S  A  M  I  L  G  G  G  N
Query                  2641      ATGCCGTATCGCACTGGCTTGTGGGCAGGAAGACTCCGCAATGATCCTCGGGGGCGGGAA  2700
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4498526   ATGCCGTATCGCACTGGCTTGTGGGCAGGAAGACTCCGCAATGATCCTCGGGGGCGGGAA  4498585
CDS:hypothetical con   560         C  R  I  A  L  A  C  G  Q  E  D  S  A  M  I  L  G  G  G  N

CDS: Putative 3        580         W  A  A  A  E  L  R  S  P  P  E  G  I  I  N  N  A  N  G  A
Query                  2701      CTGGGCAGCCGCAGAGCTGCGCAGCCCACCTGAAGGCATCATCAACAATGCTAACGGTGC  2760
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4498586   CTGGGCAGCCGCAGAGCTGCGCAGCCCACCTGAAGGCATCATCAACAATGCTAACGGTGC  4498645
CDS:hypothetical con   580         W  A  A  A  E  L  R  S  P  P  E  G  I  I  N  N  A  N  G  A

CDS: Putative 3        600         K  S  G  N  V  K  F  M  I  P  F  A  G  E  S  E  H  R  R  D
Query                  2761      CAAATCCGGCAATGTGAAGTTCATGATTCCATTCGCCGGAGAAAGCGAGCATCGACGTGA  2820
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4498646   CAAATCCGGCAATGTGAAGTTCATGATTCCATTCGCCGGAGAAAGCGAGCATCGACGTGA  4498705
CDS:hypothetical con   600         K  S  G  N  V  K  F  M  I  P  F  A  G  E  S  E  H  R  R  D

CDS: Putative 3        620         L  L  T  K  L  I  A  R  T  S  L  S  G  V  A  E  K  T  K  I
Query                  2821      TTTGTTGACGAAGTTGATAGCGCGTACATCTCTTTCTGGGGTGGCTGAAAAAACCAAAAT  2880
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4498706   TTTGTTGACGAAGTTGATAGCGCGTACATCTCTTTCTGGGGTGGCTGAAAAAACCAAAAT  4498765
CDS:hypothetical con   620         L  L  T  K  L  I  A  R  T  S  L  S  G  V  A  E  K  T  K  I

CDS: Putative 3        640         F  S  G  A  F  L  P  Q  I  P  S  P  F  E  Y  Q  T  A  C  A
Query                  2881      CTTCAGCGGTGCATTCCTTCCGCAGATACCGTCTCCCTTTGAATATCAGACAGCTTGTGC  2940
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4498766   CTTCAGCGGTGCATTCCTTCCGCAGATACCGTCTCCCTTTGAATATCAGACAGCTTGTGC  4498825
CDS:hypothetical con   640         F  S  G  A  F  L  P  Q  I  P  S  P  F  E  Y  Q  T  A  C  A

CDS: Putative 3        660         H  E  E  A  L  L  L  G  E  N  L  A  F  D  S  K  P  L  T  V
Query                  2941      GCACGAAGAAGCTCTTCTTTTGGGCGAAAACCTCGCATTCGATTCAAAACCGTTGACGGT  3000
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4498826   GCACGAAGAAGCTCTTCTTTTGGGCGAAAACCTCGCATTCGATTCAAAACCGTTGACGGT  4498885
CDS:hypothetical con   660         H  E  E  A  L  L  L  G  E  N  L  A  F  D  S  K  P  L  T  V

CDS: Putative 3        680         P  L  T  R  R  S  A  F  N  V  L  F  S  G  Y  N  D  H  I  H
Query                  3001      ACCACTTACTCGTCGATCCGCGTTCAATGTTCTATTCAGCGGCTACAACGACCACATTCA  3060
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4498886   ACCACTTACTCGTCGATCCGCGTTCAATGTTCTATTCAGCGGCTACAACGACCACATTCA  4498945
CDS:hypothetical con   680         P  L  T  R  R  S  A  F  N  V  L  F  S  G  Y  N  D  H  I  H

CDS: Putative 3        700         D  G  L  L  S  A  T  L  F  S  L  T  F  V  D  G  F  D  E  I
Query                  3061      CGATGGACTCCTGTCCGCTACGCTTTTTAGTCTGACTTTCGTCGATGGCTTTGATGAAAT  3120
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4498946   CGATGGACTCCTGTCCGCTACGCTTTTTAGTCTGACTTTCGTCGATGGCTTTGATGAAAT  4499005
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CDS:hypothetical con  700        D  G  L  L  S  A  T  L  F  S  L  T  F  V  D  G  F  D  E  I

CDS: Putative 3       720        V  Y  F  N  A  R  G  V  P  P  G  G  G  F  S  A  A  A  Q  M
Query                 3121     CGTGTACTTCAACGCGCGCGGGGTCCCCCCAGGAGGAGGATTCTCAGCCGCAGCGCAGAT  3180
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499006  CGTGTACTTCAACGCGCGCGGGGTCCCCCCAGGAGGAGGATTCTCAGCCGCAGCGCAGAT  4499065
CDS:hypothetical con  720        V  Y  F  N  A  R  G  V  P  P  G  G  G  F  S  A  A  A  Q  M

CDS: Putative 3       740        L  G  A  R  L  K  M  F  D  D  I  S  D  L  P  L  Q  A  I  S
Query                 3181     GCTCGGTGCACGCCTCAAGATGTTCGACGATATATCCGATCTACCACTTCAAGCGATATC  3240
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499066  GCTCGGTGCACGCCTCAAGATGTTCGACGATATATCCGATCTACCACTTCAAGCGATATC  4499125
CDS:hypothetical con  740        L  G  A  R  L  K  M  F  D  D  I  S  D  L  P  L  Q  A  I  S

CDS: Putative 3       760        D  D  I  G  N  R  R  V  A  L  I  I  D  G  L  D  S  E  K  A
Query                 3241     AGACGATATTGGGAATCGCCGCGTAGCATTGATTATCGATGGCCTGGATTCCGAGAAAGC  3300
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499126  AGACGATATTGGGAATCGCCGCGTAGCATTGATTATCGATGGCCTGGATTCCGAGAAAGC  4499185
CDS:hypothetical con  760        D  D  I  G  N  R  R  V  A  L  I  I  D  G  L  D  S  E  K  A

CDS: Putative 3       780        L  Q  P  A  P  A  F  R  S  L  K  P  G  E  P  P  T  P  A  D
Query                 3301     ACTACAGCCAGCCCCAGCGTTTAGATCGCTCAAGCCTGGCGAACCACCTACCCCGGCTGA  3360
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499186  ACTACAGCCAGCCCCAGCGTTTAGATCGCTCAAGCCTGGCGAACCACCTACCCCGGCTGA  4499245
CDS:hypothetical con  780        L  Q  P  A  P  A  F  R  S  L  K  P  G  E  P  P  T  P  A  D

CDS: Putative 3       800        L  L  K  R  L  A  E  D  G  P  R  K  G  T  F  V  F  I  F  V
Query                 3361     CTTGTTAAAGCGTCTCGCCGAGGACGGCCCAAGAAAGGGGACGTTTGTATTTATTTTTGT  3420
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499246  CTTGTTAAAGCGTCTCGCCGAGGACGGCCCAAGAAAGGGGACGTTTGTATTTATTTTTGT  4499305
CDS:hypothetical con  800        L  L  K  R  L  A  E  D  G  P  R  K  G  T  F  V  F  I  F  V

CDS: Putative 3       820        D  R  W  Q  R  C  A  S  A  S  K  D  L  F  S  F  F  E  L  R
Query                 3421     TGACCGTTGGCAGCGCTGTGCCAGTGCCAGCAAAGACCTTTTCTCCTTTTTCGAATTGCG  3480
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499306  TGACCGTTGGCAGCGCTGTGCCAGTGCCAGCAAAGACCTTTTCTCCTTTTTCGAATTGCG  4499365
CDS:hypothetical con  820        D  R  W  Q  R  C  A  S  A  S  K  D  L  F  S  F  F  E  L  R

CDS: Putative 3       840        V  A  Y  C  M  N  E  D  D  A  G  S  L  V  S  G  G  V  G  K
Query                 3481     CGTGGCGTACTGCATGAACGAAGACGATGCCGGATCGCTTGTGAGTGGCGGTGTTGGTAA  3540
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499366  CGTGGCGTACTGCATGAACGAAGACGATGCCGGATCGCTTGTGAGTGGCGGTGTTGGTAA  4499425
CDS:hypothetical con  840        V  A  Y  C  M  N  E  D  D  A  G  S  L  V  S  G  G  V  G  K

CDS: Putative 3       860        F  K  G  I  E  K  P  S  R  A  V  F  V  N  K  M  T  N  D  I
Query                 3541     GTTCAAAGGTATTGAAAAACCGAGCCGAGCTGTATTCGTAAACAAAATGACGAATGACAT  3600
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499426  GTTCAAAGGTATTGAAAAACCGAGCCGAGCTGTATTCGTAAACAAAATGACGAATGACAT  4499485
CDS:hypothetical con  860        F  K  G  I  E  K  P  S  R  A  V  F  V  N  K  M  T  N  D  I
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CDS: Putative 3       880        T  W  F  R  P  Y  V  Q  E  S  T  R  *
CDS: Putative 4       1                                         M  K  R  F  L  L  T  W
Query                 3601     CACATGGTTCCGGCCATATGTTCAGGAAAGCACTCGATGAAGAGATTTCTGCTCACCTGG  3660
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499486  CACATGGTTCCGGCCATATGTTCAGGAAAGCACTCGATGAAGAGATTTCTGCTCACCTGG  4499545
CDS:hypothetical con  880        T  W  F  R  P  Y  V  Q  E  S  T  R
CDS:conserved hypoth  1                                         M  K  R  F  L  L  T  W

CDS: Putative 4       9         Y  G  I  T  D  F  R  A  S  L  G  F  E  N  T  D  G  P  I  A
Query                 3661     TATGGAATCACCGATTTTCGCGCATCTCTGGGGTTTGAGAATACCGATGGCCCTATTGCG  3720
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499546  TATGGAATCACCGATTTTCGCGCATCTCTGGGGTTTGAGAATACCGATGGCCCTATTGCG  4499605
CDS:conserved hypoth  9         Y  G  I  T  D  F  R  A  S  L  G  F  E  N  T  D  G  P  I  A

CDS: Putative 4       29        S  A  L  A  G  A  S  Y  S  D  I  I  I  L  G  Y  T  R  T  D
Query                 3721     AGCGCCCTTGCGGGCGCGTCCTACTCGGACATCATTATCCTGGGTTACACCCGGACGGAT  3780
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499606  AGCGCCCTTGCGGGCGCGTCCTACTCGGACATCATTATCCTGGGTTACACCCGGACGGAT  4499665
CDS:conserved hypoth  29        S  A  L  A  G  A  S  Y  S  D  I  I  I  L  G  Y  T  R  T  D

CDS: Putative 4       49        N  D  A  S  E  L  I  E  A  Q  K  T  F  T  L  E  L  A  S  I
Query                 3781     AATGATGCCAGCGAATTGATCGAGGCACAGAAGACGTTCACGCTTGAATTGGCGTCAATA  3840
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499666  AATGATGCCAGCGAATTGATCGAGGCACAGAAGACGTTCACGCTTGAATTGGCGTCAATA  4499725
CDS:conserved hypoth  49        N  D  A  S  E  L  I  E  A  Q  K  T  F  T  L  E  L  A  S  I

CDS: Putative 4       69        R  S  M  G  Q  E  K  D  W  K  L  T  N  Q  F  V  S  R  F  A
Query                 3841     CGAAGCATGGGGCAAGAGAAAGACTGGAAGCTTACTAATCAGTTTGTCTCCAGGTTCGCT  3900
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499726  CGAAGCATGGGGCAAGAGAAAGACTGGAAGCTTACTAATCAGTTTGTCTCCAGGTTCGCT  4499785
CDS:conserved hypoth  69        R  S  M  G  Q  E  K  D  W  K  L  T  N  Q  F  V  S  R  F  A

CDS: Putative 4       89        N  T  S  V  A  H  E  H  F  E  A  W  L  K  K  K  A  A  A  L
Query                 3901     AATACCTCTGTCGCACATGAACATTTTGAAGCCTGGCTGAAAAAGAAAGCCGCCGCCCTG  3960
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499786  AATACCTCTGTCGCACATGAACATTTTGAAGCCTGGCTGAAAAAGAAAGCCGCCGCCCTG  4499845
CDS:conserved hypoth  89        N  T  S  V  A  H  E  H  F  E  A  W  L  K  K  K  A  A  A  L

CDS: Putative 4       109       G  C  N  A  R  I  R  L  N  S  E  K  L  Y  Q  L  N  D  T  E
Query                 3961     GGCTGCAACGCAAGGATCCGTTTAAATAGCGAGAAACTTTACCAGCTCAACGACACCGAA  4020
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499846  GGCTGCAACGCAAGGATCCGTTTAAATAGCGAGAAACTTTACCAGCTCAACGACACCGAA  4499905
CDS:conserved hypoth  109       G  C  N  A  R  I  R  L  N  S  E  K  L  Y  Q  L  N  D  T  E

CDS: Putative 4       129       G  I  Y  A  S  A  M  R  A  L  D  G  V  E  Q  E  P  G  E  K
Query                 4021     GGTATTTACGCTAGCGCAATGCGGGCGCTGGATGGGGTTGAACAGGAGCCAGGTGAAAAG  4080
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499906  GGTATTTACGCTAGCGCAATGCGGGCGCTGGATGGGGTTGAACAGGAGCCAGGTGAAAAG  4499965
CDS:conserved hypoth  129       G  I  Y  A  S  A  M  R  A  L  D  G  V  E  Q  E  P  G  E  K
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CDS: Putative 4       149       L  V  T  L  Y  L  S  P  G  T  P  V  M  A  F  V  W  A  L  A
Query                 4081     CTCGTCACGCTCTATCTCAGCCCAGGAACTCCGGTGATGGCCTTTGTCTGGGCGCTCGCG  4140
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4499966  CTCGTCACGCTCTATCTCAGCCCAGGAACTCCGGTGATGGCCTTTGTCTGGGCGCTCGCG  4500025
CDS:conserved hypoth  149       L  V  T  L  Y  L  S  P  G  T  P  V  M  A  F  V  W  A  L  A

CDS: Putative 4       169       A  L  S  Y  P  E  L  K  K  R  L  I  A  S  S  I  I  G  K  A
Query                 4141     GCGCTGAGCTACCCTGAACTCaaaaaaaGACTCATAGCATCGTCCATCATTGGCAAAGCA  4200
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4500026  GCGCTGAGCTACCCTGAACTCAAAAAAAGACTCATAGCATCGTCCATCATTGGCAAAGCA  4500085
CDS:conserved hypoth  169       A  L  S  Y  P  E  L  K  K  R  L  I  A  S  S  I  I  G  K  A

CDS: Putative 4       189       P  E  V  I  A  L  P  A  E  W  L  E  R  H  S  S  K  Q  A  A
Query                 4201     CCTGAAGTCATAGCGTTGCCTGCCGAGTGGCTTGAGCGACACAGCTCAAAACAGGCTGCG  4260
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4500086  CCTGAAGTCATAGCGTTGCCTGCCGAGTGGCTTGAGCGACACAGCTCAAAACAGGCTGCG  4500145
CDS:conserved hypoth  189       P  E  V  I  A  L  P  A  E  W  L  E  R  H  S  S  K  Q  A  A

CDS: Putative 4       209       I  R  D  I  S  N  G  F  D  V  T  F  H  L  F  G  E  Q  R  M
Query                 4261     ATCCGAGACATCTCCAACGGGTTCGATGTGACATTCCATCTTTTTGGTGAACAACGGATG  4320
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4500146  ATCCGAGACATCTCCAACGGGTTCGATGTGACATTCCATCTTTTTGGTGAACAACGGATG  4500205
CDS:conserved hypoth  209       I  R  D  I  S  N  G  F  D  V  T  F  H  L  F  G  E  Q  R  M

CDS: Putative 4       229       P  A  L  L  S  I  R  Q  F  E  S  A  H  H  I  F  V  N  S  K
Query                 4321     CCTGCCTTGTTGAGCATCCGGCAATTTGAGTCGGCGCATCACATTTTTGTCAACTCAAAA  4380
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4500206  CCTGCCTTGTTGAGCATCCGGCAATTTGAGTCGGCGCATCACATTTTTGTCAACTCAAAA  4500265
CDS:conserved hypoth  229       P  A  L  L  S  I  R  Q  F  E  S  A  H  H  I  F  V  N  S  K

CDS: Putative 4       249       D  F  P  A  A  C  M  R  T  F  I  G  S  R  D  L  H  E  L  T
Query                 4381     GACTTCCCTGCTGCATGTATGCGAACCTTTATTGGCTCTCGGGACCTGCATGAACTTACC  4440
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4500266  GACTTCCCTGCTGCATGTATGCGAACCTTTATTGGCTCTCGGGACCTGCATGAACTTACC  4500325
CDS:conserved hypoth  249       D  F  P  A  A  C  M  R  T  F  I  G  S  R  D  L  H  E  L  T

CDS: Putative 4       269       V  D  P  W  D  D  R  A  V  H  E  Q  I  T  K  L  A  K  Q  F
Query                 4441     GTTGACCCCTGGGATGATCGTGCTGTTCACGAACAAATCACCAAGCTGGCAAAGCAATTT  4500
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4500326  GTTGACCCCTGGGATGATCGTGCTGTTCACGAACAAATCACCAAGCTGGCAAAGCAATTT  4500385
CDS:conserved hypoth  269       V  D  P  W  D  D  R  A  V  H  E  Q  I  T  K  L  A  K  Q  F

CDS: Putative 4       289       P  E  K  T  R  I  G  I  N  L  T  G  G  T  K  L  M  F  A  G
Query                 4501     CCAGAAAAAAACACGAATTGGAATCAATTTAACTGGCGGCACAAAACTGATGTTTGCTGGC  4560
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4500386  CCAGAAAAAAACACGAATTGGAATCAATTTAACTGGCGGCACAAAACTGATGTTTGCTGGC  4500445
CDS:conserved hypoth  289       P  E  K  T  R  I  G  I  N  L  T  G  G  T  K  L  M  F  A  G

CDS: Putative 4       309       A  L  S  A  A  R  E  L  G  A  V  P  F  Y  F  D  S  K  N  R
Query                 4561     GCGCTCTCTGCTGCGCGTGAACTGGGCGCTGTTCCGTTTTATTTTGATAGCAAGAATCGT  4620
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4500446  GCGCTCTCTGCTGCGCGTGAACTGGGCGCTGTTCCGTTTTATTTTGATAGCAAGAATCGT  4500505
CDS:conserved hypoth    309       A  L  S  A  A  R  E  L  G  A  V  P  F  Y  F  D  S  K  N  R

CDS: Putative 4         329       H  V  T  F  I  D  S  V  R  R  E  K  I  R  Q  I  D  S  I  E
Query                   4621     CACGTCACATTCATTGACAGTGTTCGGCGCGAAAAAATCAGGCAGATTGATTCAATCGAA  4680
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4500506  CACGTCACATTCATTGACAGTGTTCGGCGCGAAAAAATCAGGCAGATTGATTCAATCGAA  4500565
CDS:conserved hypoth    329       H  V  T  F  I  D  S  V  R  R  E  K  I  R  Q  I  D  S  I  E

CDS: Putative 4         349       T  F  L  R  L  N  S  D  G  L  E  I  A  G  S  S  F  M  K  D
Query                   4681     ACATTTTTGCGCCTGAATAGCGACGGATTGGAGATTGCAGGCAGTTCCTTTATGAAGGAT  4740
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4500566  ACATTTTTGCGCCTGAATAGCGACGGATTGGAGATTGCAGGCAGTTCCTTTATGAAGGAT  4500625
CDS:conserved hypoth    349       T  F  L  R  L  N  S  D  G  L  E  I  A  G  S  S  F  M  K  D

CDS: Putative 4         369       I  S  P  S  R  Q  L  L  T  K  A  L  W  L  H  R  D  K  V  R
Query                   4741     ATATCGCCAAGTCGCCAACTTCTGACCAAGGCTCTTTGGTTGCATCGTGACAAGGTGCGT  4800
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4500626  ATATCGCCAAGTCGCCAACTTCTGACCAAGGCTCTTTGGTTGCATCGTGACAAGGTGCGT  4500685
CDS:conserved hypoth    369       I  S  P  S  R  Q  L  L  T  K  A  L  W  L  H  R  D  K  V  R

CDS: Putative 4         389       R  F  Y  R  E  L  T  D  Y  N  N  A  F  R  P  F  E  I  C  R
Query                   4801     AGATTTTATAGAGAACTTACCGACTATAACAATGCATTCAGGCCATTCGAGATTTGTCGT  4860
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4500686  AGATTTTATAGAGAACTTACCGACTATAACAATGCATTCAGGCCATTCGAGATTTGTCGT  4500745
CDS:conserved hypoth    389       R  F  Y  R  E  L  T  D  Y  N  N  A  F  R  P  F  E  I  C  R

CDS: Putative 4         409       D  G  F  N  F  K  L  D  D  M  E  A  V  S  V  Q  G  Y  G  L
Query                   4861     GACGGCTTCAATTTCAAGCTGGATGACATGGAGGCAGTATCCGTCCAGGGCTACGGATTG  4920
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4500746  GACGGCTTCAATTTCAAGCTGGATGACATGGAGGCAGTATCCGTCCAGGGCTACGGATTG  4500805
CDS:conserved hypoth    409       D  G  F  N  F  K  L  D  D  M  E  A  V  S  V  Q  G  Y  G  L

CDS: Putative 4         429       D  L  R  F  E  K  W  P  D  F  A  K  Y  L  S  G  G  W  F  E
Query                   4921     GATCTGAGATTTGAGAAATGGCCTGATTTCGCCAAATACCTATCTGGCGGCTGGTTCGAG  4980
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4500806  GATCTGAGATTTGAGAAATGGCCTGATTTCGCCAAATACCTATCTGGCGGCTGGTTCGAG  4500865
CDS:conserved hypoth    429       D  L  R  F  E  K  W  P  D  F  A  K  Y  L  S  G  G  W  F  E

CDS: Putative 4         449       E  F  V  Y  L  Q  C  E  P  Y  E  D  A  G  V  I  Q  D  L  R
Query                   4981     GAGTTTGTTTATTTGCAGTGCGAACCCTACGAGGATGCTGGCGTCATTCAAGACTTGCGC  5040
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4500866  GAGTTTGTTTATTTGCAGTGCGAACCCTACGAGGATGCTGGCGTCATTCAAGACTTGCGC  4500925
CDS:conserved hypoth    449       E  F  V  Y  L  Q  C  E  P  Y  E  D  A  G  V  I  Q  D  L  R

CDS: Putative 4         469       I  N  V  K  L  N  L  N  L  E  E  S  K  G  Y  S  S  F  G  V
Query                   5041     ATCAATGTCAAGCTGAACTTGAATTTAGAAGAGTCAAAAGGCTATTCGAGCTTCGGTGTT  5100
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4500926  ATCAATGTCAAGCTGAACTTGAATTTAGAAGAGTCAAAAGGCTATTCGAGCTTCGGTGTT  4500985
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CDS:conserved hypoth  469       I  N  V  K  L  N  L  N  L  E  E  S  K  G  Y  S  S  F  G  V

CDS: Putative 4       489       E  Y  N  E  L  D  I  T  F  T  D  G  Y  S  L  Y  I  V  E  C
Query                 5101     GAATACAACGAGCTGGACATCACATTCACCGACGGTTATTCGCTTTATATCGTGGAATGC  5160
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4500986  GAATACAACGAGCTGGACATCACATTCACCGACGGTTATTCGCTTTATATCGTGGAATGC  4501045
CDS:conserved hypoth  489       E  Y  N  E  L  D  I  T  F  T  D  G  Y  S  L  Y  I  V  E  C

CDS: Putative 4       509       K  A  G  N  V  T  Q  E  Q  I  M  K  L  Q  N  L  V  R  F  Y
Query                 5161     AAGGCGGGCAATGTAACGCAAGAGCAGATTATGAAGCTGCAGAACCTTGTGCGCTTCTAC  5220
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501046  AAGGCGGGCAATGTAACGCAAGAGCAGATTATGAAGCTGCAGAACCTTGTGCGCTTCTAC  4501105
CDS:conserved hypoth  509       K  A  G  N  V  T  Q  E  Q  I  M  K  L  Q  N  L  V  R  F  Y

CDS: Putative 4       529       G  G  I  E  G  R  G  I  V  A  C  C  V  P  P  N  T  E  S  A
Query                 5221     GGAGGAATTGAAGGTCGCGGTATCGTTGCCTGCTGTGTTCCGCCAAATACTGAGTCGGCC  5280
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501106  GGAGGAATTGAAGGTCGCGGTATCGTTGCCTGCTGTGTTCCGCCAAATACTGAGTCGGCC  4501165
CDS:conserved hypoth  529       G  G  I  E  G  R  G  I  V  A  C  C  V  P  P  N  T  E  S  A

CDS: Putative 4       549       K  K  K  I  K  D  A  R  L  M  L  W  S  G  A  S  L  S  E  Q
Query                 5281     AAGaaaaaaaTAAAAGATGCCAGACTGATGCTTTGGAGTGGTGCATCACTTTCTGAGCAG  5340
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501166  AAGAAAAAAATAAAAGATGCCAGACTGATGCTTTGGAGTGGTGCATCACTTTCTGAGCAG  4501225
CDS:conserved hypoth  549       K  K  K  I  K  D  A  R  L  M  L  W  S  G  A  S  L  S  E  Q

CDS: Putative 4       569       I  T  A  M  M  N  S  I  T  E  R  A  E  A  S  E  A  T  P  *
CDS: Putative 5       1                                                                  M
Query                 5341     ATAACGGCAATGATGAACAGCATCACTGAGCGGGCTGAAGCGAGTGAGGCAACGCCATGA  5400
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501226  ATAACGGCAATGATGAACAGCATCACTGAGCGGGCTGAAGCGAGTGAGGCAACGCCATGA  4501285
CDS:conserved hypoth  569       I  T  A  M  M  N  S  I  T  E  R  A  E  A  S  E  A  T  P
CDS:hypothetical pro  1                                                                  M

CDS: Putative 5       2        M  L  H  L  V  C  D  I  S  G  S  M  S  E  G  G  K  P  F  I
Query                 5401     TGCTCCATTTGGTTTGCGACATCTCCGGCAGCATGAGTGAAGGAGGCAAGCCCTTCATCC  5460
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501286  TGCTCCATTTGGTTTGCGACATCTCCGGCAGCATGAGTGAAGGAGGCAAGCCCTTCATCC  4501345
CDS:hypothetical pro  2        M  L  H  L  V  C  D  I  S  G  S  M  S  E  G  G  K  P  F  I

CDS: Putative 5       22       L  R  T  L  A  T  T  V  A  Q  W  V  R  Q  G  Y  G  K  A  E
Query                 5461     TGCGAACCTTGGCCACGACCGTGGCGCAATGGGTGCGGCAAGGGTATGGAAAGGCGGAAA  5520
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501346  TGCGAACCTTGGCCACGACCGTGGCGCAATGGGTGCGGCAAGGGTATGGAAAGGCGGAAA  4501405
CDS:hypothetical pro  22       L  R  T  L  A  T  T  V  A  Q  W  V  R  Q  G  Y  G  K  A  E

CDS: Putative 5       42       I  R  L  C  A  W  S  S  E  A  R  S  I  P  D  W  S  V  T  D
Query                 5521     TCCGCCTTTGTGCTTGGAGCAGCGAGGCACGCAGCATCCCGGACTGGAGCGTCACGGACG  5580
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501406  TCCGCCTTTGTGCTTGGAGCAGCGAGGCACGCAGCATCCCGGACTGGAGCGTCACGGACG  4501465
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CDS:hypothetical pro  42       I  R  L  C  A  W  S  S  E  A  R  S  I  P  D  W  S  V  T  D

CDS: Putative 5       62       D  L  P  V  E  M  L  V  C  H  G  S  T  N  G  Q  A  L  V  Q
Query                 5581     ATCTCCCGGTCGAAATGCTGGTTTGCCATGGAAGCACCAATGGCCAGGCGCTGGTTCAAC  5640
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501466  ATCTCCCGGTCGAAATGCTGGTTTGCCATGGAAGCACCAATGGCCAGGCGCTGGTTCAAC  4501525
CDS:hypothetical pro  62       D  L  P  V  E  M  L  V  C  H  G  S  T  N  G  Q  A  L  V  Q

CDS: Putative 5       82       L  L  G  N  E  P  D  G  K  V  L  I  L  T  D  G  F  W  T  R
Query                 5641     TGCTGGGTAACGAGCCGGATGGAAAGGTTCTGATCCTCACGGATGGATTCTGGACAAGAG  5700
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501526  TGCTGGGTAACGAGCCGGATGGAAAGGTTCTGATCCTCACGGATGGATTCTGGACAAGAG  4501585
CDS:hypothetical pro  82       L  L  G  N  E  P  D  G  K  V  L  I  L  T  D  G  F  W  T  R

CDS: Putative 5       102      D  D  V  K  T  L  S  R  W  Q  E  G  L  P  P  D  T  L  R  V
Query                 5701     ACGACGTGAAGACCCTGAGCCGCTGGCAGGAAGGTCTACCGCCGGACACGCTGCGCGTCA  5760
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501586  ACGACGTGAAGACCCTGAGCCGCTGGCAGGAAGGTCTACCGCCGGACACGCTGCGCGTCA  4501645
CDS:hypothetical pro  102      D  D  V  K  T  L  S  R  W  Q  E  G  L  P  P  D  T  L  R  V

CDS: Putative 5       122      I  Q  I  G  A  D  A  N  P  H  L  S  K  G  L  K  G  A  K  V
Query                 5761     TCCAAATCGGCGCGGATGCCAACCCACATCTTTCCAAGGGGCTCAAAGGCGCAAAGGTGT  5820
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501646  TCCAAATCGGCGCGGATGCCAACCCACATCTTTCCAAGGGGCTCAAAGGCGCAAAGGTGT  4501705
CDS:hypothetical pro  122      I  Q  I  G  A  D  A  N  P  H  L  S  K  G  L  K  G  A  K  V

CDS: Putative 5       142      F  A  A  E  E  V  L  A  V  L  D  N  W  L  Q  A  D  E  E  W
Query                 5821     TTGCCGCAGAAGAAGTGCTCGCCGTACTCGATAACTGGCTGCAGGCGGATGAGGAATGGG  5880
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501706  TTGCCGCAGAAGAAGTGCTCGCCGTACTCGATAACTGGCTGCAGGCGGATGAGGAATGGG  4501765
CDS:hypothetical pro  142      F  A  A  E  E  V  L  A  V  L  D  N  W  L  Q  A  D  E  E  W

CDS: Putative 5       162      A  *
CDS: Putative 6       1          M  T  L  W  K  S  F  G  A  S  V  R  G  P  S  H  I  A  E  G
Query                 5881     CATGACGCTTTGGAAAAGTTTTGGGGCAAGCGTTCGCGGCCCGAGCCATATCGCCGAAGG  5940
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501766  CATGACGCTTTGGAAAAGTTTTGGGGCAAGCGTTCGCGGCCCGAGCCATATCGCCGAAGG  4501825
CDS:hypothetical pro  162      A
CDS:conserved hypoth  1          M  T  L  W  K  S  F  G  A  S  V  R  G  P  S  H  I  A  E  G

CDS: Putative 6       21         L  P  N  Q  D  A  W  A  K  F  H  H  V  W  G  D  G  I  V  V
Query                 5941     TTTGCCAAATCAGGATGCATGGGCGAAGTTTCACCATGTTTGGGGTGATGGCATCGTCGT  6000
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501826  TTTGCCAAATCAGGATGCATGGGCGAAGTTTCACCATGTTTGGGGTGATGGCATCGTCGT  4501885
CDS:conserved hypoth  21         L  P  N  Q  D  A  W  A  K  F  H  H  V  W  G  D  G  I  V  V

CDS: Putative 6       41         S  D  G  V  G  S  K  P  F  S  S  F  G  S  H  A  A  C  L  A
Query                 6001     GTCCGACGGAGTTGGCTCCAAGCCCTTCTCCAGCTTCGGCAGCCATGCTGCCTGTCTCGC  6060
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501886  GTCCGACGGAGTTGGCTCCAAGCCCTTCTCCAGCTTCGGCAGCCATGCTGCCTGTCTCGC  4501945
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CDS:conserved hypoth  41          S  D  G  V  G  S  K  P  F  S  S  F  G  S  H  A  A  C  L  A

CDS: Putative 6       61          V  E  F  A  A  R  A  C  C  T  G  G  E  I  E  H  N  A  L  F
Query                 6061     CGTCGAGTTCGCAGCCCGGGCTTGTTGCACCGGTGGTGAAATCGAACACAACGCGCTGTT  6120
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4501946  CGTCGAGTTCGCAGCCCGGGCTTGTTGCACCGGTGGTGAAATCGAACACAACGCGCTGTT  4502005
CDS:conserved hypoth  61          V  E  F  A  A  R  A  C  C  T  G  G  E  I  E  H  N  A  L  F

CDS: Putative 6       81          S  N  I  Q  A  N  W  L  R  L  V  A  P  L  E  P  R  D  C  A
Query                 6121     TAGCAACATCCAAGCTAACTGGCTGAGGCTTGTCGCTCCGCTGGAACCTCGCGATTGCGC  6180
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502006  TAGCAACATCCAAGCTAACTGGCTGAGGCTTGTCGCTCCGCTGGAACCTCGCGATTGCGC  4502065
CDS:conserved hypoth  81          S  N  I  Q  A  N  W  L  R  L  V  A  P  L  E  P  R  D  C  A

CDS: Putative 6       101         A  T  C  L  F  A  L  H  L  D  G  V  I  H  L  G  M  L  G  D
Query                 6181     GGCCACCTGTCTCTTCGCACTACACCTGGATGGCGTAATCCACCTAGGGATGCTTGGCGA  6240
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502066  GGCCACCTGTCTCTTCGCACTACACCTGGATGGCGTAATCCACCTAGGGATGCTTGGCGA  4502125
CDS:conserved hypoth  101         A  T  C  L  F  A  L  H  L  D  G  V  I  H  L  G  M  L  G  D

CDS: Putative 6       121         G  L  A  A  I  A  K  S  D  G  S  V  V  S  L  S  E  N  K  T
Query                 6241     CGGACTTGCCGCTATTGCCAAGTCCGATGGATCAGTGGTTTCGCTGTCGGAAAACAAGAC  6300
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502126  CGGACTTGCCGCTATTGCCAAGTCCGATGGATCAGTGGTTTCGCTGTCGGAAAACAAGAC  4502185
CDS:conserved hypoth  121         G  L  A  A  I  A  K  S  D  G  S  V  V  S  L  S  E  N  K  T

CDS: Putative 6       141         Q  G  F  S  N  I  T  T  A  L  S  S  K  V  S  A  K  D  W  Q
Query                 6301     GCAAGGCTTCTCCAATATCACTACTGCGCTGTCCTCCAAGGTCTCCGCCAAAGACTGGCA  6360
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502186  GCAAGGCTTCTCCAATATCACTACTGCGCTGTCCTCCAAGGTCTCCGCCAAAGACTGGCA  4502245
CDS:conserved hypoth  141         Q  G  F  S  N  I  T  T  A  L  S  S  K  V  S  A  K  D  W  Q

CDS: Putative 6       161         Y  L  S  L  P  G  E  Q  C  I  A  V  L  L  C  T  D  G  V  A
Query                 6361     GTATTTGTCGCTGCCGGGGGAGCAGTGCATCGCAGTATTGCTCTGCACCGATGGGGTGGC  6420
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502246  GTATTTGTCGCTGCCGGGGGAGCAGTGCATCGCAGTATTGCTCTGCACCGATGGGGTGGC  4502305
CDS:conserved hypoth  161         Y  L  S  L  P  G  E  Q  C  I  A  V  L  L  C  T  D  G  V  A

CDS: Putative 6       181         D  D  L  D  N  A  D  G  F  V  S  S  F  A  E  T  H  R  T  L
Query                 6421     TGACGATTTGGATAACGCTGACGGGTTTGTGAGCAGTTTCGCCGAAACGCATCGAACCCT  6480
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502306  TGACGATTTGGATAACGCTGACGGGTTTGTGAGCAGTTTCGCCGAAACGCATCGAACCCT  4502365
CDS:conserved hypoth  181         D  D  L  D  N  A  D  G  F  V  S  S  F  A  E  T  H  R  T  L

CDS: Putative 6       201         A  P  V  S  A  N  R  R  I  H  E  M  L  E  N  W  P  T  P  K
Query                 6481     CGCACCGGTAAGTGCCAACCGGCGCATCCACGAGATGCTCGAAAACTGGCCCACGCCCAA  6540
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502366  CGCACCGGTAAGTGCCAACCGGCGCATCCACGAGATGCTCGAAAACTGGCCCACGCCCAA  4502425
CDS:conserved hypoth  201         A  P  V  S  A  N  R  R  I  H  E  M  L  E  N  W  P  T  P  K
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CDS: Putative 6       221        H  S  D  D  K  T  L  A  C  L  C  S  E  E  V  A  D  E  *
CDS: Putative 7       1                                                          M  S  N
Query                 6541     GCACAGCGACGATAAAACCCTCGCCTGCCTGTGCAGTGAGGAGGTTGCAGATGAGTAACG  6600
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502426  GCACAGCGACGATAAAACCCTCGCCTGCCTGTGCAGTGAGGAGGTTGCAGATGAGTAACG  4502485
CDS:conserved hypoth  221        H  S  D  D  K  T  L  A  C  L  C  S  E  E  V  A  D  E
CDS:putative protein  1                                                          M  S  N

CDS: Putative 7       4        A  E  H  Q  A  L  K  P  L  V  D  E  Y  N  N  V  H  Q  M  A
Query                 6601     CCGAACACCAGGCTCTGAAGCCACTTGTGGATGAATACAACAATGTTCATCAGATGGCCG  6660
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502486  CCGAACACCAGGCTCTGAAGCCACTTGTGGATGAATACAACAATGTTCATCAGATGGCCG  4502545
CDS:putative protein  4        A  E  H  Q  A  L  K  P  L  V  D  E  Y  N  N  V  H  Q  M  A

CDS: Putative 7       24       D  E  L  A  R  G  G  Q  G  V  V  Y  R  T  K  D  A  D  L  A
Query                 6661     ATGAGCTTGCGCGCGGTGGGCAAGGCGTGGTCTATCGCACCAAGGATGCGGATTTGGCCG  6720
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502546  ATGAGCTTGCGCGCGGTGGGCAAGGCGTGGTCTATCGCACCAAGGATGCGGATTTGGCCG  4502605
CDS:putative protein  24       D  E  L  A  R  G  G  Q  G  V  V  Y  R  T  K  D  A  D  L  A

CDS: Putative 7       44       V  K  Q  P  L  D  A  A  G  Q  P  D  K  N  A  N  L  R  E  R
Query                 6721     TCAAGCAGCCGCTGGACGCTGCCGGCCAGCCGGACAAAAACGCCAATCTGCGCGAGCGCT  6780
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502606  TCAAGCAGCCGCTGGACGCTGCCGGCCAGCCGGACAAAAACGCCAATCTGCGCGAGCGCT  4502665
CDS:putative protein  44       V  K  Q  P  L  D  A  A  G  Q  P  D  K  N  A  N  L  R  E  R

CDS: Putative 7       64       F  Q  H  V  R  L  L  P  I  P  R  R  I  P  V  S  L  P  L  A
Query                 6781     TCCAGCACGTCCGCCTGTTGCCCATACCACGGCGCATCCCCGTTTCCCTTCCACTCGCCA  6840
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502666  TCCAGCACGTCCGCCTGTTGCCCATACCACGGCGCATCCCCGTTTCCCTTCCACTCGCCA  4502725
CDS:putative protein  64       F  Q  H  V  R  L  L  P  I  P  R  R  I  P  V  S  L  P  L  A

CDS: Putative 7       84       I  L  R  D  E  P  G  Y  V  M  R  L  L  N  G  M  K  P  F  A
Query                 6841     TCCTGCGCGACGAGCCGGGCTATGTGATGCGTCTGTTGAACGGCATGAAGCCCTTCGCCA  6900
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502726  TCCTGCGCGACGAGCCGGGCTATGTGATGCGTCTGTTGAACGGCATGAAGCCCTTCGCCA  4502785
CDS:putative protein  84       I  L  R  D  E  P  G  Y  V  M  R  L  L  N  G  M  K  P  F  A

CDS: Putative 7       104      S  F  D  L  D  G  R  S  K  K  K  L  E  D  Q  S  Q  A  L  P
Query                 6901     GTTTCGATTTGGACGGCAGAAGCAAAAAGAAGCTGGAAGATCAAAGCCAAGCCTTGCCCC  6960
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502786  GTTTCGATTTGGACGGCAGAAGCAAAAAGAAGCTGGAAGATCAAAGCCAAGCCTTGCCCC  4502845
CDS:putative protein  104      S  F  D  L  D  G  R  S  K  K  K  L  E  D  Q  S  Q  A  L  P

CDS: Putative 7       124      Q  W  L  T  K  I  P  D  K  D  L  A  L  R  L  L  H  Y  A  Q
Query                 6961     AATGGCTGACGAAGATTCCTGACAAGGACCTGGCGCTGCGACTACTGCATTACGCACAAA  7020
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502846  AATGGCTGACGAAGATTCCTGACAAGGACCTGGCGCTGCGACTACTGCATTACGCACAAA  4502905
CDS:putative protein  124      Q  W  L  T  K  I  P  D  K  D  L  A  L  R  L  L  H  Y  A  Q
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CDS: Putative 7       144      T  G  S  T  R  R  R  S  L  A  L  A  K  C  A  A  I  L  A  R
Query                 7021     CTGGCTCCACCCGCCGCCGTTCGCTCGCGCTTGCCAAGTGCGCTGCCATCCTCGCCCGCC  7080
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502906  CTGGCTCCACCCGCCGCCGTTCGCTCGCGCTTGCCAAGTGCGCTGCCATCCTCGCCCGCC  4502965
CDS:putative protein  144      T  G  S  T  R  R  R  S  L  A  L  A  K  C  A  A  I  L  A  R

CDS: Putative 7       164      L  H  S  A  G  L  V  Y  G  D  I  S  T  N  N  A  F  I  G  E
Query                 7081     TGCACAGCGCTGGACTGGTCTATGGCGACATTTCCACCAACAACGCTTTCATTGGCGAAG  7140
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4502966  TGCACAGCGCTGGACTGGTCTATGGCGACATTTCCACCAACAACGCTTTCATTGGCGAAG  4503025
CDS:putative protein  164      L  H  S  A  G  L  V  Y  G  D  I  S  T  N  N  A  F  I  G  E

CDS: Putative 7       184      D  D  T  T  D  V  W  L  I  D  A  D  N  M  R  L  E  L  P  S
Query                 7141     ACGACACCACCGATGTCTGGCTCATAGATGCCGACAATATGCGCCTGGAGTTACCCAGCG  7200
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4503026  ACGACACCACCGATGTCTGGCTCATAGATGCCGACAATATGCGCCTGGAGTTACCCAGCG  4503085
CDS:putative protein  184      D  D  T  T  D  V  W  L  I  D  A  D  N  M  R  L  E  L  P  S

CDS: Putative 7       204      G  G  V  S  V  Y  T  P  G  Y  G  A  P  E  V  V  Q  G  R  D
Query                 7201     GCGGTGTGTCCGTCTATACGCCGGGCTACGGTGCACCGGAGGTAGTGCAGGGCCGTGACC  7260
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4503086  GCGGTGTGTCCGTCTATACGCCGGGCTACGGTGCACCGGAGGTAGTGCAGGGCCGTGACC  4503145
CDS:putative protein  204      G  G  V  S  V  Y  T  P  G  Y  G  A  P  E  V  V  Q  G  R  D

CDS: Putative 7       224      Q  S  R  P  R  T  D  C  W  A  F  A  V  M  T  F  K  L  L  A
Query                 7261     AATCCCGCCCGCGAACCGACTGCTGGGCTTTCGCTGTGATGACATTCAAGCTACTGGCGC  7320
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4503146  AATCCCGCCCGCGAACCGACTGCTGGGCTTTCGCTGTGATGACATTCAAGCTACTGGCGC  4503205
CDS:putative protein  224      Q  S  R  P  R  T  D  C  W  A  F  A  V  M  T  F  K  L  L  A

CDS: Putative 7       244      L  C  H  P  F  I  G  K  K  V  L  E  P  E  D  E  E  D  G  W
Query                 7321     TTTGCCACCCTTTCATTGGCAAGAAAGTACTGGAGCCCGAAGATGAAGAAGACGGCTGGG  7380
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4503206  TTTGCCACCCTTTCATTGGCAAGAAAGTACTGGAGCCCGAAGATGAAGAAGACGGCTGGG  4503265
CDS:putative protein  244      L  C  H  P  F  I  G  K  K  V  L  E  P  E  D  E  E  D  G  W

CDS: Putative 7       264      D  A  D  P  A  P  N  G  T  A  T  D  L  N  E  Q  A  F  A  G
Query                 7381     ATGCCGACCCTGCGCCCAATGGCACTGCCACCGATCTGAACGAACAGGCATTCGCTGGTT  7440
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4503266  ATGCCGACCCTGCGCCCAATGGCACTGCCACCGATCTGAACGAACAGGCATTCGCTGGTT  4503325
CDS:putative protein  264      D  A  D  P  A  P  N  G  T  A  T  D  L  N  E  Q  A  F  A  G

CDS: Putative 7       284      F  L  P  F  V  D  D  E  D  D  D  S  N  E  G  V  G  G  L  P
Query                 7441     TCTTGCCTTTCGTGGATGACGAAGATGACGATTCCAACGAAGGAGTTGGAGGCCTGCCCC  7500
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4503326  TCTTGCCTTTCGTGGATGACGAAGATGACGATTCCAACGAAGGAGTTGGAGGCCTGCCCC  4503385
CDS:putative protein  284      F  L  P  F  V  D  D  E  D  D  D  S  N  E  G  V  G  G  L  P

CDS: Putative 7       304      R  V  L  V  A  T  E  G  L  R  R  L  F  Q  E  T  F  G  A  G
Query                 7501     GTGTATTAGTCGCAACAGAAGGATTACGCCGCCTGTTTCAGGAAACTTTCGGTGCAGGAC  7560
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4503386   GTGTATTAGTCGCAACAGAAGGATTACGCCGCCTGTTTCAGGAAACTTTCGGTGCAGGAC  4503445
CDS:putative protein   304       R  V  L  V  A  T  E  G  L  R  R  L  F  Q  E  T  F  G  A  G

CDS: Putative 7        324       R  E  L  P  H  R  R  P  T  M  A  F  W  T  L  E  L  A  R  A
Query                  7561      GTGAACTGCCGCACCGCCGCCCGACAATGGCGTTCTGGACATTGGAGCTTGCGAGGGCGG  7620
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4503446   GTGAACTGCCGCACCGCCGCCCGACAATGGCGTTCTGGACATTGGAGCTTGCGAGGGCGG  4503505
CDS:putative protein   324       R  E  L  P  H  R  R  P  T  M  A  F  W  T  L  E  L  A  R  A

CDS: Putative 7        344       A  D  Q  S  L  D  C  L  E  C  G  M  S  H  F  A  D  E  Y  A
Query                  7621      CGGATCAGTCGCTGGATTGCCTCGAATGTGGCATGAGCCATTTCGCCGATGAATACGCGC  7680
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4503506   CGGATCAGTCGCTGGATTGCCTCGAATGTGGCATGAGCCATTTCGCCGATGAATACGCGC  4503565
CDS:putative protein   344       A  D  Q  S  L  D  C  L  E  C  G  M  S  H  F  A  D  E  Y  A

CDS: Putative 7        364       Q  C  P  Y  C  G  A  A  R  P  A  F  I  R  V  K  T  P  R  W
Query                  7681      AATGCCCGTATTGTGGCGCGGCGCGCCCGGCTTTCATTCGCGTCAAAACGCCACGTTGGG  7740
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4503566   AATGCCCGTATTGTGGCGCGGCGCGCCCGGCTTTCATTCGCGTCAAAACGCCACGTTGGG  4503625
CDS:putative protein   364       Q  C  P  Y  C  G  A  A  R  P  A  F  I  R  V  K  T  P  R  W

CDS: Putative 7        384       E  I  L  I  P  G  G  A  T  E  F  R  L  P  Q  R  L  F  H  P
Query                  7741      AAATCCTGATTCCTGGTGGTGCCACGGAGTTCAGATTGCCGCAGCGGCTTTTTCACCCGT  7800
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4503626   AAATCCTGATTCCTGGTGGTGCCACGGAGTTCAGATTGCCGCAGCGGCTTTTTCACCCGT  4503685
CDS:putative protein   384       E  I  L  I  P  G  G  A  T  E  F  R  L  P  Q  R  L  F  H  P

CDS: Putative 7        404       F  S  F  E  Y  F  D  N  T  A  Y  E  A  M  L  N  C  A  A  K
Query                  7801      TTTCATTCGAGTATTTCGATAACACAGCATACGAAGCCATGCTGAACTGCGCGGCCAAAA  7860
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4503686   TTTCATTCGAGTATTTCGATAACACAGCATACGAAGCCATGCTGAACTGCGCGGCCAAAA  4503745
CDS:putative protein   404       F  S  F  E  Y  F  D  N  T  A  Y  E  A  M  L  N  C  A  A  K

CDS: Putative 7        424       T  A  V  P  V  R  G  T  L  P  F  P  D  N  L  T  F  E  F  V
Query                  7861      CCGCAGTCCCCGTGCGGGGCACGCTGCCTTTCCCGGACAACCTCACCTTTGAGTTCGTGG  7920
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4503746   CCGCAGTCCCCGTGCGGGGCACGCTGCCTTTCCCGGACAACCTCACCTTTGAGTTCGTGG  4503805
CDS:putative protein   424       T  A  V  P  V  R  G  T  L  P  F  P  D  N  L  T  F  E  F  V

CDS: Putative 7        444       E  G  C  K  *
CDS: Putative 8        1                   M  K  F  Q  D  I  P  V  N  I  I  T  V  R  I  K  R
Query                  7921      AGGGCTGCAAATGAAGTTTCAGGACATTCCTGTCAACATCATAACTGTCCGCATCAAGCG  7980
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4503806   AGGGCTGCAAATGAAGTTTCAGGACATTCCTGTCAACATCATAACTGTCCGCATCAAGCG  4503865
CDS:putative protein   444       E  G  C  K
CDS:hypothetical pro   1                   M  K  F  Q  D  I  P  V  N  I  I  T  V  R  I  K  R

CDS: Putative 8        18          S  D  N  V  E  A  L  Q  E  Q  P  V  F  S  V  E  A  S  L  S
Query                  7981      GTCTGACAATGTCGAAGCCCTGCAAGAGCAGCCAGTATTCTCGGTAGAGGCCAGCCTATC  8040
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4503866   GTCTGACAATGTCGAAGCCCTGCAAGAGCAGCCAGTATTCTCGGTAGAGGCCAGCCTATC  4503925
CDS:hypothetical pro   18          S  D  N  V  E  A  L  Q  E  Q  P  V  F  S  V  E  A  S  L  S

CDS: Putative 8        38          R  A  D  E  F  E  I  R  L  R  D  A  V  V  F  V  R  P  V  A
Query                  8041      CCGCGCAGATGAATTTGAAATCCGCCTGAGAGACGCGGTTGTTTTCGTTCGCCCCGTCGC  8100
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4503926   CCGCGCAGATGAATTTGAAATCCGCCTGAGAGACGCGGTTGTTTTCGTTCGCCCCGTCGC  4503985
CDS:hypothetical pro   38          R  A  D  E  F  E  I  R  L  R  D  A  V  V  F  V  R  P  V  A

CDS: Putative 8        58          A  V  D  I  R  R  L  N  A  E  L  A  S  G  R  S  L  L  A  Q
Query                  8101      GGCTGTTGACATCCGCCGCCTCAACGCTGAACTTGCCAGTGGGCGTTCCCTGCTTGCACA  8160
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4503986   GGCTGTTGACATCCGCCGCCTCAACGCTGAACTTGCCAGTGGGCGTTCCCTGCTTGCACA  4504045
CDS:hypothetical pro   58          A  V  D  I  R  R  L  N  A  E  L  A  S  G  R  S  L  L  A  Q

CDS: Putative 8        78          L  E  N  P  A  A  D  G  S  I  E  L  K  I  G  F  F  T  G  V
Query                  8161      ACTTGAAAACCCTGCCGCCGATGGCAGCATCGAGCTGAAGATCGGTTTTTTCACCGGCGT  8220
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4504046   ACTTGAAAACCCTGCCGCCGATGGCAGCATCGAGCTGAAGATCGGTTTTTTCACCGGCGT  4504105
CDS:hypothetical pro   78          L  E  N  P  A  A  D  G  S  I  E  L  K  I  G  F  F  T  G  V

CDS: Putative 8        98          C  L  E  M  G  D  V  E  I  G  V  D  E  Y  V  Q  E  K  M  R
Query                  8221      CTGCCTGGAAATGGGCGATGTTGAAATCGGTGTGGATGAGTATGTGCAAGAAAAGATGCG  8280
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4504106   CTGCCTGGAAATGGGCGATGTTGAAATCGGTGTGGATGAGTATGTGCAAGAAAAGATGCG  4504165
CDS:hypothetical pro   98          C  L  E  M  G  D  V  E  I  G  V  D  E  Y  V  Q  E  K  M  R

CDS: Putative 8        118         T  K  G  E  A  L  Y  K  R  L  G  E  L  C  C  F  Q  Q  G  N
Query                  8281      GACGAAGGGTGAGGCACTTTACAAGAGGCTGGGCGAACTTTGCTGCTTCCAACAGGGAAA  8340
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4504166   GACGAAGGGTGAGGCACTTTACAAGAGGCTGGGCGAACTTTGCTGCTTCCAACAGGGAAA  4504225
CDS:hypothetical pro   118         T  K  G  E  A  L  Y  K  R  L  G  E  L  C  C  F  Q  Q  G  N

CDS: Putative 8        138         D  A  F  F  F  L  T  A  G  P  A  I  D  E  E  L  K  P  V  G
Query                  8341      CGACGCATTTTTCTTCCTGACTGCTGGCCCGGCGATTGATGAAGAACTGAAACCTGTCGG  8400
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4504226   CGACGCATTTTTCTTCCTGACTGCTGGCCCGGCGATTGATGAAGAACTGAAACCTGTCGG  4504285
CDS:hypothetical pro   138         D  A  F  F  F  L  T  A  G  P  A  I  D  E  E  L  K  P  V  G

CDS: Putative 8        158         E  D  T  P  R  D  A  A  A  E  P  T  R  I  N  A  F  C  V  T
Query                  8401      CGAGGACACGCCACGCGATGCAGCTGCGGAGCCGACCCGAATAAACGCTTTCTGTGTTAC  8460
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4504286   CGAGGACACGCCACGCGATGCAGCTGCGGAGCCGACCCGAATAAACGCTTTCTGTGTTAC  4504345
CDS:hypothetical pro   158         E  D  T  P  R  D  A  A  A  E  P  T  R  I  N  A  F  C  V  T

CDS: Putative 8        178         G  E  G  I  R  F  I  A  T  E  K  A  M  P  G  G  Q  T  I  Y
Query                  8461      TGGCGAAGGTATCCGCTTCATTGCCACCGAAAAAGCAATGCCAGGCGGCCAAACTATCTA  8520
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4504346   TGGCGAAGGTATCCGCTTCATTGCCACCGAAAAAGCAATGCCAGGCGGCCAAACTATCTA  4504405
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CDS:hypothetical pro  178        G  E  G  I  R  F  I  A  T  E  K  A  M  P  G  G  Q  T  I  Y

CDS: Putative 8       198        I  A  T  R  L  T  K  P  K  K  E  P  D  R  T  L  R  L  A  K
Query                 8521     CATCGCCACCCGTCTAACCAAGCCAAAGAAGGAACCTGACCGCACCTTACGCCTGGCCAA  8580
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4504406  CATCGCCACCCGTCTAACCAAGCCAAAGAAGGAACCTGACCGCACCTTACGCCTGGCCAA  4504465
CDS:hypothetical pro  198        I  A  T  R  L  T  K  P  K  K  E  P  D  R  T  L  R  L  A  K

CDS: Putative 8       218        G  R  L  R  F  V  D  W  T  Q  A  G  Q  V  Q  I  L  A  K  A
Query                 8581     AGGTCGGCTGCGTTTTGTGGACTGGACACAGGCGGGACAAGTGCAAATTCTTGCCAAAGC  8640
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4504466  AGGTCGGCTGCGTTTTGTGGACTGGACACAGGCGGGACAAGTGCAAATTCTTGCCAAAGC  4504525
CDS:hypothetical pro  218        G  R  L  R  F  V  D  W  T  Q  A  G  Q  V  Q  I  L  A  K  A

CDS: Putative 8       238        Q  M  T  A  L  T  Q  D  D  G  S  Y  L  K  K  W  D  E  F  G
Query                 8641     GCAAATGACAGCACTCACTCAGGACGATGGAAGCTATCTGAAAAAGTGGGACGAGTTTGG  8700
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4504526  GCAAATGACAGCACTCACTCAGGACGATGGAAGCTATCTGAAAAAGTGGGACGAGTTTGG  4504585
CDS:hypothetical pro  238        Q  M  T  A  L  T  Q  D  D  G  S  Y  L  K  K  W  D  E  F  G

CDS: Putative 8       258        E  V  E  G  E  L  L  L  K  Q  A  R  E  V  G  A  L  Q  F  T
Query                 8701     TGAGGTTGAAGGTGAACTGCTGCTCAAGCAAGCACGCGAAGTGGGTGCTTTGCAATTCAC  8760
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4504586  TGAGGTTGAAGGTGAACTGCTGCTCAAGCAAGCACGCGAAGTGGGTGCTTTGCAATTCAC  4504645
CDS:hypothetical pro  258        E  V  E  G  E  L  L  L  K  Q  A  R  E  V  G  A  L  Q  F  T

CDS: Putative 8       278        E  M  V  P  K  R  D  G  T  V  G  V  R  I  A  Q  A  S  D  S
Query                 8761     GGAGATGGTGCCGAAACGGGATGGAACTGTCGGAGTTCGTATTGCGCAGGCATCAGATTC  8820
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4504646  GGAGATGGTGCCGAAACGGGATGGAACTGTCGGAGTTCGTATTGCGCAGGCATCAGATTC  4504705
CDS:hypothetical pro  278        E  M  V  P  K  R  D  G  T  V  G  V  R  I  A  Q  A  S  D  S

CDS: Putative 8       298        A  W  G  A  L  R  Q  G  A  V  P  E  V  E  L  V  D  E  L  P
Query                 8821     TGCGTGGGGCGCACTGAGACAAGGCGCAGTACCTGAAGTTGAACTGGTGGACGAGTTGCC  8880
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4504706  TGCGTGGGGCGCACTGAGACAAGGCGCAGTACCTGAAGTTGAACTGGTGGACGAGTTGCC  4504765
CDS:hypothetical pro  298        A  W  G  A  L  R  Q  G  A  V  P  E  V  E  L  V  D  E  L  P

CDS: Putative 8       318        D  Y  L  Q  D  E  N  L  S  F  T  D  F  A  R  G  I  E  K  K
Query                 8881     GGACTACTTGCAGGATGAAAACCTGAGCTTCACGGATTTTGCGAGAGGGATCGaaaaaaa  8940
                               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4504766  GGACTACTTGCAGGATGAAAACCTGAGCTTCACGGATTTTGCGAGAGGGATCGAAAAAAA  4504825
CDS:hypothetical pro  318        D  Y  L  Q  D  E  N  L  S  F  T  D  F  A  R  G  I  E  K  K

CDS: Putative 8       338        E  G  E  H  S  K  L  G  E  K  R  E  L  R  E  K  N  T  Y  F
Query                 8941     GGAGGGGGAACACAGCAAGCTCGGTGAAAAACGCGAGCTGCGCGAGAAAAATACCTATTT  9000
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4504826  GGAGGGGGAACACAGCAAGCTCGGTGAAAAACGCGAGCTGCGCGAGAAAAATACCTATTT  4504885
CDS:hypothetical pro  338        E  G  E  H  S  K  L  G  E  K  R  E  L  R  E  K  N  T  Y  F
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CDS: Putative 8       358        S  V  A  E  F  D  E  E  T  R  V  L  T  L  K  A  E  A  L  P
Query                 9001     CAGTGTCGCAGAGTTTGACGAGGAAACTCGCGTACTCACGCTTAAAGCCGAGGCTCTACC  9060
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4504886  CAGTGTCGCAGAGTTTGACGAGGAAACTCGCGTACTCACGCTTAAAGCCGAGGCTCTACC  4504945
CDS:hypothetical pro  358        S  V  A  E  F  D  E  E  T  R  V  L  T  L  K  A  E  A  L  P

CDS: Putative 8       378        K  E  F  G  T  L  I  L  S  L  A  G  E  S  A  Q  I  K  R  R
Query                 9061     CAAGGAATTCGGCACGCTCATCCTGTCGCTGGCGGGCGAATCTGCTCAGATCAAGCGCCG  9120
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4504946  CAAGGAATTCGGCACGCTCATCCTGTCGCTGGCGGGCGAATCTGCTCAGATCAAGCGCCG  4505005
CDS:hypothetical pro  378        K  E  F  G  T  L  I  L  S  L  A  G  E  S  A  Q  I  K  R  R

CDS: Putative 8       398        M  A  A  R  Q  A  I  L  E  G  R  A  A  N  P  Q  L  G  L  L
Query                 9121     CATGGCCGCCCGTCAAGCCATTCTGGAAGGCCGTGCCGCCAACCCCCAGCTTGGGCTGTT  9180
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4505006  CATGGCCGCCCGTCAAGCCATTCTGGAAGGCCGTGCCGCCAACCCCCAGCTTGGGCTGTT  4505065
CDS:hypothetical pro  398        M  A  A  R  Q  A  I  L  E  G  R  A  A  N  P  Q  L  G  L  L

CDS: Putative 8       418        I  E  A  Q  G  R  I  T  Q  I  R  P  S  Q  K  V  Q  P  L  T
Query                 9181     GATTGAGGCGCAGGGGCGAATCACACAGATCCGGCCATCGCAAAAAGTTCAACCGCTCAC  9240
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4505066  GATTGAGGCGCAGGGGCGAATCACACAGATCCGGCCATCGCAAAAAGTTCAACCGCTCAC  4505125
CDS:hypothetical pro  418        I  E  A  Q  G  R  I  T  Q  I  R  P  S  Q  K  V  Q  P  L  T

CDS: Putative 8       438        A  F  V  R  N  K  V  F  R  N  P  P  T  V  M  Q  E  K  A  I
Query                 9241     GGCCTTCGTTCGCAACAAGGTCTTTCGCAATCCGCCCACCGTCATGCAGGAAAAGGCCAT  9300
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4505126  GGCCTTCGTTCGCAACAAGGTCTTTCGCAATCCGCCCACCGTCATGCAGGAAAAGGCCAT  4505185
CDS:hypothetical pro  438        A  F  V  R  N  K  V  F  R  N  P  P  T  V  M  Q  E  K  A  I

CDS: Putative 8       458        E  A  A  L  K  T  P  D  I  A  L  I  Q  G  P  P  G  T  G  K
Query                 9301     CGAGGCCGCCCTAAAAACGCCAGATATAGCGTTGATCCAAGGCCCGCCCGGTACCGGCAA  9360
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4505186  CGAGGCCGCCCTAAAAACGCCAGATATAGCGTTGATCCAAGGCCCGCCCGGTACCGGCAA  4505245
CDS:hypothetical pro  458        E  A  A  L  K  T  P  D  I  A  L  I  Q  G  P  P  G  T  G  K

CDS: Putative 8       478        T  T  V  I  A  A  I  L  E  R  L  N  E  M  A  D  K  R  G  A
Query                 9361     GACCACCGTCATCGCTGCCATTCTGGAGCGCCTGAACGAGATGGCCGACAAGCGCGGCGC  9420
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4505246  GACCACCGTCATCGCTGCCATTCTGGAGCGCCTGAACGAGATGGCCGACAAGCGCGGCGC  4505305
CDS:hypothetical pro  478        T  T  V  I  A  A  I  L  E  R  L  N  E  M  A  D  K  R  G  A

CDS: Putative 8       498        S  I  K  G  Q  I  L  L  T  G  F  Q  H  D  A  V  E  N  M  I
Query                 9421     GAGCATCAAAGGCCAAATTCTGTTGACAGGCTTTCAGCACGATGCGGTGGAAAACATGAT  9480
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4505306  GAGCATCAAAGGCCAAATTCTGTTGACAGGCTTTCAGCACGATGCGGTGGAAAACATGAT  4505365
CDS:hypothetical pro  498        S  I  K  G  Q  I  L  L  T  G  F  Q  H  D  A  V  E  N  M  I

CDS: Putative 8       518        E  R  L  S  L  N  S  L  P  V  P  K  F  G  K  R  S  G  A  T
Query                 9481     CGAGCGGCTCTCGCTCAATAGCCTGCCCGTGCCGAAATTCGGCAAACGGTCTGGCGCGAC  9540
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4505366  CGAGCGGCTCTCGCTCAATAGCCTGCCCGTGCCGAAATTCGGCAAACGGTCTGGCGCGAC  4505425
CDS:hypothetical pro   518        E  R  L  S  L  N  S  L  P  V  P  K  F  G  K  R  S  G  A  T

CDS: Putative 8        538        E  D  D  L  S  T  F  E  R  N  L  E  D  W  C  S  K  L  A  A
Query                  9541     GGAAGACGATCTCAGCACCTTCGAGCGCAATCTTGAGGATTGGTGTTCAAAGTTGGCCGC  9600
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4505426  GGAAGACGATCTCAGCACCTTCGAGCGCAATCTTGAGGATTGGTGTTCAAAGTTGGCCGC  4505485
CDS:hypothetical pro   538        E  D  D  L  S  T  F  E  R  N  L  E  D  W  C  S  K  L  A  A

CDS: Putative 8        558        E  L  R  E  R  N  P  Q  I  A  E  V  E  Q  E  R  E  I  K  N
Query                  9601     CGAACTACGTGAACGAAACCCACAGATTGCCGAAGTTGAGCAGGAACGGGAAATAAAAAA  9660
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4505486  CGAACTACGTGAACGAAACCCACAGATTGCCGAAGTTGAGCAGGAACGGGAAATAAAAAA  4505545
CDS:hypothetical pro   558        E  L  R  E  R  N  P  Q  I  A  E  V  E  Q  E  R  E  I  K  N

CDS: Putative 8        578        L  C  L  Q  Y  V  Q  A  P  S  R  V  L  A  A  S  L  A  R  K
Query                  9661     CCTGTGCCTGCAATATGTCCAAGCCCCGTCACGCGTGCTGGCCGCCAGCCTTGCTAGGAA  9720
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4505546  CCTGTGCCTGCAATATGTCCAAGCCCCGTCACGCGTGCTGGCCGCCAGCCTTGCTAGGAA  4505605
CDS:hypothetical pro   578        L  C  L  Q  Y  V  Q  A  P  S  R  V  L  A  A  S  L  A  R  K

CDS: Putative 8        598        I  A  A  L  G  S  V  I  L  G  E  D  G  A  R  R  S  T  N  L
Query                  9721     AATCGCAGCGCTCGGCAGTGTAATTCTTGGCGAAGACGGCGCTCGACGGTCGACGAATTT  9780
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4505606  AATCGCAGCGCTCGGCAGTGTAATTCTTGGCGAAGACGGCGCTCGACGGTCGACGAATTT  4505665
CDS:hypothetical pro   598        I  A  A  L  G  S  V  I  L  G  E  D  G  A  R  R  S  T  N  L

CDS: Putative 8        618        A  K  K  L  A  H  E  E  N  L  N  D  G  S  T  Q  W  L  D  A
Query                  9781     GGCGAAAAAGCTCGCGCACGAGGAAAACCTCAACGATGGCTCCACCCAATGGCTTGATGC  9840
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4505666  GGCGAAAAAGCTCGCGCACGAGGAAAACCTCAACGATGGCTCCACCCAATGGCTTGATGC  4505725
CDS:hypothetical pro   618        A  K  K  L  A  H  E  E  N  L  N  D  G  S  T  Q  W  L  D  A

CDS: Putative 8        638        A  R  R  L  R  V  R  H  E  S  F  S  D  D  G  P  E  R  A  M
Query                  9841     AGCGCGCCGTCTGCGCGTTCGCCATGAAAGCTTTTCTGACGACGGGCCAGAAAGGGCGAT  9900
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4505726  AGCGCGCCGTCTGCGCGTTCGCCATGAAAGCTTTTCTGACGACGGGCCAGAAAGGGCGAT  4505785
CDS:hypothetical pro   638        A  R  R  L  R  V  R  H  E  S  F  S  D  D  G  P  E  R  A  M

CDS: Putative 8        658        D  A  L  D  D  L  R  D  V  L  E  E  D  E  R  K  L  L  D  K
Query                  9901     GGACGCACTGGATGACCTGCGTGATGTGCTTGAAGAAGACGAACGCAAACTGCTGGACAA  9960
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4505786  GGACGCACTGGATGACCTGCGTGATGTGCTTGAAGAAGACGAACGCAAACTGCTGGACAA  4505845
CDS:hypothetical pro   658        D  A  L  D  D  L  R  D  V  L  E  E  D  E  R  K  L  L  D  K

CDS: Putative 8        678        A  S  L  W  R  N  E  D  G  P  A  P  F  L  D  N  L  V  A  L
Query                  9961     AGCCAGTCTGTGGCGCAATGAAGATGGCCCAGCGCCATTTTTGGACAACCTGGTCGCGTT  10020
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4505846  AGCCAGTCTGTGGCGCAATGAAGATGGCCCAGCGCCATTTTTGGACAACCTGGTCGCGTT  4505905
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CDS:hypothetical pro  678        A  S  L  W  R  N  E  D  G  P  A  P  F  L  D  N  L  V  A  L

CDS: Putative 8       698        K  K  R  L  L  A  R  F  T  A  P  P  I  L  R  V  E  K  Q  N
Query                 10021    GAAAAAGAGGCTCCTCGCCCGGTTCACCGCTCCACCGATTCTTCGCGTGGAAAAGCAGAA  10080
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4505906  GAAAAAGAGGCTCCTCGCCCGGTTCACCGCTCCACCGATTCTTCGCGTGGAAAAGCAGAA  4505965
CDS:hypothetical pro  698        K  K  R  L  L  A  R  F  T  A  P  P  I  L  R  V  E  K  Q  N

CDS: Putative 8       718        D  A  V  L  A  L  A  E  F  A  I  Q  R  I  K  N  A  E  Y  S
Query                 10081    CGACGCAGTGCTTGCATTGGCAGAATTCGCCATACAACGCATCAAAAACGCCGAGTATTC  10140
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4505966  CGACGCAGTGCTTGCATTGGCAGAATTCGCCATACAACGCATCAAAAACGCCGAGTATTC  4506025
CDS:hypothetical pro  718        D  A  V  L  A  L  A  E  F  A  I  Q  R  I  K  N  A  E  Y  S

CDS: Putative 8       738        A  K  D  K  K  S  A  A  L  A  E  F  L  A  E  L  E  G  N  P
Query                 10141    GGCTAAGGATAAAAAATCTGCTGCGCTGGCCGAGTTTCTAGCCGAACTGGAAGGCAACCC  10200
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4506026  GGCTAAGGATAAAAAATCTGCTGCGCTGGCCGAGTTTCTAGCCGAACTGGAAGGCAACCC  4506085
CDS:hypothetical pro  738        A  K  D  K  K  S  A  A  L  A  E  F  L  A  E  L  E  G  N  P

CDS: Putative 8       758        Y  G  M  V  D  A  L  S  E  Y  S  F  A  F  A  A  T  S  Q  Q
Query                 10201    CTATGGCATGGTAGATGCCCTGTCCGAATACAGTTTTGCCTTTGCCGCCACCAGCCAGCA  10260
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4506086  CTATGGCATGGTAGATGCCCTGTCCGAATACAGTTTTGCCTTTGCCGCCACCAGCCAGCA  4506145
CDS:hypothetical pro  758        Y  G  M  V  D  A  L  S  E  Y  S  F  A  F  A  A  T  S  Q  Q

CDS: Putative 8       778        S  V  N  R  A  M  Q  K  R  K  G  L  V  G  R  D  V  N  Q  N
Query                 10261    GAGCGTCAATCGTGCAATGCAAAAACGCAAAGGGCTTGTCGGGCGCGATGTCAATCAAAA  10320
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4506146  GAGCGTCAATCGTGCAATGCAAAAACGCAAAGGGCTTGTCGGGCGCGATGTCAATCAAAA  4506205
CDS:hypothetical pro  778        S  V  N  R  A  M  Q  K  R  K  G  L  V  G  R  D  V  N  Q  N

CDS: Putative 8       798        Q  K  G  M  E  Y  E  Y  V  I  V  D  E  A  A  R  V  S  P  R
Query                 10321    CCAGAAAGGCATGGAATACGAATATGTCATCGTGGACGAAGCCGCCCGTGTCTCGCCTCG  10380
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4506206  CCAGAAAGGCATGGAATACGAATATGTCATCGTGGACGAAGCCGCCCGTGTCTCGCCTCG  4506265
CDS:hypothetical pro  798        Q  K  G  M  E  Y  E  Y  V  I  V  D  E  A  A  R  V  S  P  R

CDS: Putative 8       818        D  L  M  V  A  M  A  Q  G  K  R  I  I  L  V  G  D  H  R  Q
Query                 10381    TGATTTGATGGTGGCTATGGCGCAAGGCAAGCGCATTATTCTGGTCGGCGACCATCGACA  10440
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4506266  TGATTTGATGGTGGCTATGGCGCAAGGCAAGCGCATTATTCTGGTCGGCGACCATCGACA  4506325
CDS:hypothetical pro  818        D  L  M  V  A  M  A  Q  G  K  R  I  I  L  V  G  D  H  R  Q

CDS: Putative 8       838        L  P  H  I  I  D  E  E  V  A  R  Q  M  E  E  G  E  T  G  E
Query                 10441    ATTGCCGCACATCATTGACGAAGAGGTGGCTCGCCAGATGGAGGAAGGCGAAACGGGTGA  10500
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4506326  ATTGCCGCACATCATTGACGAAGAGGTGGCTCGCCAGATGGAGGAAGGCGAAACGGGTGA  4506385
CDS:hypothetical pro  838        L  P  H  I  I  D  E  E  V  A  R  Q  M  E  E  G  E  T  G  E
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CDS: Putative 8       858        D  E  N  D  W  L  K  K  S  M  F  Q  Y  L  F  S  E  R  L  K
Query                 10501    GGACGAAAATGACTGGCTaaaaaaaTCCATGTTTCAGTATTTGTTCTCCGAGCGTTTAAA  10560
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4506386  GGACGAAAATGACTGGCTAAAAAAATCCATGTTTCAGTATTTGTTCTCCGAGCGTTTAAA  4506445
CDS:hypothetical pro  858        D  E  N  D  W  L  K  K  S  M  F  Q  Y  L  F  S  E  R  L  K

CDS: Putative 8       878        T  L  D  K  N  F  P  I  I  D  S  T  T  G  R  V  T  P  R  C
Query                 10561    AACACTGGACAAGAACTTCCCAATTATCGACAGCACCACTGGCCGCGTTACACCACGTTG  10620
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4506446  AACACTGGACAAGAACTTCCCAATTATCGACAGCACCACTGGCCGCGTTACACCACGTTG  4506505
CDS:hypothetical pro  878        T  L  D  K  N  F  P  I  I  D  S  T  T  G  R  V  T  P  R  C

CDS: Putative 8       898        I  T  L  D  K  Q  Y  R  M  H  P  L  L  G  S  F  I  S  R  N
Query                 10621    CATCACGCTGGACAAGCAATACCGCATGCATCCGCTGCTGGGCAGCTTTATCAGTAGAAA  10680
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4506506  CATCACGCTGGACAAGCAATACCGCATGCATCCGCTGCTGGGCAGCTTTATCAGTAGAAA  4506565
CDS:hypothetical pro  898        I  T  L  D  K  Q  Y  R  M  H  P  L  L  G  S  F  I  S  R  N

CDS: Putative 8       918        F  Y  E  R  F  D  P  E  E  Q  F  G  S  G  R  P  A  S  D  F
Query                 10681    TTTCTATGAACGCTTCGACCCGGAGGAGCAATTTGGCTCCGGGCGACCAGCAAGCGATTT  10740
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4506566  TTTCTATGAACGCTTCGACCCGGAGGAGCAATTTGGCTCCGGGCGACCAGCAAGCGATTT  4506625
CDS:hypothetical pro  918        F  Y  E  R  F  D  P  E  E  Q  F  G  S  G  R  P  A  S  D  F

CDS: Putative 8       938        A  H  D  L  P  G  T  N  G  K  S  A  V  W  M  D  V  P  A  Q
Query                 10741    CGCCCATGATCTGCCAGGCACGAACGGCAAGTCTGCCGTTTGGATGGATGTACCAGCACA  10800
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4506626  CGCCCATGATCTGCCAGGCACGAACGGCAAGTCTGCCGTTTGGATGGATGTACCAGCACA  4506685
CDS:hypothetical pro  938        A  H  D  L  P  G  T  N  G  K  S  A  V  W  M  D  V  P  A  Q

CDS: Putative 8       958        R  G  K  H  Q  K  D  G  T  S  W  T  R  P  A  E  V  T  V  I
Query                 10801    AAGAGGAAAACATCAAAAGGACGGAACCAGTTGGACGCGCCCCGCAGAAGTCACTGTCAT  10860
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4506686  AAGAGGAAAACATCAAAAGGACGGAACCAGTTGGACGCGCCCCGCAGAAGTCACTGTCAT  4506745
CDS:hypothetical pro  958        R  G  K  H  Q  K  D  G  T  S  W  T  R  P  A  E  V  T  V  I

CDS: Putative 8       978        A  R  Q  L  Q  A  W  M  S  S  D  A  G  K  D  L  S  F  G  V
Query                 10861    CGCTCGCCAGTTACAGGCGTGGATGAGTTCGGATGCAGGGAAAGATCTCTCCTTCGGTGT  10920
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4506746  CGCTCGCCAGTTACAGGCGTGGATGAGTTCGGATGCAGGGAAAGATCTCTCCTTCGGTGT  4506805
CDS:hypothetical pro  978        A  R  Q  L  Q  A  W  M  S  S  D  A  G  K  D  L  S  F  G  V

CDS: Putative 8       998        I  S  F  Y  K  A  Q  A  D  S  I  R  E  Q  L  K  R  K  F  G
Query                 10921    TATTTCATTTTATAAGGCGCAGGCCGACAGCATCAGGGAACAACTCAAAAGGAAATTCGG  10980
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4506806  TATTTCATTTTATAAGGCGCAGGCCGACAGCATCAGGGAACAACTCAAAAGGAAATTCGG  4506865
CDS:hypothetical pro  998        I  S  F  Y  K  A  Q  A  D  S  I  R  E  Q  L  K  R  K  F  G

CDS: Putative 8       1018       G  I  V  N  D  D  K  Q  L  R  V  G  T  V  D  S  F  Q  G  M
Query                 10981    CGGGATCGTGAACGATGACAAGCAACTGCGTGTTGGAACGGTGGACTCTTTCCAAGGCAT  11040
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4506866  CGGGATCGTGAACGATGACAAGCAACTGCGTGTTGGAACGGTGGACTCTTTCCAAGGCAT  4506925
CDS:hypothetical pro   1018       G  I  V  N  D  D  K  Q  L  R  V  G  T  V  D  S  F  Q  G  M

CDS: Putative 8        1038       E  F  D  V  V  F  L  S  M  V  R  T  L  P  Q  N  W  Q  P  K
Query                  11041    GGAATTCGATGTCGTCTTCCTCTCAATGGTGCGAACCTTGCCGCAAAACTGGCAGCCAAA  11100
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4506926  GGAATTCGATGTCGTCTTCCTCTCAATGGTGCGAACCTTGCCGCAAAACTGGCAGCCAAA  4506985
CDS:hypothetical pro   1038       E  F  D  V  V  F  L  S  M  V  R  T  L  P  Q  N  W  Q  P  K

CDS: Putative 8        1058       D  D  D  R  D  K  Q  A  R  A  L  F  G  H  L  C  L  Y  N  R
Query                  11101    GGATGATGACCGCGACAAACAAGCTAGAGCGCTGTTTGGCCATCTCTGTCTTTACAACCG  11160
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4506986  GGATGATGACCGCGACAAACAAGCTAGAGCGCTGTTTGGCCATCTCTGTCTTTACAACCG  4507045
CDS:hypothetical pro   1058       D  D  D  R  D  K  Q  A  R  A  L  F  G  H  L  C  L  Y  N  R

CDS: Putative 8        1078       L  N  V  A  M  S  R  Q  K  K  L  L  V  V  V  G  D  T  G  L
Query                  11161    TCTGAATGTCGCCATGAGCCGTCAGAAGAAGCTGCTGGTGGTCGTTGGAGATACGGGGTT  11220
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4507046  TCTGAATGTCGCCATGAGCCGTCAGAAGAAGCTGCTGGTGGTCGTTGGAGATACGGGGTT  4507105
CDS:hypothetical pro   1078       L  N  V  A  M  S  R  Q  K  K  L  L  V  V  V  G  D  T  G  L

CDS: Putative 8        1098       L  Q  S  E  L  A  K  E  F  V  P  G  L  V  D  F  L  Q  I  C
Query                  11221    GCTACAAAGTGAACTCGCGAAGGAGTTCGTGCCTGGACTGGTGGATTTCCTTCAGATATG  11280
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4507106  GCTACAAAGTGAACTCGCGAAGGAGTTCGTGCCTGGACTGGTGGATTTCCTTCAGATATG  4507165
CDS:hypothetical pro   1098       L  Q  S  E  L  A  K  E  F  V  P  G  L  V  D  F  L  Q  I  C

CDS: Putative 8        1118       R  E  Q  G  V  M  L  P  C  *
CDS: Putative 9        1                                   M  L  R  L  L  D  Y  G  K  P  A  P
Query                  11281    CCGCGAGCAAGGGGTGATGCTGCCATGTTGAGGCTCCTTGATTACGGCAAACCTGCCCCC  11340
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4507166  CCGCGAGCAAGGGGTGATGCTGCCATGTTGAGGCTCCTTGATTACGGCAAACCTGCCCCC  4507225
CDS:hypothetical pro   1118       R  E  Q  G  V  M  L  P  C
CDS:hypothetical pro   1                                   M  L  R  L  L  D  Y  G  K  P  A  P

CDS: Putative 9        13        F  G  E  T  I  G  R  P  R  H  L  A  W  P  L  N  A  Y  R  V
Query                  11341    TTCGGTGAGACCATCGGTAGGCCGCGCCACCTTGCGTGGCCGCTGAACGCATACCGCGTG  11400
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4507226  TTCGGTGAGACCATCGGTAGGCCGCGCCACCTTGCGTGGCCGCTGAACGCATACCGCGTG  4507285
CDS:hypothetical pro   13        F  G  E  T  I  G  R  P  R  H  L  A  W  P  L  N  A  Y  R  V

CDS: Putative 9        33        T  L  P  R  V  L  D  D  G  N  G  L  N  A  F  E  R  V  I  L
Query                  11401    ACCTTGCCCAGAGTTCTTGACGATGGCAATGGCTTGAACGCATTTGAGCGTGTCATCCTG  11460
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4507286  ACCTTGCCCAGAGTTCTTGACGATGGCAATGGCTTGAACGCATTTGAGCGTGTCATCCTG  4507345
CDS:hypothetical pro   33        T  L  P  R  V  L  D  D  G  N  G  L  N  A  F  E  R  V  I  L

CDS: Putative 9        53        K  L  L  D  A  A  G  R  M  D  A  D  A  L  A  A  E  T  R  I
Query                  11461    AAACTACTCGACGCTGCCGGTCGTATGGATGCCGATGCGCTGGCGGCTGAAACCCGCATC  11520
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4507346  AAACTACTCGACGCTGCCGGTCGTATGGATGCCGATGCGCTGGCGGCTGAAACCCGCATC  4507405
CDS:hypothetical pro   53        K  L  L  D  A  A  G  R  M  D  A  D  A  L  A  A  E  T  R  I

CDS: Putative 9        73        P  L  D  L  V  K  S  V  L  L  R  L  Q  D  K  D  L  I  D  E
Query                  11521    CCACTCGATTTGGTCAAGAGCGTTCTGCTTCGTTTGCAAGACAAGGACTTGATTGACGAA  11580
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4507406  CCACTCGATTTGGTCAAGAGCGTTCTGCTTCGTTTGCAAGACAAGGACTTGATTGACGAA  4507465
CDS:hypothetical pro   73        P  L  D  L  V  K  S  V  L  L  R  L  Q  D  K  D  L  I  D  E

CDS: Putative 9        93        H  N  A  V  I  E  R  E  R  E  D  E  R  A  P  V  F  V  T  A
Query                  11581    CACAATGCCGTCATTGAGCGGGAGCGTGAAGATGAGCGCGCGCCGGTGTTTGTCACTGCG  11640
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4507466  CACAATGCCGTCATTGAGCGGGAGCGTGAAGATGAGCGCGCGCCGGTGTTTGTCACTGCG  4507525
CDS:hypothetical pro   93        H  N  A  V  I  E  R  E  R  E  D  E  R  A  P  V  F  V  T  A

CDS: Putative 9        113       L  V  F  R  E  L  A  T  G  R  I  L  P  F  L  H  R  L  D  D
Query                  11641    CTGGTCTTTCGCGAACTCGCCACCGGGAGAATTCTGCCTTTTCTGCATCGGCTGGACGAC  11700
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4507526  CTGGTCTTTCGCGAACTCGCCACCGGGAGAATTCTGCCTTTTCTGCATCGGCTGGACGAC  4507585
CDS:hypothetical pro   113       L  V  F  R  E  L  A  T  G  R  I  L  P  F  L  H  R  L  D  D

CDS: Putative 9        133       T  N  P  M  R  K  K  E  C  E  D  K  D  F  R  V  I  R  W  D
Query                  11701    ACAAACCCCATGCGGAAAAAGGAATGCGAGGACAAAGACTTCCGGGTAATCCGCTGGGAT  11760
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4507586  ACAAACCCCATGCGGAAAAAGGAATGCGAGGACAAAGACTTCCGGGTAATCCGCTGGGAT  4507645
CDS:hypothetical pro   133       T  N  P  M  R  K  K  E  C  E  D  K  D  F  R  V  I  R  W  D

CDS: Putative 9        153       G  D  R  R  K  A  I  P  A  P  R  D  V  I  R  T  L  R  A  M
Query                  11761    GGTGACCGCAGAAAAGCGATACCAGCGCCGCGTGATGTAATCAGAACTTTGCGCGCCATG  11820
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4507646  GGTGACCGCAGAAAAGCGATACCAGCGCCGCGTGATGTAATCAGAACTTTGCGCGCCATG  4507705
CDS:hypothetical pro   153       G  D  R  R  K  A  I  P  A  P  R  D  V  I  R  T  L  R  A  M

CDS: Putative 9        173       K  K  R  S  S  A  F  G  Q  D  S  K  M  P  A  V  Q  Q  I  T
Query                  11821    AAAAAGCGTTCGTCTGCGTTCGGCCAGGACAGCAAGATGCCCGCAGTCCAACAGATCACG  11880
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4507706  AAAAAGCGTTCGTCTGCGTTCGGCCAGGACAGCAAGATGCCCGCAGTCCAACAGATCACG  4507765
CDS:hypothetical pro   173       K  K  R  S  S  A  F  G  Q  D  S  K  M  P  A  V  Q  Q  I  T

CDS: Putative 9        193       I  V  A  E  P  E  L  L  H  L  D  C  P  I  A  I  Q  K  S  D
Query                  11881    ATAGTCGCCGAGCCCGAGCTGCTTCACCTTGACTGCCCTATCGCCATCCAGAAAAGCGAT  11940
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4507766  ATAGTCGCCGAGCCCGAGCTGCTTCACCTTGACTGCCCTATCGCCATCCAGAAAAGCGAT  4507825
CDS:hypothetical pro   193       I  V  A  E  P  E  L  L  H  L  D  C  P  I  A  I  Q  K  S  D

CDS: Putative 9        213       G  E  F  R  I  A  D  P  F  G  N  G  F  S  L  I  L  E  N  A
Query                  11941    GGCGAGTTCCGTATAGCTGACCCGTTCGGCAACGGTTTCTCCTTGATTCTCGAAAATGCG  12000
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4507826  GGCGAGTTCCGTATAGCTGACCCGTTCGGCAACGGTTTCTCCTTGATTCTCGAAAATGCG  4507885
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CDS:hypothetical pro  213       G  E  F  R  I  A  D  P  F  G  N  G  F  S  L  I  L  E  N  A

CDS: Putative 9       233       F  E  K  L  L  E  Q  D  E  S  L  S  K  W  L  H  G  W  K  Q
Query                 12001    TTCGAGAAACTTTTGGAGCAGGATGAAAGCCTCAGCAAGTGGCTGCATGGTTGGAAACAG  12060
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4507886  TTCGAGAAACTTTTGGAGCAGGATGAAAGCCTCAGCAAGTGGCTGCATGGTTGGAAACAG  4507945
CDS:hypothetical pro  233       F  E  K  L  L  E  Q  D  E  S  L  S  K  W  L  H  G  W  K  Q

CDS: Putative 9       253       S  L  S  T  P  R  P  E  K  Q  D  A  T  P  K  E  P  F  D  N
Query                 12061    TCATTAAGCACTCCTCGTCCAGAAAAGCAGGATGCCACGCCAAAAGAGCCGTTCGACAAC  12120
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4507946  TCATTAAGCACTCCTCGTCCAGAAAAGCAGGATGCCACGCCAAAAGAGCCGTTCGACAAC  4508005
CDS:hypothetical pro  253       S  L  S  T  P  R  P  E  K  Q  D  A  T  P  K  E  P  F  D  N

CDS: Putative 9       273       D  A  N  R  Q  R  Y  P  K  L  V  A  N  L  R  P  L  R  N  S
Query                 12121    GATGCCAACCGGCAACGCTACCCGAAGCTCGTCGCCAATTTGCGCCCCTTGCGGAATAGC  12180
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4508006  GATGCCAACCGGCAACGCTACCCGAAGCTCGTCGCCAATTTGCGCCCCTTGCGGAATAGC  4508065
CDS:hypothetical pro  273       D  A  N  R  Q  R  Y  P  K  L  V  A  N  L  R  P  L  R  N  S

CDS: Putative 9       293       P  F  R  S  I  A  Q  I  H  A  A  I  E  W  A  L  F  Y  T  C
Query                 12181    CCGTTCCGCTCCATCGCCCAAATCCATGCCGCAATCGAATGGGCGCTGTTCTATACCTGC  12240
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4508066  CCGTTCCGCTCCATCGCCCAAATCCATGCCGCAATCGAATGGGCGCTGTTCTATACCTGC  4508125
CDS:hypothetical pro  293       P  F  R  S  I  A  Q  I  H  A  A  I  E  W  A  L  F  Y  T  C

CDS: Putative 9       313       C  R  R  P  V  D  S  V  I  A  R  L  K  F  T  T  Q  D  Q  H
Query                 12241    TGCCGCAGACCGGTTGATTCCGTTATTGCAAGGCTGAAATTCACTACGCAAGACCAACAC  12300
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4508126  TGCCGCAGACCGGTTGATTCCGTTATTGCAAGGCTGAAATTCACTACGCAAGACCAACAC  4508185
CDS:hypothetical pro  313       C  R  R  P  V  D  S  V  I  A  R  L  K  F  T  T  Q  D  Q  H

CDS: Putative 9       333       A  A  L  L  E  Q  A  A  K  A  L  G  L  E  Q  P  P  I  G  F
Query                 12301    GCAGCCCTGCTTGAGCAGGCCGCGAAAGCCCTCGGTCTTGAGCAGCCGCCGATTGGCTTC  12360
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4508186  GCAGCCCTGCTTGAGCAGGCCGCGAAAGCCCTCGGTCTTGAGCAGCCGCCGATTGGCTTC  4508245
CDS:hypothetical pro  333       A  A  L  L  E  Q  A  A  K  A  L  G  L  E  Q  P  P  I  G  F

CDS: Putative 9       353       R  P  I  R  E  G  K  L  R  E  F  E  D  G  G  A  F  Q  E  T
Query                 12361    AGGCCGATTCGGGAAGGTAAGCTGCGGGAATTTGAGGACGGCGGCGCGTTCCAAGAGACG  12420
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4508246  AGGCCGATTCGGGAAGGTAAGCTGCGGGAATTTGAGGACGGCGGCGCGTTCCAAGAGACG  4508305
CDS:hypothetical pro  353       R  P  I  R  E  G  K  L  R  E  F  E  D  G  G  A  F  Q  E  T

CDS: Putative 9       373       V  L  A  I  A  L  L  Q  A  Q  D  D  A  L  H  P  L  R  R  V
Query                 12421    GTTCTTGCCATAGCTTTGCTTCAAGCGCAAGACGACGCTTTGCATCCCTTGCGCCGTGTT  12480
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4508306  GTTCTTGCCATAGCTTTGCTTCAAGCGCAAGACGACGCTTTGCATCCCTTGCGCCGTGTT  4508365
CDS:hypothetical pro  373       V  L  A  I  A  L  L  Q  A  Q  D  D  A  L  H  P  L  R  R  V
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CDS: Putative 9       393       A  A  A  Y  S  D  L  I  T  R  L  F  A  I  N  A  K  R  N  E
Query                 12481    GCGGCCGCGTATTCAGACCTCATCACTCGCCTGTTCGCTATCAACGCCAAACGCAACGAG  12540
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4508366  GCGGCCGCGTATTCAGACCTCATCACTCGCCTGTTCGCTATCAACGCCAAACGCAACGAG  4508425
CDS:hypothetical pro  393       A  A  A  Y  S  D  L  I  T  R  L  F  A  I  N  A  K  R  N  E

CDS: Putative 9       413       K  G  H  G  K  G  G  A  D  A  P  Q  Q  A  L  T  D  D  S  F
Query                 12541    AAGGGCCACGGCAAGGGCGGCGCAGACGCACCGCAGCAGGCACTAACTGACGATTCGTTC  12600
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4508426  AAGGGCCACGGCAAGGGCGGCGCAGACGCACCGCAGCAGGCACTAACTGACGATTCGTTC  4508485
CDS:hypothetical pro  413       K  G  H  G  K  G  G  A  D  A  P  Q  Q  A  L  T  D  D  S  F

CDS: Putative 9       433       M  R  E  V  V  H  A  L  V  P  G  I  V  F  T  D  T  P  P  T
Query                 12601    ATGCGCGAAGTCGTTCATGCGCTTGTGCCAGGCATCGTGTTTACCGACACGCCTCCTACC  12660
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4508486  ATGCGCGAAGTCGTTCATGCGCTTGTGCCAGGCATCGTGTTTACCGACACGCCTCCTACC  4508545
CDS:hypothetical pro  433       M  R  E  V  V  H  A  L  V  P  G  I  V  F  T  D  T  P  P  T

CDS: Putative 9       453       A  P  D  K  D  E  Q  G  D  A  L  L  D  A  R  T  S  I  Q  E
Query                 12661    GCGCCAGACAAGGACGAGCAGGGTGATGCACTGCTGGATGCCCGCACTAGCATTCAGGAG  12720
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4508546  GCGCCAGACAAGGACGAGCAGGGTGATGCACTGCTGGATGCCCGCACTAGCATTCAGGAG  4508605
CDS:hypothetical pro  453       A  P  D  K  D  E  Q  G  D  A  L  L  D  A  R  T  S  I  Q  E

CDS: Putative 9       473       E  F  G  H  Q  L  F  N  R  L  G  A  N  L  Q  D  R  L  V  H
Query                 12721    GAGTTCGGCCACCAGTTGTTCAACCGCCTGGGCGCAAACTTGCAAGACCGGCTGGTTCAC  12780
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4508606  GAGTTCGGCCACCAGTTGTTCAACCGCCTGGGCGCAAACTTGCAAGACCGGCTGGTTCAC  4508665
CDS:hypothetical pro  473       E  F  G  H  Q  L  F  N  R  L  G  A  N  L  Q  D  R  L  V  H

CDS: Putative 9       493       A  E  R  F  F  Q  S  C  H  D  G  D  D  A  L  A  Y  V  R  D
Query                 12781    GCGGAACGTTTTTCCAGTCTTGCCATGACGGGGATGACGCTTTGGCCTATGTCCGCGAC  12840
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4508666  GCGGAACGTTTTTCCAGTCTTGCCATGACGGGGATGACGCTTTGGCCTATGTCCGCGAC  4508725
CDS:hypothetical pro  493       A  E  R  F  F  Q  S  C  H  D  G  D  D  A  L  A  Y  V  R  D

CDS: Putative 9       513       L  Y  A  A  I  Q  S  S  F  E  R  A  L  T  G  R  L  P  S  D
Query                 12841    CTTTATGCCGCAATCCAGTCATCATTTGAGAGAGCTTTGACAGGCAGGCTGCCGTCCGAT  12900
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4508726  CTTTATGCCGCAATCCAGTCATCATTTGAGAGAGCTTTGACAGGCAGGCTGCCGTCCGAT  4508785
CDS:hypothetical pro  513       L  Y  A  A  I  Q  S  S  F  E  R  A  L  T  G  R  L  P  S  D

CDS: Putative 9       533       T  S  D  A  Q  L  K  D  T  A  E  R  K  A  V  E  A  G  F  C
Query                 12901    ACCAGTGACGCGCAGCTCAAAGACACGGCTGAACGCAAGGCTGTTGAGGCTGGTTTCTGC  12960
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4508786  ACCAGTGACGCGCAGCTCAAAGACACGGCTGAACGCAAGGCTGTTGAGGCTGGTTTCTGC  4508845
CDS:hypothetical pro  533       T  S  D  A  Q  L  K  D  T  A  E  R  K  A  V  E  A  G  F  C

CDS: Putative 9       553       E  G  L  S  E  S  L  R  T  V  K  T  S  A  V  R  Q  A  L  Q
Query                 12961    GAAGGCTTGTCGGAGAGCCTGCGAACCGTCAAAACATCCGCTGTGCGCCAGGCATTGCAA  13020
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4508846   GAAGGCTTGTCGGAGAGCCTGCGAACCGTCAAAACATCCGCTGTGCGCCAGGCATTGCAA  4508905
CDS:hypothetical pro   553        E  G  L  S  E  S  L  R  T  V  K  T  S  A  V  R  Q  A  L  Q

CDS: Putative 9        573        G  G  S  Q  T  L  G  A  C  V  L  A  W  L  L  V  S  D  A  D
Query                  13021     GGCGGCAGCCAAACGCTCGGGGCTTGCGTTCTTGCATGGCTGCTGGTGAGCGATGCTGAT  13080
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4508906   GGCGGCAGCCAAACGCTCGGGGCTTGCGTTCTTGCATGGCTGCTGGTGAGCGATGCTGAT  4508965
CDS:hypothetical pro   573        G  G  S  Q  T  L  G  A  C  V  L  A  W  L  L  V  S  D  A  D

CDS: Putative 9        593        E  L  A  A  I  H  D  T  Q  P  S  L  I  G  D  M  A  N  L  I
Query                  13081     GAACTTGCCGCAATTCATGACACGCAGCCGTCCTTGATCGGCGATATGGCAAACCTTATC  13140
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4508966   GAACTTGCCGCAATTCATGACACGCAGCCGTCCTTGATCGGCGATATGGCAAACCTTATC  4509025
CDS:hypothetical pro   593        E  L  A  A  I  H  D  T  Q  P  S  L  I  G  D  M  A  N  L  I

CDS: Putative 9        613        A  R  R  G  H  G  N  E  P  L  P  L  P  K  E  N  I  A  Q  L
Query                  13141     GCTCGGCGTGGGCATGGCAACGAGCCGCTGCCATTGCCCAAAGAGAACATCGCACAGCTT  13200
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4509026   GCTCGGCGTGGGCATGGCAACGAGCCGCTGCCATTGCCCAAAGAGAACATCGCACAGCTT  4509085
CDS:hypothetical pro   613        A  R  R  G  H  G  N  E  P  L  P  L  P  K  E  N  I  A  Q  L

CDS: Putative 9        633        R  K  A  A  F  T  T  I  R  T  L  M  E  S  *
CDS: Putative 10       1                                                      M  N  S  P
Query                  13201     CGCAAAGCTGCTTTCACAACTATCAGAACACTTATGGAATCTTGAAAATGAACAGCCCCG  13260
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4509086   CGCAAAGCTGCTTTCACAACTATCAGAACACTTATGGAATCTTGAAAATGAACAGCCCCG  4509145
CDS:hypothetical pro   633        R  K  A  A  F  T  T  I  R  T  L  M  E  S
CDS:conserved hypoth   1                                                      M  N  S  P

CDS: Putative 10       5         V  Q  P  D  T  E  A  Q  R  L  A  D  L  N  A  R  E  S  W  I
Query                  13261     TCCAACCCGACACCGAAGCCCAGCGGCTTGCCGATTTGAACGCGCGTGAGAGCTGGATAA  13320
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4509146   TCCAACCCGACACCGAAGCCCAGCGGCTTGCCGATTTGAACGCGCGTGAGAGCTGGATAA  4509205
CDS:conserved hypoth   5         V  Q  P  D  T  E  A  Q  R  L  A  D  L  N  A  R  E  S  W  I

CDS: Putative 10       25        N  T  K  E  S  E  I  A  S  R  E  T  A  V  A  T  R  E  R  D
Query                  13321     ACACCAAGGAAAGCGAAATCGCCAGCCGTGAAACCGCCGTGGCTACACGTGAAAGGGATG  13380
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4509206   ACACCAAGGAAAGCGAAATCGCCAGCCGTGAAACCGCCGTGGCTACACGTGAAAGGGATG  4509265
CDS:conserved hypoth   25        N  T  K  E  S  E  I  A  S  R  E  T  A  V  A  T  R  E  R  D

CDS: Putative 10       45        A  T  A  E  R  Q  V  I  E  Q  D  K  A  K  L  A  Q  R  E  Q
Query                  13381     CGACTGCAGAGCGTCAAGTCATCGAGCAAGACAAGGCCAAGCTGGCGCAGCGCGAGCAGG  13440
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4509266   CGACTGCAGAGCGTCAAGTCATCGAGCAAGACAAGGCCAAGCTGGCGCAGCGCGAGCAGG  4509325
CDS:conserved hypoth   45        A  T  A  E  R  Q  V  I  E  Q  D  K  A  K  L  A  Q  R  E  Q

CDS: Putative 10       65        A  V  T  Q  A  E  Q  K  C  D  A  G  F  A  D  E  R  A  A  L
Query                  13441     CCGTCACGCAGGCTGAGCAAAAGTGTGATGCAGGTTTTGCCGATGAACGAGCCGCGCTGA  13500
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4509326   CCGTCACGCAGGCTGAGCAAAAGTGTGATGCAGGTTTTGCCGATGAACGAGCCGCGCTGA  4509385
CDS:conserved hypoth   65        A  V  T  Q  A  E  Q  K  C  D  A  G  F  A  D  E  R  A  A  L

CDS: Putative 10       85        N  D  E  L  R  E  K  R  A  Q  G  E  R  A  I  A  E  M  R  E
Query                  13501     ATGATGAGCTGCGTGAAAAGCGCGCCCAGGGCGAAAGAGCAATTGCCGAGATGCGAGAGA  13560
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4509386   ATGATGAGCTGCGTGAAAAGCGCGCCCAGGGCGAAAGAGCAATTGCCGAGATGCGAGAGA  4509445
CDS:conserved hypoth   85        N  D  E  L  R  E  K  R  A  Q  G  E  R  A  I  A  E  M  R  E

CDS: Putative 10       105       K  N  L  S  A  L  E  V  E  I  S  E  L  K  A  K  R  L  G  A
Query                  13561     AAAACCTTTCAGCGTTGGAGGTTGAAATTTCCGAGCTGAAAGCAAAGCGACTGGGTGCGG  13620
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4509446   AAAACCTTTCAGCGTTGGAGGTTGAAATTTCCGAGCTGAAAGCAAAGCGACTGGGTGCGG  4509505
CDS:conserved hypoth   105       K  N  L  S  A  L  E  V  E  I  S  E  L  K  A  K  R  L  G  A

CDS: Putative 10       125       V  A  H  A  E  N  A  E  R  E  R  I  R  T  E  I  A  Q  E  R
Query                  13621     TTGCCCATGCCGAAAACGCCGAACGGGAGCGCATTCGGACAGAAATCGCCCAAGAGCGCG  13680
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4509506   TTGCCCATGCCGAAAACGCCGAACGGGAGCGCATTCGGACAGAAATCGCCCAAGAGCGCG  4509565
CDS:conserved hypoth   125       V  A  H  A  E  N  A  E  R  E  R  I  R  T  E  I  A  Q  E  R

CDS: Putative 10       145       D  A  W  T  K  Q  Q  G  D  A  R  K  Q  L  N  A  E  R  T  E
Query                  13681     ATGCATGGACAAAACAACAGGGTGACGCTCGAAAGCAGTTGAATGCAGAGCGCACGGAAT  13740
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4509566   ATGCATGGACAAAACAACAGGGTGACGCTCGAAAGCAGTTGAATGCAGAGCGCACGGAAT  4509625
CDS:conserved hypoth   145       D  A  W  T  K  Q  Q  G  D  A  R  K  Q  L  N  A  E  R  T  E

CDS: Putative 10       165       F  E  K  Q  K  G  A  L  S  A  L  Q  S  E  V  E  G  R  Q  A
Query                  13741     TTGAGAAACAAAAAGGCGCACTCTCCGCCTTGCAAAGCGAAGTCGAAGGAAGACAGGCAG  13800
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4509626   TTGAGAAACAAAAAGGCGCACTCTCCGCCTTGCAAAGCGAAGTCGAAGGAAGACAGGCAG  4509685
CDS:conserved hypoth   165       F  E  K  Q  K  G  A  L  S  A  L  Q  S  E  V  E  G  R  Q  A

CDS: Putative 10       185       E  L  E  T  S  E  R  T  L  E  R  K  E  Q  R  L  E  Q  Q  N
Query                  13801     AGCTTGAGACTTCAGAGCGGACACTCGAACGCAAAGAACAACGGCTGGAACAGCAGAACC  13860
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4509686   AGCTTGAGACTTCAGAGCGGACACTCGAACGCAAAGAACAACGGCTGGAACAGCAGAACC  4509745
CDS:conserved hypoth   185       E  L  E  T  S  E  R  T  L  E  R  K  E  Q  R  L  E  Q  Q  N

CDS: Putative 10       205       Q  R  R  S  E  Q  L  D  D  E  V  E  R  R  V  E  D  R  R  K
Query                  13861     AGAGGCGCAGCGAGCAACTGGACGATGAGGTTGAGAGGCGTGTTGAGGATCGCCGAAAAT  13920
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4509746   AGAGGCGCAGCGAGCAACTGGACGATGAGGTTGAGAGGCGTGTTGAGGATCGCCGAAAAT  4509805
CDS:conserved hypoth   205       Q  R  R  S  E  Q  L  D  D  E  V  E  R  R  V  E  D  R  R  K

CDS: Putative 10       225       S  L  E  A  A  L  Q  S  A  K  E  E  N  I  R  L  R  E  A  F
Query                  13921     CGCTAGAGGCTGCTCTGCAATCTGCCAAAGAGGAAAACATTCGACTGCGCGAGGCGTTTA  13980
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4509806   CGCTAGAGGCTGCTCTGCAATCTGCCAAAGAGGAAAACATTCGACTGCGCGAGGCGTTTA  4509865
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CDS:conserved hypoth  225      S  L  E  A  A  L  Q  S  A  K  E  E  N  I  R  L  R  E  A  F

CDS: Putative 10      245      K  T  Q  D  E  L  L  G  A  F  E  Q  L  K  L  Q  L  G  G  K
Query                 13981    AAACTCAAGACGAACTTCTCGGCGCGTTCGAACAGTTAAAGTTGCAACTTGGTGGCAAAG  14040
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4509866  AAACTCAAGACGAACTTCTCGGCGCGTTCGAACAGTTAAAGTTGCAACTTGGTGGCAAAG  4509925
CDS:conserved hypoth  245      K  T  Q  D  E  L  L  G  A  F  E  Q  L  K  L  Q  L  G  G  K

CDS: Putative 10      265      D  P  A  E  I  L  R  A  L  N  S  Q  A  D  E  L  K  R  L  R
Query                 14041    ACCCTGCTGAAATTCTGCGTGCGCTGAACAGCCAGGCCGACGAACTCAAACGCCTACGAG  14100
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4509926  ACCCTGCTGAAATTCTGCGTGCGCTGAACAGCCAGGCCGACGAACTCAAACGCCTACGAG  4509985
CDS:conserved hypoth  265      D  P  A  E  I  L  R  A  L  N  S  Q  A  D  E  L  K  R  L  R

CDS: Putative 10      285      E  E  L  A  T  R  P  T  E  E  M  R  E  R  Y  Q  A  L  E  S
Query                 14101    AGGAGCTTGCTACCCGACCTACTGAGGAAATGCGCGAGCGGTATCAAGCCCTTGAATCAG  14160
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4509986  AGGAGCTTGCTACCCGACCTACTGAGGAAATGCGCGAGCGGTATCAAGCCCTTGAATCAG  4510045
CDS:conserved hypoth  285      E  E  L  A  T  R  P  T  E  E  M  R  E  R  Y  Q  A  L  E  S

CDS: Putative 10      305      E  A  K  N  Q  K  T  R  A  D  Q  L  E  R  Q  L  S  T  N  E
Query                 14161    AAGCCAAAAATCAGAAAACACGGGCAGACCAGTTAGAACGGCAACTTTCCACCAATGAGG  14220
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4510046  AAGCCAAAAATCAGAAAACACGGGCAGACCAGTTAGAACGGCAACTTTCCACCAATGAGG  4510105
CDS:conserved hypoth  305      E  A  K  N  Q  K  T  R  A  D  Q  L  E  R  Q  L  S  T  N  E

CDS: Putative 10      325      A  A  V  A  E  I  G  E  L  R  R  Q  G  S  E  L  N  A  E  N
Query                 14221    CTGCGGTCGCTGAAATTGGCGAGCTGCGCCGTCAAGGCTCGGAGCTCAACGCCGAAAACA  14280
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4510106  CTGCGGTCGCTGAAATTGGCGAGCTGCGCCGTCAAGGCTCGGAGCTCAACGCCGAAAACA  4510165
CDS:conserved hypoth  325      A  A  V  A  E  I  G  E  L  R  R  Q  G  S  E  L  N  A  E  N

CDS: Putative 10      345      K  S  L  A  Q  R  A  S  I  F  E  G  A  A  N  E  A  Q  A  E
Query                 14281    AATCTCTGGCGCAAAGGGCATCCATCTTCGAGGGAGCAGCCAACGAAGCGCAAGCCGAAC  14340
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4510166  AATCTCTGGCGCAAAGGGCATCCATCTTCGAGGGAGCAGCCAACGAAGCGCAAGCCGAAC  4510225
CDS:conserved hypoth  345      K  S  L  A  Q  R  A  S  I  F  E  G  A  A  N  E  A  Q  A  E

CDS: Putative 10      365      L  K  R  L  R  A  A  Y  E  R  P  A  E  V  T  A  R  Y  K  E
Query                 14341    TCAAGCGTTTGCGTGCAGCTTATGAGCGCCCTGCTGAAGTTACCGCTCGCTACAAAGAAA  14400
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4510226  TCAAGCGTTTGCGTGCAGCTTATGAGCGCCCTGCTGAAGTTACCGCTCGCTACAAAGAAA  4510285
CDS:conserved hypoth  365      L  K  R  L  R  A  A  Y  E  R  P  A  E  V  T  A  R  Y  K  E

CDS: Putative 10      385      I  E  M  P  H  I  S  V  D  K  V  K  Q  P  V  Q  H  E  I  D
Query                 14401    TTGAGATGCCGCACATCAGTGTGGATAAGGTCAAGCAGCCGGTGCAGCACGAGATCGATG  14460
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4510286  TTGAGATGCCGCACATCAGTGTGGATAAGGTCAAGCAGCCGGTGCAGCACGAGATCGATG  4510345
CDS:conserved hypoth  385      I  E  M  P  H  I  S  V  D  K  V  K  Q  P  V  Q  H  E  I  D
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CDS: Putative 10      405      E  L  T  W  L  T  G  I  G  N  A  C  D  T  Y  G  L  H  F  N
Query                 14461    AGCTAACTTGGCTCACTGGGATTGGTAATGCTTGCGATACATACGGACTACATTTCAATC  14520
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4510346  AGCTAACTTGGCTCACTGGGATTGGTAATGCTTGCGATACATACGGACTACATTTCAATC  4510405
CDS:conserved hypoth  405      E  L  T  W  L  T  G  I  G  N  A  C  D  T  Y  G  L  H  F  N

CDS: Putative 10      425      P  R  I  L  K  A  F  H  T  A  L  K  T  A  E  W  S  P  L  T
Query                 14521    CACGTATTTTGAAAGCTTTTCATACAGCTCTCAAAACAGCGGAATGGTCGCCGCTCACTG  14580
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4510406  CACGTATTTTGAAAGCTTTTCATACAGCTCTCAAAACAGCGGAATGGTCGCCGCTCACTG  4510465
CDS:conserved hypoth  425      P  R  I  L  K  A  F  H  T  A  L  K  T  A  E  W  S  P  L  T

CDS: Putative 10      445      V  L  A  G  V  S  G  T  G  K  S  E  L  P  R  L  Y  S  H  F
Query                 14581    TCCTGGCAGGGGTTTCCGGAACCGGAAAATCCGAACTGCCGCGCCTCTACTCGCACTTTG  14640
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4510466  TCCTGGCAGGGGTTTCCGGAACCGGAAAATCCGAACTGCCGCGCCTCTACTCGCACTTTG  4510525
CDS:conserved hypoth  445      V  L  A  G  V  S  G  T  G  K  S  E  L  P  R  L  Y  S  H  F

CDS: Putative 10      465      G  G  I  Y  F  E  P  L  S  V  Q  P  N  W  D  S  Q  E  S  M
Query                 14641    GCGGAATTTATTTCGAGCCGCTGTCTGTCCAGCCTAATTGGGATTCGCAGGAATCCATGC  14700
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4510526  GCGGAATTTATTTCGAGCCGCTGTCTGTCCAGCCTAATTGGGATTCGCAGGAATCCATGC  4510585
CDS:conserved hypoth  465      G  G  I  Y  F  E  P  L  S  V  Q  P  N  W  D  S  Q  E  S  M

CDS: Putative 10      485      L  G  F  F  N  S  I  D  N  K  F  D  A  Q  P  V  L  R  F  L
Query                 14701    TGGGCTTTTTCAATTCCATAGACAATAAATTCGATGCACAGCCGGTGCTGCGTTTTCTCG  14760
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4510586  TGGGCTTTTTCAATTCCATAGACAATAAATTCGATGCACAGCCGGTGCTGCGTTTTCTCG  4510645
CDS:conserved hypoth  485      L  G  F  F  N  S  I  D  N  K  F  D  A  Q  P  V  L  R  F  L

CDS: Putative 10      505      A  Q  S  Q  I  S  G  R  E  Q  Y  E  Q  R  I  R  R  W  Q  S
Query                 14761    CGCAAAGTCAGATATCAGGCCGCGAACAATATGAACAGCGCATTAGACGTTGGCAGAGTA  14820
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4510646  CGCAAAGTCAGATATCAGGCCGCGAACAATATGAACAGCGCATTAGACGTTGGCAGAGTA  4510705
CDS:conserved hypoth  505      A  Q  S  Q  I  S  G  R  E  Q  Y  E  Q  R  I  R  R  W  Q  S

CDS: Putative 10      525      M  S  P  D  Q  Q  I  A  L  D  P  E  K  D  K  E  L  I  E  A
Query                 14821    TGTCGCCAGATCAGCAAATAGCACTTGACCCTGAGAAGGACAAAGAGCTGATTGAAGCGT  14880
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4510706  TGTCGCCAGATCAGCAAATAGCACTTGACCCTGAGAAGGACAAAGAGCTGATTGAAGCGT  4510765
CDS:conserved hypoth  525      M  S  P  D  Q  Q  I  A  L  D  P  E  K  D  K  E  L  I  E  A

CDS: Putative 10      545      L  K  Q  A  D  Y  P  G  L  Q  D  A  V  C  L  V  L  L  D  E
Query                 14881    TGAAACAAGCAGATTATCCAGGATTGCAGGACGCAGTGTGTCTTGTTCTGCTTGATGAGA  14940
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4510766  TGAAACAAGCAGATTATCCAGGATTGCAGGACGCAGTGTGTCTTGTTCTGCTTGATGAGA  4510825
CDS:conserved hypoth  545      L  K  Q  A  D  Y  P  G  L  Q  D  A  V  C  L  V  L  L  D  E

CDS: Putative 10      565      M  N  L  A  H  P  E  L  Y  F  A  E  F  L  S  K  L  E  L  R
Query                 14941    TGAATCTGGCACACCCTGAGCTTTATTTTGCAGAGTTTTTGAGCAAGCTAGAACTGCGGC  15000
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4510826   TGAATCTGGCACACCCTGAGCTTTATTTTGCAGAGTTTTTGAGCAAGCTAGAACTGCGGC  4510885
CDS:conserved hypoth   565       M  N  L  A  H  P  E  L  Y  F  A  E  F  L  S  K  L  E  L  R

CDS: Putative 10       585       R  G  R  K  G  D  D  V  P  F  I  P  V  K  I  G  A  G  M  E
Query                  15001     GTGGCAGAAAGGGTGATGATGTTCCGTTCATACCGGTGAAAATTGGCGCCGGCATGGAAC  15060
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4510886   GTGGCAGAAAGGGTGATGATGTTCCGTTCATACCGGTGAAAATTGGCGCCGGCATGGAAC  4510945
CDS:conserved hypoth   585       R  G  R  K  G  D  D  V  P  F  I  P  V  K  I  G  A  G  M  E

CDS: Putative 10       605       P  Y  K  L  P  L  G  R  N  V  L  W  T  G  T  M  N  Q  D  E
Query                  15061     CCTATAAGCTCCCCCTCGGTCGTAATGTACTCTGGACAGGGACGATGAACCAGGACGAAA  15120
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4510946   CCTATAAGCTCCCCCTCGGTCGTAATGTACTCTGGACAGGGACGATGAACCAGGACGAAA  4511005
CDS:conserved hypoth   605       P  Y  K  L  P  L  G  R  N  V  L  W  T  G  T  M  N  Q  D  E

CDS: Putative 10       625       T  T  K  S  L  S  D  K  V  L  D  R  S  I  I  I  N  F  P  R
Query                  15121     CCACCAAGTCCCTTTCGGACAAGGTGCTTGACCGTTCCATCATCATCAACTTTCCGCGCC  15180
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4511006   CCACCAAGTCCCTTTCGGACAAGGTGCTTGACCGTTCCATCATCATCAACTTTCCGCGCC  4511065
CDS:conserved hypoth   625       T  T  K  S  L  S  D  K  V  L  D  R  S  I  I  I  N  F  P  R

CDS: Putative 10       645       P  T  E  L  K  R  R  L  K  L  A  P  L  D  D  K  N  R  G  P
Query                  15181     CGACGGAACTCAAACGCCGCCTGAAGCTTGCTCCACTTGATGACAAAAATCGAGGCCCGG  15240
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4511066   CGACGGAACTCAAACGCCGCCTGAAGCTTGCTCCACTTGATGACAAAAATCGAGGCCCGG  4511125
CDS:conserved hypoth   645       P  T  E  L  K  R  R  L  K  L  A  P  L  D  D  K  N  R  G  P

CDS: Putative 10       665       A  L  H  K  T  S  W  Q  S  W  L  A  Q  G  S  N  F  S  D  D
Query                  15241     CGCTACACAAAACGTCGTGGCAGAGTTGGCTAGCACAGGGCAGCAACTTCTCCGACGATC  15300
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4511126   CGCTACACAAAACGTCGTGGCAGAGTTGGCTAGCACAGGGCAGCAACTTCTCCGACGATC  4511185
CDS:conserved hypoth   665       A  L  H  K  T  S  W  Q  S  W  L  A  Q  G  S  N  F  S  D  D

CDS: Putative 10       685       Q  V  S  P  F  K  K  F  I  E  A  I  N  A  S  L  A  V  T  G
Query                  15301     AAGTCAGCCCGTTCAAAAAATTCATTGAAGCAATCAATGCTTCTTTAGCGGTTACAGGCC  15360
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4511186   AAGTCAGCCCGTTCAAAAAATTCATTGAAGCAATCAATGCTTCTTTAGCGGTTACAGGCC  4511245
CDS:conserved hypoth   685       Q  V  S  P  F  K  K  F  I  E  A  I  N  A  S  L  A  V  T  G

CDS: Putative 10       705       R  A  L  G  H  R  V  W  Q  S  I  E  Y  Y  M  A  N  Y  P  D
Query                  15361     GTGCCCTCGGTCACCGCGTTTGGCAATCCATTGAATACTACATGGCCAATTACCCGGATG  15420
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4511246   GTGCCCTCGGTCACCGCGTTTGGCAATCCATTGAATACTACATGGCCAATTACCCGGATG  4511305
CDS:conserved hypoth   705       R  A  L  G  H  R  V  W  Q  S  I  E  Y  Y  M  A  N  Y  P  D

CDS: Putative 10       725       V  R  A  A  R  D  K  D  A  L  A  R  A  M  H  V  A  F  E  D
Query                  15421     TCCGTGCTGCACGCGATAAAGATGCGCTTGCCAGAGCTATGCATGTCGCCTTCGAGGATC  15480
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4511306   TCCGTGCTGCACGCGATAAAGATGCGCTTGCCAGAGCTATGCATGTCGCCTTCGAGGATC  4511365
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CDS:conserved hypoth  725      V  R  A  A  R  D  K  D  A  L  A  R  A  M  H  V  A  F  E  D

CDS: Putative 10      745      Q  L  V  Q  K  V  M  P  K  L  R  G  I  D  T  R  G  K  S  K
Query                 15481    AACTCGTGCAGAAGGTCATGCCCAAATTGCGGGGTATTGATACACGCGGCAAGAGCAAGA  15540
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4511366  AACTCGTGCAGAAGGTCATGCCCAAATTGCGGGGTATTGATACACGCGGCAAGAGCAAGA  4511425
CDS:conserved hypoth  745      Q  L  V  Q  K  V  M  P  K  L  R  G  I  D  T  R  G  K  S  K

CDS: Putative 10      765      T  E  C  L  D  R  I  R  G  Q  L  V  T  G  I  G  S  N  S  F
Query                 15541    CAGAGTGCCTGGACAGGATTCGTGGACAACTCGTTACAGGAATCGGCAGTAACTCATTCA  15600
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4511426  CAGAGTGCCTGGACAGGATTCGTGGACAACTCGTTACAGGAATCGGCAGTAACTCATTCA  4511485
CDS:conserved hypoth  765      T  E  C  L  D  R  I  R  G  Q  L  V  T  G  I  G  S  N  S  F

CDS: Putative 10      785      N  L  T  E  D  F  D  L  A  C  D  L  G  Y  G  Q  F  I  W  Q
Query                 15601    ATCTGACAGAGGATTTCGACCTTGCCTGTGATCTTGGCTATGGTCAGTTTATTTGGCAGT  15660
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4511486  ATCTGACAGAGGATTTCGACCTTGCCTGTGATCTTGGCTATGGTCAGTTTATTTGGCAGT  4511545
CDS:conserved hypoth  785      N  L  T  E  D  F  D  L  A  C  D  L  G  Y  G  Q  F  I  W  Q

CDS: Putative 10      805      S  A  N  Y  L  N  V  G  D  T  E  T  N  D  R  S  T  A  S  R
Query                 15661    CGGCAAATTACCTAAACGTCGGTGACACGGAAACCAATGATAGATCCACGGCCAGTCGAG  15720
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4511546  CGGCAAATTACCTAAACGTCGGTGACACGGAAACCAATGATAGATCCACGGCCAGTCGAG  4511605
CDS:conserved hypoth  805      S  A  N  Y  L  N  V  G  D  T  E  T  N  D  R  S  T  A  S  R

CDS: Putative 10      825      D  S  D  N  A  E  L  P  H  S  L  F  M  K  D  E  P  D  S  D
Query                 15721    ACTCGGACAATGCTGAATTGCCACACTCCCTTTTTATGAAAGATGAACCAGATTCAGACA  15780
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4511606  ACTCGGACAATGCTGAATTGCCACACTCCCTTTTTATGAAAGATGAACCAGATTCAGACA  4511665
CDS:conserved hypoth  825      D  S  D  N  A  E  L  P  H  S  L  F  M  K  D  E  P  D  S  D

CDS: Putative 10      845      K  R  H  K  M  W  N  L  K  T  P  E  Q  R  D  E  L  R  V  K
Query                 15781    AGCGTCATAAAATGTGGAACTTAAAGACACCAGAGCAACGAGATGAGCTGCGCGTGAAAC  15840
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4511666  AGCGTCATAAAATGTGGAACTTAAAGACACCAGAGCAACGAGATGAGCTGCGCGTGAAAC  4511725
CDS:conserved hypoth  845      K  R  H  K  M  W  N  L  K  T  P  E  Q  R  D  E  L  R  V  K

CDS: Putative 10      865      L  E  E  N  A  R  A  G  R  I  H  A  K  Q  *
Query                 15841    TTGAAGAAAATGCCAGAGCAGGAAGGATTCACGCCAAGCAATGAGTATTACTCTGGAAAA  15900
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4511726  TTGAAGAAAATGCCAGAGCAGGAAGGATTCACGCCAAGCAATGAGTATTACTCTGGAAAA  4511785
CDS:conserved hypoth  865      L  E  E  N  A  R  A  G  R  I  H  A  K  Q

Query                 15901    AATCTATACCGACTTCCGTGCCAAAGAAAAACTTGCCAAAAAACTGCTTGAGCAAATGAA  15960
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4511786  AATCTATACCGACTTCCGTGCCAAAGAAAAACTTGCCAAAAAACTGCTTGAGCAAATGAA  4511845

Query                 15961    TTGGTTTGGTTCAATCACGGATTTCGATCCTAAGACCGGCGCGGCTCTGCCGAAATCCTT  16020
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct                4511846  TTGGTTTGGTTCAATCACGGATTTCGATCCTAAGACCGGCGCGGCTCTGCCGAAATCCTT  4511905

Query                16021    GTCAGGGTTCCTCGCCAAAGTCGCACAGCCAGAAGCGAGTGAGATAACCCGTGACCGCCT  16080
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4511906  GTCAGGGTTCCTCGCCAAAGTCGCACAGCCAGAAGCGAGTGAGATAACCCGTGACCGCCT  4511965

Query                16081    TTGGCGCATAACGGAACACTGCCGCGCTTCTGTCGAGCGATTATTTCATTCTCTCAACGA  16140
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4511966  TTGGCGCATAACGGAACACTGCCGCGCTTCTGTCGAGCGATTATTTCATTCTCTCAACGA  4512025

Query                16141    AAGTCCTCGCTGCGAACACGCTCTACTGCCTGTTCATGCTGTGCGTGAACTGGATGCCAA  16200
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4512026  AAGTCCTCGCTGCGAACACGCTCTACTGCCTGTTCATGCTGTGCGTGAACTGGATGCCAA  4512085

Query                16201    CAGTTTTATTAAGCTGAGTAATCGTCCGGGTCGTACCATTCGGGAAAAACTGGCAGGTAA  16260
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4512086  CAGTTTTATTAAGCTGAGTAATCGTCCGGGTCGTACCATTCGGGAAAAACTGGCAGGTAA  4512145

Query                16261    CCCCTACATACAGGCTGTGCGTCGTTTTCAATCCGTCGACCTGCCGGAAAATCGCTTGCT  16320
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4512146  CCCCTACATACAGGCTGTGCGTCGTTTTCAATCCGTCGACCTGCCGGAAAATCGCTTGCT  4512205

Query                16321    GAAAGCCTTTGCCATTCGCCTTGCGGAAATGCTTGATTTACGCGGTGATTGTCTCGGTCA  16380
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4512206  GAAAGCCTTTGCCATTCGCCTTGCGGAAATGCTTGATTTACGCGGTGATTGTCTCGGTCA  4512265

Query                16381    AGAGGATGAGCTTCTATCAAAAATCTACTTATGGTTGCGTTCTGATGAGGCGCAAGCCAT  16440
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4512266  AGAGGATGAGCTTCTATCAAAAATCTACTTATGGTTGCGTTCTGATGAGGCGCAAGCCAT  4512325

Query                16441    CGGCAATTGGGAAAATCTGCCACCTAACAACACGCTACTAGCACACCGAGATTACCGTCA  16500
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4512326  CGGCAATTGGGAAAATCTGCCACCTAACAACACGCTACTAGCACACCGAGATTACCGTCA  4512385

Query                16501    CGTGTGGGATGCATGGCGCTGGCTGCAAACCCTCGATGAGGACATCACCAGCGACCTTTC  16560
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4512386  CGTGTGGGATGCATGGCGCTGGCTGCAAACCCTCGATGAGGACATCACCAGCGACCTTTC  4512445

Query                16561    TCAACTGGATGTCCGCGAGAAAACCATGCGCCTTTGGCAGCAATGCGCGCAAATGTGGCT  16620
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4512446  TCAACTGGATGTCCGCGAGAAAACCATGCGCCTTTGGCAGCAATGCGCGCAAATGTGGCT  4512505

Query                16621    TGATGGAAAGCATCTTTTTGCTGAGATACCGTTACTATTCGATTATGAAAAGTTTGAGAT  16680
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4512506  TGATGGAAAGCATCTTTTTGCTGAGATACCGTTACTATTCGATTATGAAAAGTTTGAGAT  4512565

CDS: Putative 11     1                                                      M  P  R  H
Query                16681    TCTTCCGTGGACTTCCAAGCCACCTTTGTTCAAGGAAGTGAAGTACAAGATGCCCCGGCA  16740
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4512566  TCTTCCGTGGACTTCCAAGCCACCTTTGTTCAAGGAAGTGAAGTACAAGATGCCCCGGCA  4512625
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CDS:hypothetical pro  1                                                  M  P  R  H

CDS: Putative 11      5          L  R  Q  S  A  S  A  E  P  I  C  V  D  I  T  A  L  H  P  R
Query                 16741    TTTGCGACAAAGCGCGAGTGCCGAACCAATTTGTGTTGATATCACAGCCCTGCATCCCCG  16800
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4512626  TTTGCGACAAAGCGCGAGTGCCGAACCAATTTGTGTTGATATCACAGCCCTGCATCCCCG  4512685
CDS:hypothetical pro  5          L  R  Q  S  A  S  A  E  P  I  C  V  D  I  T  A  L  H  P  R

CDS: Putative 11      25         Y  A  S  G  D  G  K  G  A  Q  S  L  A  A  P  F  L  W  Q  R
Query                 16801    CTATGCCAGTGGTGACGGAAAAGGAGCGCAGTCGCTGGCGGCCCCCTTTCTTTGGCAGAG  16860
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4512686  CTATGCCAGTGGTGACGGAAAAGGAGCGCAGTCGCTGGCGGCCCCCTTTCTTTGGCAGAG  4512745
CDS:hypothetical pro  25         Y  A  S  G  D  G  K  G  A  Q  S  L  A  A  P  F  L  W  Q  R

CDS: Putative 11      45         W  Q  R  E  N  E  T  V  D  I  E  L  F  G  S  D  A  V  W  L
Query                 16861    GTGGCAGCGCGAAAATGAAACCGTTGACATCGAACTCTTTGGTTCCGATGCCGTTTGGCT  16920
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4512746  GTGGCAGCGCGAAAATGAAACCGTTGACATCGAACTCTTTGGTTCCGATGCCGTTTGGCT  4512805
CDS:hypothetical pro  45         W  Q  R  E  N  E  T  V  D  I  E  L  F  G  S  D  A  V  W  L

CDS: Putative 11      65         N  P  D  A  T  T  I  S  A  P  D  L  F  F  A  K  D  N  A  T
Query                 16921    GAATCCCGATGCGACCACCATTTCTGCGCCAGATCTGTTTTTCGCCAAAGACAACGCCAC  16980
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4512806  GAATCCCGATGCGACCACCATTTCTGCGCCAGATCTGTTTTTCGCCAAAGACAACGCCAC  4512865
CDS:hypothetical pro  65         N  P  D  A  T  T  I  S  A  P  D  L  F  F  A  K  D  N  A  T

CDS: Putative 11      85         E  L  F  D  P  A  A  R  A  F  T  T  R  L  R  E  E  F  K  N
Query                 16981    TGAGCTTTTTGACCCCGCCGCCCGCGCGTTCACTACTCGGCTACGCGAAGAGTTCAAGAA  17040
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4512866  TGAGCTTTTTGACCCCGCCGCCCGCGCGTTCACTACTCGGCTACGCGAAGAGTTCAAGAA  4512925
CDS:hypothetical pro  85         E  L  F  D  P  A  A  R  A  F  T  T  R  L  R  E  E  F  K  N

CDS: Putative 11      105        D  T  L  I  W  L  A  P  D  F  L  N  D  F  E  L  E  V  I  R
Query                 17041    CGATACACTCATCTGGCTTGCGCCTGACTTTCTCAACGATTTCGAGCTTGAAGTCATCCG  17100
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4512926  CGATACACTCATCTGGCTTGCGCCTGACTTTCTCAACGATTTCGAGCTTGAAGTCATCCG  4512985
CDS:hypothetical pro  105        D  T  L  I  W  L  A  P  D  F  L  N  D  F  E  L  E  V  I  R

CDS: Putative 11      125        R  N  L  N  A  R  F  P  N  A  E  P  L  P  R  S  V  A  A  V
Query                 17101    TCGCAACCTCAACGCGCGTTTCCCGAATGCCGAGCCGTTGCCGCGAAGTGTGGCGGCCGT  17160
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4512986  TCGCAACCTCAACGCGCGTTTCCCGAATGCCGAGCCGTTGCCGCGAAGTGTGGCGGCCGT  4513045
CDS:hypothetical pro  125        R  N  L  N  A  R  F  P  N  A  E  P  L  P  R  S  V  A  A  V

CDS: Putative 11      145        F  A  Q  A  D  P  A  K  I  T  G  E  G  Y  A  I  I  V  V  D
Query                 17161    GTTCGCTCAAGCTGACCCGGCCAAAATCACGGGCGAGGGTTACGCCATCATCGTCGTTGA  17220
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4513046  GTTCGCTCAAGCTGACCCGGCCAAAATCACGGGCGAGGGTTACGCCATCATCGTCGTTGA  4513105
CDS:hypothetical pro  145        F  A  Q  A  D  P  A  K  I  T  G  E  G  Y  A  I  I  V  V  D
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CDS: Putative 11      165        S  I  G  G  K  T  T  A  T  K  L  I  A  K  R  D  K  D  L  A
Query                 17221    TTCCATTGGCGGCAAGACGACCGCCACCAAGCTCATCGCCAAGCGCGACAAAGACCTGGC  17280
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4513106  TTCCATTGGCGGCAAGACGACCGCCACCAAGCTCATCGCCAAGCGCGACAAAGACCTGGC  4513165
CDS:hypothetical pro  165        S  I  G  G  K  T  T  A  T  K  L  I  A  K  R  D  K  D  L  A

CDS: Putative 11      185        K  R  L  P  I  T  K  G  F  Y  W  E  R  C  P  P  V  V  I  P
Query                 17281    GAAACGTCTTCCCATCACCAAAGGCTTTTATTGGGAGCGTTGCCCGCCGGTTGTTATCCC  17340
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4513166  GAAACGTCTTCCCATCACCAAAGGCTTTTATTGGGAGCGTTGCCCGCCGGTTGTTATCCC  4513225
CDS:hypothetical pro  185        K  R  L  P  I  T  K  G  F  Y  W  E  R  C  P  P  V  V  I  P

CDS: Putative 11      205        G  E  E  A  E  R  L  G  G  S  G  Y  D  I  I  T  L  D  A  N
Query                 17341    TGGCGAGGAAGCAGAAAGGCTAGGTGGCAGCGGCTACGACATCATCACGCTGGATGCCAA  17400
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4513226  TGGCGAGGAAGCAGAAAGGCTAGGTGGCAGCGGCTACGACATCATCACGCTGGATGCCAA  4513285
CDS:hypothetical pro  205        G  E  E  A  E  R  L  G  G  S  G  Y  D  I  I  T  L  D  A  N

CDS: Putative 11      225        G  R  W  H  D  A  I  R  P  A  K  P  P  F  I  E  A  A  H  L
Query                 17401    CGGGCGGTGGCACGATGCGATCCGCCCGGCAAAGCCCCCATTCATTGAGGCAGCACACCT  17460
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4513286  CGGGCGGTGGCACGATGCGATCCGCCCGGCAAAGCCCCCATTCATTGAGGCAGCACACCT  4513345
CDS:hypothetical pro  225        G  R  W  H  D  A  I  R  P  A  K  P  P  F  I  E  A  A  H  L

CDS: Putative 11      245        K  R  I  P  N
Query                 17461    GAAGCGTATTCCAAAC  17476
                               ||||||||||||||||
Sbjct                 4513346  GAAGCGTATTCCAAAC  4513361
CDS:hypothetical pro  245        K  R  I  P  N
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>gb|CP000884.1| Delftia acidovorans SPH-1, complete genome
Length=6767514

Features in this part of subject sequence:
  Cold-shock protein DNA-binding
  Chromosome segregation ATPase-like protein

Score = 3.110e+04 bits (16843), Expect = 0.0
Identities = 17266/17477 (99%), Gaps = 2/17477 (0%)
Strand=Plus/Minus

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CDS: Putative 11      1          I  E  T  Q  G  R  T  F  V  G  D  N  G  R  Y  T  K  T  D
Query                 1        GGATCGAGACGCAAGGGCGAACCTTTGTGGGCGACAACGGACGCTACACAAAAACAGATT  60
                               ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct                 4600512  GGATCGAGACGCAAGGGCGAACCTTTGTGGGCGATAACGGACGCTACACAAAAACAGATT  4600453
CDS:hypothetical pro  303      R  I  E  T  Q  G  R  T  F  V  G  D  N  G  R  Y  T  K  T  D

CDS: Putative 11      20       L  I  V  T  D  L  R  V  P  V  I  L  G  R  G  E  G  M  G  A
Query                 61       TGATAGTCACCGACTTGCGGGTTCCGGTCATTCTGGGGCGTGGTGAGGGCATGGGGGCTC  120
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                                 |||||||||| |||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct                  4600452  TGATAGTCACTGACTTGCGGGTTCCGGTCATTCTGGGACGTGGTGAGGGCATGGGGGCTC  4600393
CDS:hypothetical pro   323      L  I  V  T  D  L  R  V  P  V  I  L  G  R  G  E  G  M  G  A

CDS: Putative 11       40       P  V  G  G  S  M  A  F  E  V  K  C  G  K  A  E  Y  L  Y  S
Query                  121      CGGTGGGCGGCTCGATGGCATTCGAAGTGAAATGCGGCAAGGCGGAATACCTCTATTCGC  180
                                 | ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4600392  CTGTGGGAGGCTCGATGGCATTCGAAGTGAAATGCGGCAAGGCGGAATACCTCTATTCGC  4600333
CDS:hypothetical pro   343      P  V  G  G  S  M  A  F  E  V  K  C  G  K  A  E  Y  L  Y  S

CDS: Putative 11       60       Q  K  D  H  M  I  F  Q  A  E  G  H  K  Q  A  D  A  Q  C  T
Query                  181      AGAAAGATCACATGATTTTTCAGGCTGAAGGGCACAAGCAAGCAGATGCGCAATGCACTC  240
                                 |||||||||||||||||||||||||| |||||||||||||||||||| |||||||||||||
Sbjct                  4600332  AGAAAGATCACATGATTTTTCAGGCCGAAGGGCACAAGCAAGCAGACGCGCAATGCACTC  4600273
CDS:hypothetical pro   363      Q  K  D  H  M  I  F  Q  A  E  G  H  K  Q  A  D  A  Q  C  T

CDS: Putative 11       80       L  C  S  R  D  I  H  D  L  P  E  E  K  Q  K  E  L  R  D  A
Query                  241      TTTGCTCGCGAGATATCCACGATTTGCCAGAAGAAAAACAGAAAGAACTGCGCGACGCCT  300
                                 ||||||| ||||| |||||||||||||||||||||||||||||||||||||||||| |||
Sbjct                  4600272  TTTGCTCACGAGACATCCACGATTTGCCAGAAGAAAAACAGAAAGAACTGCGCGATGCCC  4600213
CDS:hypothetical pro   383      L  C  S  R  D  I  H  D  L  P  E  E  K  Q  K  E  L  R  D  A

CDS: Putative 11       100      L  R  E  A  G  S  P  M  V  G  M  L  P  R  K  N  E  I  D  Q
Query                  301      TGCGCGAAGCTGGCTCACCAATGGTGGGAATGTTGCCAAGGAAAAATGAAATAGATCAGT  360
                                 |||||||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||
Sbjct                  4600212  TGCGCGAAGCTGGCTCACCGATGGTGGGAATGCTGCCAAGGAAAAATGAAATAGATCAGT  4600153
CDS:hypothetical pro   403      L  R  E  A  G  S  P  M  V  G  M  L  P  R  K  N  E  I  D  Q

CDS: Putative 11       120      S  C  L  D  F  I  R  Q  N  E  E  E  Q  P  *
Query                  361      CCTGTCTTGATTTCATCCGCCAAAACGAGGAGGAGCAACCATGAAAATACGTTTCGCAAT  420
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4600152  CCTGTCTTGATTTCATCCGCCAAAACGAGGAGGAGCAACCATGAAAATACGTTTCGCAAT  4600093
CDS:hypothetical pro   423      S  C  L  D  F  I  R  Q  N  E  E  E  Q  P

Query                  421      TATTAGCCATGACCTTCTCGCACAAGTCCGGGCTGAAGTTGATGTCCTCCTGCATGCAGT  480
                                 |||||||||||||||||||||||||||||||||||| |||||||| ||||||| ||||||
Sbjct                  4600092  TATTAGCCATGACCTTCTCGCACAAGTCCGGGCTGAGGTTGATGTTCTCCTGCGTGCAGT  4600033

Query                  481      AAATGTCGGAGATATGGATGGCGTGGATGCGTCCACCGCACGCCTCTTGGAGCTGACAGT  540
                                 ||||||||| ||||||| || ||||||||||||||||||||||||||||||||||||||||
Sbjct                  4600032  CAATGTCGGAAATATGGACGGTGTGGATGCGTCCACCGCACGCCTCTTGGAGCTGACAGT  4599973

Query                  541      TGATTGCAGATCGATTGAGTTGTCCGAGGAAGAGTGGCGCGCATTTCTAAGCGAAATCAG  600
                                 | |||||||||||||||||||||||||| |||||||||||||||||||||||||| ||||
Sbjct                  4599972  TAATTGCAGATCGATTGAGTTGTCCGAGCAAGAGTGGCGCGCATTTCTAAGCGAACTCAG  4599913

Query                  601      GGCCAAGAACCCTGAGTTCGAATCGAGCTACTTGTTGCCTGGGACTATTTGCGCGCCCCT  660
                                 |||||||| ||| |||||||||||||||||| | |||||||||||||||||||| |||||
Sbjct                  4599912  GGCCAAGAGCCCGGAGTTCGAATCGAGCTACCTTTTGCCTGGGACTATTTGCGCACCCCT  4599853
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CDS: Putative 10      1                                   M  F  S  N  F  Q  S  M  V  I
Query                 661      GTTTCCAAACCTCTCGGTAGCTGACGACTATGTTCTCGAACTTCCAATCGATGGTGATAT  720
                               |||||| ||  |||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct                 4599852  GTTTCCCAAAGTCTCGGTAGCTGACCACTATGTTCTCGAACTTCCAATCGATGGTGATAT  4599793
CDS:hypothetical pro  1                                   M  F  S  N  F  Q  S  M  V  I

CDS: Putative 10      11       W  K  R  R  K  L  M  F  D  E  A  F  G  M  A  A  M  C  A  G
Query                 721      GGAAGAGGAGGAAGCTAATGTTTGATGAGGCCTTTGGAATGGCTGCGATGTGCGCTGGAA  780
                               ||||||||||||||||| ||||||||||||||| |||||||||||||||||||| |||||||
Sbjct                 4599792  GGAAGAGGAGGAAGCTGATGTTTGATGAGGCTTTTGGAATGGCTGCGATGTGTGCTGGAA  4599733
CDS:hypothetical pro  11       W  K  R  R  K  L  M  F  D  E  A  F  G  M  A  A  M  C  A  G

CDS: Putative 10      31       K  F  R  E  G  V  R  D  T  F  G  A  S  I  V  A  D  V  L  D
Query                 781      AATTTCGCGAGGGAGTGCGTGATACGTTCGGCGCGTCCATTGTTGCTGATGTACTTGATC  840
                               |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct                 4599732  AATTTCGCGAGGGAGTGCGTGATACGTTCGGCGCGTCCATTGTTGCCGATGTACTTGATC  4599673
CDS:hypothetical pro  31       K  F  R  E  G  V  R  D  T  F  G  A  S  I  V  A  D  V  L  D

CDS: Putative 10      51       P  I  L  K  E  V  D  S  L  R  I  F  N  A  A  Y  Q  Q  Q  S
Query                 841      CGATTCTCAAGGAAGTCGATTCACTCCGCATTTTCAATGCGGCTTACCAGCAGCAATCGC  900
                               |||||||||||||||||||||||||| ||||||||||||| ||||  ||||| |||||||
Sbjct                 4599672  CGATTCTCAAGGAAGTCGATTCACTCTGCATTTTCAATGCTGCTTTTCAGCAACAATCGC  4599613
CDS:hypothetical pro  51       P  I  L  K  E  V  D  S  L  C  I  F  N  A  A  F  Q  Q  Q  S

CDS: Putative 10      71       L  A  I  D  R  T  L  N  D  V  R  E  L  Q  F  K  D  S  G  W
CDS: Putative 9       1                                                                 V  E
Query                 901      TCGCCATTGATCGAACTTTGAATGACGTTCGCGAGCTCCAGTTCAAAGACAGTGGGTGGA  960
                               |||||||||||||||||||||||||||||||||||||| || ||||||||||| |||||||
Sbjct                 4599612  TCGCCATTGATCGAACTTTGAATGACGTTCGCGAGCTTCAATTCAAAGACAGCGGGTGGA  4599553
CDS:cell divisionFts  1                                                                 M  E
CDS:hypothetical pro  71       L  A  I  D  R  T  L  N  D  V  R  E  L  Q  F  K  D  S  G  W

CDS: Putative 10      91       N  Q  *
CDS: Putative 9       3          S  M  S  E  S  A  K  D  F  Q  S  V  I  F  K  L  H  K  A  I
Query                 961      ATCAATGAGTGAAAGCGCGAAGGATTTTCAGAGCGTAATTTTCAAGCTACACAAGGCAAT  1020
                               ||||||||||| |||||| |||||||||||||| | |||| |||||||||||||||| |
Sbjct                 4599552  ATCAATGAGTGGAAGCGCAAAGGATTTTCAGAGCATCATTTCCAAGCTACACAAGGCAGT  4599493
CDS:cell divisionFts  3          S  M  S  G  S  A  K  D  F  Q  S  I  I  S  K  L  H  K  A  V
CDS:hypothetical pro  91       N  Q

CDS: Putative 9       23         A  D  Y  Q  E  G  C  A  R  I  D  R  E  F  N  A  T  K  K  T
Query                 1021     TGCGGACTATCAAGAAGGTTGTGCGCGCATCGACCGCGAATTCAATGCCACTaaaaaaaC  1080
                               |||||||||||||||||||||||||||||||||||||||||||| || |||| |||||| |
Sbjct                 4599492  TGCGGACTATCAAGAAGGTTGTGCGCGCATCGACCGCGAATTCGATACCACCAAAAAAGC  4599433
CDS:cell divisionFts  23         A  D  Y  Q  E  G  C  A  R  I  D  R  E  F  D  T  T  K  K  A

CDS: Putative 9       43         L  N  E  D  Q  E  R  N  R  S  I  R  K  S  N  W  Q  A  G  F
Query                 1081     ATTGAACGAAGACCAGGAGCGCAATCGGAGCATAAGGAAGTCGAATTGGCAGGCAGGCTT  1140
                               ||| | |||||||||||| |||||||| | |||||||| |||||||||||||||||| ||
Sbjct                 4599432  ATTAAGCGAAGACCAGGAACGCAATCGAAACATAAGGAGGTCGAATTGGCAGGCAGGTTT  4599373
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CDS:cell divisionFts  43          L  S  E  D  Q  E  R  N  R  N  I  R  R  S  N  W  Q  A  G  F

CDS: Putative 9       63          V  R  E  W  E  S  N  A  T  A  I  A  N  A  S  A  Q  L  R  Q
Query                 1141     TGTCAGAGAGTGGGAAAGTAATGCAACTGCTATAGCGAACGCAAGTGCACAGCTTAGACA  1200
                               |  || ||||||||||| |||||||||||||||||||||||||||  | ||||| |||||
Sbjct                 4599372  TTCCAAAGAGTGGGAAAGAAATGCAACTGCTATAGCGAACGCAAGCTCGCAGCTCAGACA  4599313
CDS:cell divisionFts  63          S  K  E  W  E  R  N  A  T  A  I  A  N  A  S  S  Q  L  R  Q

CDS: Putative 9       83          H  Q  P  A  F  V  D  F  C  V  D  K  P  L  M  A  S  E  I  P
Query                 1201     ACATCAGCCTGCCTTCGTGGATTTTTGTGTAGACAAGCCATTGATGGCATCGGAAATTCC  1260
                               ||| || ||||||||||||||||||||||||| |||||||||||||||| ||||||||
Sbjct                 4599312  ACAACAACCTGCCTTCGTGGATTTTTGTGTAGATAAGCCATTGATGGCATCAGAAATTCC  4599253
CDS:cell divisionFts  83          Q  Q  P  A  F  V  D  F  C  V  D  K  P  L  M  A  S  E  I  P

CDS: Putative 9       103         A  G  L  V  L  G  S  E  Q  V  S  F  E  K  L  S  C  Q  S  P
Query                 1261     AGCAGGTCTTGTGCTTGGCTCGGAGCAAGTCTCTTTTGAGAAGCTCTCTTGTCAATCCCC  1320
                               ||||||||||||||||||| |||||||||||||||||||||||||| ||||||||  ||||
Sbjct                 4599252  AGCAGGTCTTGTGCTTGGCACGGAGCAAGTCTCTTTTGAGAAGCTATCTTGTCAGGCCCC  4599193
CDS:cell divisionFts  103         A  G  L  V  L  G  T  E  Q  V  S  F  E  K  L  S  C  Q  A  P

CDS: Putative 9       123         K  V  I  S  F  P  F  S  S  A  L  V  F  P  Q  G  D  A  E  K
Query                 1321     AAAAGTCATCTCTTTCCCCTTCTCCAGCGCTCTTGTTTTTCCGCAAGGCGATGCGGAGAA  1380
                                ||| ||||||| |||||||| ||||| ||||||||||| | ||||||||||| ||| |
Sbjct                 4599192  TAAATTCATCTCATTCCCCTTATCCAGTGCTCTTGTTTTTTCACAAGGCGATGCAGAGCA  4599133
CDS:cell divisionFts  123         K  F  I  S  F  P  L  S  S  A  L  V  F  S  Q  G  D  A  E  Q

CDS: Putative 9       143         K  R  L  A  H  C  L  L  L  R  L  L  S  A  L  P  A  G  Q  V
Query                 1381     GAAAAGACTCGCGCATTGTCTCTTGTTGCGGTTGCTGTCGGCTTTGCCTGCAGGTCAAGT  1440
                               |||| | |||| ||||||||||||||| |||||||||  |||||||||||||||||||||
Sbjct                 4599132  GAAACGCCTCGTGCATTGTCTCTTGTTACGGTTGCTGCAGGCTTTGCCTGCAGGTCAAGT  4599073
CDS:cell divisionFts  143         K  R  L  V  H  C  L  L  L  R  L  L  Q  A  L  P  A  G  Q  V

CDS: Putative 9       163         E  L  T  L  I  D  P  L  Q  Q  G  Q  S  V  E  P  F  L  P  L
Query                 1441     AGAGTTGACACTGATTGACCCCCTACAGCAGGGTCAATCGGTCGAGCCGTTCCTACCATT  1500
                               ||||||||||||||||||||||||| |||||||| |||||||||||||||||||  |||||
Sbjct                 4599072  AGAGTTGACACTGATTGACCCCCTGCAGCAGGGGCAATCGGTCGAGCCGTTCCGGCCATT  4599013
CDS:cell divisionFts  163         E  L  T  L  I  D  P  L  Q  Q  G  Q  S  V  E  P  F  R  P  L

CDS: Putative 9       183         L  K  V  E  Q  L  V  P  Q  G  H  V  L  T  R  A  D  E  I  E
Query                 1501     GCTGAAGGTTGAGCAATTGGTGCCGCAAGGTCATGTTCTTACTCGTGCGGACGAAATCGA  1560
                               ||||||||| |||||||||||||||||||||||||||||||||||| |||| ||||||||
Sbjct                 4599012  GCTGAAGGTAGAGCAATTGGTGCCGCAAGGTCATGTTCTTACTCGTTCGGATGAAATCGA  4598953
CDS:cell divisionFts  183         L  K  V  E  Q  L  V  P  Q  G  H  V  L  T  R  S  D  E  I  E

CDS: Putative 9       203         A  A  L  G  Q  L  T  D  E  I  E  E  L  I  Q  L  R  F  N  E
Query                 1561     AGCAGCGCTCGGACAACTGACGGACGAAATTGAGGAGCTGATCCAGCTGCGGTTCAATGA  1620
                               ||| ||||||||| | |||||||||||||||||||||| ||||||||| ||||||||||||
Sbjct                 4598952  AGCTGCGCTCGGAAAGCTGACGGACGAAATTGAGGAGTTGATCCAGCAGCGGTTCAATGA  4598893
CDS:cell divisionFts  203         A  A  L  G  K  L  T  D  E  I  E  E  L  I  Q  Q  R  F  N  D
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CDS: Putative 9       223        K  A  S  N  W  L  K  Y  N  A  V  Q   P  D  A  P  L  P  Y
Query                 1621     GAAGGCATCCAACTGGTTGAAATACAACGCAGTTCAA-CCCGATGCCCCGTTGCCTTACA  1679
                                |||||||||||||||| | |||||||||| | |||| ||||      | || |||||||
Sbjct                 4598892  CAAGGCATCCAACTGGTCGGAATACAACGC-GATCAACCCCGGCAATTCATTACCTTACA  4598834
CDS:cell divisionFts  223        K  A  S  N  W  S  E  Y  N  A   I  N  P  G  N  S  L  P  Y

CDS: Putative 9       242      K  V  V  L  L  F  D  V  P  E  Q  I  S  E  K  S  L  W  L  L
Query                 1680     AGGTAGTACTGCTCTTTGATGTGCCAGAGCAGATATCGGAAAAATCTCTTTGGCTCCTTG  1739
                               |||| ||  |||| |||||||||||||||||||| ||||||||||||| ||| | ||||
Sbjct                 4598833  AGGTGGTGGTGCTTTTTGATGTGCCAGAGCAGATGTCGGAAAAATCTCTCTGGTTTCTTG  4598774
CDS:cell divisionFts  242      K  V  V  V  L  F  D  V  P  E  Q  M  S  E  K  S  L  W  F  L

CDS: Putative 9       262      G  R  I  C  E  N  G  P  R  C  G  V  L  P  I  I  A  I  D  E
Query                 1740     GACGCATCTGCGAAAACGGTCCACGCTGCGGCGTGCTGCCCATCATTGCAATTGATGAGC  1799
                               | ||||| |  |||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct                 4598773  GCCGCATTTTTGAAAACGGTCCACGCTGCGGCGTGCTGCCCATCGTTGCAATTGATGAGC  4598714
CDS:cell divisionFts  262      G  R  I  F  E  N  G  P  R  C  G  V  L  P  I  V  A  I  D  E

CDS: Putative 9       282      Q  R  M  E  D  R  R  Y  E  K  L  N  A  T  L  K  N  S  T  T
Query                 1800     AGCGCATGGAAGACCGGCGATATGAAAAGCTCAACGCCACGCTGAAAAACTCAACCACGC  1859
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4598713  AGCGCATGGAAGACCGGCGATATGAAAAGCTCAACGCCACGCTGAAAAACTCAACCATGC  4598654
CDS:cell divisionFts  282      Q  R  M  E  D  R  R  Y  E  K  L  N  A  T  L  K  N  S  T  M

CDS: Putative 9       302      Q  L  N  D  L  L  Q  R  A  G  A  G  G  L  S  F  T  Y  Q  P
Query                 1860     AACTGAATGATCTCTTGCAACGCGCTGGGGCTGGTGGGCTGTCATTCACATATCAACCGG  1919
                               |||||||||||||| ||||| |||||||||||||| | ||||||||||||||| || ||||
Sbjct                 4598653  AACTGAATGATCTGTTGCAGCGCGCTGGGGCTGGCGAGCTGTCATTCACATACCAGCCGG  4598594
CDS:cell divisionFts  302      Q  L  N  D  L  L  Q  R  A  G  A  G  E  L  S  F  T  Y  Q  P

CDS: Putative 9       322      E  Q  W  P  R  Q  D  V  L  D  G  F  I  A  R  L  A  E  D  C
Query                 1920     AGCAATGGCCGCGACAAGATGTGCTGGATGGCTTTATCGCAAGGCTCGCTGAAGATTGTG  1979
                               |||||||||||||||| |||||||||||||||||| |||||| ||||| ||||||||||
Sbjct                 4598593  AGCAATGGCCGCGACAGGATGTGCTGGATGGCTTTCTCGCAAAGCTCGTTGAAGATTGTG  4598534
CDS:cell divisionFts  322      E  Q  W  P  R  Q  D  V  L  D  G  F  L  A  K  L  V  E  D  C

CDS: Putative 9       342      A  A  R  T  R  F  K  K  T  M  A  D  L  W  T  S  F  G  K  E
Query                 1980     CTGCTAGGACGCGCTTCAAGAAAACGATGGCTGATCTCTGGACGAGCTTCGGCAAGGAAG  2039
                               |||||| |||||||||||||||||||||| |||||||||||||||||||||||||||  |
Sbjct                 4598533  CTGCTAAGACGCGCTTCAAGAAAACGATGCCTGATCTCTGGACGAGCTTCGGCAAGGGTG  4598474
CDS:cell divisionFts  342      A  A  K  T  R  F  K  K  T  M  P  D  L  W  T  S  F  G  K  G

CDS: Putative 9       362      E  T  T  L  G  G  F  D  I  P  I  G  W  T  S  A  G  D  L  A
Query                 2040     AGACGACTCTTGGTGGCTTTGATATTCCCATCGGCTGGACGAGCGCCGGCGACCTCGCGA  2099
                               ||||||||||| |||||||||||||||||||||||||||||| | | |||||| ||||
Sbjct                 4598473  AGACGACTCTTGCTGGCTTTGATATTCCCATCGGCTGGACGACCACAGGCGACTTCGCTC  4598414
CDS:cell divisionFts  362      E  T  T  L  A  G  F  D  I  P  I  G  W  T  T  T  G  D  F  A

CDS: Putative 9       382      T  L  R  L  G  A  T  D  S  E  H  H  V  L  L  A  G  K  T  G
Query                 2100     CCCTGAGACTGGGCGCGACGGACTCCGAGCATCATGTACTGCTTGCGGGGAAGACAGGCT  2159
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4598413  CCCTGAGACTGGGCGCGACGGACTCCGAGCATCATGTACTGCTTGCGGGGAAGACAGGCT  4598354
CDS:cell divisionFts    382      P  L  R  L  G  A  T  D  S  E  H  H  V  L  L  A  G  K  T  G

CDS: Putative 9         402      S  G  K  S  N  L  L  H  V  L  I  H  T  L  C  E  K  Y  P  T
Query                   2160     CGGGAAAATCCAATCTGCTCCATGTTTTGATTCACACGTTATGCGAGAAATATCCGACCG  2219
                                 |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct                   4598353  CGGGAAAATCCAATCTGCTCCATGTTTTGATTCACACGTTATGCGAGAAATACCCGACCG  4598294
CDS:cell divisionFts    402      S  G  K  S  N  L  L  H  V  L  I  H  T  L  C  E  K  Y  P  T

CDS: Putative 9         422      E  E  L  D  L  Y  L  L  D  Y  K  E  S  T  E  F  N  I  Y  A
Query                   2220     AGGAGCTTGATCTTTATCTACTGGATTACAAGGAATCGACTGAGTTCAATATTTACGCAA  2279
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4598293  AGGAGCTTGATCTTTATCTACTGGATTACAAGGAATCGACTGAGTTCAATATTTACGCAA  4598234
CDS:cell divisionFts    422      E  E  L  D  L  Y  L  L  D  Y  K  E  S  T  E  F  N  I  Y  A

CDS: Putative 9         442      T  P  P  V  P  Q  A  R  L  V  A  T  E  S  D  P  E  Y  G  V
Query                   2280     CGCCCCCAGTCCCACAGGCCCGCCTTGTCGCTACGGAAAGTGACCCTGAATATGGCGTCA  2339
                                 | |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4598233  CTCCCCCAGTCCCACAAGCCCGCCTTGTCGCTACGGAAAGTGACCCTGAATATGGCGTCA  4598174
CDS:cell divisionFts    442      T  P  P  V  P  Q  A  R  L  V  A  T  E  S  D  P  E  Y  G  V

CDS: Putative 9         462      T  V  L  R  H  L  V  D  E  L  E  T  R  A  R  I  F  K  S  K
Query                   2340     CTGTATTAAGGCATCTTGTGGATGAACTGGAAACGCGTGCACGCATATTCAAGTCAAAAA  2399
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4598173  CTGTATTAAGGCATCTTGTGGATGAACTGGAAACGCGTGCACGCATATTCAAGTCAAAAA  4598114
CDS:cell divisionFts    462      T  V  L  R  H  L  V  D  E  L  E  T  R  A  R  I  F  K  S  K

CDS: Putative 9         482      N  V  N  D  F  S  E  Y  R  K  S  S  G  V  R  L  P  R  A  L
Query                   2400     ATGTCAACGATTTCAGCGAATACCGTAAATCAAGCGGGGTACGGTTGCCCCGCGCTCTGC  2459
                                 |||||||||||||||||||||||||| |||||||||||| |||||||||| ||||  ||||
Sbjct                   4598113  ATGTCAACGATTTCAGCGAATACCGAAAATCAAGCGGGATACGGTTGCCACGCGTCCTGC  4598054
CDS:cell divisionFts    482      N  V  N  D  F  S  E  Y  R  K  S  S  G  I  R  L  P  R  V  L

CDS: Putative 9         502      L  V  I  D  E  F  Q  I  L  F  S  E  S  R  Q  V  A  E  A  A
Query                   2460     TAGTCATAGATGAGTTCCAAATTCTGTTCTCAGAAAGTCGCCAGGTGGCAGAAGCTGCTG  2519
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4598053  TAGTCATAGATGAGTTCCAAATTCTGTTCTCAGAAAGTCGCCAGGTGGCAGAAGCTGCTG  4597994
CDS:cell divisionFts    502      L  V  I  D  E  F  Q  I  L  F  S  E  S  R  Q  V  A  E  A  A

CDS: Putative 9         522      E  Q  L  L  S  K  L  L  K  Q  G  R  S  F  G  I  H  I  L  L
Query                   2520     AGCAGCTGCTGTCGAAGCTCTTGAAACAGGGGCGCTCGTTCGGTATTCACATCCTCCTGG  2579
                                 ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4597993  AGCAGTTGCTGTCGAAGCTCTTGAAACAGGGGCGCTCGTTCGGTATTCACATCCTCCTGG  4597934
CDS:cell divisionFts    522      E  Q  L  L  S  K  L  L  K  Q  G  R  S  F  G  I  H  I  L  L

CDS: Putative 9         542      A  T  Q  T  L  K  G  I  N  A  Q  S  I  G  S  I  I  T  Q  L
Query                   2580     CTACTCAGACTTTGAAAGGCATCAACGCGCAGTCAATCGGAAGCATCATCACCCAGTTGG  2639
                                 |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct                   4597933  CTACTCAGACTTTGAAAGGCATCAACGCACAGTCAATCGGAAGCATCATCACCCAGTTGG  4597874
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CDS:cell divisionFts  542      A  T  Q  T  L  K  G  I  N  A  Q  S  I  G  S  I  I  T  Q  L

CDS: Putative 9       562      G  C  R  I  A  L  A  C  G  Q  E  D  S  A  M  I  L  G  G  G
Query                 2640     GATGCCGTATCGCACTGGCTTGTGGGCAGGAAGACTCCGCAATGATCCTCGGGGGCGGGA  2699
                               |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4597873  GATGCCGTATTGCACTGGCTTGTGGGCAGGAAGACTCCGCAATGATCCTCGGGGGCGGGA  4597814
CDS:cell divisionFts  562      G  C  R  I  A  L  A  C  G  Q  E  D  S  A  M  I  L  G  G  G

CDS: Putative 9       582      N  W  A  A  A  E  L  R  S  P  P  E  G  I  I  N  N  A  N  G
Query                 2700     ACTGGGCAGCCGCAGAGCTGCGCAGCCCACCTGAAGGCATCATCAACAATGCTAACGGTG  2759
                               | ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct                 4597813  ATTGGGCAGCCGCAGAGCTGCGCAGCCCACCTGAAGGCATCATCAACAATGCTAATGGTG  4597754
CDS:cell divisionFts  582      N  W  A  A  A  E  L  R  S  P  P  E  G  I  I  N  N  A  N  G

CDS: Putative 9       602      A  K  S  G  N  V  K  F  M  I  P  F  A  G  E  S  E  H  R  R
Query                 2760     CCAAATCCGGCAATGTGAAGTTCATGATTCCATTCGCCGGAGAAAGCGAGCATCGACGTG  2819
                               ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct                 4597753  CCAAATCCGGCAATGTGAAGTTCATGATTCCATTCGCCGGAGAAAGTGAGCATCGACGTG  4597694
CDS:cell divisionFts  602      A  K  S  G  N  V  K  F  M  I  P  F  A  G  E  S  E  H  R  R

CDS: Putative 9       622      D  L  L  T  K  L  I  A  R  T  S  L  S  G  V  A  E  K  T  K
Query                 2820     ATTTGTTGACGAAGTTGATAGCGCGTACATCTCTTTCTGGGGTGGCTGAAAAAACCAAAA  2879
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4597693  ATTTGTTGACGAAGTTGATAGCGCGTACATCTCTTTCTGGGGTGGCTGAAAAAACCAAAA  4597634
CDS:cell divisionFts  622      D  L  L  T  K  L  I  A  R  T  S  L  S  G  V  A  E  K  T  K

CDS: Putative 9       642      I  F  S  G  A  F  L  P  Q  I  P  S  P  F  E  Y  Q  T  A  C
Query                 2880     TCTTCAGCGGTGCATTCCTTCCGCAGATACCGTCTCCCTTTGAATATCAGACAGCTTGTG  2939
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4597633  TCTTCAGCGGTGCATTCCTTCCGCAGATACCGTCTCCCTTTGAATATCAGACAGCTTGTG  4597574
CDS:cell divisionFts  642      I  F  S  G  A  F  L  P  Q  I  P  S  P  F  E  Y  Q  T  A  C

CDS: Putative 9       662      A  H  E  E  A  L  L  L  G  E  N  L  A  F  D  S  K  P  L  T
Query                 2940     CGCACGAAGAAGCTCTTCTTTTGGGCGAAAACCTCGCATTCGATTCAAAACCGTTGACGG  2999
                               |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4597573  CGCATGAAGAAGCTCTTCTTTTGGGCGAAAACCTCGCATTCGATTCAAAACCGTTGACGG  4597514
CDS:cell divisionFts  662      A  H  E  E  A  L  L  L  G  E  N  L  A  F  D  S  K  P  L  T

CDS: Putative 9       682      V  P  L  T  R  R  S  A  F  N  V  L  F  S  G  Y  N  D  H  I
Query                 3000     TACCACTTACTCGTCGATCCGCGTTCAATGTTCTATTCAGCGGCTACAACGACCACATTC  3059
                               |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct                 4597513  TACCACTTACTCGTCGATCCGCGTTCAATGTTCTATTCAGCGGCTACAATGACCACATTC  4597454
CDS:cell divisionFts  682      V  P  L  T  R  R  S  A  F  N  V  L  F  S  G  Y  N  D  H  I

CDS: Putative 9       702      H  D  G  L  L  S  A  T  L  F  S  L  T  F  V  D  G  F  D  E
Query                 3060     ACGATGGACTCCTGTCCGCTACGCTTTTTAGTCTGACTTTCGTCGATGGCTTTGATGAAA  3119
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4597453  ACGATGGACTCCTGTCCGCTACGCTTTTTAGTCTGACTTTCGTCGATGGCTTTGATGAAA  4597394
CDS:cell divisionFts  702      H  D  G  L  L  S  A  T  L  F  S  L  T  F  V  D  G  F  D  E
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CDS: Putative 9       722      I  V  Y  F  N  A  R  G  V  P  P  G  G  G  F  S  A  A  A  Q
Query                 3120     TCGTGTACTTCAACGCGCGCGGGGTCCCCCCAGGAGGAGGATTCTCAGCCGCAGCGCAGA  3179
                               ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct                 4597393  TCGTGTACTTCAACGCGCGCGGGATCCCCCCAGGAGGAGGATTCTCAGCCGCAGCGCAGA  4597334
CDS:cell divisionFts  722      I  V  Y  F  N  A  R  G  I  P  P  G  G  G  F  S  A  A  A  Q

CDS: Putative 9       742      M  L  G  A  R  L  K  M  F  D  D  I  S  D  L  P  L  Q  A  I
Query                 3180     TGCTCGGTGCACGCCTCAAGATGTTCGACGATATATCCGATCTACCACTTCAAGCGATAT  3239
                               ||||||||||||||||||||||| |||||||||||||||| |||||||||||||||||||
Sbjct                 4597333  TGCTCGGTGCACGCCTCAAGATATTCGACGATATATCCGAGCTACCACTTCAAGCGATAT  4597274
CDS:cell divisionFts  742      M  L  G  A  R  L  K  I  F  D  D  I  S  E  L  P  L  Q  A  I

CDS: Putative 9       762      S  D  D  I  G  N  R  R  V  A  L  I  I  D  G  L  D  S  E  K
Query                 3240     CAGACGATATTGGGAATCGCCGCGTAGCATTGATTATCGATGGCCTGGATTCCGAGAAAG  3299
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4597273  CAGACGATATTGGGAATCGCCGCGTAGCATTGATTATCGATGGCCTGGATTCCGAGAAAG  4597214
CDS:cell divisionFts  762      S  D  D  I  G  N  R  R  V  A  L  I  I  D  G  L  D  S  E  K

CDS: Putative 9       782      A  L  Q  P  A  P  A  F  R  S  L  K  P  G  E  P  P  T  P  A
Query                 3300     CACTACAGCCAGCCCCAGCGTTTAGATCGCTCAAGCCTGGCGAACCACCTACCCCGGCTG  3359
                                |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct                 4597213  TACTACAGCCAGCCCCAGCGTTTAGATCGCCCAAGCCTGGCGAACCACCTACCCCGGCTG  4597154
CDS:cell divisionFts  782      V  L  Q  P  A  P  A  F  R  S  P  K  P  G  E  P  P  T  P  A

CDS: Putative 9       802      D  L  L  K  R  L  A  E  D  G  P  R  K  G  T  F  V  F  I  F
Query                 3360     ACTTGTTAAAGCGTCTCGCCGAGGACGGCCCAAGAAAGGGGACGTTTGTATTTATTTTTG  3419
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4597153  ACTTGTTAAAGCGTCTCGCCGAGGACGGCCCAAGAAAGGGGACGTTTGTATTTATTTTTG  4597094
CDS:cell divisionFts  802      D  L  L  K  R  L  A  E  D  G  P  R  K  G  T  F  V  F  I  F

CDS: Putative 9       822      V  D  R  W  Q  R  C  A  S  A  S  K  D  L  F  S  F  F  E  L
Query                 3420     TTGACCGTTGGCAGCGCTGTGCCAGTGCCAGCAAAGACCTTTTCTCCTTTTTCGAATTGC  3479
                               |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct                 4597093  TTGACCGTTGGCAGCGCTGTGCCAGTGCCTGCAAAGACCTTTTCTCCTTTTTCGAATTGC  4597034
CDS:cell divisionFts  822      V  D  R  W  Q  R  C  A  S  A  C  K  D  L  F  S  F  F  E  L

CDS: Putative 9       842      R  V  A  Y  C  M  N  E  D  D  A  G  S  L  V  S  G  G  V  G
Query                 3480     GCGTGGCGTACTGCATGAACGAAGACGATGCCGGATCGCTTGTGAGTGGCGGTGTTGGTA  3539
                               ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct                 4597033  GCGTGGCGTACTGCATGAATGAAGACGATGCCGGATCGCTTGTGAGTGGCGGTGTTGGTA  4596974
CDS:cell divisionFts  842      R  V  A  Y  C  M  N  E  D  D  A  G  S  L  V  S  G  G  V  G

CDS: Putative 9       862      K  F  K  G  I  E  K  P  S  R  A  V  F  V  N  K  M  T  N  D
Query                 3540     AGTTCAAAGGTATTGAAAAACCGAGCCGAGCTGTATTCGTAAACAAAATGACGAATGACA  3599
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4596973  AGTTCAAAGGTATTGAAAAACCGAGCCGAGCTGTATTCGTAAACAAAATGACGAATGACA  4596914
CDS:cell divisionFts  862      K  F  K  G  I  E  K  P  S  R  A  V  F  V  N  K  M  T  N  D

CDS: Putative 9       882      I  T  W  F  R  P  Y  V  Q  E  S  T  R  *
Query                 3600     TCACATGGTTCCGGCCATATGTTCAGGAAAGCACTCGATGAAGAGATTTCTGCTCACCTG  3659
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                            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||| ||
Sbjct                 4596913  TCACATGGTTCCGGCCATATGTTCAGGAAAGCACTCAATGAAGAGATTTCTGCTCACGTG  4596854
CDS:cell divisionFts  882      I  T  W  F  R  P  Y  V  Q  E  S  T  Q

Query                 3660     GTATGGAATCACCGATTTTCGCGCATCTCTGGGGTTTGAGAATACCGATGGCCCTATTGC  3719
                               |||||||||||||||||||||||| |||||||||||||||||||||||| ||||||||||||
Sbjct                 4596853  GTATGGAATCACCGATTTTCGCGCGTCTCTGGGGTTTGAGAATACCGACGGCCCTATTGC  4596794

Query                 3720     GAGCGCCCTTGCGGGCGCGTCCTACTCGGACATCATTATCCTGGGTTACACCCGGACGGA  3779
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4596793  GAGCGCCCTTGCGGGCGCGTCCTACTCGGACATCATTATCCTGGGTTACACCCGGACGGA  4596734

Query                 3780     TAATGATGCCAGCGAATTGATCGAGGCACAGAAGACGTTCACGCTTGAATTGGCGTCAAT  3839
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4596733  TAATGATGCCAGCGAATTGATCGAGGCACAGAAGACGTTCACGCTTGAATTGGCGTCAAT  4596674

Query                 3840     ACGAAGCATGGGGCAAGAGAAAGACTGGAAGCTTACTAATCAGTTTGTCTCCAGGTTCGC  3899
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4596673  ACGAAGCATGGGGCAAGAGAAAGACTGGAAGCTTACTAATCAGTTTGTCTCCAGGTTCGC  4596614

Query                 3900     TAATACCTCTGTCGCACATGAACATTTTGAAGCCTGGCTGAAAAAGAAAGCCGCCGCCCT  3959
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4596613  CAATACCTCTGTCGCACATGAACATTTTGAAGCCTGGCTGAAAAAGAAAGCCGCCGCCCT  4596554

Query                 3960     GGGCTGCAACGCAAGGATCCGTTTAAATAGCGAGAAACTTTACCAGCTCAACGACACCGA  4019
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4596553  GGGCTGCAACGCAAGGATCCGTTTAAATAGCGAGAAACTTTACCAGCTCAACGACACCGA  4596494

Query                 4020     AGGTATTTACGCTAGCGCAATGCGGGCGCTGGATGGGGTTGAACAGGAGCCAGGTGAAAA  4079
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4596493  AGGTATTTACGCTAGCGCAATGCGGGCGCTGGATGGGGTTGAACAGGAGCCAGGTGAAAA  4596434

Query                 4080     GCTCGTCACGCTCTATCTCAGCCCAGGAACTCCGGTGATGGCCTTTGTCTGGGCGCTCGC  4139
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4596433  GCTCGTCACGCTCTATCTCAGCCCAGGAACTCCGGTGATGGCCTTTGTCTGGGCGCTCGC  4596374

Query                 4140     GGCGCTGAGCTACCCTGAACTCaaaaaaaGACTCATAGCATCGTCCATCATTGGCAAAGC  4199
                               |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct                 4596373  GGCGCTGAGCTACCCTGAGCTCAAAAAAAGACTCATAGCATCGTCCATCATTGGCAAAGC  4596314

Query                 4200     ACCTGAAGTCATAGCGTTGCCTGCCGAGTGGCTTGAGCGACACAGCTCAAAACAGGCTGC  4259
                               ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct                 4596313  ACCTGAAGTCATAGCGTTGCCTGCTGAGTGGCTTGAGCGACACAGCTCAAAACAGGCTGC  4596254

CDS: Putative 8       1                                                                   M
Query                 4260     GATCCGAGACATCTCCAACGGGTTCGATGTGACATTCCATCTTTTTGGTGAACAACGGAT  4319
                               |||||||| |||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct                 4596253  GATCCGAGGCATCTCCAACGGGTTCGATGTGACATTCCATCTTTTTGGTGAGCAACGGAT  4596194
CDS:hypothetical pro  1                                                                   M
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CDS: Putative 8       2          P  A  L  L  S  I  R  Q  F  E  S  A  H  H  I  F  V  N  S  K
Query                 4320     GCCTGCCTTGTTGAGCATCCGGCAATTTGAGTCGGCGCATCACATTTTTGTCAACTCAAA  4379
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4596193  GCCTGCCTTGTTGAGCATCCGGCAATTTGAGTCGGCGCATCACATTTTTGTCAACTCAAA  4596134
CDS:hypothetical pro  2          P  A  L  L  S  I  R  Q  F  E  S  A  H  H  I  F  V  N  S  K

CDS: Putative 8       22         D  F  P  A  A  C  M  R  T  F  I  G  S  R  D  L  H  E  L  T
Query                 4380     AGACTTCCCTGCTGCATGTATGCGAACCTTTATTGGCTCTCGGGACCTGCATGAACTTAC  4439
                               |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct                 4596133  AGACTTCCCTGCTGCATGTATGCAAACCTTTATTGGCTCTCGGGACCTGCATGAACTTAC  4596074
CDS:hypothetical pro  22         D  F  P  A  A  C  M  Q  T  F  I  G  S  R  D  L  H  E  L  T

CDS: Putative 8       42         V  D  P  W  D  D  R  A  V  H  E  Q  I  T  K  L  A  K  Q  F
Query                 4440     CGTTGACCCCTGGGATGATCGTGCTGTTCACGAACAAATCACCAAGCTGGCAAAGCAATT  4499
                               |||||||||||||||||||||| ||||||||||||||||||||| |||||||||||||||
Sbjct                 4596073  CGTTGACCCCTGGGATGATCGCGCTGTTCACGAACAAATCACCGAGCTGGCAAAGCAATT  4596014
CDS:hypothetical pro  42         V  D  P  W  D  D  R  A  V  H  E  Q  I  T  E  L  A  K  Q  F

CDS: Putative 8       62         P  E  K  T  R  I  G  I  N  L  T  G  G  T  K  L  M  F  A  G
Query                 4500     TCCAGAAAAAACACGAATTGGAATCAATTTAACTGGCGGCACAAAACTGATGTTTGCTGG  4559
                               |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct                 4596013  TCCAGAAAAAACACGAATTGGAATCAATTTAACTGGCGGCACAAAATTGATGTTTGCTGG  4595954
CDS:hypothetical pro  62         P  E  K  T  R  I  G  I  N  L  T  G  G  T  K  L  M  F  A  G

CDS: Putative 8       82         A  L  S  A  A  R  E  L  G  A  V  P  F  Y  F  D  S  K  N  R
Query                 4560     CGCGCTCTCTGCTGCGCGTGAACTGGGCGCTGTTCCGTTTTATTTTGATAGCAAGAATCG  4619
                               ||||||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Sbjct                 4595953  CGCGCTCTCTGCTGCACGTGAACTGGGCGCTGTTCCGTTTTATTTTGACAGCAAGAATCG  4595894
CDS:hypothetical pro  82         A  L  S  A  A  R  E  L  G  A  V  P  F  Y  F  D  S  K  N  R

CDS: Putative 8       102        H  V  T  F  I  D  S  V  R  R  E  K  I  R  Q  I  D  S  I  E
Query                 4620     TCACGTCACATTCATTGACAGTGTTCGGCGCGAAAAAATCAGGCAGATTGATTCAATCGA  4679
                               || ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4595893  TCGCGTCATATTCATTGACAGTGTTCGGCGCGAAAAAATCAGGCAGATTGATTCAATCGA  4595834
CDS:hypothetical pro  102        R  V  I  F  I  D  S  V  R  R  E  K  I  R  Q  I  D  S  I  E

CDS: Putative 8       122        T  F  L  R  L  N  S  D  G  L  E  I  A  G  S  S  F  M  K  D
Query                 4680     AACATTTTTGCGCCTGAATAGCGACGGATTGGAGATTGCAGGCAGTTCCTTTATGAAGGA  4739
                                |||||||||| ||||||||||| || |||||||||||||||||||||||| ||||||||
Sbjct                 4595833  GACATTTTTGCACCTGAATAGCGATGGTTTGGAGATTGCAGGCAGTTCCTTCATGAAGGA  4595774
CDS:hypothetical pro  122        T  F  L  H  L  N  S  D  G  L  E  I  A  G  S  S  F  M  K  D

CDS: Putative 8       142        I  S  P  S  R  Q  L  L  T  K  A  L  W  L  H  R  D  K  V  R
Query                 4740     TATATCGCCAAGTCGCCAACTTCTGACCAAGGCTCTTTGGTTGCATCGTGACAAGGTGCG  4799
                               |||||||||||||||||||||||||||||| || | |||||| |||||||||||||||||||
Sbjct                 4595773  TATATCGCCAAGTCGCCAACTTCTGACCGAGACCCTTTGGCTGCATCGTGACAAGGTGCG  4595714
CDS:hypothetical pro  142        I  S  P  S  R  Q  L  L  T  E  T  L  W  L  H  R  D  K  V  R

CDS: Putative 8       162        R  F  Y  R  E  L  T  D  Y  N  N  A  F  R  P  F  E  I  C  R
Query                 4800     TAGATTTTATAGAGAACTTACCGACTATAACAATGCATTCAGGCCATTCGAGATTTGTCG  4859
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                                 |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct                  4595713  TAGATTTTATAGAGAACTGACCGACTATAACAATGCATTCAGGCCATTCGAGATTTGTCG  4595654
CDS:hypothetical pro   162        R  F  Y  R  E  L  T  D  Y  N  N  A  F  R  P  F  E  I  C  R

CDS: Putative 8        182        D  G  F  N  F  K  L  D  D  M  E  A  V  S  V  Q  G  Y  G  L
Query                  4860     TGACGGCTTCAATTTCAAGCTGGATGACATGGAGGCAGTATCCGTCCAGGGCTACGGATT  4919
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4595653  TGACGGCTTCAATTTCAAGCTGGATGACATGGAGGCAGTATCCGTCCAGGGCTACGGATT  4595594
CDS:hypothetical pro   182        D  G  F  N  F  K  L  D  D  M  E  A  V  S  V  Q  G  Y  G  L

CDS: Putative 8        202        D  L  R  F  E  K  W  P  D  F  A  K  Y  L  S  G  G  W  F  E
Query                  4920     GGATCTGAGATTTGAGAAATGGCCTGATTTCGCCAAATACCTATCTGGCGGCTGGTTCGA  4979
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4595593  GGATCTGAGATTTGAGAAATGGCCTGATTTCGCCAAATACCTATCTGGCGGCTGGTTCGA  4595534
CDS:hypothetical pro   202        D  L  R  F  E  K  W  P  D  F  A  K  Y  L  S  G  G  W  F  E

CDS: Putative 8        222        E  F  V  Y  L  Q  C  E  P  Y  E  D  A  G  V  I  Q  D  L  R
Query                  4980     GGAGTTTGTTTATTTGCAGTGCGAACCCTACGAGGATGCTGGCGTCATTCAAGACTTGCG  5039
                                 ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct                  4595533  GGAGTTTGTTTATTTGCAGTGCAAACCCTACGAGGATGCTGGCGTCATTCAAGACTTGCG  4595474
CDS:hypothetical pro   222        E  F  V  Y  L  Q  C  K  P  Y  E  D  A  G  V  I  Q  D  L  R

CDS: Putative 8        242        I  N  V  K  L  N  L  N  L  E  E  S  K  G  Y  S  S  F  G  V
Query                  5040     CATCAATGTCAAGCTGAACTTGAATTTAGAAGAGTCAAAAGGCTATTCGAGCTTCGGTGT  5099
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4595473  CATCAATGTCAAGCTGAACTTGAATTTAGAAGAGTCAAAAGGCTATTCGAGCTTCGGTGT  4595414
CDS:hypothetical pro   242        I  N  V  K  L  N  L  N  L  E  E  S  K  G  Y  S  S  F  G  V

CDS: Putative 8        262        E  Y  N  E  L  D  I  T  F  T  D  G  Y  S  L  Y  I  V  E  C
Query                  5100     TGAATACAACGAGCTGGACATCACATTCACCGACGGTTATTCGCTTTATATCGTGGAATG  5159
                                 ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct                  4595413  TGAATACAACGAGCTGGACATCACATTCACCGACGGTTATTCGCTTTATGTCGTGGAATG  4595354
CDS:hypothetical pro   262        E  Y  N  E  L  D  I  T  F  T  D  G  Y  S  L  Y  V  V  E  C

CDS: Putative 8        282        K  A  G  N  V  T  Q  E  Q  I  M  K  L  Q  N  L  V  R  F  Y
Query                  5160     CAAGGCGGGCAATGTAACGCAAGAGCAGATTATGAAGCTGCAGAACCTTGTGCGCTTCTA  5219
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4595353  CAAGGCGGGCAATGTAACGCAAGAGCAGATTATGAAGCTGCAGAACCTTGTGCGCTTCTA  4595294
CDS:hypothetical pro   282        K  A  G  N  V  T  Q  E  Q  I  M  K  L  Q  N  L  V  R  F  Y

CDS: Putative 8        302        G  G  I  E  G  R  G  I  V  A  C  C  V  P  P  N  T  E  S  A
Query                  5220     CGGAGGAATTGAAGGTCGCGGTATCGTTGCCTGCTGTGTTCCGCCAAATACTGAGTCGGC  5279
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4595293  CGGAGGAATTGAAGGTCGCGGTATCGTTGCCTGCTGTGTTCCGCCAAATACTGAGTCGGC  4595234
CDS:hypothetical pro   302        G  G  I  E  G  R  G  I  V  A  C  C  V  P  P  N  T  E  S  A

CDS: Putative 8        322        K  K  K  I  K  D  A  R  L  M  L  W  S  G  A  S  L  S  E  Q
Query                  5280     CAAGaaaaaaaTAAAAGATGCCAGACTGATGCTTTGGAGTGGTGCATCACTTTCTGAGCA  5339
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4595233  CAAGAAAAAAATAAAAGATGCCAGACTGATGCTTTGGAGTGGTGCATCACTTTCTGAGCA  4595174
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CDS:hypothetical pro  322        K  K  K  I  K  D  A  R  L  M  L  W  S  G  A  S  L  S  E  Q

CDS: Putative 8       342        I  T  A  M  M  N  S  I  T  E  R  A  E  A  S  E  A  T  P  *
CDS: Putative 7       1                                                                  M
Query                 5340     GATAACGGCAATGATGAACAGCATCACTGAGCGGGCTGAAGCGAGTGAGGCAACGCCATG  5399
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4595173  GATAACGGCAATGATGAACAGCATCACTGAGCGGGCTGAAGCGAGTGAGGCAACGCCATG  4595114
CDS:hypothetical pro  1                                                                  M
CDS:hypothetical pro  342        I  T  A  M  M  N  S  I  T  E  R  A  E  A  S  E  A  T  P

CDS: Putative 7       2         M  L  H  L  V  C  D  I  S  G  S  M  S  E  G  G  K  P  F  I
Query                 5400     ATGCTCCATTTGGTTTGCGACATCTCCGGCAGCATGAGTGAAGGAGGCAAGCCCTTCATC  5459
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4595113  ATGCTCCATTTGGTTTGCGACATCTCCGGCAGCATGAGTGAAGGAGGCAAGCCCTTCATC  4595054
CDS:hypothetical pro  2         M  L  H  L  V  C  D  I  S  G  S  M  S  E  G  G  K  P  F  I

CDS: Putative 7       22        L  R  T  L  A  T  T  V  A  Q  W  V  R  Q  G  Y  G  K  A  E
Query                 5460     CTGCGAACCTTGGCCACGACCGTGGCGCAATGGGTGCGGCAAGGGTATGGAAAGGCGGAA  5519
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4595053  CTGCGAACCTTGGCCACGACCGTGGCGCAATGGGTGCGGCAAGGGTATGGAAAGGCGGAA  4594994
CDS:hypothetical pro  22        L  R  T  L  A  T  T  V  A  Q  W  V  R  Q  G  Y  G  K  A  E

CDS: Putative 7       42        I  R  L  C  A  W  S  S  E  A  R  S  I  P  D  W  S  V  T  D
Query                 5520     ATCCGCCTTTGTGCTTGGAGCAGCGAGGCACGCAGCATCCCGGACTGGAGCGTCACGGAC  5579
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594993  ATCCGCCTTTGTGCTTGGAGCAGCGAGGCACGCAGCATCCCGGACTGGAGCGTCACGGAC  4594934
CDS:hypothetical pro  42        I  R  L  C  A  W  S  S  E  A  R  S  I  P  D  W  S  V  T  D

CDS: Putative 7       62        D  L  P  V  E  M  L  V  C  H  G  S  T  N  G  Q  A  L  V  Q
Query                 5580     GATCTCCCGGTCGAAATGCTGGTTTGCCATGGAAGCACCAATGGCCAGGCGCTGGTTCAA  5639
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594933  GATCTCCCGGTCGAAATGCTGGTTTGCCATGGAAGCACCAATGGCCAGGCGCTGGTTCAA  4594874
CDS:hypothetical pro  62        D  L  P  V  E  M  L  V  C  H  G  S  T  N  G  Q  A  L  V  Q

CDS: Putative 7       82        L  L  G  N  E  P  D  G  K  V  L  I  L  T  D  G  F  W  T  R
Query                 5640     CTGCTGGGTAACGAGCCGGATGGAAAGGTTCTGATCCTCACGGATGGATTCTGGACAAGA  5699
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594873  CTGCTGGGTAACGAGCCGGATGGAAAGGTTCTGATCCTCACGGATGGATTCTGGACAAGA  4594814
CDS:hypothetical pro  82        L  L  G  N  E  P  D  G  K  V  L  I  L  T  D  G  F  W  T  R

CDS: Putative 7       102       D  D  V  K  T  L  S  R  W  Q  E  G  L  P  P  D  T  L  R  V
Query                 5700     GACGACGTGAAGACCCTGAGCCGCTGGCAGGAAGGTCTACCGCCGGACACGCTGCGCGTC  5759
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594813  GACGACGTGAAGACCCTGAGCCGCTGGCAGGAAGGTCTACCGCCGGACACGCTGCGCGTC  4594754
CDS:hypothetical pro  102       D  D  V  K  T  L  S  R  W  Q  E  G  L  P  P  D  T  L  R  V

CDS: Putative 7       122       I  Q  I  G  A  D  A  N  P  H  L  S  K  G  L  K  G  A  K  V
Query                 5760     ATCCAAATCGGCGCGGATGCCAACCCACATCTTTCCAAGGGGCTCAAAGGCGCAAAGGTG  5819
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594753  ATCCAAATCGGCGCGGATGCCAACCCACATCTTTCCAAGGGGCTCAAAGGCGCAAAGGTG  4594694
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CDS:hypothetical pro  122       I  Q  I  G  A  D  A  N  P  H  L  S  K  G  L  K  G  A  K  V

CDS: Putative 7       142       F  A  A  E  E  V  L  A  V  L  D  N  W  L  Q  A  D  E  E  W
Query                 5820     TTTGCCGCAGAAGAAGTGCTCGCCGTACTCGATAACTGGCTGCAGGCGGATGAGGAATGG  5879
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594693  TTTGCCGCAGAAGAAGTGCTCGCCGTACTCGATAACTGGCTGCAGGCGGATGAGGAATGG  4594634
CDS:hypothetical pro  142       F  A  A  E  E  V  L  A  V  L  D  N  W  L  Q  A  D  E  E  W

CDS: Putative 7       162       A  *
CDS: Putative 6       1           M  T  L  W  K  S  F  G  A  S  V  R  G  P  S  H  I  A  E
Query                 5880     GCATGACGCTTTGGAAAAGTTTTGGGGCAAGCGTTCGCGGCCCGAGCCATATCGCCGAAG  5939
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594633  GCATGACGCTTTGGAAAAGTTTTGGGGCAAGCGTTCGCGGCCCGAGCCATATCGCCGAAG  4594574
CDS:hypothetical pro  1           M  T  L  W  K  S  F  G  A  S  V  R  G  P  S  H  I  A  E
CDS:hypothetical pro  162       A

CDS: Putative 6       20       G  L  P  N  Q  D  A  W  A  K  F  H  H  V  W  G  D  G  I  V
Query                 5940     GTTTGCCAAATCAGGATGCATGGGCGAAGTTTCACCATGTTTGGGGTGATGGCATCGTCG  5999
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594573  GTTTGCCAAATCAGGATGCATGGGCGAAGTTTCACCATGTTTGGGGTGATGGCATCGTCG  4594514
CDS:hypothetical pro  20       G  L  P  N  Q  D  A  W  A  K  F  H  H  V  W  G  D  G  I  V

CDS: Putative 6       40       V  S  D  G  V  G  S  K  P  F  S  S  F  G  S  H  A  A  C  L
Query                 6000     TGTCCGACGGAGTTGGCTCCAAGCCCTTCTCCAGCTTCGGCAGCCATGCTGCCTGTCTCG  6059
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594513  TGTCCGACGGAGTTGGCTCCAAGCCCTTCTCCAGCTTCGGCAGCCATGCTGCCTGTCTCG  4594454
CDS:hypothetical pro  40       V  S  D  G  V  G  S  K  P  F  S  S  F  G  S  H  A  A  C  L

CDS: Putative 6       60       A  V  E  F  A  A  R  A  C  C  T  G  G  E  I  E  H  N  A  L
Query                 6060     CCGTCGAGTTCGCAGCCCGGGCTTGTTGCACCGGTGGTGAAATCGAACACAACGCGCTGT  6119
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594453  CCGTCGAGTTCGCAGCCCGGGCTTGTTGCACCGGTGGTGAAATCGAACACAACGCGCTGT  4594394
CDS:hypothetical pro  60       A  V  E  F  A  A  R  A  C  C  T  G  G  E  I  E  H  N  A  L

CDS: Putative 6       80       F  S  N  I  Q  A  N  W  L  R  L  V  A  P  L  E  P  R  D  C
Query                 6120     TTAGCAACATCCAAGCTAACTGGCTGAGGCTTGTCGCTCCGCTGGAACCTCGCGATTGCG  6179
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594393  TTAGCAACATCCAAGCTAACTGGCTGAGGCTTGTCGCTCCGCTGGAACCTCGCGATTGCG  4594334
CDS:hypothetical pro  80       F  S  N  I  Q  A  N  W  L  R  L  V  A  P  L  E  P  R  D  C

CDS: Putative 6       100      A  A  T  C  L  F  A  L  H  L  D  G  V  I  H  L  G  M  L  G
Query                 6180     CGGCCACCTGTCTCTTCGCACTACACCTGGATGGCGTAATCCACCTAGGGATGCTTGGCG  6239
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594333  CGGCCACCTGTCTCTTCGCACTACACCTGGATGGCGTAATCCACCTAGGGATGCTTGGCG  4594274
CDS:hypothetical pro  100      A  A  T  C  L  F  A  L  H  L  D  G  V  I  H  L  G  M  L  G

CDS: Putative 6       120      D  G  L  A  A  I  A  K  S  D  G  S  V  V  S  L  S  E  N  K
Query                 6240     ACGGACTTGCCGCTATTGCCAAGTCCGATGGATCAGTGGTTTCGCTGTCGGAAAACAAGA  6299
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594273  ACGGACTTGCCGCTATTGCCAAGTCCGATGGATCAGTGGTTTCGCTGTCGGAAAACAAGA  4594214
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CDS:hypothetical pro  120      D  G  L  A  A  I  A  K  S  D  G  S  V  V  S  L  S  E  N  K

CDS: Putative 6       140      T  Q  G  F  S  N  I  T  T  A  L  S  S  K  V  S  A  K  D  W
Query                 6300     CGCAAGGCTTCTCCAATATCACTACTGCGCTGTCCTCCAAGGTCTCCGCCAAAGACTGGC  6359
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594213  CGCAAGGCTTCTCCAATATCACTACTGCGCTGTCCTCCAAGGTCTCCGCCAAAGACTGGC  4594154
CDS:hypothetical pro  140      T  Q  G  F  S  N  I  T  T  A  L  S  S  K  V  S  A  K  D  W

CDS: Putative 6       160      Q  Y  L  S  L  P  G  E  Q  C  I  A  V  L  L  C  T  D  G  V
Query                 6360     AGTATTTGTCGCTGCCGGGGGAGCAGTGCATCGCAGTATTGCTCTGCACCGATGGGGTGG  6419
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594153  AGTATTTGTCGCTGCCGGGGGAGCAGTGCATCGCAGTATTGCTCTGCACCGATGGGGTGG  4594094
CDS:hypothetical pro  160      Q  Y  L  S  L  P  G  E  Q  C  I  A  V  L  L  C  T  D  G  V

CDS: Putative 6       180      A  D  D  L  D  N  A  D  G  F  V  S  S  F  A  E  T  H  R  T
Query                 6420     CTGACGATTTGGATAACGCTGACGGGTTTGTGAGCAGTTTCGCCGAAACGCATCGAACCC  6479
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594093  CTGACGATTTGGATAACGCTGACGGGTTTGTGAGCAGTTTCGCCGAAACGCATCGAACCC  4594034
CDS:hypothetical pro  180      A  D  D  L  D  N  A  D  G  F  V  S  S  F  A  E  T  H  R  T

CDS: Putative 6       200      L  A  P  V  S  A  N  R  R  I  H  E  M  L  E  N  W  P  T  P
Query                 6480     TCGCACCGGTAAGTGCCAACCGGCGCATCCACGAGATGCTCGAAAACTGGCCCACGCCCA  6539
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4594033  TCGCACCGGTAAGTGCCAACCGGCGCATCCACGAGATGCTCGAAAACTGGCCCACGCCCA  4593974
CDS:hypothetical pro  200      L  A  P  V  S  A  N  R  R  I  H  E  M  L  E  N  W  P  T  P

CDS: Putative 6       220      K  H  S  D  D  K  T  L  A  C  L  C  S  E  E  V  A  D  E  *
CDS: Putative 5       1                                                                M  S  N
Query                 6540     AGCACAGCGACGATAAAACCCTCGCCTGCCTGTGCAGTGAGGAGGTTGCAGATGAGTAAC  6599
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593973  AGCACAGCGACGATAAAACCCTCGCCTGCCTGTGCAGTGAGGAGGTTGCAGATGAGTAAC  4593914
CDS:serine/threonine  1                                                                M  S  N
CDS:hypothetical pro  220      K  H  S  D  D  K  T  L  A  C  L  C  S  E  E  V  A  D  E

CDS: Putative 5       4         A  E  H  Q  A  L  K  P  L  V  D  E  Y  N  N  V  H  Q  M  A
Query                 6600     GCCGAACACCAGGCTCTGAAGCCACTTGTGGATGAATACAACAATGTTCATCAGATGGCC  6659
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593913  GCCGAACACCAGGCTCTGAAGCCACTTGTGGATGAATACAACAATGTTCATCAGATGGCC  4593854
CDS:serine/threonine  4         A  E  H  Q  A  L  K  P  L  V  D  E  Y  N  N  V  H  Q  M  A

CDS: Putative 5       24        D  E  L  A  R  G  G  Q  G  V  V  Y  R  T  K  D  A  D  L  A
Query                 6660     GATGAGCTTGCGCGCGGTGGGCAAGGCGTGGTCTATCGCACCAAGGATGCGGATTTGGCC  6719
                               |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct                 4593853  GATGAGCTTGCGCGCGGTGGACAAGGCGTGGTCTATCGCACCAAGGATGCGGATTTGGCC  4593794
CDS:serine/threonine  24        D  E  L  A  R  G  G  Q  G  V  V  Y  R  T  K  D  A  D  L  A

CDS: Putative 5       44        V  K  Q  P  L  D  A  A  G  Q  P  D  K  N  A  N  L  R  E  R
Query                 6720     GTCAAGCAGCCGCTGGACGCTGCCGGCCAGCCGGACAAAAACGCCAATCTGCGCGAGCGC  6779
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593793  GTCAAGCAGCCGCTGGACGCTGCCGGCCAGCCGGACAAAAACGCCAATCTGCGCGAGCGC  4593734
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CDS:serine/threonine  44        V  K  Q  P  L  D  A  A  G  Q  P  D  K  N  A  N  L  R  E  R

CDS: Putative 5       64        F  Q  H  V  R  L  L  P  I  P  R  R  I  P  V  S  L  P  L  A
Query                 6780     TTCCAGCACGTCCGCCTGTTGCCCATACCACGGCGCATCCCCGTTTCCCTTCCACTCGCC  6839
                               ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct                 4593733  TTCCAGCACGTCCGCCTGTTGCCCATACCACGGCGCATCCCCGTTTCCCTGCCACTCGCC  4593674
CDS:serine/threonine  64        F  Q  H  V  R  L  L  P  I  P  R  R  I  P  V  S  L  P  L  A

CDS: Putative 5       84        I  L  R  D  E  P  G  Y  V  M  R  L  L  N  G  M  K  P  F  A
Query                 6840     ATCCTGCGCGACGAGCCGGGCTATGTGATGCGTCTGTTGAACGGCATGAAGCCCTTCGCC  6899
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593673  ATCCTGCGCGACGAGCCGGGCTATGTGATGCGTCTGTTGAACGGCATGAAGCCCTTCGCC  4593614
CDS:serine/threonine  84        I  L  R  D  E  P  G  Y  V  M  R  L  L  N  G  M  K  P  F  A

CDS: Putative 5       104       S  F  D  L  D  G  R  S  K  K  K  L  E  D  Q  S  Q  A  L  P
Query                 6900     AGTTTCGATTTGGACGGCAGAAGCAAAAAGAAGCTGGAAGATCAAAGCCAAGCCTTGCCC  6959
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593613  AGTTTCGATTTGGACGGCAGAAGCAAAAAGAAGCTGGAAGATCAAAGCCAAGCCTTGCCC  4593554
CDS:serine/threonine  104       S  F  D  L  D  G  R  S  K  K  K  L  E  D  Q  S  Q  A  L  P

CDS: Putative 5       124       Q  W  L  T  K  I  P  D  K  D  L  A  L  R  L  L  H  Y  A  Q
Query                 6960     CAATGGCTGACGAAGATTCCTGACAAGGACCTGGCGCTGCGACTACTGCATTACGCACAA  7019
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593553  CAATGGCTGACGAAGATTCCTGACAAGGACCTGGCGCTGCGACTACTGCATTACGCACAA  4593494
CDS:serine/threonine  124       Q  W  L  T  K  I  P  D  K  D  L  A  L  R  L  L  H  Y  A  Q

CDS: Putative 5       144       T  G  S  T  R  R  R  S  L  A  L  A  K  C  A  A  I  L  A  R
Query                 7020     ACTGGCTCCACCCGCCGCCGTTCGCTCGCGCTTGCCAAGTGCGCTGCCATCCTCGCCCGC  7079
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593493  ACTGGCTCCACCCGCCGCCGTTCGCTCGCGCTTGCCAAGTGCGCTGCCATCCTCGCCCGC  4593434
CDS:serine/threonine  144       T  G  S  T  R  R  R  S  L  A  L  A  K  C  A  A  I  L  A  R

CDS: Putative 5       164       L  H  S  A  G  L  V  Y  G  D  I  S  T  N  N  A  F  I  G  E
Query                 7080     CTGCACAGCGCTGGACTGGTCTATGGCGACATTTCCACCAACAACGCTTTCATTGGCGAA  7139
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593433  CTGCACAGCGCTGGACTGGTCTATGGCGACATTTCCACCAACAACGCTTTCATTGGCGAA  4593374
CDS:serine/threonine  164       L  H  S  A  G  L  V  Y  G  D  I  S  T  N  N  A  F  I  G  E

CDS: Putative 5       184       D  D  T  T  D  V  W  L  I  D  A  D  N  M  R  L  E  L  P  S
Query                 7140     GACGACACCACCGATGTCTGGCTCATAGATGCCGACAATATGCGCCTGGAGTTACCCAGC  7199
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593373  GACGACACCACCGATGTCTGGCTCATAGATGCCGACAATATGCGCCTGGAGTTACCCAGC  4593314
CDS:serine/threonine  184       D  D  T  T  D  V  W  L  I  D  A  D  N  M  R  L  E  L  P  S

CDS: Putative 5       204       G  G  V  S  V  Y  T  P  G  Y  G  A  P  E  V  V  Q  G  R  D
Query                 7200     GGCGGTGTGTCCGTCTATACGCCGGGCTACGGTGCACCGGAGGTAGTGCAGGGCCGTGAC  7259
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593313  GGCGGTGTGTCCGTCTATACGCCGGGCTACGGTGCACCGGAGGTAGTGCAGGGCCGTGAC  4593254
CDS:serine/threonine  204       G  G  V  S  V  Y  T  P  G  Y  G  A  P  E  V  V  Q  G  R  D
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CDS: Putative 5       224       Q  S  R  P  R  T  D  C  W  A  F  A  V  M  T  F  K  L  L  A
Query                 7260     CAATCCCGCCCGCGAACCGACTGCTGGGCTTTCGCTGTGATGACATTCAAGCTACTGGCG  7319
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593253  CAATCCCGCCCGCGAACCGACTGCTGGGCTTTCGCTGTGATGACATTCAAGCTACTGGCG  4593194
CDS:serine/threonine  224       Q  S  R  P  R  T  D  C  W  A  F  A  V  M  T  F  K  L  L  A

CDS: Putative 5       244       L  C  H  P  F  I  G  K  K  V  L  E  P  E  D  E  E  D  G  W
Query                 7320     CTTTGCCACCCTTTCATTGGCAAGAAAGTACTGGAGCCCGAAGATGAAGAAGACGGCTGG  7379
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593193  CTTTGCCACCCTTTCATTGGCAAGAAAGTACTGGAGCCCGAAGATGAAGAAGACGGCTGG  4593134
CDS:serine/threonine  244       L  C  H  P  F  I  G  K  K  V  L  E  P  E  D  E  E  D  G  W

CDS: Putative 5       264       D  A  D  P  A  P  N  G  T  A  T  D  L  N  E  Q  A  F  A  G
Query                 7380     GATGCCGACCCTGCGCCCAATGGCACTGCCACCGATCTGAACGAACAGGCATTCGCTGGT  7439
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593133  GATGCCGACCCTGCGCCCAATGGCACTGCCACCGATCTGAACGAACAGGCATTCGCTGGT  4593074
CDS:serine/threonine  264       D  A  D  P  A  P  N  G  T  A  T  D  L  N  E  Q  A  F  A  G

CDS: Putative 5       284       F  L  P  F  V  D  D  E  D  D  D  S  N  E  G  V  G  G  L  P
Query                 7440     TTCTTGCCTTTCGTGGATGACGAAGATGACGATTCCAACGAAGGAGTTGGAGGCCTGCCC  7499
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593073  TTCTTGCCTTTCGTGGATGACGAAGATGACGATTCCAACGAAGGAGTTGGAGGCCTGCCC  4593014
CDS:serine/threonine  284       F  L  P  F  V  D  D  E  D  D  D  S  N  E  G  V  G  G  L  P

CDS: Putative 5       304       R  V  L  V  A  T  E  G  L  R  R  L  F  Q  E  T  F  G  A  G
Query                 7500     CGTGTATTAGTCGCAACAGAAGGATTACGCCGCCTGTTTCAGGAAACTTTCGGTGCAGGA  7559
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4593013  CGTGTATTAGTCGCAACAGAAGGATTACGCCGCCTGTTTCAGGAAACTTTCGGTGCAGGA  4592954
CDS:serine/threonine  304       R  V  L  V  A  T  E  G  L  R  R  L  F  Q  E  T  F  G  A  G

CDS: Putative 5       324       R  E  L  P  H  R  R  P  T  M  A  F  W  T  L  E  L  A  R  A
Query                 7560     CGTGAACTGCCGCACCGCCGCCCGACAATGGCGTTCTGGACATTGGAGCTTGCGAGGGCG  7619
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4592953  CGTGAACTGCCGCACCGCCGCCCGACAATGGCGTTCTGGACATTGGAGCTTGCGAGGGCG  4592894
CDS:serine/threonine  324       R  E  L  P  H  R  R  P  T  M  A  F  W  T  L  E  L  A  R  A

CDS: Putative 5       344       A  D  Q  S  L  D  C  L  E  C  G  M  S  H  F  A  D  E  Y  A
Query                 7620     GCGGATCAGTCGCTGGATTGCCTCGAATGTGGCATGAGCCATTTCGCCGATGAATACGCG  7679
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4592893  GCGGATCAGTCGCTGGATTGCCTCGAATGTGGCATGAGCCATTTCGCCGATGAATACGCG  4592834
CDS:serine/threonine  344       A  D  Q  S  L  D  C  L  E  C  G  M  S  H  F  A  D  E  Y  A

CDS: Putative 5       364       Q  C  P  Y  C  G  A  A  R  P  A  F  I  R  V  K  T  P  R  W
Query                 7680     CAATGCCCGTATTGTGGCGCGGCGCGCCCGGCTTTCATTCGCGTCAAAACGCCACGTTGG  7739
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4592833  CAATGCCCGTATTGTGGCGCGGCGCGCCCGGCTTTCATTCGCGTCAAAACGCCACGTTGG  4592774
CDS:serine/threonine  364       Q  C  P  Y  C  G  A  A  R  P  A  F  I  R  V  K  T  P  R  W

CDS: Putative 5       384       E  I  L  I  P  G  G  A  T  E  F  R  L  P  Q  R  L  F  H  P
Query                 7740     GAAATCCTGATTCCTGGTGGTGCCACGGAGTTCAGATTGCCGCAGCGGCTTTTTCACCCG  7799
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4592773  GAAATCCTGATTCCTGGTGGTGCCACGGAGTTCAGATTGCCGCAGCGGCTTTTTCACCCG  4592714
CDS:serine/threonine    384       E  I  L  I  P  G  G  A  T  E  F  R  L  P  Q  R  L  F  H  P

CDS: Putative 5         404       F  S  F  E  Y  F  D  N  T  A  Y  E  A  M  L  N  C  A  A  K
Query                   7800     TTTTCATTCGAGTATTTCGATAACACAGCATACGAAGCCATGCTGAACTGCGCGGCCAAA  7859
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4592713  TTTTCATTCGAGTATTTCGATAACACAGCATACGAAGCCATGCTGAACTGCGCGGCCAAA  4592654
CDS:serine/threonine    404       F  S  F  E  Y  F  D  N  T  A  Y  E  A  M  L  N  C  A  A  K

CDS: Putative 5         424       T  A  V  P  V  R  G  T  L  P  F  P  D  N  L  T  F  E  F  V
Query                   7860     ACCGCAGTCCCCGTGCGGGGCACGCTGCCTTTCCCGGACAACCTCACCTTTGAGTTCGTG  7919
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4592653  ACCGCAGTCCCCGTGCGGGGCACGCTGCCTTTCCCGGACAACCTCACCTTTGAGTTCGTG  4592594
CDS:serine/threonine    424       T  A  V  P  V  R  G  T  L  P  F  P  D  N  L  T  F  E  F  V

CDS: Putative 5         444       E  G  C  K  *
CDS: Putative 4         1                   M  K  F  Q  D  I  P  V  N  I  I  T  V  R  I  K
Query                   7920     GAGGGCTGCAAATGAAGTTTCAGGACATTCCTGTCAACATCATAACTGTCCGCATCAAGC  7979
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4592593  GAGGGCTGCAAATGAAGTTTCAGGACATTCCTGTCAACATCATAACTGTCCGCATCAAGC  4592534
CDS:AAA ATPase [Delf    1                   M  K  F  Q  D  I  P  V  N  I  I  T  V  R  I  K
CDS:serine/threonine    444       E  G  C  K

CDS: Putative 4         17       R  S  D  N  V  E  A  L  Q  E  Q  P  V  F  S  V  E  A  S  L
Query                   7980     GGTCTGACAATGTCGAAGCCCTGCAAGAGCAGCCAGTATTCTCGGTAGAGGCCAGCCTAT  8039
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4592533  GGTCTGACAATGTCGAAGCCCTGCAAGAGCAGCCAGTATTCTCGGTAGAGGCCAGCCTAT  4592474
CDS:AAA ATPase [Delf    17       R  S  D  N  V  E  A  L  Q  E  Q  P  V  F  S  V  E  A  S  L

CDS: Putative 4         37       S  R  A  D  E  F  E  I  R  L  R  D  A  V  V  F  V  R  P  V
Query                   8040     CCCGCGCAGATGAATTTGAAATCCGCCTGAGAGACGCGGTTGTTTTCGTTCGCCCCGTCG  8099
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4592473  CCCGCGCAGATGAATTTGAAATCCGCCTGAGAGACGCGGTTGTTTTCGTTCGCCCCGTCG  4592414
CDS:AAA ATPase [Delf    37       S  R  A  D  E  F  E  I  R  L  R  D  A  V  V  F  V  R  P  V

CDS: Putative 4         57       A  A  V  D  I  R  R  L  N  A  E  L  A  S  G  R  S  L  L  A
Query                   8100     CGGCTGTTGACATCCGCCGCCTCAACGCTGAACTTGCCAGTGGGCGTTCCCTGCTTGCAC  8159
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4592413  CGGCTGTTGACATCCGCCGCCTCAACGCTGAACTTGCCAGTGGGCGTTCCCTGCTTGCAC  4592354
CDS:AAA ATPase [Delf    57       A  A  V  D  I  R  R  L  N  A  E  L  A  S  G  R  S  L  L  A

CDS: Putative 4         77       Q  L  E  N  P  A  A  D  G  S  I  E  L  K  I  G  F  F  T  G
Query                   8160     AACTTGAAAACCCTGCCGCCGATGGCAGCATCGAGCTGAAGATCGGTTTTTTCACCGGCG  8219
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4592353  AACTTGAAAACCCTGCCGCCGATGGCAGCATCGAGCTGAAGATCGGTTTTTTCACCGGCG  4592294
CDS:AAA ATPase [Delf    77       Q  L  E  N  P  A  A  D  G  S  I  E  L  K  I  G  F  F  T  G

CDS: Putative 4         97       V  C  L  E  M  G  D  V  E  I  G  V  D  E  Y  V  Q  E  K  M
Query                   8220     TCTGCCTGGAAATGGGCGATGTTGAAATCGGTGTGGATGAGTATGTGCAAGAAAAGATGC  8279
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4592293   TCTGCCTGGAAATGGGCGATGTTGAAATCGGTGTGGATGAGTATGTGCAAGAAAAGATGC  4592234
CDS:AAA ATPase [Delf   97        V  C  L  E  M  G  D  V  E  I  G  V  D  E  Y  V  Q  E  K  M

CDS: Putative 4        117       R  T  K  G  E  A  L  Y  K  R  L  G  E  L  C  C  F  Q  Q  G
Query                  8280      GGACGAAGGGTGAGGCACTTTACAAGAGGCTGGGCGAACTTTGCTGCTTCCAACAGGGAA  8339
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4592233   GGACGAAGGGTGAGGCACTTTACAAGAGGCTGGGCGAACTTTGCTGCTTCCAACAGGGAA  4592174
CDS:AAA ATPase [Delf   117       R  T  K  G  E  A  L  Y  K  R  L  G  E  L  C  C  F  Q  Q  G

CDS: Putative 4        137       N  D  A  F  F  F  L  T  A  G  P  A  I  D  E  E  L  K  P  V
Query                  8340      ACGACGCATTTTTCTTCCTGACTGCTGGCCCGGCGATTGATGAAGAACTGAAACCTGTCG  8399
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4592173   ACGACGCATTTTTCTTCCTGACTGCTGGCCCGGCGATTGATGAAGAACTGAAACCTGTCG  4592114
CDS:AAA ATPase [Delf   137       N  D  A  F  F  F  L  T  A  G  P  A  I  D  E  E  L  K  P  V

CDS: Putative 4        157       G  E  D  T  P  R  D  A  A  A  E  P  T  R  I  N  A  F  C  V
Query                  8400      GCGAGGACACGCCACGCGATGCAGCTGCGGAGCCGACCCGAATAAACGCTTTCTGTGTTA  8459
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4592113   GCGAGGACACGCCACGCGATGCAGCTGCGGAGCCGACCCGAATAAACGCTTTCTGTGTTA  4592054
CDS:AAA ATPase [Delf   157       G  E  D  T  P  R  D  A  A  A  E  P  T  R  I  N  A  F  C  V

CDS: Putative 4        177       T  G  E  G  I  R  F  I  A  T  E  K  A  M  P  G  G  Q  T  I
Query                  8460      CTGGCGAAGGTATCCGCTTCATTGCCACCGAAAAAGCAATGCCAGGCGGCCAAACTATCT  8519
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4592053   CTGGCGAAGGTATCCGCTTCATTGCCACCGAAAAAGCAATGCCAGGCGGCCAAACTATCT  4591994
CDS:AAA ATPase [Delf   177       T  G  E  G  I  R  F  I  A  T  E  K  A  M  P  G  G  Q  T  I

CDS: Putative 4        197       Y  I  A  T  R  L  T  K  P  K  K  E  P  D  R  T  L  R  L  A
Query                  8520      ACATCGCCACCCGTCTAACCAAGCCAAAGAAGGAACCTGACCGCACCTTACGCCTGGCCA  8579
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4591993   ACATCGCCACCCGTCTAACCAAGCCAAAGAAGGAACCTGACCGCACCTTACGCCTGGCCA  4591934
CDS:AAA ATPase [Delf   197       Y  I  A  T  R  L  T  K  P  K  K  E  P  D  R  T  L  R  L  A

CDS: Putative 4        217       K  G  R  L  R  F  V  D  W  T  Q  A  G  Q  V  Q  I  L  A  K
Query                  8580      AAGGTCGGCTGCGTTTTGTGGACTGGACACAGGCGGGACAAGTGCAAATTCTTGCCAAAG  8639
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4591933   AAGGTCGGCTGCGTTTTGTGGACTGGACACAGGCGGGACAAGTGCAAATTCTTGCCAAAG  4591874
CDS:AAA ATPase [Delf   217       K  G  R  L  R  F  V  D  W  T  Q  A  G  Q  V  Q  I  L  A  K

CDS: Putative 4        237       A  Q  M  T  A  L  T  Q  D  D  G  S  Y  L  K  K  W  D  E  F
Query                  8640      CGCAAATGACAGCACTCACTCAGGACGATGGAAGCTATCTGAAAAAGTGGGACGAGTTTG  8699
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4591873   CGCAAATGACAGCACTCACTCAGGACGATGGAAGCTATCTGAAAAAGTGGGACGAGTTTG  4591814
CDS:AAA ATPase [Delf   237       A  Q  M  T  A  L  T  Q  D  D  G  S  Y  L  K  K  W  D  E  F

CDS: Putative 4        257       G  E  V  E  G  E  L  L  L  K  Q  A  R  E  V  G  A  L  Q  F
Query                  8700      GTGAGGTTGAAGGTGAACTGCTGCTCAAGCAAGCACGCGAAGTGGGTGCTTTGCAATTCA  8759
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4591813   GTGAGGTTGAAGGTGAACTGCTGCTCAAGCAAGCACGCGAAGTGGGTGCTTTGCAATTCA  4591754
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CDS:AAA ATPase [Delf  257      G  E  V  E  G  E  L  L  L  K  Q  A  R  E  V  G  A  L  Q  F

CDS: Putative 4       277      T  E  M  V  P  K  R  D  G  T  V  G  V  R  I  A  Q  A  S  D
Query                 8760     CGGAGATGGTGCCGAAACGGGATGGAACTGTCGGAGTTCGTATTGCGCAGGCATCAGATT  8819
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4591753  CGGAGATGGTGCCGAAACGGGATGGAACTGTCGGAGTTCGTATTGCGCAGGCATCAGATT  4591694
CDS:AAA ATPase [Delf  277      T  E  M  V  P  K  R  D  G  T  V  G  V  R  I  A  Q  A  S  D

CDS: Putative 4       297      S  A  W  G  A  L  R  Q  G  A  V  P  E  V  E  L  V  D  E  L
Query                 8820     CTGCGTGGGGCGCACTGAGACAAGGCGCAGTACCTGAAGTTGAACTGGTGGACGAGTTGC  8879
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4591693  CTGCGTGGGGCGCACTGAGACAAGGCGCAGTACCTGAAGTTGAACTGGTGGACGAGTTGC  4591634
CDS:AAA ATPase [Delf  297      S  A  W  G  A  L  R  Q  G  A  V  P  E  V  E  L  V  D  E  L

CDS: Putative 4       317      P  D  Y  L  Q  D  E  N  L  S  F  T  D  F  A  R  G  I  E  K
Query                 8880     CGGACTACTTGCAGGATGAAAACCTGAGCTTCACGGATTTTGCGAGAGGGATCGaaaaaa  8939
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4591633  CGGACTACTTGCAGGATGAAAACCTGAGCTTCACGGATTTTGCGAGAGGGATCGAAAAAA  4591574
CDS:AAA ATPase [Delf  317      P  D  Y  L  Q  D  E  N  L  S  F  T  D  F  A  R  G  I  E  K

CDS: Putative 4       337      K  E  G  E  H  S  K  L  G  E  K  R  E  L  R  E  K  N  T  Y
Query                 8940     aGGAGGGGGAACACAGCAAGCTCGGTGAAAAACGCGAGCTGCGCGAGAAAAATACCTATT  8999
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4591573  AGGAGGGGGAACACAGCAAGCTCGGTGAAAAACGCGAGCTGCGCGAGAAAAATACCTATT  4591514
CDS:AAA ATPase [Delf  337      K  E  G  E  H  S  K  L  G  E  K  R  E  L  R  E  K  N  T  Y

CDS: Putative 4       357      F  S  V  A  E  F  D  E  E  T  R  V  L  T  L  K  A  E  A  L
Query                 9000     TCAGTGTCGCAGAGTTTGACGAGGAAACTCGCGTACTCACGCTTAAAGCCGAGGCTCTAC  9059
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4591513  TCAGTGTCGCAGAGTTTGACGAGGAAACTCGCGTACTCACGCTTAAAGCCGAGGCTCTAC  4591454
CDS:AAA ATPase [Delf  357      F  S  V  A  E  F  D  E  E  T  R  V  L  T  L  K  A  E  A  L

CDS: Putative 4       377      P  K  E  F  G  T  L  I  L  S  L  A  G  E  S  A  Q  I  K  R
Query                 9060     CCAAGGAATTCGGCACGCTCATCCTGTCGCTGGCGGGCGAATCTGCTCAGATCAAGCGCC  9119
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4591453  CCAAGGAATTCGGCACGCTCATCCTGTCGCTGGCGGGCGAATCTGCTCAGATCAAGCGCC  4591394
CDS:AAA ATPase [Delf  377      P  K  E  F  G  T  L  I  L  S  L  A  G  E  S  A  Q  I  K  R

CDS: Putative 4       397      R  M  A  A  R  Q  A  I  L  E  G  R  A  A  N  P  Q  L  G  L
Query                 9120     GCATGGCCGCCCGTCAAGCCATTCTGGAAGGCCGTGCCGCCAACCCCCAGCTTGGGCTGT  9179
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4591393  GCATGGCCGCCCGTCAAGCCATTCTGGAAGGCCGTGCCGCCAACCCCCAGCTTGGGCTGT  4591334
CDS:AAA ATPase [Delf  397      R  M  A  A  R  Q  A  I  L  E  G  R  A  A  N  P  Q  L  G  L

CDS: Putative 4       417      L  I  E  A  Q  G  R  I  T  Q  I  R  P  S  Q  K  V  Q  P  L
Query                 9180     TGATTGAGGCGCAGGGGCGAATCACACAGATCCGGCCATCGCAAAAAGTTCAACCGCTCA  9239
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4591333  TGATTGAGGCGCAGGGGCGAATCACACAGATCCGGCCATCGCAAAAAGTTCAACCGCTCA  4591274
CDS:AAA ATPase [Delf  417      L  I  E  A  Q  G  R  I  T  Q  I  R  P  S  Q  K  V  Q  P  L
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CDS: Putative 4       437      T  A  F  V  R  N  K  V  F  R  N  P  P  T  V  M  Q  E  K  A
Query                 9240     CGGCCTTCGTTCGCAACAAGGTCTTTCGCAATCCGCCCACCGTCATGCAGGAAAAGGCCA  9299
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4591273  CGGCCTTCGTTCGCAACAAGGTCTTTCGCAATCCGCCCACCGTCATGCAGGAAAAGGCCA  4591214
CDS:AAA ATPase [Delf  437      T  A  F  V  R  N  K  V  F  R  N  P  P  T  V  M  Q  E  K  A

CDS: Putative 4       457      I  E  A  A  L  K  T  P  D  I  A  L  I  Q  G  P  P  G  T  G
Query                 9300     TCGAGGCCGCCCTAAAAACGCCAGATATAGCGTTGATCCAAGGCCCGCCCGGTACCGGCA  9359
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4591213  TCGAGGCCGCCCTAAAAACGCCAGATATAGCGTTGATCCAAGGCCCGCCCGGTACCGGCA  4591154
CDS:AAA ATPase [Delf  457      I  E  A  A  L  K  T  P  D  I  A  L  I  Q  G  P  P  G  T  G

CDS: Putative 4       477      K  T  T  V  I  A  A  I  L  E  R  L  N  E  M  A  D  K  R  G
Query                 9360     AGACCACCGTCATCGCTGCCATTCTGGAGCGCCTGAACGAGATGGCCGACAAGCGCGGCG  9419
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4591153  AGACCACCGTCATCGCTGCCATTCTGGAGCGCCTGAACGAGATGGCCGACAAGCGCGGCG  4591094
CDS:AAA ATPase [Delf  477      K  T  T  V  I  A  A  I  L  E  R  L  N  E  M  A  D  K  R  G

CDS: Putative 4       497      A  S  I  K  G  Q  I  L  L  T  G  F  Q  H  D  A  V  E  N  M
Query                 9420     CGAGCATCAAAGGCCAAATTCTGTTGACAGGCTTTCAGCACGATGCGGTGGAAAACATGA  9479
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4591093  CGAGCATCAAAGGCCAAATTCTGTTGACAGGCTTTCAGCACGATGCGGTGGAAAACATGA  4591034
CDS:AAA ATPase [Delf  497      A  S  I  K  G  Q  I  L  L  T  G  F  Q  H  D  A  V  E  N  M

CDS: Putative 4       517      I  E  R  L  S  L  N  S  L  P  V  P  K  F  G  K  R  S  G  A
Query                 9480     TCGAGCGGCTCTCGCTCAATAGCCTGCCCGTGCCGAAATTCGGCAAACGGTCTGGCGCGA  9539
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4591033  TCGAGCGGCTCTCGCTCAATAGCCTGCCCGTGCCGAAATTCGGCAAACGGTCTGGCGCGA  4590974
CDS:AAA ATPase [Delf  517      I  E  R  L  S  L  N  S  L  P  V  P  K  F  G  K  R  S  G  A

CDS: Putative 4       537      T  E  D  D  L  S  T  F  E  R  N  L  E  D  W  C  S  K  L  A
Query                 9540     CGGAAGACGATCTCAGCACCTTCGAGCGCAATCTTGAGGATTGGTGTTCAAAGTTGGCCG  9599
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4590973  CGGAAGACGATCTCAGCACCTTCGAGCGCAATCTTGAGGATTGGTGTTCAAAGTTGGCCG  4590914
CDS:AAA ATPase [Delf  537      T  E  D  D  L  S  T  F  E  R  N  L  E  D  W  C  S  K  L  A

CDS: Putative 4       557      A  E  L  R  E  R  N  P  Q  I  A  E  V  E  Q  E  R  E  I  K
Query                 9600     CCGAACTACGTGAACGAAACCCACAGATTGCCGAAGTTGAGCAGGAACGGGAAATAAAAA  9659
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4590913  CCGAACTACGTGAACGAAACCCACAGATTGCCGAAGTTGAGCAGGAACGGGAAATAAAAA  4590854
CDS:AAA ATPase [Delf  557      A  E  L  R  E  R  N  P  Q  I  A  E  V  E  Q  E  R  E  I  K

CDS: Putative 4       577      N  L  C  L  Q  Y  V  Q  A  P  S  R  V  L  A  A  S  L  A  R
Query                 9660     ACCTGTGCCTGCAATATGTCCAAGCCCCGTCACGCGTGCTGGCCGCCAGCCTTGCTAGGA  9719
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4590853  ACCTGTGCCTGCAATATGTCCAAGCCCCGTCACGCGTGCTGGCCGCCAGCCTTGCTAGGA  4590794
CDS:AAA ATPase [Delf  577      N  L  C  L  Q  Y  V  Q  A  P  S  R  V  L  A  A  S  L  A  R

CDS: Putative 4       597      K  I  A  A  L  G  S  V  I  L  G  E  D  G  A  R  R  S  T  N
Query                 9720     AAATCGCAGCGCTCGGCAGTGTAATTCTTGGCGAAGACGGCGCTCGACGGTCGACGAATT  9779
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4590793   AAATCGCAGCGCTCGGCAGTGTAATTCTTGGCGAAGACGGCGCTCGACGGTCGACGAATT  4590734
CDS:AAA ATPase [Delf   597       K  I  A  A  L  G  S  V  I  L  G  E  D  G  A  R  R  S  T  N

CDS: Putative 4        617       L  A  K  K  L  A  H  E  E  N  L  N  D  G  S  T  Q  W  L  D
Query                  9780      TGGCGAAAAAGCTCGCGCACGAGGAAAACCTCAACGATGGCTCCACCCAATGGCTTGATG  9839
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4590733   TGGCGAAAAAGCTCGCGCACGAGGAAAACCTCAACGATGGCTCCACCCAATGGCTTGATG  4590674
CDS:AAA ATPase [Delf   617       L  A  K  K  L  A  H  E  E  N  L  N  D  G  S  T  Q  W  L  D

CDS: Putative 4        637       A  A  R  R  L  R  V  R  H  E  S  F  S  D  D  G  P  E  R  A
Query                  9840      CAGCGCGCCGTCTGCGCGTTCGCCATGAAAGCTTTTCTGACGACGGGCCAGAAAGGGCGA  9899
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4590673   CAGCGCGCCGTCTGCGCGTTCGCCATGAAAGCTTTTCTGACGACGGGCCAGAAAGGGCGA  4590614
CDS:AAA ATPase [Delf   637       A  A  R  R  L  R  V  R  H  E  S  F  S  D  D  G  P  E  R  A

CDS: Putative 4        657       M  D  A  L  D  D  L  R  D  V  L  E  E  D  E  R  K  L  L  D
Query                  9900      TGGACGCACTGGATGACCTGCGTGATGTGCTTGAAGAAGACGAACGCAAACTGCTGGACA  9959
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4590613   TGGACGCACTGGATGACCTGCGTGATGTGCTTGAAGAAGACGAACGCAAACTGCTGGACA  4590554
CDS:AAA ATPase [Delf   657       M  D  A  L  D  D  L  R  D  V  L  E  E  D  E  R  K  L  L  D

CDS: Putative 4        677       K  A  S  L  W  R  N  E  D  G  P  A  P  F  L  D  N  L  V  A
Query                  9960      AAGCCAGTCTGTGGCGCAATGAAGATGGCCCAGCGCCATTTTTGGACAACCTGGTCGCGT  10019
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4590553   AAGCCAGTCTGTGGCGCAATGAAGATGGCCCAGCGCCATTTTTGGACAACCTGGTCGCGT  4590494
CDS:AAA ATPase [Delf   677       K  A  S  L  W  R  N  E  D  G  P  A  P  F  L  D  N  L  V  A

CDS: Putative 4        697       L  K  K  R  L  L  A  R  F  T  A  P  P  I  L  R  V  E  K  Q
Query                  10020     TGAAAAAGAGGCTCCTCGCCCGGTTCACCGCTCCACCGATTCTTCGCGTGGAAAAGCAGA  10079
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4590493   TGAAAAAGAGGCTCCTCGCCCGGTTCACCGCTCCACCGATTCTTCGCGTGGAAAAGCAGA  4590434
CDS:AAA ATPase [Delf   697       L  K  K  R  L  L  A  R  F  T  A  P  P  I  L  R  V  E  K  Q

CDS: Putative 4        717       N  D  A  V  L  A  L  A  E  F  A  I  Q  R  I  K  N  A  E  Y
Query                  10080     ACGACGCAGTGCTTGCATTGGCAGAATTCGCCATACAACGCATCAAAAACGCCGAGTATT  10139
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4590433   ACGACGCAGTGCTTGCATTGGCAGAATTCGCCATACAACGCATCAAAAACGCCGAGTATT  4590374
CDS:AAA ATPase [Delf   717       N  D  A  V  L  A  L  A  E  F  A  I  Q  R  I  K  N  A  E  Y

CDS: Putative 4        737       S  A  K  D  K  K  S  A  A  L  A  E  F  L  A  E  L  E  G  N
Query                  10140     CGGCTAAGGATAAAAAATCTGCTGCGCTGGCCGAGTTTCTAGCCGAACTGGAAGGCAACC  10199
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4590373   CGGCTAAGGATAAAAAATCTGCTGCGCTGGCCGAGTTTCTAGCCGAACTGGAAGGCAACC  4590314
CDS:AAA ATPase [Delf   737       S  A  K  D  K  K  S  A  A  L  A  E  F  L  A  E  L  E  G  N

CDS: Putative 4        757       P  Y  G  M  V  D  A  L  S  E  Y  S  F  A  F  A  A  T  S  Q
Query                  10200     CCTATGGCATGGTAGATGCCCTGTCCGAATACAGTTTTGCCTTTGCCGCCACCAGCCAGC  10259
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4590313   CCTATGGCATGGTAGATGCCCTGTCCGAATACAGTTTTGCCTTTGCCGCCACCAGCCAGC  4590254
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CDS:AAA ATPase [Delf  757      P  Y  G  M  V  D  A  L  S  E  Y  S  F  A  F  A  A  T  S  Q

CDS: Putative 4       777      Q  S  V  N  R  A  M  Q  K  R  K  G  L  V  G  R  D  V  N  Q
Query                 10260    AGAGCGTCAATCGTGCAATGCAAAAACGCAAAGGGCTTGTCGGGCGCGATGTCAATCAAA  10319
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4590253  AGAGCGTCAATCGTGCAATGCAAAAACGCAAAGGGCTTGTCGGGCGCGATGTCAATCAAA  4590194
CDS:AAA ATPase [Delf  777      Q  S  V  N  R  A  M  Q  K  R  K  G  L  V  G  R  D  V  N  Q

CDS: Putative 4       797      N  Q  K  G  M  E  Y  E  Y  V  I  V  D  E  A  A  R  V  S  P
Query                 10320    ACCAGAAAGGCATGGAATACGAATATGTCATCGTGGACGAAGCCGCCCGTGTCTCGCCTC  10379
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4590193  ACCAGAAAGGCATGGAATACGAATATGTCATCGTGGACGAAGCCGCCCGTGTCTCGCCTC  4590134
CDS:AAA ATPase [Delf  797      N  Q  K  G  M  E  Y  E  Y  V  I  V  D  E  A  A  R  V  S  P

CDS: Putative 4       817      R  D  L  M  V  A  M  A  Q  G  K  R  I  I  L  V  G  D  H  R
Query                 10380    GTGATTTGATGGTGGCTATGGCGCAAGGCAAGCGCATTATTCTGGTCGGCGACCATCGAC  10439
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4590133  GTGATTTGATGGTGGCTATGGCGCAAGGCAAGCGCATTATTCTGGTCGGCGACCATCGAC  4590074
CDS:AAA ATPase [Delf  817      R  D  L  M  V  A  M  A  Q  G  K  R  I  I  L  V  G  D  H  R

CDS: Putative 4       837      Q  L  P  H  I  I  D  E  E  V  A  R  Q  M  E  E  G  E  T  G
Query                 10440    AATTGCCGCACATCATTGACGAAGAGGTGGCTCGCCAGATGGAGGAAGGCGAAACGGGTG  10499
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4590073  AATTGCCGCACATCATTGACGAAGAGGTGGCTCGCCAGATGGAGGAAGGCGAAACGGGTG  4590014
CDS:AAA ATPase [Delf  837      Q  L  P  H  I  I  D  E  E  V  A  R  Q  M  E  E  G  E  T  G

CDS: Putative 4       857      E  D  E  N  D  W  L  K  K  S  M  F  Q  Y  L  F  S  E  R  L
Query                 10500    AGGACGAAAATGACTGGCTaaaaaaaTCCATGTTTCAGTATTTGTTCTCCGAGCGTTTAA  10559
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4590013  AGGACGAAAATGACTGGCTAAAAAAATCCATGTTTCAGTATTTGTTCTCCGAGCGTTTAA  4589954
CDS:AAA ATPase [Delf  857      E  D  E  N  D  W  L  K  K  S  M  F  Q  Y  L  F  S  E  R  L

CDS: Putative 4       877      K  T  L  D  K  N  F  P  I  I  D  S  T  T  G  R  V  T  P  R
Query                 10560    AAACACTGGACAAGAACTTCCCAATTATCGACAGCACCACTGGCCGCGTTACACCACGTT  10619
                               ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4589953  AAACACTGGACAAGAGCTTCCCAATTATCGACAGCACCACTGGCCGCGTTACACCACGTT  4589894
CDS:AAA ATPase [Delf  877      K  T  L  D  K  S  F  P  I  I  D  S  T  T  G  R  V  T  P  R

CDS: Putative 4       897      C  I  T  L  D  K  Q  Y  R  M  H  P  L  L  G  S  F  I  S  R
Query                 10620    GCATCACGCTGGACAAGCAATACCGCATGCATCCGCTGCTGGGCAGCTTTATCAGTAGAA  10679
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4589893  GCATCACGCTGGACAAGCAATACCGCATGCATCCGCTGCTGGGCAGCTTTATCAGTAGAA  4589834
CDS:AAA ATPase [Delf  897      C  I  T  L  D  K  Q  Y  R  M  H  P  L  L  G  S  F  I  S  R

CDS: Putative 4       917      N  F  Y  E  R  F  D  P  E  E  Q  F  G  S  G  R  P  A  S  D
Query                 10680    ATTTCTATGAACGCTTCGACCCGGAGGAGCAATTTGGCTCCGGGCGACCAGCAAGCGATT  10739
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4589833  ATTTCTATGAACGCTTCGACCCGGAGGAGCAATTTGGCTCCGGGCGACCAGCAAGCGATT  4589774
CDS:AAA ATPase [Delf  917      N  F  Y  E  R  F  D  P  E  E  Q  F  G  S  G  R  P  A  S  D
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CDS: Putative 4       937      F  A  H  D  L  P  G  T  N  G  K  S  A  V  W  M  D  V  P  A
Query                 10740    TCGCCCATGATCTGCCAGGCACGAACGGCAAGTCTGCCGTTTGGATGGATGTACCAGCAC  10799
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4589773  TCGCCCATGATCTGCCAGGCACGAACGGCAAGTCTGCCGTTTGGATGGATGTACCAGCAC  4589714
CDS:AAA ATPase [Delf  937      F  A  H  D  L  P  G  T  N  G  K  S  A  V  W  M  D  V  P  A

CDS: Putative 4       957      Q  R  G  K  H  Q  K  D  G  T  S  W  T  R  P  A  E  V  T  V
Query                 10800    AAAGAGGAAAACATCAAAAGGACGGAACCAGTTGGACGCGCCCCGCAGAAGTCACTGTCA  10859
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4589713  AAAGAGGAAAACATCAAAAGGACGGAACCAGTTGGACGCGCCCCGCAGAAGTCACTGTCA  4589654
CDS:AAA ATPase [Delf  957      Q  R  G  K  H  Q  K  D  G  T  S  W  T  R  P  A  E  V  T  V

CDS: Putative 4       977      I  A  R  Q  L  Q  A  W  M  S  S  D  A  G  K  D  L  S  F  G
Query                 10860    TCGCTCGCCAGTTACAGGCGTGGATGAGTTCGGATGCAGGGAAAGATCTCTCCTTCGGTG  10919
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4589653  TCGCTCGCCAGTTACAGGCGTGGATGAGTTCGGATGCAGGGAAAGATCTCTCCTTCGGTG  4589594
CDS:AAA ATPase [Delf  977      I  A  R  Q  L  Q  A  W  M  S  S  D  A  G  K  D  L  S  F  G

CDS: Putative 4       997      V  I  S  F  Y  K  A  Q  A  D  S  I  R  E  Q  L  K  R  K  F
Query                 10920    TTATTTCATTTTATAAGGCGCAGGCCGACAGCATCAGGGAACAACTCAAAAGGAAATTCG  10979
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4589593  TTATTTCATTTTATAAGGCGCAGGCCGACAGCATCAGGGAACAACTCAAAAGGAAATTCG  4589534
CDS:AAA ATPase [Delf  997      V  I  S  F  Y  K  A  Q  A  D  S  I  R  E  Q  L  K  R  K  F

CDS: Putative 4       1017     G  G  I  V  N  D  D  K  Q  L  R  V  G  T  V  D  S  F  Q  G
Query                 10980    GCGGGATCGTGAACGATGACAAGCAACTGCGTGTTGGAACGGTGGACTCTTTCCAAGGCA  11039
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4589533  GCGGGATCGTGAACGATGACAAGCAACTGCGTGTTGGAACGGTGGACTCTTTCCAAGGCA  4589474
CDS:AAA ATPase [Delf  1017     G  G  I  V  N  D  D  K  Q  L  R  V  G  T  V  D  S  F  Q  G

CDS: Putative 4       1037     M  E  F  D  V  V  F  L  S  M  V  R  T  L  P  Q  N  W  Q  P
Query                 11040    TGGAATTCGATGTCGTCTTCCTCTCAATGGTGCGAACCTTGCCGCAAAACTGGCAGCCAA  11099
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4589473  TGGAATTCGATGTCGTCTTCCTCTCAATGGTGCGAACCTTGCCGCAAAACTGGCAGCCAA  4589414
CDS:AAA ATPase [Delf  1037     M  E  F  D  V  V  F  L  S  M  V  R  T  L  P  Q  N  W  Q  P

CDS: Putative 4       1057     K  D  D  D  R  D  K  Q  A  R  A  L  F  G  H  L  C  L  Y  N
Query                 11100    AGGATGATGACCGCGACAAACAAGCTAGAGCGCTGTTTGGCCATCTCTGTCTTTACAACC  11159
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4589413  AGGATGATGACCGCGACAAACAAGCTAGAGCGCTGTTTGGCCATCTCTGTCTTTACAACC  4589354
CDS:AAA ATPase [Delf  1057     K  D  D  D  R  D  K  Q  A  R  A  L  F  G  H  L  C  L  Y  N

CDS: Putative 4       1077     R  L  N  V  A  M  S  R  Q  K  K  L  L  V  V  V  G  D  T  G
Query                 11160    GTCTGAATGTCGCCATGAGCCGTCAGAAGAAGCTGCTGGTGGTCGTTGGAGATACGGGGT  11219
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4589353  GTCTGAATGTCGCCATGAGCCGTCAGAAGAAGCTGCTGGTGGTCGTTGGAGATACGGGGT  4589294
CDS:AAA ATPase [Delf  1077     R  L  N  V  A  M  S  R  Q  K  K  L  L  V  V  V  G  D  T  G

CDS: Putative 4       1097     L  L  Q  S  E  L  A  K  E  F  V  P  G  L  V  D  F  L  Q  I
Query                 11220    TGCTACAAAGTGAACTCGCGAAGGAGTTCGTGCCTGGACTGGTGGATTTCCTTCAGATAT  11279
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4589293   TGCTACAAAGTGAACTCGCGAAGGAGTTCGTGCCTGGACTGGTGGATTTCCTTCAGATAT  4589234
CDS:AAA ATPase [Delf   1097      L  L  Q  S  E  L  A  K  E  F  V  P  G  L  V  D  F  L  Q  I

CDS: Putative 4        1117      C  R  E  Q  G  V  M  L  P  C  *
Query                  11280     GCCGCGAGCAAGGGGTGATGCTGCCATGTTGAGGCTCCTTGATTACGGCAAACCTGCCCC  11339
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4589233   GCCGCGAGCAAGGGGTGATGCTGCCATGTTGAGGCTCCTTGATTACGGCAAACCTGCCCC  4589174
CDS:AAA ATPase [Delf   1117      C  R  E  Q  G  V  M  L  P  C

Query                  11340     CTTCGGTGAGACCATCGGTAGGCCGCGCCACCTTGCGTGGCCGCTGAACGCATACCGCGT  11399
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4589173   CTTCGGTGAGACCATCGGTAGGCCGCGCCACCTTGCGTGGCCGCTGAACGCATACCGCGT  4589114

Query                  11400     GACCTTGCCCAGAGTTCTTGACGATGGCAATGGCTTGAACGCATTTGAGCGTGTCATCCT  11459
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4589113   GACCTTGCCCAGAGTTCTTGACGATGGCAATGGCTTGAACGCATTTGAGCGTGTCATCCT  4589054

Query                  11460     GAAACTACTCGACGCTGCCGGTCGTATGGATGCCGATGCGCTGGCGGCTGAAACCCGCAT  11519
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4589053   GAAACTACTCGACGCTGCCGGTCGTATGGATGCCGATGCGCTGGCGGCTGAAACCCGCAT  4588994

Query                  11520     CCCACTCGATTTGGTCAAGAGCGTTCTGCTTCGTTTGCAAGACAAGGACTTGATTGACGA  11579
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588993   CCCACTCGATTTGGTCAAGAGCGTTCTGCTTCGTTTGCAAGACAAGGACTTGATTGACGA  4588934

Query                  11580     ACACAATGCCGTCATTGAGCGGGAGCGTGAAGATGAGCGCGCGCCGGTGTTTGTCACTGC  11639
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588933   ACACAATGCCGTCATTGAGCGGGAGCGTGAAGATGAGCGCGCGCCGGTGTTTGTCACTGC  4588874

Query                  11640     GCTGGTCTTTCGCGAACTCGCCACCGGGAGAATTCTGCCTTTTCTGCATCGGCTGGACGA  11699
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588873   GCTGGTCTTTCGCGAACTCGCCACCGGGAGAATTCTGCCTTTTCTGCATCGGCTGGACGA  4588814

Query                  11700     CACAAACCCCATGCGGAAAAAGGAATGCGAGGACAAAGACTTCCGGGTAATCCGCTGGGA  11759
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588813   CACAAACCCCATGCGGAAAAAGGAATGCGAGGACAAAGACTTCCGGGTAATCCGCTGGGA  4588754

Query                  11760     TGGTGACCGCAGAAAAGCGATACCAGCGCCGCGTGATGTAATCAGAACTTTGCGCGCCAT  11819
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588753   TGGTGACCGCAGAAAAGCGATACCAGCGCCGCGTGATGTAATCAGAACTTTGCGCGCCAT  4588694

Query                  11820     GAAAAAGCGTTCGTCTGCGTTCGGCCAGGACAGCAAGATGCCCGCAGTCCAACAGATCAC  11879
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588693   GAAAAAGCGTTCGTCTGCGTTCGGCCAGGACAGCAAGATGCCCGCAGTCCAACAGATCAC  4588634

Query                  11880     GATAGTCGCCGAGCCCGAGCTGCTTCACCTTGACTGCCCTATCGCCATCCAGAAAAGCGA  11939
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588633   GATAGTCGCCGAGCCCGAGCTGCTTCACCTTGACTGCCCTATCGCCATCCAGAAAAGCGA  4588574
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Query                  11940    TGGCGAGTTCCGTATAGCTGACCCGTTCGGCAACGGTTTCTCCTTGATTCTCGAAAATGC  11999
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Sbjct                  4588573  TGGCGAGTTCCGTATAGCTGACCCGTTCGGCAACGGTTTCTCCTTGATTCTCGAAAATGC  4588514

Query                  12000    GTTCGAGAAACTTTTGGAGCAGGATGAAAGCCTCAGCAAGTGGCTGCATGGTTGGAAACA  12059
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588513  GTTCGAGAAACTTTTGGAGCAGGATGAAAGCCTCAGCAAGTGGCTGCATGGTTGGAAACA  4588454

CDS: Putative 3        126          *  A  S  R  T  W  F  L  L  I  G  R  W  F  L  R  E  V  V
Query                  12060    GTCATTAAGCACTCCTCGTCCAGAAAAGCAGGATGCCACGCCAAAAGAGCCGTTCGACAA  12119
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588453  GTCATTAAGCACTCCTCGTCCAGAAAAGCAGGATGCCACGCCAAAAGAGCCGTTCGACAA  4588394
CDS:hypothetical pro   126             A  S  R  T  W  F  L  L  I  G  R  W  F  L  R  E  V  V

CDS: Putative 3        108        I  G  V  P  L  A  V  R  L  E  D  G  I  Q  A  G  Q  P  I  A
Query                  12120    CGATGCCAACCGGCAACGCTACCCGAAGCTCGTCGCCAATTTGCGCCCCTTGCGGAATAG  12179
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588393  CGATGCCAACCGGCAACGCTACCCGAAGCTCGTCGCCAATTTGCGCCCCTTGCGGAATAG  4588334
CDS:hypothetical pro   108        I  G  V  P  L  A  V  R  L  E  D  G  I  Q  A  G  Q  P  I  A

CDS: Putative 3        88         R  E  A  G  D  G  L  D  M  G  C  D  F  P  R  Q  E  I  G  A
Query                  12180    CCCGTTCCGCTCCATCGCCCAAATCCATGCCGCAATCGAATGGGCGCTGTTCTATACCTG  12239
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588333  CCCGTTCCGCTCCATCGCCCAAATCCATGCCGCAATCGAATGGGCGCTGTTCTATACCTG  4588274
CDS:hypothetical pro   88         R  E  A  G  D  G  L  D  M  G  C  D  F  P  R  Q  E  I  G  A

CDS: Putative 3        68         A  A  S  R  N  I  G  N  N  C  P  Q  F  E  S  R  L  V  L  V
Query                  12240    CTGCCGCAGACCGGTTGATTCCGTTATTGCAAGGCTGAAATTCACTACGCAAGACCAACA  12299
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588273  CTGCCGCAGACCGGTTGATTCCGTTATTGCAAGGCTGAAATTCACTACGCAAGACCAACA  4588214
CDS:hypothetical pro   68         A  A  S  R  N  I  G  N  N  C  P  Q  F  E  S  R  L  V  L  V

CDS: Putative 3        48         C  G  Q  K  L  L  G  R  F  G  E  T  K  L  L  R  R  N  A  E
Query                  12300    CGCAGCCCTGCTTGAGCAGGCCGCGAAAGCCCTCGGTCTTGAGCAGCCGCCGATTGGCTT  12359
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588213  CGCAGCCCTGCTTGAGCAGGCCGCGAAAGCCCTCGGTCTTGAGCAGCCGCCGATTGGCTT  4588154
CDS:hypothetical pro   48         C  G  Q  K  L  L  G  R  F  G  E  T  K  L  L  R  R  N  A  E

CDS: Putative 3        28         P  R  N  P  F  T  L  Q  P  F  K  L  V  A  A  R  E  L  L  R
Query                  12360    CAGGCCGATTCGGGAAGGTAAGCTGCGGGAATTTGAGGACGGCGGCGCGTTCCAAGAGAC  12419
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588153  CAGGCCGATTCGGGAAGGTAAGCTGCGGGAATTTGAGGACGGCGGCGCGTTCCAAGAGAC  4588094
CDS:hypothetical pro   28         P  R  N  P  F  T  L  Q  P  F  K  L  V  A  A  R  E  L  L  R

CDS: Putative 3        8          N  K  G  Y  S  Q  K  L
Query                  12420    GGTTCTTGCCATAGCTTTGCTTCAAGCGCAAGACGACGCTTTGCATCCCTTGCGCCGTGT  12479
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4588093  GGTTCTTGCCATAGCTTTGCTTCAAGCGCAAGACGACGCTTTGCATCCCTTGCGCCGTGT  4588034
CDS:hypothetical pro   8          N  K  G  Y  S  Q  K  M
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Query                 12480    TGCGGCCGCGTATTCAGACCTCATCACTCGCCTGTTCGCTATCAACGCCAAACGCAACGA  12539
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Sbjct                 4588033  TGCGGCCGCGTATTCAGACCTCATCACTCGCCTGTTCGCTATCAACGCCAAACGCAACGA  4587974

Query                 12540    GAAGGGCCACGGCAAGGGCGGCGCAGACGCACCGCAGCAGGCACTAACTGACGATTCGTT  12599
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4587973  GAAGGGCCACGGCAAGGGCGGCGCAGACGCACCGCAGCAGGCACTAACTGACGATTCGTT  4587914

Query                 12600    CATGCGCGAAGTCGTTCATGCGCTTGTGCCAGGCATCGTGTTTACCGACACGCCTCCTAC  12659
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4587913  CATGCGCGAAGTCGTTCATGCGCTTGTGCCAGGCATCGTGTTTACCGACACGCCTCCTAC  4587854

Query                 12660    CGCGCCAGACAAGGACGAGCAGGGTGATGCACTGCTGGATGCCCGCACTAGCATTCAGGA  12719
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4587853  CGCGCCAGACAAGGACGAGCAGGGTGATGCACTGCTGGATGCCCGCACTAGCATTCAGGA  4587794

Query                 12720    GGAGTTCGGCCACCAGTTGTTCAACCGCCTGGGCGCAAACTTGCAAGACCGGCTGGTTCA  12779
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4587793  GGAGTTCGGCCACCAGTTGTTCAACCGCCTGGGCGCAAACTTGCAAGACCGGCTGGTTCA  4587734

Query                 12780    CGCGGAACGTTTTTTCCAGTCTTGCCATGACGGGGATGACGCTTTGGCCTATGTCCGCGA  12839
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4587733  CGCGGAACGTTTTTTCCAGTCTTGCCATGACGGGGATGACGCTTTGGCCTATGTCCGCGA  4587674

Query                 12840    CCTTTATGCCGCAATCCAGTCATCATTTGAGAGAGCTTTGACAGGCAGGCTGCCGTCCGA  12899
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4587673  CCTTTATGCCGCAATCCAGTCATCATTTGAGAGAGCTTTGACAGGCAGGCTGCCGTCCGA  4587614

Query                 12900    TACCAGTGACGCGCAGCTCAAAGACACGGCTGAACGCAAGGCTGTTGAGGCTGGTTTCTG  12959
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4587613  TACCAGTGACGCGCAGCTCAAAGACACGGCTGAACGCAAGGCTGTTGAGGCTGGTTTCTG  4587554

Query                 12960    CGAAGGCTTGTCGGAGAGCCTGCGAACCGTCAAAACATCCGCTGTGCGCCAGGCATTGCA  13019
                               ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct                 4587553  CGAAGGCTTGTCGGAGAGCCTGCGAACCGTCAAAACATCGGCTGTGCGCCAGGCATTGCA  4587494

Query                 13020    AGGCGGCAGCCAAACGCTCGGGGCTTGCGTTCTTGCATGGCTGCTGGTGAGCGATGCTGA  13079
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4587493  AGGCGGCAGCCAAACGCTCGGGGCTTGCGTTCTTGCATGGCTGCTGGTGAGCGATGCTGA  4587434

Query                 13080    TGAACTTGCCGCAATTCATGACACGCAGCCGTCCTTGATCGGCGATATGGCAAACCTTAT  13139
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4587433  TGAACTTGCCGCAATTCATGACACGCAGCCGTCCTTGATCGGCGATATGGCAAACCTTAT  4587374

Query                 13140    CGCTCGGCGTGGGCATGGCAACGAGCCGCTGCCATTGCCCAAAGAGAACATCGCACAGCT  13199
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4587373  CGCTCGGCGTGGGCATGGCAACGAGCCGCTGCCATTGCCCAAAGAGAACATCGCACAGCT  4587314

CDS: Putative 2       1                                                L  K  M  N  S  P
Query                 13200    TCGCAAAGCTGCTTTCACAACTATCAGAACACTTATGGAATCTTGAAAATGAACAGCCCC  13259
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Sbjct                   4587313  TCGCAAAGCTGCTTTCACAACTATCAGAACACTTATGGAATCTTGAAAATGAACAGCCCC  4587254
CDS:Chromosome segre    1                                                M  K  M  N  S  P

CDS: Putative 2         7         V  Q  P  D  T  E  A  Q  R  L  A  D  L  N  A  R  E  S  W  I
Query                   13260    GTCCAACCCGACACCGAAGCCCAGCGGCTTGCCGATTTGAACGCGCGTGAGAGCTGGATA  13319
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4587253  GTCCAACCCGACACCGAAGCCCAGCGGCTTGCCGATTTGAACGCGCGTGAGAGCTGGATA  4587194
CDS:Chromosome segre    7         V  Q  P  D  T  E  A  Q  R  L  A  D  L  N  A  R  E  S  W  I

CDS: Putative 2         27        N  T  K  E  S  E  I  A  S  R  E  T  A  V  A  T  R  E  R  D
Query                   13320    AACACCAAGGAAAGCGAAATCGCCAGCCGTGAAACCGCCGTGGCTACACGTGAAAGGGAT  13379
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4587193  AACACCAAGGAAAGCGAAATCGCCAGCCGTGAAACCGCCGTGGCTACACGTGAAAGGGAT  4587134
CDS:Chromosome segre    27        N  T  K  E  S  E  I  A  S  R  E  T  A  V  A  T  R  E  R  D

CDS: Putative 2         47        A  T  A  E  R  Q  V  I  E  Q  D  K  A  K  L  A  Q  R  E  Q
Query                   13380    GCGACTGCAGAGCGTCAAGTCATCGAGCAAGACAAGGCCAAGCTGGCGCAGCGCGAGCAG  13439
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4587133  GCGACTGCAGAGCGTCAAGTCATCGAGCAAGACAAGGCCAAGCTGGCGCAGCGCGAGCAG  4587074
CDS:Chromosome segre    47        A  T  A  E  R  Q  V  I  E  Q  D  K  A  K  L  A  Q  R  E  Q

CDS: Putative 2         67        A  V  T  Q  A  E  Q  K  C  D  A  G  F  A  D  E  R  A  A  L
Query                   13440    GCCGTCACGCAGGCTGAGCAAAAGTGTGATGCAGGTTTTGCCGATGAACGAGCCGCGCTG  13499
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4587073  GCCGTCACGCAGGCTGAGCAAAAGTGTGATGCAGGTTTTGCCGATGAACGAGCCGCGCTG  4587014
CDS:Chromosome segre    67        A  V  T  Q  A  E  Q  K  C  D  A  G  F  A  D  E  R  A  A  L

CDS: Putative 2         87        N  D  E  L  R  E  K  R  A  Q  G  E  R  A  I  A  E  M  R  E
Query                   13500    AATGATGAGCTGCGTGAAAAGCGCGCCCAGGGCGAAAGAGCAATTGCCGAGATGCGAGAG  13559
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4587013  AATGATGAGCTGCGTGAAAAGCGCGCCCAGGGCGAAAGAGCAATTGCCGAGATGCGAGAG  4586954
CDS:Chromosome segre    87        N  D  E  L  R  E  K  R  A  Q  G  E  R  A  I  A  E  M  R  E

CDS: Putative 2         107       K  N  L  S  A  L  E  V  E  I  S  E  L  K  A  K  R  L  G  A
Query                   13560    AAAAACCTTTCAGCGTTGGAGGTTGAAATTTCCGAGCTGAAAGCAAAGCGACTGGGTGCG  13619
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4586953  AAAAACCTTTCAGCGTTGGAGGTTGAAATTTCCGAGCTGAAAGCAAAGCGACTGGGTGCG  4586894
CDS:Chromosome segre    107       K  N  L  S  A  L  E  V  E  I  S  E  L  K  A  K  R  L  G  A

CDS: Putative 2         127       V  A  H  A  E  N  A  E  R  E  R  I  R  T  E  I  A  Q  E  R
Query                   13620    GTTGCCCATGCCGAAAACGCCGAACGGGAGCGCATTCGGACAGAAATCGCCCAAGAGCGC  13679
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4586893  GTTGCCCATGCCGAAAACGCCGAACGGGAGCGCATTCGGACAGAAATCGCCCAAGAGCGC  4586834
CDS:Chromosome segre    127       V  A  H  A  E  N  A  E  R  E  R  I  R  T  E  I  A  Q  E  R

CDS: Putative 2         147       D  A  W  T  K  Q  Q  G  D  A  R  K  Q  L  N  A  E  R  T  E
Query                   13680    GATGCATGGACAAAACAACAGGGTGACGCTCGAAAGCAGTTGAATGCAGAGCGCACGGAA  13739
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                   4586833  GATGCATGGACAAAACAACAGGGTGACGCTCGAAAGCAGTTGAATGCAGAGCGCACGGAA  4586774
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CDS:Chromosome segre  147       D  A  W  T  K  Q  Q  G  D  A  R  K  Q  L  N  A  E  R  T  E

CDS: Putative 2       167       F  E  K  Q  K  G  A  L  S  A  L  Q  S  E  V  E  G  R  Q  A
Query                 13740    TTTGAGAAACAAAAAGGCGCACTCTCCGCCTTGCAAAGCGAAGTCGAAGGAAGACAGGCA  13799
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Sbjct                 4586773  TTTGAGAAACAAAAAGGCGCACTCTCCGCCTTGCAAAGCGAAGTCGAAGGAAGACAGGCA  4586714
CDS:Chromosome segre  167       F  E  K  Q  K  G  A  L  S  A  L  Q  S  E  V  E  G  R  Q  A

CDS: Putative 2       187       E  L  E  T  S  E  R  T  L  E  R  K  E  Q  R  L  E  Q  Q  N
Query                 13800    GAGCTTGAGACTTCAGAGCGGACACTCGAACGCAAAGAACAACGGCTGGAACAGCAGAAC  13859
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4586713  GAGCTTGAGACTTCAGAGCGGACACTCGAACGCAAAGAACAACGGCTGGAACAGCAGAAC  4586654
CDS:Chromosome segre  187       E  L  E  T  S  E  R  T  L  E  R  K  E  Q  R  L  E  Q  Q  N

CDS: Putative 2       207       Q  R  R  S  E  Q  L  D  D  E  V  E  R  R  V  E  D  R  R  K
Query                 13860    CAGAGGCGCAGCGAGCAACTGGACGATGAGGTTGAGAGGCGTGTTGAGGATCGCCGAAAA  13919
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4586653  CAGAGGCGCAGCGAGCAACTGGACGATGAGGTTGAGAGGCGTGTTGAGGATCGCCGAAAA  4586594
CDS:Chromosome segre  207       Q  R  R  S  E  Q  L  D  D  E  V  E  R  R  V  E  D  R  R  K

CDS: Putative 2       227       S  L  E  A  A  L  Q  S  A  K  E  E  N  I  R  L  R  E  A  F
Query                 13920    TCGCTAGAGGCTGCTCTGCAATCTGCCAAAGAGGAAAACATTCGACTGCGCGAGGCGTTT  13979
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Sbjct                 4586593  TCGCTAGAGGCTGCTCTGCAATCTGCCAAAGAGGAAAACATTCGACTGCGCGAGGCGTTT  4586534
CDS:Chromosome segre  227       S  L  E  A  A  L  Q  S  A  K  E  E  N  I  R  L  R  E  A  F

CDS: Putative 2       247       K  T  Q  D  E  L  L  G  A  F  E  Q  L  K  L  Q  L  G  G  K
Query                 13980    AAAACTCAAGACGAACTTCTCGGCGCGTTCGAACAGTTAAAGTTGCAACTTGGTGGCAAA  14039
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Sbjct                 4586533  AAAACTCAAGACGAACTTCTCGGCGCGTTCGAACAGTTAAAGTTGCAACTTGGTGGCAAA  4586474
CDS:Chromosome segre  247       K  T  Q  D  E  L  L  G  A  F  E  Q  L  K  L  Q  L  G  G  K

CDS: Putative 2       267       D  P  A  E  I  L  R  A  L  N  S  Q  A  D  E  L  K  R  L  R
Query                 14040    GACCCTGCTGAAATTCTGCGTGCGCTGAACAGCCAGGCCGACGAACTCAAACGCCTACGA  14099
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Sbjct                 4586473  GACCCTGCTGAAATTCTGCGTGCGCTGAACAGCCAGGCCGACGAACTCAAACGCCTACGA  4586414
CDS:Chromosome segre  267       D  P  A  E  I  L  R  A  L  N  S  Q  A  D  E  L  K  R  L  R

CDS: Putative 2       287       E  E  L  A  T  R  P  T  E  E  M  R  E  R  Y  Q  A  L  E  S
Query                 14100    GAGGAGCTTGCTACCCGACCTACTGAGGAAATGCGCGAGCGGTATCAAGCCCTTGAATCA  14159
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Sbjct                 4586413  GAGGAGCTTGCTACCCGACCTACTGAGGAAATGCGCGAGCGGTATCAAGCCCTTGAATCA  4586354
CDS:Chromosome segre  287       E  E  L  A  T  R  P  T  E  E  M  R  E  R  Y  Q  A  L  E  S

CDS: Putative 2       307       E  A  K  N  Q  K  T  R  A  D  Q  L  E  R  Q  L  S  T  N  E
Query                 14160    GAAGCCAAAAATCAGAAAACACGGGCAGACCAGTTAGAACGGCAACTTTCCACCAATGAG  14219
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Sbjct                 4586353  GAAGCCAAAAATCAGAAAACACGGGCAGACCAGTTAGAACGGCAACTTTCCACCAATGAG  4586294
CDS:Chromosome segre  307       E  A  K  N  Q  K  T  R  A  D  Q  L  E  R  Q  L  S  T  N  E
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CDS: Putative 2       327       A  A  V  A  E  I  G  E  L  R  R  Q  G  S  E  L  N  A  E  N
Query                 14220    GCTGCGGTCGCTGAAATTGGCGAGCTGCGCCGTCAAGGCTCGGAGCTCAACGCCGAAAAC  14279
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Sbjct                 4586293  GCTGCGGTCGCTGAAATTGGCGAGCTGCGCCGTCAAGGCTCGGAGCTCAACGCCGAAAAC  4586234
CDS:Chromosome segre  327       A  A  V  A  E  I  G  E  L  R  R  Q  G  S  E  L  N  A  E  N

CDS: Putative 2       347       K  S  L  A  Q  R  A  S  I  F  E  G  A  A  N  E  A  Q  A  E
Query                 14280    AAATCTCTGGCGCAAAGGGCATCCATCTTCGAGGGAGCAGCCAACGAAGCGCAAGCCGAA  14339
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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CDS:Chromosome segre  347       K  S  L  A  Q  R  A  S  I  F  E  G  A  A  N  E  A  Q  A  E

CDS: Putative 2       367       L  K  R  L  R  A  A  Y  E  R  P  A  E  V  T  A  R  Y  K  E
Query                 14340    CTCAAGCGTTTGCGTGCAGCTTATGAGCGCCCTGCTGAAGTTACCGCTCGCTACAAAGAA  14399
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Sbjct                 4586173  CTCAAGCGTTTGCGTGCAGCTTATGAGCGCCCTGCTGAAGTTACCGCTCGCTACAAAGAA  4586114
CDS:Chromosome segre  367       L  K  R  L  R  A  A  Y  E  R  P  A  E  V  T  A  R  Y  K  E

CDS: Putative 2       387       I  E  M  P  H  I  S  V  D  K  V  K  Q  P  V  Q  H  E  I  D
Query                 14400    ATTGAGATGCCGCACATCAGTGTGGATAAGGTCAAGCAGCCGGTGCAGCACGAGATCGAT  14459
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Sbjct                 4586113  ATTGAGATGCCGCACATCAGTGTGGATAAGGTCAAGCAGCCGGTGCAGCACGAGATCGAT  4586054
CDS:Chromosome segre  387       I  E  M  P  H  I  S  V  D  K  V  K  Q  P  V  Q  H  E  I  D

CDS: Putative 2       407       E  L  T  W  L  T  G  I  G  N  A  C  D  T  Y  G  L  H  F  N
Query                 14460    GAGCTAACTTGGCTCACTGGGATTGGTAATGCTTGCGATACATACGGACTACATTTCAAT  14519
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4586053  GAGCTAACTTGGCTCACTGGGATTGGTAATGCTTGCGATACATACGGACTACATTTCAAT  4585994
CDS:Chromosome segre  407       E  L  T  W  L  T  G  I  G  N  A  C  D  T  Y  G  L  H  F  N

CDS: Putative 2       427       P  R  I  L  K  A  F  H  T  A  L  K  T  A  E  W  S  P  L  T
Query                 14520    CCACGTATTTTGAAAGCTTTTCATACAGCTCTCAAAACAGCGGAATGGTCGCCGCTCACT  14579
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Sbjct                 4585993  CCACGTATTTTGAAAGCTTTTCATACAGCTCTCAAAACAGCGGAATGGTCGCCGCTCACT  4585934
CDS:Chromosome segre  427       P  R  I  L  K  A  F  H  T  A  L  K  T  A  E  W  S  P  L  T

CDS: Putative 2       447       V  L  A  G  V  S  G  T  G  K  S  E  L  P  R  L  Y  S  H  F
Query                 14580    GTCCTGGCAGGGGTTTCCGGAACCGGAAAATCCGAACTGCCGCGCCTCTACTCGCACTTT  14639
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Sbjct                 4585933  GTCCTGGCAGGGGTTTCCGGAACCGGAAAATCCGAACTGCCGCGCCTCTACTCGCACTTT  4585874
CDS:Chromosome segre  447       V  L  A  G  V  S  G  T  G  K  S  E  L  P  R  L  Y  S  H  F

CDS: Putative 2       467       G  G  I  Y  F  E  P  L  S  V  Q  P  N  W  D  S  Q  E  S  M
Query                 14640    GGCGGAATTTATTTCGAGCCGCTGTCTGTCCAGCCTAATTGGGATTCGCAGGAATCCATG  14699
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Sbjct                 4585873  GGCGGAATTTATTTCGAGCCGCTGTCTGTCCAGCCTAATTGGGATTCGCAGGAATCCATG  4585814
CDS:Chromosome segre  467       G  G  I  Y  F  E  P  L  S  V  Q  P  N  W  D  S  Q  E  S  M

CDS: Putative 2       487       L  G  F  F  N  S  I  D  N  K  F  D  A  Q  P  V  L  R  F  L
Query                 14700    CTGGGCTTTTTCAATTCCATAGACAATAAATTCGATGCACAGCCGGTGCTGCGTTTTCTC  14759
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CDS:Chromosome segre    487       L  G  F  F  N  S  I  D  N  K  F  D  A  Q  P  V  L  R  F  L

CDS: Putative 2         507       A  Q  S  Q  I  S  G  R  E  Q  Y  E  Q  R  I  R  R  W  Q  S
Query                   14760    GCGCAAAGTCAGATATCAGGCCGCGAACAATATGAACAGCGCATTAGACGTTGGCAGAGT  14819
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Sbjct                   4585753  GCGCAAAGTCAGATATCAGGCCGCGAACAATATGAACAGCGCATTAGACGTTGGCAGAGT  4585694
CDS:Chromosome segre    507       A  Q  S  Q  I  S  G  R  E  Q  Y  E  Q  R  I  R  R  W  Q  S

CDS: Putative 2         527       M  S  P  D  Q  Q  I  A  L  D  P  E  K  D  K  E  L  I  E  A
Query                   14820    ATGTCGCCAGATCAGCAAATAGCACTTGACCCTGAGAAGGACAAAGAGCTGATTGAAGCG  14879
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Sbjct                   4585693  ATGTCGCCAGATCAGCAAATAGCACTTGACCCTGAGAAGGACAAAGAGCTGATTGAAGCG  4585634
CDS:Chromosome segre    527       M  S  P  D  Q  Q  I  A  L  D  P  E  K  D  K  E  L  I  E  A

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Query                   14880    TTGAAACAAGCAGATTATCCAGGATTGCAGGACGCAGTGTGTCTTGTTCTGCTTGATGAG  14939
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Sbjct                   4585633  TTGAAACAAGCAGATTATCCAGGATTGCAGGACGCAGTGTGTCTTGTTCTGCTTGATGAG  4585574
CDS:Chromosome segre    547       L  K  Q  A  D  Y  P  G  L  Q  D  A  V  C  L  V  L  L  D  E

CDS: Putative 2         567       M  N  L  A  H  P  E  L  Y  F  A  E  F  L  S  K  L  E  L  R
Query                   14940    ATGAATCTGGCACACCCTGAGCTTTATTTTGCAGAGTTTTTGAGCAAGCTAGAACTGCGG  14999
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Sbjct                   4585573  ATGAATCTGGCACACCCTGAGCTTTATTTTGCAGAGTTTTTGAGCAAGCTAGAACTGCGG  4585514
CDS:Chromosome segre    567       M  N  L  A  H  P  E  L  Y  F  A  E  F  L  S  K  L  E  L  R

CDS: Putative 2         587       R  G  R  K  G  D  D  V  P  F  I  P  V  K  I  G  A  G  M  E
Query                   15000    CGTGGCAGAAAGGGTGATGATGTTCCGTTCATACCGGTGAAAATTGGCGCCGGCATGGAA  15059
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CDS:Chromosome segre    587       R  G  R  K  G  D  D  V  P  F  I  P  V  K  I  G  A  G  M  E

CDS: Putative 2         607       P  Y  K  L  P  L  G  R  N  V  L  W  T  G  T  M  N  Q  D  E
Query                   15060    CCCTATAAGCTCCCCCTCGGTCGTAATGTACTCTGGACAGGGACGATGAACCAGGACGAA  15119
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Sbjct                   4585453  CCCTATAAGCTCCCCCTCGGTCGTAATGTACTCTGGACAGGGACGATGAACCAGGACGAA  4585394
CDS:Chromosome segre    607       P  Y  K  L  P  L  G  R  N  V  L  W  T  G  T  M  N  Q  D  E

CDS: Putative 2         627       T  T  K  S  L  S  D  K  V  L  D  R  S  I  I  I  N  F  P  R
Query                   15120    ACCACCAAGTCCCTTTCGGACAAGGTGCTTGACCGTTCCATCATCATCAACTTTCCGCGC  15179
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CDS:Chromosome segre    627       T  T  K  S  L  S  D  K  V  L  D  R  S  I  I  I  N  F  P  R

CDS: Putative 2         647       P  T  E  L  K  R  R  L  K  L  A  P  L  D  D  K  N  R  G  P
Query                   15180    CCGACGGAACTCAAACGCCGCCTGAAGCTTGCTCCACTTGATGACAAAAATCGAGGCCCG  15239
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Sbjct                   4585333  CCGACGGAACTCAAACGTCGCCTGAAGCTTGCTCCACTTGATGACAAAAATCGAGGCCCG  4585274
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CDS:Chromosome segre  647       P  T  E  L  K  R  R  L  K  L  A  P  L  D  D  K  N  R  G  P

CDS: Putative 2       667       A  L  H  K  T  S  W  Q  S  W  L  A  Q  G  S  N  F  S  D  D
Query                 15240    GCGCTACACAAAACGTCGTGGCAGAGTTGGCTAGCACAGGGCAGCAACTTCTCCGACGAT  15299
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Sbjct                 4585273  GCGCTACACAAAACGTCGTGGCAGAGTTGGCTAGCACAGGGCAGCAACTTCTCCGACGAT  4585214
CDS:Chromosome segre  667       A  L  H  K  T  S  W  Q  S  W  L  A  Q  G  S  N  F  S  D  D

CDS: Putative 2       687       Q  V  S  P  F  K  K  F  I  E  A  I  N  A  S  L  A  V  T  G
Query                 15300    CAAGTCAGCCCGTTCAAAAAATTCATTGAAGCAATCAATGCTTCTTTAGCGGTTACAGGC  15359
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CDS:Chromosome segre  687       Q  V  S  P  F  K  K  F  I  E  A  I  N  A  S  L  A  V  T  G

CDS: Putative 2       707       R  A  L  G  H  R  V  W  Q  S  I  E  Y  Y  M  A  N  Y  P  D
Query                 15360    CGTGCCCTCGGTCACCGCGTTTGGCAATCCATTGAATACTACATGGCCAATTACCCGGAT  15419
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4585153  CGTGCCCTCGGTCACCGCGTTTGGCAATCCATTGAATACTACATGGCCAATTACCCGGAT  4585094
CDS:Chromosome segre  707       R  A  L  G  H  R  V  W  Q  S  I  E  Y  Y  M  A  N  Y  P  D

CDS: Putative 2       727       V  R  A  A  R  D  K  D  A  L  A  R  A  M  H  V  A  F  E  D
Query                 15420    GTCCGTGCTGCACGCGATAAAGATGCGCTTGCCAGAGCTATGCATGTCGCCTTCGAGGAT  15479
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Sbjct                 4585093  GTCCGTGCTGCACGCGATAAAGATGCGCTTGCCAGAGCTATGCATGTCGCCTTCGAGGAT  4585034
CDS:Chromosome segre  727       V  R  A  A  R  D  K  D  A  L  A  R  A  M  H  V  A  F  E  D

CDS: Putative 2       747       Q  L  V  Q  K  V  M  P  K  L  R  G  I  D  T  R  G  K  S  K
Query                 15480    CAACTCGTGCAGAAGGTCATGCCCAAATTGCGGGGTATTGATACACGCGGCAAGAGCAAG  15539
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Sbjct                 4585033  CAACTCGTGCAGAAGGTCATGCCCAAATTGCGGGGTATTGATACACGCGGCAAGAGCAAG  4584974
CDS:Chromosome segre  747       Q  L  V  Q  K  V  M  P  K  L  R  G  I  D  T  R  G  K  S  K

CDS: Putative 2       767       T  E  C  L  D  R  I  R  G  Q  L  V  T  G  I  G  S  N  S  F
Query                 15540    ACAGAGTGCCTGGACAGGATTCGTGGACAACTCGTTACAGGAATCGGCAGTAACTCATTC  15599
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Sbjct                 4584973  ACAGAGTGCCTGGACAGGATTCGTGGACAACTCGTTACAGGAATCGGCAGTAACTCATTC  4584914
CDS:Chromosome segre  767       T  E  C  L  D  R  I  R  G  Q  L  V  T  G  I  G  S  N  S  F

CDS: Putative 2       787       N  L  T  E  D  F  D  L  A  C  D  L  G  Y  G  Q  F  I  W  Q
Query                 15600    AATCTGACAGAGGATTTCGACCTTGCCTGTGATCTTGGCTATGGTCAGTTTATTTGGCAG  15659
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584913  AATCTGACAGAGGATTTCGACCTTGCCTGTGATCTTGGCTATGGTCAGTTTATTTGGCAG  4584854
CDS:Chromosome segre  787       N  L  T  E  D  F  D  L  A  C  D  L  G  Y  G  Q  F  I  W  Q

CDS: Putative 2       807       S  A  N  Y  L  N  V  G  D  T  E  T  N  D  R  S  T  A  S  R
Query                 15660    TCGGCAAATTACCTAAACGTCGGTGACACGGAAACCAATGATAGATCCACGGCCAGTCGA  15719
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584853  TCGGCAAATTACCTAAACGTCGGTGACACGGAAACCAATGATAGATCCACGGCCAGTCGA  4584794
CDS:Chromosome segre  807       S  A  N  Y  L  N  V  G  D  T  E  T  N  D  R  S  T  A  S  R
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CDS: Putative 2       827       D  S  D  N  A  E  L  P  H  S  L  F  M  K  D  E  P  D  S  D
Query                 15720    GACTCGGACAATGCTGAATTGCCACACTCCCTTTTTATGAAAGATGAACCAGATTCAGAC  15779
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584793  GACTCGGACAATGCTGAATTGCCACACTCCCTTTTTATGAAAGATGAACCAGATTCAGAC  4584734
CDS:Chromosome segre  827       D  S  D  N  A  E  L  P  H  S  L  F  M  K  D  E  P  D  S  D

CDS: Putative 2       847       K  R  H  K  M  W  N  L  K  T  P  E  Q  R  D  E  L  R  V  K
Query                 15780    AAGCGTCATAAAATGTGGAACTTAAAGACACCAGAGCAACGAGATGAGCTGCGCGTGAAA  15839
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584733  AAGCGTCATAAAATGTGGAACTTAAAGACACCAGAGCAACGAGATGAGCTGCGCGTGAAA  4584674
CDS:Chromosome segre  847       K  R  H  K  M  W  N  L  K  T  P  E  Q  R  D  E  L  R  V  K

CDS: Putative 2       867       L  E  E  N  A  R  A  G  R  I  H  A  K  Q  *
CDS: Putative 1       1                                                   M  S  I  T  L  E
Query                 15840    CTTGAAGAAAATGCCAGAGCAGGAAGGATTCACGCCAAGCAATGAGTATTACTCTGGAAA  15899
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584673  CTTGAAGAAAATGCCAGAGCAGGAAGGATTCACGCCAAGCAATGAGTATTACTCTGGAAA  4584614
CDS:Cold-shock prote  1                                                   M  S  I  T  L  E
CDS:Chromosome segre  867       L  E  E  N  A  R  A  G  R  I  H  A  K  Q

CDS: Putative 1       7        K  I  Y  T  D  F  R  A  K  E  K  L  A  K  K  L  L  E  Q  M
Query                 15900    AAATCTATACCGACTTCCGTGCCAAAGAAAAACTTGCCAAAAAACTGCTTGAGCAAATGA  15959
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584613  AAATCTATACCGACTTCCGTGCCAAAGAAAAACTTGCCAAAAAACTGCTTGAGCAAATGA  4584554
CDS:Cold-shock prote  7        K  I  Y  T  D  F  R  A  K  E  K  L  A  K  K  L  L  E  Q  M

CDS: Putative 1       27       N  W  F  G  S  I  T  D  F  D  P  K  T  G  A  A  L  P  K  S
Query                 15960    ATTGGTTTGGTTCAATCACGGATTTCGATCCTAAGACCGGCGCGGCTCTGCCGAAATCCT  16019
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584553  ATTGGTTTGGTTCAATCACGGATTTCGATCCTAAGACCGGCGCGGCTCTGCCGAAATCCT  4584494
CDS:Cold-shock prote  27       N  W  F  G  S  I  T  D  F  D  P  K  T  G  A  A  L  P  K  S

CDS: Putative 1       47       L  S  G  F  L  A  K  V  A  Q  P  E  A  S  E  I  T  R  D  R
Query                 16020    TGTCAGGGTTCCTCGCCAAAGTCGCACAGCCAGAAGCGAGTGAGATAACCCGTGACCGCC  16079
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584493  TGTCAGGGTTCCTCGCCAAAGTCGCACAGCCAGAAGCGAGTGAGATAACCCGTGACCGCC  4584434
CDS:Cold-shock prote  47       L  S  G  F  L  A  K  V  A  Q  P  E  A  S  E  I  T  R  D  R

CDS: Putative 1       67       L  W  R  I  T  E  H  C  R  A  S  V  E  R  L  F  H  S  L  N
Query                 16080    TTTGGCGCATAACGGAACACTGCCGCGCTTCTGTCGAGCGATTATTTCATTCTCTCAACG  16139
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584433  TTTGGCGCATAACGGAACACTGCCGCGCTTCTGTCGAGCGATTATTTCATTCTCTCAACG  4584374
CDS:Cold-shock prote  67       L  W  R  I  T  E  H  C  R  A  S  V  E  R  L  F  H  S  L  N

CDS: Putative 1       87       E  S  P  R  C  E  H  A  L  L  P  V  H  A  V  R  E  L  D  A
Query                 16140    AAAGTCCTCGCTGCGAACACGCTCTACTGCCTGTTCATGCTGTGCGTGAACTGGATGCCA  16199
                               ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584373  AAAGTCCTCGCCGCGAACACGCTCTACTGCCTGTTCATGCTGTGCGTGAACTGGATGCCA  4584314
CDS:Cold-shock prote  87       E  S  P  R  R  E  H  A  L  L  P  V  H  A  V  R  E  L  D  A
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CDS: Putative 1       107      N  S  F  I  K  L  S  N  R  P  G  R  T  I  R  E  K  L  A  G
Query                 16200    ACAGTTTTATTAAGCTGAGTAATCGTCCGGGTCGTACCATTCGGGAAAAACTGGCAGGTA  16259
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584313  ACAGTTTTATTAAGCTGAGTAATCGTCCGGGTCGTACCATTCGGGAAAAACTGGCAGGTA  4584254
CDS:Cold-shock prote  107      N  S  F  I  K  L  S  N  R  P  G  R  T  I  R  E  K  L  A  G

CDS: Putative 1       127      N  P  Y  I  Q  A  V  R  R  F  Q  S  V  D  L  P  E  N  R  L
Query                 16260    ACCCCTACATACAGGCTGTGCGTCGTTTTCAATCCGTCGACCTGCCGGAAAATCGCTTGC  16319
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584253  ACCCCTACATACAGGCTGTGCGTCGTTTTCAATCCGTCGACCTGCCGGAAAATCGCTTGC  4584194
CDS:Cold-shock prote  127      N  P  Y  I  Q  A  V  R  R  F  Q  S  V  D  L  P  E  N  R  L

CDS: Putative 1       147      L  K  A  F  A  I  R  L  A  E  M  L  D  L  R  G  D  C  L  G
Query                 16320    TGAAAGCCTTTGCCATTCGCCTTGCGGAAATGCTTGATTTACGCGGTGATTGTCTCGGTC  16379
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584193  TGAAAGCCTTTGCCATTCGCCTTGCGGAAATGCTTGATTTACGCGGTGATTGTCTCGGTC  4584134
CDS:Cold-shock prote  147      L  K  A  F  A  I  R  L  A  E  M  L  D  L  R  G  D  C  L  G

CDS: Putative 1       167      Q  E  D  E  L  L  S  K  I  Y  L  W  L  R  S  D  E  A  Q  A
Query                 16380    AAGAGGATGAGCTTCTATCAAAAATCTACTTATGGTTGCGTTCTGATGAGGCGCAAGCCA  16439
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584133  AAGAGGATGAGCTTCTATCAAAAATCTACTTATGGTTGCGTTCTGATGAGGCGCAAGCCA  4584074
CDS:Cold-shock prote  167      Q  E  D  E  L  L  S  K  I  Y  L  W  L  R  S  D  E  A  Q  A

CDS: Putative 1       187      I  G  N  W  E  N  L  P  P  N  N  T  L  L  A  H  R  D  Y  R
Query                 16440    TCGGCAATTGGGAAAATCTGCCACCTAACAACACGCTACTAGCACACCGAGATTACCGTC  16499
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584073  TCGGCAATTGGGAAAATCTGCCACCTAACAACACGCTACTAGCACACCGAGATTACCGTC  4584014
CDS:Cold-shock prote  187      I  G  N  W  E  N  L  P  P  N  N  T  L  L  A  H  R  D  Y  R

CDS: Putative 1       207      H  V  W  D  A  W  R  W  L  Q  T  L  D  E  D  I  T  S  D  L
Query                 16500    ACGTGTGGGATGCATGGCGCTGGCTGCAAACCCTCGATGAGGACATCACCAGCGACCTTT  16559
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4584013  ACGTGTGGGATGCATGGCGCTGGCTGCAAACCCTCGATGAGGACATCACCAGCGACCTTT  4583954
CDS:Cold-shock prote  207      H  V  W  D  A  W  R  W  L  Q  T  L  D  E  D  I  T  S  D  L

CDS: Putative 1       227      S  Q  L  D  V  R  E  K  T  M  R  L  W  Q  Q  C  A  Q  M  W
Query                 16560    CTCAACTGGATGTCCGCGAGAAAACCATGCGCCTTTGGCAGCAATGCGCGCAAATGTGGC  16619
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4583953  CTCAACTGGATGTCCGCGAGAAAACCATGCGCCTTTGGCAGCAATGCGCGCAAATGTGGC  4583894
CDS:Cold-shock prote  227      S  Q  L  D  V  R  E  K  T  M  R  L  W  Q  Q  C  A  Q  M  W

CDS: Putative 1       247      L  D  G  K  H  L  F  A  E  I  P  L  L  F  D  Y  E  K  F  E
Query                 16620    TTGATGGAAAGCATCTTTTTGCTGAGATACCGTTACTATTCGATTATGAAAAGTTTGAGA  16679
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4583893  TTGATGGAAAGCATCTTTTTGCTGAGATACCGTTACTATTCGATTATGAAAAGTTTGAGA  4583834
CDS:Cold-shock prote  247      L  D  G  K  H  L  F  A  E  I  P  L  L  F  D  Y  E  K  F  E

CDS: Putative 1       267      I  L  P  W  T  S  K  P  P  L  F  K  E  V  K  Y  K  M  P  R
Query                 16680    TTCTTCCGTGGACTTCCAAGCCACCTTTGTTCAAGGAAGTGAAGTACAAGATGCCCCGGC  16739
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4583833   TTCTTCCGTGGACTTCCAAGCCACCTTTGTTCAAGGAAGTGAAGTACAAGATGCCCCGGC  4583774
CDS:Cold-shock prote   267       I  L  P  W  T  S  K  P  P  L  F  K  E  V  K  Y  K  M  P  R

CDS: Putative 1        287       H  L  R  Q  S  A  S  A  E  P  I  C  V  D  I  T  A  L  H  P
Query                  16740     ATTTGCGACAAAGCGCGAGTGCCGAACCAATTTGTGTTGATATCACAGCCCTGCATCCCC  16799
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4583773   ATTTGCGACAAAGCGCGAGTGCCGAACCAATTTGTGTTGATATCACAGCCCTGCATCCCC  4583714
CDS:Cold-shock prote   287       H  L  R  Q  S  A  S  A  E  P  I  C  V  D  I  T  A  L  H  P

CDS: Putative 1        307       R  Y  A  S  G  D  G  K  G  A  Q  S  L  A  A  P  F  L  W  Q
Query                  16800     GCTATGCCAGTGGTGACGGAAAAGGAGCGCAGTCGCTGGCGGCCCCCTTTCTTTGGCAGA  16859
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4583713   GCTATGCCAGTGGTGACGGAAAAGGAGCGCAGTCGCTGGCGGCCCCCTTTCTTTGGCAGA  4583654
CDS:Cold-shock prote   307       R  Y  A  S  G  D  G  K  G  A  Q  S  L  A  A  P  F  L  W  Q

CDS: Putative 1        327       R  W  Q  R  E  N  E  T  V  D  I  E  L  F  G  S  D  A  V  W
Query                  16860     GGTGGCAGCGCGAAAATGAAACCGTTGACATCGAACTCTTTGGTTCCGATGCCGTTTGGC  16919
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4583653   GGTGGCAGCGCGAAAATGAAACCGTTGACATCGAACTCTTTGGTTCCGATGCCGTTTGGC  4583594
CDS:Cold-shock prote   327       R  W  Q  R  E  N  E  T  V  D  I  E  L  F  G  S  D  A  V  W

CDS: Putative 1        347       L  N  P  D  A  T  T  I  S  A  P  D  L  F  F  A  K  D  N  A
Query                  16920     TGAATCCCGATGCGACCACCATTTCTGCGCCAGATCTGTTTTTCGCCAAAGACAACGCCA  16979
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4583593   TGAATCCCGATGCGACCACCATTTCTGCGCCAGATCTGTTTTTCGCCAAAGACAACGCCA  4583534
CDS:Cold-shock prote   347       L  N  P  D  A  T  T  I  S  A  P  D  L  F  F  A  K  D  N  A

CDS: Putative 1        367       T  E  L  F  D  P  A  A  R  A  F  T  T  R  L  R  E  E  F  K
Query                  16980     CTGAGCTTTTTGACCCCGCCGCCCGCGCGTTCACTACTCGGCTACGCGAAGAGTTCAAGA  17039
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4583533   CTGAGCTTTTTGACCCCGCCGCCCGCGCGTTCACTACTCGGCTACGCGAAGAGTTCAAGA  4583474
CDS:Cold-shock prote   367       T  E  L  F  D  P  A  A  R  A  F  T  T  R  L  R  E  E  F  K

CDS: Putative 1        387       N  D  T  L  I  W  L  A  P  D  F  L  N  D  F  E  L  E  V  I
Query                  17040     ACGATACACTCATCTGGCTTGCGCCTGACTTTCTCAACGATTTCGAGCTTGAAGTCATCC  17099
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4583473   ACGATACACTCATCTGGCTTGCGCCTGACTTTCTCAACGATTTCGAGCTTGAAGTCATCC  4583414
CDS:Cold-shock prote   387       N  D  T  L  I  W  L  A  P  D  F  L  N  D  F  E  L  E  V  I

CDS: Putative 1        407       R  R  N  L  N  A  R  F  P  N  A  E  P  L  P  R  S  V  A  A
Query                  17100     GTCGCAACCTCAACGCGCGTTTCCCGAATGCCGAGCCGTTGCCGCGAAGTGTGGCGGCCG  17159
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4583413   GTCGCAACCTCAACGCGCGTTTCCCGAATGCCGAGCCGTTGCCGCGAAGTGTGGCGGCCG  4583354
CDS:Cold-shock prote   407       R  R  N  L  N  A  R  F  P  N  A  E  P  L  P  R  S  V  A  A

CDS: Putative 1        427       V  F  A  Q  A  D  P  A  K  I  T  G  E  G  Y  A  I  I  V  V
Query                  17160     TGTTCGCTCAAGCTGACCCGGCCAAAATCACGGGCGAGGGTTACGCCATCATCGTCGTTG  17219
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  4583353   TGTTCGCTCAAGCTGACCCGGCCAAAATCACGGGCGAGGGTTACGCCATCATCGTCGTTG  4583294
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CDS:Cold-shock prote  427      V  F  A  Q  A  D  P  A  K  I  T  G  E  G  Y  A  I  I  V  V

CDS: Putative 1       447      D  S  I  G  G  K  T  T  A  T  K  L  I  A  K  R  D  K  D  L
Query                 17220    ATTCCATTGGCGGCAAGACGACCGCCACCAAGCTCATCGCCAAGCGCGACAAAGACCTGG  17279
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4583293  ATTCCATTGGCGGCAAGACGACCGCCACCAAGCTCATCGCCAAGCGCGACAAAGACCTGG  4583234
CDS:Cold-shock prote  447      D  S  I  G  G  K  T  T  A  T  K  L  I  A  K  R  D  K  D  L

CDS: Putative 1       467      A  K  R  L  P  I  T  K  G  F  Y  W  E  R  C  P  P  V  V  I
Query                 17280    CGAAACGTCTTCCCATCACCAAAGGCTTTTATTGGGAGCGTTGCCCGCCGGTTGTTATCC  17339
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4583233  CGAAACGTCTTCCCATCACCAAAGGCTTTTATTGGGAGCGTTGCCCGCCGGTTGTTATCC  4583174
CDS:Cold-shock prote  467      A  K  R  L  P  I  T  K  G  F  Y  W  E  R  C  P  P  V  V  I

CDS: Putative 1       487      P  G  E  E  A  E  R  L  G  G  S  G  Y  D  I  I  T  L  D  A
Query                 17340    CTGGCGAGGAAGCAGAAAGGCTAGGTGGCAGCGGCTACGACATCATCACGCTGGATGCCA  17399
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4583173  CTGGCGAGGAAGCAGAAAGGCTAGGTGGCAGCGGCTACGACATCATCACGCTGGATGCCA  4583114
CDS:Cold-shock prote  487      P  G  E  E  A  E  R  L  G  G  S  G  Y  D  I  I  T  L  D  A

CDS: Putative 1       507      N  G  R  W  H  D  A  I  R  P  A  K  P  P  F  I  E  A  A  H
Query                 17400    ACGGGCGGTGGCACGATGCGATCCGCCCGGCAAAGCCCCCATTCATTGAGGCAGCACACC  17459
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 4583113  ACGGGCGGTGGCACGATGCGATCCGCCCGGCAAAGCCCCCATTCATTGAGGCAGCACACC  4583054
CDS:Cold-shock prote  507      N  G  R  W  H  D  A  I  R  P  A  K  P  P  F  I  E  A  A  H

CDS: Putative 1       527      L  K  R  I  P  N
Query                 17460    TGAAGCGTATTCCAAAC  17476
                               |||||||||||||||||
Sbjct                 4583053  TGAAGCGTATTCCAAAC  4583037
CDS:Cold-shock prote  527      L  K  R  I  P  N
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>dbj|AP012280.1| Pseudomonas aeruginosa NCGM2.S1 DNA, complete genome
Length=6764661

Features in this part of subject sequence:
  hypothetical protein
  cell division protein

Score = 1.658e+04 bits (8980), Expect = 0.0
Identities = 9994/10497 (95%), Gaps = 15/10497 (0%)
Strand=Plus/Plus

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CDS: Putative 1       1           I  E  T  Q  G  R  T  F  V  G  D  N  G  R  Y  T  K  T  D
Query                 1        GGATCGAGACGCAAGGGCGAACCTTTGTGGGCGACAACGGACGCTACACAAAAACAGATT  60
                               ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct                 1529286  GGATCGAGACGCAAGGGCGAACCTTTGTGGGCGATAACGGACGCTACACAAAAACAGATT  1529345
CDS:hypothetical pro  372      R  I  E  T  Q  G  R  T  F  V  G  D  N  G  R  Y  T  K  T  D
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CDS: Putative 1       20       L  I  V  T  D  L  R  V  P  V  I  L  G  R  G  E  G  M  G  A
Query                 61       TGATAGTCACCGACTTGCGGGTTCCGGTCATTCTGGGGCGTGGTGAGGGCATGGGGGCTC  120
                               |||||||||| |||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct                 1529346  TGATAGTCACTGACTTGCGGGTTCCGGTCATTCTGGGACGTGGTGAGGGCATGGGGGCTC  1529405
CDS:hypothetical pro  392      L  I  V  T  D  L  R  V  P  V  I  L  G  R  G  E  G  M  G  A

CDS: Putative 1       40       P  V  G  G  S  M  A  F  E  V  K  C  G  K  A  E  Y  L  Y  S
Query                 121      CGGTGGGCGGCTCGATGGCATTCGAAGTGAAATGCGGCAAGGCGGAATACCTCTATTCGC  180
                               | ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1529406  CTGTGGGAGGCTCGATGGCATTCGAAGTGAAATGCGGCAAGGCGGAATACCTCTATTCGC  1529465
CDS:hypothetical pro  412      P  V  G  G  S  M  A  F  E  V  K  C  G  K  A  E  Y  L  Y  S

CDS: Putative 1       60       Q  K  D  H  M  I  F  Q  A  E  G  H  K  Q  A  D  A  Q  C  T
Query                 181      AGAAAGATCACATGATTTTTCAGGCTGAAGGGCACAAGCAAGCAGATGCGCAATGCACTC  240
                               |||||||||||||||||||||||||| ||||||||||||||||||||| |||||||||||||
Sbjct                 1529466  AGAAAGATCACATGATTTTTCAGGCCGAAGGGCACAAGCAAGCAGACGCGCAATGCACTC  1529525
CDS:hypothetical pro  432      Q  K  D  H  M  I  F  Q  A  E  G  H  K  Q  A  D  A  Q  C  T

CDS: Putative 1       80       L  C  S  R  D  I  H  D  L  P  E  E  K  Q  K  E  L  R  D  A
Query                 241      TTTGCTCGCGAGATATCCACGATTTGCCAGAAGAAAAACAGAAAGAACTGCGCGACGCCT  300
                               ||||||| ||||| |||||||||||||||||||||||||||||||||||||||| |||
Sbjct                 1529526  TTTGCTCACGAGACATCCACGATTTGCCAGAAGAAAAACAGAAAGAACTGCGCGATGCCC  1529585
CDS:hypothetical pro  452      L  C  S  R  D  I  H  D  L  P  E  E  K  Q  K  E  L  R  D  A

CDS: Putative 1       100      L  R  E  A  G  S  P  M  V  G  M  L  P  R  K  N  E  I  D  Q
Query                 301      TGCGCGAAGCTGGCTCACCAATGGTGGGAATGTTGCCAAGGAAAAATGAAATAGATCAGT  360
                               |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct                 1529586  TGCGCGAAGCTGGCTCACCGATGGTGGGAATGTTGCCAAGGAAAAATGAAATAGATCAGT  1529645
CDS:hypothetical pro  472      L  R  E  A  G  S  P  M  V  G  M  L  P  R  K  N  E  I  D  Q

CDS: Putative 1       120      S  C  L  D  F  I  R  Q  N  E  E  E  Q  P  *
Query                 361      CCTGTCTTGATTTCATCCGCCAAAACGAGGAGGAGCAACCATGAAAATACGTTTCGCAAT  420
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1529646  CCTGTCTTGATTTCATCCGCCAAAACGAGGAGGAGCAACCATGAAAATACGTTTCGCAAT  1529705
CDS:hypothetical pro  492      S  C  L  D  F  I  R  Q  N  E  E  E  Q  P

Query                 421      TATTAGCCATGACCTTCTCGCACAAGTCCGGGCTGAAGTTGATGTCCTCCTGCATGCAGT  480
                               |||||||||||||||||||||| ||||| || ||||| |||||||| ||||||| ||||||
Sbjct                 1529706  TATTAGCCATGACCTTCTCGCGCAAGTTCGAGCTGAGGTTGATGTTCTCCTGCGTGCAGT  1529765

Query                 481      AAATGTCGGAGATATGGATGGCGTGGATGCGTCCACCGCACGCCTCTTGGAGCTGACAGT  540
                                |||||||||| ||||||| || |||||||||||||||||||||||||||||||||||||||
Sbjct                 1529766  CAATGTCGGAAATATGGACGGTGTGGATGCGTCCACCGCACGCCTCTTGGAGCTGACAGT  1529825

Query                 541      TGATTGCAGATCGATTGAGTTGTCCGAGGAAGAGTGGCGCGCATTTCTAAGCGAAATCAG  600
                               | |||||||||||||||||||||||||| |||||||||||||||||||||||||| ||||
Sbjct                 1529826  TAATTGCAGATCGATTGAGTTGTCCGAGCAAGAGTGGCGCGCATTTCTAAGCGAACTCAG  1529885

Query                 601      GGCCAAGAACCCTGAGTTCGAATCGAGCTACTTGTTGCCTGGGACTATTTGCGCGCCCCT  660
                               |||||||| ||| |||||||||||||||||| | ||||||||||||||||||||| |||||
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Sbjct                 1529886  GGCCAAGAGCCCGGAGTTCGAATCGAGCTACCTTTTGCCTGGGACTATTTGCGCACCCCT  1529945

Query                 661      GTTTCCAAACCTCTCGGTAGCTGACGACTATGTTCTCGAACTTCCAATCGATGGTGATAT  720
                               |||||| ||  |||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct                 1529946  GTTTCCCAAAGTCTCGGTAGCTGACCACTATGTTCTCGAACTTCCAATCGATGGTGATAT  1530005

Query                 721      GGAAGAGGAGGAAGCTAATGTTTGATGAGGCCTTTGGAATGGCTGCGATGTGCGCTGGAA  780
                               ||||||||||||||||| |||||||||||||| |||||||||||||||||||| |||||||
Sbjct                 1530006  GGAAGAGGAGGAAGCTGATGTTTGATGAGGCTTTTGGAATGGCTGCGATGTGTGCTGGAA  1530065

Query                 781      AATTTCGCGAGGGAGTGCGTGATACGTTCGGCGCGTCCATTGTTGCTGATGTACTTGATC  840
                               |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct                 1530066  AATTTCGCGAGGGAGTGCGTGATACGTTCGGCGCGTCCATTGTTGCCGATGTACTTGATC  1530125

Query                 841      CGATTCTCAAGGAAGTCGATTCACTCCGCATTTTCAATGCGGCTTACCAGCAGCAATCGC  900
                               ||||||||||||||||||||||||||| ||||||||||||| ||||  ||||| |||||||
Sbjct                 1530126  CGATTCTCAAGGAAGTCGATTCACTCTGCATTTTCAATGCTGCTTTTCAGCAACAATCGC  1530185

Query                 901      TCGCCATTGATCGAACTTTGAATGACGTTCGCGAGCTCCAGTTCAAAGACAGTGGGTGGA  960
                               |||||||||||||||||||||||||||||||||||||| || ||||||||||| |||||||
Sbjct                 1530186  TCGCCATTGATCGAACTTTGAATGACGTTCGCGAGCTTCAATTCAAAGACAGCGGGTGGA  1530245

CDS: Putative 2       1            M  S  E  S  A  K  D  F  Q  S  V  I  F  K  L  H  K  A  I
Query                 961      ATCAATGAGTGAAAGCGCGAAGGATTTTCAGAGCGTAATTTTCAAGCTACACAAGGCAAT  1020
                               ||||||||||| |||||| ||||||||||||||| | |||| |||||||||||||||| |
Sbjct                 1530246  ATCAATGAGTGGAAGCGCAAAGGATTTTCAGAGCATCATTTCCAAGCTACACAAGGCAGT  1530305
CDS:cell division pr  1            M  S  G  S  A  K  D  F  Q  S  I  I  S  K  L  H  K  A  V

CDS: Putative 2       20         A  D  Y  Q  E  G  C  A  R  I  D  R  E  F  N  A  T  K  K  T
Query                 1021     TGCGGACTATCAAGAAGGTTGTGCGCGCATCGACCGCGAATTCAATGCCACTaaaaaaaC  1080
                               |||||||||||||||||||||||||||||||||||||||||||| || |||| |||||| |
Sbjct                 1530306  TGCGGACTATCAAGAAGGTTGTGCGCGCATCGACCGCGAATTCGATACCACCAAAAAAGC  1530365
CDS:cell division pr  20         A  D  Y  Q  E  G  C  A  R  I  D  R  E  F  D  T  T  K  K  A

CDS: Putative 2       40         L  N  E  D  Q  E  R  N  R  S  I  R  K  S  N  W  Q  A  G  F
Query                 1081     ATTGAACGAAGACCAGGAGCGCAATCGGAGCATAAGGAAGTCGAATTGGCAGGCAGGCTT  1140
                               ||| | ||||||||||| |||||||| | |||||||| |||||||||||||||||| ||
Sbjct                 1530366  ATTAAGCGAAGACCAGGAACGCAATCGAAACATAAGGAGGTCGAATTGGCAGGCAGGTTT  1530425
CDS:cell division pr  40         L  S  E  D  Q  E  R  N  R  N  I  R  R  S  N  W  Q  A  G  F

CDS: Putative 2       60         V  R  E  W  E  S  N  A  T  A  I  A  N  A  S  A  Q  L  R  Q
Query                 1141     TGTCAGAGAGTGGGAAAGTAATGCAACTGCTATAGCGAACGCAAGTGCACAGCTTAGACA  1200
                               |  || ||||||||||| |||||||||||||||||||||||||  | ||||| |||||
Sbjct                 1530426  TTCCAAAGAGTGGGAAAGAAATGCAACTGCTATAGCGAACGCAAGCTCGCAGCTCAGACA  1530485
CDS:cell division pr  60         S  K  E  W  E  R  N  A  T  A  I  A  N  A  S  S  Q  L  R  Q

CDS: Putative 2       80         H  Q  P  A  F  V  D  F  C  V  D  K  P  L  M  A  S  E  I  P
Query                 1201     ACATCAGCCTGCCTTCGTGGATTTTTGTGTAGACAAGCCATTGATGGCATCGGAAATTCC  1260
                               ||| || |||||||||||||||||||||||||| |||||||||||||||| ||||||||
Sbjct                 1530486  ACAACAACCTGCCTTCGTGGATTTTTGTGTAGATAAGCCATTGATGGCATCAGAAATTCC  1530545
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CDS:cell division pr  80        Q  Q  P  A  F  V  D  F  C  V  D  K  P  L  M  A  S  E  I  P

CDS: Putative 2       100       A  G  L  V  L  G  S  E  Q  V  S  F  E  K  L  S  C  Q  S  P
Query                 1261    AGCAGGTCTTGTGCTTGGCTCGGAGCAAGTCTCTTTTGAGAAGCTCTCTTGTCAATCCCC  1320
                              ||||||||||||||||||| |||||||||||||||||||||||||| ||||||||  ||||
Sbjct                 1530546 AGCAGGTCTTGTGCTTGGCACGGAGCAAGTCTCTTTTGAGAAGCTATCTTGTCAGGCCCC  1530605
CDS:cell division pr  100       A  G  L  V  L  G  T  E  Q  V  S  F  E  K  L  S  C  Q  A  P

CDS: Putative 2       120       K  V  I  S  F  P  F  S  S  A  L  V  F  P  Q  G  D  A  E  K
Query                 1321    AAAAGTCATCTCTTTCCCCTTCTCCAGCGCTCTTGTTTTTCCGCAAGGCGATGCGGAGAA  1380
                               ||| ||||||| |||||||| ||||| ||||||||||| | ||||||||||| ||| |
Sbjct                 1530606 TAAATTCATCTCATTCCCCTTATCCAGTGCTCTTGTTTTTTCACAAGGCGATGCAGAGCA  1530665
CDS:cell division pr  120       K  F  I  S  F  P  L  S  S  A  L  V  F  S  Q  G  D  A  E  Q

CDS: Putative 2       140       K  R  L  A  H  C  L  L  L  R  L  L  S  A  L  P  A  G  Q  V
Query                 1381    GAAAAGACTCGCGCATTGTCTCTTGTTGCGGTTGCTGTCGGCTTTGCCTGCAGGTCAAGT  1440
                              ||||   |||| ||||||||||||||| |||||||||  ||||||||| | |||||||||
Sbjct                 1530666 GAAACACCTCGTGCATTGTCTCTTGTTACGGTTGCTGCAGGCTTTGCCAGTAGGTCAAGT  1530725
CDS:cell division pr  140       K  H  L  V  H  C  L  L  L  R  L  L  Q  A  L  P  V  G  Q  V

CDS: Putative 2       160       E  L  T  L  I  D  P  L  Q  Q  G  Q  S  V  E  P  F  L  P  L
Query                 1441    AGAGTTGACACTGATTGACCCCCTACAGCAGGGTCAATCGGTCGAGCCGTTCCTACCATT  1500
                              |||||||||||||||||||||||| |||||||| |||||||||||||||||||  |||||
Sbjct                 1530726 AGAGTTGACACTGATTGACCCCCTGCAGCAGGGGCAATCGGTCGAGCCGTTCCGGCCATT  1530785
CDS:cell division pr  160       E  L  T  L  I  D  P  L  Q  Q  G  Q  S  V  E  P  F  R  P  L

CDS: Putative 2       180       L  K  V  E  Q  L  V  P  Q  G  H  V  L  T  R  A  D  E  I  E
Query                 1501    GCTGAAGGTTGAGCAATTGGTGCCGCAAGGTCATGTTCTTACTCGTGCGGACGAAATCGA  1560
                              ||||||||| |||||||||||||||||||||||||||||||||||| |||| ||||||||
Sbjct                 1530786 GCTGAAGGTAGAGCAATTGGTGCCGCAAGGTCATGTTCTTACTCGTTCGGATGAAATCGA  1530845
CDS:cell division pr  180       L  K  V  E  Q  L  V  P  Q  G  H  V  L  T  R  S  D  E  I  E

CDS: Putative 2       200       A  A  L  G  Q  L  T  D  E  I  E  E  L  I  Q  L  R  F  N  E
Query                 1561    AGCAGCGCTCGGACAACTGACGGACGAAATTGAGGAGCTGATCCAGCTGCGGTTCAATGA  1620
                              ||| ||||||||| | |||||||||||||||||||||| ||||||||| ||||||||||||
Sbjct                 1530846 AGCTGCGCTCGGAAAGCTGACGGACGAAATTGAGGAGTTGATCCAGCAGCGGTTCAATGA  1530905
CDS:cell division pr  200       A  A  L  G  K  L  T  D  E  I  E  E  L  I  Q  Q  R  F  N  D

CDS: Putative 2       220       K  A  S  N  W  L  K  Y  N  A  V  Q  P  D  A   P  L  P  Y
Query                 1621    GAAGGCATCCAACTGGTTGAAATACAACGCAGTTCAACCCGATGC--CCCGTTGCCTTAC  1678
                               |||||||||||||||| | |||||||||| | |||||||   ||    | || ||||||
Sbjct                 1530906 CAAGGCATCCAACTGGTCGGAATACAACGC-GATCAACCCCG-GCAATTCATTACCTTAC  1530963
CDS:cell division pr  220       K  A  S  N  W  S  E  Y  N  A  I  N  P  G  N  S  L  P  Y

CDS: Putative 2       239      K  V  V  L  L  F  D  V  P  E  Q  I  S  E  K  S  L  W  L  L
Query                 1679    AAGGTAGTACTGCTCTTTGATGTGCCAGAGCAGATATCGGAAAAATCTCTTTGGCTCCTT  1738
                              ||||| ||  |||| |||||||||||||||||||| |||||||||||||| ||| | |||
Sbjct                 1530964 AAGGTGGTGGTGCTTTTTGATGTGCCAGAGCAGATGTCGGAAAAATCTCTCTGGTTTCTT  1531023
CDS:cell division pr  239      K  V  V  V  L  F  D  V  P  E  Q  M  S  E  K  S  L  W  F  L
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CDS: Putative 2       259       G  R  I  C  E  N  G  P  R  C  G  V  L  P  I  I  A  I  D  E
Query                 1739     GGACGCATCTGCGAAAACGGTCCACGCTGCGGCGTGCTGCCCATCATTGCAATTGATGAG  1798
                               || ||||| |  |||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct                 1531024  GGCCGCATTTTTGAAAACGGTCCACGCTGCGGCGTGCTGCCCATCGTTGCAATTGATGAG  1531083
CDS:cell division pr  259       G  R  I  F  E  N  G  P  R  C  G  V  L  P  I  V  A  I  D  E

CDS: Putative 2       279       Q  R  M  E  D  R  R  Y  E  K  L  N  A  T  L  K  N  S  T  T
Query                 1799     CAGCGCATGGAAGACCGGCGATATGAAAAGCTCAACGCCACGCTGAAAAACTCAACCACG  1858
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct                 1531084  CAGCGCATGGAAGACCGGCGATATGAAAAGCTCAACGCCACGCTGAAAAACTCAACCATG  1531143
CDS:cell division pr  279       Q  R  M  E  D  R  R  Y  E  K  L  N  A  T  L  K  N  S  T  M

CDS: Putative 2       299       Q  L  N  D  L  L  Q  R  A  G  A  G  G  L  S  F  T  Y  Q  P
Query                 1859     CAACTGAATGATCTCTTGCAACGCGCTGGGGCTGGTGGGCTGTCATTCACATATCAACCG  1918
                               ||||||||||||||| |||||||||||||||||||||| | ||||||||||||||| || |||
Sbjct                 1531144  CAACTGAATGATCTGTTGCAACGCGCTGGGGCTGGCGAGCTGTCATTCACATACCAGCCG  1531203
CDS:cell division pr  299       Q  L  N  D  L  L  Q  R  A  G  A  G  E  L  S  F  T  Y  Q  P

CDS: Putative 2       319       E  Q  W  P  R  Q  D  V  L  D  G  F  I  A  R  L  A  E  D  C
Query                 1919     GAGCAATGGCCGCGACAAGATGTGCTGGATGGCTTTATCGCAAGGCTCGCTGAAGATTGT  1978
                               |||||||||||||||||| |||||||||||||||||||| |||||| ||||| ||||||||||
Sbjct                 1531204  GAGCAATGGCCGCGACAGGATGTGCTGGATGGCTTTCTCGCAAAGCTCGTTGAAGATTGT  1531263
CDS:cell division pr  319       E  Q  W  P  R  Q  D  V  L  D  G  F  L  A  K  L  V  E  D  C

CDS: Putative 2       339       A  A  R  T  R  F  K  K  T  M  A  D  L  W  T  S  F  G  K  E
Query                 1979     GCTGCTAGGACGCGCTTCAAGAAAACGATGGCTGATCTCTGGACGAGCTTCGGCAAGGAA  2038
                               ||||||| |||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct                 1531264  GCTGCTAAGACGCGCTTCAAGAAAACGATGCCTGATCTCTGGACGAGCTTCGGCAAGGGT  1531323
CDS:cell division pr  339       A  A  K  T  R  F  K  K  T  M  P  D  L  W  T  S  F  G  K  G

CDS: Putative 2       359       E  T  T  L  G  G  F  D  I  P  I  G  W  T  S  A  G  D  L  A
Query                 2039     GAGACGACTCTTGGTGGCTTTGATATTCCCATCGGCTGGACGAGCGCCGGCGACCTCGCG  2098
                               ||||||||||||| |||||||||||||||||||||||||||||| | | |||||| ||||
Sbjct                 1531324  GAGACGACTCTTGCTGGCTTTGATATTCCCATCGGCTGGACGACCACAGGCGACTTCGCT  1531383
CDS:cell division pr  359       E  T  T  L  A  G  F  D  I  P  I  G  W  T  T  T  G  D  F  A

CDS: Putative 2       379       T  L  R  L  G  A  T  D  S  E  H  H  V  L  L  A  G  K  T  G
Query                 2099     ACCCTGAGACTGGGCGCGACGGACTCCGAGCATCATGTACTGCTTGCGGGGAAGACAGGC  2158
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1531384  CCCCTGAGACTGGGCGCGACGGACTCCGAGCATCATGTACTGCTTGCGGGGAAGACAGGC  1531443
CDS:cell division pr  379       P  L  R  L  G  A  T  D  S  E  H  H  V  L  L  A  G  K  T  G

CDS: Putative 2       399       S  G  K  S  N  L  L  H  V  L  I  H  T  L  C  E  K  Y  P  T
Query                 2159     TCGGGAAAATCCAATCTGCTCCATGTTTTGATTCACACGTTATGCGAGAAATATCCGACC  2218
                               |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct                 1531444  TCGGGAAAATCCAATCTGCTCCATGTTTTGATTCACACGTTATGCGAGAAATACCCGACC  1531503
CDS:cell division pr  399       S  G  K  S  N  L  L  H  V  L  I  H  T  L  C  E  K  Y  P  T

CDS: Putative 2       419       E  E  L  D  L  Y  L  L  D  Y  K  E  S  T  E  F  N  I  Y  A
Query                 2219     GAGGAGCTTGATCTTTATCTACTGGATTACAAGGAATCGACTGAGTTCAATATTTACGCA  2278
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1531504  GAGGAGCTTGATCTTTATCTACTGGATTACAAGGAATCGACTGAGTTCAATATTTACGCA  1531563
CDS:cell division pr   419       E  E  L  D  L  Y  L  L  D  Y  K  E  S  T  E  F  N  I  Y  A

CDS: Putative 2        439       T  P  P  V  P  Q  A  R  L  V  A  T  E  S  D  P  E  Y  G  V
Query                  2279     ACGCCCCCAGTCCCACAGGCCCGCCTTGTCGCTACGGAAAGTGACCCTGAATATGGCGTC  2338
                                 || |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1531564  ACTCCCCCAGTCCCACAAGCCCGCCTTGTCGCTACGGAAAGTGACCCTGAATATGGCGTC  1531623
CDS:cell division pr   439       T  P  P  V  P  Q  A  R  L  V  A  T  E  S  D  P  E  Y  G  V

CDS: Putative 2        459       T  V  L  R  H  L  V  D  E  L  E  T  R  A  R  I  F  K  S  K
Query                  2339     ACTGTATTAAGGCATCTTGTGGATGAACTGGAAACGCGTGCACGCATATTCAAGTCAAAA  2398
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1531624  ACTGTATTAAGGCATCTTGTGGATGAACTGGAAACGCGTGCACGCATATTCAAGTCAAAA  1531683
CDS:cell division pr   459       T  V  L  R  H  L  V  D  E  L  E  T  R  A  R  I  F  K  S  K

CDS: Putative 2        479       N  V  N  D  F  S  E  Y  R  K  S  S  G  V  R  L  P  R  A  L
Query                  2399     AATGTCAACGATTTCAGCGAATACCGTAAATCAAGCGGGGTACGGTTGCCCCGCGCTCTG  2458
                                 ||||||||||||||||||||||||||| |||||||| ||| |||||||||| ||||  |||
Sbjct                  1531684  AATGTCAACGATTTCAGCGAATACCGAAAATCAAGTGGGATACGGTTGCCACGCGTCCTG  1531743
CDS:cell division pr   479       N  V  N  D  F  S  E  Y  R  K  S  S  G  I  R  L  P  R  V  L

CDS: Putative 2        499       L  V  I  D  E  F  Q  I  L  F  S  E  S  R  Q  V  A  E  A  A
Query                  2459     CTAGTCATAGATGAGTTCCAAATTCTGTTCTCAGAAAGTCGCCAGGTGGCAGAAGCTGCT  2518
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1531744  CTAGTCATAGATGAGTTCCAAATTCTGTTCTCAGAAAGTCGCCAGGTGGCAGAAGCTGCT  1531803
CDS:cell division pr   499       L  V  I  D  E  F  Q  I  L  F  S  E  S  R  Q  V  A  E  A  A

CDS: Putative 2        519       E  Q  L  L  S  K  L  L  K  Q  G  R  S  F  G  I  H  I  L  L
Query                  2519     GAGCAGCTGCTGTCGAAGCTCTTGAAACAGGGGCGCTCGTTCGGTATTCACATCCTCCTG  2578
                                 |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1531804  GAGCAGTTGCTGTCGAAGCTCTTGAAACAGGGGCGCTCGTTCGGTATTCACATCCTCCTG  1531863
CDS:cell division pr   519       E  Q  L  L  S  K  L  L  K  Q  G  R  S  F  G  I  H  I  L  L

CDS: Putative 2        539       A  T  Q  T  L  K  G  I  N  A  Q  S  I  G  S  I  I  T  Q  L
Query                  2579     GCTACTCAGACTTTGAAAGGCATCAACGCGCAGTCAATCGGAAGCATCATCACCCAGTTG  2638
                                 |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct                  1531864  GCTACTCAGACTTTGAAAGGCATCAACGCACAGTCAATCGGAAGCATCATCACCCAGTTG  1531923
CDS:cell division pr   539       A  T  Q  T  L  K  G  I  N  A  Q  S  I  G  S  I  I  T  Q  L

CDS: Putative 2        559       G  C  R  I  A  L  A  C  G  Q  E  D  S  A  M  I  L  G  G  G
Query                  2639     GGATGCCGTATCGCACTGGCTTGTGGGCAGGAAGACTCCGCAATGATCCTCGGGGGCGGG  2698
                                 ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1531924  GGATGCCGTATTGCACTGGCTTGTGGGCAGGAAGACTCCGCAATGATCCTCGGGGGCGGG  1531983
CDS:cell division pr   559       G  C  R  I  A  L  A  C  G  Q  E  D  S  A  M  I  L  G  G  G

CDS: Putative 2        579       N  W  A  A  A  E  L  R  S  P  P  E  G  I  I  N  N  A  N  G
Query                  2699     AACTGGGCAGCCGCAGAGCTGCGCAGCCCACCTGAAGGCATCATCAACAATGCTAACGGT  2758
                                 || |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct                  1531984  AATTGGGCAGCCGCAGAGCTGCGCAGCCCACCTGAAGGCATCATCAACAATGCTAATGGT  1532043
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CDS:cell division pr  579       N  W  A  A  A  E  L  R  S  P  P  E  G  I  I  N  N  A  N  G

CDS: Putative 2       599       A  K  S  G  N  V  K  F  M  I  P  F  A  G  E  S  E  H  R  R
Query                 2759     GCCAAATCCGGCAATGTGAAGTTCATGATTCCATTCGCCGGAGAAAGCGAGCATCGACGT  2818
                               ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct                 1532044  GCCAAATCCGGCAATGTGAAGTTCATGATTCCATTCGCCGGAGAAAGTGAGCATCGACGT  1532103
CDS:cell division pr  599       A  K  S  G  N  V  K  F  M  I  P  F  A  G  E  S  E  H  R  R

CDS: Putative 2       619       D  L  L  T  K  L  I  A  R  T  S  L  S  G  V  A  E  K  T  K
Query                 2819     GATTTGTTGACGAAGTTGATAGCGCGTACATCTCTTTCTGGGGTGGCTGAAAAAACCAAA  2878
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1532104  GATTTGTTGACGAAGTTGATAGCGCGTACATCTCTTTCTGGGGTGGCTGAAAAAACCAAA  1532163
CDS:cell division pr  619       D  L  L  T  K  L  I  A  R  T  S  L  S  G  V  A  E  K  T  K

CDS: Putative 2       639       I  F  S  G  A  F  L  P  Q  I  P  S  P  F  E  Y  Q  T  A  C
Query                 2879     ATCTTCAGCGGTGCATTCCTTCCGCAGATACCGTCTCCCTTTGAATATCAGACAGCTTGT  2938
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1532164  ATCTTCAGCGGTGCATTCCTTCCGCAGATACCGTCTCCCTTTGAATATCAGACAGCTTGT  1532223
CDS:cell division pr  639       I  F  S  G  A  F  L  P  Q  I  P  S  P  F  E  Y  Q  T  A  C

CDS: Putative 2       659       A  H  E  E  A  L  L  L  G  E  N  L  A  F  D  S  K  P  L  T
Query                 2939     GCGCACGAAGAAGCTCTTCTTTTGGGCGAAAACCTCGCATTCGATTCAAAACCGTTGACG  2998
                               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1532224  GCGCATGAAGAAGCTCTTCTTTTGGGCGAAAACCTCGCATTCGATTCAAAACCGTTGACG  1532283
CDS:cell division pr  659       A  H  E  E  A  L  L  L  G  E  N  L  A  F  D  S  K  P  L  T

CDS: Putative 2       679       V  P  L  T  R  R  S  A  F  N  V  L  F  S  G  Y  N  D  H  I
Query                 2999     GTACCACTTACTCGTCGATCCGCGTTCAATGTTCTATTCAGCGGCTACAACGACCACATT  3058
                               ||| |||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct                 1532284  GTATCACTTACTCGTCGATCCGCGTTCAATGTTCTATTCAGCGGCTACAATGACCACATT  1532343
CDS:cell division pr  679       V  S  L  T  R  R  S  A  F  N  V  L  F  S  G  Y  N  D  H  I

CDS: Putative 2       699       H  D  G  L  L  S  A  T  L  F  S  L  T  F  V  D  G  F  D  E
Query                 3059     CACGATGGACTCCTGTCCGCTACGCTTTTTAGTCTGACTTTCGTCGATGGCTTTGATGAA  3118
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1532344  CACGATGGACTCCTGTCCGCTACGCTTTTTAGTCTGACTTTCGTCGATGGCTTTGATGAA  1532403
CDS:cell division pr  699       H  D  G  L  L  S  A  T  L  F  S  L  T  F  V  D  G  F  D  E

CDS: Putative 2       719       I  V  Y  F  N  A  R  G  V  P  P  G  G  G  F  S  A  A  A  Q
Query                 3119     ATCGTGTACTTCAACGCGCGCGGGGTCCCCCCAGGAGGAGGATTCTCAGCCGCAGCGCAG  3178
                               |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct                 1532404  ATCGTGTACTTCAACGCGCGCGGGATCCCCCCAGGAGGAGGATTCTCAGCCGCAGCGCAG  1532463
CDS:cell division pr  719       I  V  Y  F  N  A  R  G  I  P  P  G  G  G  F  S  A  A  A  Q

CDS: Putative 2       739       M  L  G  A  R  L  K  M  F  D  D  I  S  D  L  P  L  Q  A  I
Query                 3179     ATGCTCGGTGCACGCCTCAAGATGTTCGACGATATATCCGATCTACCACTTCAAGCGATA  3238
                               ||||||||||||||||||||||| |||||||||||||||| |||||||||||||||||||
Sbjct                 1532464  ATGCTCGGTGCACGCCTCAAGATATTCGACGATATATCCGAGCTACCACTTCAAGCGATA  1532523
CDS:cell division pr  739       M  L  G  A  R  L  K  I  F  D  D  I  S  E  L  P  L  Q  A  I
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CDS: Putative 2       759       S  D  D  I  G  N  R  R  V  A  L  I  I  D  G  L  D  S  E  K
Query                 3239     TCAGACGATATTGGGAATCGCCGCGTAGCATTGATTATCGATGGCCTGGATTCCGAGAAA  3298
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1532524  TCAGACGATATTGGGAATCGCCGCGTAGCATTGATTATCGATGGCCTGGATTCCGAGAAA  1532583
CDS:cell division pr  759       S  D  D  I  G  N  R  R  V  A  L  I  I  D  G  L  D  S  E  K

CDS: Putative 2       779       A  L  Q  P  A  P  A  F  R  S  L  K  P  G  E  P  P  T  P  A
Query                 3299     GCACTACAGCCAGCCCCAGCGTTTAGATCGCTCAAGCCTGGCGAACCACCTACCCCGGCT  3358
                               | |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct                 1532584  GTACTACAGCCAGCCCCAGCGTTTAGATCGCCCAAGCCTGGCGAACCACCTACCCCGGCT  1532643
CDS:cell division pr  779       V  L  Q  P  A  P  A  F  R  S  P  K  P  G  E  P  P  T  P  A

CDS: Putative 2       799       D  L  L  K  R  L  A  E  D  G  P  R  K  G  T  F  V  F  I  F
Query                 3359     GACTTGTTAAAGCGTCTCGCCGAGGACGGCCCAAGAAAGGGGACGTTTGTATTTATTTTT  3418
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1532644  GACTTGTTAAAGCGTCTCGCCGAGGACGGCCCAAGAAAGGGGACGTTTGTATTTATTTTT  1532703
CDS:cell division pr  799       D  L  L  K  R  L  A  E  D  G  P  R  K  G  T  F  V  F  I  F

CDS: Putative 2       819       V  D  R  W  Q  R  C  A  S  A  S  K  D  L  F  S  F  F  E  L
Query                 3419     GTTGACCGTTGGCAGCGCTGTGCCAGTGCCAGCAAAGACCTTTTCTCCTTTTTCGAATTG  3478
                               ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct                 1532704  GTTGACCGTTGGCAGCGCTGTGCCAGTGCCTGCAAAGACCTTTTCTCCTTTTTCGAATTG  1532763
CDS:cell division pr  819       V  D  R  W  Q  R  C  A  S  A  C  K  D  L  F  S  F  F  E  L

CDS: Putative 2       839       R  V  A  Y  C  M  N  E  D  D  A  G  S  L  V  S  G  G  V  G
Query                 3479     CGCGTGGCGTACTGCATGAACGAAGACGATGCCGGATCGCTTGTGAGTGGCGGTGTTGGT  3538
                               ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct                 1532764  CGCGTGGCGTACTGCATGAATGAAGACGATGCCGGATCGCTTGTGAGTGGCGGTGTTGGT  1532823
CDS:cell division pr  839       R  V  A  Y  C  M  N  E  D  D  A  G  S  L  V  S  G  G  V  G

CDS: Putative 2       859       K  F  K  G  I  E  K  P  S  R  A  V  F  V  N  K  M  T  N  D
Query                 3539     AAGTTCAAAGGTATTGAAAAACCGAGCCGAGCTGTATTCGTAAACAAAATGACGAATGAC  3598
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1532824  AAGTTCAAAGGTATTGAAAAACCGAGCCGAGCTGTATTCGTAAACAAAATGACGAATGAC  1532883
CDS:cell division pr  859       K  F  K  G  I  E  K  P  S  R  A  V  F  V  N  K  M  T  N  D

CDS: Putative 2       879       I  T  W  F  R  P  Y  V  Q  E  S  T  R  *
CDS: Putative 3       1            M  V  P  A  I  C  S  G  K  H  S  M  K  R  F  L  L  T
Query                 3599     ATCACATGGTTCCGGCCATATGTTCAGGAAAGCACTCGATGAAGAGATTTCTGCTCACCT  3658
                               |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||| |
Sbjct                 1532884  ATCACATGGTTCCGGCCATATGTTCAGGAAAGCACTCAATGAAGAGATTTCTGCTCACGT  1532943
CDS:cell division pr  879       I  T  W  F  R  P  Y  V  Q  E  S  T  Q
CDS:hypothetical pro  1            M  V  P  A  I  C  S  G  K  H  S  M  K  R  F  L  L  T

CDS: Putative 3       19       W  Y  G  I  T  D  F  R  A  S  L  G  F  E  N  T  D  G  P  I
Query                 3659     GGTATGGAATCACCGATTTTCGCGCATCTCTGGGGTTTGAGAATACCGATGGCCCTATTG  3718
                               |||||||||||||||||||||||||| |||||||||||||||||||||||| ||||||||||
Sbjct                 1532944  GGTATGGAATCACCGATTTTCGCGCGTCTCTGGGGTTTGAGAATACCGACGGCCCTATTG  1533003
CDS:hypothetical pro  19       W  Y  G  I  T  D  F  R  A  S  L  G  F  E  N  T  D  G  P  I
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CDS: Putative 3       39       A  S  A  L  A  G  A  S  Y  S  D  I  I  I  L  G  Y  T  R  T
Query                 3719     CGAGCGCCCTTGCGGGCGCGTCCTACTCGGACATCATTATCCTGGGTTACACCCGGACGG  3778
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1533004  CGAGCGCCCTTGCGGGCGCGTCCTACTCGGACATCATTATCCTGGGTTACACCCGGACGG  1533063
CDS:hypothetical pro  39       A  S  A  L  A  G  A  S  Y  S  D  I  I  I  L  G  Y  T  R  T

CDS: Putative 3       59       D  N  D  A  S  E  L  I  E  A  Q  K  T  F  T  L  E  L  A  S
Query                 3779     ATAATGATGCCAGCGAATTGATCGAGGCACAGAAGACGTTCACGCTTGAATTGGCGTCAA  3838
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1533064  ATAATGATGCCAGCGAATTGATCGAGGCACAGAAGACGTTCACGCTTGAATTGGCGTCAA  1533123
CDS:hypothetical pro  59       D  N  D  A  S  E  L  I  E  A  Q  K  T  F  T  L  E  L  A  S

CDS: Putative 3       79       I  R  S  M  G  Q  E  K  D  W  K  L  T  N  Q  F  V  S  R  F
Query                 3839     TACGAAGCATGGGGCAAGAGAAAGACTGGAAGCTTACTAATCAGTTTGTCTCCAGGTTCG  3898
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1533124  TACGAAGCATGGGGCAAGAGAAAGACTGGAAGCTTACTAATCAGTTTGTCTCCAGGTTCG  1533183
CDS:hypothetical pro  79       I  R  S  M  G  Q  E  K  D  W  K  L  T  N  Q  F  V  S  R  F

CDS: Putative 3       99       A  N  T  S  V  A  H  E  H  F  E  A  W  L  K  K  K  A  A  A
Query                 3899     CTAATACCTCTGTCGCACATGAACATTTTGAAGCCTGGCTGAAAAAGAAAGCCGCCGCCC  3958
                               | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1533184  CCAATACCTCTGTCGCACATGAACATTTTGAAGCCTGGCTGAAAAAGAAAGCCGCCGCCC  1533243
CDS:hypothetical pro  99       A  N  T  S  V  A  H  E  H  F  E  A  W  L  K  K  K  A  A  A

CDS: Putative 3       119      L  G  C  N  A  R  I  R  L  N  S  E  K  L  Y  Q  L  N  D  T
Query                 3959     TGGGCTGCAACGCAAGGATCCGTTTAAATAGCGAGAAACTTTACCAGCTCAACGACACCG  4018
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1533244  TGGGCTGCAACGCAAGGATCCGTTTAAATAGCGAGAAACTTTACCAGCTCAACGACACCG  1533303
CDS:hypothetical pro  119      L  G  C  N  A  R  I  R  L  N  S  E  K  L  Y  Q  L  N  D  T

CDS: Putative 3       139      E  G  I  Y  A  S  A  M  R  A  L  D  G  V  E  Q  E  P  G  E
Query                 4019     AAGGTATTTACGCTAGCGCAATGCGGGCGCTGGATGGGGTTGAACAGGAGCCAGGTGAAA  4078
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1533304  AAGGTATTTACGCTAGCGCAATGCGGGCGCTGGATGGGGTTGAACAGGAGCCAGGTGAAA  1533363
CDS:hypothetical pro  139      E  G  I  Y  A  S  A  M  R  A  L  D  G  V  E  Q  E  P  G  E

CDS: Putative 3       159      K  L  V  T  L  Y  L  S  P  G  T  P  V  M  A  F  V  W  A  L
Query                 4079     AGCTCGTCACGCTCTATCTCAGCCCAGGAACTCCGGTGATGGCCTTTGTCTGGGCGCTCG  4138
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1533364  AGCTCGTCACGCTCTATCTCAGCCCAGGAACTCCGGTGATGGCCTTTGTCTGGGCGCTCG  1533423
CDS:hypothetical pro  159      K  L  V  T  L  Y  L  S  P  G  T  P  V  M  A  F  V  W  A  L

CDS: Putative 3       179      A  A  L  S  Y  P  E  L  K  K  R  L  I  A  S  S  I  I  G  K
Query                 4139     CGGCGCTGAGCTACCCTGAACTCaaaaaaaGACTCATAGCATCGTCCATCATTGGCAAAG  4198
                               |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct                 1533424  CGGCGCTGAGCTACCCTGAGCTCAAAAAAAGACTCATAGCATCGTCCATCATTGGCAAAG  1533483
CDS:hypothetical pro  179      A  A  L  S  Y  P  E  L  K  K  R  L  I  A  S  S  I  I  G  K

CDS: Putative 3       199      A  P  E  V  I  A  L  P  A  E  W  L  E  R  H  S  S  K  Q  A
Query                 4199     CACCTGAAGTCATAGCGTTGCCTGCCGAGTGGCTTGAGCGACACAGCTCAAAACAGGCTG  4258
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                                 |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct                  1533484  CACCTGAAGTCATAGCGTTGCCTGCTGAGTGGCTTGAGCGACACAGCTCAAAACAGGCTG  1533543
CDS:hypothetical pro   199      A  P  E  V  I  A  L  P  A  E  W  L  E  R  H  S  S  K  Q  A

CDS: Putative 3        219      A  I  R  D  I  S  N  G  F  D  V  T  F  H  L  F  G  E  Q  R
Query                  4259     CGATCCGAGACATCTCCAACGGGTTCGATGTGACATTCCATCTTTTTGGTGAACAACGGA  4318
                                 ||||||||| |||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct                  1533544  CGATCCGAGGCATCTCCAACGGGTTCGATGTGACATTCCATCTTTTTGGTGAGCAACGGA  1533603
CDS:hypothetical pro   219      A  I  R  G  I  S  N  G  F  D  V  T  F  H  L  F  G  E  Q  R

CDS: Putative 3        239      M  P  A  L  L  S  I  R  Q  F  E  S  A  H  H  I  F  V  N  S
Query                  4319     TGCCTGCCTTGTTGAGCATCCGGCAATTTGAGTCGGCGCATCACATTTTTGTCAACTCAA  4378
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1533604  TGCCTGCCTTGTTGAGCATCCGGCAATTTGAGTCGGCGCATCACATTTTTGTCAACTCAA  1533663
CDS:hypothetical pro   239      M  P  A  L  L  S  I  R  Q  F  E  S  A  H  H  I  F  V  N  S

CDS: Putative 3        259      K  D  F  P  A  A  C  M  R  T  F  I  G  S  R  D  L  H  E  L
Query                  4379     AAGACTTCCCTGCTGCATGTATGCGAACCTTTATTGGCTCTCGGGACCTGCATGAACTTA  4438
                                 |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct                  1533664  AAGACTTCCCTGCTGCATGTATGCAAACCTTTATTGGCTCTCGGGACCTGCATGAACTTA  1533723
CDS:hypothetical pro   259      K  D  F  P  A  A  C  M  Q  T  F  I  G  S  R  D  L  H  E  L

CDS: Putative 3        279      T  V  D  P  W  D  D  R  A  V  H  E  Q  I  T  K  L  A  K  Q
Query                  4439     CCGTTGACCCCTGGGATGATCGTGCTGTTCACGAACAAATCACCAAGCTGGCAAAGCAAT  4498
                                 |||||||||||||||||||||| ||||||||||||||||||||| |||||||||||||||
Sbjct                  1533724  CCGTTGACCCCTGGGATGATCGCGCTGTTCACGAACAAATCACCGAGCTGGCAAAGCAAT  1533783
CDS:hypothetical pro   279      T  V  D  P  W  D  D  R  A  V  H  E  Q  I  T  E  L  A  K  Q

CDS: Putative 3        299      F  P  E  K  T  R  I  G  I  N  L  T  G  G  T  K  L  M  F  A
Query                  4499     TTCCAGAAAAAACACGAATTGGAATCAATTTAACTGGCGGCACAAAACTGATGTTTGCTG  4558
                                 |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct                  1533784  TTCCAGAAAAAACACGAATTGGAATCAATTTAACTGGCGGCACAAAATTGATGTTTGCTG  1533843
CDS:hypothetical pro   299      F  P  E  K  T  R  I  G  I  N  L  T  G  G  T  K  L  M  F  A

CDS: Putative 3        319      G  A  L  S  A  A  R  E  L  G  A  V  P  F  Y  F  D  S  K  N
Query                  4559     GCGCGCTCTCTGCTGCGCGTGAACTGGGCGCTGTTCCGTTTTATTTTGATAGCAAGAATC  4618
                                 |||||||||||||||| |||||||||||||||||||||||||||||||| |||||||||||
Sbjct                  1533844  GCGCGCTCTCTGCTGCACGTGAACTGGGCGCTGTTCCGTTTTATTTTGACAGCAAGAATC  1533903
CDS:hypothetical pro   319      G  A  L  S  A  A  R  E  L  G  A  V  P  F  Y  F  D  S  K  N

CDS: Putative 3        339      R  H  V  T  F  I  D  S  V  R  R  E  K  I  R  Q  I  D  S  I
Query                  4619     GTCACGTCACATTCATTGACAGTGTTCGGCGCGAAAAAATCAGGCAGATTGATTCAATCG  4678
                                 ||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1533904  GTCGCGTCATATTCATTGACAGTGTTCGGCGCGAAAAAATCAGGCAGATTGATTCAATCG  1533963
CDS:hypothetical pro   339      R  R  V  I  F  I  D  S  V  R  R  E  K  I  R  Q  I  D  S  I

CDS: Putative 3        359      E  T  F  L  R  L  N  S  D  G  L  E  I  A  G  S  S  F  M  K
Query                  4679     AAACATTTTTGCGCCTGAATAGCGACGGATTGGAGATTGCAGGCAGTTCCTTTATGAAGG  4738
                                 | |||||||||| ||||||||||| || |||||||||||||||||||||||| |||||||
Sbjct                  1533964  AGACATTTTTGCACCTGAATAGCGATGGTTTGGAGATTGCAGGCAGTTCCTTCATGAAGG  1534023
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CDS:hypothetical pro  359      E  T  F  L  H  L  N  S  D  G  L  E  I  A  G  S  S  F  M  K

CDS: Putative 3       379      D  I  S  P  S  R  Q  L  L  T  K  A  L  W  L  H  R  D  K  V
Query                 4739     ATATATCGCCAAGTCGCCAACTTCTGACCAAGGCTCTTTGGTTGCATCGTGACAAGGTGC  4798
                               ||||||||||||||||||||||||||||| || | |||||| |||||||||||||||||
Sbjct                 1534024  ATATATCGCCAAGTCGCCAACTTCTGACCGAGACCCTTTGGCTGCATCGTGACAAGGTGC  1534083
CDS:hypothetical pro  379      D  I  S  P  S  R  Q  L  L  T  E  T  L  W  L  H  R  D  K  V

CDS: Putative 3       399      R  R  F  Y  R  E  L  T  D  Y  N  N  A  F  R  P  F  E  I  C
Query                 4799     GTAGATTTTATAGAGAACTTACCGACTATAACAATGCATTCAGGCCATTCGAGATTTGTC  4858
                               ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct                 1534084  GTAGATTTTATAGAGAACTGACCGACTATAACAATGCATTCAGGCCATTCGAGATTTGTC  1534143
CDS:hypothetical pro  399      R  R  F  Y  R  E  L  T  D  Y  N  N  A  F  R  P  F  E  I  C

CDS: Putative 3       419      R  D  G  F  N  F  K  L  D  D  M  E  A  V  S  V  Q  G  Y  G
Query                 4859     GTGACGGCTTCAATTTCAAGCTGGATGACATGGAGGCAGTATCCGTCCAGGGCTACGGAT  4918
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1534144  GTGACGGCTTCAATTTCAAGCTGGATGACATGGAGGCAGTATCCGTCCAGGGCTACGGAT  1534203
CDS:hypothetical pro  419      R  D  G  F  N  F  K  L  D  D  M  E  A  V  S  V  Q  G  Y  G

CDS: Putative 3       439      L  D  L  R  F  E  K  W  P  D  F  A  K  Y  L  S  G  G  W  F
Query                 4919     TGGATCTGAGATTTGAGAAATGGCCTGATTTCGCCAAATACCTATCTGGCGGCTGGTTCG  4978
                               | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1534204  TAGATCTGAGATTTGAGAAATGGCCTGATTTCGCCAAATACCTATCTGGCGGCTGGTTCG  1534263
CDS:hypothetical pro  439      L  D  L  R  F  E  K  W  P  D  F  A  K  Y  L  S  G  G  W  F

CDS: Putative 3       459      E  E  F  V  Y  L  Q  C  E  P  Y  E  D  A  G  V  I  Q  D  L
Query                 4979     AGGAGTTTGTTTATTTGCAGTGCGAACCCTACGAGGATGCTGGCGTCATTCAAGACTTGC  5038
                               |||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||||||
Sbjct                 1534264  AGGAGTTTGTTTATTTGCAGTGCAAACCCTACGAGGATGCTGGAGTCATTCAAGACTTGC  1534323
CDS:hypothetical pro  459      E  E  F  V  Y  L  Q  C  K  P  Y  E  D  A  G  V  I  Q  D  L

CDS: Putative 3       479      R  I  N  V  K  L  N  L  N  L  E  E  S  K  G  Y  S  S  F  G
Query                 5039     GCATCAATGTCAAGCTGAACTTGAATTTAGAAGAGTCAAAAGGCTATTCGAGCTTCGGTG  5098
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1534324  GCATCAATGTCAAGCTGAACTTGAATTTAGAAGAGTCAAAAGGCTATTCGAGCTTCGGTG  1534383
CDS:hypothetical pro  479      R  I  N  V  K  L  N  L  N  L  E  E  S  K  G  Y  S  S  F  G

CDS: Putative 3       499      V  E  Y  N  E  L  D  I  T  F  T  D  G  Y  S  L  Y  I  V  E
Query                 5099     TTGAATACAACGAGCTGGACATCACATTCACCGACGGTTATTCGCTTTATATCGTGGAAT  5158
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1534384  TTGAATACAACGAGCTGGACATCACATTCACCGACGGTTATTCGCTTTATATCGTGGAAT  1534443
CDS:hypothetical pro  499      V  E  Y  N  E  L  D  I  T  F  T  D  G  Y  S  L  Y  I  V  E

CDS: Putative 3       519      C  K  A  G  N  V  T  Q  E  Q  I  M  K  L  Q  N  L  V  R  F
Query                 5159     GCAAGGCGGGCAATGTAACGCAAGAGCAGATTATGAAGCTGCAGAACCTTGTGCGCTTCT  5218
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1534444  GCAAGGCGGGCAATGTAACGCAAGAGCAGATTATGAAGCTGCAGAACCTTGTGCGCTTCT  1534503
CDS:hypothetical pro  519      C  K  A  G  N  V  T  Q  E  Q  I  M  K  L  Q  N  L  V  R  F
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CDS: Putative 3       539      Y  G  G  I  E  G  R  G  I  V  A  C  C  V  P  P  N  T  E  S
Query                 5219     ACGGAGGAATTGAAGGTCGCGGTATCGTTGCCTGCTGTGTTCCGCCAAATACTGAGTCGG  5278
                               ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Sbjct                 1534504  ACGGAGGAATTGAAGGTCGCGGTATCGTTGCCTGCTGTGTTCTCCCAAATACTGAGTCGG  1534563
CDS:hypothetical pro  539      Y  G  G  I  E  G  R  G  I  V  A  C  C  V  L  P  N  T  E  S

CDS: Putative 3       559      A  K  K  K  I  K  D  A  R  L  M  L  W  S  G  A  S  L  S  E
Query                 5279     CCAAGaaaaaaaTAAAAGATGCCAGACTGATGCTTTGGAGTGGTGCATCACTTTCTGAGC  5338
                                |||||||||||||||||||||||| |||||||||||||||||||||||| |||||||||
Sbjct                 1534564  TCAAGAAAAAAATAAAAGATGCCAGGCTGATGCTTTGGAGTGGTGCATCATTTTCTGAGC  1534623
CDS:hypothetical pro  559      V  K  K  K  I  K  D  A  R  L  M  L  W  S  G  A  S  F  S  E

CDS: Putative 3       579      Q  I  T  A  M  M  N  S  I  T  E  R  A  E  A  S  E  A  T  P
Query                 5339     AGATAACGGCAATGATGAACAGCATCACTGAGCGGGCTGAAGCGAGTGAGGCAACGCCAT  5398
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1534624  AGATAACGGCAATGATGAACAGCATCACTGAGCGGGCTGAAGCGAGTGAGGCAACGCCAT  1534683
CDS:hypothetical pro  579      Q  I  T  A  M  M  N  S  I  T  E  R  A  E  A  S  E  A  T  P

CDS: Putative 3                *
Query                 5399     GATGCTCCATTTGGTTTGCGACATCTCCGGCAGCATGAGTGAAGGAGGCAAGCCCTTCAT  5458
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1534684  GATGCTCCATTTGGTTTGCGACATCTCCGGCAGCATGAGTGAAGGAGGCAAGCCCTTCAT  1534743

Query                 5459     CCTGCGAACCTTGGCCACGACCGTGGCGCAATGGGTGCGGCAAGGGTATGGAAAGGCGGA  5518
                               |||||||||||||||||||||||||||||||||||||||||||| ||||||||| |||||||
Sbjct                 1534744  CCTGCGAACCTTGGCCACGACCGTGGCGCAATGGGTGCGGCATGGGTATGGACAGGCGGA  1534803

Query                 5519     AATCCGCCTTTGTGCTTGGAGCAGCGAGGCACGCAGCATCCCGGACTGGAGCGTCACGGA  5578
                               |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct                 1534804  AATCCGCCTTTGTGCTTGGAGCAGCGAGGCACGCAGCATCCCGAACTGGAGCGTCACGGA  1534863

Query                 5579     CGATCTCCCGGTCGAAATGCTGGTTTGCCATGGAAGCACCAATGGCCAGGCGCTGGTTCA  5638
                               |||||||||||| |||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct                 1534864  CGATCTCCCGGTGGAAATGCTGGTTTGCCATGGAAGCACCAATGGCGAGGCGCTGGTTCA  1534923

Query                 5639     ACTGCTGGGTAACGAGCCGGATGGAAAGGTTCTGATCCTCACGGATGGATTCTGGACAAG  5698
                               |||| |||||| ||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct                 1534924  ACTGTTGGGTAGCGAGCCGGATGGAAAGGTTCTGATTCTCACGGATGGATTCTGGACAAG  1534983

CDS: Putative 4       1                V  K  T  L  S  R  W  Q  E  G  L  P  P  D  T  L  R  V
Query                 5699     AGACGACGTGAAGACCCTGAGCCGCTGGCAGGAAGGTCTACCGCCGGACACGCTGCGCGT  5758
                               ||||| ||||||||| |||||||||||||||||||| |||||||||||| ||||||||||||
Sbjct                 1534984  AGACGGCGTGAAGACTCTGAGCCGCTGGCAGGAAGGCCTACCGCCGGATACGCTGCGCGT  1535043
CDS:hypothetical pro  1                M  K  T  L  S  R  W  Q  E  G  L  P  P  D  T  L  R  V

CDS: Putative 4       19                I  Q  I  G  A  D  A  N  P  H  L  S  K  G  L  K  G  A  K  V
Query                 5759     CATCCAAATCGGCGCGGATGCCAACCCACATCTTTCCAAGGGGCTCAAAGGCGCAAAGGT  5818
                               ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct                 1535044  CATCCAAATCGGCGCGGATGCCAACCCGCATCTTTCCAAGGGGCTCAAAGGCGCAAAGGT  1535103
CDS:hypothetical pro  19                I  Q  I  G  A  D  A  N  P  H  L  S  K  G  L  K  G  A  K  V
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CDS: Putative 4       39         F  A  A  E  E  V  L  A  V  L  D  N  W  L  Q  A  D  E  E  W
Query                 5819     GTTTGCCGCAGAAGAAGTGCTCGCCGTACTCGATAACTGGCTGCAGGCGGATGAGGAATG  5878
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1535104  GTTTGCCGCAGAAGAAGTGCTCGCCGTACTCGATAACTGGCTGCAGGCGGATGAGGAATG  1535163
CDS:hypothetical pro  39         F  A  A  E  E  V  L  A  V  L  D  N  W  L  Q  A  D  E  E  W

CDS: Putative 4       59         A  *
Query                 5879     GGCATGACGCTTTGGAAAAGTTTTGGGGCAAGCGTTCGCGGCCCGAGCCATATCGCCGAA  5938
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1535164  GGCATGACGCTTTGGAAAAGTTTTGGGGCAAGCGTTCGCGGCCCGAGCCATATCGCCGAA  1535223
CDS:hypothetical pro  59         A

Query                 5939     GGTTTGCCAAATCAGGATGCATGGGCGAAGTTTCACCATGTTTGGGGTGATGGCATCGTC  5998
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1535224  GGTTTGCCAAATCAGGATGCATGGGCGAAGTTTCACCATGTTTGGGGTGATGGCATCGTC  1535283

Query                 5999     GTGTCCGACGGAGTTGGCTCCAAGCCCTTCTCCAGCTTCGGCAGCCATGCTGCCTGTCTC  6058
                               ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1535284  GTGTCCGACGGGGTTGGCTCCAAGCCCTTCTCCAGCTTCGGCAGCCATGCTGCCTGTCTC  1535343

Query                 6059     GCCGTCGAGTTCGCAGCCCGGGCTTGTTGCACCGGTGGTGAAATCGAACACAACGCGCTG  6118
                               |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct                 1535344  GCCGTCGAGTTCGCAGCCCGGGCTTGTTGCACCAGTGGTGAAATCGAACACAACGCGCTG  1535403

Query                 6119     TTTAGCAACATCCAAGCTAACTGGCTGAGGCTTGTCGCTCCGCTGGAACCTCGCGATTGC  6178
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1535404  TTTAGCAACATCCAAGCTAACTGGCTGAGGCTTGTCGCTCCGCTGGAACCTCGCGATTGC  1535463

Query                 6179     GCGGCCACCTGTCTCTTCGCACTACACCTGGATGGCGTAATCCACCTAGGGATGCTTGGC  6238
                               ||||||||||||||| |||||||||| |||||||||||||||||||||||||||||||||
Sbjct                 1535464  GCGGCCACCTGTCTTTTCGCACTACGCCTGGATGGCGTAATCCACCTAGGGATGCTTGGC  1535523

Query                 6239     GACGGACTTGCCGCTATTGCCAAGTCCGATGGATCAGTGGTTTCGCTGTCGGAAAACAAG  6298
                               |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct                 1535524  GACGGACTTGCCGCTATTGCCAAGTCCGATGGATCAGTCGTTTCGCTGTCGGAAAACAAG  1535583

Query                 6299     ACGCAAGGCTTCTCCAATATCACTACTGCGCTGTCCTCCAAGGTCTCCGCCAAAGACTGG  6358
                               || |||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct                 1535584  ACACAAGGCTTCTCCAATATCACCATTGCGCTGTCCTCCAAGGTCTCCGCCAAAGACTGG  1535643

Query                 6359     CAGTATTTGTCGCTGCCGGGGGAGCAGTGCATCGCAGTATTGCTCTGCACCGATGGGGTG  6418
                               |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct                 1535644  CAGTATTTGTCGCTGCCGGGGGAGCAGTGCATCGCAGTATTGCTCTGCACTGATGGGGTG  1535703

Query                 6419     GCTGACGATTTGGATAACGCTGACGGGTTTGTGAGCAGTTTCGCCGAAACGCATCGAACC  6478
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1535704  GCTGACGATTTGGATAACGCTGACGGGTTTGTGAGCAGTTTCGCCGAAACGCATCGAACC  1535763

Query                 6479     CTCGCACCGGTAAGTGCCAACCGGCGCATCCACGAGATGCTCGAAAACTGGCCCACGCCC  6538
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                            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1535764  CTCGCGCCGGTAAGTGCCAACCGGCGCATCCACGAGATGCTCGAAAACTGGCCCACGCCC  1535823

CDS: Putative 5       1                                                                M  S  N
Query                 6539     AAGCACAGCGACGATAAAACCCTCGCCTGCCTGTGCAGTGAGGAGGTTGCAGATGAGTAA  6598
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1535824  AAGCACAGCGACGATAAAACCCTCGCCTGCCTGTGCAGTGAGGAGGTTGCAGATGAGTAA  1535883
CDS:serine/threonine  1                                                                M  S  N

CDS: Putative 5       4          A  E  H  Q  A  L  K  P  L  V  D  E  Y  N  N  V  H  Q  M  A
Query                 6599     CGCCGAACACCAGGCTCTGAAGCCACTTGTGGATGAATACAACAATGTTCATCAGATGGC  6658
                               |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct                 1535884  CGCCGAACACCAGGCTCTGAAGCCACTTGTGGATGAATACGACAATGTTCATCAGATGGC  1535943
CDS:serine/threonine  4          A  E  H  Q  A  L  K  P  L  V  D  E  Y  D  N  V  H  Q  M  A

CDS: Putative 5       24         D  E  L  A  R  G  G  Q  G  V  V  Y  R  T  K  D  A  D  L  A
Query                 6659     CGATGAGCTTGCGCGCGGTGGGCAAGGCGTGGTCTATCGCACCAAGGATGCGGATTTGGC  6718
                               ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct                 1535944  CGATGAGCTTGCGCGCGGTGGACAAGGCGTGGTCTATCGCACCAAGGATGCGGATTTGGC  1536003
CDS:serine/threonine  24         D  E  L  A  R  G  G  Q  G  V  V  Y  R  T  K  D  A  D  L  A

CDS: Putative 5       44         V  K  Q  P  L  D  A  A  G  Q  P  D  K  N  A  N  L  R  E  R
Query                 6719     CGTCAAGCAGCCGCTGGACGCTGCCGGCCAGCCGGACAAAAACGCCAATCTGCGCGAGCG  6778
                               ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct                 1536004  CGTCAAGCAGCCGCTGGACGCAGCCGGCCAGCCGGACAAAAACGCCAATCTGCGCGAGCG  1536063
CDS:serine/threonine  44         V  K  Q  P  L  D  A  A  G  Q  P  D  K  N  A  N  L  R  E  R

CDS: Putative 5       64         F  Q  H  V  R  L  L  P  I  P  R  R  I  P  V  S  L  P  L  A
Query                 6779     CTTCCAGCACGTCCGCCTGTTGCCCATACCACGGCGCATCCCCGTTTCCCTTCCACTCGC  6838
                               |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct                 1536064  CTTCCAGCACGTCCGCCTGTTGCCCATACCACGGCGCATCCCCGTTTCCCTGCCACTCGC  1536123
CDS:serine/threonine  64         F  Q  H  V  R  L  L  P  I  P  R  R  I  P  V  S  L  P  L  A

CDS: Putative 5       84         I  L  R  D  E  P  G  Y  V  M  R  L  L  N  G  M  K  P  F  A
Query                 6839     CATCCTGCGCGACGAGCCGGGCTATGTGATGCGTCTGTTGAACGGCATGAAGCCCTTCGC  6898
                               |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct                 1536124  CATCCTGCGCGACGAGCCGGGCTATGTGATGCGTCTGTTGAGCGGCATGAAGCCCTTCGC  1536183
CDS:serine/threonine  84         I  L  R  D  E  P  G  Y  V  M  R  L  L  S  G  M  K  P  F  A

CDS: Putative 5       104        S  F  D  L  D  G  R  S  K  K  K  L  E  D  Q  S  Q  A  L  P
Query                 6899     CAGTTTCGATTTGGACGGCAGAAGCAAAAAGAAGCTGGAAGATCAAAGCCAAGCCTTGCC  6958
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1536184  CAGTTTCGATTTGGACGGCAGAAGCAAAAAGAAGCTGGAAGATCAAAGCCAAGCCTTGCC  1536243
CDS:serine/threonine  104        S  F  D  L  D  G  R  S  K  K  K  L  E  D  Q  S  Q  A  L  P

CDS: Putative 5       124        Q  W  L  T  K  I  P  D  K  D  L  A  L  R  L  L  H  Y  A  Q
Query                 6959     CCAATGGCTGACGAAGATTCCTGACAAGGACCTGGCGCTGCGACTACTGCATTACGCACA  7018
                               |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct                 1536244  CCAATGGCTGACGAAGATTCCTGACAAGGACCTGGCGCTGCGACTGCTGCATTACGCACA  1536303
CDS:serine/threonine  124        Q  W  L  T  K  I  P  D  K  D  L  A  L  R  L  L  H  Y  A  Q
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CDS: Putative 5       144        T  G  S  T  R  R  R  S  L  A  L  A  K  C  A  A  I  L  A  R
Query                 7019     AACTGGCTCCACCCGCCGCCGTTCGCTCGCGCTTGCCAAGTGCGCTGCCATCCTCGCCCG  7078
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1536304  AACTGGCTCCACCCGCCGCCGTTCGCTCGCGCTTGCCAAGTGCGCTGCCATCCTCGCCCG  1536363
CDS:serine/threonine  144        T  G  S  T  R  R  R  S  L  A  L  A  K  C  A  A  I  L  A  R

CDS: Putative 5       164        L  H  S  A  G  L  V  Y  G  D  I  S  T  N  N  A  F  I  G  E
Query                 7079     CCTGCACAGCGCTGGACTGGTCTATGGCGACATTTCCACCAACAACGCTTTCATTGGCGA  7138
                               ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1536364  CCTGCACAGCGCGGGACTGGTCTATGGCGACATTTCCACCAACAACGCTTTCATTGGCGA  1536423
CDS:serine/threonine  164        L  H  S  A  G  L  V  Y  G  D  I  S  T  N  N  A  F  I  G  E

CDS: Putative 5       184        D  D  T  T  D  V  W  L  I  D  A  D  N  M  R  L  E  L  P  S
Query                 7139     AGACGACACCACCGATGTCTGGCTCATAGATGCCGACAATATGCGCCTGGAGTTACCCAG  7198
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1536424  AGACGACACCACCGATGTCTGGCTCATAGATGCCGACAATATGCGCCTGGAGTTACCCAG  1536483
CDS:serine/threonine  184        D  D  T  T  D  V  W  L  I  D  A  D  N  M  R  L  E  L  P  S

CDS: Putative 5       204        G  G  V  S  V  Y  T  P  G  Y  G  A  P  E  V  V  Q  G  R  D
Query                 7199     CGGCGGTGTGTCCGTCTATACGCCGGGCTACGGTGCACCGGAGGTAGTGCAGGGCCGTGA  7258
                               |||||| ||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct                 1536484  CGGCGGCGTGTCCGTCTATACGCCGGGCTACGGTGCACCGGAGGTAGTGCTGGGCCGTGA  1536543
CDS:serine/threonine  204        G  G  V  S  V  Y  T  P  G  Y  G  A  P  E  V  V  L  G  R  D

CDS: Putative 5       224        Q  S  R  P  R  T  D  C  W  A  F  A  V  M  T  F  K  L  L  A
Query                 7259     CCAATCCCGCCCGCGAACCGACTGCTGGGCTTTCGCTGTGATGACATTCAAGCTACTGGC  7318
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1536544  CCAATCCCGCCCGCGAACCGACTGCTGGGCTTTCGCTGTGATGACATTCAAGCTACTGGC  1536603
CDS:serine/threonine  224        Q  S  R  P  R  T  D  C  W  A  F  A  V  M  T  F  K  L  L  A

CDS: Putative 5       244        L  C  H  P  F  I  G  K  K  V  L  E  P  E  D  E  E  D  G  W
Query                 7319     GCTTTGCCACCCTTTCATTGGCAAGAAAGTACTGGAGCCCGAAGATGAAGAAGACGGCTG  7378
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1536604  GCTTTGCCACCCTTTCATTGGCAAGAAAGTACTGGAGCCCGAAGATGAAGAAGACGGCTG  1536663
CDS:serine/threonine  244        L  C  H  P  F  I  G  K  K  V  L  E  P  E  D  E  E  D  G  W

CDS: Putative 5       264        D  A  D  P  A  P  N  G  T  A  T  D  L  N  E  Q  A  F  A  G
Query                 7379     GGATGCCGACCCTGCGCCCAATGGCACTGCCACCGATCTGAACGAACAGGCATTCGCTGG  7438
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1536664  GGATGCCGACCCTGCGCCCAATGGCACTGCCACCGATCTGAACGAACAGGCATTCGCTGG  1536723
CDS:serine/threonine  264        D  A  D  P  A  P  N  G  T  A  T  D  L  N  E  Q  A  F  A  G

CDS: Putative 5       284        F  L  P  F  V  D  D  E  D  D  D  S  N  E  G  V  G  G  L  P
Query                 7439     TTTCTTGCCTTTCGTGGATGACGAAGATGACGATTCCAACGAAGGAGTTGGAGGCCTGCC  7498
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1536724  TTTCTTGCCTTTCGTGGATGACGAAGATGACGATTCCAACGAAGGAGTTGGAGGCCTGCC  1536783
CDS:serine/threonine  284        F  L  P  F  V  D  D  E  D  D  D  S  N  E  G  V  G  G  L  P

CDS: Putative 5       304        R  V  L  V  A  T  E  G  L  R  R  L  F  Q  E  T  F  G  A  G
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Query                  7499     CCGTGTATTAGTCGCAACAGAAGGATTACGCCGCCTGTTTCAGGAAACTTTCGGTGCAGG  7558
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1536784  CCGTGTATTAGTCGCAACAGAAGGATTACGCCGCCTGTTTCAGGAAACTTTCGGTGCAGG  1536843
CDS:serine/threonine   304        R  V  L  V  A  T  E  G  L  R  R  L  F  Q  E  T  F  G  A  G

CDS: Putative 5        324        R  E  L  P  H  R  R  P  T  M  A  F  W  T  L  E  L  A  R  A
Query                  7559     ACGTGAACTGCCGCACCGCCGCCCGACAATGGCGTTCTGGACATTGGAGCTTGCGAGGGC  7618
                                ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct                  1536844  ACGTGAACTGCCGCACCGCCGCCCGACAATGGCGTTCTGGATATTGGAGCTTGCGAGGGC  1536903
CDS:serine/threonine   324        R  E  L  P  H  R  R  P  T  M  A  F  W  I  L  E  L  A  R  A

CDS: Putative 5        344        A  D  Q  S  L  D  C  L  E  C  G  M  S  H  F  A  D  E  Y  A
Query                  7619     GGCGGATCAGTCGCTGGATTGCCTCGAATGTGGCATGAGCCATTTCGCCGATGAATACGC  7678
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1536904  GGCGGATCAGTCGCTGGATTGCCTCGAATGTGGCATGAGCCATTTCGCCGATGAATACGC  1536963
CDS:serine/threonine   344        A  D  Q  S  L  D  C  L  E  C  G  M  S  H  F  A  D  E  Y  A

CDS: Putative 5        364        Q  C  P  Y  C  G  A  A  R  P  A  F  I  R  V  K  T  P  R  W
Query                  7679     GCAATGCCCGTATTGTGGCGCGGCGCGCCCGGCTTTCATTCGCGTCAAAACGCCACGTTG  7738
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1536964  GCAATGCCCGTATTGTGGCGCGGCGCGCCCGGCTTTCATTCGCGTCAAAACGCCACGTTG  1537023
CDS:serine/threonine   364        Q  C  P  Y  C  G  A  A  R  P  A  F  I  R  V  K  T  P  R  W

CDS: Putative 5        384        E  I  L  I  P  G  G  A  T  E  F  R  L  P  Q  R  L  F  H  P
Query                  7739     GGAAATCCTGATTCCTGGTGGTGCCACGGAGTTCAGATTGCCGCAGCGGCTTTTTCACCC  7798
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1537024  GGAAATCCTGATTCCTGGTGGTGCCACGGAGTTCAGATTGCCGCAGCGGCTTTTTCACCC  1537083
CDS:serine/threonine   384        E  I  L  I  P  G  G  A  T  E  F  R  L  P  Q  R  L  F  H  P

CDS: Putative 5        404        F  S  F  E  Y  F  D  N  T  A  Y  E  A  M  L  N  C  A  A  K
Query                  7799     GTTTTCATTCGAGTATTTCGATAACACAGCATACGAAGCCATGCTGAACTGCGCGGCCAA  7858
                                ||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct                  1537084  GTTTTCATTCGAGTATTTCGATAACACAGCATACGAAGCCATGCTGAACTTCGCGGCCAA  1537143
CDS:serine/threonine   404        F  S  F  E  Y  F  D  N  T  A  Y  E  A  M  L  N  F  A  A  K

CDS: Putative 5        424        T  A  V  P  V  R  G  T  L  P  F  P  D  N  L  T  F  E  F  V
Query                  7859     AACCGCAGTCCCCGTGCGGGGCACGCTGCCTTTCCCGGACAACCTCACCTTTGAGTTCGT  7918
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1537144  AACCGCAGTCCCCGTGCGGGGCACGCTGCCTTTCCCGGACAACCTCACCTTTGAGTTCGT  1537203
CDS:serine/threonine   424        T  A  V  P  V  R  G  T  L  P  F  P  D  N  L  T  F  E  F  V

CDS: Putative 5        444        E  G  C  K  *
CDS: Putative 6        1                     M  K  F  Q  D  I  P  V  N  I  I  T  V  R  I  K
Query                  7919     GGAGGGCTGCAAATGAAGTTTCAGGACATTCCTGTCAACATCATAACTGTCCGCATCAAG  7978
                                ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1537204  GGAGGCCTGCAAATGAAGTTTCAGGACATTCCTGTCAACATCATAACTGTCCGCATCAAG  1537263
CDS:serine/threonine   444        E  A  C  K
CDS:AAA ATPase [Pseu   1                     M  K  F  Q  D  I  P  V  N  I  I  T  V  R  I  K

CDS: Putative 6        17        R  S  D  N  V  E  A  L  Q  E  Q  P  V  F  S  V  E  A  S  L
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Query                  7979     CGGTCTGACAATGTCGAAGCCCTGCAAGAGCAGCCAGTATTCTCGGTAGAGGCCAGCCTA  8038
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1537264  CGGTCTGACAATGTCGAAGCCCTGCAAGAGCAGCCAGTATTCTCGGTAGAGGCCAGCCTA  1537323
CDS:AAA ATPase [Pseu  17        R  S  D  N  V  E  A  L  Q  E  Q  P  V  F  S  V  E  A  S  L

CDS: Putative 6        37        S  R  A  D  E  F  E  I  R  L  R  D  A  V  V  F  V  R  P  V
Query                  8039     TCCCGCGCAGATGAATTTGAAATCCGCCTGAGAGACGCGGTTGTTTTCGTTCGCCCCGTC  8098
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1537324  TCCCGCGCAGATGAATTTGAAATCCGCCTGAGAGACGCGGTTGTTTTCGTTCGCCCCGTC  1537383
CDS:AAA ATPase [Pseu  37        S  R  A  D  E  F  E  I  R  L  R  D  A  V  V  F  V  R  P  V

CDS: Putative 6        57        A  A  V  D  I  R  R  L  N  A  E  L  A  S  G  R  S  L  L  A
Query                  8099     GCGGCTGTTGACATCCGCCGCCTCAACGCTGAACTTGCCAGTGGGCGTTCCCTGCTTGCA  8158
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1537384  GCGGCTGTTGACATCCGCCGCCTCAACGCTGAACTTGCCAGTGGGCGTTCCCTGCTTGCA  1537443
CDS:AAA ATPase [Pseu  57        A  A  V  D  I  R  R  L  N  A  E  L  A  S  G  R  S  L  L  A

CDS: Putative 6        77        Q  L  E  N  P  A  A  D  G  S  I  E  L  K  I  G  F  F  T  G
Query                  8159     CAACTTGAAAACCCTGCCGCCGATGGCAGCATCGAGCTGAAGATCGGTTTTTTCACCGGC  8218
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1537444  CAACTTGAAAACCCTGCCGCCGATGGCAGCATCGAGCTGAAGATCGGTTTTTTCACCGGC  1537503
CDS:AAA ATPase [Pseu  77        Q  L  E  N  P  A  A  D  G  S  I  E  L  K  I  G  F  F  T  G

CDS: Putative 6        97        V  C  L  E  M  G  D  V  E  I  G  V  D  E  Y  V  Q  E  K  M
Query                  8219     GTCTGCCTGGAAATGGGCGATGTTGAAATCGGTGTGGATGAGTATGTGCAAGAAAAGATG  8278
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1537504  GTCTGCCTGGAAATGGGCGATGTTGAAATCGGTGTGGATGAGTATGTGCAAGAAAAGATG  1537563
CDS:AAA ATPase [Pseu  97        V  C  L  E  M  G  D  V  E  I  G  V  D  E  Y  V  Q  E  K  M

CDS: Putative 6        117       R  T  K  G  E  A  L  Y  K  R  L  G  E  L  C  C  F  Q  Q  G
Query                  8279     CGGACGAAGGGTGAGGCACTTTACAAGAGGCTGGGCGAACTTTGCTGCTTCCAACAGGGA  8338
                                ||||||||||| |||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct                  1537564  CGGACGAAGGGCGAGGCACTTTACAAGAGGCTGGGCGAACTTTGCTGCTTCCAACTGGGA  1537623
CDS:AAA ATPase [Pseu  117       R  T  K  G  E  A  L  Y  K  R  L  G  E  L  C  C  F  Q  L  G

CDS: Putative 6        137       N  D  A  F  F  F  L  T  A  G  P  A  I  D  E  E  L  K  P  V
Query                  8339     AACGACGCATTTTTCTTCCTGACTGCTGGCCCGGCGATTGATGAAGAACTGAAACCTGTC  8398
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1537624  AACGACGCATTTTTCTTCCTGACTGCTGGCCCGGCGATTGATGAAGAACTGAAACCTGTC  1537683
CDS:AAA ATPase [Pseu  137       N  D  A  F  F  F  L  T  A  G  P  A  I  D  E  E  L  K  P  V

CDS: Putative 6        157       G  E  D  T  P  R  D  A  A  A  E  P  T  R  I  N  A  F  C  V
Query                  8399     GGCGAGGACACGCCACGCGATGCAGCTGCGGAGCCGACCCGAATAAACGCTTTCTGTGTT  8458
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1537684  GGCGAGGACACGCCACGCGATGCAGCTGCGGAGCCGACCCGAATAAACGCTTTCTGTGTT  1537743
CDS:AAA ATPase [Pseu  157       G  E  D  T  P  R  D  A  A  A  E  P  T  R  I  N  A  F  C  V

CDS: Putative 6        177       T  G  E  G  I  R  F  I  A  T  E  K  A  M  P  G  G  Q  T  I
Query                  8459     ACTGGCGAAGGTATCCGCTTCATTGCCACCGAAAAAGCAATGCCAGGCGGCCAAACTATC  8518
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
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Sbjct                  1537744  ACTGGCGAAGGTATCCGCTTCATTGCCACCGAAAAAGCAATGCCAGGCGGCCAAACCATC  1537803
CDS:AAA ATPase [Pseu   177       T  G  E  G  I  R  F  I  A  T  E  K  A  M  P  G  G  Q  T  I

CDS: Putative 6        197       Y  I  A  T  R  L  T  K   P  K  K  E  P  D  R  T  L  R  L  A
Query                  8519     TACATCGCCACCCGTCTAACCAAG-CCAAAGAAGGAACCTGACCGCACCTTACGCCTGGC  8577
                                ||||||||||| ||  |||||| | ||||| ||| |||| |||||| || | ||||| ||
Sbjct                  1537804  TACATCGCCACACGCATAACCAGGACCAAAAAAG-AACCCGACCGCGCCCTGCGCCTCGC  1537862
CDS:AAA ATPase [Pseu   197       Y  I  A  T  R  I  T  R  T  K  K   E  P  D  R  A  L  R  L  A

CDS: Putative 6        217        K  G  R  L  R  F  V  D  W  T  Q  A  G  Q  V  Q  I  L  A  K
Query                  8578     CAAAGGTCGGCTGCGTTTTGTGGACTGGACACAGGCGGGACAAGTGCAAATTCTTGCCAA  8637
                                |||||| |||||||||||||  || |||||||| || || |||||||||| |||||||||
Sbjct                  1537863  CAAAGGCCGGCTGCGTTTTGCCGATTGGACACAAGCAGGGCAAGTGCAAACTCTTGCCAA  1537922
CDS:AAA ATPase [Pseu   217        K  G  R  L  R  F  A  D  W  T  Q  A  G  Q  V  Q  T  L  A  K

CDS: Putative 6        237        A  Q  M  T  A  L   T  Q  D  D  G  S  Y  L  K  K  W  D  E
Query                  8638     AGCGCAAATGACAGCACTC--ACTCAGGACGATGGAAGCTATCTGAAAAAGTGGGACGAG  8695
                                |||||||||| | || |||  || || |||||    ||||| |||||||||||||| ||
Sbjct                  1537923  AGCGCAAATG-C-GCGCTCTTACCCAAGACGACAACAGCTACCTGAAAAAGTGGGATGAA  1537980
CDS:AAA ATPase [Pseu   237        A  Q  M   R  A  L  T  Q  D  D  N  S  Y  L  K  K  W  D  E

CDS: Putative 6        256       F  G  E  V  E  G  E  L  L  L  K  Q  A  R  E  V  G  A  L  Q
Query                  8696     TTTGGTGAGGTTGAAGGTGAACTGCTGCTCAAGCAAGCACGCGAAGTGGGTGCTTTGCAA  8755
                                ||||||||  | || || ||| ||||||||||||||||| ||||||||||| ||||| |||
Sbjct                  1537981  TTTGGTGACATGGAGGGCGAATTGCTGCTCAAGCAAGCGCGCGAAGTGGGGGCTTTACAA  1538040
CDS:AAA ATPase [Pseu   256       F  G  D  M  E  G  E  L  L  L  K  Q  A  R  E  V  G  A  L  Q

CDS: Putative 6        276       F  T  E  M  V  P  K  R  D  G  T  V  G  V  R  I  A  Q  A  S
Query                  8756     TTCACGGAGATGGTGCCGAAACGGGATGGAACTGTCGGAGTTCGTATTGCGCAGGCATCA  8815
                                ||||| |||||||  | | | |||||||||||| |||   ||||| ||| | ||||||
Sbjct                  1538041  TTCACAGAGATGGCTCAGGAGCGGGATGGAACCGTCACGGTTCGCATTTCACAGGCACTT  1538100
CDS:AAA ATPase [Pseu   276       F  T  E  M  A  Q  E  R  D  G  T  V  T  V  R  I  S  Q  A  L

CDS: Putative 6        296       D  S  A  W  G  A  L  R  Q  G  A  V  P  E  V  E  L  V  D  E
Query                  8816     GATTCTGCGTGGGGCGCACTGAGACAAGGCGCAGTACCTGAAGTTGAACTGGTGGACGAG  8875
                                || ||||| | |   || ||| |  | || || |||||||||||  ||  ||||||| ||
Sbjct                  1538101  GACTCTGCATTGAAAGCGCTGGGGAACGGTGCCGTACCTGAAGTCGAGTTGGTGGATGAA  1538160
CDS:AAA ATPase [Pseu   296       D  S  A  L  K  A  L  G  N  G  A  V  P  E  V  E  L  V  D  E

CDS: Putative 6        316       L  P  D  Y  L  Q  D  E  N  L  S  F  T  D  F  A  R  G  I  E
Query                  8876     TTGCCGGACTACTTGCAGGATGAAAACCTGAGCTTCACGGATTTTGCGAGAGGGATCGaa  8935
                                |||||||||| ||| | ||||||  | ||||||||| ||||||||| || || || ||
Sbjct                  1538161  CTGCCGGACTATTTGAAAGATGAACGCTTGAGCTTCAAGGATTTTGCAAGTGGAATTGAG  1538220
CDS:AAA ATPase [Pseu   316       L  P  D  Y  L  K  D  E  R  L  S  F  K  D  F  A  S  G  I  E

CDS: Putative 6        336       K  K  E  G  E  H  S  K  L  G  E  K  R  E  L  R  E  K  N  T
Query                  8936     aaaaaGGAGGGGGAACACAGCAAGCTCGGTGAAAAACGCGAGCTGCGCGAGAAAAATACC  8995
                                 ||  ||||  | | || |||| |  ||  | ||| |||||||  || ||   ||| |||
Sbjct                  1538221  CAAGCGGAGAAG-ATCA-AGCAGGG-CGACGGAAATCGCGAGCAACGTGAAGGAAAGACC  1538277
CDS:AAA ATPase [Pseu   336       Q  A  E  K   I   K  Q  G   D  G  N  R  E  Q  R  E  G  K  T
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CDS: Putative 6       356       Y   F  S  V  A  E  F  D  E  E  T  R  V  L  T  L  K  A  E  A
Query                 8996     TAT-TTCAGTGTCGCAGAGTTTGACGAGGAAACTCGCGTACTCACGCTTAAAGCCGAGGC  9054
                               ||  || | |||||  | ||||||| ||||||| || ||||| ||||| |||  ||||||
Sbjct                 1538278  TACCTTGA-TGTCGTCGGGTTTGACCAGGAAACCCGTGTACTTACGCTCAAAATCGAGGC  1538336
CDS:AAA ATPase [Pseu  355       Y  L  D   V  V  G  F  D  Q  E  T  R  V  L  T  L  K  I  E  A

CDS: Putative 6       376       L  P  K  E  F  G  T  L  I  L  S  L  A  G  E  S  A  Q  I  K
Query                 9055     TCTACCCAAGGAATTCGGCACGCTCATCCTGTCGCTGGCGGGCGAATCTGCTCAGATCAA  9114
                               ||| |||||||||| |||||||||||||||||||||||| || ||| |  | ||||||||
Sbjct                 1538337  TCTGCCCAAGGAATCCGGCACGCTCATCCTGTCGCTGGCCGGTGAAACCACCCAGATCAA  1538396
CDS:AAA ATPase [Pseu  375       L  P  K  E  S  G  T  L  I  L  S  L  A  G  E  T  T  Q  I  K

CDS: Putative 6       396       R  R  M  A  A  R  Q  A  I  L  E  G  R  A  A  N  P  Q  L  G
Query                 9115     GCGCCGCATGGCCGCCCGTCAAGCCATTCTGGAAGGCCGTGCCGCCAACCCCCAGCTTGG  9174
                                || || ||||| |||||||||||||||||||||||||||| ||||||| || ||||||||
Sbjct                 1538397  ACGGCGTATGGCGGCCCGTCAAGCCATTCTGGAAGGCCGTTCCGCCAATCCACAGCTTGG  1538456
CDS:AAA ATPase [Pseu  395       R  R  M  A  A  R  Q  A  I  L  E  G  R  S  A  N  P  Q  L  G

CDS: Putative 6       416       L  L  I  E  A  Q  G  R  I  T  Q  I  R  P  S  Q  K  V  Q  P
Query                 9175     GCTGTTGATTGAGGCGCAGGGGCGAATCACACAGATCCGGCCATCGCAAAAAGTTCAACC  9234
                               ||| ||||||||||  ||||||| |||||||||  |||| ||  |||||||||| ||  |
Sbjct                 1538457  GCTATTGATTGAGGAACAGGGGCAAATCACACAAGTCCGCCCGCCGCAAAAAGTCCAGTC  1538516
CDS:AAA ATPase [Pseu  415       L  L  I  E  E  Q  G  Q  I  T  Q  V  R  P  P  Q  K  V  Q  S

CDS: Putative 6       436       L  T  A  F  V  R  N  K  V  F  R  N  P  P  T  V  M  Q  E  K
Query                 9235     GCTCACGGCCTTCGTTCGCAACAAGGTCTTTCGCAATCCGCCCACCGTCATGCAGGAAAA  9294
                                ||||| || |||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct                 1538517  ACTCACCGCATTCGTTCGCAACAAGGTCTTTCGCAATCCGCCAACCGTCATGCAGGAAAG  1538576
CDS:AAA ATPase [Pseu  435       L  T  A  F  V  R  N  K  V  F  R  N  P  P  T  V  M  Q  E  R

CDS: Putative 6       456       A  I  E  A  A  L  K  T  P  D  I  A  L  I  Q  G  P  P  G  T
Query                 9295     GGCCATCGAGGCCGCCCTAAAAACGCCAGATATAGCGTTGATCCAAGGCCCGCCCGGTAC  9354
                               ||| || ||||  || || || ||||||||| | ||| | || || || ||||| || ||
Sbjct                 1538577  GGCTATTGAGGTTGCGCTGAATACGCCAGATCTCGCGCTTATTCAGGGGCCGCCGGGAAC  1538636
CDS:AAA ATPase [Pseu  455       A  I  E  V  A  L  N  T  P  D  L  A  L  I  Q  G  P  P  G  T

CDS: Putative 6       476       G  K  T  T  V  I  A  A  I  L  E  R  L  N  E  M  A  D  K  R
Query                 9355     CGGCAAGACCACCGTCATCGCTGCCATTCTGGAGCGCCTGAACGAGATGGCCGACAAGCG  9414
                                || || |||||||||||||| |||||||||||||| |||||||||||||||||||||||
Sbjct                 1538637  GGGAAAAACCACCGTCATCGCCGCCATTCTGGAGCGGCTGAACGAGATGGCCGACAAGCG  1538696
CDS:AAA ATPase [Pseu  475       G  K  T  T  V  I  A  A  I  L  E  R  L  N  E  M  A  D  K  R

CDS: Putative 6       496       G  A  S  I  K  G  Q  I  L  L  T  G  F  Q  H  D  A  V  E  N
Query                 9415     CGGCGCGAGCATCAAAGGCCAAATTCTGTTGACAGGCTTTCAGCACGATGCGGTGGAAAA  9474
                               |||||||| ||||||||||||| | ||| |||| |||||||||||||||||||||||||
Sbjct                 1538697  CGGCGCGAACATCAAAGGCCAAGTGCTGCTGACCGGCTTTCAGCACGATGCGGTGGAAAA  1538756
CDS:AAA ATPase [Pseu  495       G  A  N  I  K  G  Q  V  L  L  T  G  F  Q  H  D  A  V  E  N

CDS: Putative 6       516       M  I  E  R  L  S  L  N  S  L  P  V  P  K  F  G  K  R  S  G
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Query                  9475     CATGATCGAGCGGCTCTCGCTCAATAGCCTGCCCGTGCCGAAATTCGGCAAACGGTCTGG  9534
                                ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct                  1538757  CATGATCGAGCGGCTCTCGCTCAACAGCCTGCCCGTGCCGAAATTCGGCAAACGGTCTGG  1538816
CDS:AAA ATPase [Pseu   515        M  I  E  R  L  S  L  N  S  L  P  V  P  K  F  G  K  R  S  G

CDS: Putative 6        536        A  T  E  D  D  L  S  T  F  E  R  N  L  E  D  W  C  S  K  L
Query                  9535     CGCGACGGAAGACGATCTCAGCACCTTCGAGCGCAATCTTGAGGATTGGTGTTCAAAGTT  9594
                                ||||||||||||||||||||||||||||||||||||||||| |  |||||      | |
Sbjct                  1538817  CGCGACGGAAGACGATCTCAGCACCTTCGAGCGCAATCTTGAAGCCTGGTGCAGCTCGCT  1538876
CDS:AAA ATPase [Pseu   535        A  T  E  D  D  L  S  T  F  E  R  N  L  E  A  W  C  S  S  L

CDS: Putative 6        556        A  A  E  L  R  E  R  N  P  Q  I  A  E  V  E  Q  E  R  E  I
Query                  9595     GGCCGCCGAACTACGTGAACGAAACCCACAGATTGCCGAAGTTGAGCAGGAACGGGAAAT  9654
                                 ||| ||||||| || || || || || |||||||| ||||  |||||||| ||||||||
Sbjct                  1538877  TGCCACCGAACTGCGCGAGCGCAATCCCCAGATTGCGGAAGCCGAGCAGGAGCGGGAAAT  1538936
CDS:AAA ATPase [Pseu   555        A  T  E  L  R  E  R  N  P  Q  I  A  E  A  E  Q  E  R  E  I

CDS: Putative 6        576        K  N  L  C  L  Q  Y  V  Q  A  P  S  R  V  L  A  A  S  L  A
Query                  9655     AAAAAACCTGTGCCTGCAATATGTCCAAGCCCCGTCACGCGTGCTGGCCGCCAGCCTTGC  9714
                                ||||||||||||||||||||||||||||||||||||||||| ||| ||||||| ||||||
Sbjct                  1538937  AAAAAACCTGTGCCTGCAATATGTCCAAGCCCCGTCACGCGCGCTCGCCGCCAACCTTGC  1538996
CDS:AAA ATPase [Pseu   575        K  N  L  C  L  Q  Y  V  Q  A  P  S  R  A  L  A  A  N  L  A

CDS: Putative 6        596        R  K  I  A  A  L  G  S  V  I  L  G  E  D  G  A  R  R  S  T
Query                  9715     TAGGAAAATCGCAGCGCTCGGCAGTGTAATTCTTGGCGAAGACGGCGCTCGACGGTCGAC  9774
                                | |||||||| ||||||||||||||||||||||||||||||||||||||| |||||| |
Sbjct                  1538997  TGGGAAAATCACAGCGCTCGGCAGTGTAATTCTTGGCGAAGACGGCGCTCGGCGGTCGGC  1539056
CDS:AAA ATPase [Pseu   595        G  K  I  T  A  L  G  S  V  I  L  G  E  D  G  A  R  R  S  A

CDS: Putative 6        616        N  L  A  K  K  L  A  H  E  E  N  L  N  D  G  S  T  Q  W  L
Query                  9775     GAATTTGGCGAAAAAGCTCGCGCACGAGGAAAACCTCAACGATGGCTCCACCCAATGGCT  9834
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1539057  GAATTTGGCGAAAAAGCTCGCGCACGAGGAAAACCTCAACGATGGCTCCACCCAATGGCT  1539116
CDS:AAA ATPase [Pseu   615        N  L  A  K  K  L  A  H  E  E  N  L  N  D  G  S  T  Q  W  L

CDS: Putative 6        636        D  A  A  R  R  L  R  V  R  H  E  S  F  S  D  D  G  P  E  R
Query                  9835     TGATGCAGCGCGCCGTCTGCGCGTTCGCCATGAAAGCTTTTCTGACGACGGGCCAGAAAG  9894
                                ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct                  1539117  TGATGCAGCGCGCCGTCTGCGTGTTCGCCATGAAAGCTTTTCTGACGACGGGCCAGAAAG  1539176
CDS:AAA ATPase [Pseu   635        D  A  A  R  R  L  R  V  R  H  E  S  F  S  D  D  G  P  E  R

CDS: Putative 6        656        A  M  D  A  L  D  D  L  R  D  V  L  E  E  D  E  R  K  L  L
Query                  9895     GGCGATGGACGCACTGGATGACCTGCGTGATGTGCTTGAAGAAGACGAACGCAAACTGCT  9954
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1539177  GGCGATGGACGCACTGGATGACCTGCGTGATGTGCTTGAAGAAGACGAACGCAAACTGCT  1539236
CDS:AAA ATPase [Pseu   655        A  M  D  A  L  D  D  L  R  D  V  L  E  E  D  E  R  K  L  L

CDS: Putative 6        676        D  K  A  S  L  W  R  N  E  D  G  P  A  P  F  L  D  N  L  V
Query                  9955     GGACAAAGCCAGTCTGTGGCGCAATGAAGATGGCCCAGCGCCATTTTTGGACAACCTGGT  10014
                                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct                 1539237  GGACAAAGCCAGTCTGTGGCGCAATGAAGATGGCCCAGCGCCATTTTTGGACAACCTGGT  1539296
CDS:AAA ATPase [Pseu  675        D  K  A  S  L  W  R  N  E  D  G  P  A  P  F  L  D  N  L  V

CDS: Putative 6       696        A  L  K  K  R  L  L  A  R  F  T  A  P  P  I  L  R  V  E  K
Query                 10015    CGCGTTGAAAAAGAGGCTCCTCGCCCGGTTCACCGCTCCACCGATTCTTCGCGTGGAAAA  10074
                               ||||||||||||||||||| |||||||||||||||||||||||||| |||||||||||||
Sbjct                 1539297  CGCGTTGAAAAAGAGGCTCTTCGCCCGGTTCACCGCTCCACCGATTTTTCGCGTGGAAAA  1539356
CDS:AAA ATPase [Pseu  695        A  L  K  K  R  L  F  A  R  F  T  A  P  P  I  F  R  V  E  K

CDS: Putative 6       716        Q  N  D  A  V  L  A  L  A  E  F  A  I  Q  R  I  K  N  A  E
Query                 10075    GCAGAACGACGCAGTGCTTGCATTGGCAGAATTCGCCATACAACGCATCAAAAACGCCGA  10134
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1539357  GCAGAACGACGCAGTGCTTGCATTGGCAGAATTCGCCATACAACGCATCAAAAACGCCGA  1539416
CDS:AAA ATPase [Pseu  715        Q  N  D  A  V  L  A  L  A  E  F  A  I  Q  R  I  K  N  A  E

CDS: Putative 6       736        Y  S  A  K  D  K  K  S  A  A  L  A  E  F  L  A  E  L  E  G
Query                 10135    GTATTCGGCTAAGGATAAAAAATCTGCTGCGCTGGCCGAGTTTCTAGCCGAACTGGAAGG  10194
                               |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct                 1539417  GTATTCGGCTAAGGATAAAAAATCTGCTGCGCTGGCCGAGTTTCTGGCCGAACTGGAAGG  1539476
CDS:AAA ATPase [Pseu  735        Y  S  A  K  D  K  K  S  A  A  L  A  E  F  L  A  E  L  E  G

CDS: Putative 6       756        N  P  Y  G  M  V  D  A  L  S  E  Y  S  F  A  F  A  A  T  S
Query                 10195    CAACCCCTATGGCATGGTAGATGCCCTGTCCGAATACAGTTTTGCCTTTGCCGCCACCAG  10254
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1539477  CAACCCCTATGGCATGGTAGATGCCCTGTCCGAATACAGTTTTGCCTTTGCCGCCACCAG  1539536
CDS:AAA ATPase [Pseu  755        N  P  Y  G  M  V  D  A  L  S  E  Y  S  F  A  F  A  A  T  S

CDS: Putative 6       776        Q  Q  S  V  N  R  A  M  Q  K  R  K  G  L  V  G  R  D  V  N
Query                 10255    CCAGCAGAGCGTCAATCGTGCAATGCAAAAACGCAAAGGGCTTGTCGGGCGCGATGTCAA  10314
                               ||| |||||||||||||||  |||||||| ||||||||||||||||||||||| |||||
Sbjct                 1539537  CCAACAGAGCGTCAATCGTGATATGCAAAAGCGCAAAGGGCTTGTCGGGCGCGACGTCAA  1539596
CDS:AAA ATPase [Pseu  775        Q  Q  S  V  N  R  D  M  Q  K  R  K  G  L  V  G  R  D  V  N

CDS: Putative 6       796        Q  N  Q  K  G  M  E  Y  E  Y  V  I  V  D  E  A  A  R  V  S
Query                 10315    TCAAAACCAGAAAGGCATGGAATACGAATATGTCATCGTGGACGAAGCCGCCCGTGTCTC  10374
                               | |||||||||||||||||||||||||||||||||||||||||| |||||||| || || ||
Sbjct                 1539597  TGAAAACCAGAAAGGCATGGAATACGAATATGTCATCGTGGATGAAGCCGCTCGCGTTTC  1539656
CDS:AAA ATPase [Pseu  795        E  N  Q  K  G  M  E  Y  E  Y  V  I  V  D  E  A  A  R  V  S

CDS: Putative 6       816        P  R  D  L  M  V  A  M  A  Q  G  K  R  I  I  L  V  G  D  H
Query                 10375    GCCTCGTGATTTGATGGTGGCTATGGCGCAAGGCAAGCGCATTATTCTGGTCGGCGACCA  10434
                                || || ||  |||||||  | |||||||||||||||||||| |||||||| ||||||||
Sbjct                 1539657  ACCCCGCGACCTGATGGTTCCGATGGCGCAAGGCAAGCGCATCATTCTGGTGGGCGACCA  1539716
CDS:AAA ATPase [Pseu  815        P  R  D  L  M  V  P  M  A  Q  G  K  R  I  I  L  V  G  D  H

CDS: Putative 6       836        R  Q  L  P  H  I  I  D  E  E  V  A  R  Q  M  E  E  G
Query                 10435    TCGACAATTGCCGCACATCATTGACGAAGAGGTGGCTCGCCAGATGGAGGAAGGCGA  10491
                               ||| || |||||||| |||||||| || ||||| || ||||| |||||||  |||||
Sbjct                 1539717  TCGGCAGTTGCCGCATATCATTGATGAGGAGGTAGCACGCCAAATGGAGGCTGGCGA  1539773
CDS:AAA ATPase [Pseu  835        R  Q  L  P  H  I  I  D  E  E  V  A  R  Q  M  E  A  G  E
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 Features in this part of subject sequence:
   AAA ATPase
   hypothetical protein

 Score = 1.138e+04 bits (6161),  Expect = 0.0
 Identities = 6630/6859 (97%), Gaps = 22/6859 (0%)
 Strand=Plus/Plus

CDS: Putative 1       1          T  L  D  K  Q  Y  R  M  H  P  L  L  G  S  F  I  S  R  N
Query                 10623    TCACGCTGGACAAGCAATACCGCATGCATCCGCTGCTGGGCAGCTTTATCAGTAGAAATT  10682
                               ||||||| |||||||| || || ||||| || ||||| |||||||||||||  | ||||
Sbjct                 1539896  TCACGCTCGACAAGCAGTATCGGATGCACCCACTGCTCGGCAGCTTTATCAGCCGCAATT  1539955
CDS:AAA ATPase [Pseu  894      V  T  L  D  K  Q  Y  R  M  H  P  L  L  G  S  F  I  S  R  N

CDS: Putative 1       20       F  Y  E  R  F  D  P  E  E  Q  F  G  S  G  R  P  A  S  D  F
Query                 10683    TCTATGAACGCTTCGACCCGGAGGAGCAATTTGGCTCCGGGCGACCAGCAAGCGATTTCG  10742
                               | ||||||||||||||| |||  ||| ||||| ||||| || || || | |||||||||||
Sbjct                 1539956  TTTATGAACGCTTCGATCCGACGGAACAATTCGGCTCTGGACGGCCTGAAAGCGATTTCG  1540015
CDS:AAA ATPase [Pseu  914      F  Y  E  R  F  D  P  T  E  Q  F  G  S  G  R  P  E  S  D  F

CDS: Putative 1       40       A  H  D  L  P  G  T  N  G  K  S  A  V  W  M  D  V  P  A   Q
Query                 10743    CCCATGATCTGCCAGGCACGAACGGCAAGTCTGCCGTTTGGATGGATGTACCAGC-ACAA  10801
                               ||||  | ||||| ||||  ||||| ||  |||| || ||| |||| || |||||  | |
Sbjct                 1540016  CCCACAACCTGCCCGGCATAAACGGTAAACCTGCTGTGTGGCTGGACGTGCCAGCGGCGA  1540075
CDS:AAA ATPase [Pseu  934      A  H  N  L  P  G  I  N  G  K  P  A  V  W  L  D  V  P  A  A

CDS: Putative 1       60        R  G  K  H  Q  K  D   G  T  S  W  T  R  P  A  E  V  T  V  I
Query                 10802    AGAGGAAAACATCAAAAGGA-CGGAACCAGTTGGACGCGCCCCGCAGAAGTCACTGTCAT  10860
                               | ||| | ||| | |  | | |||||||||||||||||||||| ||||| | ||| || ||
Sbjct                 1540076  A-AGGCAGACA-CCAGCGCAGCGGAACCAGTTGGACGCGCCCGGCAGAGGCCACCGTTAT  1540133
CDS:AAA ATPase [Pseu  954      K   G  R  H   Q  R  S  G  T  S  W  T  R  P  A  E  A  T  V  I

CDS: Putative 1       80         A  R  Q  L  Q  A  W  M  S  S  D  A  G  K  D  L  S  F  G  V
Query                 10861    CGCTCGCCAGTTACAGGCGTGGATGAGTTCGGATGCAGGGAAAGATCTCTCCTTCGGTGT  10920
                                || ||||| || |||||||||||||||||| |||||||| ||||| ||||| ||||| ||
Sbjct                 1540134  TGCCCGCCAATTGCAGGCGTGGATGAGTTCAGATGCAGGCAAAGACCTCTCGTTCGGCGT  1540193
CDS:AAA ATPase [Pseu  974        A  R  Q  L  Q  A  W  M  S  S  D  A  G  K  D  L  S  F  G  V

CDS: Putative 1       100        I  S  F  Y  K  A  Q  A  D  S  I  R  E  Q  L  K  R  K  F  G
Query                 10921    TATTTCATTTTATAAGGCGCAGGCCGACAGCATCAGGGAACAACTCAAAAGGAAATTCGG  10980
                                |||||| || || |||||||||||||||   ||||| |  |||||||   | |  | || |
Sbjct                 1540194  GATTTCGTTCTACAAGGCGCAGGCCGAACTCATCAAGAGACAACTCGGCA-G-CA-TC-G  1540249
CDS:AAA ATPase [Pseu  994        I  S  F  Y  K  A  Q  A  E  L  I  K  R  Q  L  G   S    I

CDS: Putative 1       120        G  I  V  N  D  D  K  Q  L  R  V  G  T  V  D  S  F  Q  G  M
Query                 10981    CGGGATCGTGAACGATGACAAGCAACTGCGTGTTGGAACGGTGGACTCTTTCCAAGGCAT  11040
                               | ||| |  | |||| || ||  |||| || || || ||||||||||| ||||| |||||
Sbjct                 1540250  C-GGA-C--G-ACGA-GAGAA--AACTCCGCGTCGGCACGGTGGACTCATTCCAGGGCAT  1540301
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CDS:AAA ATPase [Pseu  1012     A   D      D  E   R    K  L  R  V  G  T  V  D  S  F  Q  G  M

CDS: Putative 1       140        E  F  D  V  V  F  L  S  M  V  R  T  L  P  Q  N  W  Q  P  K
Query                 11041    GGAATTCGATGTCGTCTTCCTCTCAATGGTGCGAACCTTGCCGCAAAACTGGCAGCCAAA  11100
                               ||| ||||||||||||||||||||||||||||||||||||||||||| |||||| |  | ||
Sbjct                 1540302  GGAGTTCGATGTCGTCTTCCTCTCAATGGTGCGAACCTTGCCGCATAACTGGAAATCCAA  1540361
CDS:AAA ATPase [Pseu  1030       E  F  D  V  V  F  L  S  M  V  R  T  L  P  H  N  W  K  S  K

CDS: Putative 1       160        D  D  D  R  D  K  Q  A  R  A  L  F  G  H  L  C  L  Y  N  R
Query                 11101    GGATGATGACCGCGACAAACAAGCTAGAGCGCTGTTTGGCCATCTCTGTCTTTACAACCG  11160
                               |   |||||||| || || || || | || | |||| || || || || ||||||||||
Sbjct                 1540362  GAGCGATGACCGTGAAAAGCAGGCCACAGGGTTGTTCGGACACCTTTGCCTTTACAACCG  1540421
CDS:AAA ATPase [Pseu  1050       S  D  D  R  E  K  Q  A  T  G  L  F  G  H  L  C  L  Y  N  R

CDS: Putative 1       180        L  N  V  A  M  S  R  Q  K  K  L  L  V  V  V  G  D  T  G  L
Query                 11161    TCTGAATGTCGCCATGAGCCGTCAGAAGAAGCTGCTGGTGGTCGTTGGAGATACGGGGTT  11220
                                ||||||||| | ||||| |||||||||||||| |||||||||||||| |||||||| ||
Sbjct                 1540422  CCTGAATGTCTCGATGAGTCGTCAGAAGAAGCTACTGGTGGTCGTTGGCGATACGGGTTT  1540481
CDS:AAA ATPase [Pseu  1070       L  N  V  S  M  S  R  Q  K  K  L  L  V  V  V  G  D  T  G  L

CDS: Putative 1       200        L  Q  S  E  L  A  K  E  F  V  P  G  L  V  D  F  L  Q   I
CDS: Putative 2       1                                                                  M
Query                 11221    GCTACAAAGTGAACTCGCGAAGGAGTTCGTGCCTGGACTGGTGGATTTCCTTCAGA-TAT  11279
                               ||| |||||||||||||||  ||| || ||||| |||||||||||||||||| || |||
Sbjct                 1540482  GCTGCAAAGTGAACTCGCGGCGGACTTTGTGCCGGGACTGGTGGATTTCCTTC-GACTAT  1540540
CDS:AAA ATPase [Pseu  1090       L  Q  S  E  L  A  A  D  F  V  P  G  L  V  D  F  L   R  L
CDS:hypothetical pro  1                                                                  M

CDS: Putative 1       219      C  R  E  Q  G  V  M  L  P  C  *
CDS: Putative 2       2          P  R  A  R  G  D  A  A  M  L  R  L  L  D  Y  G  K  P  A  P
Query                 11280    GCCGCGAGCAAGGGGTGATGCTGCCATGTTGAGGCTCCTTGATTACGGCAAACCTGCCCC  11339
                               |||||||||||| ||| |||||||||| ||| ||||||||||||||| ||||||||||||
Sbjct                 1540541  GCCGCGAGCAAGGAGTGGTGCTGCCATGCTGAAGCTCCTTGATTACGGTAAACCTGCCCC  1540600
CDS:AAA ATPase [Pseu  1109     C  R  E  Q  G  V  V  L  P  C
CDS:hypothetical pro  2          P  R  A  R  S  G  A  A  M  L  K  L  L  D  Y  G  K  P  A  P

CDS: Putative 2       22         F  G  E  T  I  G  R  P  R  H  L  A  W  P  L  N  A  Y  R  V
Query                 11340    CTTCGGTGAGACCATCGGTAGGCCGCGCCACCTTGCGTGGCCGCTGAACGCATACCGCGT  11399
                               |||||| | || |||||| ||||| |||||||| ||||||||| |||||| |||||||||
Sbjct                 1540601  CTTCGGAGGGATCATCGGCAGGCCTCGCCACCTCGCGTGGCCGGTGAACGTATACCGCGT  1540660
CDS:hypothetical pro  22         F  G  G  I  I  G  R  P  R  H  L  A  W  P  V  N  V  Y  R  V

CDS: Putative 2       42         T  L  P  R  V  L  D  D  G  N  G  L  N  A  F  E  R  V  I  L
Query                 11400    GACCTTGCCCAGAGTTCTTGACGATGGCAATGGCTTGAACGCATTTGAGCGTGTCATCCT  11459
                               ||||||||||||||||||||||||||||| ||||||||||||||||||| || ||||||||
Sbjct                 1540661  GACCTTGCCCAGAGTTCTTGACGATGGCGATGGCTTGAACGCATTTGAACGCGTCATCCT  1540720
CDS:hypothetical pro  42         T  L  P  R  V  L  D  D  G  D  G  L  N  A  F  E  R  V  I  L

CDS: Putative 2       62         K  L  L  D  A  A  G  R   M  D  A  D  A  L  A  A  E  T  R
Query                 11460    GAAACTACTCGACGCTGCCGGTCGT-ATGGATGCCGATGCGCTGGCGGCTGAAACCCGCA  11518
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                                 |||||| || ||  ||| ||| | | ||| | ||||||||||||||||| ||||||||||
Sbjct                  1540721   GAAACTGCTTGAAACTGTCGG-CTTGATGAACGCCGATGCGCTGGCGGATGAAACCCGCA  1540779
CDS:hypothetical pro   62          K  L  L  E  T  V  G   L  M  N  A  D  A  L  A  D  E  T  R

CDS: Putative 2        81        I  P  L  D  L  V  K  S  V  L  L  R  L  Q  D  K  D  L  I  D
Query                  11519     TCCCACTCGATTTGGTCAAGAGCGTTCTGCTTCGTTTGCAAGACAAGGACTTGATTGACG  11578
                                 | ||| ||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct                  1540780   TTCCAGTCGATTTGGTCAAGAGCGTTCTGCTCCGTTTGCAAGACAAGGACTTGATTGACG  1540839
CDS:hypothetical pro   81        I  P  V  D  L  V  K  S  V  L  L  R  L  Q  D  K  D  L  I  D

CDS: Putative 2        101       E  H  N  A  V  I  E  R  E  R  E  D  E  R  A  P  V  F  V  T
Query                  11579     AACACAATGCCGTCATTGAGCGGGAGCGTGAAGATGAGCGCGCGCCGGTGTTTGTCACTG  11638
                                 | ||| ||||| ||||||||||||||||| ||||| ||  | || ||||  || || || |
Sbjct                  1540840   ACCACCATGCCATCATTGAGCGGGAGCGCGAAGAAGAATGTGCCCCGGCATTCGTTACCG  1540899
CDS:hypothetical pro   101       D  H  H  A  I  I  E  R  E  R  E  E  E  C  A  P  A  F  V  T

CDS: Putative 2        121       A  L  V  F  R  E  L  A  T  G  R  I  L  P  F  L  H  R  L  D
Query                  11639     CGCTGGTCTTTCGCGAACTCGCCACCGGGAGAATTCTGCCTTTTCTGCATCGGCTGGACG  11698
                                 ||||  | || ||||||||||||||| || | ||||||||| || |||||| |||||||||
Sbjct                  1540900   CGCTTTTGTTCCGCGAACTCGCCACTGGAAAAATTCTGCCCTTCCTGCATTGGCTGGACG  1540959
CDS:hypothetical pro   121       A  L  L  F  R  E  L  A  T  G  K  I  L  P  F  L  H  W  L  D

CDS: Putative 2        141       D  T  N  P  M  R  K  K  E  C  E  D  K  D  F  R  V  I  R  W
Query                  11699     ACACAAACCCCATGCGGAAAAAGGAATGCGAGGACAAAGACTTCCGGGTAATCCGCTGGG  11758
                                 ||| |||||||||||||||||||||  |||||||||||||||||||| ||||||||||||
Sbjct                  1540960   ACAGAAACCCCATGCGGAAAAAGGAAAACGAGGACAAAGACTTCCGGATAATCCGCTGGG  1541019
CDS:hypothetical pro   141       D  R  N  P  M  R  K  K  E  N  E  D  K  D  F  R  I  I  R  W

CDS: Putative 2        161       D  G  D  R  R  K  A  I  P  A  P  R  D  V  I  R  T  L  R  A
Query                  11759     ATGGTGACCGCAGAAAAGCGATACCAGCGCCGCGTGATGTAATCAGAACTTTGCGCGCCA  11818
                                 |||||| ||  |||||||||||||| |||||||||||||||||||||||||||||||||| |
Sbjct                  1541020   ATGGTGTCCAAAGAAAAGCGATACCCGCGCCGCGTGATGTAATCAGAACTTTGCGCGCAA  1541079
CDS:hypothetical pro   161       D  G  V  Q  R  K  A  I  P  A  P  R  D  V  I  R  T  L  R  A

CDS: Putative 2        181       M  K  K  R  S  S  A  F  G  Q  D  S  K  M  P  A  V  Q  Q  I
Query                  11819     TGAAAAAGCGTTCGTCTGCGTTCGGCCAGGACAGCAAGATGCCCGCAGTCCAACAGATCA  11878
                                 |||||||||| ||||||||||||||| |||||| ||||||||||| |||||| |||||||
Sbjct                  1541080   TGAAAAAGCGCTCGTCTGCGTTCGGCAAGGACACCAAGATGCCCGTAGTCCAGCAGATCA  1541139
CDS:hypothetical pro   181       M  K  K  R  S  S  A  F  G  K  D  T  K  M  P  V  V  Q  Q  I

CDS: Putative 2        201       T  I  V  A  E  P  E  L  L  H  L  D  C  P  I  A  I  Q  K  S
Query                  11879     CGATAGTCGCCGAGCCCGAGCTGCTTCACCTTGACTGCCCTATCGCCATCCAGAAAAGCG  11938
                                 |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct                  1541140   CGATAGTCGCCGAGCCCGACCTGCTTCACCTTGACTGCCCTATCGCCATCCAGAAAAGCG  1541199
CDS:hypothetical pro   201       T  I  V  A  E  P  D  L  L  H  L  D  C  P  I  A  I  Q  K  S

CDS: Putative 2        221       D  G  E  F  R  I  A  D  P  F  G  N  G  F  S  L  I  L  E  N
Query                  11939     ATGGCGAGTTCCGTATAGCTGACCCGTTCGGCAACGGTTTCTCCTTGATTCTCGAAAATG  11998
                                 ||||||| ||||| || || ||||| |||||||||||||| |||||||||||||||||
Sbjct                  1541200   ATGGCGAATTCCGCATCGCCGACCCATTCGGCAACGGTTTTTCCTTGATTCTCGAAAAAT  1541259
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CDS:hypothetical pro  221      D  G  E  F  R  I  A  D  P  F  G  N  G  F  S  L  I  L  E  K

CDS: Putative 2       241      A  F  E  K  L   L  E  Q  D  E  S  L  S  K  W  L  H  G  W  K
Query                 11999    CGTTCGAGAAACTT-TTGGAGCAGGATGAAAGCCTCAGCAAGTGGCTGCATGGTTGGAAA  12057
                               ||||||| | | ||  | |||||||| |||||||| | || |||||||||||||||||
Sbjct                 1541260  CGTTCGA-ACAGTTGCTTGAGCAGGAGGAAAGCCTGACCACGTGGCTGCATGGTTGGAAG  1541318
CDS:hypothetical pro  241      S  F  E   Q  L  L  E  Q  E  E  S  L  T  T  W  L  H  G  W  K

CDS: Putative 2       261       Q  S  L  S  T  P  R  P  E  K  Q  D  A  T  P  K  E  P  F  D
Query                 12058    CAGTCATTAAGCACTCCTCGTCCAGAAAAGCAGGATGCCACGCCAAAAGAGCCGTTCGAC  12117
                               |||||||| |||||||||||||||||||||||||||||||   |||||||||||||||
Sbjct                 1541319  CAGTCATTGAGCACTCCTCGTCCAGAAAAGCAGGATGCCACGGTCAAAGAGCCGTTCGAC  1541378
CDS:hypothetical pro  261       Q  S  L  S  T  P  R  P  E  K  Q  D  A  T  V  K  E  P  F  D

CDS: Putative 2       281       N  D  A  N  R  Q  R  Y  P  K  L  V  A  N  L  R  P  L  R  N
Query                 12118    AACGATGCCAACCGGCAACGCTACCCGAAGCTCGTCGCCAATTTGCGCCCCTTGCGGAAT  12177
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1541379  AACGATGCCAACCGGCAACGCTACCCGAAGCTCGTCGCCAATTTGCGCCCCTTGCGGAAT  1541438
CDS:hypothetical pro  281       N  D  A  N  R  Q  R  Y  P  K  L  V  A  N  L  R  P  L  R  N

CDS: Putative 2       301       S  P  F  R  S  I  A  Q  I  H  A  A  I  E  W  A  L  F  Y  T
Query                 12178    AGCCCGTTCCGCTCCATCGCCCAAATCCATGCCGCAATCGAATGGGCGCTGTTCTATACC  12237
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1541439  AGCCCGTTCCGCTCCATCGCCCAAATCCATGCCGCAATCGAATGGGCGCTGTTCTATACC  1541498
CDS:hypothetical pro  301       S  P  F  R  S  I  A  Q  I  H  A  A  I  E  W  A  L  F  Y  T

CDS: Putative 2       321       C  C  R  R  P  V  D  S  V  I  A  R  L  K  F  T  T  Q  D  Q
Query                 12238    TGCTGCCGCAGACCGGTTGATTCCGTTATTGCAAGGCTGAAATTCACTACGCAAGACCAA  12297
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1541499  TGCTGCCGCAGACCGGTTGATTCCGTTATTGCAAGGCTGAAATTCACTACGCAAGACCAA  1541558
CDS:hypothetical pro  321       C  C  R  R  P  V  D  S  V  I  A  R  L  K  F  T  T  Q  D  Q

CDS: Putative 2       341       H  A  A  L  L  E  Q  A  A  K  A  L  G  L  E  Q  P  P  I  G
Query                 12298    CACGCAGCCCTGCTTGAGCAGGCCGCGAAAGCCCTCGGTCTTGAGCAGCCGCCGATTGGC  12357
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1541559  CACGCAGCCCTGCTTGAGCAGGCCGCGAAAGCCCTCGGTCTTGAGCAGCCGCCGATTGGC  1541618
CDS:hypothetical pro  341       H  A  A  L  L  E  Q  A  A  K  A  L  G  L  E  Q  P  P  I  G

CDS: Putative 2       361       F  R  P  I  R  E  G  K  L  R  E  F  E  D  G  G  A  F  Q  E
Query                 12358    TTCAGGCCGATTCGGGAAGGTAAGCTGCGGGAATTTGAGGACGGCGGCGCGTTCCAAGAG  12417
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1541619  TTCAGGCCGATTCGGGAAGGTAAGCTGCGGGAATTTGAGGACGGCGGCGCGTTCCAAGAG  1541678
CDS:hypothetical pro  361       F  R  P  I  R  E  G  K  L  R  E  F  E  D  G  G  A  F  Q  E

CDS: Putative 2       381       T  V  L  A  I  A  L  L  Q  A  Q  D  D  A  L  H  P  L  R  R
Query                 12418    ACGGTTCTTGCCATAGCTTTGCTTCAAGCGCAAGACGACGCTTTGCATCCCTTGCGCCGT  12477
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Sbjct                 1541679  ACGGTTCTTGCCATAGCTTTGCTTCAAGCGCAAGACGACGCTTTGCATCCCTTGCGCCGT  1541738
CDS:hypothetical pro  381       T  V  L  A  I  A  L  L  Q  A  Q  D  D  A  L  H  P  L  R  R
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CDS: Putative 2       401       V  A  A  A  Y  S  D  L  I  T  R  L  F  A  I  N  A  K  R  N
Query                 12478    GTTGCGGCCGCGTATTCAGACCTCATCACTCGCCTGTTCGCTATCAACGCCAAACGCAAC  12537
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Sbjct                 1541739  GTTGCGGCCGCGTATTCAGACCTCATCACTCGCCTGTTCGCTATCAACGCCAAACGCAAC  1541798
CDS:hypothetical pro  401       V  A  A  A  Y  S  D  L  I  T  R  L  F  A  I  N  A  K  R  N

CDS: Putative 2       421       E  K  G  H  G  K  G  G  A  D  A  P  Q  Q  A  L  T  D  D  S
Query                 12538    GAGAAGGGCCACGGCAAGGGCGGCGCAGACGCACCGCAGCAGGCACTAACTGACGATTCG  12597
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1541799  GAGAAGGGCCACGGCAAGGGCGGCGCAGACGCACCGCAGCAGGCACTAACTGACGATTCG  1541858
CDS:hypothetical pro  421       E  K  G  H  G  K  G  G  A  D  A  P  Q  Q  A  L  T  D  D  S

CDS: Putative 2       441       F  M  R  E  V  V  H  A  L  V  P  G  I  V  F  T  D  T  P  P
Query                 12598    TTCATGCGCGAAGTCGTTCATGCGCTTGTGCCAGGCATCGTGTTTACCGACACGCCTCCT  12657
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1541859  TTCATGCGCGAAGTCGTTCATGCGCTTGTGCCAGGCATCGTGTTTACCGACACGCCTCCT  1541918
CDS:hypothetical pro  441       F  M  R  E  V  V  H  A  L  V  P  G  I  V  F  T  D  T  P  P

CDS: Putative 2       461       T  A  P  D  K  D  E  Q  G  D  A  L  L  D  A  R  T  S  I  Q
Query                 12658    ACCGCGCCAGACAAGGACGAGCAGGGTGATGCACTGCTGGATGCCCGCACTAGCATTCAG  12717
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1541919  ACCGCGCCAGACAAGGACGAGCAGGGTGATGCACTGCTGGATGCCCGCACTAGCATTCAG  1541978
CDS:hypothetical pro  461       T  A  P  D  K  D  E  Q  G  D  A  L  L  D  A  R  T  S  I  Q

CDS: Putative 2       481       E  E  F  G  H  Q  L  F  N  R  L  G  A  N  L  Q  D  R  L  V
Query                 12718    GAGGAGTTCGGCCACCAGTTGTTCAACCGCCTGGGCGCAAACTTGCAAGACCGGCTGGTT  12777
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1541979  GAGGAGTTCGGCCACCAGTTGTTCAACCGCCTGGGCGCAAACTTGCAAGACCGGCTGGTT  1542038
CDS:hypothetical pro  481       E  E  F  G  H  Q  L  F  N  R  L  G  A  N  L  Q  D  R  L  V

CDS: Putative 2       501       H  A  E  R  F  F  Q  S  C  H  D  G  D  D  A  L  A  Y  V  R
Query                 12778    CACGCGGAACGTTTTTTCCAGTCTTGCCATGACGGGGATGACGCTTTGGCCTATGTCCGC  12837
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Sbjct                 1542039  CACGCGGAACGTTTTTTCCAGTCTTGCCATGACGGGGATGACGCTTTGGCCTATGTCCGC  1542098
CDS:hypothetical pro  501       H  A  E  R  F  F  Q  S  C  H  D  G  D  D  A  L  A  Y  V  R

CDS: Putative 2       521       D  L  Y  A  A  I  Q  S  S  F  E  R  A  L  T  G  R  L  P  S
Query                 12838    GACCTTTATGCCGCAATCCAGTCATCATTTGAGAGAGCTTTGACAGGCAGGCTGCCGTCC  12897
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1542099  GACCTTTATGCCGCAATCCAGTCATCATTTGAGAGAGCTTTGACAGGCAGGCTGCCGTCC  1542158
CDS:hypothetical pro  521       D  L  Y  A  A  I  Q  S  S  F  E  R  A  L  T  G  R  L  P  S

CDS: Putative 2       541       D  T  S  D  A  Q  L  K  D  T  A  E  R  K  A  V  E  A  G  F
Query                 12898    GATACCAGTGACGCGCAGCTCAAAGACACGGCTGAACGCAAGGCTGTTGAGGCTGGTTTC  12957
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Sbjct                 1542159  GATACCAGTGACGCGCAGCTCAAAGACACGGCTGAACGCAAGGCTGTTGAGGCTGGTTTC  1542218
CDS:hypothetical pro  541       D  T  S  D  A  Q  L  K  D  T  A  E  R  K  A  V  E  A  G  F

CDS: Putative 2       561       C  E  G  L  S  E  S  L  R  T  V  K  T  S  A  V  R  Q  A  L
Query                 12958    TGCGAAGGCTTGTCGGAGAGCCTGCGAACCGTCAAAACATCCGCTGTGCGCCAGGCATTG  13017
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CDS:hypothetical pro     561       C  E  G  L  S  E  S  L  R  T  V  K  T  S  A  V  R  Q  A  L

CDS: Putative 2          581       Q  G  G  S  Q  T  L  G  A  C  V  L  A  W  L  L  V  S  D  A
Query                    13018    CAAGGCGGCAGCCAAACGCTCGGGGCTTGCGTTCTTGCATGGCTGCTGGTGAGCGATGCT  13077
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Sbjct                    1542279  CAAGGCGGCAGCCAAACGCTCGGGGCTTGCGTTCTTGCATGGCTGCTGGTGAGCGATGCT  1542338
CDS:hypothetical pro     581       Q  G  G  S  Q  T  L  G  A  C  V  L  A  W  L  L  V  S  D  A

CDS: Putative 2          601       D  E  L  A  A  I  H  D  T  Q  P  S  L  I  G  D  M  A  N  L
Query                    13078    GATGAACTTGCCGCAATTCATGACACGCAGCCGTCCTTGATCGGCGATATGGCAAACCTT  13137
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Sbjct                    1542339  GATGAACTTGCCGCAATTCATGACACGCAGCCGTCCTTGATCGGCGATATGGCAAACCTT  1542398
CDS:hypothetical pro     601       D  E  L  A  A  I  H  D  T  Q  P  S  L  I  G  D  M  A  N  L

CDS: Putative 2          621       I  A  R  R  G  H  G  N  E  P  L  P  L  P  K  E  N  I  A  Q
Query                    13138    ATCGCTCGGCGTGGGCATGGCAACGAGCCGCTGCCATTGCCCAAAGAGAACATCGCACAG  13197
                                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                    1542399  ATCGCTCGGCGTGGGCATGGCAACGAGCCGCTGCCATTGCCCAAAGAGAACATCGCACAG  1542458
CDS:hypothetical pro     621       I  A  R  R  G  H  G  N  E  P  L  P  L  P  K  E  N  I  A  Q

CDS: Putative 2          641       L  R  K  A  A  F  T  T  I  R  T  L  M  E  S  *
CDS: Putative 3          1                                                          M  N  S
Query                    13198    CTTCGCAAAGCTGCTTTCACAACTATCAGAACACTTATGGAATCTTGAAAATGAACAGCC  13257
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Sbjct                    1542459  CTTCGCAAAGCTGCTTTCACAACTATCAGAACACTTATGGAATCTTGAAAATGAACAGCC  1542518
CDS:hypothetical pro     641       L  R  K  A  A  F  T  T  I  R  T  L  M  E  S
CDS:chromosome segre     1                                                          M  N  S

CDS: Putative 3          4        P  V  Q  P  D  T  E  A  Q  R  L  A  D  L  N  A  R  E  S  W
Query                    13258    CCGTCCAACCCGACACCGAAGCCCAGCGGCTTGCCGATTTGAACGCGCGTGAGAGCTGGA  13317
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Sbjct                    1542519  CCGTCCAACCCGACACCGAAGCCCAGCGGCTTGCCGATTTGAACGCGCGTGAGAGCTGGA  1542578
CDS:chromosome segre     4        P  V  Q  P  D  T  E  A  Q  R  L  A  D  L  N  A  R  E  S  W

CDS: Putative 3          24       I  N  T  K  E  S  E  I  A  S  R  E  T  A  V  A  T  R  E  R
Query                    13318    TAAACACCAAGGAAAGCGAAATCGCCAGCCGTGAAACCGCCGTGGCTACACGTGAAAGGG  13377
                                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                    1542579  TAAACACCAAGGAAAGCGAAATCGCCAGCCGTGAAACCGCCGTGGCTACACGTGAAAGGG  1542638
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CDS: Putative 3          44       D  A  T  A  E  R  Q  V  I  E  Q  D  K  A  K  L  A  Q  R  E
Query                    13378    ATGCGACTGCAGAGCGTCAAGTCATCGAGCAAGACAAGGCCAAGCTGGCGCAGCGCGAGC  13437
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CDS:chromosome segre     44       D  A  T  A  E  R  Q  V  I  E  Q  D  K  A  K  L  A  Q  R  E

CDS: Putative 3          64       Q  A  V  T  Q  A  E  Q  K  C  D  A  G  F  A  D  E  R  A  A
Query                    13438    AGGCCGTCACGCAGGCTGAGCAAAAGTGTGATGCAGGTTTTGCCGATGAACGAGCCGCGC  13497
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CDS:chromosome segre   64        Q  A  V  T  Q  A  E  Q  K  C  D  A  G  F  A  D  E  R  A  A

CDS: Putative 3        84        L  N  D  E  L  R  E  K  R  A  Q  G  E  R  A  I  A  E  M  R
Query                  13498     TGAATGATGAGCTGCGTGAAAAGCGCGCCCAGGGCGAAAGAGCAATTGCCGAGATGCGAG  13557
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Sbjct                  1542759   TGAATGATGAGCTGCGTGAAAAGCGCGCCCAGGGCGAAAGAGCAATTGCCGAGATGCGAG  1542818
CDS:chromosome segre   84        L  N  D  E  L  R  E  K  R  A  Q  G  E  R  A  I  A  E  M  R

CDS: Putative 3        104       E  K  N  L  S  A  L  E  V  E  I  S  E  L  K  A  K  R  L  G
Query                  13558     AGAAAAACCTTTCAGCGTTGGAGGTTGAAATTTCCGAGCTGAAAGCAAAGCGACTGGGTG  13617
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Sbjct                  1542819   AGAAAAACCTTTCAGCGTTGGAGGTTGAAATTTCCGAGCTGAAAGCAAAGCGACTGGGTG  1542878
CDS:chromosome segre   104       E  K  N  L  S  A  L  E  V  E  I  S  E  L  K  A  K  R  L  G

CDS: Putative 3        124       A  V  A  H  A  E  N  A  E  R  E  R  I  R  T  E  I  A  Q  E
Query                  13618     CGGTTGCCCATGCCGAAAACGCCGAACGGGAGCGCATTCGGACAGAAATCGCCCAAGAGC  13677
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Sbjct                  1542879   CGGTTGCCCATGCCGAAAACGCCGAACGGGAGCGCATTCGGACAGAAATCGCCCAAGAGC  1542938
CDS:chromosome segre   124       A  V  A  H  A  E  N  A  E  R  E  R  I  R  T  E  I  A  Q  E

CDS: Putative 3        144       R  D  A  W  T  K  Q  Q  G  D  A  R  K  Q  L  N  A  E  R  T
Query                  13678     GCGATGCATGGACAAAACAACAGGGTGACGCTCGAAAGCAGTTGAATGCAGAGCGCACGG  13737
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Sbjct                  1542939   GCGATGCATGGACAAAACAACAGGGTGACGCTCGAAAGCAGTTGAATGCAGAGCGCACGG  1542998
CDS:chromosome segre   144       R  D  A  W  T  K  Q  Q  G  D  A  R  K  Q  L  N  A  E  R  T

CDS: Putative 3        164       E  F  E  K  Q  K  G  A  L  S  A  L  Q  S  E  V  E  G  R  Q
Query                  13738     AATTTGAGAAACAAAAAGGCGCACTCTCCGCCTTGCAAAGCGAAGTCGAAGGAAGACAGG  13797
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Sbjct                  1542999   AATTTGAGAAACAAAAAGGCGCACTCTCCGCCTTGCAAAGCGAAGTCGAAGGAAGACAGG  1543058
CDS:chromosome segre   164       E  F  E  K  Q  K  G  A  L  S  A  L  Q  S  E  V  E  G  R  Q

CDS: Putative 3        184       A  E  L  E  T  S  E  R  T  L  E  R  K  E  Q  R  L  E  Q  Q
Query                  13798     CAGAGCTTGAGACTTCAGAGCGGACACTCGAACGCAAAGAACAACGGCTGGAACAGCAGA  13857
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Sbjct                  1543059   CAGAGCTTGAGACTTCAGAGCGGACACTCGAACGCAAAGAACAACGGCTGGAACAGCAGA  1543118
CDS:chromosome segre   184       A  E  L  E  T  S  E  R  T  L  E  R  K  E  Q  R  L  E  Q  Q

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Query                  13858     ACCAGAGGCGCAGCGAGCAACTGGACGATGAGGTTGAGAGGCGTGTTGAGGATCGCCGAA  13917
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Sbjct                  1543119   ACCAGAGGCGCAGCGAGCAACTGGACGATGAGGTTGAGAGGCGTGTTGAGGATCGCCGAA  1543178
CDS:chromosome segre   204       N  Q  R  R  S  E  Q  L  D  D  E  V  E  R  R  V  E  D  R  R

CDS: Putative 3        224       K  S  L  E  A  A  L  Q  S  A  K  E  E  N  I  R  L  R  E  A
Query                  13918     AATCGCTAGAGGCTGCTCTGCAATCTGCCAAAGAGGAAAACATTCGACTGCGCGAGGCGT  13977
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Sbjct                  1543179   AATCGCTAGAGGCTGCTCTGCAATCTGCCAAAGAGGAAAACATTCGACTGCGCGAGGCGT  1543238
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CDS:chromosome segre  224      K  S  L  E  A  A  L  Q  S  A  K  E  E  N  I  R  L  R  E  A

CDS: Putative 3       244      F  K  T  Q  D  E  L  L  G  A  F  E  Q  L  K  L  Q  L  G  G
Query                 13978    TTAAAACTCAAGACGAACTTCTCGGCGCGTTCGAACAGTTAAAGTTGCAACTTGGTGGCA  14037
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Sbjct                 1543239  TTAAAACTCAAGACGAACTTCTCGGCGCGTTCGAACAGTTAAAGTTGCAACTTGGTGGCA  1543298
CDS:chromosome segre  244      F  K  T  Q  D  E  L  L  G  A  F  E  Q  L  K  L  Q  L  G  G

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Query                 14038    AAGACCCTGCTGAAATTCTGCGTGCGCTGAACAGCCAGGCCGACGAACTCAAACGCCTAC  14097
                               ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct                 1543299  AAGACCCTGCTGAAATTCTGCGTGCGCTGAACAGCCAGGCTGACGAACTCAAACGCCTAC  1543358
CDS:chromosome segre  264      K  D  P  A  E  I  L  R  A  L  N  S  Q  A  D  E  L  K  R  L

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Query                 14098    GAGAGGAGCTTGCTACCCGACCTACTGAGGAAATGCGCGAGCGGTATCAAGCCCTTGAAT  14157
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Sbjct                 1543359  GAGAGGAGCTTGCTACCCGACCTACTGAGGAAATGCGCGAGCGGTATCAAGCCCTTGAAT  1543418
CDS:chromosome segre  284      R  E  E  L  A  T  R  P  T  E  E  M  R  E  R  Y  Q  A  L  E

CDS: Putative 3       304      S  E  A  K  N  Q  K  T  R  A  D  Q  L  E  R  Q  L  S  T  N
Query                 14158    CAGAAGCCAAAAATCAGAAAACACGGGCAGACCAGTTAGAACGGCAACTTTCCACCAATG  14217
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Sbjct                 1543419  CAGAAGCCAAAAATCAGAAAACACGGGCAGACCAGTTAGAACGGCAACTTTCCACCAATG  1543478
CDS:chromosome segre  304      S  E  A  K  N  Q  K  T  R  A  D  Q  L  E  R  Q  L  S  T  N

CDS: Putative 3       324      E  A  A  V  A  E  I  G  E  L  R  R  Q  G  S  E  L  N  A  E
Query                 14218    AGGCTGCGGTCGCTGAAATTGGCGAGCTGCGCCGTCAAGGCTCGGAGCTCAACGCCGAAA  14277
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Sbjct                 1543479  AGGCTGCGGTCGCTGAAATTGGCGAGCTGCGCCGTCAAGGCTCGGAGCTCAACGCCGAAA  1543538
CDS:chromosome segre  324      E  A  A  V  A  E  I  G  E  L  R  R  Q  G  S  E  L  N  A  E

CDS: Putative 3       344      N  K  S  L  A  Q  R  A  S  I  F  E  G  A  A  N  E  A  Q  A
Query                 14278    ACAAATCTCTGGCGCAAAGGGCATCCATCTTCGAGGGAGCAGCCAACGAAGCGCAAGCCG  14337
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Sbjct                 1543539  ACAAATCTCTGGCGCAAAGGGCATCCATCTTCGAGGGAGCAGCCAACGAAGCGCAAGCCG  1543598
CDS:chromosome segre  344      N  K  S  L  A  Q  R  A  S  I  F  E  G  A  A  N  E  A  Q  A

CDS: Putative 3       364      E  L  K  R  L  R  A  A  Y  E  R  P  A  E  V  T  A  R  Y  K
Query                 14338    AACTCAAGCGTTTGCGTGCAGCTTATGAGCGCCCTGCTGAAGTTACCGCTCGCTACAAAG  14397
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1543599  AACTCAAGCGTTTGCGTGCAGCTTATGAGCGCCCTGCTGAAGTTACCGCTCGCTACAAAG  1543658
CDS:chromosome segre  364      E  L  K  R  L  R  A  A  Y  E  R  P  A  E  V  T  A  R  Y  K

CDS: Putative 3       384      E  I  E  M  P  H  I  S  V  D  K  V  K  Q  P  V  Q  H  E  I
Query                 14398    AAATTGAGATGCCGCACATCAGTGTGGATAAGGTCAAGCAGCCGGTGCAGCACGAGATCG  14457
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Sbjct                 1543659  AAATTGAGATGCCGCACATCAGTGTGGATAAGGTCCAGCAGCCGGTGCAGCACGAGATCG  1543718
CDS:chromosome segre  384      E  I  E  M  P  H  I  S  V  D  K  V  Q  Q  P  V  Q  H  E  I
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CDS: Putative 3       404      D  E  L  T  W  L  T  G  I  G  N  A  C  D  T  Y  G  L  H  F
Query                 14458    ATGAGCTAACTTGGCTCACTGGGATTGGTAATGCTTGCGATACATACGGACTACATTTCA  14517
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Sbjct                 1543719  ATGAGCTAACTTGGCTCACTGGGATTGGTAATGCTTGCGATACATACGGACTACATTTCA  1543778
CDS:chromosome segre  404      D  E  L  T  W  L  T  G  I  G  N  A  C  D  T  Y  G  L  H  F

CDS: Putative 3       424      N  P  R  I  L  K  A  F  H  T  A  L  K  T  A  E  W  S  P  L
Query                 14518    ATCCACGTATTTTGAAAGCTTTTCATACAGCTCTCAAAACAGCGGAATGGTCGCCGCTCA  14577
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Sbjct                 1543779  ATCCACGTATTTTGAAAGCTTTTCATACAGCTCTCAAAACAGCGGAATGGTCGCCGCTCA  1543838
CDS:chromosome segre  424      N  P  R  I  L  K  A  F  H  T  A  L  K  T  A  E  W  S  P  L

CDS: Putative 3       444      T  V  L  A  G  V  S  G  T  G  K  S  E  L  P  R  L  Y  S  H
Query                 14578    CTGTCCTGGCAGGGGTTTCCGGAACCGGAAAATCCGAACTGCCGCGCCTCTACTCGCACT  14637
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1543839  CTGTCCTGGCAGGGGTTTCCGGAACCGGAAAATCCGAACTGCCGCGCCTCTACTCGCACT  1543898
CDS:chromosome segre  444      T  V  L  A  G  V  S  G  T  G  K  S  E  L  P  R  L  Y  S  H

CDS: Putative 3       464      F  G  G  I  Y  F  E  P  L  S  V  Q  P  N  W  D  S  Q  E  S
Query                 14638    TTGGCGGAATTTATTTCGAGCCGCTGTCTGTCCAGCCTAATTGGGATTCGCAGGAATCCA  14697
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1543899  TTGGCGGAATTTATTTCGAGCCGCTGTCTGTCCAGCCTAATTGGGATTCGCAGGAATCCA  1543958
CDS:chromosome segre  464      F  G  G  I  Y  F  E  P  L  S  V  Q  P  N  W  D  S  Q  E  S

CDS: Putative 3       484      M  L  G  F  F  N  S  I  D  N  K  F  D  A  Q  P  V  L  R  F
Query                 14698    TGCTGGGCTTTTTCAATTCCATAGACAATAAATTCGATGCACAGCCGGTGCTGCGTTTTC  14757
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1543959  TGCTGGGCTTTTTCAATTCCATAGACAATAAATTCGATGCACAGCCGGTGCTGCGTTTTC  1544018
CDS:chromosome segre  484      M  L  G  F  F  N  S  I  D  N  K  F  D  A  Q  P  V  L  R  F

CDS: Putative 3       504      L  A  Q  S  Q  I  S  G  R  E  Q  Y  E  Q  R  I  R  R  W  Q
Query                 14758    TCGCGCAAAGTCAGATATCAGGCCGCGAACAATATGAACAGCGCATTAGACGTTGGCAGA  14817
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1544019  TCGCGCAAAGTCAGATATCAGGCCGCGAACAATATGAACAGCGCATTAGACGTTGGCAGA  1544078
CDS:chromosome segre  504      L  A  Q  S  Q  I  S  G  R  E  Q  Y  E  Q  R  I  R  R  W  Q

CDS: Putative 3       524      S  M  S  P  D  Q  Q  I  A  L  D  P  E  K  D  K  E  L  I  E
Query                 14818    GTATGTCGCCAGATCAGCAAATAGCACTTGACCCTGAGAAGGACAAAGAGCTGATTGAAG  14877
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1544079  GTATGTCGCCAGATCAGCAAATAGCACTTGACCCTGAGAAGGACAAAGAGCTGATTGAAG  1544138
CDS:chromosome segre  524      S  M  S  P  D  Q  Q  I  A  L  D  P  E  K  D  K  E  L  I  E

CDS: Putative 3       544      A  L  K  Q  A  D  Y  P  G  L  Q  D  A  V  C  L  V  L  L  D
Query                 14878    CGTTGAAACAAGCAGATTATCCAGGATTGCAGGACGCAGTGTGTCTTGTTCTGCTTGATG  14937
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1544139  CGTTGAAACAAGCAGATTATCCAGGATTGCAGGACGCAGTGTGTCTTGTTCTGCTTGATG  1544198
CDS:chromosome segre  544      A  L  K  Q  A  D  Y  P  G  L  Q  D  A  V  C  L  V  L  L  D

CDS: Putative 3       564      E  M  N  L  A  H  P  E  L  Y  F  A  E  F  L  S  K  L  E  L
Query                 14938    AGATGAATCTGGCACACCCTGAGCTTTATTTTGCAGAGTTTTTGAGCAAGCTAGAACTGC  14997
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1544199   AGATGAATCTGGCACACCCTGAGCTTTATTTTGCAGAGTTTTTGAGCAAGCTAGAACTGC  1544258
CDS:chromosome segre   564       E  M  N  L  A  H  P  E  L  Y  F  A  E  F  L  S  K  L  E  L

CDS: Putative 3        584       R  R  G  R  K  G  D  D  V  P  F  I  P  V  K  I  G  A  G  M
Query                  14998     GGCGTGGCAGAAAGGGTGATGATGTTCCGTTCATACCGGTGAAAATTGGCGCCGGCATGG  15057
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1544259   GGCGTGGCAGAAAGGGTGATGATGTTCCGTTCATACCGGTGAAAATTGGCGCCGGCATGG  1544318
CDS:chromosome segre   584       R  R  G  R  K  G  D  D  V  P  F  I  P  V  K  I  G  A  G  M

CDS: Putative 3        604       E  P  Y  K  L  P  L  G  R  N  V  L  W  T  G  T  M  N  Q  D
Query                  15058     AACCCTATAAGCTCCCCCTCGGTCGTAATGTACTCTGGACAGGGACGATGAACCAGGACG  15117
                                 |||||||||||||  |||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1544319   AACCCTATAAGCTTCCCCTCGGTCGTAATGTACTCTGGACAGGGACGATGAACCAGGACG  1544378
CDS:chromosome segre   604       E  P  Y  K  L  P  L  G  R  N  V  L  W  T  G  T  M  N  Q  D

CDS: Putative 3        624       E  T  T  K  S  L  S  D  K  V  L  D  R  S  I  I  I  N  F  P
Query                  15118     AAACCACCAAGTCCCTTTCGGACAAGGTGCTTGACCGTTCCATCATCATCAACTTTCCGC  15177
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1544379   AAACCACCAAGTCCCTTTCGGACAAGGTGCTTGACCGTTCCATCATCATCAACTTTCCGC  1544438
CDS:chromosome segre   624       E  T  T  K  S  L  S  D  K  V  L  D  R  S  I  I  I  N  F  P

CDS: Putative 3        644       R  P  T  E  L  K  R  R  L  K  L  A  P  L  D  D  K  N  R  G
Query                  15178     GCCCGACGGAACTCAAACGCCGCCTGAAGCTTGCTCCACTTGATGACAAAAATCGAGGCC  15237
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1544439   GCCCGACGGAACTCAAACGCCGCCTGAAGCTTGCTCCACTTGATGACAAAAATCGAGGCC  1544498
CDS:chromosome segre   644       R  P  T  E  L  K  R  R  L  K  L  A  P  L  D  D  K  N  R  G

CDS: Putative 3        664       P  A  L  H  K  T  S  W  Q  S  W  L  A  Q  G  S  N  F  S  D
Query                  15238     CGGCGCTACACAAAACGTCGTGGCAGAGTTGGCTAGCACAGGGCAGCAACTTCTCCGACG  15297
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1544499   CGGCGCTACACAAAACGTCGTGGCAGAGTTGGCTAGCACAGGGCAGCAACTTCTCCGACG  1544558
CDS:chromosome segre   664       P  A  L  H  K  T  S  W  Q  S  W  L  A  Q  G  S  N  F  S  D

CDS: Putative 3        684       D  Q  V  S  P  F  K  K  F  I  E  A  I  N  A  S  L  A  V  T
Query                  15298     ATCAAGTCAGCCCGTTCAAAAAATTCATTGAAGCAATCAATGCTTCTTTAGCGGTTACAG  15357
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1544559   ATCAAGTCAGCCCGTTCAAAAAATTCATTGAAGCAATCAATGCTTCTTTAGCGGTTACAG  1544618
CDS:chromosome segre   684       D  Q  V  S  P  F  K  K  F  I  E  A  I  N  A  S  L  A  V  T

CDS: Putative 3        704       G  R  A  L  G  H  R  V  W  Q  S  I  E  Y  Y  M  A  N  Y  P
Query                  15358     GCCGTGCCCTCGGTCACCGCGTTTGGCAATCCATTGAATACTACATGGCCAATTACCCGG  15417
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1544619   GCCGTGCCCTCGGTCACCGCGTTTGGCAATCCATTGAATACTACATGGCCAATTACCCGG  1544678
CDS:chromosome segre   704       G  R  A  L  G  H  R  V  W  Q  S  I  E  Y  Y  M  A  N  Y  P

CDS: Putative 3        724       D  V  R  A  A  R  D  K  D  A  L  A  R  A  M  H  V  A  F  E
Query                  15418     ATGTCCGTGCTGCACGCGATAAAGATGCGCTTGCCAGAGCTATGCATGTCGCCTTCGAGG  15477
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1544679   ATGTCCGTGCTGCACGCGATAAAGATGCGCTTGCCAGAGCTATGCATGTCGCCTTCGAGG  1544738
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CDS:chromosome segre  724      D  V  R  A  A  R  D  K  D  A  L  A  R  A  M  H  V  A  F  E

CDS: Putative 3       744      D  Q  L  V  Q  K  V  M  P  K  L  R  G  I  D  T  R  G  K  S
Query                 15478    ATCAACTCGTGCAGAAGGTCATGCCCAAATTGCGGGGTATTGATACACGCGGCAAGAGCA  15537
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1544739  ATCAACTCGTGCAGAAGGTCATGCCCAAATTGCGGGGTATTGATACACGCGGCAAGAGCA  1544798
CDS:chromosome segre  744      D  Q  L  V  Q  K  V  M  P  K  L  R  G  I  D  T  R  G  K  S

CDS: Putative 3       764      K  T  E  C  L  D  R  I  R  G  Q  L  V  T  G  I  G  S  N  S
Query                 15538    AGACAGAGTGCCTGGACAGGATTCGTGGACAACTCGTTACAGGAATCGGCAGTAACTCAT  15597
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1544799  AGACAGAGTGCCTGGACAGGATTCGTGGACAACTCGTTACAGGAATCGGCAGTAACTCAT  1544858
CDS:chromosome segre  764      K  T  E  C  L  D  R  I  R  G  Q  L  V  T  G  I  G  S  N  S

CDS: Putative 3       784      F  N  L  T  E  D  F  D  L  A  C  D  L  G  Y  G  Q  F  I  W
Query                 15598    TCAATCTGACAGAGGATTTCGACCTTGCCTGTGATCTTGGCTATGGTCAGTTTATTTGGC  15657
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1544859  TCAATCTGACAGAGGATTTCGACCTTGCCTGTGATCTTGGCTATGGTCAGTTTATTTGGC  1544918
CDS:chromosome segre  784      F  N  L  T  E  D  F  D  L  A  C  D  L  G  Y  G  Q  F  I  W

CDS: Putative 3       804      Q  S  A  N  Y  L  N  V  G  D  T  E  T  N  D  R  S  T  A  S
Query                 15658    AGTCGGCAAATTACCTAAACGTCGGTGACACGGAAACCAATGATAGATCCACGGCCAGTC  15717
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1544919  AGTCGGCAAATTACCTAAACGTCGGTGACACGGAAACCAATGATAGATCCACGGCCAGTC  1544978
CDS:chromosome segre  804      Q  S  A  N  Y  L  N  V  G  D  T  E  T  N  D  R  S  T  A  S

CDS: Putative 3       824      R  D  S  D  N  A  E  L  P  H  S  L  F  M  K  D  E  P  D  S
Query                 15718    GAGACTCGGACAATGCTGAATTGCCACACTCCCTTTTTATGAAAGATGAACCAGATTCAG  15777
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1544979  GAGACTCGGACAATGCTGAATTGCCACACTCCCTTTTTATGAAAGATGAACCAGATTCAG  1545038
CDS:chromosome segre  824      R  D  S  D  N  A  E  L  P  H  S  L  F  M  K  D  E  P  D  S

CDS: Putative 3       844      D  K  R  H  K  M  W  N  L  K  T  P  E  Q  R  D  E  L  R  V
Query                 15778    ACAAGCGTCATAAAATGTGGAACTTAAAGACACCAGAGCAACGAGATGAGCTGCGCGTGA  15837
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545039  ACAAGCGTCATAAAATGTGGAACTTAAAGACACCAGAGCAACGAGATGAGCTGCGCGTGA  1545098
CDS:chromosome segre  844      D  K  R  H  K  M  W  N  L  K  T  P  E  Q  R  D  E  L  R  V

CDS: Putative 3       864      K  L  E  E  N  A  R  A  G  R  I  H  A  K  Q  *
CDS: Putative 4       1                                                      M  S  I  T  L  E
Query                 15838    AACTTGAAGAAAATGCCAGAGCAGGAAGGATTCACGCCAAGCAATGAGTATTACTCTGGA  15897
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct                 1545099  AACTTGAAGAAAATGCCAGAGCAGGAAGGATTCACGCCAAGCAATGAGTATTACTCTAGA  1545158
CDS:chromosome segre  864      K  L  E  E  N  A  R  A  G  R  I  H  A  K  Q
CDS:Cold-shock DNA-b  1                                                      M  S  I  T  L  E

CDS: Putative 4       7          K  I  Y  T  D  F  R  A  K  E  K  L  A  K  K  L  L  E  Q  M
Query                 15898    AAAAATCTATACCGACTTCCGTGCCAAAGAAAAACTTGCCAAAAAACTGCTTGAGCAAAT  15957
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545159  AAAAATCTATACCGACTTCCGTGCCAAAGAAAAACTTGCCAAAAAACTGCTTGAGCAAAT  1545218
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CDS:Cold-shock DNA-b  7          K  I  Y  T  D  F  R  A  K  E  K  L  A  K  K  L  L  E  Q  M

CDS: Putative 4       27         N  W  F  G  S  I  T  D  F  D  P  K  T  G  A  A  L  P  K  S
Query                 15958    GAATTGGTTTGGTTCAATCACGGATTTCGATCCTAAGACCGGCGCGGCTCTGCCGAAATC  16017
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545219  GAATTGGTTTGGTTCAATCACGGATTTCGATCCTAAGACCGGCGCGGCTCTGCCGAAATC  1545278
CDS:Cold-shock DNA-b  27         N  W  F  G  S  I  T  D  F  D  P  K  T  G  A  A  L  P  K  S

CDS: Putative 4       47         L  S  G  F  L  A  K  V  A  Q  P  E  A  S  E  I  T  R  D  R
Query                 16018    CTTGTCAGGGTTCCTCGCCAAAGTCGCACAGCCAGAAGCGAGTGAGATAACCCGTGACCG  16077
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545279  CTTGTCAGGGTTCCTCGCCAAAGTCGCACAGCCAGAAGCGAGTGAGATAACCCGTGACCG  1545338
CDS:Cold-shock DNA-b  47         L  S  G  F  L  A  K  V  A  Q  P  E  A  S  E  I  T  R  D  R

CDS: Putative 4       67         L  W  R  I  T  E  H  C  R  A  S  V  E  R  L  F  H  S  L  N
Query                 16078    CCTTTGGCGCATAACGGAACACTGCCGCGCTTCTGTCGAGCGATTATTTCATTCTCTCAA  16137
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545339  CCTTTGGCGCATAACGGAACACTGCCGCGCTTCTGTCGAGCGATTATTTCATTCTCTCAA  1545398
CDS:Cold-shock DNA-b  67         L  W  R  I  T  E  H  C  R  A  S  V  E  R  L  F  H  S  L  N

CDS: Putative 4       87         E  S  P  R  C  E  H  A  L  L  P  V  H  A  V  R  E  L  D  A
Query                 16138    CGAAAGTCCTCGCTGCGAACACGCTCTACTGCCTGTTCATGCTGTGCGTGAACTGGATGC  16197
                               ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545399  CGAAAGTCCTCGCCGCGAACACGCTCTACTGCCTGTTCATGCTGTGCGTGAACTGGATGC  1545458
CDS:Cold-shock DNA-b  87         E  S  P  R  R  E  H  A  L  L  P  V  H  A  V  R  E  L  D  A

CDS: Putative 4       107        N  S  F  I  K  L  S  N  R  P  G  R  T  I  R  E  K  L  A  G
Query                 16198    CAACAGTTTTATTAAGCTGAGTAATCGTCCGGGTCGTACCATTCGGGAAAAACTGGCAGG  16257
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545459  CAACAGTTTTATTAAGCTGAGTAATCGTCCGGGTCGTACCATTCGGGAAAAACTGGCAGG  1545518
CDS:Cold-shock DNA-b  107        N  S  F  I  K  L  S  N  R  P  G  R  T  I  R  E  K  L  A  G

CDS: Putative 4       127        N  P  Y  I  Q  A  V  R  R  F  Q  S  V  D  L  P  E  N  R  L
Query                 16258    TAACCCCTACATACAGGCTGTGCGTCGTTTTCAATCCGTCGACCTGCCGGAAAATCGCTT  16317
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545519  TAACCCCTACATACAGGCTGTGCGTCGTTTTCAATCCGTCGACCTGCCGGAAAATCGCTT  1545578
CDS:Cold-shock DNA-b  127        N  P  Y  I  Q  A  V  R  R  F  Q  S  V  D  L  P  E  N  R  L

CDS: Putative 4       147        L  K  A  F  A  I  R  L  A  E  M  L  D  L  R  G  D  C  L  G
Query                 16318    GCTGAAAGCCTTTGCCATTCGCCTTGCGGAAATGCTTGATTTACGCGGTGATTGTCTCGG  16377
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545579  GCTGAAAGCCTTTGCCATTCGCCTTGCGGAAATGCTTGATTTACGCGGTGATTGTCTCGG  1545638
CDS:Cold-shock DNA-b  147        L  K  A  F  A  I  R  L  A  E  M  L  D  L  R  G  D  C  L  G

CDS: Putative 4       167        Q  E  D  E  L  L  S  K  I  Y  L  W  L  R  S  D  E  A  Q  A
Query                 16378    TCAAGAGGATGAGCTTCTATCAAAAATCTACTTATGGTTGCGTTCTGATGAGGCGCAAGC  16437
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545639  TCAAGAGGATGAGCTTCTATCAAAAATCTACTTATGGTTGCGTTCTGATGAGGCGCAAGC  1545698
CDS:Cold-shock DNA-b  167        Q  E  D  E  L  L  S  K  I  Y  L  W  L  R  S  D  E  A  Q  A
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CDS: Putative 4       187        I  G  N  W  E  N  L  P  P  N  N  T  L  L  A  H  R  D  Y  R
Query                 16438    CATCGGCAATTGGGAAAATCTGCCACCTAACAACACGCTACTAGCACACCGAGATTACCG  16497
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545699  CATCGGCAATTGGGAAAATCTGCCACCTAACAACACGCTACTAGCACACCGAGATTACCG  1545758
CDS:Cold-shock DNA-b  187        I  G  N  W  E  N  L  P  P  N  N  T  L  L  A  H  R  D  Y  R

CDS: Putative 4       207        H  V  W  D  A  W  R  W  L  Q  T  L  D  E  D  I  T  S  D  L
Query                 16498    TCACGTGTGGGATGCATGGCGCTGGCTGCAAACCCTCGATGAGGACATCACCAGCGACCT  16557
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545759  TCACGTGTGGGATGCATGGCGCTGGCTGCAAACCCTCGATGAGGACATCACCAGCGACCT  1545818
CDS:Cold-shock DNA-b  207        H  V  W  D  A  W  R  W  L  Q  T  L  D  E  D  I  T  S  D  L

CDS: Putative 4       227        S  Q  L  D  V  R  E  K  T  M  R  L  W  Q  Q  C  A  Q  M  W
Query                 16558    TTCTCAACTGGATGTCCGCGAGAAAACCATGCGCCTTTGGCAGCAATGCGCGCAAATGTG  16617
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545819  TTCTCAACTGGATGTCCGCGAGAAAACCATGCGCCTTTGGCAGCAATGCGCGCAAATGTG  1545878
CDS:Cold-shock DNA-b  227        S  Q  L  D  V  R  E  K  T  M  R  L  W  Q  Q  C  A  Q  M  W

CDS: Putative 4       247        L  D  G  K  H  L  F  A  E  I  P  L  L  F  D  Y  E  K  F  E
Query                 16618    GCTTGATGGAAAGCATCTTTTTGCTGAGATACCGTTACTATTCGATTATGAAAAGTTTGA  16677
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545879  GCTTGATGGAAAGCATCTTTTTGCTGAGATACCGTTACTATTCGATTATGAAAAGTTTGA  1545938
CDS:Cold-shock DNA-b  247        L  D  G  K  H  L  F  A  E  I  P  L  L  F  D  Y  E  K  F  E

CDS: Putative 4       267        I  L  P  W  T  S  K  P  P  L  F  K  E  V  K  Y  K  M  P  R
Query                 16678    GATTCTTCCGTGGACTTCCAAGCCACCTTTGTTCAAGGAAGTGAAGTACAAGATGCCCCG  16737
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545939  GATTCTTCCGTGGACTTCCAAGCCACCTTTGTTCAAGGAAGTGAAGTACAAGATGCCCCG  1545998
CDS:Cold-shock DNA-b  267        I  L  P  W  T  S  K  P  P  L  F  K  E  V  K  Y  K  M  P  R

CDS: Putative 4       287        H  L  R  Q  S  A  S  A  E  P  I  C  V  D  I  T  A  L  H  P
Query                 16738    GCATTTGCGACAAAGCGCGAGTGCCGAACCAATTTGTGTTGATATCACAGCCCTGCATCC  16797
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1545999  GCATTTGCGACAAAGCGCGAGTGCCGAACCAATTTGTGTTGATATCACAGCCCTGCATCC  1546058
CDS:Cold-shock DNA-b  287        H  L  R  Q  S  A  S  A  E  P  I  C  V  D  I  T  A  L  H  P

CDS: Putative 4       307        R  Y  A  S  G  D  G  K  G  A  Q  S  L  A  A  P  F  L  W  Q
Query                 16798    CCGCTATGCCAGTGGTGACGGAAAAGGAGCGCAGTCGCTGGCGGCCCCCTTTCTTTGGCA  16857
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1546059  CCGCTATGCCAGTGGTGACGGAAAAGGAGCGCAGTCGCTGGCGGCCCCCTTTCTTTGGCA  1546118
CDS:Cold-shock DNA-b  307        R  Y  A  S  G  D  G  K  G  A  Q  S  L  A  A  P  F  L  W  Q

CDS: Putative 4       327        R  W  Q  R  E  N  E  T  V  D  I  E  L  F  G  S  D  A  V  W
Query                 16858    GAGGTGGCAGCGCGAAAATGAAACCGTTGACATCGAACTCTTTGGTTCCGATGCCGTTTG  16917
                               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1546119  GAGGTGGCAGCGCGAAAATGAAACCGTTGACATCGAACTCTTTGGTTCCGATGCCGTTTG  1546178
CDS:Cold-shock DNA-b  327        R  W  Q  R  E  N  E  T  V  D  I  E  L  F  G  S  D  A  V  W

CDS: Putative 4       347        L  N  P  D  A  T  T  I  S  A  P  D  L  F  F  A  K  D  N  A
Query                 16918    GCTGAATCCCGATGCGACCACCATTTCTGCGCCAGATCTGTTTTTCGCCAAAGACAACGC  16977
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                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1546179  GCTGAATCCCGATGCGACCACCATTTCTGCGCCAGATCTGTTTTTCGCCAAAGACAACGC  1546238
CDS:Cold-shock DNA-b   347        L  N  P  D  A  T  T  I  S  A  P  D  L  F  F  A  K  D  N  A

CDS: Putative 4        367        T  E  L  F  D  P  A  A  R  A  F  T  T  R  L  R  E  E  F  K
Query                  16978    CACTGAGCTTTTTGACCCCGCCGCCCGCGCGTTCACTACTCGGCTACGCGAAGAGTTCAA  17037
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1546239  CACTGAGCTTTTTGACCCCGCCGCCCGCGCGTTCACTACTCGGCTACGCGAAGAGTTCAA  1546298
CDS:Cold-shock DNA-b   367        T  E  L  F  D  P  A  A  R  A  F  T  T  R  L  R  E  E  F  K

CDS: Putative 4        387        N  D  T  L  I  W  L  A  P  D  F  L  N  D  F  E  L  E  V  I
Query                  17038    GAACGATACACTCATCTGGCTTGCGCCTGACTTTCTCAACGATTTCGAGCTTGAAGTCAT  17097
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1546299  GAACGATACACTCATCTGGCTTGCGCCTGACTTTCTCAACGATTTCGAGCTTGAAGTCAT  1546358
CDS:Cold-shock DNA-b   387        N  D  T  L  I  W  L  A  P  D  F  L  N  D  F  E  L  E  V  I

CDS: Putative 4        407        R  R  N  L  N  A  R  F  P  N  A  E  P  L  P  R  S  V  A  A
Query                  17098    CCGTCGCAACCTCAACGCGCGTTTCCCGAATGCCGAGCCGTTGCCGCGAAGTGTGGCGGC  17157
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1546359  CCGTCGCAACCTCAACGCGCGTTTCCCGAATGCCGAGCCGTTGCCGCGAAGTGTGGCGGC  1546418
CDS:Cold-shock DNA-b   407        R  R  N  L  N  A  R  F  P  N  A  E  P  L  P  R  S  V  A  A

CDS: Putative 4        427        V  F  A  Q  A  D  P  A  K  I  T  G  E  G  Y  A  I  I  V  V
Query                  17158    CGTGTTCGCTCAAGCTGACCCGGCCAAAATCACGGGCGAGGGTTACGCCATCATCGTCGT  17217
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1546419  CGTGTTCGCTCAAGCTGACCCGGCCAAAATCACGGGCGAGGGTTACGCCATCATCGTCGT  1546478
CDS:Cold-shock DNA-b   427        V  F  A  Q  A  D  P  A  K  I  T  G  E  G  Y  A  I  I  V  V

CDS: Putative 4        447        D  S  I  G  G  K  T  T  A  T  K  L  I  A  K  R  D  K  D  L
Query                  17218    TGATTCCATTGGCGGCAAGACGACCGCCACCAAGCTCATCGCCAAGCGCGACAAAGACCT  17277
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1546479  TGATTCCATTGGCGGCAAGACGACCGCCACCAAGCTCATCGCCAAGCGCGACAAAGACCT  1546538
CDS:Cold-shock DNA-b   447        D  S  I  G  G  K  T  T  A  T  K  L  I  A  K  R  D  K  D  L

CDS: Putative 4        467        A  K  R  L  P  I  T  K  G  F  Y  W  E  R  C  P  P  V  V  I
Query                  17278    GGCGAAACGTCTTCCCATCACCAAAGGCTTTTATTGGGAGCGTTGCCCGCCGGTTGTTAT  17337
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1546539  GGCGAAACGTCTTCCCATCACCAAAGGCTTTTATTGGGAGCGTTGCCCGCCGGTTGTTAT  1546598
CDS:Cold-shock DNA-b   467        A  K  R  L  P  I  T  K  G  F  Y  W  E  R  C  P  P  V  V  I

CDS: Putative 4        487        P  G  E  E  A  E  R  L  G  G  S  G  Y  D  I  I  T  L  D  A
Query                  17338    CCCTGGCGAGGAAGCAGAAAGGCTAGGTGGCAGCGGCTACGACATCATCACGCTGGATGC  17397
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1546599  CCCTGGCGAGGAAGCAGAAAGGCTAGGTGGCAGCGGCTACGACATCATCACGCTGGATGC  1546658
CDS:Cold-shock DNA-b   487        P  G  E  E  A  E  R  L  G  G  S  G  Y  D  I  I  T  L  D  A

CDS: Putative 4        507        N  G  R  W  H  D  A  I  R  P  A  K  P  P  F  I  E  A  A  H
Query                  17398    CAACGGGCGGTGGCACGATGCGATCCGCCCGGCAAAGCCCCCATTCATTGAGGCAGCACA  17457
                                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                  1546659  CAACGGGCGGTGGCACGATGCGATCCGCCCGGCAAAGCCCCCATTCATTGAGGCAGCACA  1546718
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CDS:Cold-shock DNA-b  507        N  G  R  W  H  D  A  I  R  P  A  K  P  P  F  I  E  A  A  H

CDS: Putative 4       527        L  K  R  I  P  N
Query                 17458    CCTGAAGCGTATTCCAAAC  17476
                               ||||||||||||||||||
Sbjct                 1546719  CCTGAAGCGTATTCCAAAC  1546737
CDS:Cold-shock DNA-b  527        L  K  R  I  P  N


&gt;gb|CP002738.1| Methylomonas methanica MC09, complete genome
Length=5051681

 Features in this part of subject sequence:
   hypothetical protein
   hypothetical protein

 Score = 4486 bits (2429),  Expect = 0.0
 Identities = 4504/5526 (82%), Gaps = 62/5526 (1%)
 Strand=Plus/Minus

CDS: Putative 6       1           I  E  T  Q  G  R  T  F  V  G  D  N  G  R  Y  T  K  T  D
Query                 1        GGATCGAGACGCAAGGGCGAACCTTTGTGGGCGACAACGGACGCTACACAAAAACAGATT  60
                               |||||||||| || || ||||| ||||| ||||||||||||||| ||||||||||| ||||
Sbjct                 2526996  GGATCGAGACACAGGGTCGAACTTTTGTTGGCGACAACGGACGGTACACAAAAACGGATT  2526937
CDS:hypothetical pro  303      R  I  E  T  Q  G  R  T  F  V  G  D  N  G  R  Y  T  K  T  D

CDS: Putative 6       20       L  I  V  T  D  L  R  V  P  V  I  L  G  R  G  E  G  M  G  A
Query                 61       TGATAGTCACCGACTTGCGGGTTCCGGTCATTCTGGGGCGTGGTGAGGGCATGGGGGCTC  120
                               |  |||| || || || |  ||||| |||||| ||||||| || |||||||||||||||
Sbjct                 2526936  TACTAGTGACGGAATTACAAGTTCCAGTCATTTTGGGGCGCGGCGAGGGCATGGGGGCTT  2526877
CDS:hypothetical pro  323      L  L  V  T  E  L  Q  V  P  V  I  L  G  R  G  E  G  M  G  A

CDS: Putative 6       40       P  V  G  G  S  M  A  F  E  V  K  C  G  K  A  E  Y  L  Y  S
Query                 121      CGGTGGGCGGCTCGATGGCATTCGAAGTGAAATGCGGCAAGGCGGAATACCTCTATTCGC  180
                               ||||||| |||||||||||||||| |||||||| |||||||||||||||||||| ||||
Sbjct                 2526876  CGGTGGGAGGCTCGATGGCATTCGAGGTGAAATGTGGCAAGGCGGAATACCTCTACTCGC  2526817
CDS:hypothetical pro  343      S  V  G  G  S  M  A  F  E  V  K  C  G  K  A  E  Y  L  Y  S

CDS: Putative 6       60       Q  K  D  H  M  I  F  Q  A  E  G  H  K  Q  A  D  A  Q  C  T
Query                 181      AGAAAGATCACATGATTTTTCAGGCTGAAGGGCACAAGCAAGCAGATGCGCAATGCACTC  240
                               ||||||||||||||||| || |||||  ||||||||||||| ||||| |||||||||||||
Sbjct                 2526816  AGAAAGATCACATGATCTTCCAGGCCAAAGGGCACAAGCATGCAGACGCGCAATGCACTC  2526757
CDS:hypothetical pro  363      Q  K  D  H  M  I  F  Q  A  K  G  H  K  H  A  D  A  Q  C  T

CDS: Putative 6       80       L  C  S  R  D  I  H  D  L  P  E  E  K  Q  K  E  L  R  D  A
Query                 241      TTTGCTCGCGAGATATCCACGATTTGCCAGAAGAAAAACAGAAAGAACTGCGCGACGCCT  300
                               ||||||||||||| |||||||| ||||||| |||||||||||||||||||||||  ||
Sbjct                 2526756  TTTGCTCGCGAGACATCCACGACTTGCCAGCAGAAAAACAGAAAGAACTGCGCGATACCC  2526697
CDS:hypothetical pro  383      L  C  S  R  D  I  H  D  L  P  A  E  K  Q  K  E  L  R  D  T
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CDS: Putative 6       100      L  R  E  A  G  S  P  M  V  G  M  L  P  R  K  N  E  I  D  Q
Query                 301      TGCGCGAAGCTGGCTCACCAATGGTGGGAATGTTGCCAAGGAAAAATGAAATAGATCAGT  360
                               |||||||||| |||||||||||||||||| ||||||||||| |||||||||||||||||||
Sbjct                 2526696  TGCGCGAAGCAGGCTCACCAATGGTGGGGATGTTGCCAAGAAAAAATGAAATAGATCAGT  2526637
CDS:hypothetical pro  403      L  R  E  A  G  S  P  M  V  G  M  L  P  R  K  N  E  I  D  Q

CDS: Putative 6       120      S  C  L  D  F  I  R  Q  N  E  E  E  Q  P  *
CDS: Putative 5       1                                                M  K  I  R  F  A  I
Query                 361      CCTGTCTTGATTTCATCCGCCAAAACGAGGAGGAGCAACCATGAAAATACGTTTCGCAAT  420
                               |||||||||||||||||||||||||||||||||||||||| |||||| ||||||||| |||||
Sbjct                 2526636  CCTGTCTTGATTTCATCCGCCAAAACGAGGAGGAGCAGCCATGAGAATACGTTTTGCAAT  2526577
CDS:hypothetical pro  1                                                M  R  I  R  F  A  I
CDS:hypothetical pro  423      S  C  L  D  F  I  R  Q  N  E  E  E  Q  P

CDS: Putative 5       8          I  S   H  D  L  L  A  Q  V  R  A  E  V  D  V  L  L  H  A
Query                 421      TATTAGC-CATGACCTTCTCGCACAAGTCCGGGCTGAAGTTGATGTCCTCCTGCATGCAG  479
                               | ||||  || ||||||||| | ||||||||| |||| |||||  | || |||| |||||
Sbjct                 2526576  TGTTAGTTCA-GACCTTCTCTCGCAAGTCCGGACTGACGTTGACATTCTTCTGCGTGCAG  2526518
CDS:hypothetical pro  8          V  S  S   D  L  L  S  Q  V  R  T  D  V  D  I  L  L  R  A

CDS: Putative 5       27       V  N  V  G  D  M  D  G  V  D  A  S  T  A  R  L  L  E  L  T
Query                 480      TAAATGTCGGAGATATGGATGGCGTGGATGCGTCCACCGCACGCCTCTTGGAGCTGACAG  539
                               | |||| ||| |||||||||||||||||||  |||| | || |||||||||||||||||
Sbjct                 2526517  TCAATGCCGGGGATATGGATGGCGTGGATGCAGCCACGGAACACCTCTTGGAGCTGACAG  2526458
CDS:hypothetical pro  27       V  N  A  G  D  M  D  G  V  D  A  A  T  E  H  L  L  E  L  T

CDS: Putative 5       47       V  D  C  R  S  I  E  L  S  E  E  E  W  R  A  F  L  S  E  I
Query                 540      TTGATTGCAGATCGATTGAGTTGTCCGAGGAAGAGTGGCGCGCATTTCTAAGCGAAATCA  599
                               || ||||||||||||||| || |||||||| || |||||| | ||||| |  |||||||
Sbjct                 2526457  TTAATTGCAGATCGATTGACTTATCCGAGGATGAATGGCGCACGTTTCTGAATGAAATCA  2526398
CDS:hypothetical pro  47       V  N  C  R  S  I  D  L  S  E  D  E  W  R  T  F  L  N  E  I

CDS: Putative 5       67       R  A  K  N  P  E  F  E  S  S  Y  L  L  P  G   T  I  C  A  P
Query                 600      GGGCCAAGAACCCTGAGTTCGAATCGAGCTACTTGTTGCCTGG-GACTATTTGCGCGCCC  658
                               |||||||||| |||| |||||||||  ||||| |||||||||| ||   ||||||| | |
Sbjct                 2526397  GGGCCAAGAATCCTGCGTTCGAATCCCGCTACCTGTTGCCTGGCGAGG-TTTGCGCTCAC  2526339
CDS:hypothetical pro  67       R  A  K  N  P  A  F  E  S  R  Y  L  L  P  G  E   V  C  A  H

CDS: Putative 5       87        L  F  P  N  L  S  V  A  D  D  Y  V  L  E  L  P  I  D  G  D
Query                 659      CTGTTTCCAAACCTCTCGGTAGCTGACGACTATGTTCTCGAACTTCCAATCGATGGTGAT  718
                               || |||||||   || |   ||||| |||||||||||||||||||||||| ||||| |||
Sbjct                 2526338  CTATTTCCAACAATCAC---AGCTGGCGACTATGTTCTCGAACTTCCAATTGATGGAGAT  2526282
CDS:hypothetical pro  87        L  F  P  T  I  T    A  G  D  Y  V  L  E  L  P  I  D  G  D

CDS: Putative 5       107       M  E  E  E  E  A  N  V  *
CDS: Putative 4       1                          M  F  D  E  A  F  G  M  A  A  M  C  A  G
Query                 719      ATGGAAGAGGAGGAAGCTAATGTTTGATGAGGCCTTTGGAATGGCTGCGATGTGCGCTGG  778
                               |||| |||||| |||| | |||||||||||||  || ||||||||  || ||||  |||
Sbjct                 2526281  ATGGGAGAGGAAGAAGTTGATGTTTGATGAGGTTTTAGGAATGGCGACGCTGTGTACTGA  2526222
CDS:hypothetical pro  1                          M  F  D  E  V  L  G  M  A  T  L  C  T  E
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CDS:hypothetical pro  106       M  G  E  E  E  V  D  V

CDS: Putative 4       15        K  F  R  E  G  V  R  D  T  F  G  A  S  I  V  A  D  V  L  D
Query                 779      AAAATTTCGCGAGGGAGTGCGTGATACGTTCGGCGCGTCCATTGTTGCTGATGTACTTGA  838
                               ||| || ||||| || ||||| ||| |||||||||| ||||||||||| ||||||||||
Sbjct                 2526221  AAACTTCCGCGACGGTGTGCGCGATTCGTTCGGCGCATCCATTGTTGCCGATGTACTTGA  2526162
CDS:hypothetical pro  15        N  F  R  D  G  V  R  D  S  F  G  A  S  I  V  A  D  V  L  D

CDS: Putative 4       35        P  I  L  K  E  V  D  S  L  R  I  F  N  A  A  Y  Q  Q  Q  S
Query                 839      TCCGATTCTCAAGGAAGTCGATTCACTCCGCATTTTCAATGCGGCTTACCAGCAGCAATC  898
                               ||||||||||||||| ||||||||||||| ||||| ||||| |||| |||||||||||
Sbjct                 2526161  TCCGATTCTCAAGGAAATCGATTCACTCCGTATTTTTAATGCCGCTTTCCAGCAGCAATC  2526102
CDS:hypothetical pro  35        P  I  L  K  E  I  D  S  L  R  I  F  N  A  A  F  Q  Q  Q  S

CDS: Putative 4       55        L  A  I  D  R  T  L  N  D  V  R   E   L  Q  F  K  D  S  G
Query                 899      GCTCGCCATTGATCGAACTTTGAATGACGTTCGCG-A-GCTCCAGTTCAAAGACAGTGGG  956
                               ||||  |||||||| ||| |||  ||| |  |||| | |||||||||||||||||| ||
Sbjct                 2526101  GCTCAGCATTGATCAAACCTTGGCTGATG--CGCGTACGCTCCAGTTCAAAGACAGTAGG  2526044
CDS:hypothetical pro  55        L  S  I  D  Q  T  L  A  D   A  R  T  L  Q  F  K  D  S  R

CDS: Putative 4       74       W  N  Q  *
CDS: Putative 3       1                M  S  E  S  A  K  D  F  Q  S  V  I  F  K  L  H  K
Query                 957      TGGAATCAATGAGTGAAAGCGCGAAGGATTTTCAGAGCGTAATTTTCAAGCTACACAAGG  1016
                               ||||  |||||| || ||| || ||    ||||||   || | |   ||  ||||||||
Sbjct                 2526043  TGGACGCAATGAATGGAAGAGCAAAATCGTTTCAGGATGTGACTGCTAAATTACACAAGA  2525984
CDS:cell division pr  1                M  N  G  R  A  K  S  F  Q  D  V  T  A  K  L  H  K
CDS:hypothetical pro  74       W  T  Q

CDS: Putative 3       18       A  I  A  D  Y  Q  E  G   C  A  R  I  D  R  E  F  N  A  T  K
Query                 1017     CAATTGCGGACTATCAAGAAGG--TTGTGCGCGCATCGACCGCGAATTCAATGCCACTaa  1074
                               |||| | ||||||||| |||||  ||||||||  || |||||||| ||||||||||| ||
Sbjct                 2525983  CAATCGTGGACTATCACGAAGGCCTTGTGCGC--ATTGACCGCGATTTCAATGCCACCAA  2525926
CDS:cell division pr  18       T  I  V  D  Y  H  E  G  L  V  R   I  D  R  D  F  N  A  T  K

CDS: Putative 3       38        K  T  L  N  E  D  Q  E  R  N  R  S  I  R  K  S  N  W  Q  A
Query                 1075     aaaaaCATTGAACGAAGACCAGGAGCGCAATCGGAGCATAAGGAAGTCGAATTGGCAGGC  1134
                               ||||||||| |||||||| |||||||| || |||   || ||||||||||||||| || |
Sbjct                 2525925  AAAAACATTAAACGAAGATCAGGAGCGTAACCGGGAAATCAGGAAGTCGAATTGGAAGTC  2525866
CDS:cell division pr  38        K  T  L  N  E  D  Q  E  R  N  R  E  I  R  K  S  N  W  K  S

CDS: Putative 3       58        G  F  V  R  E  W  E  S  N   A  T  A  I  A  N  A  S  A  Q
Query                 1135     AGGCTTTGTCAGAGAGTGGGAAAGTAAT-GCAACTGCTATAGCGAACGCAAGTGCACAGC  1193
                               |||||| |||||||| ||||| |  ||| |||||||  |||||||||| |||| | ||||
Sbjct                 2525865  AGGCTTCGTCAGAGAATGGGAGAA-AATCGCAACTGAAATAGCGAACGTAAGTTCGCAGC  2525807
CDS:cell division pr  58        G  F  V  R  E  W  E  K   I  A  T  E  I  A  N  V  S  S  Q

CDS: Putative 3       77       L  R  Q  H  Q  P  A  F  V  D  F  C  V  D  K  P  L  M  A  S
Query                 1194     TTAGACAACATCAGCCTGCCTTCGTGGATTTTTGTGTAGACAAGCCATTGATGGCATCGG  1253
                               ||||||| |  ||||| ||  |||| |||||| |   |||||||||||||||||||||||
Sbjct                 2525806  TTAGACAGCGCCAGCCCGCTCTCGTAGATTTTGGCAAAGACAAGCCATTGATGGCATCGG  2525747
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CDS:cell division pr  77       L  R  Q  R  Q  P  A  L  V  D  F  G  K  D  K  P  L  M  A  S

CDS: Putative 3       97       E  I  P  A  G  L  V  L  G  S  E  Q  V  S  F  E  K  L  S  C
Query                 1254     AAATTCCAGCAGGTCTTGTGCTTGGCTCGGAGCAAGTCTCTTTTGAGAAGCTCTCTTGTC  1313
                               | |||||||| |||||||| ||||||||  |||| || ||||| ||  |||| |||||||
Sbjct                 2525746  AGATTCCAGCTGGTCTTGTCCTTGGCTCTCAGCAGGTTTCTTTCGATCAGCTTTCTTGTC  2525687
CDS:cell division pr  97       E  I  P  A  G  L  V  L  G  S  Q  Q  V  S  F  D  Q  L  S  C

CDS: Putative 3       117      Q  S  P  K  V  I  S  F  P  F  S  S  A  L  V  F  P  Q  G  D
Query                 1314     AATCCCCAAAAGTCATCTCTTTCCCCTTCTCCAGCGCTCTTGTTTTTCCGCAAGGCGATG  1373
                               |    ||||| |||||| | ||||||||| | ||||| |||||||| ||||||||| |||
Sbjct                 2525686  ATGTTCCAAAGGTCATCCCATTCCCCTTCGCTAGCGCCCTTGTTTTGCCGCAAGGCAATG  2525627
CDS:cell division pr  117      H  V  P  K  V  I  P  F  P  F  A  S  A  L  V  L  P  Q  G  N

CDS: Putative 3       137      A  E  K  K  R  L  A  H  C  L  L  L  R  L  L  S  A  L  P  A
Query                 1374     CGGAGAAGAAAAGACTCGCGCATTGTCTCTTGTTGCGGTTGCTGTCGGCTTTGCCTGCAG  1433
                                 ||| | ||  | ||||| ||||| || ||||||||| |||||||||||||||  | |
Sbjct                 2525626  TAGAGCAAAAGCGGCTCGCACATTGCCTTTTGTTGCGGCTGCTGTCGGCTTTGCCGCCGG  2525567
CDS:cell division pr  137      V  E  Q  K  R  L  A  H  C  L  L  L  R  L  L  S  A  L  P  P

CDS: Putative 3       157      G  Q  V  E  L  T  L  I  D  P  L  Q  Q  G  Q  S  V  E  P  F
Query                 1434     GTCAAGTAGAGTTGACACTGATTGACCCCCTACAGCAGGGTCAATCGGTCGAGCCGTTCC  1493
                               | |||||||||||||||||||||| || || || | ||| |||||||||||||||||||
Sbjct                 2525566  GACAAGTAGAGTTGACACTGATTGATCCACTGCAACTGGGGCAATCGGTCGAGCCGTTCC  2525507
CDS:cell division pr  157      G  Q  V  E  L  T  L  I  D  P  L  Q  L  G  Q  S  V  E  P  F

CDS: Putative 3       177      L  P  L  L  K  V  E  Q  L  V  P  Q  G  H  V  L  T  R  A  D
Query                 1494     TACCATTGCTGAAGGTTGAGCAATTGGTGCCGCAAGGTCATGTTCTTACTCGTGCGGACG  1553
                               ||||  |||||||||| |||||||||||||||||||||||||||||| |||||  |||| |
Sbjct                 2525506  TACCTCTGCTGAAGGTAGAGCAATTGGTGCCGCAAGGTCATGTTCTCACTCGCTCGGATG  2525447
CDS:cell division pr  177      L  P  L  L  K  V  E  Q  L  V  P  Q  G  H  V  L  T  R  S  D

CDS: Putative 3       197      E  I  E  A  A  L  G  Q  L  T  D  E  I  E  E  L  I  Q  L  R
Query                 1554     AAATCGAAGCAGCGCTCGGACAACTGACGGACGAAATTGAGGAGCTGATCCAGCTGCGGT  1613
                               | ||||| |  ||||||||  |||||||||||||  |||||||| | |||||||  ||||
Sbjct                 2525446  AGATCGAGGGCGCGCTCGGCAAACTGACGGACGAGGTTGAGGAGATCATCCAGCACCGGT  2525387
CDS:cell division pr  197      E  I  E  G  A  L  G  K  L  T  D  E  V  E  E  I  I  Q  H  R

CDS: Putative 3       217      F  N  E  K  A  S  N  W  L  K  Y  N  A  V  Q   P  D  A  P  L
Query                 1614     TCAATGAGAAGGCATCCAACTGGTTGAAATACAACGCAGTTCAAC-CCGATGCCCCGTTG  1672
                               ||||||| ||| ||||||| ||||     |||||||| | ||||| |||| ||||| |||
Sbjct                 2525386  TCAATGACAAGTCATCCAATTGGTCAGGCTACAACGC-GATCAACGCCGACGCCCCCTTG  2525328
CDS:cell division pr  217      F  N  D  K  S  S  N  W  S  G  Y  N  A   I  N  A  D  A  P  L

CDS: Putative 3       237       P  Y  K  V  V  L  L  F  D  V  P  E  Q  I  S  E   K  S  L  W
Query                 1673     CCTTACAAGGTAGTACTGCTCTTTGATGTGCCAGAGCAGATATCGGA-AAAATCTCTTTG  1731
                                |||||||||| ||  |||| |||||||||||||||| || || || |||| | || ||
Sbjct                 2525327  ACTTACAAGGTTGTGGTGCTTTTTGATGTGCCAGAGCAAATCTCCGACAAAAGC-CTCTG  2525269
CDS:cell division pr  237       T  Y  K  V  V  V  L  F  D  V  P  E  Q  I  S  D  K  S   L  W
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CDS: Putative 3       257        L  L  G  R  I  C  E  N  G  P  R  C  G  V  L  P  I  I  A  I
Query                 1732     GCTCCTTGGACGCATCTGCGAAAACGGTCCACGCTGCGGCGTGCTGCCCATCATTGCAAT  1791
                               | ||||||| ||  | ||||| ||||| ||||| ||||| ||||||||| ||||||||||
Sbjct                 2525268  GTTCCTTGGGCGGCTTTGCGAGAACGGCCCACGATGCGGTGTGCTGCCCGTCATTGCAAT  2525209
CDS:cell division pr  257        F  L  G  R  L  C  E  N  G  P  R  C  G  V  L  P  V  I  A  I

CDS: Putative 3       277        D  E  Q  R  M  E  D  R  R  Y  E  K  L  N  A  T  L  K  N  S
Query                 1792     TGATGAGCAGCGCATGGAAGACCGGCGATATGAAAAGCTCAACGCCACGCTGAAAAACTC  1851
                               ||||| ||| |||||||| ||  ||||||| || ||| |       |  |||| |||  ||
Sbjct                 2525208  TGATGGGCAACGCATGGACGAGAGGCGATACGAGAAGTTTGGTTGCGTGCTGGAAACTTC  2525149
CDS:cell division pr  277        D  G  Q  R  M  D  E  R  R  Y  E  K  F  G  C  V  L  E  T  S

CDS: Putative 3       297        T  T  Q  L   N  D  L  L  Q  R  A  G  A  G  G  L  S  F  T
Query                 1852     AACCACGCAACT-GA-ATGATCTCTTGCAACGCGCTGGGGCTGGTGGGCTGTCATTCACA  1909
                                 ||| ||  || || | | | | || || ||| | | | | || |  || || | ||||
Sbjct                 2525148  GGCCATGCGGCTTGATACGCTGT-TT-CAGCGCTCAGAGACAGGGGATCTTTCGTGCACA  2525091
CDS:cell division pr  297        A  M  R  L  D  T  L   F   Q  R  S  E  T  G  D  L  S  C  T

CDS: Putative 3       316       Y  Q  P  E  Q  W  P  R  Q  D  V  L  D  G  F  I  A  R  L  A
Query                 1910     TATCAACCGGAGCAATGGCCGCGACAAGATGTGCTGGATGGCTTTATCGCAAGGCTCGCT  1969
                               || || ||||| |||||||| ||||| |||||||||||  | ||||| |||| ||| ||
Sbjct                 2525090  TACCAGCCGGAACAATGGCCCCGACAGGATGTGCTGGACAGTTTTATGGCAACGCTTGCC  2525031
CDS:cell division pr  316       Y  Q  P  E  Q  W  P  R  Q  D  V  L  D  S  F  M  A  T  L  A

CDS: Putative 3       336       E  D  C  A  A  R  T  R  F  K  K  T  M  A  D  L  W  T  S  F
Query                 1970     GAAGATTGTGCTGCTAGGACGCGCTTCAAGAAAACGATGGCTGATCTCTGGACGAGCTTC  2029
                               ||  |||| ||||| | || ||||||||| ||||||||| | || |||||||| | ||||
Sbjct                 2525030  GAGCATTGCGCTGCAAAGAGGCGCTTCAAAAAAACGATGCCCGACCTCTGGACAAACTTC  2524971
CDS:cell division pr  336       E  H  C  A  A  K  R  R  F  K  K  T  M  P  D  L  W  T  N  F

CDS: Putative 3       356       G  K  E  E  T  T  L  G  G  F  D  I  P  I  G  W  T  S  A  G
Query                 2030     GGCAAGGAAGAGACGACTCTTGGTGGCTTTGATATTCCCATCGGCTGGACGAGCGCCGGC  2089
                                |||||  |||||||| |||||||| ||||||||||| | || |||||    || ||
Sbjct                 2524970  ACCAAGGGGGAGACGACACTTGGTGGTTTTGATATTCCCGTTGGATGGACTCCTGCTGGT  2524911
CDS:cell division pr  356       T  K  G  E  T  T  L  G  G  F  D  I  P  V  G  W  T  P  A  G

CDS: Putative 3       376       D  L  A  T  L  R  L  G  A  T  D  S  E  H  H  V  L  L  A  G
Query                 2090     GACCTCGCGACCCTGAGACTGGGCGCGACGGACTCCGAGCATCATGTACTGCTTGCGGGG  2149
                               ||  |  ||| |||  || |||| || || ||||| |||||||| ||  ||||||| ||
Sbjct                 2524910  GAGATTACGAACCTACGATTGGGTGCAACCGACTCAGAGCATCACGTTTTGCTTGCTGGC  2524851
CDS:cell division pr  376       E  I  T  N  L  R  L  G  A  T  D  S  E  H  H  V  L  L  A  G

CDS: Putative 3       396       K  T  G  S  G  K  S  N  L  L  H  V  L  I  H  T  L  C  E  K
Query                 2150     AAGACAGGCTCGGGAAAATCCAATCTGCTCCATGTTTTGATTCACACGTTATGCGAGAAA  2209
                               ||||| ||||| || |||||||||||||||||||| |||||||||  |  |||||||||||
Sbjct                 2524850  AAGACCGGCTCAGGTAAATCCAATCTGCTCCATGTCTTGATTCACTCACTATGCGAGAAA  2524791
CDS:cell division pr  396       K  T  G  S  G  K  S  N  L  L  H  V  L  I  H  S  L  C  E  K

CDS: Putative 3       416       Y  P  T  E  E  L  D  L  Y  L  L  D  Y  K  E  S  T  E  F  N
Query                 2210     TATCCGACCGAGGAGCTTGATCTTTATCTACTGGATTACAAGGAATCGACTGAGTTCAAT  2269
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                                || ||| |||| |||||||||||||||| |||||||||||||| ||||| |||||||||
Sbjct                  2524790  TACCCGCCCGAAGAGCTTGATCTTTATCTGCTGGATTACAAGGAGTCGACGGAGTTCAAT  2524731
CDS:cell division pr   416       Y  P  P  E  E  L  D  L  Y  L  L  D  Y  K  E  S  T  E  F  N

CDS: Putative 3        436       I  Y  A  T  P    P  V  P  Q  A  R  L  V  A  T  E  S  D  P
Query                  2270     ATTTACGCAACGCC-C-CCAGTCCCACAGGCCCGCCTTGTCGCTACGGAAAGTGACCCTG  2327
                                || || |||  ||| | ||| |||| || |||||  | |||||||||||||||| ||||
Sbjct                  2524730  ATCTATGCA--GCCTCGCCACTCCCGCATGCCCGTTTGGTCGCTACGGAAAGTGATCCTG  2524673
CDS:cell division pr   436       I  Y  A    A  S  P  L  P  H  A  R  L  V  A  T  E  S  D  P

CDS: Putative 3        455      E  Y  G  V  T  V  L  R  H  L  V  D  E  L  E  T  R  A  R  I
Query                  2328     AATATGGCGTCACTGTATTAAGGCATCTTGTGGATGAACTGGAAACGCGTGCACGCATAT  2387
                                |||| || ||||| ||| || |||||||||| |||||| | || | ||| |||||||| |
Sbjct                  2524672  AATACGGTGTCACGGTACTACGGCATCTTGTAGATGAATTAGAGAAGCGAGCACGCATCT  2524613
CDS:cell division pr   455      E  Y  G  V  T  V  L  R  H  L  V  D  E  L  E  K  R  A  R  I

CDS: Putative 3        475      F  K  S  K  N  V  N  D  F  S  E  Y  R  K  S  S  G  V  R  L
Query                  2388     TCAAGTCAAAAAATGTCAACGATTTCAGCGAATACCGTAAATCAAGCGGGGTACGGTTGC  2447
                                |||||||    | || |   ||||||  |||||| || ||  |||||||||| | ||| |
Sbjct                  2524612  TCAAGTCCTCGAGTGCCCGAGATTTCGCCGAATATCGCAATGCAAGCGGGGTGCAGTTAC  2524553
CDS:cell division pr   475      F  K  S  S  S  A  R  D  F  A  E  Y  R  N  A  S  G  V  Q  L

CDS: Putative 3        495      P  R  A  L  L  V  I  D  E  F  Q  I  L  F  S  E  S  R  Q  V
Query                  2448     CCCGCGCTCTGCTAGTCATAGATGAGTTCCAAATTCTGTTCTCAGAAAGTCGCCAGGTGG  2507
                                |||||| |||| | |||||||||||||||||  ||||||| |||||| | ||||| || |
Sbjct                  2524552  CCCGCGTTCTGTTGGTCATAGATGAGTTCCAGGTTCTGTTTTCAGAAGGCCGCCAAGTAG  2524493
CDS:cell division pr   495      P  R  V  L  L  V  I  D  E  F  Q  V  L  F  S  E  G  R  Q  V

CDS: Putative 3        515      A  E  A  A  E  Q  L  L  S  K  L  L  K  Q  G  R  S  F  G  I
Query                  2508     CAGAAGCTGCTGAGCAGCTGCTGTCGAAGCTCTTGAAACAGGGGCGCTCGTTCGGTATTC  2567
                                | ||| | |||||||||||||| ||| | ||||||||||||||||| || || || ||||
Sbjct                  2524492  CCGAAACCGCTGAGCAGCTGCTCTCGCAACTCTTGAAACAGGGGCGTTCATTTGGCATTC  2524433
CDS:cell division pr   515      A  E  T  A  E  Q  L  L  S  Q  L  L  K  Q  G  R  S  F  G  I

CDS: Putative 3        535      H  I  L  L  A  T  Q  T  L  K  G  I  N  A  Q  S  I  G  S  I
Query                  2568     ACATCCTCCTGGCTACTCAGACTTTGAAAGGCATCAACGCGCAGTCAATCGGAAGCATCA  2627
                                ||||||| ||||| || |||||  ||||||| || || ||||| || |||||||||||||
Sbjct                  2524432  ACATCCTTCTGGCAACACAGACACTGAAAGGTATTAATGCGCAATCCATCGGAAGCATCA  2524373
CDS:cell division pr   535      H  I  L  L  A  T  Q  T  L  K  G  I  N  A  Q  S  I  G  S  I

CDS: Putative 3        555      I  T  Q  L  G  C  R  I  A  L  A  C  G  Q  E  D  S  A  M  I
Query                  2628     TCACCCAGTTGGGATGCCGTATCGCACTGGCTTGTGGGCAGGAAGACTCCGCAATGATCC  2687
                                | |||||||||||||||||||||||| ||||| |||||||| ||||| |||||| ||||||
Sbjct                  2524372  TTACCCAGTTGGGATGCCGTATCGCGCTGGCCTGTGGGCAAGAAGATTCCGCACTGATCC  2524313
CDS:cell division pr   555      I  T  Q  L  G  C  R  I  A  L  A  C  G  Q  E  D  S  A  L  I

CDS: Putative 3        575      L  G  G  G  N  W  A  A  A  E  L  R  S  P  P  E  G  I  I  N
Query                  2688     TCGGGGGCGGGAACTGGGCAGCCGCAGAGCTGCGCAGCCCACCTGAAGGCATCATCAACA  2747
                                | || ||||| |||||||| || || || || |||||||||||||| ||||| |||||||
Sbjct                  2524312  TGGGCGGCGGCAACTGGGCTGCGGCTGAACTTCGCAGCCCACCTGAGGGCATTATCAACA  2524253
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CDS:cell division pr  575      L  G  G  G  N  W  A  A  A  E  L  R  S  P  P  E  G  I  I  N

CDS: Putative 3       595      N  A  N  G  A  K  S  G  N  V  K  F  M  I  P  F  A  G  E  S
Query                 2748     ATGCTAACGGTGCCAAATCCGGCAATGTGAAGTTCATGATTCCATTCGCCGGAGAAAGCG  2807
                               | || |||||||||||||||||||||||||||||||||||| ||||| ||||||||||| |
Sbjct                 2524252  ACGCCAACGGTGCCAAATCCGGCAATGTGAAGTTCATGATCCCATTTGCCGGAGAAAGTG  2524193
CDS:cell division pr  595      N  A  N  G  A  K  S  G  N  V  K  F  M  I  P  F  A  G  E  S

CDS: Putative 3       615      E  H  R  R  D  L  L  T  K  L  I  A  R  T  S  L  S  G  V  A
Query                 2808     AGCATCGACGTGATTTGTTGACGAAGTTGATAGCGCGTACATCTCTTTCTGGGGTGGCTG  2867
                               | ||||| || || ||| | |||||| |||||| ||||| ||| ||||  ||||   | |
Sbjct                 2524192  AACATCGGCGAGAGTTGCTTACGAAGCTGATAGAGCGTAAATCACTTTTCGGGGCTACCG  2524133
CDS:cell division pr  615      E  H  R  R  E  L  L  T  K  L  I  E  R  K  S  L  F  G  A  T

CDS: Putative 3       635      E  K  T  K  I  F  S  G  A  F  L  P   Q  I  P  S  P  F  E  Y
Query                 2868     AAAAAACCAAAATCTTCAGCGGTGCATTCCTTCC-GCAGATACCGTCTCCCTTTGAATAT  2926
                                 ||||| ||||| |||||||| |||| ||| || || ||| |||||| | | |||||||
Sbjct                 2524132  CCAAAACGAAAATTTTCAGCGGAGCATCCCTCCCTGC-GATGCCGTCTTCTTCTGAATAT  2524074
CDS:cell division pr  635      A  K  T  K  I  F  S  G  A  S  L  P  A   M  P  S  S  S  E  Y

CDS: Putative 3       655       Q  T  A  C  A  H  E  E   A  L  L  L  G  E  N  L  A  F  D
Query                 2927     CAGACAGCTTGTGCGCACGAAGA-AG-CTCTTCTTTTGGGCGAAAACCTCGCATTCGATT  2984
                               |||| ||||||  ||||| ||   || ||||||||||||| ||    ||| |||||||
Sbjct                 2524073  CAGATAGCTTG--CGCACAAAATCAGGCTCTTCTTTTGGGTGAGCGACTCACATTCGAAG  2524016
CDS:cell division pr  655       Q  I  A  C   A  Q  N  Q  A  L  L  L  G  E  R  L  T  F  E

CDS: Putative 3       674      S  K  P   L  T  V  P  L  T  R  R  S  A  F  N  V  L  F  S  G
Query                 2985     CAAAACCGT--TGACGGTACCACTTACTCGTCGATCCGCGTTCAATGTTCTATTCAGCGG  3042
                               |  | | ||  | ||  | || |||||||| ||  | || |||||||||||  |||||||
Sbjct                 2524015  CCGA-C-GTGCTAACTATCCCGCTTACTCGCCGCACTGCATTCAATGTTCTTCTCAGCGG  2523958
CDS:cell division pr  674      A  D   V  L  T  I  P  L  T  R  R  T  A  F  N  V  L  L  S  G

CDS: Putative 3       694        Y  N  D  H  I  H  D  G  L  L  S  A  T  L  F  S  L  T  F  V
Query                 3043     CTACAACGACCACATTCACGATGGACTCCTGTCCGCTACGCTTTTTAGTCTGACTTTCGT  3102
                                |||||||| || |||||||| ||||| ||| | ||||  ||||  ||| || ||| |
Sbjct                 2523957  TTACAACGATCAAATTCACGACGGACTGCTGGCAGCTATCCTTTCAAGTATGGCTTACCA  2523898
CDS:cell division pr  694        Y  N  D  Q  I  H  D  G  L  L  A  A  I  L  S  S  M  A  Y  H

CDS: Putative 3       714        D   G   F  D  E  I  V  Y  F  N  A  R  G  V  P   P  G  G
Query                 3103     CGATG--G-CTTTGATGAAATCGTGTACTTCAACGCGCGCGGGGTCCC-CCCAGGAGGAG  3158
                               || ||  | |||||| ||| |||| || ||||||||||| || ||||| ||| |  || |
Sbjct                 2523897  CGCTGACGGCTTTGACGAAGTCGTATATTTCAACGCGCGTGGAGTCCCTCCCTGTGGG-G  2523839
CDS:cell division pr  714        A  D  G  F  D  E  V  V  Y  F  N  A  R  G  V  P  P  C  G

CDS: Putative 3       732      G  F  S  A  A  A  Q  M  L  G  A  R  L  K  M  F  D  D  I  S
Query                 3159     GATTCTCAGCCGCAGCGCAGATGCTCGGTGCACGCCTCAAGATGTTCGACGATATATCCG  3218
                               |||||||  |  || |||||   |||||||||||| ||| ||| ||||||||||| |||
Sbjct                 2523838  GATTCTCCACATCATCGCAGGCCCTCGGTGCACGCTTCAGGATCTTCGACGATATTTCCA  2523779
CDS:cell division pr  733      G  F  S  T  S  S  Q  A  L  G  A  R  F  R  I  F  D  D  I  S
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CDS: Putative 3       752      D  L  P  L  Q  A  I  S  D  D  I  G  N  R  R  V  A  L  I  I
Query                 3219     ATCTACCACTTCAAGCGATATCAGACGATATTGGGAATCGCCGCGTAGCATTGATTATCG  3278
                                ||| ||  | || ||||||||||||||||||||   |||||| | ||  |||| ||||
Sbjct                 2523778  CTCTGCCGTTACAGGCGATATCAGACGATATTGGGTCCCGCCGCATCGCGCTGATCATCG  2523719
CDS:cell division pr  753      T  L  P  L  Q  A  I  S  D  D  I  G  S  R  R  I  A  L  I  I

CDS: Putative 3       772      D  G  L  D  S  E  K  A  L  Q  P  A  P  A  F  R  S  L  K  P
Query                 3279     ATGGCCTGGATTCCGAGAAAGCACTACAGCCAGCCCCAGCGTTTAGATCGCTCAAGCCTG  3338
                               | || || || |||||||||| |||||| ||| || | |||||||||||| | ||||||||
Sbjct                 2523718  ACGGTCTTGACTCCGAGAAAGTACTACATCCAACCGCTGCGTTTAGATCCCCCAAGCCTG  2523659
CDS:cell division pr  773      D  G  L  D  S  E  K  V  L  H  P  T  A  A  F  R  S  P  K  P

CDS: Putative 3       792      G  E  P  P  T  P  A  D  L  L  K  R  L  A  E  D  G  P  R  K
Query                 3339     GCGAACCACCTACCCCGGCTGACTTGTTAAAGCGTCTCGCCGAGGACGGCCCAAGAAAGG  3398
                               ||||||||||  | ||||||||| |||||||| ||||||| || || |||||  | || |
Sbjct                 2523658  GCGAACCACCATCTCCGGCTGACCTGTTAAAGTGTCTCGCAGAAGAAGGCCCGCGGAAAG  2523599
CDS:cell division pr  793      G  E  P  P  S  P  A  D  L  L  K  C  L  A  E  E  G  P  R  K

CDS: Putative 3       812      G  T  F  V  F  I  F  V  D  R  W  Q  R  C  A  S  A  S  K  D
Query                 3399     GGACGTTTGTATTTATTTTTGTTGACCGTTGGCAGCGCTGTGCCAGTGCCAGCAAAGACC  3458
                               |||| |||||||||   |||||||||||| |||||||||||||| || ||  | ||||| |
Sbjct                 2523598  GGACATTTGTATTTGCCTTTGTTGACCGATGGCAGCGCTGTGCTAGCGCATGTAAAGATC  2523539
CDS:cell division pr  813      G  T  F  V  F  A  F  V  D  R  W  Q  R  C  A  S  A  C  K  D

CDS: Putative 3       832      L  F  S  F  F  E  L  R  V  A  Y  C  M  N  E  D  D  A  G  S
Query                 3459     TTTTCTCCTTTTTCGAATTGCGCGTGGCGTACTGCATGAACGAAGACGATGCCGGATCGC  3518
                               |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||| |
Sbjct                 2523538  TTTTCTCCTTTTTCGAATTGCGCGTGGCGTATTGCATGAACGAAGACGATGCCGGATCAC  2523479
CDS:cell division pr  833      L  F  S  F  F  E  L  R  V  A  Y  C  M  N  E  D  D  A  G  S

CDS: Putative 3       852      L  V  S  G  G  V  G  K  F  K  G  I  E  K  P  S  R  A  V  F
Query                 3519     TTGTGAGTGGCGGTGTTGGTAAGTTCAAAGGTATTGAAAAACCGAGCCGAGCTGTATTCG  3578
                               | |||||||| ||  |||| ||||||||||| ||||||||||||| |||||||||||||
Sbjct                 2523478  TAGTGAGTGGTGGCATTGGCAAGTTCAAAGGCATTGAAAAACCGAACCGAGCTGTATTCG  2523419
CDS:cell division pr  853      L  V  S  G  G  I  G  K  F  K  G  I  E  K  P  N  R  A  V  F

CDS: Putative 3       872      V  N  K  M  T  N  D   I  T  W  F  R  P  Y  V  Q  E  S  T  R
Query                 3579     TAAACAAAATGACGAATGACA-TCACATGGTTCCGGCCATATGTTCAGGAAAGCACTCGA  3637
                               ||||||| ||||||||||||  | | ||||||| | ||||||||||| ||||||||||||
Sbjct                 2523418  TAAACAAGATGACGAATGACCGTGA-ATGGTTCTGCCCATATGTTCAAGAAAGCACTCGA  2523360
CDS:cell division pr  873      V  N  K  M  T  N  D  R  E   W  F  C  P  Y  V  Q  E  S  T  R

CDS: Putative 3                *
CDS: Putative 2       1        M  K  R  F  L  L  T  W  Y  G  I  T  D  F  R  A  S  L  G  F
Query                 3638     TGAAGAGATTTCTGCTCACCTGGTATGGAATCACCGATTTTCGCGCATCTCTGGGGTTTG  3697
                               |||||| ||||||||||||  ||||| |||||||| ||||| ||||||||| |||| || |
Sbjct                 2523359  TGAAGAAATTTCTGCTCACATGGTACGGAATCACGGATTTCCGCGCATCTTTGGGATTCG  2523300
CDS:hypothetical pro  1        M  K  K  F  L  L  T  W  Y  G  I  T  D  F  R  A  S  L  G  F

CDS: Putative 2       21       E  N  T  D  G  P  I  A  S  A  L  A  G  A  S  Y  S  D  I  I
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Query                  3698     AGAATACCGATGGCCCTATTGCGAGCGCCCTTGCGGGCGCGTCCTACTCGGACATCATTA  3757
                                ||||| |||||||||| || || || ||| | ||||| | ||| ||||| ||  || |||
Sbjct                  2523299  AGAATGCCGATGGCCCCATCGCAAGTGCCATCGCGGGGGGGTCTTACTCAGATGTCGTTA  2523240
CDS:hypothetical pro   21       E  N  A  D  G  P  I  A  S  A  I  A  G  G  S  Y  S  D  V  V

CDS: Putative 2        41       I  L  G  Y  T  R  T  D  N  D  A  S  E  L  I  E  A  Q  K  T
Query                  3758     TCCTGGGTTACACCCGGACGGATAATGATGCCAGCGAATTGATCGAGGCACAGAAGACGT  3817
                                || |||||||||||||| | ||||||||| ||| |||||  |||||||  |||||||| |
Sbjct                  2523239  TCTTGGGTTACACCCGGGCCGATAATGATTCCAACGAATCTATCGAGGTTCAGAAGACAT  2523180
CDS:hypothetical pro   41       I  L  G  Y  T  R  A  D  N  D  S  N  E  S  I  E  V  Q  K  T

CDS: Putative 2        61       F  T  L  E  L  A  S  I  R  S  M  G  Q  E  K  D  W  K  L  T
Query                  3818     TCACGCTTGAATTGGCGTCAATACGAAGCATGGGGCAAGAGAAAGACTGGAAGCTTACTA  3877
                                |  |||| |||||||| || || || | || ||| |||||||||||  |||||  ||||||
Sbjct                  2523179  TTGCGCTCGAATTGGCCTCTATTCGGAACACGGGTCAAGAGAAAGATTGGAAAGTTACTA  2523120
CDS:hypothetical pro   61       F  A  L  E  L  A  S  I  R  N  T  G  Q  E  K  D  W  K  V  T

CDS: Putative 2        81       N  Q  F  V  S  R  F  A  N  T  S  V  A  H  E  H  F  E  A  W
Query                  3878     ATCAGTTTGTCTCCAGGTTCGCTAATACCTCTGTCGCACATGAACATTTTGAAGCCTGGC  3937
                                 ||||||||| || ||||| || |||||| | ||||| || |||||||| || |  ||||
Sbjct                  2523119  GTCAGTTTGTATCTAGGTTTGCCAATACCGCCGTCGCCCACGAACATTTCGAGGTTTGGC  2523060
CDS:hypothetical pro   81       S  Q  F  V  S  R  F  A  N  T  A  V  A  H  E  H  F  E  V  W

CDS: Putative 2        101      L  K  K  K  A  A  A  L  G  C  N  A   R   I  R  L  N  S  E  K
Query                  3938     TGAAAAAGAAAGCCGCCGCCCTGGGCTGCAACGC-AAGG-ATCCGTTTAAATAGCGAGAA  3995
                                |||| || |||| |||     | ||| ||   || |||  || | || |||  | || ||
Sbjct                  2523059  TGAAGAATAAAGTCGCAAGAATAGGCAGCGCTGCGAAGATATTC-TTCAAAG-GTGAAAA  2523002
CDS:hypothetical pro   101      L  K  N  K  V  A  R  I  G  S  A  A  K  I  F   F  K   G  E  K

CDS: Putative 2        121        L  Y  Q  L  N  D  T  E  G  I  Y  A  S  A  M  R  A  L  D  G
Query                  3996     ACTTTACCAGCTCAACGACACCGAAGGTATTTACGCTAGCGCAATGCGGGCGCTGGATGG  4055
                                ||||    | ||||||||||||||| ||||| |||  ||||||||| ||| ||||| |
Sbjct                  2523001  ACTTCGTGAACTCAACGACACCGAAGGAATTTATGCTGCCGCAATGCGTGCGTTGGATTG  2522942
CDS:hypothetical pro   121        L  R  E  L  N  D  T  E  G  I  Y  A  A  A  M  R  A  L  D  C

CDS: Putative 2        141        V  E  Q  E  P  G  E  K  L  V  T  L  Y  L  S  P  G  T  P  V
Query                  4056     GGTTGAACAGGAGCCAGGTGAAAAGCTCGTCACGCTCTATCTCAGCCCAGGAACTCCGGT  4115
                                 || || | ||| || ||||||||| | ||||| || |||||||| || |||||||||||
Sbjct                  2522941  TGTGGAGCGGGAACCTGGTGAAAAGTTAGTCACTCTTTATCTCAGTCCGGGAACTCCGGT  2522882
CDS:hypothetical pro   141        V  E  R  E  P  G  E  K  L  V  T  L  Y  L  S  P  G  T  P  V

CDS: Putative 2        161        M  A  F  V  W  A  L  A  A  L  S  Y  P  E  L  K  K  R  L  I
Query                  4116     GATGGCCTTTGTCTGGGCGCTCGCGGCGCTGAGCTACCCTGAACTCaaaaaaaGACTCAT  4175
                                |||||| ||||| |||||||| || ||  ||||||| |||||||||||||| | |||||
Sbjct                  2522881  GATGGCTTTTGTATGGGCGCTTGCAGCTTTGAGCTATCCTGAACTCAAAAAACGGCTCAT  2522822
CDS:hypothetical pro   161        M  A  F  V  W  A  L  A  A  L  S  Y  P  E  L  K  K  R  L  I

CDS: Putative 2        181        A  S  S  I  I  G  K  A  P  E  V  I  A  L  P  A  E  W  L  E
Query                  4176     AGCATCGTCCATCATTGGCAAAGCACCTGAAGTCATAGCGTTGCCTGCCGAGTGGCTTGA  4235
                                 ||||||||| || || |||| || ||||| |  ||| |||||||||||||||||||  |
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Sbjct                  2522821  TGCATCGTCCGTCGTTAGCAAGGCTCCTGAGGCTATATCGTTGCCTGCCGAGTGGCTCAA  2522762
CDS:hypothetical pro   181        A  S  S  V  V  S  K  A  P  E  A  I  S  L  P  A  E  W  L  K

CDS: Putative 2        201        R  H  S  S  K  Q  A  A  I  R  D  I  S  N  G  F  D  V  T  F
Query                  4236     GCGACACAGCTCAAAACAGGCTGCGATCCGAGACATCTCCAACGGGTTCGATGTGACATT  4295
                                | |||||||| | ||||||| ||||||||||||||||| ||||||| || |||||||| ||
Sbjct                  2522761  GAGACACAGCGCGAAACAGGATGCGATCCGAGACATCCCCAACGGATTTGATGTGACCTT  2522702
CDS:hypothetical pro   201        R  H  S  A  K  Q  D  A  I  R  D  I  P  N  G  F  D  V  T  F

CDS: Putative 2        221        H  L  F  G  E  Q  R  M  P  A  L  L  S  I  R  Q  F  E  S  A
Query                  4296     CCATCTTTTTGGTGAACAACGGATGCCTGCCTTGTTGAGCATCCGGCAATTTGAGTCGGC  4355
                                ||||||||||||||| ||||||||||| || ||| | |||||||| ||||||||||||
Sbjct                  2522701  CCATCTTTTTGGTGAGCAACGGATGCCAGCTTTGCTCAGCATCCGACAATTTGAGTCGGA  2522642
CDS:hypothetical pro   221        H  L  F  G  E  Q  R  M  P  A  L  L  S  I  R  Q  F  E  S  E

CDS: Putative 2        241        H  H  I  F  V  N  S  K  D  F  P  A  A  C  M  R  T  F  I  G
Query                  4356     GCATCACATTTTTGTCAACTCAAAAGACTTCCCTGCTGCATGTATGCGAACCTTTATTGG  4415
                                ||||||||||||  || ||||||||||||| ||| ||| ||||||||||| | ||  ||||
Sbjct                  2522641  GCATCACATTTTCGTTAACTCAAAAGACTACCCGGCTACATGTATGCGAGCGTTCCTTGG  2522582
CDS:hypothetical pro   241        H  H  I  F  V  N  S  K  D  Y  P  A  T  C  M  R  A  F  L  G

CDS: Putative 2        261        S  R  D  L  H  E  L  T  V  D  P  W  D  D  R  A  V  H  E  Q
Query                  4416     CTCTCGGGACCTGCATGAACTTACCGTTGACCCCTGGGATGATCGTGCTGTTCACGAACA  4475
                                ||||||  || ||||| |||||| |||||||||| |||||||||||||||||  || |  |
Sbjct                  2522581  CTCTCGCGATCTGCACGAACTTTCCGTTGACCCTTGGGATGATCGTGCTGTCCATGTGCG  2522522
CDS:hypothetical pro   261        S  R  D  L  H  E  L  S  V  D  P  W  D  D  R  A  V  H  V  R

CDS: Putative 2        281        I  T  K  L  A  K  Q  F  P  E  K  T  R  I  G  I  N  L  T  G
Query                  4476     AATCACCAAGCTGGCAAAGCAATTTCCAGAAAAAAACACGAATTGGAATCAATTTAACTGG  4535
                                 ||  |  |||| || || ||||||||||| ||||| || || || |||||| | |||||
Sbjct                  2522521  GATTGCAGAGCTTGCCAAACAATTTCCAGAGAAAACGCGCATCGGCATCAATCTGACTGG  2522462
CDS:hypothetical pro   281        I  A  E  L  A  K  Q  F  P  E  K  T  R  I  G  I  N  L  T  G

CDS: Putative 2        301        G  T  K  L  M  F  A  G  A  L  S  A  A  R  E  L  G  A  V  P
Query                  4536     CGGCACAAAACTGATGTTTGCTGGCGCGCTCTCTGCTGCGCGTGAACTGGGCGCTGTTCC  4595
                                ||| |||||| | |||||||| ||||| |||||||| ||||| || || || || |||||
Sbjct                  2522461  CGGAACAAAATTAATGTTTGCAGGCGCACTCTCTGCCGCGCGCGAGCTTGGTGCCGTTCC  2522402
CDS:hypothetical pro   301        G  T  K  L  M  F  A  G  A  L  S  A  A  R  E  L  G  A  V  P

CDS: Putative 2        321        F  Y  F  D  S  K  N  R  H  V  T  F  I  D  S  V  R  R  E  K
Query                  4596     GTTTTATTTTGATAGCAAGAATCGTCACGTCACATTCATTGACAGTGTTCGGCGCGAAAA  4655
                                 |||||||||||||||||||||||||  || || ||  |||| ||| |||||||||||||
Sbjct                  2522401  ATTTTATTTTGATAGCAAGAATCGTCGGGTAACCTTTGTTGATAGTCTTCGGCGCGAAAA  2522342
CDS:hypothetical pro   321        F  Y  F  D  S  K  N  R  R  V  T  F  V  D  S  L  R  R  E  K

CDS: Putative 2        341        I  R  Q  I  D  S  I  E  T  F  L  R  L  N  S  D  G  L  E  I
Query                  4656     AATCAGGCAGATTGATTCAATCGAAACATTTTTGCGCCTGAATAGCGACGGATTGGAGAT  4715
                                ||||||||| |||||||| |||||||| ||||| || || |||||||| ||||||||| |
Sbjct                  2522341  AATCAGGCAAATTGATTCGATCGAAACCTTTTTACGTCTCAATAGCGATGGATTGGAGTT  2522282
CDS:hypothetical pro   341        I  R  Q  I  D  S  I  E  T  F  L  R  L  N  S  D  G  L  E  F
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CDS: Putative 2       361        A  G   S  S  F  M  K  D  I  S  P  S  R  Q  L  L  T  K  A
Query                 4716     TGCAGGC-AGTTCCTTTATGAAGGATATATCGCCAAGTCGCCAACTTCTGACCAAGGCTC  4774
                               | | | | |   ||   ||||| || ||||||||    || ||| | ||||||||  |||
Sbjct                 2522281  TTCTGACGACG-CCGCGATGAATGAGATATCGCCGGACCGTCAATTCCTGACCAATACTC  2522223
CDS:hypothetical pro  361        S  D  D   A  A  M  N  E  I  S  P  D  R  Q  F  L  T  N  T

CDS: Putative 2       380      L  W  L  H  R  D  K  V  R  R  F  Y  R  E  L  T  D  Y  N  N
Query                 4775     TTTGGTTGCATCGTGACAAGGTGCGTAGATTTTATAGAGAACTTACCGACTATAACAATG  4834
                               | ||| | ||||||||||| |||| || || || | |||||| || |||||||||||||
Sbjct                 2522222  TCTGGGTACATCGTGACAAGATGCGCAGGTTCTACAAAGAACTGACAGACTATAACAATG  2522163
CDS:hypothetical pro  380      L  W  V  H  R  D  K  M  R  R  F  Y  K  E  L  T  D  Y  N  N

CDS: Putative 2       400      A  F  R  P  F  E  I  C  R  D  G  F  N  F  K  L  D  D  M   E
Query                 4835     CATTCAGGCCATTCGAGATTTGTCGTGACGGCTTCAATTTCAAGCTGGATGACATG--GA  4892
                               | ||||  |||||||| || |||||||| |||||  |||||||||||||  | |||  ||
Sbjct                 2522162  CGTTCAAACCATTCGAAATATGTCGTGATGGCTTTCATTTCAAGCTGGAC-A-ATGCTGA  2522105
CDS:hypothetical pro  400      A  F  K  P  F  E  I  C  R  D  G  F  H  F  K  L  D   N  A  E

CDS: Putative 2       420        A  V  S  V  Q  G  Y  G  L  D  L  R   F  E  K  W  P  D  F
Query                 4893     GGCAGTATCCGTCCAGGGCTACGGATTGGATCTGAGA-TTTGAGAAATGGCCTGATTTCG  4951
                               |  || | |  |||| ||||||||| ||||||| ||  ||||| || |||||||||||||
Sbjct                 2522104  GAGAGCAACAATCCAAGGCTACGGACTGGATCT-AGCCTTTGAAAACTGGCCTGATTTCG  2522046
CDS:hypothetical pro  420        R  A  T  I  Q  G  Y  G  L  D  L   A  F  E  N  W  P  D  F

CDS: Putative 2       439      A  K  Y  L  S  G  G  W  F  E  E  F  V  Y  L  Q  C  E  P  Y
Query                 4952     CCAAATACCTATCTGGCGGCTGGTTCGAGGAGTTTGTTTATTTGCAGTGCGAACCCTACG  5011
                               ||||||||||||| |||||||||||||||||| ||||| |||||||| ||| | |||||||
Sbjct                 2522045  CCAAATACCTATCCGGCGGCTGGTTCGAGGAATTTGTCTATTTGCAATGCAAGCCCTACG  2521986
CDS:hypothetical pro  439      A  K  Y  L  S  G  G  W  F  E  E  F  V  Y  L  Q  C  K  P  Y

CDS: Putative 2       459      E  D  A  G  V  I  Q  D  L  R  I  N  V  K  L  N  L  N  L  E
Query                 5012     AGGATGCTGGCGTCATTCAAGACTTGCGCATCAATGTCAAGCTGAACTTGAATTTAGAA-  5070
                               | ||| |||||||||| |||||||||||||||||||||||||||||||| ||||   ||||
Sbjct                 2521985  AAGATACTGGCGTCATCCAAGACTTGCGCATCAATGTCAAGCTGAACCTGAAGCAAGAAA  2521926
CDS:hypothetical pro  459      E  D  T  G  V  I  Q  D  L  R  I  N  V  K  L  N  L  K  Q  E

CDS: Putative 2       479       E  S  K  G  Y  S  S  F  G   V  E  Y  N  E  L  D  I  T  F  T
Query                 5071     GAGTCAAAAGGCTATTCGAGCTTCGGT-GTTGAATACAACGAGCTGGACATCACATTCAC  5129
                               | | |   |  | |||||| ||| ||  || ||||||||||| ||||| |||||||||||
Sbjct                 2521925  GCGCCTGGAATC-ATTCGA-CTTGGGGCGTCGAATACAACGAACTGGATATCACATTCAC  2521868
CDS:hypothetical pro  479      S  A  W  N   H  S   T  W  G  V  E  Y  N  E  L  D  I  T  F  T

CDS: Putative 2       499        D  G  Y  S  L  Y  I  V  E  C  K  A  G  N  V  T  Q  E  Q  I
Query                 5130     CGACGGTTATTCGCTTTATATCGTGGAATGCAAGGCGGGCAATGTAACGCAAGAGCAGAT  5189
                               |||||| || |||||||| |||||||||||||||||| |||||||||||||| || ||  |
Sbjct                 2521867  CGACGGCTACTCGCTTTACATCGTGGAATGCAAGGCAGGCAATGTAACGCAGGAACAAGT  2521808
CDS:hypothetical pro  499        D  G  Y  S  L  Y  I  V  E  C  K  A  G  N  V  T  Q  E  Q  V

CDS: Putative 2       519        M  K  L  Q  N  L  V  R  F  Y  G  G  I  E  G  R  G  I  V  A
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Query                  5190     TATGAAGCTGCAGAACCTTGTGCGCTTCTACGGAGGAATTGAAGGTCGCGGTATCGTTGC  5249
                                 ||||| ||||| ||||||||||||||||| ||||||||||||||||| || ||||| ||
Sbjct                  2521807  CATGAAACTGCAAAACCTTGTGCGCTTCTATGGAGGAATTGAAGGTCGTGGCATCGTCGC  2521748
CDS:hypothetical pro   519        M  K  L  Q  N  L  V  R  F  Y  G  G  I  E  G  R  G  I  V  A

CDS: Putative 2        539        C  C  V  P  P  N  T  E  S  A  K  K  K  I  K  D  A  R  L  M
Query                  5250     CTGCTGTGTTCCGCCAAATACTGAGTCGGCCAAGaaaaaaaTAAAAGATGCCAGACTGAT  5309
                                ||| |||||||| |||||||| ||||||||||||||||| || || |||||  | |||||
Sbjct                  2521747  CTGTTGTGTTCCACCAAATACAGAGTCGGCCAAGAAAAAGATCAAGGATGCTCGGCTGAT  2521688
CDS:hypothetical pro   539        C  C  V  P  P  N  T  E  S  A  K  K  K  I  K  D  A  R  L  M

CDS: Putative 2        559        L  W  S  G  A  S  L  S  E  Q  I  T  A  M  M  N  S  I  T  E
Query                  5310     GCTTTGGAGTGGTGCATCACTTTCTGAGCAGATAACGGCAATGATGAACAGCATCACTGA  5369
                                ||||||||| || || |||||| |||||||||| | || |||||||||||||||||| |
Sbjct                  2521687  GCTTTGGAGCGGAGCGTCACTTCCTGAGCAGATCAAGGAAATGATGAACAGCATCACCGC  2521628
CDS:hypothetical pro   559        L  W  S  G  A  S  L  P  E  Q  I  K  E  M  M  N  S  I  T  A

CDS: Putative 2        579        R  A  E  A  S  E  A  T  P  *
CDS: Putative 1        1                                   M  M  L  H  L  V  C  D  I  S  G
Query                  5370     GCGGGCTGAAGCGAGTGAGGCAACGCCATGATGCTCCATTTGGTTTGCGACATCTCCGGC  5429
                                ||| || ||||| | ||||| |||  | |||  |||||| ||||||||||||| ||||||
Sbjct                  2521627  GCGAGCCGAAGCAATTGAGGGAACTACGTGACACTCCATCTGGTTTGCGACATTTCCGGC  2521568
CDS:hypothetical pro   1                                   M  T  L  H  L  V  C  D  I  S  G
CDS:hypothetical pro   579        R  A  E  A  I  E  G  T  T

CDS: Putative 1        12         S  M  S  E  G  G  K  P  F  I  L  R  T  L  A  T  T  V  A  Q
Query                  5430     AGCATGAGTGAAGGAGGCAAGCCCTTCATCCTGCGAACCTTGGCCACGACCGTGGCGCAA  5489
                                |||||||| || || || ||||| |||||  || ||||  |||  || ||||| || |||
Sbjct                  2521567  AGCATGAGCGACGGCGGAAAGCCGTTCATTATGAGAACACTGGTTACAACCGTTGCTCAA  2521508
CDS:hypothetical pro   12         S  M  S  D  G  G  K  P  F  I  M  R  T  L  V  T  T  V  A  Q

CDS: Putative 1        32         W  V
Query                  5490     TGGGTG  5495
                                ||||||
Sbjct                  2521507  TGGGTG  2521502
CDS:hypothetical pro   32         W  V


 Features in this part of subject sequence:
   AAA ATPase
   serine/threonine protein kinase

 Score = 2843 bits (1539),  Expect = 0.0
 Identities = 3865/4987 (78%), Gaps = 163/4987 (3%)
 Strand=Plus/Minus

CDS: Putative 3        1          L  E  P  R  D  C  A  A  T  C  L  F  A  L   H   L   D  G  V
Query                  6161     CTGGAACCTCGCGATTGCGCGGCCACCTGTCTCTTCGCACTAC-A-CCTG-GATGGCGTA  6217
                                ||||| || || |||||  | || |||||||| |||||  | | |  | | || ||| ||
Sbjct                  2520833  CTGGAGCCGCGAGATTGTTCTGCAACCTGTCTGTTCGCGTTCCGATTCGGAGACGGCTTA  2520774
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CDS:hypothetical pro  99        L  E  P  R  D  C  S  A  T  C  L  F  A  F  R  F  G  D  G  L

CDS: Putative 3       20        I  H  L  G  M  L  G  D  G  L  A  A  I  A  K  S  D  G  S  V
Query                 6218     ATCCACCTAGGGATGCTTGGCGACGGACTTGCCGCTATTGCCAAGTCCGATGGATCAGTG  6277
                               |||||| | |||||||||||||| || |||  |||   |  ||| || ||| | || ||
Sbjct                 2520773  ATCCACTTGGGGATGCTTGGCGATGGGCTTATCGCAGCTCTCAAATCTGATAGCTCTGTC  2520714
CDS:hypothetical pro  119       I  H  L  G  M  L  G  D  G  L  I  A  A  L  K  S  D  S  S  V

CDS: Putative 3       40        V  S  L  S  E  N  K  T  Q  G  F  S  N  I  T  T  A  L  S  S
Query                 6278     GTTTCGCTGTCGGAAAACAAGACGCAAGGCTTCTCCAATATCACTACTGCGCTGTCCTCC  6337
                               || ||||| |||||| |||||   || || || || || ||||| |||||||| ||| |
Sbjct                 2520713  GTATCGCTCTCGGAAGACAAGGGCCACGGTTTTTCAAACATCACCACTGCGCTATCCCCG  2520654
CDS:hypothetical pro  139       V  S  L  S  E  D  K  G  H  G  F  S  N  I  T  T  A  L  S  P

CDS: Putative 3       60        K  V  S  A   K  D  W  Q  Y  L  S  L  P  G  E  Q  C  I  A  V
Query                 6338     AAGGTCTCCGCC-AAAGACTGGCAGTATTTGTCGCTGCCGGGGGAGCAGTGCATCGCAGT  6396
                               || || | |||| || || ||||   |||| ||||| |||| |||  |||| || || ||
Sbjct                 2520653  AATGTAT-CGCCGAATGAATGGCGACATTTTTCGCTTCCGGAGGAAGAGTGTATTGCTGT  2520595
CDS:hypothetical pro  159       N  V   S  P  N  E  W  R  H  F  S  L  P  E  E  E  C  I  A  V

CDS: Putative 3       80         L  L  C  T  D  G  V  A  D  D  L  D  N  A  D  G  F  V  S
Query                 6397     ATTGCTCTGCACCGATGGGGTGGCTGACGATTTGGATAACGCTGACGGGTTTGTGAGC-A  6455
                                |||||| || |||||||| || ||||| || |||||| | |  || || ||||| | |
Sbjct                 2520594  CTTGCTGTGTACCGATGGCGTAGCTGATGACTTGGATGATGTCGATGGTTTTGT-ATCGG  2520536
CDS:hypothetical pro  179         L  L  C  T  D  G  V  A  D  D  L  D  D  V  D  G  F  V   S

CDS: Putative 3       99       S  F  A  E  T  H  R  T  L  A  P  V  S  A  N  R  R  I  H  E
Query                 6456     GTTTCGCCGAAACGCATCGAACCCTCGCACCGGTAAGTGCCAACCGGCGCATCCACGAG-  6514
                               | ||   |||  | ||| |  || | ||     |||||||||| || |||| || ||||
Sbjct                 2520535  GCTTTATCGAGGCACATTGCTCCATTGCCGAAATAAGTGCCAATCGCCGCA-CC-CGAGC  2520478
CDS:hypothetical pro  198      G  F  I  E  A  H  C  S  I  A  E  I  S  A  N  R  R   T   R  A

CDS: Putative 3       119        M  L  E  N  W  P  T  P  K  H  S  D  D  K  T  L  A  C  L  C
Query                 6515     -ATGCTCGAAAACTGGCCCACGCCCAAGCACAGCGACGATAAAACCCTCGCCTGCCTGTG  6573
                                |||||||||||| ||||| || |||||||||||||||||| |||||| |||| ||||| |
Sbjct                 2520477  AATGCTCGAAAAATGGCCTACTCCCAAGCACAGCGACGACAAAACCATCGCTTGCCTTTT  2520418
CDS:hypothetical pro  218        M  L  E  K  W  P  T  P  K  H  S  D  D  K  T  I  A  C  L  F

CDS: Putative 3       139        S  E  E  V  A  D   E
CDS: Putative 2       1                        M   S  N  A   E  H  Q  A  L  K  P  L  V
Query                 6574     CAGTGAGGAGGTTGCAGATG-AGTAACGCC--GAACACCAGGCTCTGAAGCCACTTGTGG  6630
                                 ||||||| ||  | |||| |  ||  |   |||||||| |||| |||    ||||| |
Sbjct                 2520417  TCGTGAGGACGTCCCGGATGCATGAATCCATTGAACACCAAGCTCCGAAAGTTCTTGTAG  2520358
CDS:serine/threonine  1                        M  H  E  S  I  E  H  Q  A  P  K  V  L  V
CDS:hypothetical pro  238        R  E  D  V  P  D  A

CDS: Putative 2       14       D  E  Y  N  N  V  H  Q  M  A  D  E  L  A  R  G  G  Q  G  V
Query                 6631     ATGAATACAACAATGTTCATCAGATGGCCGATGAGCTTGCGCGCGGTGGGCAAGGCGTGG  6690
                               |||| ||   |||| | |||||||| |||||||| ||||| |||||||| |||||||||
Sbjct                 2520357  ATGAGTATGGCAATTTCCATCAGATTGCCGATGAACTTGCTCGCGGTGGACAAGGCGTGG  2520298
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CDS:serine/threonine  15       D  E  Y  G  N  F  H  Q  I  A  D  E  L  A  R  G  G  Q  G  V

CDS: Putative 2       34       V  Y  R  T  K  D  A  D  L  A  V  K  Q  P  L  D  A  A  G  Q
Query                 6691     TCTATCGCACCAAGGATGCGGATTTGGCCGTCAAGCAGCCGCTGGACGCTGCCGGCCAGC  6750
                               ||||||||||||||||||||||||||||| |||||||| || ||||||||| |||||||||
Sbjct                 2520297  TCTATCGCACCAAGGATGCGGATTTGGCTGTCAAGCAACCACTGGACGCTTCCGGCCAGC  2520238
CDS:serine/threonine  35       V  Y  R  T  K  D  A  D  L  A  V  K  Q  P  L  D  A  S  G  Q

CDS: Putative 2       54       P  D  K  N  A  N  L  R  E  R  F  Q  H  V  R  L  L  P  I  P
Query                 6751     CGGACAAAAACGCCAATCTGCGCGAGCGCTTCCAGCACGTCCGCCTGTTGCCCATACCAC  6810
                               ||||||||||||||||||||||||||||| ||||||| | |||||||| ||||||| ||||
Sbjct                 2520237  CGGACAAAAACGCCAATCTGCGCGAGCGTTTCCAGCGCATCCGCCTGCTGCCCATGCCAC  2520178
CDS:serine/threonine  55       P  D  K  N  A  N  L  R  E  R  F  Q  R  I  R  L  L  P  M  P

CDS: Putative 2       74       R  R  I  P  V  S  L  P  L  A  I  L  R  D  E  P  G  Y  V  M
Query                 6811     GGCGCATCCCCGTTTCCCTTCCACTCGCCATCCTGCGCGACGAGCCGGGCTATGTGATGC  6870
                                |||||||||| |||||||| ||||||||||||| | || |||||||||||||||||||||
Sbjct                 2520177  AGCGCATCCCTGTTTCCCTACCACTCGCCATCTTACGAGACGAGCCGGGCTATGTGATGC  2520118
CDS:serine/threonine  75       Q  R  I  P  V  S  L  P  L  A  I  L  R  D  E  P  G  Y  V  M

CDS: Putative 2       94       R  L  L  N  G  M  K  P  F  A  S  F  D  L  D  G  R  S  K  K
Query                 6871     GTCTGTTGAACGGCATGAAGCCCTTCGCCAGTTTCGATTTGGACGGCAGAAGCAAAAAGA  6930
                               |||| |||||||  |||| ||| ||||||  ||||||||||||| |||||||| || ||||
Sbjct                 2520117  GTCTTTTGAACGATATGAGGCCATTCGCCGTTTTCGATTTGGATGGCAGAAGTAAGAAGA  2520058
CDS:serine/threonine  95       R  L  L  N  D  M  R  P  F  A  V  F  D  L  D  G  R  S  K  K

CDS: Putative 2       114      K  L  E  D  Q  S  Q  A  L  P  Q  W  L  T  K  I  P  D  K  D
Query                 6931     AGCTGGAAGATCAAAGCCAAGCCTTGCCCCAATGGCTGACGAAGATTCCTGACAAGGACC  6990
                               ||||||||||| |||| || |||||||| ||||||||| |||||||||||||||| ||||
Sbjct                 2520057  AGCTGGAAGATGAAAGACACGCCTTGCCACAATGGCTGGCGAAGATTCCTGACAAAGACC  2519998
CDS:serine/threonine  115      K  L  E  D  E  R  H  A  L  P  Q  W  L  A  K  I  P  D  K  D

CDS: Putative 2       134      L  A  L  R  L  L  H  Y  A  Q   T  G  S  T  R  R  R  S  L  A
Query                 6991     TGGCGCTGCGACTACTGCATTACGCACA-AACTGGCTCCACCCGCCGCCGTTCGCTCGCG  7049
                                |||||| || || ||||||||||| ||  || ||||| || || ||||||  || ||||
Sbjct                 2519997  AGGCGCTTCGGCTGCTGCATTACGC-CAGCACAGGCTCTACACGTCGCCGTCTGCGCGCG  2519939
CDS:serine/threonine  135      Q  A  L  R  L  L  H  Y  A   S  T  G  S  T  R  R  R  L  R  A

CDS: Putative 2       154       L  A  K  C  A  A  I  L  A  R  L  H  S  A  G  L  V  Y  G  D
Query                 7050     CTTGCCAAGTGCGCTGCCATCCTCGCCCGCCTGCACAGCGCTGGACTGGTCTATGGCGAC  7109
                               || || |||||||| ||||||||||||||||| |||| ||| ||| |||||||||| |||
Sbjct                 2519938  CTGGCGAAGTGCGCCGCCATCCTCGCCCGCCTCCACAACGCGGGAATGGTCTATGGTGAC  2519879
CDS:serine/threonine  155       L  A  K  C  A  A  I  L  A  R  L  H  N  A  G  M  V  Y  G  D

CDS: Putative 2       174       I  S  T  N  N  A  F  I  G  E  D  D  T  T  D  V  W  L  I  D
Query                 7110     ATTTCCACCAACAACGCTTTCATTGGCGAAGACGACACCACCGATGTCTGGCTCATAGAT  7169
                               |||||| ||||||| ||||||||||||||||| ||||||| ||||||||||||| ||||||
Sbjct                 2519878  ATTTCCCCCAACAATGCTTTCATTGGCGAAGGCGACACCCCCGATGTCTGGCTGATAGAT  2519819
CDS:serine/threonine  175       I  S  P  N  N  A  F  I  G  E  G  D  T  P  D  V  W  L  I  D
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CDS: Putative 2       194       A  D  N  M  R  L  E  L  P  S  G  G  V  S  V  Y  T  P  G  Y
Query                 7170     GCCGACAATATGCGCCTGGAGTTACCCAGCGGCGGTGTGTCCGTCTATACGCCGGGCTAC  7229
                               |||||||| |||||||  ||||||| ||||||||| | ||| |||||||||||||| |||
Sbjct                 2519818  GCCGACAACATGCGCCCTGAGTTACTCAGCGGCGGCGCGTCGGTCTATACGCCGGGTTAC  2519759
CDS:serine/threonine  195       A  D  N  M  R  P  E  L  L  S  G  G  A  S  V  Y  T  P  G  Y

CDS: Putative 2       214       G  A  P  E  V  V  Q  G  R  D  Q  S  R  P  R  T  D  C  W  A
Query                 7230     GGTGCACCGGAGGTAGTGCAGGGCCGTGACCAATCCCGCCCGCGAACCGACTGCTGGGCT  7289
                               || || ||||| || ||||| || || || || |||||||| ||||| || || ||||||
Sbjct                 2519758  GGCGCGCCGGAAGTGGTGCAAGGTCGCGATCAGTCCCGCCCACGAACGGATTGTTGGGCT  2519699
CDS:serine/threonine  215       G  A  P  E  V  V  Q  G  R  D  Q  S  R  P  R  T  D  C  W  A

CDS: Putative 2       234       F  A  V  M  T  F  K  L  L  A  L  C  H  P  F  I  G  K  K  V
Query                 7290     TTCGCTGTGATGACATTCAAGCTACTGGCGCTTTGCCACCCTTTCATTGGCAAGAAAGTA  7349
                               |||||||| ||| | ||||||||  | ||||| |||||||| ||||| ||||| |||||
Sbjct                 2519698  TTCGCTGTCATGGCCTTCAAGCTGTTAGCGCTGTGCCACCCATTCATCGGCAACAAAGTG  2519639
CDS:serine/threonine  235       F  A  V  M  A  F  K  L  L  A  L  C  H  P  F  I  G  N  K  V

CDS: Putative 2       254       L  E  P  E  D  E  E  D  G  W  D  A  D  P  A   P  N  G   T
Query                 7350     CTGGAGCCCGAAGATGAAGAAGACGGCTGGGATGCCGACCCTGC-GCCCAATGGC-AC--  7405
                               ||| |  | || || || || | ||||||||| || || || || | | | |||| ||
Sbjct                 2519638  CTGCAAACTGAGGACGACGATGGCGGCTGGGACGCTGAGCC-GCAGGCGAGTGGCGACGG  2519580
CDS:serine/threonine  255       L  Q  T  E  D  D  D  G  G  W  D  A  E  P   Q  A  S  G  D  G

CDS: Putative 2       273        A  T   D   L   N  E  Q  A  F  A  G  F  L  P  F  V  D  D
Query                 7406     TGCCACCG--ATC-T-GAACGAACAGGCATTCGCTGGTTTCTTGCCTTTCGTGGATGACG  7461
                               |||  |||  | | | ||| || ||||||| |||||| | | |||||||||||||||||
Sbjct                 2519579  TGCGCCCGCCAGCATAGAA-GATCAGGCATACGCTGGGTACCTGCCTTTCGTGGATGACG  2519521
CDS:serine/threonine  275        A  P  A  S  I  E   D  Q  A  Y  A  G  Y  L  P  F  V  D  D

CDS: Putative 2       291      E  D  D  D  S  N  E  G  V  G  G  L  P  R  V  L  V  A  T  E
Query                 7462     AAGATGACGATTCCAACGAAGGAGTTGGAGGCCTGCCCCGTGTATTAGTCGCAACAGAAG  7521
                               ||||| |||||||||| | ||   ||| ||  |||| || ||  | ||| |||||   |
Sbjct                 2519520  AAGATAACGATTCCAACAAGGGCACTGGTGGTTTGCCACGCGTCCTGGTCACAACACCGG  2519461
CDS:serine/threonine  294      E  D  N  D  S  N  K  G  T  G  G  L  P  R  V  L  V  T  T  P

CDS: Putative 2       311      G  L  R  R  L  F  Q  E  T  F  G  A  G  R  E  L  P  H  R  R
Query                 7522     GATTACGCCGCCTGTTTCAGGAAACTTTCGGTGCAGGACGTGAACTGCCGCACCGCCGCC  7581
                               |||| || ||||| ||||| | ||||||||| || || || ||||  ||||   ||||||
Sbjct                 2519460  GATTGCGTCGCCTTTTTCAAGCAACTTTCGGAGCTGGCCGAGAACACCCGCCTAGCCGCC  2519401
CDS:serine/threonine  314      G  L  R  R  L  F  Q  A  T  F  G  A  G  R  E  H  P  P  S  R

CDS: Putative 2       331      P  T  M  A  F  W  T  L  E  L  A  R  A  A  D  Q  S   L  D  C
Query                 7582     CGACAATGGCGTTCTGGACATTGGAGCTTGCGAGGGCGGCGGATCAGTCGC--TGGATTG  7639
                               | || |||||||| ||| | ||||| |||   |  || || || | | |||  |||||||
Sbjct                 2519400  CCACGATGGCGTTTTGGGCGTTGGAACTTATCAAAGCAGCCGA-CCG-CGCGTTGGATTG  2519343
CDS:serine/threonine  334      P  T  M  A  F  W  A  L  E  L  I  K  A  A  D   R   A  L  D  C

CDS: Putative 2       351        L  E  C  G  M  S  H  F  A  D  E  Y  A  Q   C  P  Y  C  G
Query                 7640     CCTCGAATGTGGCATGAGCCATTTCGCCGATGAATACGCGCAA--TGCCCGTATTGTGGC  7697
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                                 || |||||||| ||||||| ||||||| |||| || |  | ||  ||||| |||||  |
Sbjct                   2519342  CCCCGAATGTGCCATGAGCTATTTCGCTGATG-AT-CATGAAAGCTGCCCTTATTG-CG-  2519287
CDS:serine/threonine    354        P  E  C  A  M  S  Y  F  A  D   D   H  E  S  C  P  Y  C

CDS: Putative 2         370       A  A    R  P  A  F  I  R  V  K  T  P  R  W  E  I  L  I   P
Query                   7698     GCGGCG--CGCCCGGCTTTCATTCGCGTCAAAACGCCACGTTGGGAAATCCTGAT-TCCT  7754
                                 ||||||  | ||| || ||||||||  |  |||| |||||||||| || | ||   |||
Sbjct                   2519286  GCGGCGAACACCCCGCATTCATTCGTATTCAAACACCACGTTGGG-AA-CGTGTCATCCC  2519229
CDS:serine/threonine    372      G  G  E  H  P  A  F  I  R  I  Q  T  P  R  W   E   R  V  I  P

CDS: Putative 2         389       G  G  A   T  E  F  R  L  P  Q  R  L  F  H  P  F  S  F  E
Query                   7755     GGTGGTGC-C-ACGGAGTTCAGATTGCCGCAGCGGCTTTTTCACCCGTTTTCATTCGAGT  7812
                                 ||    || | || ||  | |   ||||||  || || ||  |||| ||||||||||||
Sbjct                   2519228  GG-CCAGCACAACAGAACTAACCCTGCCGCGCCGTCTGTTCTACCCATTTTCATTCGAG-  2519171
CDS:serine/threonine    392         A  S  T  T  E  L  T  L  P  R  R  L  F  Y  P  F  S  F  E

CDS: Putative 2         408      Y  F  D  N   T   A   Y  E  A  M  L  N  C  A  A  K  T  A  V
Query                   7813     ATTTCGATAAC-ACA-GCA-TACGAAGCCATGCTGAACTGCGCGGCCAAAACCGCAGTCC  7869
                                 |  || |  ||  || | | |||||  || ||||||| | | |||||||||| ||||| |
Sbjct                   2519170  A-GTC-ACGACGTCATGGAGTACGAGTCCGTGCTGAATTTCTCGGCCAAAACGGCAGTTC  2519113
CDS:serine/threonine    411        S   H  D  V  M  E  Y  E  S  V  L  N  F  S  A  K  T  A  V

CDS: Putative 2         427      P  V  R  G   T  L  P  F  P  D  N  L  T  F  E  F  V  E  G  C
Query                   7870     CCGTGCGGGGC-ACGCTGCCTTTCCCGGACAACCTCACCTTTGAGTTCGTGGAGGGCTGC  7928
                                 ||| ||||||| |   || |||| || || | ||| || ||  |||| ||   |||| ||
Sbjct                   2519112  CCGCGCGGGGCGAAAATG-CTTTTCCTGAAAGCCTGACTTTCAAGTTTGTAAGGGGCGGC  2519054
CDS:serine/threonine    430      P  A  R  G  E  N   A  F  P  E  S  L  T  F  K  F  V  R  G  G

CDS: Putative 2         447       K  *
CDS: Putative 1         1           M  K  F  Q  D  I  P  V  N  I  I  T  V  R  I  K   R  S  D
Query                   7929     AAATGAAGTTTCAGGACATTCCTGTCAACATCATAACTGTCCGCATCAAG-CGGTCTGAC  7987
                                 ||||||| |||| ||||||||| | |   ||| | |   | ||  ||||| || | |  |
Sbjct                   2519053  AAATGAATTTTCGGGACATTCCCGCCCGTATCCTGAGCATACGTGTCAAGTCGAT-TACC  2518995
CDS:AAA ATPase [Meth    1           M  N  F  R  D  I  P  A  R  I  L  S  I  R  V  K  S  I   T
CDS:serine/threonine    450       K

CDS: Putative 1         20        N  V  E  A  L  Q  E  Q  P  V  F  S  V  E  A  S  L  S  R  A
Query                   7988     AATGTCGAAGCCCTGCAAGAGCAGCCAGTATTCTCGGTAGAGGCCAGCCTATCCCGCGCA  8047
                                 ||  ||   ||  | |||||||||||| |||| |||||| || ||||  |||  ||| ||
Sbjct                   2518994  AAAATCCCGGCTTTACAAGAGCAGCCCGTATCCTCGGTGGAAGCCAAGCTAAGCCGTGCG  2518935
CDS:AAA ATPase [Meth    20        K  I  P  A  L  Q  E  Q  P  V  S  S  V  E  A  K  L  S  R  A

CDS: Putative 1         40        D  E  F  E  I  R  L  R  D  A  V  V  F  V  R  P  V  A  A  V
Query                   8048     GATGAATTTGAAATCCGCCTGAGAGACGCGGTTGTTTTCGTTCGCCCCGTCGCGGCTGTT  8107
                                 || |||||||||||  ||  | | |||  | ||||| ||||| ||||| |||| |||||
Sbjct                   2518934  GACGAATTTGAAATTCGTATAAAAGATTCTGTTGTATTCGTCCGCCCTGTCGTGGCTGCA  2518875
CDS:AAA ATPase [Meth    40        D  E  F  E  I  R  I  K  D  S  V  V  F  V  R  P  V  V  A  A

CDS: Putative 1         60        D  I  R  R  L  N  A  E  L  A  S  G  R  S  L  L  A  Q  L  E
Query                   8108     GACATCCGCCGCCTCAACGCTGAACTTGCCAGTGGGCGTTCCCTGCTTGCACAACTTGAA  8167
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                                 |||||||||||||||||| || || || ||||| || ||| ||||||| || ||||| |
Sbjct                  2518874  GACATCCGCCGCCTCAATGCCGAGCTCGCCAGCGGACGTGCCCTGCTGGCGCAACTAGCC  2518815
CDS:AAA ATPase [Meth   60        D  I  R  R  L  N  A  E  L  A  S  G  R  A  L  L  A  Q  L  A

CDS: Putative 1        80        N  P  A  A  D  G  S  I  E  L  K  I  G  F  F  T  G  V  C  L
Query                  8168     AACCCTGCCGCCGATGGCAGCATCGAGCTGAAGATCGGTTTTTTCACCGGCGTCTGCCTG  8227
                                 | |||||| || ||||||||  |||| ||| | || |  |||||||| |||| |||  ||
Sbjct                  2518814  AGCCCTGCTGCTGATGGCAGTGTCGAACTGCAAATAGCATTTTTCACGGGCGACTGTTTG  2518755
CDS:AAA ATPase [Meth   80        S  P  A  A  D  G  S  V  E  L  Q  I  A  F  F  T  G  D  C  L

CDS: Putative 1        100       E  M  G  D  V  E  I  G  V  D  E  Y  V    Q    E       K  M
Query                  8228     GAAATGGGCGATGTTGAAATCGGTGTGGATGAGTATGT-G-CAA--GA-----AAAGATG  8278
                                 |||||||||||||| ||||||||||||||||| ||||| |  ||  ||     |||||||
Sbjct                  2518754  GAAATGGGCGATGTCGAAATCGGTGTGGATGAATATGTGGAAAACGGACTGGCAAAGATG  2518695
CDS:AAA ATPase [Meth   100       E  M  G  D  V  E  I  G  V  D  E  Y  V  E  N  G  L  A  K  M

CDS: Putative 1        117       R     T   K  G  E  A  L   Y  K  R  L  G  E  L  C  C  F  Q
Query                  8279     CG----GACG-AAGGGTGAGGCACT-TTACAAGAGGCTGGGCGAACTTTGCTGCTTCCAA  8332
                                 ||    | || || ||  | || || |||| |||  || ||| || | ||||| ||||||
Sbjct                  2518694  CGCCTTGGCGAAAAGGGCAAGCGCTCTTACGAGACTCTCGGCCAAATCTGCTGTTTCCAA  2518635
CDS:AAA ATPase [Meth   120       R  L  G  E  K  G  K  R  S  Y  E  T  L  G  Q  I  C  C  F  Q

CDS: Putative 1        135       Q  G  N  D  A  F  F  F  L  T  A  G  P  A  I  D  E  E  L  K
Query                  8333     CAGGGAAACGACGCATTTTTCTTCCTGACTGCTGGCCCGGCGATTGATGAAGAACTGAAA  8392
                                 || ||  || |||| |  ||||| ||||| |||||||| || ||||||  ||| ||||||
Sbjct                  2518634  CAAGGCGACAACGCCTACTTCTTTCTGACCGCTGGCCCAGCCATTGATAGAGACCTGAAA  2518575
CDS:AAA ATPase [Meth   140       Q  G  D  N  A  Y  F  F  L  T  A  G  P  A  I  D  R  D  L  K

CDS: Putative 1        155       P  V  G  E  D  T  P  R  D  A  A  A  E  P  T   R  I  N  A  F
Query                  8393     CCTGTCGGCGAGGACACGCCACGCGATGCAGCTGCGGAGCCGAC-CCGAATAAACGCTTT  8451
                                 || | || ||| ||  |||||||||| | |   || || || ||  | || |||| ||||
Sbjct                  2518574  CCAGACGCCGATGAAGCGCCACGCGAAGTAAGGGCAGAACCAACTTCCAA-AAACTCTTT  2518516
CDS:AAA ATPase [Meth   160       P  D  A  D  E  A  P  R  E  V  R  A  E  P  T  S  K   N  S  F

CDS: Putative 1        175         C  V  T  G  E  G  I  R  F  I  A  T  E  K  A  M  P  G  G  Q
Query                  8452     CTGTGTTACTGGCGAAGGTATCCGCTTCATTGCCACCGAAAAAGCAATGCCAGGCGGCCA  8511
                                 | |  |||| || || ||||||||||| |||  || ||||| |||||||| |||||  |
Sbjct                  2518515  CGGCATTACCGGAGATGGTATCCGCTTCGTTGTTACGGAAAAGGCAATGCCGGGCGGTAA  2518456
CDS:AAA ATPase [Meth   180         G  I  T  G  D  G  I  R  F  V  V  T  E  K  A  M  P  G  G  N

CDS: Putative 1        195         T  I  Y  I  A  T  R  L  T  K  P  K  K  E  P  D  R  T  L  R
Query                  8512     AACTATCTACATCGCCACCCGTCTAACCAAGCCAAAGAAGGAACCTGACCGCACCTTACG  8571
                                   | |||| ||||||  |||| || |   ||| || ||| || ||||||||| || | ||
Sbjct                  2518455  TTCCATCTTCATCGCATCCCGCCTGAAGGAGCAAAGGAATGACCCTGACCGCGCCCTGCG  2518396
CDS:AAA ATPase [Meth   200         S  I  F  I  A  S  R  L  K  E  Q  R  N  D  P  D  R  A  L  R

CDS: Putative 1        215         L  A  K  G  R  L  R  F  V  D  W  T  Q  A  G  Q  V  Q  I  L
Query                  8572     CCTGGCCAAAGGTCGGCTGCGTTTTGTGGACTGGACACAGGCGGGACAAGTGCAAATTCT  8631
                                 | |||| |||||||||||||||| ||||| |||||  |||| ||||| ||||||||||
Sbjct                  2518395  CTTGGCGAAAGGTCGGCTGCGTTTCGTGGATTGGACGGAGGCAGGACAGGTGCAAATTCT  2518336
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CDS:AAA ATPase [Meth  220        L  A  K  G  R  L  R  F  V  D  W  T  E  A  G  Q  V  Q  I  L

CDS: Putative 1       235        A  K  A  Q  M  T  A  L  T  Q  D  D  G  S  Y  L  K  K  W  D
Query                 8632     TGCCAAAGCGCAAATGACAGCACTCACTCAGGACGATGGAAGCTATCTGAAAAAGTGGGA  8691
                               ||||||||| |||||||| |||||||| ||||||||||| ||||||||||||||| |||||
Sbjct                 2518335  TGCCAAAGCCCAAATGACTGCACTCACGCAGGACGATGGCAGCTATCTGAAAAAATGGGA  2518276
CDS:AAA ATPase [Meth  240        A  K  A  Q  M  T  A  L  T  Q  D  D  G  S  Y  L  K  K  W  D

CDS: Putative 1       255        E  F  G  E  V  E  G  E  L  L  L  K  Q  A  R  E  V  G  A  L
Query                 8692     CGAGTTTGGTGAGGTTGAAGGTGAACTGCTGCTCAAGCAAGCACGCGAAGTGGGTGCTTT  8751
                               ||||||||| ||  | ||||| ||||| || ||||||||||| |||| ||| ||| | ||
Sbjct                 2518275  CGAGTTTGGCGATCTCGAAGGCGAACTTCTACTCAAGCAAGCCCGCGCAGTCGGTACGTT  2518216
CDS:AAA ATPase [Meth  260        E  F  G  D  L  E  G  E  L  L  L  K  Q  A  R  A  V  G  T  L

CDS: Putative 1       275        Q  F  T  E  M  V  P  K  R  D  G  T  V  G  V  R  I   A  Q
Query                 8752     GCAATTCACGGAGATGGTGCCGAAACGGGATGGAACTGTCGGAGTTCGTATTG-CGCAGG  8810
                               ||||||||||||| |||  || ||||||||| || |||||   ||| || |||| || | |
Sbjct                 2518215  GCAATTCACGGACATGACGCAGAAACGGGACGGGACTGTTACAGTCCGCATTGTCG-AAG  2518157
CDS:AAA ATPase [Meth  280        Q  F  T  D  M  T  Q  K  R  D  G  T  V  T  V  R  I  V   E

CDS: Putative 1       294      A  S  D  S  A  W  G  A  L  R  Q  G  A  V  P  E  V  E  L  V
Query                 8811     CATCAGATTCTGCGTGGGGCGCACTGAGACAAGGCGCAGTACCTGAAGTTGAACTGGTGG  8870
                               | || || || || | |  |||| ||    |||| | ||| |  ||||| || || || |
Sbjct                 2518156  CCTCTGACTCAGCCTTGACCGCATTGGTTGAAGGTGAAGTGCTGGAAGTCGAGCTCGTAG  2518097
CDS:AAA ATPase [Meth  299      A  S  D  S  A  L  T  A  L  V  E  G  E  V  L  E  V  E  L  V

CDS: Putative 1       314      D  E  L  P  D  Y  L  Q  D  E  N  L  S  F  T  D  F  A  R  G
Query                 8871     ACGAGTTGCCGGACTACTTGCAGGATGAAAACCTGAGCTTCACGGATTTTGCGAGAGGGA  8930
                               ||||   ||||||||| || | ||| |||| | |||| |||| | | |||||||| || |
Sbjct                 2518096  ACGAACCGCCGGACTATTTACTGGACGAAACCTTGAGTTTCAAGAACTTTGCGAGCGGAA  2518037
CDS:AAA ATPase [Meth  319      D  E  P  P  D  Y  L  L  D  E  T  L  S  F  K  N  F  A  S  G

CDS: Putative 1       334      I  E  K  K  E  G  E  H  S  K  L  G  E  K  R  E  L  R  E  K
Query                 8931     TCGaaaaaaaGGAGGGGGAACACAGCAAGCTCGGTGAAAAACGCGAGCTGCGCGAGAAAA  8990
                               |||    ||| |  | ||  |  || ||| |||| |  ||||  |||| |||||||| ||
Sbjct                 2518036  TCG----AAA-G-CGCGG--CGGAGGAAG-TCGG-G--AAACTTGAGCAGCGCGAGACAA  2517989
CDS:AAA ATPase [Meth  339      I      E   S   A    A  E  E   V  G    K  L  E  Q  R  E  T

CDS: Putative 1       354      N  T  Y  F    S  V  A  E  F  D  E  E  T  R  V  L  T  L  K  A
Query                 8991     ATACCTATTTC-A-GTGTCGCAGAGTTTGACGAGGAAACTCGCGTACTCACGCTTAAAGC  9048
                               | ||||||||| | || || |||  |||||| |||| || |||   |||||||| ||| |
Sbjct                 2517988  AGACCTATTTCAATGTATC-CAG-CTTTGACAAGGAGACCCGCTCGCTCACGCTCAAAAC  2517931
CDS:AAA ATPase [Meth  355      K  T  Y  F  N  V  S   S   F  D  K  E  T  R  S  L  T  L  K  T

CDS: Putative 1       374        E  A  L  P  K   E  F  G  T  L  I  L  S  L  A  G  E  S  A
Query                 9049     CGAGGCTCTACCCAAG-GAATTCGGCACGCTCATCCTGTCGCTGGCGGGCGAATCTGCTC  9107
                                ||| ||||  | |||  || | |||| ||| ||||||||||||||||||||| | || |
Sbjct                 2517930  TGAGACTCTGTCAAAGACAAAT-GGCAGGCTTATCCTGTCGCTGGCGGGCGAAACCGCCC  2517872
CDS:AAA ATPase [Meth  375        E  T  L  S  K  T  N   G  R  L  I  L  S  L  A  G  E  T  A
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CDS: Putative 1       393      Q  I  K  R  R  M  A  A  R  Q  A  I  L  E  G  R  A  A  N  P
Query                 9108     AGATCAAGCGCCGCATGGCCGCCCGTCAAGCCATTCTGGAAGGCCGTGCCGCCAACCCCC  9167
                               | |||||||||||| ||||| || ||||| |||||||||||||||||||| ||||||||||
Sbjct                 2517871  AAATCAAGCGCCGTATGGCGGCTCGTCAGGCCATTCTGGAAGGCCGTGCTGCCAACCCCC  2517812
CDS:AAA ATPase [Meth  394      Q  I  K  R  R  M  A  A  R  Q  A  I  L  E  G  R  A  A  N  P

CDS: Putative 1       413      Q  L  G   L  L  I  E  A  Q  G  R  I  T  Q  I  R   P  S  Q  K
Query                 9168     AGCTTGGG-CTGTTGATTGAGGCGCAGGGGCGAATCACACAGATCCGGC-CATCGCAAAA  9225
                               || ||||| |||||||||||||| |||||| | |||||  | || || ||  | |||||||
Sbjct                 2517811  AG-TTGGGACTGTTGATTGAGGAGCAGGGACAAATCA-TCCGAACCCGCGAACCGCAAAA  2517754
CDS:AAA ATPase [Meth  414      Q   L  G  L  L  I  E  E  Q  G  Q  I   I  R  T  R  E  P  Q  K

CDS: Putative 1       433        V  Q  P  L  T  A  F  V  R  N  K  V  F  R  N  P  P   T  V
Query                 9226     AGTTCAACCGCTCACGGCCTTCGTTCGCAACAAGGTCTTTCGCAATCCGCCC-ACCGTCA  9284
                               | | | |||  | ||||| || || ||||| || |||||||| |||   ||| || || |
Sbjct                 2517753  AATCCCACCAATTACGGCATTTGTCCGCAAGAAAGTCTTTCGTAAT-GACCCAACTGTAA  2517695
CDS:AAA ATPase [Meth  434        I  P  P  I  T  A  F  V  R  K  K  V  F  R  N   D  P  T  V

CDS: Putative 1       452      M  Q  E  K  A  I  E  A  A  L  K  T  P  D  I  A  L  I  Q  G
Query                 9285     TGCAGGAAAAGGCCATCGAGGCCGCCCTAAAAACGCCAGATATAGCGTTGATCCAAGGCC  9344
                               ||||||||||||| || || || ||| |||| || ||||| |||||| | |||||||||
Sbjct                 2517694  TGCAGGAAAAGGCTATTGATGCGGCCTTAAACACACCAGACATAGCGCTAATCCAAGGCT  2517635
CDS:AAA ATPase [Meth  453      M  Q  E  K  A  I  D  A  A  L  N  T  P  D  I  A  L  I  Q  G

CDS: Putative 1       472      P  P  G  T  G  K  T  T  V  I  A  A  I  L  E  R  L  N  E  M
Query                 9345     CGCCCGGTACCGGCAAGACCACCGTCATCGCTGCCATTCTGGAGCGCCTGAACGAGATGG  9404
                               | || |||||||||||||||| ||||||||||| ||||| ||| || ||||||||||||
Sbjct                 2517634  CACCGGGTACCGGCAAGACCACTGTCATCGCTGCGATTCTAGAGAGCTTGAACGAGATGG  2517575
CDS:AAA ATPase [Meth  473      S  P  G  T  G  K  T  T  V  I  A  A  I  L  E  S  L  N  E  M

CDS: Putative 1       492      A  D  K  R  G  A  S  I  K  G  Q  I  L  L  T  G  F  Q  H  D
Query                 9405     CCGACAAGCGCGGCGCGAGCATCAAAGGCCAAATTCTGTTGACAGGCTTTCAGCACGATG  9464
                               | ||||| || || ||| | |||||||| ||||| ||||||||||| |||||||||||||
Sbjct                 2517574  CAGACAAACGAGGTGCGCGTATCAAAGGTCAAATCCTGTTGACAGGGTTTCAGCACGATG  2517515
CDS:AAA ATPase [Meth  493      A  D  K  R  G  A  R  I  K  G  Q  I  L  L  T  G  F  Q  H  D

CDS: Putative 1       512      A  V  E  N  M  I  E  R  L  S  L  N  S  L  P  V  P  K  F  G
Query                 9465     CGGTGGAAAACATGATCGAGCGGCTCTCGCTCAATAGCCTGCCCGTGCCGAAATTCGGCA  9524
                               | ||||| |||||||||||||||||||||||||||  || | ||||| || ||||| ||||
Sbjct                 2517514  CCGTGGAGAACATGATCGAGCGGCTCTCGCTCAACGGCATCCCCGTCCCTAAATTTGGCA  2517455
CDS:AAA ATPase [Meth  513      A  V  E  N  M  I  E  R  L  S  L  N  G  I  P  V  P  K  F  G

CDS: Putative 1       532      K  R  S  G  A  T  E  D  D  L   S  T  F  E  R  N  L  E  D  W
Query                 9525     AACGGTCTGGCGCGACGGAAGACGATCT-CAGCACCTTCGAGCGCAATCTTGAGGATTGG  9583
                               | |||||||||||| | ||||| || || |||| |||||||||||||||||| || |||
Sbjct                 2517454  AGCGGTCTGGCGCGGCTGAAGATGA-CTACAGCGCCTTCGAGCGCAATCTTGAAGACTGG  2517396
CDS:AAA ATPase [Meth  533      K  R  S  G  A  A  E  D  D   Y  S  A  F  E  R  N  L  E  D  W

CDS: Putative 1       552       C  S  K  L  A  A  E  L  R  E  R  N  P  Q  I  A  E  V  E  Q
Query                 9584     TGTTCAAAGTTGGCCGCCGAACTACGTGAACGAAACCCACAGATTGCCGAAGTTGAGCAG  9643
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                                || || || ||||| ||||||||||||| || ||||| ||||| || ||||| ||||||
Sbjct                  2517395  TGCTCCAAATTGGCAGCCGAACTACGTGAGCGGAACCCGCAGATAGCAGAAGTGGAGCAG  2517336
CDS:AAA ATPase [Meth   553       C  S  K  L  A  A  E  L  R  E  R  N  P  Q  I  A  E  V  E  Q

CDS: Putative 1        572       E  R  E  I  K  N  L  C  L  Q  Y  V  Q  A  P  S  R  V    L
Query                  9644     GAACGGGAAATAAAAAACCTGTGCCTGCAATATGTCCAAGCCCCGTCACGCGTGC--TGG  9701
                                ||| ||||||| ||||||||||  || ||||| || ||||| ||   |||||  |  |||
Sbjct                  2517335  GAAAGGGAAATCAAAAACCTGTTTCTCCAATACGTTCAAGCACC--AACGCGCCCATTGG  2517278
CDS:AAA ATPase [Meth   573       E  R  E  I  K  N  L  F  L  Q  Y  V  Q  A  P    T  R  P  L

CDS: Putative 1        591      A  A  S  L  A  R  K  I  A  A  L  G  S  V  I  L  G  E  D  G
Query                  9702     CCGCCAGCCTTGCTAGGAAAATCGCAGCGCTCGGCAGTGTAATTCTTGGCGAAGACGGCG  9761
                                | |  |||||||||||||||||||  | || |||  |||  | || || |||| ||||
Sbjct                  2517277  CGGGGAGCCTTGCTAGGAAAATCGCTTCACTTGGCGTTGTGGTGCTAGGTGAAGGCGGCA  2517218
CDS:AAA ATPase [Meth   592      A  G  S  L  A  R  K  I  A  S  L  G  V  V  V  L  G  E  G  G

CDS: Putative 1        611      A  R  R  S  T  N  L  A  K  K  L  A  H  E  E  N  L  N  D  G
Query                  9762     CTCGACGGTCGACGAATTTGGCGAAAAAGCTCGCGCACGAGGAAAACCTCAACGATGGCT  9821
                                | || ||| ||  ||| |||||||| || |||  ||  || || || || ||||| |  |
Sbjct                  2517217  CGCGGCGGGCGGAGAACTTGGCGAAGAACCTCAAGCGTGAAGAGAAGCTTAACGAAGATT  2517158
CDS:AAA ATPase [Meth   612      T  R  R  A  E  N  L  A  K  N  L  K  R  E  E  K  L  N  E  D

CDS: Putative 1        631      S  T  Q  W  L  D  A  A  R  R  L  R  V   R  H  E  S  F  S  D
Query                  9822     CCACCCAATGGCTTGATGCAGCGCGCCGTCTGCGCGTTC-GCCATGAAAGCTTTTCTGAC  9880
                                | |  ||||||||  |||| || || ||||| || || | |||| ||||| ||    |||
Sbjct                  2517157  CAAGTCAATGGCTAAATGCCGCACGTCGTCTTCGTGTCCGGCCA-GAAAGTTTCAGCGAC  2517099
CDS:AAA ATPase [Meth   632      S  S  Q  W  L  N  A  A  R  R  L  R  V  R  P   E  S  F  S  D

CDS: Putative 1        651       D  G  P  E  R  A  M  D  A  L  D  D  L  R  D  V  L  E  E  D
Query                  9881     GACGGGCCAGAAAGGGCGATGGACGCACTGGATGACCTGCGTGATGTGCTTGAAGAAGAC  9940
                                ||||| || ||| || || ||||||  ||||| || ||||| ||||| ||||||||||||
Sbjct                  2517098  GACGGCCCGGAACGGTCGGTGGACGTGCTGGAAGATCTGCGCGATGTTCTTGAAGAAGAC  2517039
CDS:AAA ATPase [Meth   652       D  G  P  E  R  S  V  D  V  L  E  D  L  R  D  V  L  E  E  D

CDS: Putative 1        671       E  R  K  L  L  D  K  A  S  L  W  R  N  E  D  G  P  A  P  F
Query                  9941     GAACGCAAACTGCTGGACAAAGCCAGTCTGTGGCGCAATGAAGATGGCCCAGCGCCATTT  10000
                                || |||||| ||||||||| ||||||||| |||||||  |||||||||||| || | ||
Sbjct                  2517038  GAGCGCAAATTGCTGGACACAGCCAGTCTTTGGCGCAGCGAAGATGGCCCACCGTCGTTC  2516979
CDS:AAA ATPase [Meth   672       E  R  K  L  L  D  T  A  S  L  W  R  S  E  D  G  P  P  S  F

CDS: Putative 1        691       L  D   N  L  V  A  L  K  K  R  L  L  A  R  F  T   A  P  P
Query                  10001    TTGGACA-ACCTGGTCGCGTTGAAAAAGAGGCTCCTCGCCCGGTTCACC-GCTCCACCGA  10058
                                 ||| || |  |||  ||| ||||||||||||| || | |||| | ||| || || |||
Sbjct                  2516978  CTGG-CAGATTTGGCGGCGCTGAAAAAGAGGCTTCTTGTCCGGCTTACCAGC-CCGCCGG  2516921
CDS:AAA ATPase [Meth   692       L   A  D  L  A  A  L  K  K  R  L  L  V  R  L  T  S   P  P

CDS: Putative 1        710      I  L  R  V  E  K  Q  N  D  A  V  L  A  L  A  E  F  A  I  Q
Query                  10059    TTCTTCGCGTGGAAAAGCAGAACGACGCAGTGCTTGCATTGGCAGAATTCGCCATACAAC  10118
                                |  |||||||||||||||| |||||||  ||| ||||  |||| ||||| ||||| || |
Sbjct                  2516920  TCTTTCGCGTGGAAAAGCAAAACGACGAGGTGATTGCGCTGGCGGAATTTGCCATTCAGC  2516861
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CDS:AAA ATPase [Meth  711      V  F  R  V  E  K  Q  N  D  E  V  I  A  L  A  E  F  A  I  Q

CDS: Putative 1       730      R  I  K  N  A  E  Y  S  A  K  D  K  K  S  A  A  L  A  E  F
Query                 10119    GCATCAAAAACGCCGAGTATTCGGCTAAGGATAAAAAATCTGCTGCGCTGGCCGAGTTTC  10178
                               |||| || | ||| | | | || |||||| |||||||||||||||| |||||||||||
Sbjct                 2516860  GCATAAAGACCGCAGGGCACTCAGCTAAGAATAAAAAATCTGCTGCGTTGGCCGAGTTTT  2516801
CDS:AAA ATPase [Meth  731      R  I  K  T  A  G  H  S  A  K  N  K  K  S  A  A  L  A  E  F

CDS: Putative 1       750      L  A  E  L  E  G  N  P  Y  G  M  V  D  A  L  S  E  Y  S  F
Query                 10179    TAGCCGAACTGGAAGGCAACCCCTATGGCATGGTAGATGCCCTGTCCGAATACAGTTTTG  10238
                               | || ||| |||||||||||| ||||| ||| | ||||| ||||| || ||||| ||||
Sbjct                 2516800  TGGCTGAATTGGAAGGCAACCCTTATGGAATGATGGATGCACTGTCTGATTACAGCTTTG  2516741
CDS:AAA ATPase [Meth  751      L  A  E  L  E  G  N  P  Y  G  M  M  D  A  L  S  D  Y  S  F

CDS: Putative 1       770      A  F  A  A  T  S  Q  Q  S  V  N  R  A  M  Q  K  R  K  G  L
Query                 10239    CCTTTGCCGCCACCAGCCAGCAGAGCGTCAATCGTGCAATGCAAAAACGCAAAGGGCTTG  10298
                               | |||||||| ||  ||||||| ||||| | |||    |||| |   |  ||||||  ||
Sbjct                 2516740  CTTTTGCCGCTACTTGCCAGCAAAGCGTGAGTCGAAGGATGC-AGGCCCAAAAGGGGATG  2516682
CDS:AAA ATPase [Meth  771      A  F  A  A  T  C  Q  Q  S  V  S  R  R  M   Q  A  Q  K  G  M

CDS: Putative 1       790      V   G  R  D  V  N  Q  N  Q  K  G  M  E  Y  E  Y  V  I  V  D
Query                 10299    TC-GGGCGCGATGTCAATCAAAACCAGAAAGGCATGGAATACGAATATGTCATCGTGGAC  10357
                                | ||||  |||||||||        || ||| ||||| ||||||||||| |||||||||
Sbjct                 2516681  ACTGGGCATGATGTCAAT--------GAGAGG-ATGGAGTACGAATATGTGATCGTGGAC  2516631
CDS:AAA ATPase [Meth  791       T  G  H  D  V  N          E  R   M  E  Y  E  Y  V  I  V  D

CDS: Putative 1       810       E  A  A  R  V  S  P  R  D  L  M  V  A  M  A  Q  G  K  R  I
Query                 10358    GAAGCCGCCCGTGTCTCGCCTCGTGATTTGATGGTGGCTATGGCGCAAGGCAAGCGCATT  10417
                               ||||| || || || ||||| ||||| ||||||| ||| |||||||||||||||| ||
Sbjct                 2516630  GAAGCTGCTCGCGTATCGCCCCGTGACTTGATGGGGGCCATGGCGCAAGGCAAGCGGATC  2516571
CDS:AAA ATPase [Meth  808       E  A  A  R  V  S  P  R  D  L  M  G  A  M  A  Q  G  K  R  I

CDS: Putative 1       830       I  L  V  G  D  H  R  Q  L  P  H  I  I  D  E  E  V  A  R  Q
Query                 10418    ATTCTGGTCGGCGACCATCGACAATTGCCGCACATCATTGACGAAGAGGTGGCTCGCCAG  10477
                               |||||||| ||||||||||| || |||||||||||||||||||||||||||||||||||
Sbjct                 2516570  ATTCTGGTGGGCGACCATCGGCAGTTGCCGCACATCATTGACGAAGAGGTGGCTCGCCAG  2516511
CDS:AAA ATPase [Meth  828       I  L  V  G  D  H  R  Q  L  P  H  I  I  D  E  E  V  A  R  Q

CDS: Putative 1       850       M  E  E  G  E  T  G  E  D  E  N  D  W  L  K  K  S  M  F  Q
Query                 10478    ATGGAGGAAGGCGAAACGGGTGAGGACGAAAATGACTGGCTaaaaaaaTCCATGTTTCAG  10537
                               |||||||||||||||   ||| |||||||||||||||||||||||||||||||||| |||
Sbjct                 2516510  ATGGAGGAAGGCGAAGGTGGTCAGGACGAAAATGACTGGCTAAAAAAATCCATGTTCCAG  2516451
CDS:AAA ATPase [Meth  848       M  E  E  G  E  G  G  Q  D  E  N  D  W  L  K  K  S  M  F  Q

CDS: Putative 1       870       Y  L  F  S  E  R  L  K  T  L  D  K  N  F  P  I  I  D  S  T
Query                 10538    TATTTGTTCTCCGAGCGTTTAAAAACACTGGACAAGAACTTCCCAATTATCGACAGCACC  10597
                               |||||||||  |   ||| | |||||  ||||   ||| | |  |     || || ||||
Sbjct                 2516450  TATTTGTTCAGCACCCGTCTGAAAACGTTGGAG--GAA-TGCG-A-----CGGCATCACC  2516400
CDS:AAA ATPase [Meth  868       Y  L  F  S  T  R  L  K  T  L  E    E   C   D       G  I  T
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CDS: Putative 1       890       T  G  R  V  T  P  R  C  I  T  L  D  K  Q  Y  R  M  H  P  L
Query                 10598    ACTGGCCGCGTTACACCACGTTGCATCACGCTGGACAAGCAATACCGCATGCATCCGCTG  10657
                                | | ||||||  ||| || | |      |    ||||||||||||||||||||||||||
Sbjct                 2516399  -C-G-CCGCGT--CAC-AC-T-G------G----ACAAGCAATACCGCATGCATCCGCTG  2516358
CDS:AAA ATPase [Meth  885         R   R  V    T    L            D  K  Q  Y  R  M  H  P  L

CDS: Putative 1       910       L  G  S  F  I  S  R  N  F  Y  E  R  F  D  P  E  E  Q  F  G
Query                 10658    CTGGGCAGCTTTATCAGTAGAAATTTCTATGAACGCTTCGACCCGGAGGAGCAATTTGGC  10717
                               ||||| ||||| |||||  | || ||||| ||||||||||| |||  ||||||||| |||
Sbjct                 2516357  CTGGGTAGCTTCATCAGCCGTAACTTCTACGAACGCTTCGATCCGACGGAGCAATTCGGC  2516298
CDS:AAA ATPase [Meth  899       L  G  S  F  I  S  R  N  F  Y  E  R  F  D  P  T  E  Q  F  G

CDS: Putative 1       930       S  G  R  P  A  S  D  F  A  H  D   L  P  G  T  N  G  K  S
Query                 10718    TCCGGGCGACCAGCAAGCGATTTCGCCCATGA--TCTGCCAGGCACGAACGGCAAGTCTG  10775
                               || ||||| || | |||||||||||||||||   ||| |||| |||| | |||||| ||
Sbjct                 2516297  TCAGGGCGGCCTGTAAGCGATTTCGCCCATGCGCTCT-CCAG-CACGGATGGCAAGCCTA  2516240
CDS:AAA ATPase [Meth  919       S  G  R  P  V  S  D  F  A  H  A  L   S  S   T  D  G  K  P

CDS: Putative 1       949      A  V  W  M  D  V  P  A  Q  R  G  K  H  Q  K  D  G  T  S  W
Query                 10776    CCGTTTGGATGGATGTACCAGCACAAAGAGGAAAACATCAAAAGGACGGAACCAGTTGGA  10835
                               | |||||| |||||||||||||||| | ||||| ||||||||| || |||||||||||||
Sbjct                 2516239  CGGTTTGGCTGGATGTACCAGCACAGATAGGAAGACATCAAAAAGATGGAACCAGTTGGA  2516180
CDS:AAA ATPase [Meth  938      T  V  W  L  D  V  P  A  Q  I  G  R  H  Q  K  D  G  T  S  W

CDS: Putative 1       969      T  R  P  A  E  V  T  V  I  A  R  Q  L  Q  A  W  M  S  S  D
Query                 10836    CGCGCCCCGCAGAAGTCACTGTCATCGCTCGCCAGTTACAGGCGTGGATGAGTTCGGATG  10895
                               ||||||| ||||| | |||||||||||  ||| |||| || | |||||||||||||||||
Sbjct                 2516179  CGCGCCCTGCAGAGGCCACTGTCATCGTCCGCAAGTTGCATGAGTGGATGAGTTCGGATG  2516120
CDS:AAA ATPase [Meth  958      T  R  P  A  E  A  T  V  I  V  R  K  L  H  E  W  M  S  S  D

CDS: Putative 1       989      A  G  K  D  L  S  F  G  V  I  S  F  Y  K  A  Q  A  D  S  I
Query                 10896    CAGGGAAAGATCTCTCCTTCGGTGTTATTTCATTTTATAAGGCGCAGGCCGACAGCATCA  10955
                               | || ||||  ||||||||||||| ||||| || || || || || ||||||  |||||
Sbjct                 2516119  CGGGAAAAGGACTCTCCTTCGGTGTGATTTCCTTCTACAAAGCTCAAGCCGACCTCATCA  2516060
CDS:AAA ATPase [Meth  978      A  G  K  G  L  S  F  G  V  I  S  F  Y  K  A  Q  A  D  L  I

CDS: Putative 1       1009     R  E  Q  L  K  R  K  F  G  G  I  V  N  D  D  K  Q  L  R  V
Query                 10956    GGGAACAACTCAAAAGGAAATTCGGCGGGATCGTGAACGATGACAAGCAACTGCGTGTTG  11015
                               || ||| |||     |  |  ||| ||| | ||  | |||   |||| || |||| || |
Sbjct                 2516059  GGAAACGACTG---GGCCACATCG-CGG-A-CG--A-CGA---CAAGAAATTGCGCGTCG  2516012
CDS:AAA ATPase [Meth  998      R  K  R  L    G  H  I   A   D    D   D    K  K  L  R  V

CDS: Putative 1       1029     G  T  V  D  S  F  Q  G  M  E  F  D  V  V  F  L  S  M  V  R
Query                 11016    GAACGGTGGACTCTTTCCAAGGCATGGAATTCGATGTCGTCTTCCTCTCAATGGTGCGAA  11075
                               | |||||||||||||||||||| |||||||||||||||||| ||||| || |||||| |||
Sbjct                 2516011  GGACGGTGGACTCTTTCCAAGGAATGGAATTCGATGTCGTATTCCTATCCATGGTGAGAA  2515952
CDS:AAA ATPase [Meth  1014     G  T  V  D  S  F  Q  G  M  E  F  D  V  V  F  L  S  M  V  R

CDS: Putative 1       1049     T  L  P
Query                 11076    CCTTGCC  11082
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                                || ||||
Sbjct                  2515951  CCATGCC  2515945
CDS:AAA ATPase [Meth   1034     T  M  P


 Features in this part of subject sequence:
   chromosome segregation ATPase-like protein

 Score = 2039 bits (1104),  Expect = 0.0
 Identities = 2910/3793 (77%), Gaps = 80/3793 (2%)
 Strand=Plus/Minus

CDS: Putative 1        1          K  L  A  Q  R  E  Q  A  V  T  Q   A  E  Q  K  C  D  A  G
Query                  13417    CCAAGCTGGCGCAGCGCGAGCAGGCCGTCACGCA-GGCTGAGCAAAAGTGTGATGCAGGT  13475
                                ||||||||  |  |||| ||| | |||||||| ||  || ||||||||  |||| || |||
Sbjct                  2513619  CCAAGCTGACAGAGCGTGAGAAAGCCGTCAC-CATTGCCGAGCAAAATCGTGACGCTGGT  2513561
CDS:chromosome segre   39       S  K  L  T  E  R  E  K  A  V  T   I  A  E  Q  N  R  D  A  G

CDS: Putative 1        20        F  A  D  E  R  A  A  L  N  D  E  L  R  E  K  R  A  Q  G  E
Query                  13476    TTTGCCGATGAACGAGCCGCGCTGAATGATGAGCTGCGTGAAAAGCGCGCCCAGGGCGAA  13535
                                ||||| || || || || ||  ||||  ||||| |||| || || ||||| || |||  |
Sbjct                  2513560  TTTGCTGACGACCGTGCTGCTTTGAACCATGAGTTGCGCGACAAACGCGCTCA-GGCAGA  2513502
CDS:chromosome segre   59        F  A  D  D  R  A  A  L  N  H  E  L  R  D  K  R  A  Q   A  E

CDS: Putative 1        40        R  A   I  A  E  M  R  E  K  N  L  S  A  L  E  V  E  I  S  E
Query                  13536    AGAGCA-ATTGCCGAGATGCGAGAGAAAAACCTTTCAGCGTTGGAGGTTGAAATTTCCGA  13594
                                || | | ||  |  |  |  |||  ||||| ||||| | | | || | ||||||| || |
Sbjct                  2513501  AGCGGAGATATCAAACTTTAGAGCCAAAAAACTTTCCGAGATTGATGATGAAATTGCCAA  2513442
CDS:chromosome segre   79         A  E  I  S  N  F  R  A  K  K  L  S  E  I  D  D  E  I  A  K

CDS: Putative 1        60         L  K  A  K  R  L  G  A  V  A  H  A  E  N  A  E  R  E  R  I
Query                  13595    GCTGAAAGCAAAGCGACTGGGTGCGGTTGCCCATGCCGAAAACGCCGAACGGGAGCGCAT  13654
                                  | ||| |  ||||||| | ||   |  || | || |||||||  || || || |||||
Sbjct                  2513441  ATTAAAAACCGAGCGACTAGATGACATCTCCAACGCTGAAAACGTGGAGCGTGAACGCAT  2513382
CDS:chromosome segre   99         L  K  T  E  R  L  D  D  I  S  N  A  E  N  V  E  R  E  R  I

CDS: Putative 1        80         R  T  E  I  A  Q  E  R  D  A  W  T  K  Q  Q  G  D  A  R  K
Query                  13655    TCGGACAGAAATCGCCCAAGAGCGCGATGCATGGACAAAACAACAGGGTGACGCTCGAAA  13714
                                |||    ||||| ||| | |||||||| |||||||| || ||||||| |||  |||| ||
Sbjct                  2513381  TCGTGTGGAAATTGCCAAGGAGCGCGAAGCATGGACGAAGCAACAGGATGATACTCGCAA  2513322
CDS:chromosome segre   119        R  V  E  I  A  K  E  R  E  A  W  T  K  Q  Q  D  D  T  R  K

CDS: Putative 1        100        Q  L  N  A  E  R  T  E  F  E  K  Q  K  G  A  L  S  A  L  Q
Query                  13715    GCAGTTGAATGCAGAGCGCACGGAATTTGAGAAACAAAAAGGCGCACTCTCCGCCTTGCA  13774
                                |||||||||| | || |||||||| |||||||||||   || || || || |  |||||
Sbjct                  2513321  GCAGTTGAATACCGAACGCACGGAGTTTGAGAAACAACGGGGTGCGCTATCTGTTTTGCA  2513262
CDS:chromosome segre   139        Q  L  N  T  E  R  T  E  F  E  K  Q  R  G  A  L  S  V  L  Q

CDS: Putative 1        120        S  E  V  E  G  R  Q  A  E  L   E  T  S  E  R  T  L  E  R
Query                  13775    AAGCGAAGTCGAAGGAAGACAGGCAGAGCTTG-AGACTTCAGAGCGGACACTCGAACGCA  13833
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                                  ||||||  | || ||  || ||   ||||||| || |  | ||| |||  ||||||||||
Sbjct                   2513261  AAGCGAGCTTGAGGGTCGAAAGATCGAGCTTGAAGGC-GCCGAGAGGATGCTCGAACGCA  2513203
CDS:chromosome segre    159        S  E  L  E  G  R  K  I  E  L  E  G   A  E  R  M  L  E  R

CDS: Putative 1         139      K  E  Q  R  L  E  Q  Q  N  Q  R  R  S  E  Q  L  D  D  E  V
Query                   13834    AAGAACAACGGCTGGAACAGCAGAACCAGAGGCGCAGCGAGCAACTGGACGATGAGGTTG  13893
                                 ||||||| || || || |||||    ||||| ||||  ||||||||| | ||||| || |
Sbjct                   2513202  AAGAACAGCGACTAGAGCAGCAATGGCAGAGACGCAATGAGCAACTGCAGGATGAAGTAG  2513143
CDS:chromosome segre    178      K  E  Q  R  L  E  Q  Q  W  Q  R  R  N  E  Q  L  Q  D  E  V

CDS: Putative 1         159      E   R  R  V  E  D  R  R  K  S  L  E  A  A   L   Q  S  A  K
Query                   13894    A-GAGGCGTGTTGAGGATCGCCGAAAATCGCTAGAGGCTGC-TCTGC-AATCTGCCAAAG  13950
                                 | ||  |   ||  ||| ||||| || || || ||||||||    || ||| |   ||||
Sbjct                   2513142  ATGA-ACAGATTAGGGAACGCCGCAAGTCACTGGAGGCTGCGGAGGCAAATAT--TAAAG  2513086
CDS:chromosome segre    198      D  E   Q  I  R  E  R  R  K  S  L  E  A  A  E  A  N  I    K

CDS: Putative 1         178      E  E  N  I  R  L  R  E  A  F  K  T  Q  D   E  L  L  G  A  F
Query                   13951    AGGAAAACATTCGACTGCGCGAGGCGTTTAAAACTCAAGAC-GAACTTCTCGGCGCGTTC  14009
                                  |||||| |||||  |||| |||||| |  |   || |||| | |||| || | || |||
Sbjct                   2513085  TGGAAAATATTCGGTTGCGTGAGGCGCTGCACGTTC-AGACTGGACTTGTCAGTGCATTC  2513027
CDS:chromosome segre    217      V  E  N  I  R  L  R  E  A  L  H  V   Q  T  G  L  V  S  A  F

CDS: Putative 1         198       E  Q  L  K  L  Q  L  G  G  K  D  P  A  E  I  L  R  A  L  N
Query                   14010    GAACAGTTAAAGTTGCAACTTGGTGGCAAAGACCCTGCTGAAATTCTGCGTGCGCTGAAC  14069
                                 || || |||||   ||| || |||||||||||||| || || || ||||| ||  |||||
Sbjct                   2513026  GAGCAATTAAAACAGCAGCTCGGTGGCAAAGACCCAGCAGAGATCCTGCGCGCATTGAAC  2512967
CDS:chromosome segre    237       E  Q  L  K  Q  Q  L  G  G  K  D  P  A  E  I  L  R  A  L  N

CDS: Putative 1         218       S  Q  A  D  E  L  K  R  L  R  E  E  L  A  T  R  P  T  E  E
Query                   14070    AGCCAGGCCGACGAACTCAAACGCCTACGAGAGGAGCTTGCTACCCGACCTACTGAGGAA  14129
                                 || ||  | ||||||||||||||||| || || |||||||| |||||||| || ||||||
Sbjct                   2512966  AGTCAAACTGACGAACTCAAACGCCTGCGTGAAGAGCTTGCCACCCGACCCACCGAGGAA  2512907
CDS:chromosome segre    257       S  Q  T  D  E  L  K  R  L  R  E  E  L  A  T  R  P  T  E  E

CDS: Putative 1         238       M  R  E  R  Y  Q  A  L  E  S  E  A  K  N  Q  K  T  R  A  D
Query                   14130    ATGCGCGAGCGGTATCAAGCCCTTGAATCAGAAGCCAAAAATCAGAAAACACGGGCAGAC  14189
                                 |||||||||||||||||  | |||||||| |||||||  || ||||| |  ||||| |||
Sbjct                   2512906  ATGCGCGAGCGGTATCAGACGCTTGAATCGGAAGCCAGGAACCAGAAGATGCGGGCTGAC  2512847
CDS:chromosome segre    277       M  R  E  R  Y  Q  T  L  E  S  E  A  R  N  Q  K  M  R  A  D

CDS: Putative 1         258       Q  L  E  R  Q  L  S  T  N  E  A  A  V  A  E  I  G  E  L  R
Query                   14190    CAGTTAGAACGGCAACTTTCCACCAATGAGGCTGCGGTCGCTGAAATTGGCGAGCTGCGC  14249
                                  |||| || |||||| || |||  ||||| || || || || ||||||||||| ||||||
Sbjct                   2512846  GAGTTGGAGCGGCAAATTGCCAGTAATGAAGCGGCTGTAGCCGAAATTGGCGACCTGCGC  2512787
CDS:chromosome segre    297       E  L  E  R  Q  I  A  S  N  E  A  A  V  A  E  I  G  D  L  R

CDS: Putative 1         278       R  Q  G  S  E  L  N  A  E  N  K  S  L  A  Q  R  A  S  I  F
Query                   14250    CGTCAAGGCTCGGAGCTCAACGCCGAAAACAAATCTCTGGCGCAAAGGGCATCCATCTTC  14309
                                 || ||   ||| || ||||||||||| ||||| ||| |||||||||| || |||||||||
Sbjct                   2512786  CGCCAGAACTCCGAACTCAACGCCGAGAACAAGTCTTTGGCGCAAAGAGCGTCCATCTTC  2512727
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CDS:chromosome segre  317       R  Q  N  S  E  L  N  A  E  N  K  S  L  A  Q  R  A  S  I  F

CDS: Putative 1       298       E  G  A  A  N  E  A  Q  A  E  L  K  R  L  R  A  A  Y  E  R
Query                 14310    GAGGGAGCAGCCAACGAAGCGCAAGCCGAACTCAAGCGTTTGCGTGCAGCTTATGAGCGC  14369
                               ||||| |||||||||||||||||| |||||||||| ||| ||||||| |||||||||||
Sbjct                 2512726  GAGGGGGCAGCCAACGAAGCGCAATCCGAACTCAACCGTCTGCGTGCGGCTTATGAGCGT  2512667
CDS:chromosome segre  337       E  G  A  A  N  E  A  Q  S  E  L  N  R  L  R  A  A  Y  E  R

CDS: Putative 1       318       P  A  E  V  T  A  R  Y  K  E  I  E  M  P  H  I  S  V  D  K
Query                 14370    CCTGCTGAAGTTACCGCTCGCTACAAAGAAATTGAGATGCCGCACATCAGTGTGGATAAG  14429
                               || || |||||| | || || |||||||||||||||||||||||||||||||||||| ||
Sbjct                 2512666  CCCGCCGAAGTTGCAGCCCGTTACAAAGAAATTGAGATGCCGCACATCAGTGTGGACAAA  2512607
CDS:chromosome segre  357       P  A  E  V  A  A  R  Y  K  E  I  E  M  P  H  I  S  V  D  K

CDS: Putative 1       338       V  K  Q  P  V  Q  H  E  I  D  E  L  T  W  L  T  G  I  G  N
Query                 14430    GTCAAGCAGCCGGTGCAGCACGAGATCGATGAGCTAACTTGGCTCACTGGGATTGGTAAT  14489
                               |||||  |||| ||| | || || || || ||| | ||||||||||| || ||||| |||
Sbjct                 2512606  GTCAAAGAGCCCGTGAAACATGATATTGACGAGATGACTTGGCTCACGGGCATTGGCAAT  2512547
CDS:chromosome segre  377       V  K  E  P  V  K  H  D  I  D  E  M  T  W  L  T  G  I  G  N

CDS: Putative 1       358       A  C  D  T  Y  G  L  H  F  N  P  R  I  L  K  A  F  H  T  A
Query                 14490    GCTTGCGATACATACGGACTACATTTCAATCCACGTATTTTGAAAGCTTTTCATACAGCT  14549
                               || ||||| ||||||||  | || ||||| || || || |||||||| ||||| || ||
Sbjct                 2512546  GCCTGCGACACATACGGGTTGCACTTCAACCCGCGCATCTTGAAAGCATTTCACACTGCG  2512487
CDS:chromosome segre  397       A  C  D  T  Y  G  L  H  F  N  P  R  I  L  K  A  F  H  T  A

CDS: Putative 1       378       L  K  T  A  E  W  S  P  L  T  V  L  A  G  V  S  G  T  G  K
Query                 14550    CTCAAAACAGCGGAATGGTCGCCGCTCACTGTCCTGGCAGGGGTTTCCGGAACCGGAAAA  14609
                               ||||||||||| |||||||| || |||||||| ||||| || ||||||||||||||||||
Sbjct                 2512486  CTCAAAACAGCTGAATGGTCACCTCTCACTGTACTGGCGGGTGTTTCCGGAACCGGAAAA  2512427
CDS:chromosome segre  417       L  K  T  A  E  W  S  P  L  T  V  L  A  G  V  S  G  T  G  K

CDS: Putative 1       398       S  E  L  P  R  L  Y  S  H  F  G  G  I  Y  F  E  P  L  S  V
Query                 14610    TCCGAACTGCCGCGCCTCTACTCGCACTTTGGCGGAATTTATTTCGAGCCGCTGTCTGTC  14669
                               ||||| ||||| || || |||||||||||||||| || || || |||||||| || |||
Sbjct                 2512426  TCCGAGCTGCCACGTCTATACTCGCACTTTGGCGGCATCTACTTTGAGCCGCTTTCAGTC  2512367
CDS:chromosome segre  437       S  E  L  P  R  L  Y  S  H  F  G  G  I  Y  F  E  P  L  S  V

CDS: Putative 1       418       Q  P  N  W  D  S  Q  E  S  M  L  G  F  F  N  S  I  D  N  K
Query                 14670    CAGCCTAATTGGGATTCGCAGGAATCCATGCTGGGCTTTTTCAATTCCATAGACAATAAA  14729
                               ||||| || ||||| || ||||| |||||||||||||| ||||| ||||||||||| |||
Sbjct                 2512366  CAGCCGAACTGGGACTCACAGGAGTCCATGCTGGGCTTCTTCAACTCCATAGACAACAAA  2512307
CDS:chromosome segre  457       Q  P  N  W  D  S  Q  E  S  M  L  G  F  F  N  S  I  D  N  K

CDS: Putative 1       438       F  D  A  Q  P  V  L  R  F  L  A  Q  S  Q  I  S  G  R  E  Q
Query                 14730    TTCGATGCACAGCCGGTGCTGCGTTTTCTCGCGCAAAGTCAGATATCAGGCCGCGAACAA  14789
                               |||||||| ||||| ||||| ||||| ||||||||||| || ||| |||| | |||  ||
Sbjct                 2512306  TTCGATGCGCAGCCTGTGCTACGTTTCCTCGCGCAAAGCCAAATACCAGGACACGAGAAA  2512247
CDS:chromosome segre  477       F  D  A  Q  P  V  L  R  F  L  A  Q  S  Q  I  P  G  H  E  K
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CDS: Putative 1       458       Y  E   Q  R  I  R  R  W  Q   S  M  S  P  D  Q  Q  I  A  L
Query                 14790    TATGAAC-AGCGCATTAGACGTTGGCA-GAGTATGTCGCCAGATCAGCAAATAGCACTTG  14847
                               ||||||| | || |||||||||||||| ||| ||||| || ||| | |  ||| | ||||
Sbjct                 2512246  TATGAACAAACG-ATTAGACGTTGGCAGGAG-ATGTCACCGGAT-A-C-GATAACTCTTG  2512192
CDS:chromosome segre  497       Y  E  Q  T   I  R  R  W  Q  E   M  S  P  D   T   I  T  L

CDS: Putative 1       477      D  P  E  K  D  K   E  L  I  E  A  L  K  Q  A  D  Y  P  G  L
Query                 14848    ACCCTGAGAAGGACAAAG-AGCTGATTGAAGCGTTGAAACAAGCAGATTATCCAGGATTG  14906
                               |||| || |||| | ||| | |||||||| || |||||||  ||||||||||| ||  |
Sbjct                 2512191  ACCCCGAAAAGG-CTAAGAAACTGATTGATGCTTTGAAACTGGCAGATTATCCGGGGCTA  2512133
CDS:chromosome segre  515      D  P  E  K   A  K  K  L  I  D  A  L  K  L  A  D  Y  P  G  L

CDS: Putative 1       497       Q  D  A  V  C  L  V  L  L  D  E  M  N  L  A  H  P  E  L  Y
Query                 14907    CAGGACGCAGTGTGTCTTGTTCTGCTTGATGAGATGAATCTGGCACACCCTGAGCTTTAT  14966
                               || || ||||| ||||||||||| |||||||| ||||| || || ||||| || || |||
Sbjct                 2512132  CAAGATGCAGTCTGTCTTGTTCTACTTGATGAAATGAACCTAGCGCACCCAGAACTGTAT  2512073
CDS:chromosome segre  535       Q  D  A  V  C  L  V  L  L  D  E  M  N  L  A  H  P  E  L  Y

CDS: Putative 1       517       F  A  E  F  L  S  K  L  E  L  R  R  G  R  K  G  D  D  V   P
Query                 14967    TTTGCAGAGTTTTTGAGCAAGCTAGAACTGCGGCGTGGCAGAAAGGGTGATGATGT-TCC  15025
                               || || || || ||||||||||| || || ||| | ||  | ||||| |  |||||  ||
Sbjct                 2512072  TTCGCGGACTTCTTGAGCAAGCTTGAGCTACGGAGAGGTCGGAAGGGGGGCGATGTACCC  2512013
CDS:chromosome segre  555       F  A  D  F  L  S  K  L  E  L  R  R  G  R  K  G  G  D  V  P

CDS: Putative 1       537         F  I  P  V  K  I  G  A  G  M  E  P  Y  K  L  P  L  G  R  N
Query                 15026    GTTCATACCGGTGAAAATTGGCGCCGGCATGGAACCCTATAAGCTCCCCCTCGGTCGTAA  15085
                               |||| | || |||||||| || || || |||   || ||| | |||||||| || |||||
Sbjct                 2512012  GTTC-TTCCCGTGAAAATAGGTGCTGGGATGTCCCCTTATCAACTCCCCCTAGGACGTAA  2511954
CDS:chromosome segre  575       V   L  P  V  K  I  G  A  G  M  S  P  Y  Q  L  P  L  G  R  N

CDS: Putative 1       557         V  L  W  T  G  T  M  N  Q  D  E  T  T  K  S  L  S  D  K  V
Query                 15086    TGTACTCTGGACAGGGACGATGAACCAGGACGAAACCACCAAGTCCCTTTCGGACAAGGT  15145
                               ||| |||||||| ||||||||||||||||||||| || ||||| ||||| ||||||||
Sbjct                 2511953  TGTTCTCTGGACGGGGACGATGAACCAGGACGAAACAACTAAGTCACTTTCAGACAAGGT  2511894
CDS:chromosome segre  595         V  L  W  T  G  T  M  N  Q  D  E  T  T  K  S  L  S  D  K  V

CDS: Putative 1       577         L  D  R  S  I  I  I  N  F  P  R  P  T  E  L  K  R  R  L  K
Query                 15146    GCTTGACCGTTCCATCATCATCAACTTTCCGCGCCCGACGGAACTCAAACGCCGCCTGAA  15205
                                || || || |||||||| |||||||| || || ||||| |||||||||||||| || ||
Sbjct                 2511893  CCTCGATCGCTCCATCATTATCAACTTCCCTCGACCGACAGAACTCAAACGCCGTCTAAA  2511834
CDS:chromosome segre  615         L  D  R  S  I  I  I  N  F  P  R  P  T  E  L  K  R  R  L  K

CDS: Putative 1       597         L  A  P  L  D  D  K  N  R  G  P  A  L  H  K  T  S  W  Q  S
Query                 15206    GCTTGCTCCACTTGATGACAAAAATCGAGGCCCGGCGCTACACAAAACGTCGTGGCAGAG  15265
                               |||||| || ||||||||||| ||| |  | || ||||||||||||||| ||||||||||
Sbjct                 2511833  GCTTGCGCCGCTTGATGACAAGAATTGCAGTCCTGCGCTACACAAAACATCGTGGCAGAG  2511774
CDS:chromosome segre  635         L  A  P  L  D  D  K  N  C  S  P  A  L  H  K  T  S  W  Q  S

CDS: Putative 1       617         W  L  A  Q  G  S  N  F  S  D  D  Q  V  S  P  F  K  K  F  I
Query                 15266    TTGGCTAGCACAGGGCAGCAACTTCTCCGACGATCAAGTCAGCCCGTTCAAAAAATTCAT  15325
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                                 |||| |||| || |||||| | |||||||| || || ||||  |||||||| |||||||
Sbjct                  2511773  TTGGGTAGCGCAAGGCAGCGATTTCTCCGATGACCAGGTCAAACCGTTCAAAGAATTCAT  2511714
CDS:chromosome segre   655        W  V  A  Q  G  S  D  F  S  D  D  Q  V  K  P  F  K  E  F  I

CDS: Putative 1        637        E  A  I  N  A  S  L  A  V  T  G  R  A  L  G  H  R  V  W  Q
Query                  15326    TGAAGCAATCAATGCTTCTTTAGCGGTTACAGGCCGTGCCCTCGGTCACCGCGTTTGGCA  15385
                                 |||| ||| ||||| ||| |  |||| ||||| ||||||||||| |||||||| |||||
Sbjct                  2511713  CGAAGGAATGAATGCCTCTCTCTCGGTCACAGGTCGTGCCCTCGGCCACCGCGTATGGCA  2511654
CDS:chromosome segre   675        E  G  M  N  A  S  L  S  V  T  G  R  A  L  G  H  R  V  W  Q

CDS: Putative 1        657        S  I  E  Y  Y  M  A  N  Y  P  D  V  R  A  A   R  D   K  D
Query                  15386    ATCCATTGAATACTACATGGCCAATTACCCGGATGTCCGTGCTGCAC-GCGAT--AAAGA  15442
                                 |||||||||||||||||||||||||||||||||| ||||||||| |||    |||||
Sbjct                  2511653  GTCCATTGAATACTACATGGCCAATTACCCGGATGTTCGTGCTGCACAGCGGGCGAAAGA  2511594
CDS:chromosome segre   695        S  I  E  Y  Y  M  A  N  Y  P  D  V  R  A  A  Q  R  A  K  D

CDS: Putative 1        676              A  L  A  R  A  M  H  V  A  F  E  D  Q  L  V  Q  K  V
Query                  15443    T--G----CGCTTGCCAGAGCTATGCATGTCGCCTTCGAGGATCAACTCGTGCAGAAGGT  15496
                                |  |    ||||||| |  || |||||| |||| |||||||||||||||||||||||||
Sbjct                  2511593  TAAGGATTCGCTTGCTAAGGCAATGCATATCGCTTTCGAGGATCAACTCGTGCAGAAGGT  2511534
CDS:chromosome segre   715        K  D  S  L  A  K  A  M  H  I  A  F  E  D  Q  L  V  Q  K  V

CDS: Putative 1        694        M  P  K  L  R  G  I  D  T  R  G  K  S  K  T  E  C  L  D  R
Query                  15497    CATGCCCAAATTGCGGGGTATTGATACACGCGGCAAGAGCAAGACAGAGTGCCTGGACAG  15556
                                 |||||||| || ||||| || || || |||||||||||||||| |||||||||||||
Sbjct                  2511533  TATGCCCAAGTTACGGGGCATAGACACGCGCGGCAAGAGCAAGACGGAGTGCCTGGACAA  2511474
CDS:chromosome segre   735        M  P  K  L  R  G  I  D  T  R  G  K  S  K  T  E  C  L  D  K

CDS: Putative 1        714        I  R  G  Q  L  V  T  G  I  G  S  N  S  F  N  L  T  E  D  F
Query                  15557    GATTCGTGGACAACTCGTTACAGGAATCGGCAGTAACTCATTCAATCTGACAGAGGATTT  15616
                                 ||||  || ||  | ||||| || |||||| | |||   ||||||||  | ||||||||
Sbjct                  2511473  AATTCTCGGGCAGATTGTTACTGGGATCGGCGGCAACAAGTTCAATCTTGCCGAGGATTT  2511414
CDS:chromosome segre   755        I  L  G  Q  I  V  T  G  I  G  G  N  K  F  N  L  A  E  D  F

CDS: Putative 1        734        D  L  A  C  D  L  G  Y  G  Q  F  I  W  Q  S  A  N  Y  L  N
Query                  15617    CGACCTTGCCTGTGATCTTGGCTATGGTCAGTTTATTTGGCAGTCGGCAAATTACCTAAA  15676
                                 ||| || |||||  ||||||| ||||| ||||| || |||||||| || ||||| || ||
Sbjct                  2511413  CGATCTCGCCTGCTATCTTGGTTATGGACAGTTCATCTGGCAGTCAGCTAATTATCTTAA  2511354
CDS:chromosome segre   775        D  L  A  C  Y  L  G  Y  G  Q  F  I  W  Q  S  A  N  Y  L  N

CDS: Putative 1        754        V  G  D  T  E  T  N  D  R  S  T  A  S  R   D  S  D    N
Query                  15677    CGTCGGTGACACGGAAACCAATGATAGATCCACGGCCAGTCGA-GACTCGGAC---AATG  15732
                                 |||||| || |||||   |||||  | ||  | | | || | | | ||||||    || |
Sbjct                  2511353  CGTCGGCGATACGGACGTCAATGGAAAATATATGAC-AGCCCAAGCCTCGGATGGGAACG  2511295
CDS:chromosome segre   795        V  G  D  T  D  V  N  G  K  Y  M  T   A  Q  A  S  D  G  N

CDS: Putative 1        772      A  E  L  P  H  S   L  F  M  K  D  E  P  D  S  D  K  R  H  K
Query                  15733    CTGAATTGCCACACTCC-CTTTTTATGAAAGATGAACCAGATTCAGACAAGCGTCATAAA  15791
                                  |||   ||||| ||| |||||||||| | |||||||||||   | |||||||| ||||
Sbjct                  2511294  AAGAA---CCACA-TCCGCTTTTTATGATAAATGAACCAGATATGGCCAAGCGTCGTAAA  2511239
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CDS:chromosome segre  814      E  E    P  H   P  L  F  M  I  N  E  P  D  M  A  K  R  R  K

CDS: Putative 1       792       M  W  N  L  K  T  P  E  Q  R  D  E  L  R  V  K  L  E  E  N
Query                 15792    ATGTGGAACTTAAAGACACCAGAGCAACGAGATGAGCTGCGCGTGAAACTTGAAGAAAAT  15851
                                 ||||||   |||||||||||||||||||| || ||  | |   | || ||||  |||
Sbjct                 2511238  GCGTGGAATGCAAAGACACCAGAGCAACGAGACGAACTTAGTGATCAGCTAGAAGCGAAT  2511179
CDS:chromosome segre  833       A  W  N  A  K  T  P  E  Q  R  D  E  L  S  D  Q  L  E  A  N

CDS: Putative 1       812       A  R  A  G  R  I  H   A
Query                 15852    GCCAGAGCAGGAAGGATTCAC-GCCAAGCAATGAGTATTACTCTGGAAAAAATCTATACC  15910
                               | ||  || |||||||||| | || |  || |||  || | |||| ||||| | |||  |
Sbjct                 2511178  GACAAGGCTGGAAGGATTCCCCGCTAGACA-TGACAATAAATCTGCAAAAAGTATATTTC  2511120
CDS:chromosome segre  853       D  K  A  G  R  I  P  R

Query                 15911    GACTTCCGTGCCAAAGAAAAACTTGCCAAAAAACTGCTTGAGCAAATGAATTGGTTTGGT  15970
                               ||||  || ||| ||||  ||   |||     |||||||| |||| || |||||||| ||
Sbjct                 2511119  GACTATCGCGCCGAAGAGGAAAAGGCCTGTGCACTGCTTGGGCAATTGGATTGGTTTTGT  2511060

Query                 15971    T-CAAT-CACGGATTTCGATCCTAAGACCGGCGCGGCTCTGCCGAAATCCTTGTCAGGGT  16028
                                || | || | |||||||||| || || ||   |||  ||||  || | || ||    |
Sbjct                 2511059  CGCATTGCA-G-ATTTCGATCCGAAAACTGGTTTGGCGTTGCCACAAGCATTATCTATTT  2511002

Query                 16029    TCCTCGCCAAAGTCGCAC-AGCCAGAA--G-CGAGTGAGATAACCCGTGACCGCCTTTGG  16084
                               ||||||  | |||||||| | | | ||  | || ||| | |  |   |||| | ||||||
Sbjct                 2511001  TCCTCGAAAGAGTCGCACTACCGAAAAATGGCG-GTGTGGTT-CT--TGACAGACTTTGG  2510946

Query                 16085    CGCATAACGGAACACTGCCGCGCTTCTGTCGAGCGATTATTTCATTCTCTCAACGAAAGT  16144
                               || || ||||| ||| |||| ||||| ||||||||  ||||||| || ||||| ||||||
Sbjct                 2510945  CGTATCACGGAGCACAGCCGTGCTTCAGTCGAGCGGCTATTTCACTCGCTCAATGAAAGT  2510886

Query                 16145    CCTCGCTGCGAACACGCTCTACTGCCTGTTCATGCTGTGCGTGAACTGGATGCCAACAGT  16204
                               || ||| | || |||||  | || || || || || ||||||||||| ||||||| |||
Sbjct                 2510885  CCACGCCGTGAGCACGCCTTGCTACCCGTACACGCCGTGCGTGAACTCGATGCCAGCAGC  2510826

Query                 16205    TTTATTAAGCTGAGTAATCGTCCGGGTCGTACCATTCGGGAAAAACTGGCAGGTAACCCC  16264
                               || || ||||| || || ||||| || || || |||||||||||||| || || || |||
Sbjct                 2510825  TTCATCAAGCTCAGCAACCGTCCAGGACGCACTATTCGGGAAAAACTTGCGGGCAAACCC  2510766

Query                 16265    TACATACAGGCTGTGCGTCGTTTTCAATCCGTCGACCTGCCGGAAAATCGCTTGCTGAAA  16324
                               || || ||||| |||||||| || ||||| |||||  ||||||| || ||  |||||||
Sbjct                 2510765  TATATGCAGGCCGTGCGTCGGTTCCAATCTGTCGATTTGCCGGAGAACCGTCTGCTGAAG  2510706

Query                 16325    GCCTTTGCCATTCGCCTTGCGGAAATGCTTGATTTACGCGGTGATTGTCTCGGTCAAGAG  16384
                               || ||||     | ||| | |||| |||| || || ||| | ||||||||| | || ||
Sbjct                 2510705  GCATTTGTGCGGCACCTAGGGGAACTGCTCGAATTGCGCCGAGATTGTCTCAGCCATGAA  2510646

Query                 16385    GATGAGCTTCTATCAAAAATCTACTTATGGTTGCGTTCTGATGAGGCGCAAGCCATCGGC  16444
                               || || |||||  |||||||  | || ||| | ||||| || || || || ||||| |||
Sbjct                 2510645  GACGAACTTCTGCCAAAAATACAATTGTGGCTACGTTCAGAGGAAGCACAGGCCATTGGC  2510586
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Query                 16445    AATTGGGAAAATCTGCCACCTAACAACACGCTACTAGCACACCGAGATTACCGTCACGTG  16504
                               |||||||| || ||||| || ||||| ||||| ||  | ||||| |||||||| |  ||
Sbjct                 2510585  AATTGGGACAACCTGCCGCCCAACAATACGCTGCTCTCGCACCGCGATTACCGGCGAGTT  2510526

Query                 16505    TGGGATGCATGGCGCTGGCTGCAAACCCTCGATGAGGACATCACCAGCGACCTTTCTCAA  16564
                               |||||  ||||||||||||| || ||| | || || ||  || |  |||||||| ||||
Sbjct                 2510525  TGGGACTCATGGCGCTGGCTACAGACCTTGGACGATGATGTCGCTGGCGACCTTGCTCAG  2510466

Query                 16565    CTGGATGTCCGCGAGAAAACCATGCGCCTTTGGCAGCAATGCGCGCAAATGTGG-CTTGA  16623
                               || || |  ||||  || || |||||||| ||| |||||||||||||||||| || ||
Sbjct                 2510465  CTTGAAGCGCGCGGCAAGACAATGCGCCTATGGAAGCAATGCGCGCAAATGTGGGCTGGA  2510406

Query                 16624    TGGAAAGCATCTTTTTGCTGAGATACCGTTACTATTCGATTATGAAAAGTTTGAGATTCT  16683
                                || |||||||| ||||| ||||| ||| | || |||||||| || ||||| ||||||||
Sbjct                 2510405  -GGCAAGCATCTCTTTGCAGAGATGCCGCTTCTTTTCGATTACGAGAAGTTCGAGATTCT  2510347

Query                 16684    TCCGTGGACTTCCAAGCCACC-TTTGTTCAAGGAAGTGAAGT-ACAAGATGCCCCGGCAT  16741
                               ||| ||| |||||||||| ||  || || ||  |  | |||  | || || ||  ||| |
Sbjct                 2510346  TCCTTGGTCTTCCAAGCCGCCCCTTTTT-AAT-ACATCAAGGCAGAATATTCCAAGGCGT  2510289

Query                 16742    TTGCGACAAAGC-GCGAG-TG-CCGAACCAATTTGTGTTGATATCACAGCCCTGCATCCC  16798
                                | |  |||||  | ||  |  |||| ||| |||||||||| ||||  || | |  ||
Sbjct                 2510288  AT-C--CAAAGGTGTGAAATCACCGAGCCAGTTTGTGTTGATTTCACGTCCTTACGCCCG  2510232

Query                 16799    CGCTATGCCAGTGGTGACGGAAAAGGAGCGCAGTCGCTGGCGGCCCCCTTTCTTTGGCAG  16858
                               ||||| |||||||| ||||| ||||  || |||||  || | |   | || || ||||||
Sbjct                 2510231  CGCTACGCCAGTGGCGACGGTAAAGTCGCACAGTCATTGCCAGAGGCGTTCCTGTGGCAG  2510172

Query                 16859    AGGTGGCAG-CGCGAAAATGAAACCGTTGACATCGAACTCTTTGGTTCCGATGCCGTTTG  16917
                                  ||| || |||||  |||| | ||| |||||||||||||   ||| ||||||||||
Sbjct                 2510171  CAATGG-AGACGCGATGATGAGAGCGTGGACATCGAACTCTTCCATTCTGATGCCGTTTG  2510113

Query                 16918    GCTGAATCC-CGATGCGACCACCATTTCTGCGCCAGATCTGTTTTTCGCCAAAGACAACG  16976
                               |||  |||| | || |||| ||||| ||||||||||||||| || ||||| || ||||||
Sbjct                 2510112  GCTTCATCCGCAAT-CGACTACCATCTCTGCGCCAGATCTCTTATTCGCAAAGGACAACA  2510054

Query                 16977    CCACTGAGCTTTTTGACCCCGCCGCCCGCGCGTTCACTACTCGGCTACGCGAAGAGTTCA  17036
                               |  | |||   |  ||||  |||||||||||||||| |  |||  ||  |||| | |||
Sbjct                 2510053  CGTCAGAGAACTGCGACCGTGCCGCCCGCGCGTTCGCATCTCATCT--GCGAGGCGTTTT  2509996

Query                 17037    -AGA-ACGATACACTCATCTGGCTTGCGCCTGACTTTCTCAACGATTTCGAGCTTGAAGT  17094
                                ||  |||| || ||||| ||||||||||| ||||  || ||||| |||||||| |||||
Sbjct                 2509995  TAGGCACGACACGCTCATTTGGCTTGCGCCAGACTACCTTAACGACTTCGAGCTCGAAGT  2509936

Query                 17095    CATCCGTCGCAACCTCAACGCGCGTTTC-CCGAATGCCGAGCCGTTGCCGCGAAGTGTGG  17153
                               |||||| ||||||||||||||| |||||| |||| ||| ||||| |||||||| || || |
Sbjct                 2509935  CATCCGCCGCAACCTCAACGCACGTTTCACCGA-TGCAGAGCCATTGCCGCGTAGCGTAG  2509877

Query                 17154    CGGCCGTGTTCGC  17166
                               ||||||| |||||
```

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Sbjct                 2509876  CGGCCGTCTTCGC  2509864


 Features in this part of subject sequence:
   hypothetical protein
   hypothetical protein

 Score =  171 bits (92),  Expect = 6e-38
 Identities = 154/184 (84%), Gaps = 4/184 (2%)
 Strand=Plus/Minus

CDS: Putative 2       1          W  L  Q  A  D  E  E  W  A  *
CDS: Putative 1       1                                  M  T  L  W  K  S  F  G  A  S  V
Query                 5855     CTGGCTGCAGGCGGATGAGGAATGGGCATGACGCTTTGGAAAAGTTTTGGGGCAAGCGTT  5914
                               |||||| || | |||||||||||||||||||||||||||||||||||||| || |||||||||
Sbjct                 2521154  CTGGCTCCAAGAGGATGAGGAATGGGCATGACGCTTTGGAAAAGTTTCGGCGCAAGCGTT  2521095
CDS:hypothetical pro  1                                  M  T  L  W  K  S  F  G  A  S  V
CDS:hypothetical pro  150        W  L  Q  E  D  E  E  W  A

CDS: Putative 1       12        R  G  P   S   H  I  A  E  G  L  P  N  Q  D  A  W  A  K  F
Query                 5915     CGCGGCCC-GAGC-CATATCGCCGAAGGTTTGCCAAATCAGGATGCATGGGCGAAGTTTC  5972
                               |||||||| | || ||| | || |||||||||||||| || ||||| |||  |   ||||
Sbjct                 2521094  CGCGGCCCAGGGCACAT-T-GCTGAAGGTTTGCCAAACCAAGATGCGTGGATGTCATTTC  2521037
CDS:hypothetical pro  12        R  G  P  G  H  I    A  E  G  L  P  N  Q  D  A  W  M  S  F

CDS: Putative 1       31       H  H  V  W  G  D  G  I  V  V  S  D  G  V  G  S  K  P  F  S
Query                 5973     ACCATGTTTGGGGTGATGGCATCGTCGTGTCCGACGGAGTTGGCTCCAAGCCCTTCTCCA  6032
                               |||||| |||||| |||||| | || || ||||| ||||||||||| ||||| || ||||
Sbjct                 2521036  ACCATGCTTGGGGGGATGGCGTTGTAGTTTCCGATGGAGTTGGCTCAAAGCCATTTTCCA  2520977
CDS:hypothetical pro  31       H  H  A  W  G  D  G  V  V  V  S  D  G  V  G  S  K  P  F  S

CDS: Putative 1       51       S
Query                 6033     GCTT  6036
                                |||
Sbjct                 2520976  ACTT  2520973
CDS:hypothetical pro  51       N  F


&gt;gb|CP002475.1| Streptomyces flavogriseus ATCC 33331, complete genome
Length=7337497

 Features in this part of subject sequence:
   AAA ATPase central domain protein

 Score = 56.5 bits (30),  Expect = 0.002
 Identities = 30/30 (100%), Gaps = 0/30 (0%)
 Strand=Plus/Minus

CDS: Putative 1       1         G  P  P  G  T  G  K  T  T  V
Query                 9341     GGCCCGCCCGGTACCGGCAAGACCACCGTC  9370
```

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                                ||||||||||||||||||||||||||||||
Sbjct                  1764471  GGCCCGCCCGGTACCGGCAAGACCACCGTC  1764442
CDS:AAA ATPase centr   882       G  P  P  G  T  G  K  T  T  V
```

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
Posted date: Jun 10, 2012 4:43 PM
Number of letters in database: 10,243,265,045
Number of sequences in database: 4,087,780

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.28	0.460	0.850

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 4087780
Number of Hits to DB: 164689
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 17476
Length of database: 10243265045
Length adjustment: 35
Effective length of query: 17441
Effective length of database: 10100192745
Effective search space: 176157461665545
Effective search space used: 176157461665545
A: 0
X1: 14 (26.9 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 14 (27.0 bits)
S2: 24 (45.4 bits)

</pre></body></html>