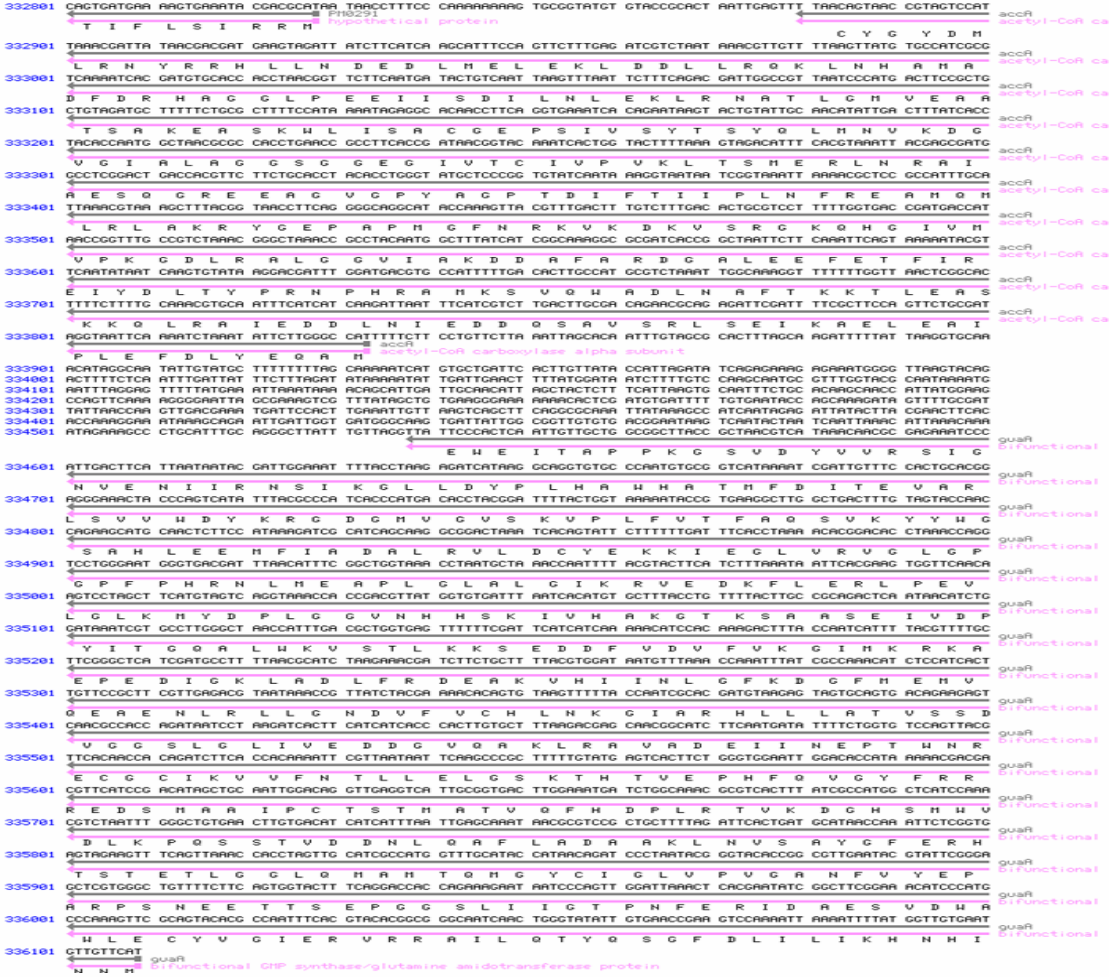
A.



B.

```
Pm70                TTTCTTTAGATATAAAAATATTGATTGAACTTTTATGGATAATCTTTTGTCCAAGCAATG 334079
ePST47              ------------------------------------------------------------ATG 3
HD_1218             ------------------------------------------------------------ATTCTAG 7
                                                                                 *    *

Pm70                CGTTTGGTACGCAATAAAATGAATTTAGGAGTTTTTATGAAATTAAATAAAACAGCATTG 334139
ePST47              CGTTTGGTACGCAATAAAATGAATTTAGGAGTTTTTATGAAATTAAATAAAACAGCATTG 63
HD_1218             TGTGCATTCTTCAATGA--TTGGTTTATCGTTGGCTAGGAGTGTTGCTGTGTTTCCTTTT 65
                     **    *   **** *  *   ****    *   ** **   *  *       * **

Pm70                ATTGCAACAT--TAGCTACTCTTTCATTAAGTGCAATTTCTGCACAAGCAACCATTATGG 334197
ePST47              ATTGCAACAT--TAGCTACTCTTTCATTAAGTGCAATTTCTGCACAAGCAACCATTATGG 121
HD_1218             GTGGCTAATTCATAGTCGTAATTCGGGTTAATG-GGTTTATACACC-GCACCTGAGGCAG 123
                     * ** *  *  ***       **    * * **   *** * ***  *** *       *

Pm70                AAGCCA-GTTCAAAAGGGGAATTAGCGAAAGTCGTTTATAGCTGTGAAGGGAAAAAAACA 334255
                                                                              T
                                                                              T
ePST47              AAGCCA-GTTCAAAAGGGGAATTAGCGAAAGTCGTTTATAGCTGTGAAGGGAAAAAAACA 180
HD_1218             ATTTTACATTTTTCATTGGGATCATTTCATCTACTTGATTG--ATGATCGCATAAGAATC 181
                    *    *  **    *  ** ** * *   *  *  ** ** *   ***  * * ** **

Pm70                CTCGATGTGATTTTTGTGAATACCAGCAAAGATAGTTTTGCGATTATTAACCAAGTTGAC 334315
                                                  D  S  F  A  I  I  N  Q  V  D
                    L  D  V  I  F  V  N  T  S  K
                    L  D  V  I  F  V  N  T  S  K  D  S  F  A  I  I  N  Q  V  D
ePST47              CTCGATGTGATTTTTGTGAATACCAGCAAAGATAGTTTTGCGATTATTAACCAAGTTGAC 240
HD_1218             TTTATCGGTATTCACGAAAATAACATCGAGTGTATTTTTATCTTTA-----CAAGCATAT 236
                     *    *  ***   *  **** ** * *   ** ****    ***      ****   *

Pm70                GAAATGATTCCACTTGAAATTGTTAAGTCAGCTTCAGGCGCAAATTATAAAGCCATCAAT 334375
                    E  M  I  P  L  E  I  V  K
                                                                        A  I  N
                    E  M  I  P  L  E  I  V  K                           A  I  N
ePST47              GAAATGATTCCACTTGAAATTGTTAAGTCAGCTTCAGGCGCAAATTATAAAGCCATCAAT 300
HD_1218             ACAAC--TTTGG--TGATTTCATTCTCTGAGCTTT-GTTGCA--TTATGGTTGCGTGTGC 289
                      **    **      ***  *  **    * *****  *  ***  ****      * *

Pm70                AGAGATTAT-ACTTACGAACTTCACACCAAAGGAAATAAAGCAGAATTGATTGGTGATGG 334434
                       D  Y    T  Y  E  L  H  T  K
                    R  D  Y    T  Y  E  L  H  T  K
                    R  D  Y    T  Y  E  L  H  T  K  G  N  K
ePST47              AGAGATTAT-ACTTACGAACTTCACACCAAAGGAAATAAAGCAGAATTGATTGGTGATGG 359
HD_1218             AGAGATGGTTGCTAACAAGCCT---ATCATTGAGAATAGCGC-GGTTTGTATTTTCAT-- 343
                    ******  *  ** ** * * *   * **  *  ****  ** *  ***  *  * **

Pm70                GCAAGTGATTATTGGCGGTTGTGTGACGGAATAAGTCAATACTAATCAATTAAACATTAA 334494
ePST47              GCAAGTGATTATTGGCGGTTGTGTGACGGAATAA---------------------------- 393
HD_1218             ------------------------------------------------------------
```