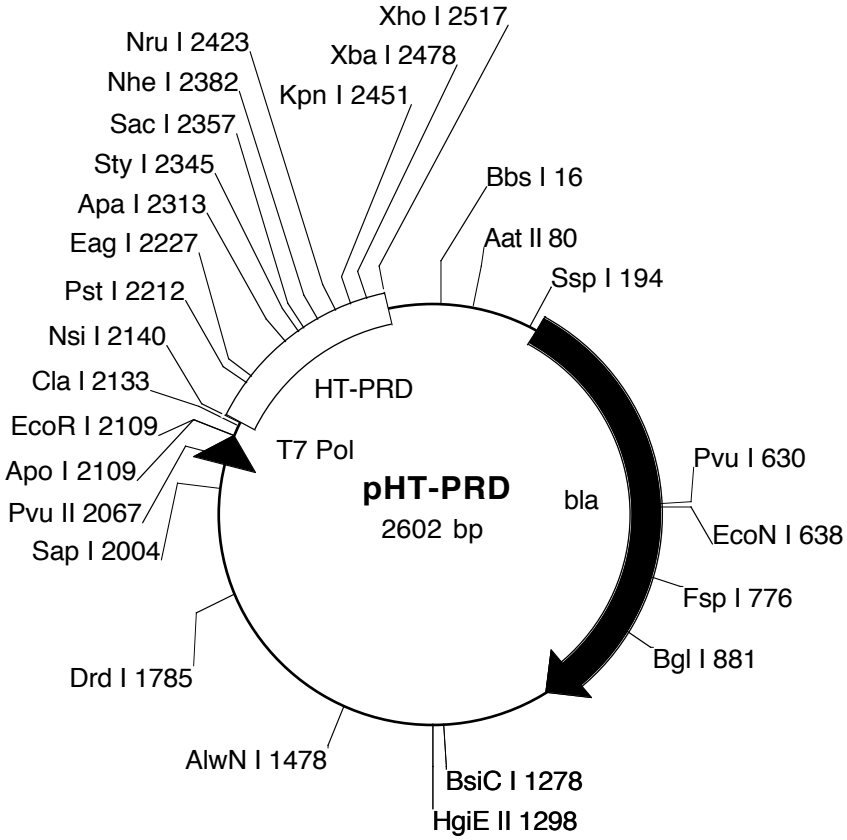

Bacterial expression vector pHT-PRD (pHT-DY1aPRD)
Product: 6X His-tagged dynamin 1a PRD (residues 746-864)
Product calculated MW: 12954.5
Promoter: T7 RNA polymerase promoter
Parent vector: modified pND1, Amp^R
Required host for expression: BL21 or strains containing T7 RNA polymerase

Reference:
Liu, Y., Adayev, T., and Hwang, Y. W. (2017) An ELISA DYRK1A Non Radioactive Assay Suitable for the Characterization of Inhibitors. F1000Research (https://f1000research.com/articles/6-42/)

pHT-PRD sites and sequence

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                Bbs I
         ◊      |   ◊         ◊         ◊         ◊         ◊
ATTTCTTGAAGACGAAAGGGCCTCGTGTTACGCCTATTTTTATAGGTTAATGTCATGATA  60
TAAAGAACTTCTGCTTTCCCGGAGCACAATGCGGATAAAAATATCCAATTACAGTACTAT

                   Aat II
         ◊         |         ◊         ◊         ◊         ◊
ATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATT  120
TATTACCAAAGAATCTGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAA


TGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAA  180
ACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATT


            Ssp I
         ◊  |     ◊         ◊         ◊         ◊         ◊
ATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTT  240
TACGAAGTTATTATAACTTTTTCCTTCTCATACTCATAAGTTGTAAAGGCACAGCGGGAA
                            M  S  I  Q  H  F  R  V  A  L
                            I>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>


ATTCCCTTTTTTCCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAA  300
TAAGGGAAAAAAGGCCGTAAAACGGAAGGACAAAAACGAGTGGGTCTTTGCGACCACTTT
I  P  F  F  P  A  F  C  L  P  V  F  A  H  P  E  T  L  V  K
>>>>>>>>>>>>>>>>>>>>>>>>>>>bla>>>>>>>>>>>>>>>>>>>>>>>>>>>>>


GTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAAC  360
CATTTTCTACGACTTCTAGTCAACCCACGTGCTCACCCAATGTAGCTTGACCTAGAGTTG
V  K  D  A  E  D  Q  L  G  A  R  V  G  Y  I  E  L  D  L  N
>>>>>>>>>>>>>>>>>>>>>>>>>>>bla>>>>>>>>>>>>>>>>>>>>>>>>>>>>>


AGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTT  420
TCGCCATTCTAGGAACTCTCAAAAGCGGGGCTTCTTGCAAAAGGTTACTACTCGTGAAAA
S  G  K  I  L  E  S  F  R  P  E  E  R  F  P  M  M  S  T  F
>>>>>>>>>>>>>>>>>>>>>>>>>>>bla>>>>>>>>>>>>>>>>>>>>>>>>>>>>>


AAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGT  480
TTTCAAGACGATACACCGCGCCATAATAGGGCATAACTGCGGCCCGTTCTCGTTGAGCCA
K  V  L  L  C  G  A  V  L  S  R  I  D  A  G  Q  E  Q  L  G
>>>>>>>>>>>>>>>>>>>>>>>>>>>bla>>>>>>>>>>>>>>>>>>>>>>>>>>>>>


CGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCAT  540
GCGGCGTATGTGATAAGAGTCTTACTGAACCAACTCATGAGTGGTCAGTGTCTTTTCGTA
R  R  I  H  Y  S  Q  N  D  L  V  E  Y  S  P  V  T  E  K  H
>>>>>>>>>>>>>>>>>>>>>>>>>>>bla>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
```

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CTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAAC  600
GAATGCCTACCGTACTGTCATTCTCTTAATACGTCACGACGGTATTGGTACTCACTATTG
L  T  D  G  M  T  V  R  E  L  C  S  A  A  I  T  M  S  D  N
>>>>>>>>>>>>>>>>>>>>>>>>>>>bla>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>

                           Pvu I   EcoN I
         ◊         ◊         |       | ◊         ◊         ◊
ACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTG  660
TGACGCCGGTTGAATGAAGACTGTTGCTAGCCTCCTGGCTTCCTCGATTGGCGAAAAAAC
T  A  A  N  L  L  L  T  T  I  G  G  P  K  E  L  T  A  F  L
>>>>>>>>>>>>>>>>>>>>>>>>>>>bla>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>


CACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCC  720
GTGTTGTACCCCCTAGTACATTGAGCGGAACTAGCAACCCTTGGCCTCGACTTACTTCGG
H  N  M  G  D  H  V  T  R  L  D  R  W  E  P  E  L  N  E  A
>>>>>>>>>>>>>>>>>>>>>>>>>>>bla>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>

                                                        Fsp I
         ◊         ◊         ◊         ◊         ◊     |   ◊
ATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAA  780
TATGGTTTGCTGCTCGCACTGTGGTGCTACGGACATCGTTACCGTTGTTGCAACGCGTTT
I  P  N  D  E  R  D  T  T  M  P  V  A  M  A  T  T  L  R  K
>>>>>>>>>>>>>>>>>>>>>>>>>>>bla>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>


CTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAG  840
GATAATTGACCGCTTGATGAATGAGATCGAAGGGCCGTTGTTAATTATCTGACCTACCTC
L  L  T  G  E  L  L  T  L  A  S  R  Q  Q  L  I  D  W  M  E
>>>>>>>>>>>>>>>>>>>>>>>>>>>bla>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>

                                       Bgl I
         ◊         ◊         ◊         ◊|        ◊         ◊
GCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCT  900
CGCCTATTTCAACGTCCTGGTGAAGACGCGAGCCGGGAAGGCCGACCGACCAAATAACGA
A  D  K  V  A  G  P  L  L  R  S  A  L  P  A  G  W  F  I  A
>>>>>>>>>>>>>>>>>>>>>>>>>>>bla>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>


GATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGAT  960
CTATTTAGACCTCGGCCACTCGCACCCAGAGCGCCATAGTAACGTCGTGACCCCGGTCTA
D  K  S  G  A  G  E  R  G  S  R  G  I  I  A  A  L  G  P  D
>>>>>>>>>>>>>>>>>>>>>>>>>>>bla>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>


GGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAA  1020
CCATTCGGGAGGGCATAGCATCAATAGATGTGCTGCCCCTCAGTCCGTTGATACCTACTT
G  K  P  S  R  I  V  V  I  Y  T  T  G  S  Q  A  T  M  D  E
>>>>>>>>>>>>>>>>>>>>>>>>>>>bla>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>


CGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGAC  1080
GCTTTATCTGTCTAGCGACTCTATCCACGGAGTGACTAATTCGTAACCATTGACAGTCTG
R  N  R  Q  I  A  E  I  G  A  S  L  I  K  H  W  .
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 >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>I

CAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATC  1140
GTTCAAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAG


TAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTC  1200
ATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAG


CACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTG  1260
GTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGAC


                BsiC I              HgiE II
        ◊       | ◊         ◊       | ◊         ◊         ◊
CGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCG  1320
GCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGC


GATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCA  1380
CTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGT


AATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCG  1440
TTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGC


                                  AlwN I
        ◊         ◊         ◊       | ◊         ◊         ◊
CCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCG  1500
GGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGC


TGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGA  1560
ACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACT


ACGGGGGGTTCGTGCACAGAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATAC  1620
TGCCCCCCAAGCACGTGTCTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATG


CTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTAT  1680
GATGTCGCACTCGTAACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATA


CCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCC  1740
GGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGG


                                        Drd I
        ◊         ◊         ◊         ◊    |    ◊         ◊
TGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGA  1800
ACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACT
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TGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTC  1860
ACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAG

CTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTG  1920
GACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACAC

GATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAG  1980
CTATTGGCATAATGGCGGAAACTCACTCGACTATGGCGAGCGGCGTCGGCTTGCTGGCTC

                      Sap I
         ◊         ◊   |     ◊         ◊         ◊         ◊
CGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCC  2040
GCGTCGCTCAGTCACTCGCTCCTTCGCCTTCTCGCGGGTTATGCGTTTGGCGGAGAGGGG

                        Pvu II
         ◊         ◊      |  ◊         ◊         ◊         ◊
GCGCGTTGGCCGATTCATTAATGCAGCTGGCTTATCGAAATTAATACGACTCACTATAGG  2100
CGCGCAACCGGCTAAGTAATTACGTCGACCGAATAGCTTTAATTATGCTGAGTGATATCC
                                          I>>>>>>>>T7 Pol

        EcoR I
        Apo I                   Cla I  Nsi I
        |◊         ◊         ◊  |      |         ◊         ◊
GAGACCGGAATTCAAAATTAAGGAGGATCCATCGATGCATCATCATCATCATCATAACAC  2160
CTCTGGCCTTAAGTTTTAATTCCTCCTAGGTAGCTACGTAGTAGTAGTAGTAGTATTGTG
                                 M  H  H  H  H  H  H  N  T
>>>>>>>>>I
                                 I>>>>>>>>>>>>>>>>>>>>>>>>

                                                    Pst I
         ◊         ◊         ◊         ◊         ◊ |       ◊
GACCACCGTCAGCACGCCCATGCCCCCGCCCGTGGACGACTCCTGGCTGCAGGTGCAGAG  2220
CTGGTGGCAGTCGTGCGGGTACGGGGGCGGGCACCTGCTGAGGACCGACGTCCACGTCTC
 T  T  V  S  T  P  M  P  P  P  V  D  D  S  W  L  Q  V  Q  S
>>>>>>>>>>>>>>>>>>>>>>>>>>HT-PRD>>>>>>>>>>>>>>>>>>>>>>>>>>

      Eag I
      |  ◊         ◊         ◊         ◊         ◊         ◊
CGTACCGGCCGGACGCAGGTCGCCCACGTCCAGCCCCACGCCGCAGCGCCGAGCCCCCGC  2280
GCATGGCCGGCCTGCGTCCAGCGGGTGCAGGTCGGGGTGCGGCGTCGCGGCTCGGGGGCG
 V  P  A  G  R  R  S  P  T  S  S  P  T  P  Q  R  R  A  P  A
>>>>>>>>>>>>>>>>>>>>>>>>>>HT-PRD>>>>>>>>>>>>>>>>>>>>>>>>>>

                                 Apa I
         ◊         ◊         ◊  |      ◊         ◊         ◊
CGTGCCCCCAGCCCGGCCCGGGTCGCGGGGCCCTGCTCCTGGGCCTCCGCCTGCTGGATC  2340
GCACGGGGGTCGGGCCGGGCCCAGCGCCCCGGGACGAGGACCCGGAGGCGGACGACCTAG
 V  P  P  A  R  P  G  S  R  G  P  A  P  G  P  P  P  A  G  S
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>>>>>>>>>>>>>>>>>>>>>>>>>>>HT-PRD>>>>>>>>>>>>>>>>>>>>>>>>>>>

    Sty I       Sac I                    Nhe I
    |    ◊      |  ◊         ◊         ◊ |       ◊         ◊
CGCCCTAGGAGGAGCTCCTCCTGTTCCATCCAGACCAGGAGCTAGCCCTGATCCTTTTGG  2400
GCGGGATCCTCCTCGAGGAGGACAAGGTAGGTCTGGTCCTCGATCGGGACTAGGAAAACC
 A  L  G  G  A  P  P  V  P  S  R  P  G  A  S  P  D  P  F  G
>>>>>>>>>>>>>>>>>>>>>>>>>>>HT-PRD>>>>>>>>>>>>>>>>>>>>>>>>>>>

                      Nru I                      Kpn I
         ◊         ◊  |      ◊         ◊         ◊|        ◊
TCCTCCTCCTCAAGTACCTTCGCGACCAAACCGCGCTCCTCCTGGGGTACCAAGTCGTTC  2460
AGGAGGAGGAGTTCATGGAAGCGCTGGTTTGGCGCGAGGAGGACCCCATGGTTCAGCAAG
 P  P  P  Q  V  P  S  R  P  N  R  A  P  P  G  V  P  S  R  S
>>>>>>>>>>>>>>>>>>>>>>>>>>>HT-PRD>>>>>>>>>>>>>>>>>>>>>>>>>>>

                 Xba I                                    Xho I
         ◊       | ◊         ◊         ◊         ◊      |  ◊
AGGACAAGCATCACCTTCTAGACCAGAATCTCCACGACCACCTTTTGACCTATGACTCGA  2520
TCCTGTTCGTAGTGGAAGATCTGGTCTTAGAGGTGCTGGTGGAAAACTGGATACTGAGCT
 G  Q  A  S  P  S  R  P  E  S  P  R  P  P  F  D  L  .
>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>I


GTAGCTTGCATCTATGGTCTCTCCCTTTAGTGAGGGTTAATTAGAAACTGGAGTCGATGA  2580
CATCGAACGTAGATACCAGAGAGGGAAATCACTCCCAATTAATCTTTGACCTCAGCTACT



TAAGCTGTCAAACATGAGAATT  2602
ATTCGACAGTTTGTACTCTTAA
```

pHT-PRD Sequence

ATTTCTTGAAGACGAAAGGGCCTCGTGTTACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGT
CAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCT
CATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCC
CTTATTCCCTTTTTTCCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAG
ATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGA
ACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAA
CTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCA
TGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGATCGG
AGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTG
AATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTG
GCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCG
CTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCA
CTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATA
GACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTCATATATACTTTAGAT
TGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAA
CGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCG
TAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTT
TCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTC
AAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGT
GTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACAGA
GCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCCGAA
GGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACG
CCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCG
GAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTT
CCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGA
CCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGAT
TCATTAATGCAGCTGGCTTATCGAAATTAATACGACTCACTATAGGGAGACCGGAATTCAAAATTAAGGAGGATCCATC
GATGCATCATCATCATCATCATAACACGACCACCGTCAGCACGCCCATGCCCCCGCCCGTGGACGACTCCTGGCTGCAG
GTGCAGAGCGTACCGGCCGGACGCAGGTCGCCCACGTCCAGCCCCACGCCGCAGCGCCGAGCCCCCGCCGTGCCCCCAG
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CAGACCAGGAGCTAGCCCTGATCCTTTTGGTCCTCCTCCTCAAGTACCTTCGCGACCAAACCGCGCTCCTCCTGGGGTA
CCAAGTCGTTCAGGACAAGCATCACCTTCTAGACCAGAATCTCCACGACCACCTTTTGACCTATGACTCGAGTAGCTTG
CATCTATGGTCTCTCCCTTTAGTGAGGGTTAATTAGAAACTGGAGTCGATGATAAGCTGTCAAACATGAGAATT