

Gene Abbreviation	Accession No. (NCBI)	Percentage of Identity	E value	Contig number (BioProject 541449)
ACT	MF405765.1	95%	0.00	CTG107765
TUB	U76558.1	93%	0.00	CTG25086
CYP	EU035525.1	92%	0.00	CTG81232
GAPDH	KR029492.1	≥87%	≤6.38*10 ⁻¹⁸	CTG108160
UBC	M62720.1	≥93%	≤1.74 x 10 ⁻³⁰	CTG29477
EF1	M90077.2	92%	0.00	CTG31755
TBP	L07604.1	≥90%	≤5.56*10 ⁻⁰⁷	CTG9379
ADPR	Ta2291 (Unigene cluster)	≥92%	1.03 x 10 ⁻²²	CTG25287
PGD	Ta30797 (Unigene cluster)	≥90%	≤1.58 × 10 ⁻²⁸	CTG22048
PAL	MT150275.1	91%	0.00	CTG14153

Actin (ACT)

reference sequence: MF405765.1

forward primer: **CGAGCGGGAAATTGTAAGGG**

reverse primer: **CGATCATGGATGGCTGGAAG**

product size: 191 bp

contig number: CTG107765, percentage identity: 95%, E value: 0.00, Gaps (0/615)

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Query      454  GGTATCGTTCTCGACTCTGGTGTGATGGTGTGTCAGCCACACCGTGCCATTTACGAAGGATAC 513
          |||||  |||||  |||||||||||||||||||||||||||||||||||  |||||  ||  |||||||||
Subject 18164  GGTATTGTTCTTACTCTGGTGTGATGGTGTGTCAGCCACACTGTGCCATCTATGAAGGATAC 18223

Query      514  GCGCTTCCTCATGCCATTCTTCGTTTGGATCTCGCTGGTCGGGATCTCACGGACTCCCTC 573
          |||||||||||  |||||||||||||||||||||||||||||||  |||||  ||  |||||||||  ||  ||  |||
Subject 18224  GCGCTTCCTCACGCCATTCTTCGTTTGGATCTTGTCTGGCCGTGATCTCACTGATTCTCTC 18283

Query      574  ATGAAGATCCTCACTGAGAGAGGTTACTCCTTCACAACCTCAGCCGAGCGGGAAATTGTA 633
          |||||||||  |||||||||||||||||||||||||||||||  |||||||  ||  |||||||||  ||  ||  |||
Subject 18284  ATGAAGATTCTCACTGAGAGAGGTTACTCCTTCACAACCTCAGCCGAGCGGGAAATTGTA 18343

Query      634  AGGGACATCAAGGAGAAGCTTGCGTATGTTGCCCTTGATTATGAACAGGAGCTGGAGACT 693
          |||||||||||  |||||||||||||||||||||||||||||||  ||  |||||||||||  |||||||||  |||
Subject 18344  AGGGACATCAAGGAGAAGCTTGCGTACGTAGCCCTTGATTATGAACAAGAGCTGGAGACT 18403

Query      694  GCCAAGAACAGCTCCTCAGTTGAGAAGAGCTACGAGCTTCCTGATGGTCAGGTCATCACG 753
          |||||||||||  |||||||||||||||||||||||||||||||  |||||||  |||||  |||||||  |||||
Subject 18404  GCCAAGAACAGCTCCTCAGTTGAGAAGAGCTACGAGCTACCTGACGGTCAGGTCATCACG 18463

Query      754  ATTGGCGCAGAGAGGTTTCAGGTGCCCTGAGGTCTCTTCCAGCCATCCATGATCGGCATG 813
          |||||||||  |||||||||||||||||||||||||||||||  |||||||||||  |||||||  |||||||
Subject 18464  ATTGGCGCTGAGAGGTTTCAGGTGCCCTGAGGTCTCTTCCAGCCATCCATGATCGGCATG 18523

Query      814  GAGTCTTCTGGAATCCATGAGACGACCTACAACCTCCATCATGAAGTGTGACGTGGATATC 873
          |||||||||||  |||||||||||||||||||||||||||||||  |||||||||||  |||||||  |||||||
Subject 18524  GAGTCTTCTGGAATCCATGAGACAACCTACAACCTCCATCATGAAGTGTGACGTGGATATC 18583

Query      874  AGGAAGGACCTGTACGGCAACATTGTGCTCAGTGGTGGCACAACTATGTTCCCAGGTATC 933
          |||||||||||  |||||||||||||||||||||||||||||||  ||  |||||  |||||  |||||  |||||
Subject 18584  AGGAAGGACCTGTATGGCAACATTGTGCTCAGTGGAGGTACAACCATGTTCCCAGGTATC 18643

Query      934  GCTGACCGTATGAGCAAGGAGATCACCGCGCTTGCTCCGAGCAGCATGAAGATCAAGGTT 993
          |||||||||||  |||||||||||||||||||||||||||||||  |||||||||||  |||||||  |||||||
Subject 18644  GCTGACCGTATGAGCAAGGAGATCACCGCGCTTGCTCCGAGCAGCATGAAGATCAAGGTT 18703

Query      994  GTCGCCCCACCTGAGAGGAAGTACAGTGTCTGGATCGGAGGGTCCATCCTAGCCTCACTC 1053
          ||  ||  ||  ||  |||||||||||||||||||||||||||||||  |||||||  |||||  |||||  |||
Subject 18704  GTTGTCTCCTCTGAGAGGAAGTACAGTGTCTGGATCGGAGGGTCCATTCTAGCCTCGCTC 18763

Query      1054  AGCACTTTCCAACAG 1068
          |||||||||||||
Subject 18764  AGCACTTTCCAACAG 18778
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oat sequence:

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GGTATTGTTCTTACTCTGGTGTGATGGTGTGTCAGCCACACTGTGCCATCTATGAAGGATACGCGCTTCTCAGCCATTCTTCG
TTTGGATCTTGTCTGGCCGTGATCTCACTGATTCTCTCATGAAGATTCTCACTGAGAGAGGTTACTCCTTCACAACCTCAGCCG
AGCGGGAAATTGTAAGGGACATCAAGGAGAAGCTTGCGTACGTAGCCCTTGATTATGAACAAGAGCTGGAGACTSGCCAAGAA
CAGCTCCTCAGTTGAGAAGAGCTACGAGCTACCTGACGGTCAGGTGATCACGATTGGCGCTGAGAGGTTCAAGTGCCTGAGG
TCCTCTTCCAGCCATCCATGATCCGCATGGAGTCTTCTGGAATCCATGAGACAACCTACAACCTCCATCATGAAGTGTGACGTG
GATATCAGGAAGGACCTGTATGGCAACATTGTGCTCAGTGGAGGTACAACCATGTTCCCAGGTATCGCTGACCGTATGAGCAA
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GGAGATCACCGCGCTTGCTCCGAGCAGCATGAAGATCAAGGTTGTTGCTCCTCCTGAGAGGAAGTACAGTGTCTGGATCGGAG
GGTCATTCTAGCCTCGCTCAGCACTTCCAACAG

Ubiquitin conjugating enzyme (UBC)

reference sequence: M62720.1

forward primer: CAAGCTGACCCTGCAATTCA

reverse primer: GGGCTCCACTGGTTCTGTA

product size: 135 bp

contig number: CTG29477, percentage identity: $\geq 93\%$, E value: $\leq 1.74 \times 10^{-30}$

E value 2.75×10^{-34} Identities: 96% Gaps: 0/92

```
Query      132  AGGTACGTTCAAGCTGACCCTGCAATTCACAGAAGATTACCCCAACAAGCCACCAACTGT  191
          |||
Subject 65992  AGGTACGTTCAAGCTGACCCTGCAATTCACAGAAGATTATCCCAACAACCACCAACTGT  65933
```

```
Query      192  TCGGTTTGTCTCAAGGATGTTTCACCCAAACANN  223
          |||
Subject 65932  TCGGTTTGTCTCAAGGATGTTTCACCCGAACA  65901
```

E value 1.74×10^{-30} Identities: 95% Gaps: 0/87

```
Query      226  TATGCAGATGGAAGCATCTGCTTGGACATCCTACAGAACCAGTGGAGCCCTATATATGAT  285
          |||
Subject 65783  TATGCAGATGGAAGCATCTGCTTGGATATCTTACAGAACCAGTGGAGCCCCATATATGAT  65724
```

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Query      286  GTTGCAGCAATATTGACCTCTATCCAG  312
          |||
Subject 65723  GTTGCAGCAATATTGACCTCTGTCCAG  65697
```

E value 1.52×10^{-37} Identities: 93% Gaps: 0/108

```
Query 310      CAGTCCCTGCTGTGCGACCCGAACCCGAATTCTCCTGCGAACTCTGAAGCAGCCAGAATG  369
          |||
Subject 65027  CAGTCCCTGCTGTGCGACCCGAATCCAAATTCTCCGGCGAACTCTGAAGCAGCCAGGATG  64968
```

```
Query      370  TACAGCGAGAACAAGCGCGAGTACAACCGCAAGGTTTCGTGAGGTCGTG  417
          |||
Subject 64967  TATAGCGAGAACAAGCGCGAGTACAACCGCAAAGTTCGTGAGATCGTG  64920
```

oat sequence:

```
AGGTACGTTCAAGCTGACCCTGCAATTCA CAGAAGATTATCCCAACAACCACCAACTGTTTCGGTTTGTCTCAAGGATGTTTC
ACCCGAACANNATGCAGATGGAAGCATCTGCTTGGATATCTTACAGAACCAGTGGAGCCC CATATATGATGTTGCAGCAATA
TTGACCTCTGTCCAGTCCCTGCTGTGCGACCCGAATCCAAATTCTCCGGCGAACTCTGAAGCAGCCAGGATGTATAGCGAGAA
CAAGCGGAGTACAACCGCAAAGTTCGTGAGATCGTG
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AGATGGATGCCACCACTCCCAAGTACTCGAAGGCACGTTATGAAGAAATGTGAAGGAAGTCTCTTCTTACCTGAAGAAGTTGGCTACAACCCTGACAAGGTGCCA
TTTGTCCCACATCTCTGGGTTTGAGGGTGACAACATGATTGAGAGGTCAACCAACCTTGACTGGTACAAGGGCCCCACCTTGCTTGAGGGCGCTTGACCAGATCAACGA
GCCCCAAGAGGCCCTCAGACAAGCCCCTCCGTCTTCCCCTCCAGGATGTTTACAAGATTGGTGGCATTGGAAGTGTGCCTGTTGGCCGTGTTGAGACCGGTGTCATCA
AGCCTGGCATGGTTGTACCTTTGGTCCAAGTGGTCTGACCACTGAGGTTAAGTCCGTTGAGATGCACCACGAGTCTCTCCTGGAGGGCGCTCCCTGGTGACAACGTC
GGGTTCAATGTCAAGAATGTGCTGTGAAGGATCTCAAGCGTGGGTTTGTGGCGTCCAACCTCAAGGATGACCCTGCAAGAGGGCAGCCAACTTCACTCCAGGT
CATCATCATGAACCAACCTGGTCAGATAGGCAACGGCTATGCCCCAGTGTGGACTGCCACACTTCGCACATTCTGTCAAGTTGCTGAGCTGGTGACCAAGATTG
ACAGACGATCTGGCAAGGAGATTGAGAAGGAGCCCAAGTTCTGAAGAATGGTATGCTGGGATAGTGAAGATGATFCCACCAAGCCCATGGTTGTGGAGACCTTT
TCTACTTACCCCTCTTGGTCGCTTGTGTGCGTGACATGAGACAAACGGTGTCTGTGGTGTATCAAGGCCGTGGAGAAGAAGGACCTACCCGGTGCCAAGGT
GACCAAGGCTGCTGCCAAGAAGAAATGAGGTGTTTACCT-TATCGTCCATGTCTGGTTTTGAGATACCCTAGTAGTTTTGT

ADP-ribosylation factor (ADPR)

reference sequence: AB050957.1

forward primer: CTCATGGTTGGTCTCGATGC

reverse primer: ACATCCCAAACAGTGAAGCT

product size: 143 bp

contig number: CTG25287, percentage identity: $\geq 92\%$, E value: $\leq 1.03 \times 10^{-22}$

E value: 5.56×10^{-64} , Identities: 97%, gaps 0/149

```
Query      1  ATGGGGCTCACGTTACCAAGCTGTTTCAGCCGCCTCTTCGCCAAGAAGGAGATGAGGATT  60
          |||
Subject 21896 ATGGGGCTCACGTTTCAGCCGCCTCTTCGCCAAGAAGGAGATGAGGATT  21955

Query      61  CTCATGGTTGGTCTCGATGCCGCTGGTAAGACCACCATCCTCTACAAGCTCAAGCTCGGA  120
          |||
Subject 21956 CTCATGGTTGGTCTCGATGCCGCTGGTAAGACCACCATCCTCTACAAGCTCAAGCTCGGC  22015

Query     121  GAGATCGTCACCACCATCCCAACCATCGG  149
          |||
Subject 22016 GAGATCGTCACCACCATCCCTACCATCGG  22044
```

E value: 1.03×10^{-22} , Identities: 92%, gaps 0/78

```
Query     148  GGATTCACGTCGAAACTGTTGAATACAAGAACATCAGCTTCACTGTTTGGGATGTGGGG  207
          |||
Subject 22349 GGATTTAACGTCGAGACTGTTCGAATACAAGAACATCAGCTTCACTGTTTGGGATGTGGGG  22408

Query     208  GGCCAAGACAAGATCAGG  225
          ||
Subject 22409 GGTC AAGACAAGTAAGG  22426
```

E value 1.45×10^{-45} Identities: 94% Gaps: 0/123

```
Query     218  AGATCAGGCCCTGTGGAGGCCTACTTCCAGAATACCCAAGGGCTCATTTTTGTTGTTG  277
          |||
Subject 22602 AGATCAGGCCCTTTGGAGGCCTACTTCCAGAATACACAGGGACTCATCTTTGTTGTTG  22661

Query     278  ACAGCAATGATAGGGAACGTGTTGTTGAGGCTAGAGATGAGCTCCACAGAATGCTGAATG  337
          |||
Subject 22662 ACAGCAATGATAGGGAGCGTGTTGTTGAGGCTAGAGATGAGCTCCACAGGATGCTGAATG  22721

Query     338  AGG  340
          |||
Subject 22722 AGG  22724
```

E value 1.89×10^{-50} Identities: 96% Gaps: 0/124

```
Query     338  AGGATGAGCTGCGTGATGCTGTGTTGCTTGTATTTGCAAACAACAAGATCTTCCCTAATG  397
          |||
Subject 22999 AGGATGAGCTACGTGATGCTGTGTTGCTTGTATTTGCAAACAACAAGATCTTCCCAATG  23058

Query     398  CCATGAATGCTGCTGAAATCACCACAAGCTTGGTCTGCACTCCCTGCGCCAGCGGCACT  457
          |||
Subject 23059 CCATGAATGCGGCTGAAATCACTGACAAGCTTGGTCTGCACTCCCTGCGCCAGCGGCACT  23118

Query     458  GGTA  461
          |||
Subject 23119 GGTA  23122
```

oat sequence:

ATGGGGCTCACGTTCTGGCAAGCTGTTTCAGCCGCCTCTTCGCCAAGAAGGAGATGAGGATTCTCATGGTTGGTCTCGATGCGCTGGTAAGACCA
CCATCCTCTACAAGCTCAAGCTCGGCGAGATCGTCACCACCATCCCTACCATCGGATTTAACGTCGAGACTGTCGAATACAAGAACATCAGCTT
CACTGTTGGGATGTGGGGGTCAAGACAAGATCAGGCCCTTTGGAGGCACTACTTCCAGAATACACAGGGACTCATCTTTGTTGTTGACAGC
AATGATAGGGAGCGTGTGTTGAGGCTAGAGATGAGCTCCACAGGATGCTGAATGAGGATGAGCTACGTGATGCTGTGTTGCTTGTATTTGCAA
ACAAACAAGATCTCCCAATGCCATGAATGCGGCTGAAATCACTGACAAGCTTGGTCTGCACTCCCTGCGCCAGCGGCACTGGTA

Similar to phosphogluconate dehydrogenase (PGD)

reference sequence: Ta30797 (Unigene Cluster)

forward primer: **GCAAAGATGAAACTGGTGGTCA**

reverse primer: **CAACCCACTTTTGTCCGCC**

product size: 90 bp

contig number: CTG22048 percentage identity: $\geq 90\%$, E value: $\leq 1.58 \times 10^{-28}$

E value 1.06×10^{-30} Identities: 90% Gaps: 0/103

```
Query      217  GTTGTTCGACAAGGATGGCGTGCTCGAGCAAATCGGAGAGGGCAAGGGCTACGTGGAT  276
          |||
Subject 40058 GTTGTTCGACAAGGATGGCGTGCTCGAGCAAATCGGGGAAGGGAAGGGCTATGTGGAC  39999

Query      277  ATGTCCACTGTTGATGCTGCAACTTCTTGCAAGATAAGCGAGG  319
          |||
Subject 39998 ATGTCCACCCTGATGCCGCGACCTCTTGCAAGATAAGTGAGG  39956
```

E value 7.16×10^{-33} Identities: 91% Gaps: 0/105

```
Query      317  AGGCGGTTAAACAAAAGGGCGGAGCTTTTGTGAAGCTCCAGTTTCAGGGAGCAAGAAGC  376
          |||
Subject 39013 AGGCGGTTAAACAAAAGCTGGAGCTTTTGTGAAGCTCCAGTTTCAGGGAGCAAGAAGC  38954

Query      377  CAGCTGAAGATGGCCAATTGGTCAATTCTTGCTGCAGGCGACAAG  421
          |||
Subject 38953 CAGCTGAAGATGGTCAATTGGTTATTCTTGCAAGATAAGTGAGG  38909
```

E value 1.48×10^{-41} Identities: 93% Gaps: 0/118

```
Query      419  AGGCACTATATGATGATATGGTCCCTGCATTTGATGTACTTGGGAAGAAGTCATTCTTTC  478
          |||
Subject 37645 AGGCACTATATGACGACATGGTCCCTGCCTTTGATGTACTTGGGAAAAGTCGTCTTCT  37586

Query      479  TGGGGGAGATGGGAAATGGAGCAAAGATGAACTGGTGGTCAACATGATCATGGGAAG  536
          |||
Subject 37585 TGGGGGAGATGGGAAATGGAGCAAAGATGAACTGGTGGTCAACATGATCATGGGAAG  37528
```

E value 1.58×10^{-28} Identities: 96% Gaps: 0/82

```
Query      535  AGTATGATGAATGCTTTTTCTGAGGGACTCTGTTTGGCTGACAAAAGTGGGTTGAGCCCC  594
          |||
Subject 37031 AGTACGATGAATGCCTTTTTCTGAGGGACTCTGTTTGGCGGACAAAAGTGGGTTGAGCCCC  36972

Query      595  CAGACGCTTCTTGATGTCCTGG  616
          |||
Subject 36971 CAGACGCTTCTTGATGTCCTGG  36950
```

oat sequence:

```
AGTGCAGCAGCTCGCCGCGCTGGGCGCTACCGTCGGGGACACGCCCGGAAGGTCGTCGCCAAGTGCACCTACACCATCGCC
ATGCTCTCCGATCCCAGCGCCGCGCTATCCGTTGTTTTCGACAAGGATGGCGTGCTCGAGCAAATCGGGGAAGGGAAGGGCTA
TGTGGACATGTCCACCGTTGATGCCGCGACCTCTTGCAAGATAAGTGAGGCAGTTAAACAGAAAGCTGGAGCTTTTGTGAAG
CTCCAGTTTCAGGGAGCAAGAAGCCAGCTGAAGATGGTCAATTGGTTATTCTTGCAAGATAAGTGAGGCAGTTAAACAGAAAGCTGGAGCTTTTGTGAAG
ATGGTCCCTGCCTTTGATGTACTTGGGAAAAGTCTTCTTCTTGGGGGAGATTGGAAATGGAGCAAAGATGAAACTGGTGGT
CAACATGATCATGGGAAGTACGATGAATGCCTTTTTCTGAGGGACTCTGTTTGGCGGACAAAAGTGGGTTGAGCCCCCAGACGC
TTCTTGATGTCCTGG
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Subject 141857 GATGAAGGGCGCTGAGATCGCCATGGCGTCTGACTGCTCTGAGCTGCAGTTCTTGGGCAA 141798
 Query 1021 CCCGGTGACTAACCATGTCCAGAGCGCGGAGCAGCACAACCAGGATGTGAACTCACTTGG 1080
 Subject 141797 CCCGGTGACCAACCATGTGCAGAGCGCGGAGCAGCACAACCAGGACGTGAACTCACTCGG 141738
 Query 1081 TCTGATCTCATCCAGGAAGACC CGCGGAGGCTATTGACATCTTGAAGATCATGTCTTCCAC 1140
 Subject 141737 CCTGATCTCGTCCCGAAGACC CGCGGAGGCGATCGACATCTTGAAGATCATGTCTTCCAC 141678
 Query 1141 GTTCCTGGTGGCTCTGTGCGCAGGCCATTGACCTTCGCCACATTGAGGAGAACATGAAGAC 1200
 Subject 141677 GTTCCTGATCGCTCTGTGCGCAGGCCATTGACCTTCGCCACCTCGAGGAGAACATGAAGAC 141618
 Query 1201 AGCGGTGAGGAAC TGCCTGATGCAGGTGGCCAAGAAGACCTTGAGCATGAACAACATGGG 1260
 Subject 141617 AGCTGTGAGGAAC TGCCTGATGCAGGTGGCCAAGAAGACCTTGAGCATGAACAAC TGGG 141558
 Query 1261 CGGCCTCCACATCGCCCGCTTCTGCGAGAAGGATCTGCTGACCGGATCGACCGCGAGGC 1320
 Subject 141557 CGGCCTCCACATCGCCCGCTTCTGCGAGAAGGATCTGCTACCGCCATCGACCGCGAGGC 141498
 Query 1321 GGTGTTTCGCTACGCGGACGACCCGTCAGCCCAACTACCCGCTGATGCAGAAGCTGCG 1380
 Subject 141497 GGTGTTTCGCTACGCGGACGACCCGTCAGCCCAACTACCCGCTCATGCAGAAGCTCAG 141438
 Query 1381 GGCGGTGCTGGTGGAGCAGCGCTGGCCAACGGCGACGGCGAGCGCCCTGGAGACCTC 1440
 Subject 141437 GGCCGTGCTGATCGAGCACGCGCTGGCCAACGGCGAAGGGAGCGCGCCCTGGAGACCTC 141378
 Query 1441 CATCTTCGCCAAGGTGGCGGAGTTCGAGCAGAACATCCGCGCGGTGCTGCCAAGGAGGT 1500
 Subject 141377 CATCTTCGCCAAGGTTCGCGGAGTTCGAGCAGAATGTCCGCGCCGCTGCCAAGGAGGT 141318
 Query 1501 GGAGGCCGCGCGCGCTCCGTGGAGAACGGCACGCGCTGGCTCCCAACCGGATCAAGGA 1560
 Subject 141317 GGAGGCCGCGCGCGCTCCGTGGAGAACGGCACGCGCTGGCTCCCAACCGGATCAAGGA 141258
 Query 1561 CTGCCGCTCTACCCGCTGTACCAGTTCGTGCGCGAGGTGTGCGGCACCGAGTACCTGAC 1620
 Subject 141257 CTGCCGCTCTACCCGCTGTACCAGTTCGTGCGCGAGGTGTGCGGCACCGAGTACCTCAC 141198
 Query 1621 CGGCGAGAAGACGCGTTCGCCCGGGAGGAGCTGAACAAGGTGCTGGTGGCCATGAACGA 1680
 Subject 141197 GGGCGAGAAGACCGGTTCGCCCGGGAGGAGCTGAACAAGGTCTGGTGGCCATGAACGA 141138
 Query 1681 GCG 1683
 Subject 141137 GCG 141137

oat sequence:

CAGGTTCTCAACGCGGTGCTTCGGAACCGGCACGGACGACGCTCTGCGGCGGAGGCAACGCGCGCCCATGTGGTCCGCATCAACACCCCTCTGCAGG
 GTTACTCGGGATCCGCTTCGAGATCCTCGAGGCCATCACCAGCTGCTCAACGCGCAACGTCAACCCCGTGCCTCCCGCTCCGCGGACCATCACCGCTCGGGCGAC
 CTCGTGCCGCTCTCTACATTGCGGGCTTATCACCAGTTCGCCAGAACTCCGTCGCGGTGGCCCCGATGGCACCAGGTGACCCGCTGCCGAGGCGTTCAAGATCGC
 CGGCATCGAGCACGGGTTCTTTGAGCTGCAGCCCAAGGAAGGCTTGCATGGTGAACGGGACAGCCGTGGGTTCGGGACTTGCCTCGACCGTGTGTTGAGGCCA
 ACATCTCGCCATACCTCGCTGAGGCTCTGTCGCGGTCTTCTGCGAGGTGATGACCGGCAAGCCGAGTTACGCGACACCTGACCCACAAGTGAAGCACCACCT
 GGGCAGATCGAGGCGCGCGATCATGGAGCACATCTTGAAGGGAGCTCGTACATGAAGCAGGCCAAGATACAGGGCGAGCTCGACCCGCTGATGAAGCCGAAGCA
 GGACCGGTACGCGCTCCGCACGTCGCGCGAGTGGCTTGGCCCTCAGATCGAGGTTATCCGCTTCGCCACCAAGTTCGATCGAGCGGAGATCAACTCCGCTCAACGACA
 ACCCGCTCATCGATGTCTCCCGTGGCAAGGCGATCCATGGGGCAACTTCCAGGGCACCCCATCGGTGCTCCATGGACAACACCCGCTTGCATCGCTGCTATT
 GGCAAGCTCATGTTCCGCGAGTCTCGGAGCTGGTGAACGACTTCTACAACACCGGCTCCCGTCCAACCTGTCCGGTGGGCGCAACCCGAGCTTGGACTACGGGAT
 GAAGGGCGCTGAGATCGCCATGGCGTCTGACTGCTCTGAGTGCAGTTCCTTGGGCAACCCGCTGACCAACCATGTGCAGAGCGCGGAGCAGCACAACCAGGACGTGA
 ACTCACTCGGCCTGATCTCGTCCCGAAGACCGCGGAGGCGATCGACATCCTGAAGATCATGTCTCCACGTTCCCTGATCGCTCTGTGCCAGGCCATTGACCTTCG
 CACCTCGAGGAGAACATGAAGACAGTGTGAGGAAGTGCCTGATGCAGGTGGCCAAGAAGACCCCTGAGCATGAACAAGTGGGCGGCTCCACATCGCCCGCTTCTG
 CGAGAAGGATCTGCTACCCGCTCGACCGCGAGGCGGTTCGCTACCGGACGACCCCTGCAGCGCAACTACCCGCTCATGCAGAAGCTCAGGGCCGTGCTGA
 TCGAGCAGCGCTGGCCAACGGCGAAGGCGAGCGCCCTGGAGACCTCCATCTTCGCCAAGGTTCGCGGAGTTCGAGCAGAAATGTCCGCGCCCGCTGCCAAGGAG
 GTGGAGGCCGCGCGCTGCTCCGTGGAGAACGGGACGCGGCTGGCGCGCAACCGGATCAAGGACTGCGCTCTTACCCGCTGTACCAGTTCGTGCGCGAGGTGTGCGG
 CACGGAGTACCTCACGGGCGAGAAGACCCGCTCGCGGGGAGGAGCTCAACAAGTCTGTTGGCCATGAACGAGCG