


```

0 ----- 0
151 AGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTG 200
0 ----- 0
201 ATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGAT 250
0 ----- 0
251 TGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGG 300
0 ----- 0
301 CCGAGGATGCCAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTG 350
0 ----- 0
351 GACAACCTGCTGGCCCAGATCGGGCACCAGTACGCCGACCTGTTTCTGGC 400
0 ----- 0
401 CGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGA 450
0 ----- 0
451 ACACCGAGATCACCAAGGCCCCCTGAGCGCCTCTATGATCAAGAGATAC 500
0 ----- 0
501 GACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCA 550
0 ----- 0
551 GCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCT 600
0 ----- 0
601 ACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTC 650
1 ----- 6
          ||          |.||
          GG          GATC
651 ATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAA 700
7 AT-----CTGGAA---GTGGACGGCACCGAGGAACTGCTCGTGAA 43
701 GCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCA 750
44 GCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCA 93
751 GCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGG 800
94 GCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGG 143
801 CAGGAAGATTTTTACCCATTCTGAAGGACAACCGGGAAAAGATCGAGAA 850
144 CAGGAAGATTTTTACCCATTCTGAAGGACAACCGGGAAAAGATCGAGAA 193
851 GATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGGCCAGGGGA 900
194 GATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCT--GGCCAGGGGA 242
901 AACAGCAGATTTCGCCTGGATGACCAG--AAGAGCGAGGAAACCATCACCCC 949
243 AACAGCAGATTTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCC 292
950 CT-GCACTTCGAGGAAGT-GTGGACA--GGCGCT--CG-CCAGAGC-TCA 991
293 CTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCAGAGCTTCA 342
992 TCGAGC-GATGAC--AC-TCGAT-AGA--CTG-CCAACGAG-AGGTGCTG 1032
343 TCGAGCGGATGACCAACTTCGATAAAGAACCTGCCAACGAGAAGGTGCTG 392
1033 CC--AGCACAG-CTGCTGTA----- 1049
393 CCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGAC 442
1049 ----- 1049
443 CAAAGTGAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCG 492

```

```

1049 ----- 1049
493 GCGAGCAGAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAA 542
1049 ----- 1049
543 GTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTT 592
1049 ----- 1049
593 CGACTCCGTGGAAATCTCCGGCGTGAAGATCGGTTCAACGCCTCCCTGG 642
1049 ----- 1049
643 GCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGAC 692
1049 ----- 1049
693 AATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACT 742
1049 ----- 1049
743 GTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCACC 792
1049 ----- 1049
793 TGTTGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGC 842
1049 ----- 1049
843 TGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTC 892
1049 ----- 1049
893 CGGGCAGACATCCTGGATTTCTGAAGTCCGACGGCTTCGCAACAGAAAC 942
1049 ----- 1049
943 TCATGCAGCTGATCACGACGACAGCTGACTTAAGAGACATCAGATGCCAG 992
1049 ----- 1049
993 TGTCGCAGGCGATAGCTGCACGAGCAATGGCATCTGTGCAGGCCGCATAG 1042
1049 ----- 1049
1043 AGCATCTGCGACTGAGTGTGACAGCTCTGAATGATGACCGCCAAGCCGAA 1092
1049 ----- 1049
1093 AACTCTGGTATTCTG 1106

```

```

#-----
#-----
The beginning of excellent alignment is shown below.

```

```

701 GCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCA 750
44 GCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCA 93

```

```

needle -outfile=002F003F.needle -asequence=002F.seq -bsequence=003F.seq -gapopen=10 -gapextend=0.5
Needleman-Wunsch global alignment of two sequences

```

```

#####
# Program: needle
# Rundate: Thu 28 Jan 2021 08:06:05
# Commandline: needle
# -outfile 002F003F.needle
# -asequence 002F.seq
# -bsequence 003F.seq
# -gapopen 10
# -gapextend 0.5
# Align_format: srspair
# Report_file: 002F003F.needle
#####

```

```

#=====
#
# Aligned_sequences: 2

```

1:
 # 2:
 # Matrix: EDNAFULL
 # Gap_penalty: 10.0
 # Extend_penalty: 0.5
 #
 # Length: 1789
 # Identity: 441/1789 (24.7%)
 # Similarity: 441/1789 (24.7%)
 # Gaps: 1332/1789 (74.5%)
 # Score: 1787.5
 #
 #

#####

1	GGGATCATCTGGAAGTGGACGGCACCGAGGAACTGCTCGTGAAGCTGAAC	50
0	-----	0
51	AGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCC	100
0	-----	0
101	CCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAG	150
0	-----	0
151	ATTTTTACCCATTCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTG	200
0	-----	0
201	ACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAG	250
0	-----	0
251	ATTGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCTGGA	300
0	-----	0
301	TCGAGGAAGTGGTGGACAAGGGCGCTTCGCCCAGAGCTTCATCGAGCGG	350
0	-----	0
351	ATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCA	400
0	-----	0
401	CAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGA	450
0	-----	0
451	AATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAG	500
0	-----	0
501	AAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGT	550
0	-----	0
551	GAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCG	600
0	-----	0
601	TGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACA---	647
1	-----GGC-CAGGC	8
648	TACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCTGGACAATGA	697
9	TA-CACGATCTGCTG--AATTATCAAGGACAAGGACTTCTGGACAATGA	55
698	GGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTG	747
56	GGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTG	105
748	AGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTC	797
106	AGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTC	155
798	GACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGG	847

156 GACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGG 205
 848 CAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGGC 897
 |||||
 206 CAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCA 255
 898 AGAC-ATCCTGGATTTCTGAAGTCCGACGGCTTCG-CAACAGAAAC-TC 944
 |||||
 256 AGACAATCCTGGATTTCTGAAGTCCGACGGCTTCGCCAACAGAACTTC 305
 945 ATGCAGCTGAT-CACGACGACAG-CTGAC---TTAAGA-GACATC---AG 985
 |||||
 306 ATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAA 355
 986 ATGCCA-GTGTC--GC--AGGCGATAG-CTGCACGAGCA-ATGGC--ATC 1026
 |.|.|||
 356 AGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATC 405
 1027 TGTGCAGGCCG-----CAT-----AGAGCAT-CTGC-GAC--TGA----- 1057
 |||.|||.|||
 406 TG-GCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGT 454
 1058 -GTGTGAC-AGCTC-TGAA--TGAT-GACCG--CCAAG-CCGAAAAC-TC 1097
 |||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||
 455 GGTG-GACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATC 503
 1098 TGGTATTCTG----- 1106
 |||.|||
 504 --GTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAG 551
 1106 ----- 1106
 552 AACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGG 601
 1106 ----- 1106
 602 CAGCCAGATCCTGAAAGAACACCCCGTGGAACACCCAGCTGCAGAACG 651
 1106 ----- 1106
 652 AGAAGCTGTACTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGAC 701
 1106 ----- 1106
 702 CAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACCATATCGT 751
 1106 ----- 1106
 752 GCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAAGTGCTGACCA 801
 1106 ----- 1106
 802 GAAGCGACAAGAACCGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTC 851
 1106 ----- 1106
 852 GTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCCAAGCTGA 901
 1106 ----- 1106
 902 TTACCCAGAGAAAGTTCGACATCTGACCAACGCCGAGAGAGGGCGGCCTGA 951
 1106 ----- 1106
 952 GCGAACTGGATAATGCGCTTCATCAGGAGACAGCTGATGAACCCCGCAGA 1001
 1106 ----- 1106
 1002 TCACAAAGCACGTGGCACAGATCTGACTCCCGGATGACACTTAGTACGAC 1051
 1106 ----- 1106
 1052 GAGATGACAGCCTGATCGGCAGTGAAGTGATCACCTTGAGTTCAGCTTG 1101
 1106 ----- 1106
 1102 GGTTCGGATTCGAAAGAATTCCTAGCTTACCAAATTGC 1140

#-----
 #-----

The beginning of excellent alignment is shown below.

698 GGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACTGTTT 747
 56 GGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACTGTTT 105

needle -outfile=003F004R.needle -asequence=003F.seq -bsequence=004R.seq -gapopen=10 -gapextend=0.5
 Needleman-Wunsch global alignment of two sequences

```
#####
# Program: needle
# Rundate: Thu 28 Jan 2021 08:06:05
# Commandline: needle
# -outfile 003F004R.needle
# -asequence 003F.seq
# -bsequence 004R.seq
# -gapopen 10
# -gapextend 0.5
# Align_format: srspair
# Report_file: 003F004R.needle
#####
```

```
#=====
#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1181
# Identity: 1081/1181 (91.5%)
# Similarity: 1081/1181 (91.5%)
# Gaps: 70/1181 ( 5.9%)
# Score: 5021.5
#
#
#=====
```

```

1 -----GGCCAGGCTACACGA-TCTGCTGAA-T 25
              ||.||..|..|...  |||||...
1 GATGGTCTGATTCAACGCCTCCTGGGCACACATCACGATTCTGCTGAAGC 50

26 TATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGG 75
  .||| |... |.||||.|..|..|...  |||||... ||| |...
51 AATC-AGGAC-ATGACTGCTTGACCAATGA-GAAAACGA-GACA-TCTGA 95

76 AAGATATCGTGCTGACCCTGACTGTTTGGAGACAGAGAGATGATCGAG 125
  |||||...  |||||...  |||||...  |||||...  |||||...  |||||...
96 AAGATATCGTGCTGA-CCTGACTGTTTGGAGACAGAGAGATGATCGA- 143

126 GAACGGCTGAAAACCTATG-CCCACCTGTTCGACGACAAAGTGATGAAGC 174
  |||||...  |||||...  |||||...  |||||...  |||||...  |||||...
144 GAACGGCTGAAAACCTATGCCCCACCTGTTCGACGACAAAGTGATGAAGC 193

175 AGCTGAAGCGGCGGAGATACACCGCTGGGGCAGGCTGAGCCGGAAGCTG 224
  |||||...  |||||...  |||||...  |||||...  |||||...  |||||...
194 AGCTGAAGCGGCGGAGATACACCGCTGGGGCAGGCTGAGCCGGAAGCTG 243

225 ATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTCCT 274
  |||||...  |||||...  |||||...  |||||...  |||||...  |||||...
244 ATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTT-CT 292

275 GAAGTCCGACGGCTTCGCCAACAGAACTTCATGCAGCTGATCCACGACG 324
  |||||...  |||||...  |||||...  |||||...  |||||...  |||||...
293 GAAGTCCGACGGCTTCGCCAACAGAACTTCATGCAGCTGATCCACGACG 342

325 ACAGCCTGACCTTTAAAGAGGACATCCAGAAAG-CCCAGGTGTCCGGCCA 373
  |||||.  |||||...  |||||...  |||||...  |||||...  |||||...
343 ACAGCGTGACCTTTAAAGAGGACATCCAGAAAGCCCCAGGTGTCCGGCCA 392

374 GGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCA 423
  |||||...  |||||...  |||||...  |||||...  |||||...  |||||...
393 GGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCA 442

424 TTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAA 473
  |||||...  |||||...  |||||...  |||||...  |||||...  |||||...
443 TTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAA 492

474 GTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGA 523
```

```

|||||
493 GTGATGGGCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGA 542
|||||
524 GAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGC 573
|||||
543 GAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGC 592
|||||
574 GGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACAC 623
|||||
593 GGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACAC 642
|||||
624 CCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCT 673
|||||
643 CCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCT 692
|||||
674 GCAGAATGGGCGGGATATGTACGTGGACCAGGAAGTGGACATCAACCGGC 723
|||||
693 GCAGAATGGGCGGGATATGTACGTGGACCAGGAAGTGGACATCAACCGGC 742
|||||
724 TGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAGGAC 773
|||||
743 TGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAGGAC 792
|||||
774 GACTCCATCGACAACAAAGTGCTGACCAGAAGCGACAAGAACCGGGGCAA 823
|||||
793 GACTCCATCGACAACAAAGTGCTGACCAGAAGCGACAAGAACCGGGGCAA 842
|||||
824 GAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAAGTACT 873
|||||
843 GAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAAGTACT 892
|||||
874 GGCAGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGAC-A 922
|||||
893 GGCAGCAGCTGCTGAACG-CCAAGCTGATTACCCAGAGAAAGTTCGACAA 941
|||||
923 TCTGACCAACGCCGAGAGAGGGCGGCTGAGCGAACTGGATAATGC--GCT 970
|||||
942 TCTGACCAAGGCCGAGAGAGGGCGGCTGAGCGAACTGGATAAAGGCCGGCT 991
|||||
971 TCATCAGGAGACAGCTGATG--AACCCCGCAGATCACAAAGCACGTGGCA 1018
|||||
992 TCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCA 1041
|||||
1019 CAGATC--TGAATCCCGGATG-ACACTTAGTACGACGAG-ATGACAGCCT 1064
|||||
1042 CAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCT 1091
|||||
1065 GATC--GGCAGTG-AAGTGATCACCTTGAGTTC-AGCTTGGGT-TCCGA 1109
|||||
1092 GATCCGGAAGTGAAAGTGATCACCTGAAGTCCAAGCT--GGTGTCCGA 1139
|||||
1110 TTCGCAAAGAATTCCTAGCTTACCAAATTGC 1140
|||.||
1140 TCCG--AAGAA--CCGA----- 1152

```

```

#-----
#-----
The beginning of excellent alignment is shown below.

```

```

175 AGCTGAAGCGGCGGAGATACACCGCTGGGGCAGGCTGAGCCGGAAGCTG 224
194 AGCTGAAGCGGCGGAGATACACCGCTGGGGCAGGCTGAGCCGGAAGCTG 243

```

```

needle -outfile=004R005R.needle -asequence=004R.seq -bsequence=005R.seq -gapopen=10 -gapextend=0.5
Needleman-Wunsch global alignment of two sequences

```

```

#####
# Program: needle
# Rundate: Thu 28 Jan 2021 08:06:05
# Commandline: needle
# -outfile 004R005R.needle
# -asequence 004R.seq
# -bsequence 005R.seq
# -gapopen 10
# -gapextend 0.5
# Align_format: srspair
# Report_file: 004R005R.needle
#####

```

```

#=====

```

```

#
# Aligned_sequences: 2
# 1:
# 2:
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1814
# Identity: 360/1814 (19.8%)
# Similarity: 360/1814 (19.8%)
# Gaps: 1452/1814 (80.0%)
# Score: 1679.0
#
#
#=====

```

```

      1 GATGGTCTGATTCAACGCCTCCTGGGCACACATCACGATTCTGCTGAAGC      50
      0 ----- 0
     51 AATCAGGACATGACTGCTTGACCAATGAGAAAACGAGACATCTGAAAGAT     100
      0 ----- 0
    101 ATCGTGCTGACCTGACACTGTTTGAGGACAGAGAGATGATCGAGAACGGC     150
      0 ----- 0
    151 TGAAAACCTATGCCCCACCTGTTTCGACGACAAAGTGATGAAGCAGCTGAA     200
      0 ----- 0
    201 GCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACG     250
      0 ----- 0
    251 GCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCTGAAGTCCG     300
      0 ----- 0
    301 ACGGCTTCGCCAACAGAACTTCATGCAGCTGATCCACGACGACAGCGTG     350
      0 ----- 0
    351 ACCTTTAAAGAGGACATCCAGAAAGCCCCAGGTGTCCGGCCAGGGCGATA     400
      0 ----- 0
    401 GCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAG     450
      0 ----- 0
    451 GGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGG     500
      0 ----- 0
    501 CCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGA     550
      0 ----- 0
    551 CCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAA     600
      0 ----- 0
    601 GAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGGA     650
      0 ----- 0
    651 AAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATG     700
      0 ----- 0
    701 GGCGGGATATGTACGTGGACCAGGAAGTGGACATCAACCGGCTGTCCGAC     750
      0 ----- 0
    751 TACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCAT     800
      1 -----GCTTTCTGAAGGACGACTCCAT      22

```


801 CGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGCAAGAGCGACA 850
 ||||| ||||||||||||||||||||||||| . ||||||| |||||||
 23 CGAC-ACAAGGTGCTGACCAGAAGCGACA--GACCGGGC-AGAGCGAC- 67

 851 ACGTGCCCTCCGAAGAGGTGCTGAAGAAGATGAAGAACTACTGGCGGCAG 900
 |||||||||||||||| ||||||| |||||||||||||||||||||||||||
 68 ACGTGCCCTCCGAAGA-GTCGTG-AGAAGATGAAGAACTACTGGCGGCAG 115

 901 CTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAA 950
 |||||||||||||||||||||||||||||||||||||||||||||||
 116 CTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAA 165

 951 GG-CCGAGAGAGGCGGCCTGAGCGAACTGGATAAGG-CCGGCTTCATCAA 998
 || ||||||||||||||| ||||||||||||||||||| |||||||||||
 166 GGCCCGAGAGAGGCGG-CTGAGCGAACTGGATAAGGCCCGGCTTCATCAA 214

 999 GAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCC 1048
 |||||||||||||||||||||||||||||||||||||||||||||||
 215 GAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCC 264

 1049 TGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGG 1098
 |||||||||||||||||||||||||||||||||||||||||||||||
 265 TGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGG 314

 1099 GAAGTGAAAGTGATCACCCCTGAAGTCCAAGCTGGTGTCCGAT---CCGAA 1145
 |||||||||||||||||||||||||||||||||||||||||||||.|||
 315 GAAGTGAAAGTGATCACCCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAA 364

 1146 GAACCGA----- 1152
 | ||
 365 G----GATTTCCAGTTTTACAAAGTGC GCGAGATCAACA ACTACCACCAC 410

 1152 ----- 1152

 411 GCCCAGGACGCCTACTGAACGCCGTGCGTGGGAACCGCCCTGATCAAAAA 460

 1152 ----- 1152

 461 GTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACG 510

 1152 ----- 1152

 511 ACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACC 560

 1152 ----- 1152

 561 GCCAAGTACTTCTTCTACAGCAACATCATGAACCTTTTCAAGACCGAGAT 610

 1152 ----- 1152

 611 TACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACG 660

 1152 ----- 1152

 661 GCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCACCGTG 710

 1152 ----- 1152

 711 CGGAAAGTGTGAGCATGCCCAAGTGAATATCGTGAAAAGACCGAGGT 760

 1152 ----- 1152

 761 GCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCG 810

 1152 ----- 1152

 811 ATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGC 860

 1152 ----- 1152

 861 TTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGA 910

 1152 ----- 1152

 911 AAAGGGCAAGTCCAAGAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCA 960

 1152 ----- 1152

 961 CCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTCTGAAGC 1010

 1152 ----- 1152

#-----
#-----

The beginning of excellent alignment is shown below.

901 CTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTGACAATCTGACCAA 950
116 CTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTGACAATCTGACCAA 165

needle -outfile=005R006R.needle -asequence=005R.seq -bsequence=006R.seq -gapopen=10 -gapextend=0.5
Needleman-Wunsch global alignment of two sequences

Program: needle
Rndate: Thu 28 Jan 2021 08:06:05
Commandline: needle
-outfile 005R006R.needle
-asequence 005R.seq
-bsequence 006R.seq
-gapopen 10
-gapextend 0.5
Align_format: srspair
Report_file: 005R006R.needle
#####

#=====

Aligned_sequences: 2
1:
2:
Matrix: EDNAFULL
Gap_penalty: 10.0
Extend_penalty: 0.5

Length: 1676
Identity: 528/1676 (31.5%)
Similarity: 528/1676 (31.5%)
Gaps: 1129/1676 (67.4%)
Score: 2368.5

#=====
#

```

1 GCTTTCTGAAGGACGACTCCATCGACACAAGGTGCTGACCAGAAGCGACA 50
0 ----- 0
51 GACCGGGGCAGAGCGACACGTGCCCTCCGAAGAGTCGTGAGAAGATGAAG 100
0 ----- 0
101 AACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTT 150
0 ----- 0
151 CGACAATCTGACCAAGGCCCGAGAGAGGCGGCTGAGCGAACTGGATAAGG 200
0 ----- 0
201 CCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCA 250
0 ----- 0
251 CGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATG 300
0 ----- 0
301 ACAAGCTGATCCGGGAAGTGAAAGTGATCACCTGAAGTCCAAGCTGGTG 350
0 ----- 0
351 TCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAA 400
0 ----- 0
401 CTACCACCACGCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCC 450
0 ----- 0
```

451	TGATCAAAAAGTACCCTAAGCTGGAAAGCGA--GTTCGTG-TACGGC-GA	496
1	-----GCT-GAAGGCGAAGTTTCGAGTTACGACGGA	30
497	CTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCG-AGCAGGAA	545
31	CTACAA-GAGTACGACGTAC-GAAGATGATCGGCAAGAGCGAAGCCAGAA	78
546	ATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAG-CAACATCATGAACT	594
79	ATCCGCCAAGCTA-CGCCAAGTACTTCTTCTACAGCCACCATCATGAACT	127
595	TTTTCAAGACCGAGATTACCCTGGCCAACG-GCGAGATCC-GGAAGCGGC	642
128	TTTTCAAGA-CGAGATTACCCT-GCCAACGAGCGAGATCCAGAAAGCGGC	175
643	CTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGC	692
176	CTCTGATCGAGAC-ATCGGCGAAACCCGGGAGATCGTGTGGGATAAGAGC	224
693	CGGGATTTTGCCACCGTGCAGGAAAGTGCTGAGCATGCCCAAGTGAATAT	742
225	CGGGATTTTG-CACCGTGCAGGAAAGTGCTGAGCATGCCCAAGTGAATAT	273
743	CGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCC	792
274	CGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCC	323
793	TGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGAC	842
324	TGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGAC	373
843	CCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCT	892
374	CCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCT	423
893	GGTGGTGGCCAAAGTGAAAAAGGGCAAGTCCAAGAACTGAAGAGTGTGA	942
424	GGTGGTGGCCAAAGTGAAAAAGGGCAAGTCCAAGAACTGAAGAGTGTGA	473
943	AAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAAT	992
474	AAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAAT	523
993	CCCATCGAC-TTCT-GAAGCCAAGCAC-----AGTG----AGG----	1024
524	CCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCT	573
1024	-----	1024
574	GATCATCAAGCTGCCTAAGTACTCCCTGTTTCGAGCTGGAAAACGGCCGGA	623
1024	-----	1024
624	AGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCC	673
1024	-----	1024
674	CTGCCCTCAAATATGTGAACTTCTGTACCTGGCCAGCCACTATGAGAA	723
1024	-----	1024
724	GCTGAAGGGCTCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAAC	773
1024	-----	1024
774	AGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCC	823
1024	-----	1024
824	AAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTA	873
1024	-----	1024
874	CAACAAGCACCGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCC	923
1024	-----	1024
924	ACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCTTCAAGTACTTT	973

```

1024 ----- 1024
974 GACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGA 1023
1024 ----- 1024
1024 CGCCACCCTGATCCACCAGAGCATCACCGGCTGTACGAGACACGGATCG 1073
1024 ----- 1024
1074 ACCTGTCTCAGCTGGGAGGCGACCCAAAGAAGAAGCGGAAGGTCTGAAAG 1123
1024 ----- 1024
1124 CTTGCGGCCGCACTCGAGCACCACCACCACCACCCTGAGATCCGGCTGC 1173
1024 ----- 1024
1174 TAACAAAGCCCGAAAGAGCGATTTCC 1199

```

```

#-----
#-----

```

The beginning of excellent alignment is shown below.

```

743 CGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCC 792
274 CGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCC 323

```

The merged DNA sequence is shown below.

```

CTGTATTTTCGATCAGTTCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTTCATCCAGCTGGTGCAGACCTA
CAACCAGCTGTTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTG
ATCGCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTTCGAAAACCTGATTGCCCTGAGCCTGGGCTGACCCCACTTCAAGAGCAACTTCGACCTGG
CCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGC
CGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCTGAGCGCCTCTATGATCAAGAGATAC
GACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCT
ACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAAGTCTCGTGAA
GCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGG
CAGGAAGATTTTTACCCATTCTGAAGGACAACCGGAAAAGATCGAGAAGATCCTGACCTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAA
ACAGCAGATTCGCTGGATGACCAGAAAAGAGCGAGGAAACCATCACCCCTGGAACCTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCAGAGCTTCAT
CGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACC
AAAGTGAATACGTGACCGAGGGAATGAGAAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAG
TGACCGTGAAGCAGCTGAAAAGGACTACTTCAAGAAAATCGAGTGTTCGACTCCGTGGAAATCTCCGGCGTGGAAAGATCGGTTCAACGCCTCCCTGGG
CACATACCAGATCTGCTGAAAATTATCAAGGACAAGGACTTCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGTGACCCCTGACACTG
TTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCACCTGTTTCGACGACAAAAGTGAAGCAGCTGAAGCGGCGGAGATACACCGGCT
GGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCTGAAGTCCGACGGCTTCCGCAACAGAAAC
TTCATGCAGCTGATCCACGACGACAGCGTGACCTTTAAAGAGGACATCCAGAAAAGCCCGAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCC
AATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAGTGAAGTGGGCGGCAAGCCCGAGAACA
TCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAAGCAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGG
CAGCCAGATCCTGAAAAGAACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGAC
CAGGAAGTGGACATCAACCGGCTGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCA
GAAGCGACAAGAACCAGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTGCTGAAGAAGATGAAGAACTACTGGCGGCGAGCTGCTGAACGCCAAGCTGAT
TACCCAGAGAAAAGTTCGACAATCTGACCAAGGCCCGAGAGAGGCGGCTGAGCGAACTGGATAAGGCCCGGCTTCATCAAGAGACAGCTGGTGGAAAACCCG
GCAGATCACAAGCACGTTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAGTGAATCACCTG
AAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCAGGAGATCAACAACCTACCACCACGCCACGACGCCTACCTGAACGCCG
TCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAG
CGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGG
AAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGGCACCGTGCAGGAAAGTGTGAGCATGCCCAAG
TGAATATCGTGA AAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAAGGA
CTGGGACCCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAACTGAAG
AGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGA AAA
AGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCAACTGCAGAAGGGAAACGA
ACTGGCCCTGCCCTCCAAATATGTGAACCTTCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCGAGGATAATGAGCAGAAAACAGCTGTTT
GTGGAACAGCACAAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCCTCAAGAGAGTGTATCCTGGCCGACGCTAATCTGGACAAAAGTGTGT
CCGCCTACAACAAGCACCGGATAAGCCATCAGAGAGCAGGCGGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAA
GTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCTGTACGAGACA
CGGATCGACCTGTCTCAGCTGGGAGGCGACCCAAAGAAGAAGCGGAAGGTCTGAAAGCTTGGCGGCCACTCGAGCACCACCACCACCACCCTGAGATC
CGGCTGCTAACAAGCCCGAAAGAGCGATTTCC

```