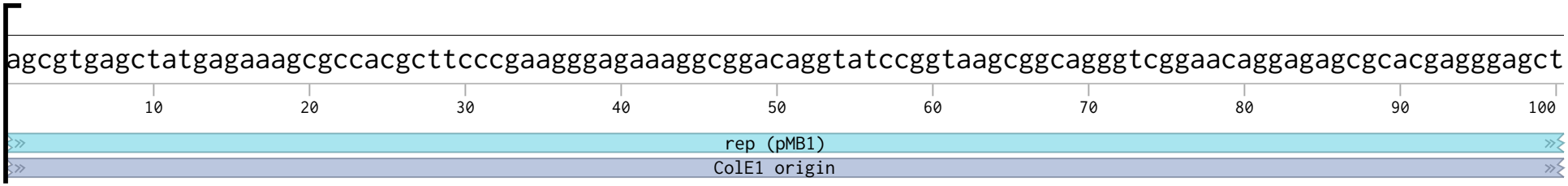
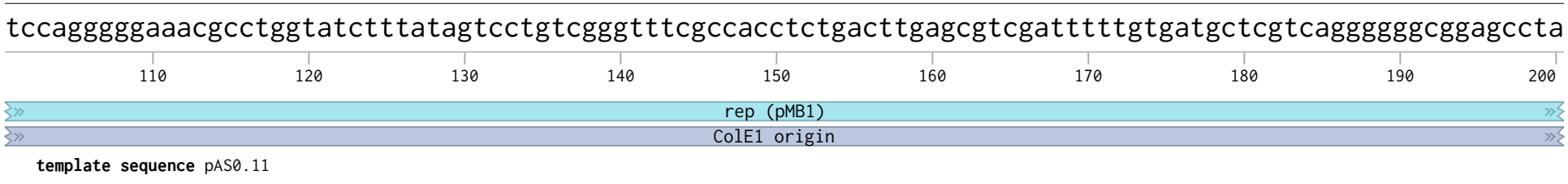
# Template Alignment: 2020-11-03_A02_ASASO11ASP1



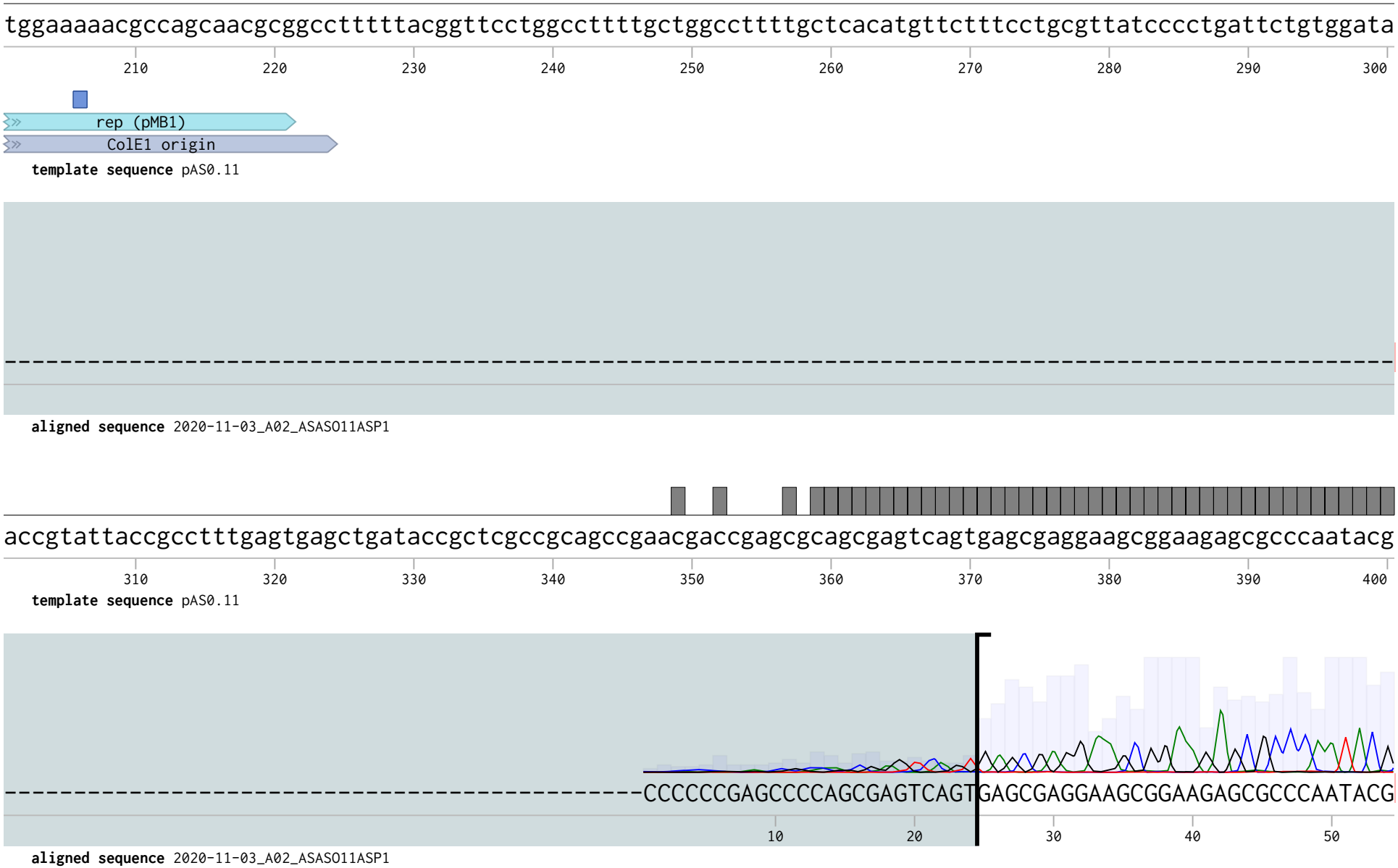

**template sequence** pAS0.11

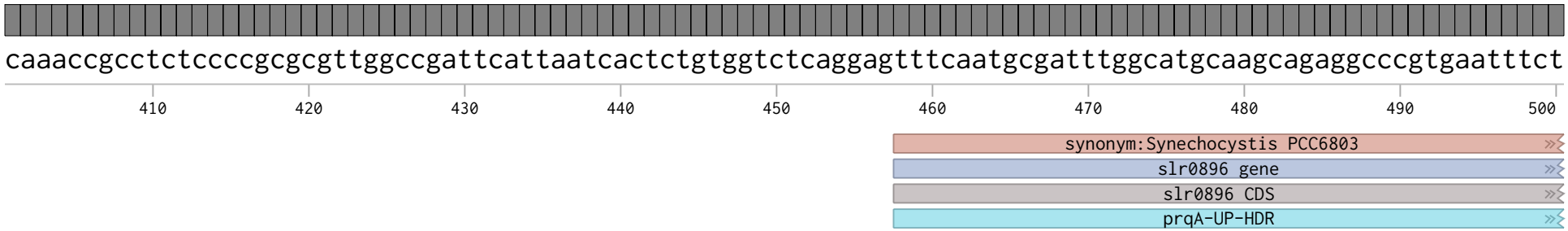
**aligned sequence** 2020-11-03_A02_ASASO11ASP1



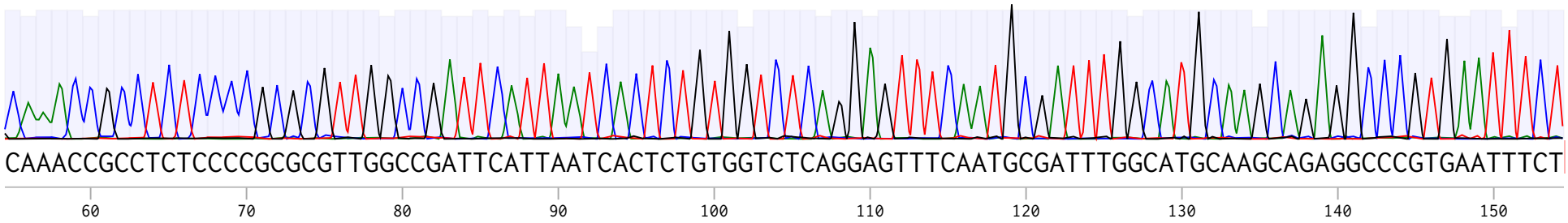

**template sequence** pAS0.11

**aligned sequence** 2020-11-03_A02_ASASO11ASP1

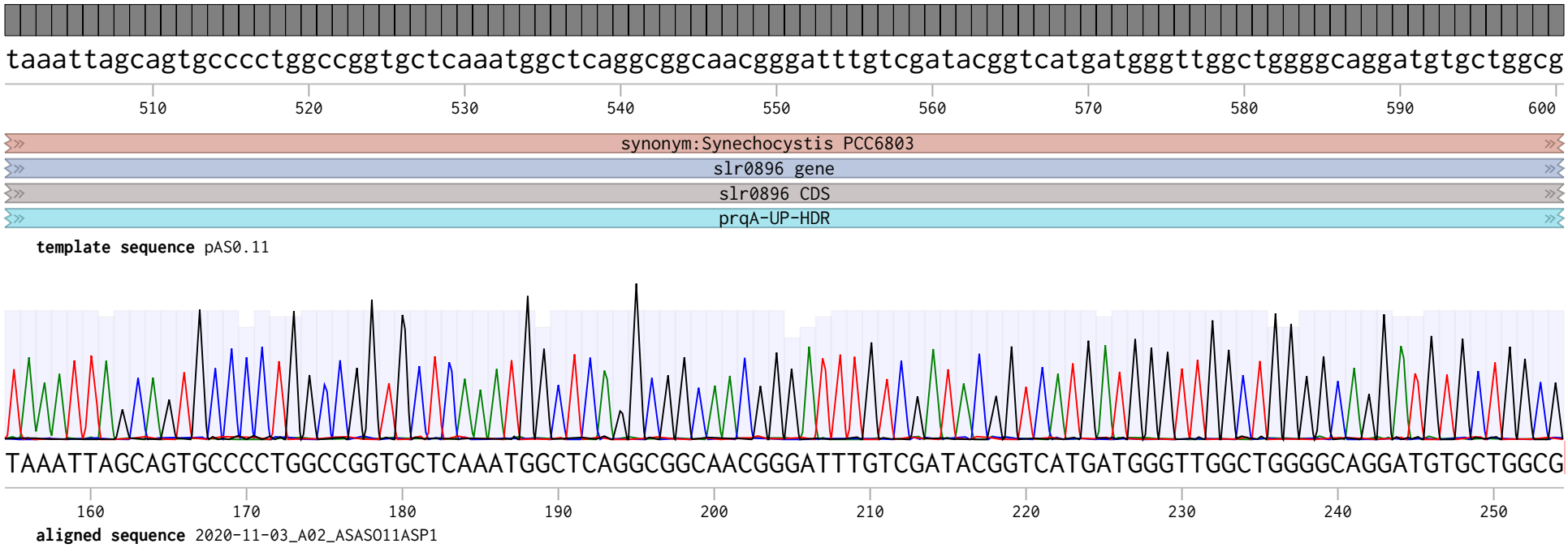

tggaaaaacgccagcaacgcggccttttacggttcctggccttttgctggccttttgctcacatgttctttcctgcgttatcccctgattctgtggata
210
220
230
240
250
260
270
280
290
300
rep (pMB1)
ColE1 origin
template sequence pAS0.11
aligned sequence 2020-11-03_A02_ASASO11ASP1
accgtattaccgcctttgagtgagctgataccgctcgccgcagccgaacgaccgagcgcagcgagtcagtgagcgaggaagcggaagagcgcccaatacg
310
320
330
340
350
360
370
380
390
400
template sequence pAS0.11
CCCCCCGAGCCCCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACG
10
20
30
40
50
aligned sequence 2020-11-03_A02_ASASO11ASP1

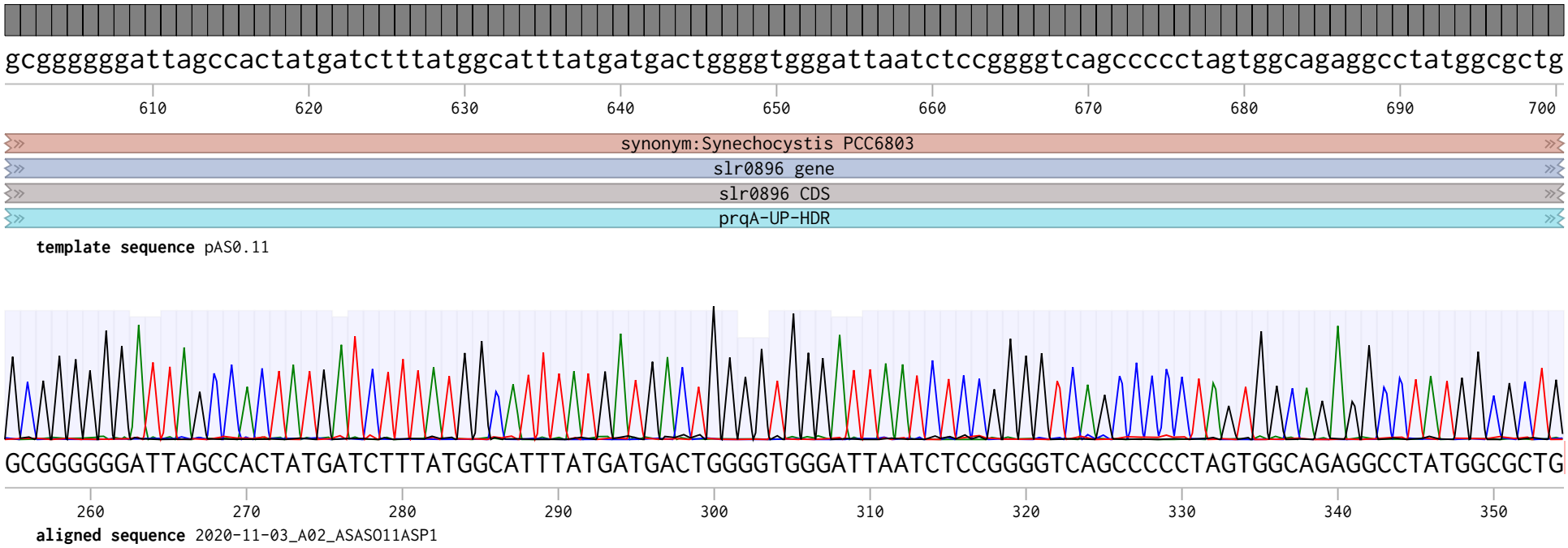


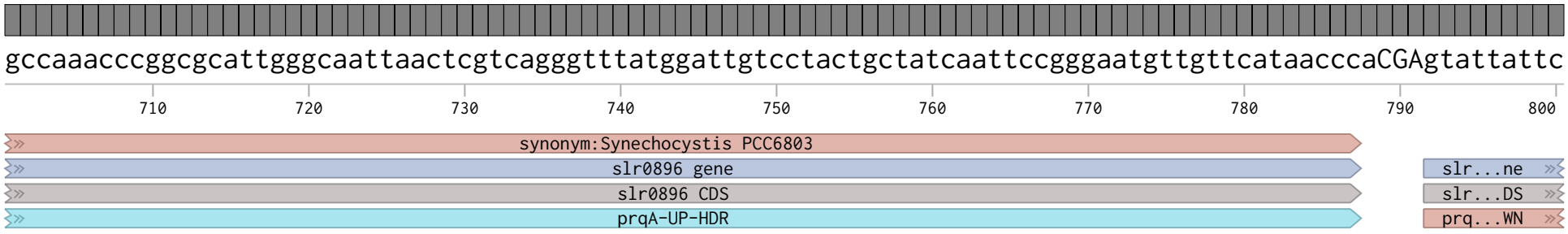

**template sequence** pAS0.11



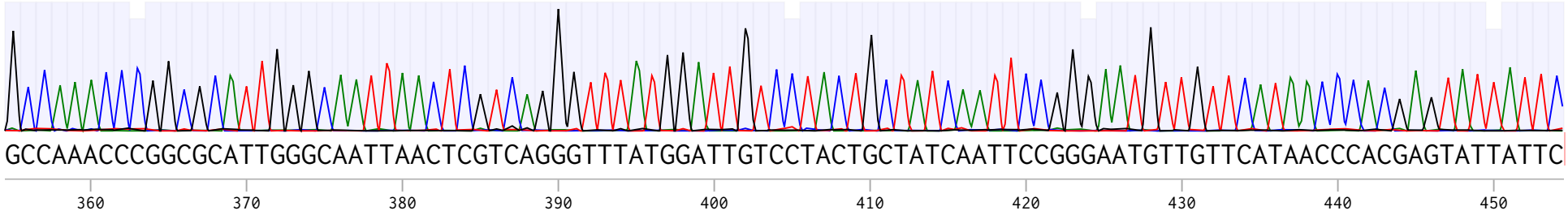

**aligned sequence** 2020-11-03_A02_ASASO11ASP1


taaattagcagtgcccctggccggtgctcaaatggctcaggcggcaacgggatttgtcgatacggtcatgatgggttggctggggcaggatgtgctggcg
510
520
530
540
550
560
570
580
590
600
synonym:Synechocystis PCC6803
slr0896 gene
slr0896 CDS
prqA-UP-HDR
template sequence pAS0.11
TAAATTAGCAGTGCCCCTGGCCGGTGCTCAAATGGCTCAGGCGGCAACGGGATTTGTCGATACGGTCATGATGGGTTGGCTGGGGCAGGATGTGCTGGCG
160
170
180
190
200
210
220
230
240
250
aligned sequence 2020-11-03_A02_ASASO11ASP1

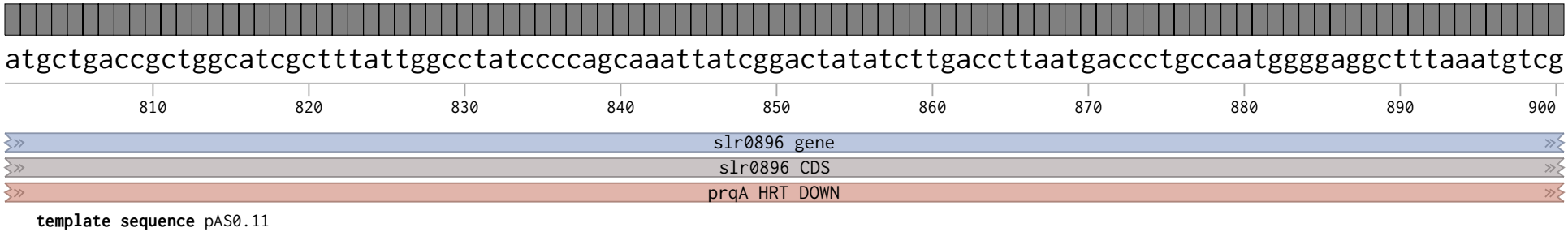

gcgggggggattagccactatgatctttatggcatttatgatgactggggtgggattaatctccggggtcagccccctagtggcagaggcctatggcgctg
610
620
630
640
650
660
670
680
690
700
synonym:Synechocystis PCC6803
slr0896 gene
slr0896 CDS
prqA-UP-HDR
template sequence pAS0.11
GCGGGGGGATTAGCCACTATGATCTTTATGGCATTTATGATGACTGGGGTGGGATTAATCTCCGGGGTCAGCCCCCTAGTGGCAGAGGCCTATGGCGCTG
260
270
280
290
300
310
320
330
340
350
aligned sequence 2020-11-03_A02_ASASO11ASP1



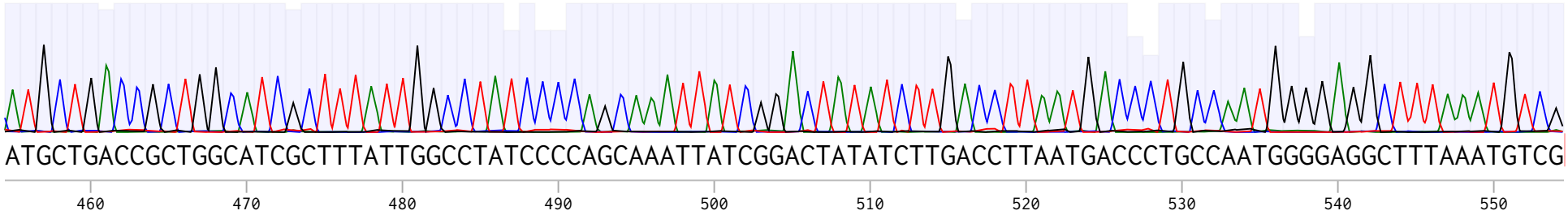

**template sequence** pAS0.11



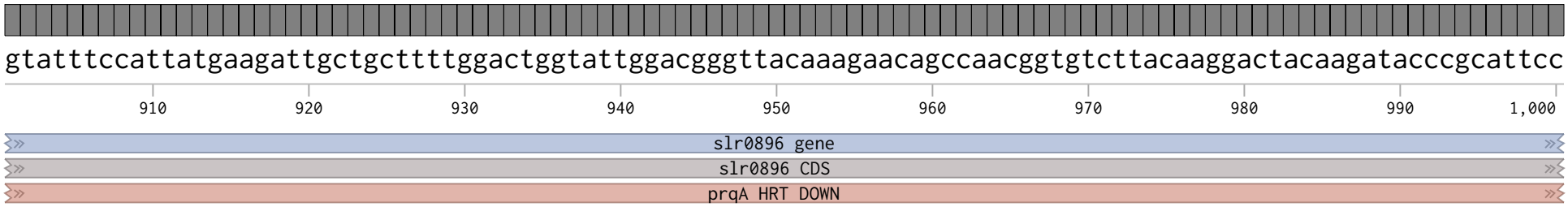

**aligned sequence** 2020-11-03_A02_ASASO11ASP1



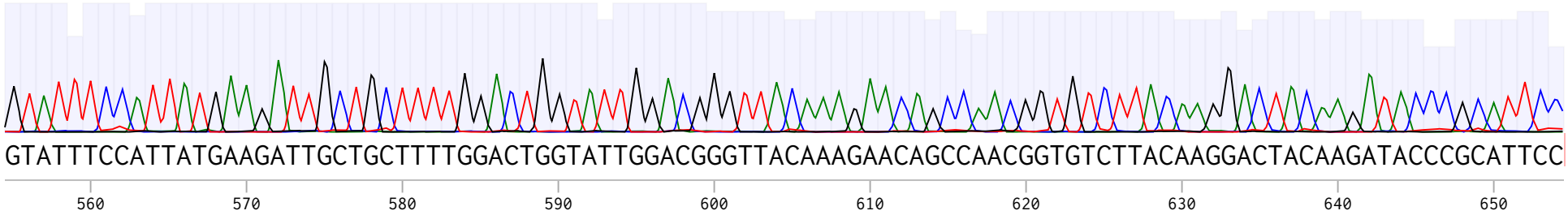

**template sequence** pAS0.11



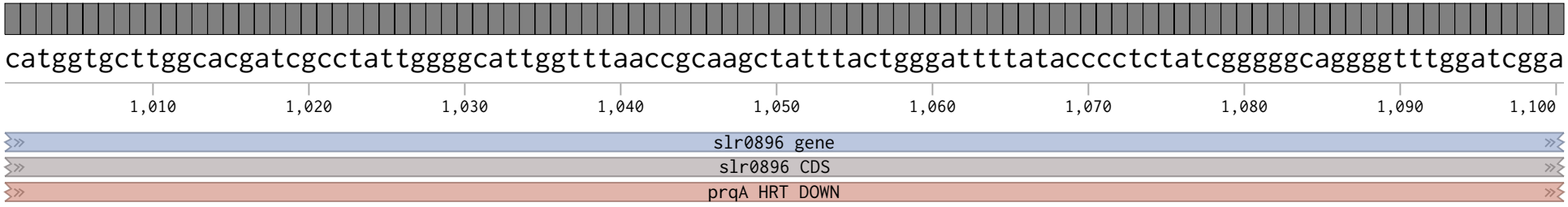

**aligned sequence** 2020-11-03_A02_ASASO11ASP1



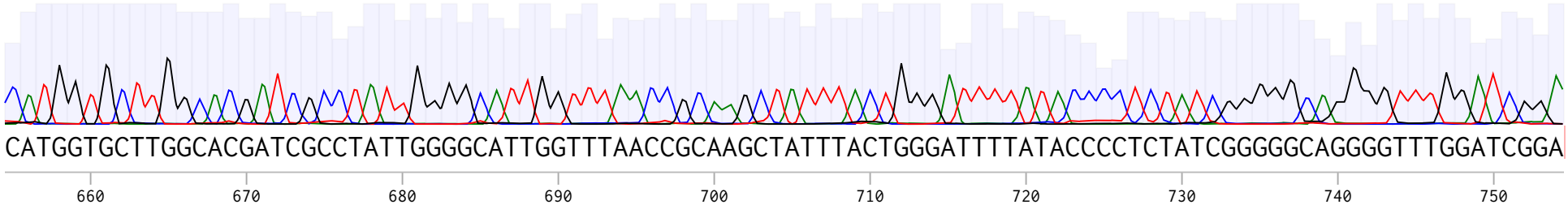

**template sequence** pAS0.11



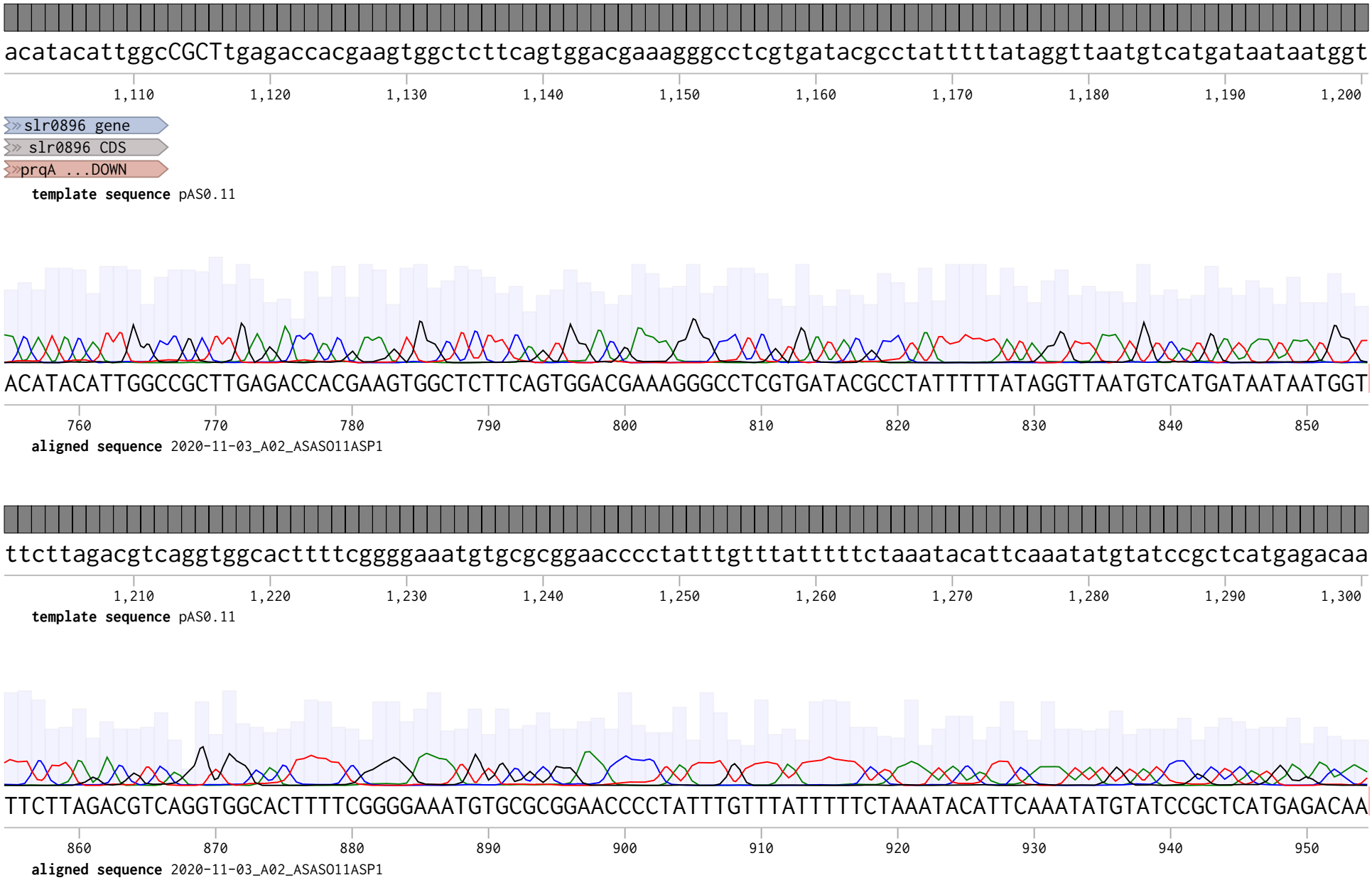

**aligned sequence** 2020-11-03_A02_ASASO11ASP1

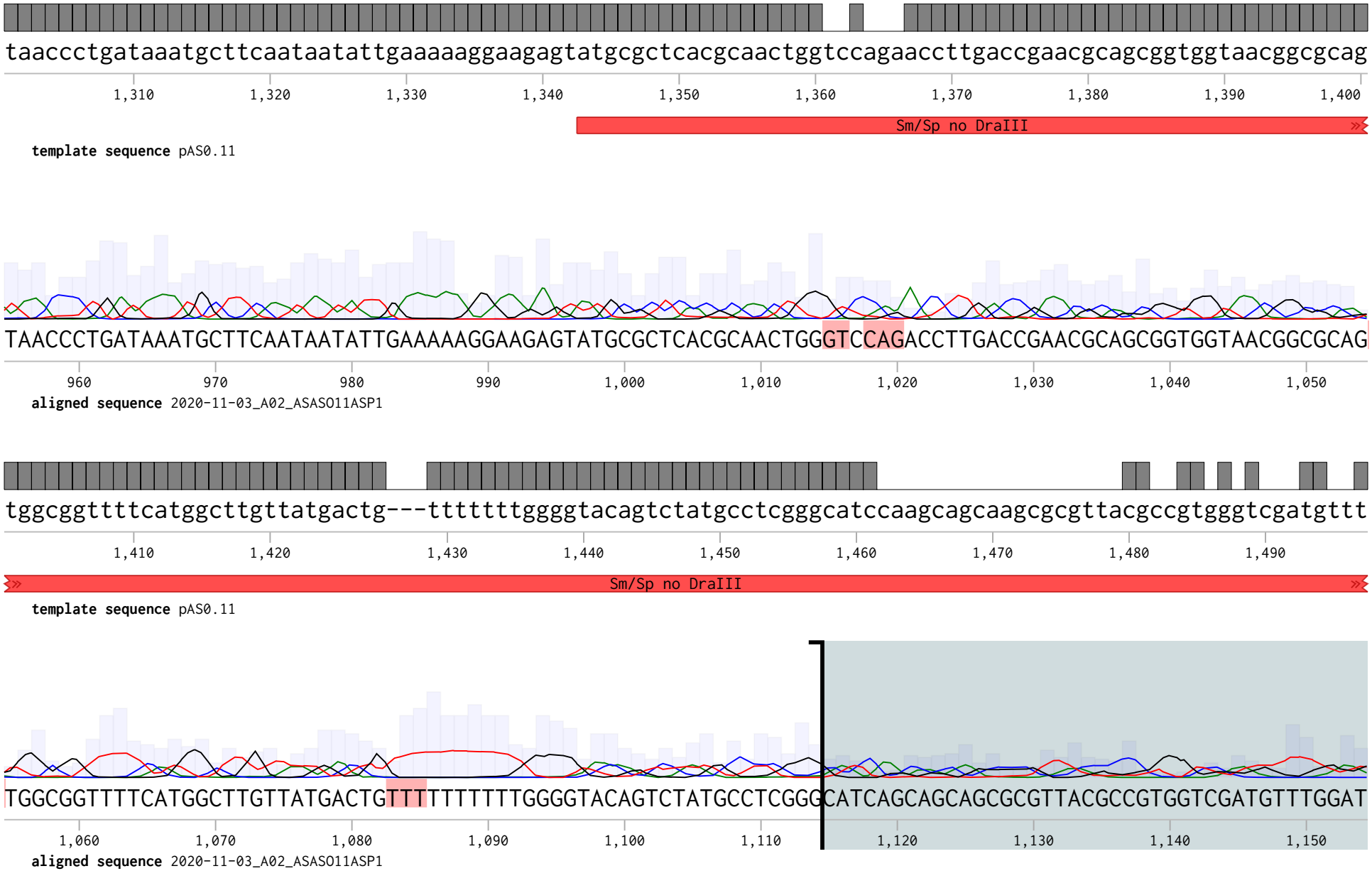


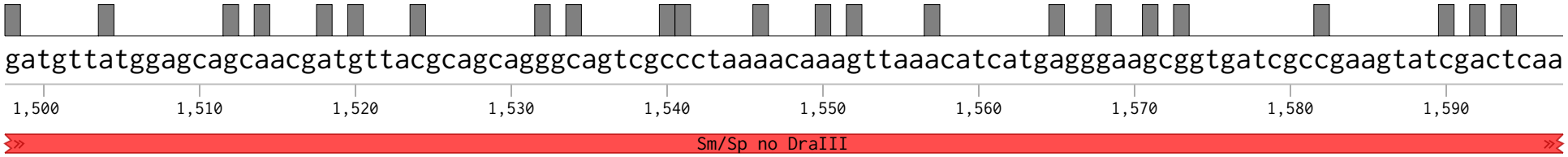

**template sequence** pAS0.11



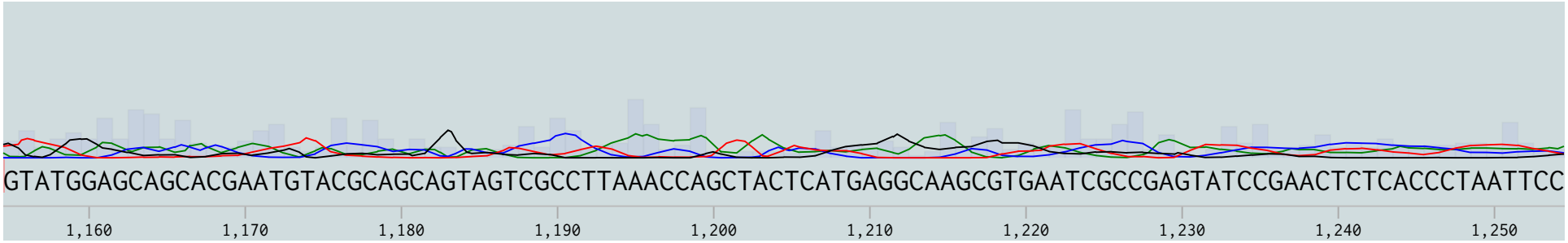

**aligned sequence** 2020-11-03_A02_ASASO11ASP1


acatacattggcCGCTtgagaccacgaagtggctcttcagtggacgaaagggcctcgtgatacgcctatttttataggttaatgtcatgataataatggt
1,110
1,120
1,130
1,140
1,150
1,160
1,170
1,180
1,190
1,200
slr0896 gene
slr0896 CDS
prqA ...DOWN
template sequence pAS0.11
ACATACATTGGCCGCTTGAGACCACGAAGTGGCTCTTCAGTGGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGT
760
770
780
790
800
810
820
830
840
850
aligned sequence 2020-11-03_A02_ASASO11ASP1
ttcttagacgtcaggtggcacttttcggggaaatgtgcgcggaacccctatttgtttatttttctaaatacattcaaatatgtatccgctcatgagacaa
1,210
1,220
1,230
1,240
1,250
1,260
1,270
1,280
1,290
1,300
template sequence pAS0.11
TTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAA
860
870
880
890
900
910
920
930
940
950
aligned sequence 2020-11-03_A02_ASASO11ASP1

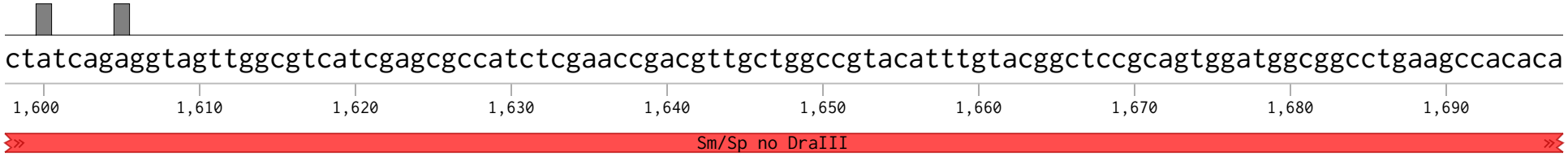

taaccctgataaatgcttcaataatattgaaaaaggaagagtatgcgctcacgcaactggtccagaaccttgaccgaacgcagcggtggtaacggcgcag
1,310
1,320
1,330
1,340
1,350
1,360
1,370
1,380
1,390
1,400
Sm/Sp no DraIII
template sequence pAS0.11
TAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGCGCTCACGCAACTGGGTCCAGACCTTGACCGAACGCAGCGGTGGTAACGGCGCAG
960
970
980
990
1,000
1,010
1,020
1,030
1,040
1,050
aligned sequence 2020-11-03_A02_ASASO11ASP1
tggcggttttcatggcttgttatgactg---ttttttggggtacagtctatgcctcgggcatccaagcagcaagcgcgttacgccgtgggtcgatgttt
1,410
1,420
1,430
1,440
1,450
1,460
1,470
1,480
1,490
Sm/Sp no DraIII
template sequence pAS0.11
TGGCGGTTTTCATGGCTTGTTATGACTGTTTTTTTTTTGGGGTACAGTCTATGCCTCGGGCATCAGCAGCAGCGCGTTACGCCGTGGTCGATGTTTGGAT
1,060
1,070
1,080
1,090
1,100
1,110
1,120
1,130
1,140
1,150
aligned sequence 2020-11-03_A02_ASASO11ASP1




**template sequence** pAS0.11




**aligned sequence** 2020-11-03_A02_ASASO11ASP1




**template sequence** pAS0.11

**aligned sequence** 2020-11-03_A02_ASASO11ASP1

gcgatattgatttgctggttacggtgaccgtaaggcttgatgaaacaacgcggcgagctttgatcaacgacctttttggaaacttcggcttcccctggaga

1,700 1,710 1,720 1,730 1,740 1,750 1,760 1,770 1,780 1,790

Sm/Sp no DraIII

**template sequence** pAS0.11

**aligned sequence** 2020-11-03_A02_ASASO11ASP1

gagcgagattctccgcgctgtagaagtcaccattgttgtgcacgacgacatcattccgtggcgttatccagctaagcgcgaactgcaatttggagaatgg

1,800 1,810 1,820 1,830 1,840 1,850 1,860 1,870 1,880 1,890

Sm/Sp no DraIII

**template sequence** pAS0.11

**aligned sequence** 2020-11-03_A02_ASASO11ASP1

cagcgcaatgacattcttgcaggtatcttcgagccagccacgatcgacattgatctggctatcttgctgacaaaagcaagagaacatagcgttgccttgg

1,900 1,910 1,920 1,930 1,940 1,950 1,960 1,970 1,980 1,990

Sm/Sp no DraIII

**template sequence** pAS0.11

**aligned sequence** 2020-11-03_A02_ASASO11ASP1

taggtccagcggcggaggaactctttgatccggttcctgaacaggatctatttgaggcgctaaatgaaaccttaacgctatggaactcgccgcccgactg

2,000 2,010 2,020 2,030 2,040 2,050 2,060 2,070 2,080 2,090

Sm/Sp no DraIII

**template sequence** pAS0.11

**aligned sequence** 2020-11-03_A02_ASASO11ASP1

ggctggcgatgagcgaaatgtagtgcttacgttgtcccgcatttggtacagcgcagtaaccggcaaaatcgcgccgaaggatgtcgctgccgactgggca

2,100 2,110 2,120 2,130 2,140 2,150 2,160 2,170 2,180 2,190

Sm/Sp no DraIII

**template sequence** pAS0.11

**aligned sequence** 2020-11-03_A02_ASASO11ASP1

atggagcgcctgccggcccagtatcagcccgtcatacttgaagctagacaggcttatcttggacaagaagaagatcgcttggcctcgcgcgcagatcagt

2,200 2,210 2,220 2,230 2,240 2,250 2,260 2,270 2,280 2,290

Sm/Sp no DraIII

**template sequence** pAS0.11

**aligned sequence** 2020-11-03_A02_ASASO11ASP1

tggaagaatttgtccattacgtaaaaggcgagatcaccaaggtagtcggcaaataactgtcagaccaagtttactcatatatactttagattgatttaaa

**template sequence** pAS0.11

**aligned sequence** 2020-11-03_A02_ASASO11ASP1

acttcatttttaatttaaaaggatctaggtgaagatccttttgataatctcatgaccaaaatcccttaacgtgagttttcgttccactgagcgtcagac

**template sequence** pAS0.11

**aligned sequence** 2020-11-03_A02_ASASO11ASP1

cccgtagaaaagatcaaaggatcttcttgagatccttttttctgcgcgtaatctgctgcttgcaaacaaaaaaaccaccgctaccagcggtggtttgtt

2,500 2,510 2,520 2,530 2,540 2,550 2,560 2,570 2,580 2,590

rep (pMB1)

ColE1 origin

**template sequence** pAS0.11

**aligned sequence** 2020-11-03_A02_ASASO11ASP1

tgccggatcaagagctaccaactctttttccgaaggtaactggcttcagcagagcgcagataccaaatactgtccttctagtgtagccgtagttaggcca

2,600 2,610 2,620 2,630 2,640 2,650 2,660 2,670 2,680 2,690

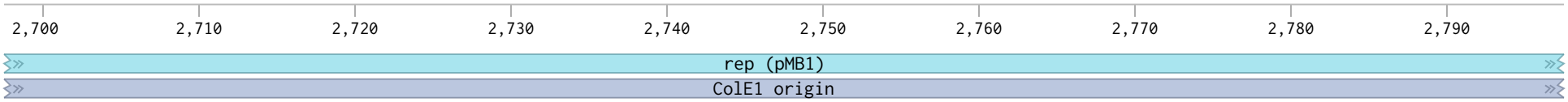
rep (pMB1)

ColE1 origin

**template sequence** pAS0.11

**aligned sequence** 2020-11-03_A02_ASASO11ASP1

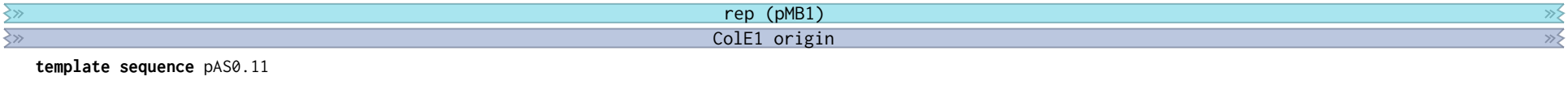
ccacttcaagaactctgtagcaccgcctacatacctcgctctgctaatcctgttaccagtggctgctgccagtggcgataagtcgtgtcttaccgggttg




**template sequence** pAS0.11

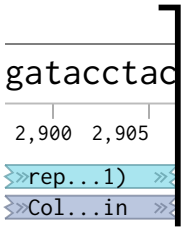
**aligned sequence** 2020-11-03_A02_ASASO11ASP1

gactcaagacgatagttaccggataaggcgcagcggtcgggctgaacgggggttcgtgcacacagcccagcttggagcgaacgacctacaccgaactga

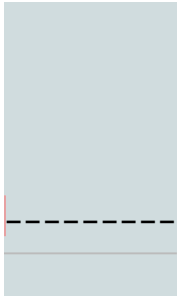



**template sequence** pAS0.11

**aligned sequence** 2020-11-03_A02_ASASO11ASP1




**template sequence** pAS0.11




**aligned sequence** 2020-11-03_A02_ASASO11ASP1