

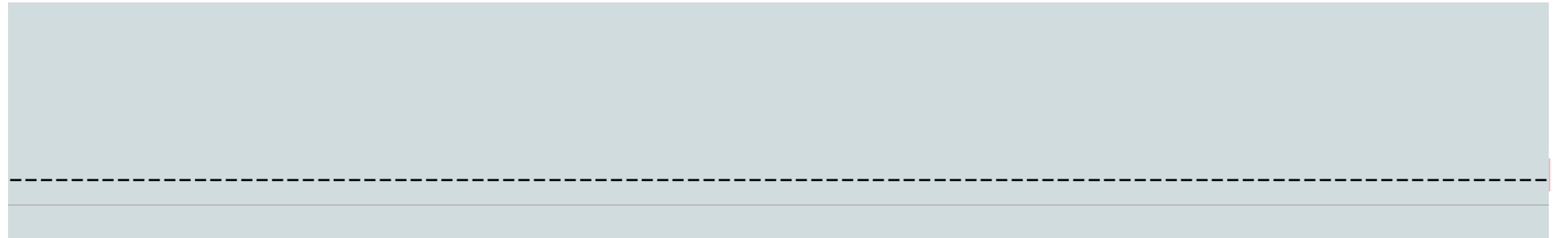
Template Alignment: 2020-11-03_G01_ASASO6ASP1

ccgtcatacttgaagctagacaggcttatcttggacaagaagaagatcgcttggcctcgcgcgagatcagttggaagaatttgtccattacgtaaaagg

10 20 30 40 50 60 70 80 90 100

SmR

template sequence pAS0.6 (PprqR)



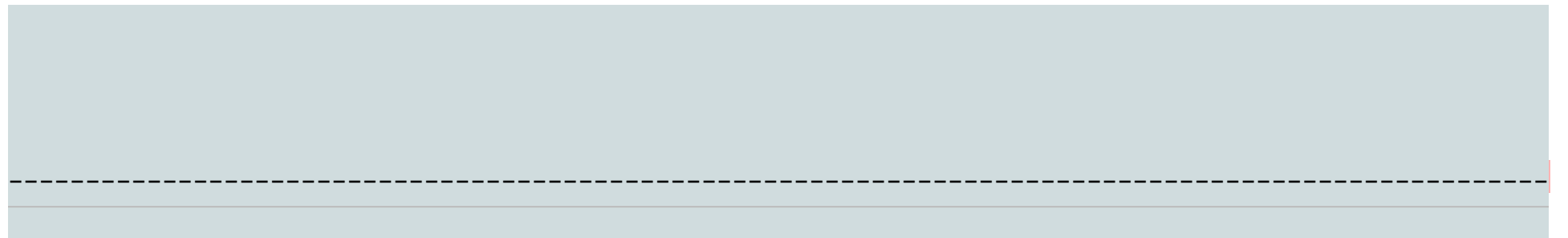
aligned sequence 2020-11-03_G01_ASASO6ASP1

cgagatcaccaaggtagtcggcaaataactgtcagaccaagtttactcatatatactttagattgattttaaacttcatttttaatttaaaggatctag

110 120 130 140 150 160 170 180 190 200

SmR

template sequence pAS0.6 (PprqR)

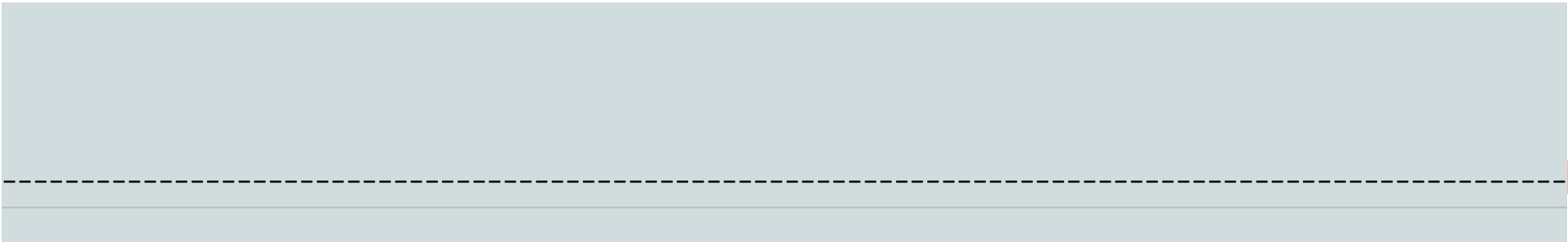


aligned sequence 2020-11-03_G01_ASASO6ASP1

gtgaagatcctttttgataatctcatgaccaaaatcccttaacgtgagttttcgttccactgagcgtcagaccccgtagaaaagatcaaaggatcttctt

210 220 230 240 250 260 270 280 290 300

template sequence pAS0.6 (PprqR)



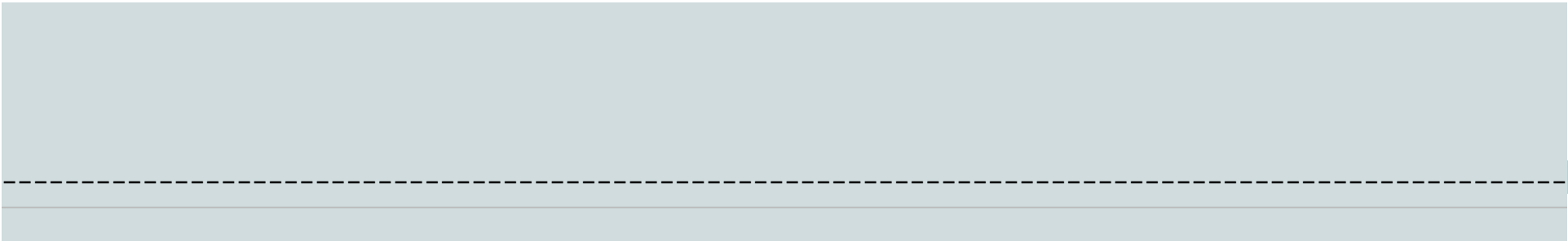
aligned sequence 2020-11-03_G01_ASAS06ASP1

gagatccttttttctgcgcgtaatctgctgcttgcaaacaaaaaaaccaccgctaccagcggtggtttgtttgccggatcaagagctaccaactctttt

310 320 330 340 350 360 370 380 390 400

>> ori >>

template sequence pAS0.6 (PprqR)



aligned sequence 2020-11-03_G01_ASAS06ASP1

tccgaaggtaactggcttcagcagagcgcagataccaaatactgtccttctagtgtagccgtagttaggccaccacttcaagaactctgtagcaccgcct

410

420

430

440

450

460

470

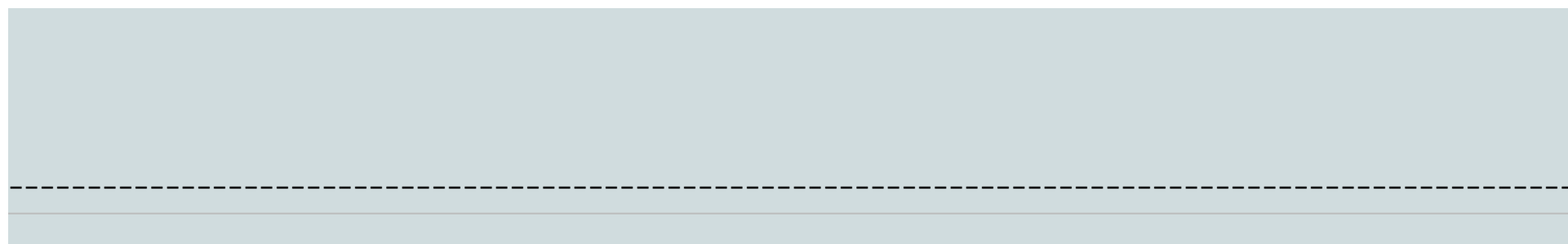
480

490

500

>> ori >>

template sequence pAS0.6 (PprqR)



aligned sequence 2020-11-03_G01_ASAS06ASP1

acatacctcgctctgctaactctgtttaccagtggtgctgccagtgggcgataagtcgtgtcttaccgggttggactcaagacgatagttaccggataagg

510

520

530

540

550

560

570

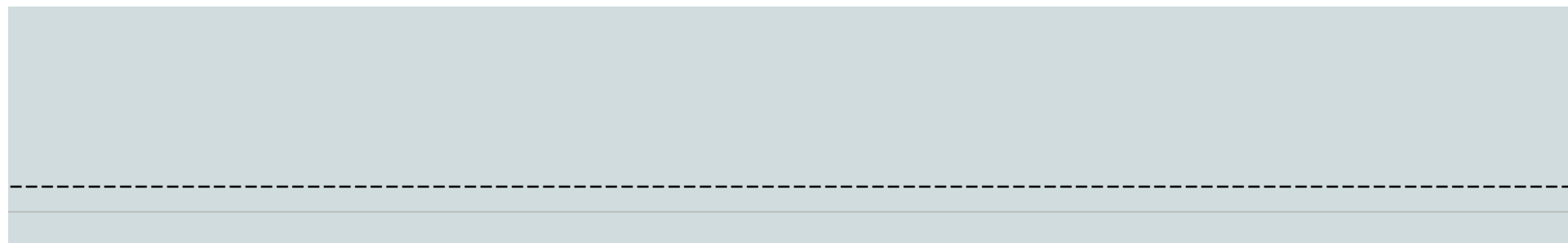
580

590

600

>> ori >>

template sequence pAS0.6 (PprqR)



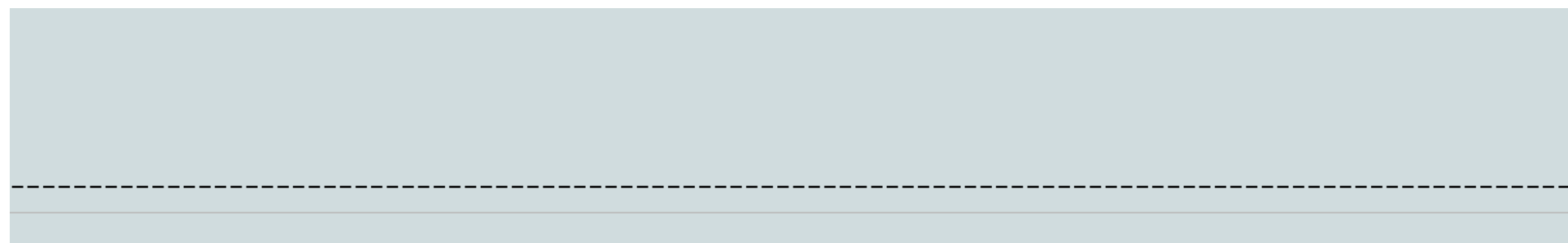
aligned sequence 2020-11-03_G01_ASAS06ASP1

cgcagcggtcgggctgaacggggggttcgtgcacacagcccagcttggagcgaacgacctacaccgaactgagatacctacagcgtgagctatgagaaag

610 620 630 640 650 660 670 680 690 700

>> ori >>

template sequence pAS0.6 (PprqR)

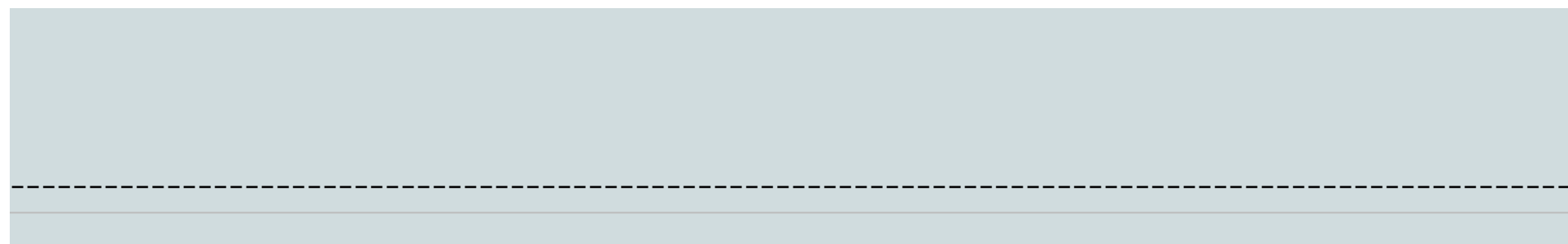


cgccacgcttcccgaaggagaaaggcggacaggtatccggtaagcggcagggtcggaacaggagagcgcacgaggagcttccagggggaaacgcctgg

710 720 730 740 750 760 770 780 790 800

>> ori >> pBR322ori-F >>

template sequence pAS0.6 (PprqR)



tatctttatagtcctgtcgggtttcgccacctctgacttgagcgtcgatttttgtgatgctcgtcaggggggcggagcctatggaaaaacgccagcaacg

810

820

830

840

850

860

870

880

890

900

>>pB...F

ori

template sequence pAS0.6 (PprqR)

aligned sequence 2020-11-03_G01_ASAS06ASP1

cggcctttttacggttcctggccttttgctggccttttgctcacatgttctttcctgcgttatccctgattctgtggataaccgtattaccgcctttga

910

920

930

940

950

960

970

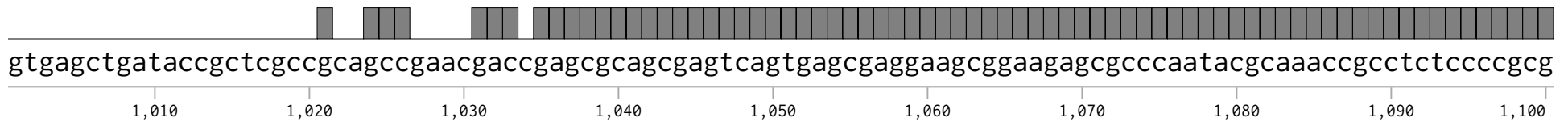
980

990

1,000

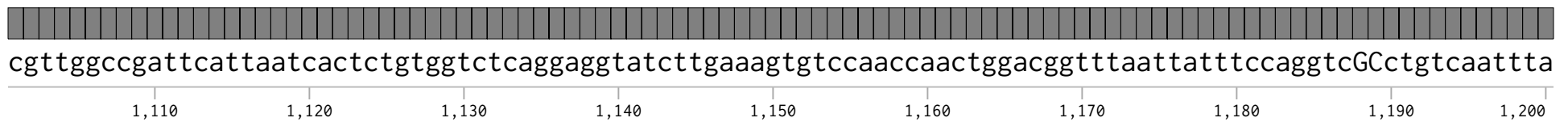
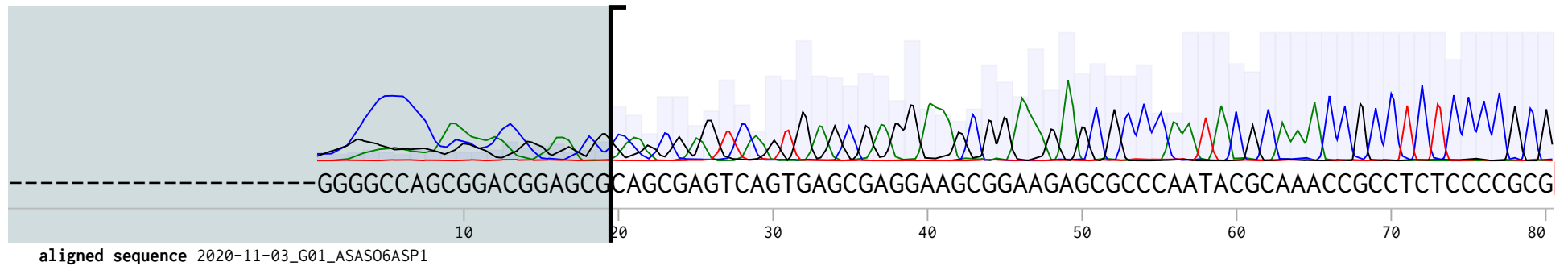
template sequence pAS0.6 (PprqR)

aligned sequence 2020-11-03_G01_ASAS06ASP1



L4440

template sequence pAS0.6 (PprqR)



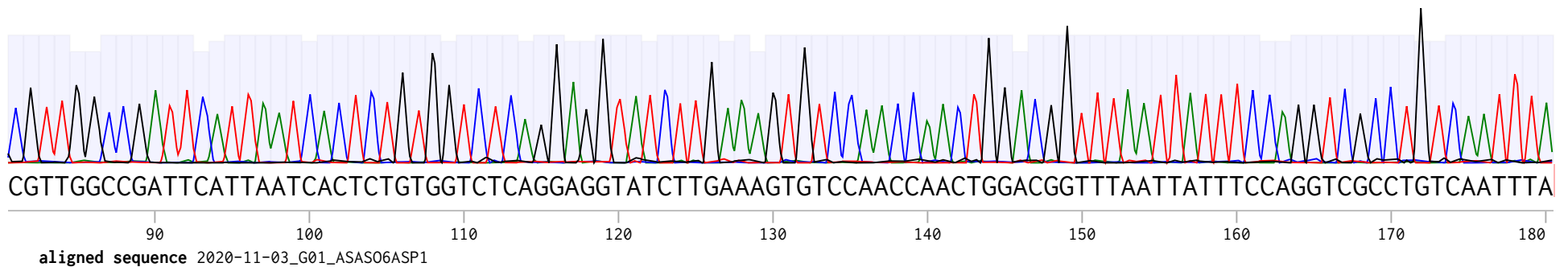
predicted promoter (sigma54, f...server/iPro54PseKNC/Pre.php) >>

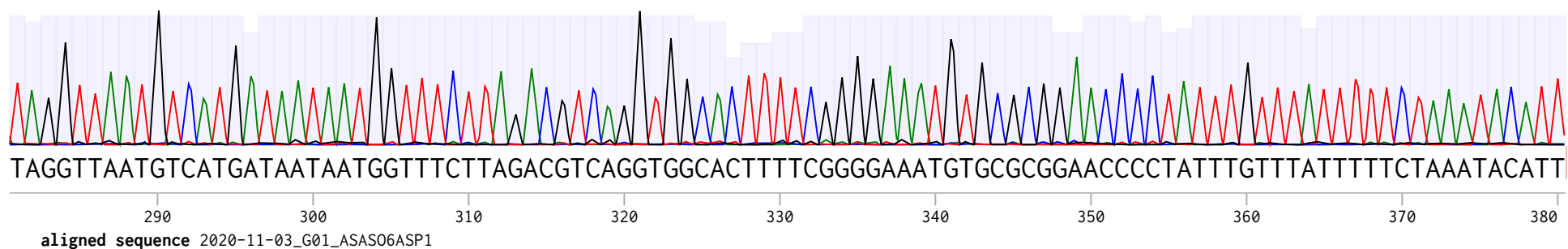
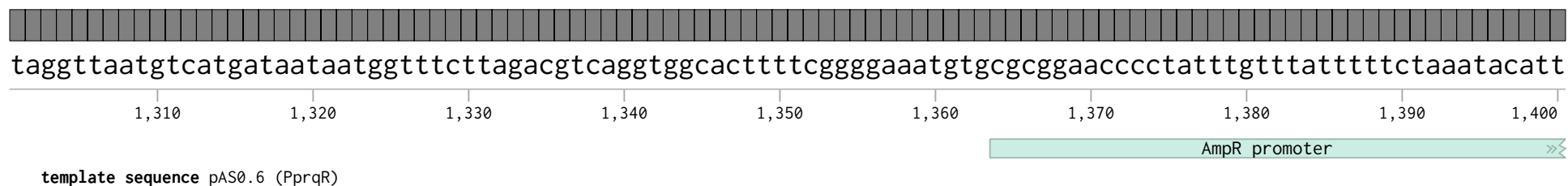
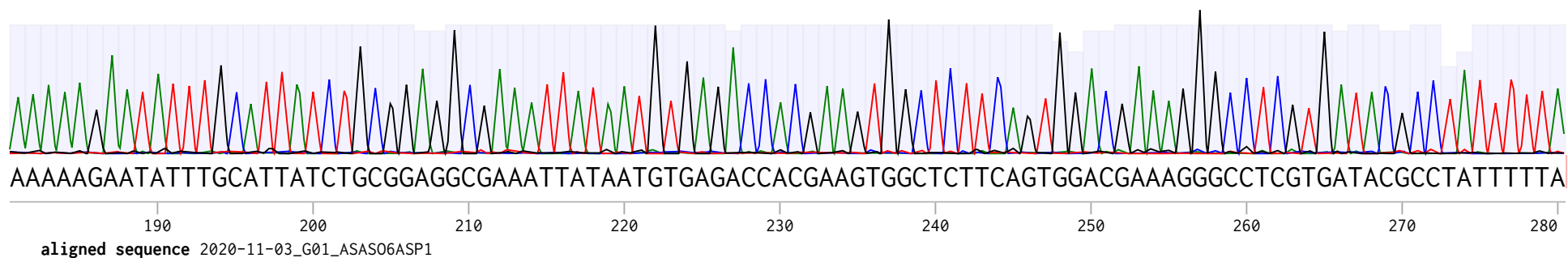
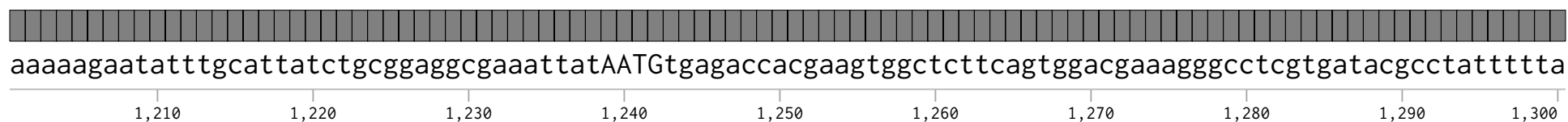
predicted promoter (sigma 70, from ht...up.cn/server/iPro70PseZNC/pro70.php) >>

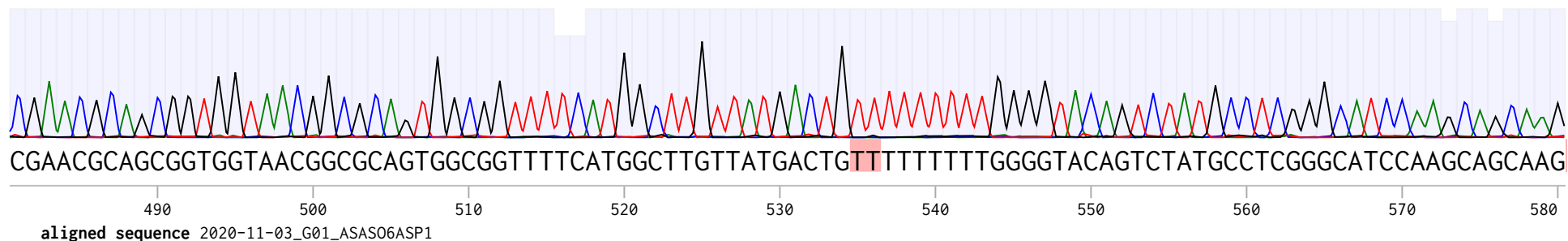
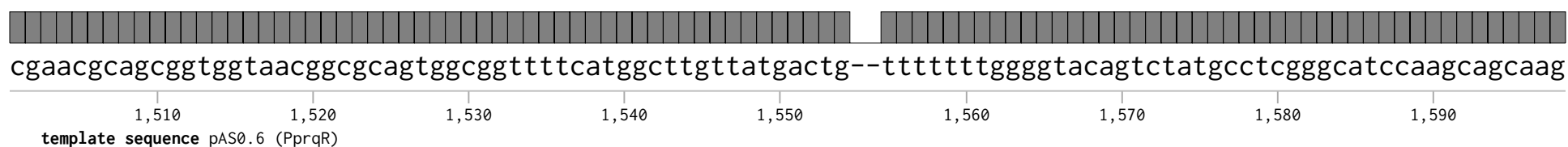
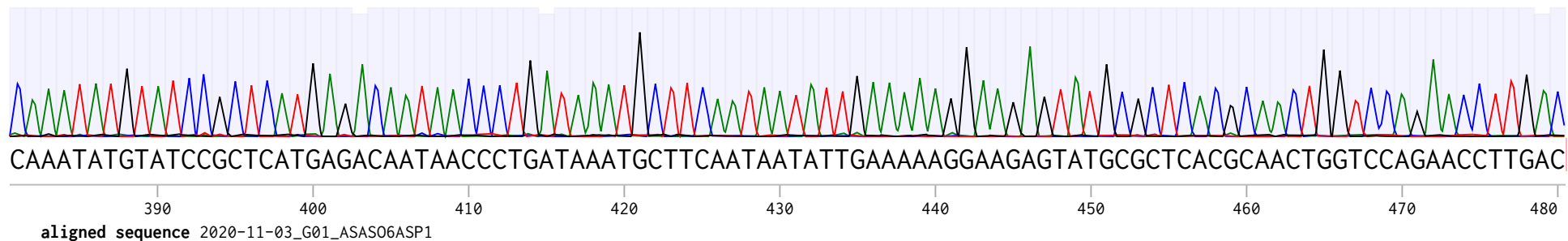
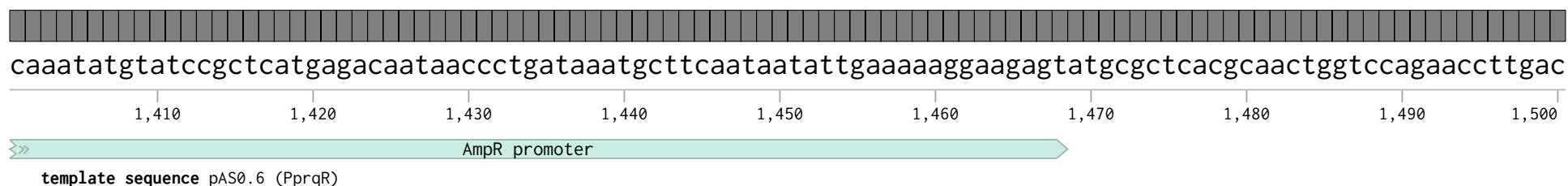
synonym: Synechocystis PCC6803 >>

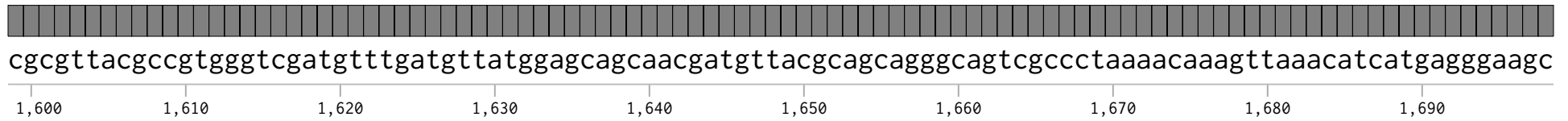
prqR-5'UTR+TSS - dom >>

template sequence pAS0.6 (PprqR)

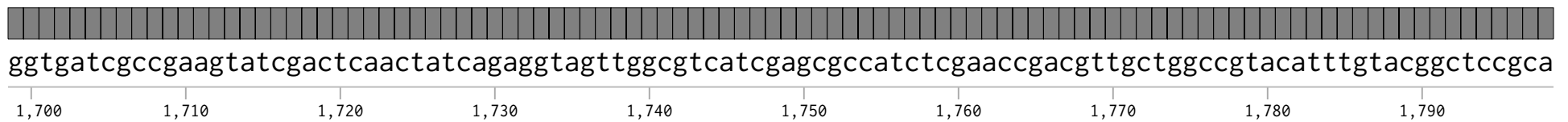
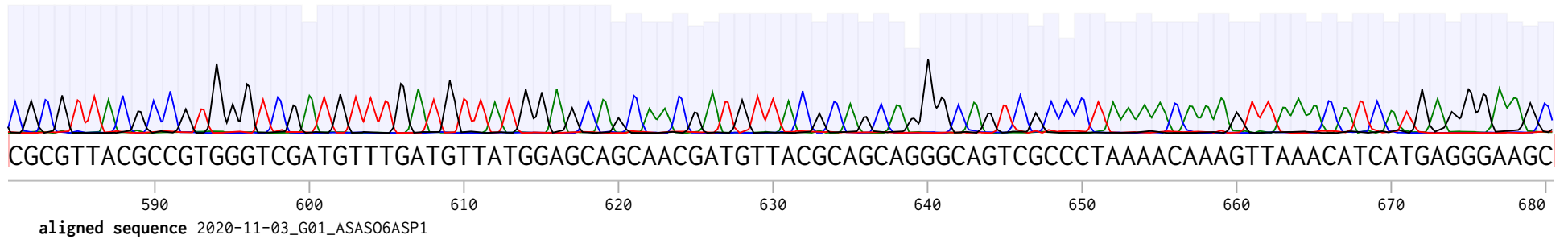








template sequence pAS0.6 (PprqR)



template sequence pAS0.6 (PprqR)

