```
                            10        20        30        40        50        60
                             |         |         |         |         |         |
MG1655 (1229483)..  GGCTATCAATATTTGTCGCTGCATAGGCTGCTGATTTTTCGTTCTCTTATCTTGTGCTCA
MDS42               GGCTATCAATATTTGTCGCTGCATAGGCTGCTGATTTTTCGTTCTCTTATCTTGTGCTCA
W3110               GGCTATCAATATTTGTCGCTGCATAGGCTGCTGATTTTTCGTTCTCTTATCTTGTGCTCA
DH1                 GGCTATCAATATTTGTCGCTGCATAGGCTGCTGATTTTTCGTTCTCTTATCTTGTGCTCA
ETEC                GGCTATCAATATTTGTCGCTGCATAGGCTGCTGATTTTTCGTTCTCTTATCTTGTGCTCA
P12b                GGCTATCAATATTTGTCGCTGCATAGGCTGCTGATTTTTCGTTCTCTTATCTTGTGCTCA
BW2952              GGCTATCAATATTTGTCGCTGCATAGGCTGCTGATTTTTCGTTCTCTTATCTTGTGCTCA
DH10B               GGCTATCAATATTTGTCGCTGCATAGGCTGCTGATTTTTCGTTCTCTTATCTTGTGCTCA
C321                GGCTATCAATATTTGTCGCTGCATAGGCTGCTGATTTTTCGTTCTCTTATCTTGTGCTCA
Wxxxxx20            GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
KO11FL              GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
LY180x19            GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
E24377A             GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
SE11xx14            GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
2009EL              GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
2011C_3493          GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
55989x18            GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
IAI1xx13            GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
O103H2              GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
APECxx11            GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
UMNK88              GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
HSxxxx39            GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
BL21DE3             GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
REL606              GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
BL21_GoldDE3pLysS   GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
ATCCxx37            GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
O111H_              GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
O26H11              GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
UMN026              GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
042NC_0176261       GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
IAI39x23            GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
O7K1xx29            GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
SMS_3_5             GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTATCTTATCCTGTGCTCA
RM12579             GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
CB9615              GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
Xuzhou21            GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
TW14359             GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
EC4115              GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
EDL933              GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
Sakaix28            GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA
                    ************************** **************** ******* ********

Prim.cons.          GGCTATCAATATTTGTCGCTGCATAGACTGCTGATTTTTCGTTCTCTTATCCTGTGCTCA

                            70        80        90       100       110       120
                             |         |         |         |         |         |
MG1655              CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
MDS42x1             CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
W3110x2             CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
DH1NC_0176381       CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
ETECxx4             CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
P12bxx5             CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
BW2952              CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
DH10Bx7             CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
C321deltaA          CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
Wxxxxx20            CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
KO11FL              CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
LY180x19            CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
E24377A             CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
SE11xx14            CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
2009EL_2050         CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
2011C_3493          CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
55989x18            CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
IAI1xx13            CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
O103H2              CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
APECxx11            CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
UMNK88              CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
```

```
HSxxxx39            CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
BL21DE3             CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
REL606              CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
BL21_GoldDE3pLysS   CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
ATCCxx37            CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCAAAAAA
O111H_              CGCGGCCTTCTGGCGACTACGCTCATCCAGCAGAAATGAAAAATATTACCCGGCTAAAAA
O26H11              CGCGGCCTTCTGGCGACTACGCTCATCCAGCAGAAATGAAAAATATTACCCGGCTAAAAA
UMN026              CGCGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
042NC_0176261       CGCGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
IAI39x23            CGCG-CCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
O7K1xx29            CGCG-CCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
SMS_3_5             CGCG-CCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
RM12579             CGCGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
CB9615              CGCGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
Xuzhou21            CGCGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
TW14359             CGCGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
EC4115              CGCGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
EDL933              CGCGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
Sakaix28            CGCGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA
                    ** * ************ **************************** ******* *****

Prim.cons.          CGTGGCCTTCTGGCGACGACGCTCATCCAGCAGAAATGAAAAATATCACCCGGCTAAAAA

                           130       140       150       160       170       180
                             |         |         |         |         |         |
MG1655              ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
MDS42x1             ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
W3110x2             ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
DH1NC_0176381       ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
ETECxx4             ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
P12bxx5             ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
BW2952              ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
DH10Bx7             ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
C321deltaA          ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
Wxxxxx20            ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
KO11FL              ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
LY180x19            ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
E24377A             ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
SE11xx14            ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
2009EL_2050         ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
2011C_3493          ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
55989x18            ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
IAI1xx13            ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
O103H2              ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
APECxx11            ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
UMNK88              ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
HSxxxx39            ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
BL21DE3             ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
REL606              ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
BL21_GoldDE3pLysS   ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
ATCCxx37            ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
O111H_              ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
O26H11              ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
UMN026              -TAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
042NC_0176261       ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
IAI39x23            ATAGAATAGAAGCATCAGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
O7K1xx29            ATAGAATAGAAGCATCAGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
SMS_3_5             ATAGAATAGAAGCATCAGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
RM12579             ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
CB9615              ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
Xuzhou21            ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
TW14359             ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
EC4115              ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
EDL933              ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
Sakaix28            ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT
                     **************  *******************************************

Prim.cons.          ATAGAATAGAAGCATTCGCCATAATGACATTAAACATTGTTTGATATTTATCATATTAAT

                           190       200       210       220       230       240
```

```
                                 |         |         |         |         |         |
MG1655                  AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
MDS42x1                 AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
W3110x2                 AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
DH1NC_0176381           AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
ETECxx4                 AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
P12bxx5                 AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
BW2952                  AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
DH10Bx7                 AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
C321deltaA              AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
Wxxxxx20                AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
KO11FL                  AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
LY180x19                AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
E24377A                 AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
SE11xx14                AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
2009EL_2050             AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
2011C_3493              AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
55989x18                AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
IAI1xx13                AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
O103H2                  AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
APECxx11                AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
UMNK88                  AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
HSxxxx39                AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
BL21DE3                 AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
REL606                  AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
BL21_GoldDE3pLysS       AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
ATCCxx37                AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
O111H_                  AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
O26H11                  AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT
UMN026                  AGAAATAAAGACATTGACGCATCTCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTC
042NC_0176261           AGAAATAAAGACATTGACGCATCTCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTC
IAI39x23                AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTC
O7K1xx29                AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTC
SMS_3_5                 AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGATGTAAAATTC
RM12579                 AGAAATAAAGACATTGACGCATCTCTCCCGGCTAACTATGAATTAGATGAAGTAAAATTC
CB9615                  AGAAATAAAGACATTGACGCATCTCTCCCGGCTAACTATGAATTAGATGAAGTAAAATTC
Xuzhou21                AGAAATAAAGACATTGACGCATCTCTCCCGGCTAACTATGAATTAGATGAAGTAAAATTC
TW14359                 AGAAATAAAGACATTGACGCATCTCTCCCGGCTAACTATGAATTAGATGAAGTAAAATTC
EC4115                  AGAAATAAAGACATTGACGCATCTCTCCCGGCTAACTATGAATTAGATGAAGTAAAATTC
EDL933                  AGAAATAAAGACATTGACGCATCTCTCCCGGCTAACTATGAATTAGATGAAGTAAAATTC
Sakaix28                AGAAATAAAGACATTGACGCATCTCTCCCGGCTAACTATGAATTAGATGAAGTAAAATTC
                        *********************** * ************************ ******** 

Prim.cons.              AGAAATAAAGACATTGACGCATCCCGCCCGGCTAACTATGAATTAGATGAAGTAAAATTT

                                250       260       270       280       290       300
                                 |         |         |         |         |         |
MG1655                  ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
MDS42x1                 ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
W3110x2                 ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
DH1NC_0176381           ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
ETECxx4                 ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
P12bxx5                 ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
BW2952                  ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
DH10Bx7                 ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
C321deltaA              ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
Wxxxxx20                ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
KO11FL                  ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
LY180x19                ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
E24377A                 ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
SE11xx14                ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
2009EL_2050             ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
2011C_3493              ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
55989x18                ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
IAI1xx13                ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
O103H2                  ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
APECxx11                ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
UMNK88                  ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
HSxxxx39                ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
```

```
BL21DE3             ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
REL606              ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
BL21_GoldDE3pLysS   ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
ATCCxx37            ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
O111H_              ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
O26H11              ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
UMN026              ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
042NC_0176261       ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
IAI39x23            TTTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
O7K1xx29            TTTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
SMS_3_5             TTTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
RM12579             ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
CB9615              ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
Xuzhou21            ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
TW14359             ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
EC4115              ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
EDL933              ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
Sakaix28            ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT
                     ***********************************************************

Prim.cons.          ATTAATAGTTGTAAAACAGGAGTTTCATTACAATTTATATATTTAAAGAGGCGAATGATT

                           310       320       330       340       350       360
                             |         |         |         |         |         |
MG1655              ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
MDS42x1             ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
W3110x2             ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
DH1NC_0176381       ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
ETECxx4             ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
P12bxx5             ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
BW2952              ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
DH10Bx7             ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
C321deltaA          ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
Wxxxxx20            ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACTGCA
KO11FL              ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACTGCA
LY180x19            ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACTGCA
E24377A             ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACTGCA
SE11xx14            ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACTGCA
2009EL_2050         ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACTGCA
2011C_3493          ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACTGCA
55989x18            ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACTGCA
IAI1xx13            ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACTGCA
O103H2              ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACTGCA
APECxx11            ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACTGCA
UMNK88              ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
HSxxxx39            ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
BL21DE3             ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
REL606              ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
BL21_GoldDE3pLysS   ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
ATCCxx37            ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
O111H_              ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
O26H11              ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA
UMN026              ATGACTGAAATCGTTGCAGATAAAACGGTAGAGGTAGTTAAAAACGCAATCGAAACCGCA
042NC_0176261       ATGACTGAAATCGTTGCAGATAAAACGGTAGAGGTAGTTAAAAACGCAATCGAAACCGCA
IAI39x23            ATGACTGAAATCGTTGCAGATAAAACGGTAGAGGTAGTTAAAAACGCAATCGAAACCGCA
O7K1xx29            ATGACTGAAATCGTTGCAGATAAAACGGTAGAGGTAGTTAAAAACGCAATCGAAACCGCA
SMS_3_5             ATGACTGAAATCGTTGCAGATAAAACGGTAGAGGTAGTTAAAAACGCAATCGAAACCGCA
RM12579             ATGACTGAAATCGTTGCAGATAAAACGGTAGAGGTAGTTAAAAACGCAATCGAAACCGCA
CB9615              ATGACTGAAATCGTTGCAGATAAAACGGTAGAGGTAGTTAAAAACGCAATCGAAACCGCA
Xuzhou21            ATGACTGAAATCGTTGCAGATAAAACGGTAGAGGTAGTTAAAAACGCAATCGAAACCGCA
TW14359             ATGACTGAAATCGTTGCAGATAAAACGGTAGAGGTAGTTAAAAACGCAATCGAAACCGCA
EC4115              ATGACTGAAATCGTTGCAGATAAAACGGTAGAGGTAGTTAAAAACGCAATCGAAACCGCA
EDL933              ATGACTGAAATCGTTGCAGATAAAACGGTAGAGGTAGTTAAAAACGCAATCGAAACCGCA
Sakaix28            ATGACTGAAATCGTTGCAGATAAAACGGTAGAGGTAGTTAAAAACGCAATCGAAACCGCA
                    ******************************** *********************** ***

Prim.cons.          ATGACTGAAATCGTTGCAGATAAAACGGTAGAAGTAGTTAAAAACGCAATCGAAACCGCA


                           370       380       390       400       410       420
```

```
                             |         |         |         |         |         |
MG1655              GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
MDS42x1             GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
W3110x2             GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
DH1NC_0176381       GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
ETECxx4             GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
P12bxx5             GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
BW2952              GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
DH10Bx7             GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
C321deltaA          GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
Wxxxxx20            GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
KO11FL              GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
LY180x19            GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
E24377A             GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
SE11xx14            GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
2009EL_2050         GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTAGCAGACCTTT
2011C_3493          GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTAGCAGACCTTT
55989x18            GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTAGCAGACCTTT
IAI1xx13            GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
O103H2              GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
APECxx11            GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
UMNK88              GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
HSxxxx39            GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
BL21DE3             GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
REL606              GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
BL21_GoldDE3pLysS   GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
ATCCxx37            GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
O111H_              GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
O26H11              GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
UMN026              GATGGAGCATTAGACCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTC
042NC_0176261       GATGGAGCATTAGACCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTC
IAI39x23            GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
O7K1xx29            GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
SMS_3_5             GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
RM12579             GATGGAGCATTGGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
CB9615              GATGGAGCATTGGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
Xuzhou21            GATGGAGCATTGGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
TW14359             GATGGAGCATTGGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
EC4115              GATGGAGCATTGGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
EDL933              GATGGAGCATTGGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
Sakaix28            GATGGAGCATTGGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT
                    *********** ** ********************************** ********* 

Prim.cons.          GATGGAGCATTAGATCTTTATAATAAATATCTCGATCAGGTCATCCCCTGGCAGACCTTT

                           430       440       450       460       470       480
                             |         |         |         |         |         |
MG1655              GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
MDS42x1             GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
W3110x2             GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
DH1NC_0176381       GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
ETECxx4             GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
P12bxx5             GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
BW2952              GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
DH10Bx7             GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
C321deltaA          GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
Wxxxxx20            GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
KO11FL              GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
LY180x19            GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
E24377A             GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
SE11xx14            GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
2009EL_2050         GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
2011C_3493          GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
55989x18            GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
IAI1xx13            GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
O103H2              GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
APECxx11            GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
UMNK88              GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
HSxxxx39            GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTAACAGGCAGCCTCCGTT
```

```
BL21DE3             GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
REL606              GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
BL21_GoldDE3pLysS   GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
ATCCxx37            GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
O111H_              GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
O26H11              GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
UMN026              GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
042NC_0176261       GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
IAI39x23            GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
O7K1xx29            GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
SMS_3_5             GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
RM12579             GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
CB9615              GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
Xuzhou21            GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
TW14359             GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
EC4115              GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
EDL933              GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
Sakaix28            GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT
                    ******************************************* ****************

Prim.cons.          GATGAAACCATAAAAGAGTTAAGTCGCTTTAAACAGGAGTATTCACAGGCAGCCTCCGTT

                           490       500       510       520       530       540
                             |         |         |         |         |         |
MG1655              TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
MDS42x1             TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
W3110x2             TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
DH1NC_0176381       TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
ETECxx4             TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
P12bxx5             TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
BW2952              TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
DH10Bx7             TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
C321deltaA          TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
Wxxxxx20            TTAGTCGGCGATATTAAAACCTTACTTATGGATAGC-AGGATAAGTATTTTGAAGCAACC
KO11FL              TTAGTCGGCGATATTAAAACCTTACTTATGGATAGC-AGGATAAGTATTTTGAAGCAACC
LY180x19            TTAGTCGGCGATATTAAAACCTTACTTATGGATAGC-AGGATAAGTATTTTGAAGCAACC
E24377A             TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
SE11xx14            TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
2009EL_2050         TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
2011C_3493          TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
55989x18            TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
IAI1xx13            TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
O103H2              TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
APECxx11            TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
UMNK88              TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
HSxxxx39            TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
BL21DE3             TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
REL606              TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
BL21_GoldDE3pLysS   TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
ATCCxx37            TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
O111H_              TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
O26H11              TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
UMN026              TTAGTTGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
042NC_0176261       TTAGTTGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
IAI39x23            TTAGTTGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
O7K1xx29            TTAGTTGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
SMS_3_5             TTAGTTGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
RM12579             TTAGTTGGCAATATTAAAACCTTACTAATGGATAGCCAGGATAAGTATTTTGAAGCAACC
CB9615              TTAGTTGGCAATATTAAAACCTTACTAATGGATAGCCAGGATAAGTATTTTGAAGCAACC
Xuzhou21            TTAGTTGGCAATATTAAAACCTTACTAATGGATAGCCAGGATAAGTATTTTGAAGCAACC
TW14359             TTAGTTGGCAATATTAAAACCTTACTAATGGATAGCCAGGATAAGTATTTTGAAGCAACC
EC4115              TTAGTTGGCAATATTAAAACCTTACTAATGGATAGCCAGGATAAGTATTTTGAAGCAACC
EDL933              TTAGTTGGCAATATTAAAACCTTACTAATGGATAGCCAGGATAAGTATTTTGAAGCAACC
Sakaix28            TTAGTTGGCAATATTAAAACCTTACTAATGGATAGCCAGGATAAGTATTTTGAAGCAACC
                    ***** *** **************** ********* ***********************

Prim.cons.          TTAGTCGGCGATATTAAAACCTTACTTATGGATAGCCAGGATAAGTATTTTGAAGCAACC
```

```
                               550       560       570       580       590       600
                                 |         |         |         |         |         |
MG1655                  CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
MDS42x1                 CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
W3110x2                 CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
DH1NC_0176381           CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
ETECxx4                 CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
P12bxx5                 CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
BW2952                  CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
DH10Bx7                 CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
C321deltaA              CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
Wxxxxx20                CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTTCTA
KO11FL                  CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTTCTA
LY180x19                CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTTCTA
E24377A                 CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTTCTA
SE11xx14                CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTTCTA
2009EL_2050             CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTTCTA
2011C_3493              CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTTCTA
55989x18                CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTTCTA
IAI1xx13                CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTTCTA
O103H2                  CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTTCTA
APECxx11                CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTTCTA
UMNK88                  CAAACAGTGTATGAATGGTTTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
HSxxxx39                CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
BL21DE3                 CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
REL606                  CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
BL21_GoldDE3pLysS       CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
ATCCxx37                CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
O111H_                  CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
O26H11                  CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
UMN026                  CAAACGGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
042NC_0176261           CAAACGGTGTATGAATGGTGTGGTGTTGCGACACAATTGCTCGCAGCATATATTTTGCTA
IAI39x23                CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
O7K1xx29                CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
SMS_3_5                 CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
RM12579                 CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
CB9615                  CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
Xuzhou21                CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
TW14359                 CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
EC4115                  CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
EDL933                  CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
Sakaix28                CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA
                        ***** ************* ************ ************** ******** ***

Prim.cons.              CAAACAGTGTATGAATGGTGTGGTGTTGCGACGCAATTGCTCGCAGCGTATATTTTGCTA

                               610       620       630       640       650       660
                                 |         |         |         |         |         |
MG1655                  TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
MDS42x1                 TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
W3110x2                 TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
DH1NC_0176381           TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
ETECxx4                 TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
P12bxx5                 TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
BW2952                  TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
DH10Bx7                 TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
C321deltaA              TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
Wxxxxx20                TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
KO11FL                  TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
LY180x19                TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
E24377A                 TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
SE11xx14                TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
2009EL_2050             TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
2011C_3493              TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
55989x18                TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
IAI1xx13                TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
O103H2                  TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
APECxx11                TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
UMNK88                  TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
```

```
HSxxxx39            TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
BL21DE3             TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
REL606              TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
BL21_GoldDE3pLysS   TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
ATCCxx37            TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
O111H_              TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
O26H11              TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
UMN026              TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
042NC_0176261       TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
IAI39x23            TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
O7K1xx29            TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
SMS_3_5             TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
RM12579             TTTGATGAGTATAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGTTACTG
CB9615              TTTGATGAGTATAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGTTACTG
Xuzhou21            TTTGATGAGTATAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
TW14359             TTTGATGAGTATAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
EC4115              TTTGATGAGTATAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
EDL933              TTTGATGAGTATAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
Sakaix28            TTTGATGAGTATAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG
                    *********** ****************************************** *****

Prim.cons.          TTTGATGAGTACAATGAGAAGAAAGCATCCGCCCAGAAAGACATTCTCATTAAGGTACTG

                           670       680       690       700       710       720
                             |         |         |         |         |         |
MG1655              GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
MDS42x1             GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
W3110x2             GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
DH1NC_0176381       GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
ETECxx4             GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
P12bxx5             GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
BW2952              GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
DH10Bx7             GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
C321deltaA          GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
Wxxxxx20            GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
KO11FL              GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
LY180x19            GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
E24377A             GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
SE11xx14            GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
2009EL_2050         GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
2011C_3493          GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
55989x18            GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
IAI1xx13            GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
O103H2              GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
APECxx11            GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
UMNK88              GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
HSxxxx39            GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
BL21DE3             GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
REL606              GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
BL21_GoldDE3pLysS   GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
ATCCxx37            GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
O111H_              GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
O26H11              GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
UMN026              GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
042NC_0176261       GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCTCTGCTGGTAAGCTCACAAAGT
IAI39x23            GATGACGGTATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
O7K1xx29            GATGACGGTATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
SMS_3_5             GATGACGGTATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
RM12579             GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
CB9615              GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
Xuzhou21            GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
TW14359             GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
EC4115              GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
EDL933              GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
Sakaix28            GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
                    ******** ****************************** ********************

Prim.cons.          GATGACGGCATCACGAAGCTGAATGAAGCGCAAAAATCCCTGCTGGTAAGCTCACAAAGT
```

```
                           730       740       750       760       770       780
                             |         |         |         |         |         |
MG1655              TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
MDS42x1             TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
W3110x2             TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
DH1NC_0176381       TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
ETECxx4             TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
P12bxx5             TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
BW2952              TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
DH10Bx7             TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
C321deltaA          TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
Wxxxxx20            TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
KO11FL              TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
LY180x19            TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
E24377A             TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
SE11xx14            TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
2009EL_2050         TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
2011C_3493          TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
55989x18            TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
IAI1xx13            TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
O103H2              TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
APECxx11            TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
UMNK88              TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
HSxxxx39            TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
BL21DE3             TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
REL606              TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
BL21_GoldDE3pLysS   TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
ATCCxx37            TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
O111H_              TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
O26H11              TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
UMN026              TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
042NC_0176261       TTCAACAACGCTTCCGGAAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
IAI39x23            TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
O7K1xx29            TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
SMS_3_5             TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
RM12579             TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
CB9615              TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
Xuzhou21            TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
TW14359             TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
EC4115              TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
EDL933              TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
Sakaix28            TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA
                    ***************** ******************************************

Prim.cons.          TTCAACAACGCTTCCGGGAAACTGCTGGCGTTAGATAGCCAGTTAACCAATGATTTTTCA

                           790       800       810       820       830       840
                             |         |         |         |         |         |
MG1655              GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCATATGCCG
MDS42x1             GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCATATGCCG
W3110x2             GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCATATGCCG
DH1NC_0176381       GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCATATGCCG
ETECxx4             GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCATATGCCG
P12bxx5             GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCATATGCCG
BW2952              GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCATATGCCG
DH10Bx7             GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCATATGCCG
C321deltaA          GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCATATGCCG
Wxxxxx20            GAAAAAAG--CAGCT-TTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
KO11FL              GAAAAAAG--CAGCT-TTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
LY180x19            GAAAAAAG--CAGCT-TTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
E24377A             GAAAAAAG--CAGCT-TTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
SE11xx14            GAAAAAAG--CAGCT-TTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
2009EL_2050         GAAAAAAG--CAGCT-TTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
2011C_3493          GAAAAAAG--CAGCT-TTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
55989x18            GAAAAAAG--CAGCT-TTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
IAI1xx13            GAAAAAAG--CAGCT-TTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
O103H2              GAAAAAAG--CAGCT-TTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
APECxx11            GAAAAAAG--CAGCT-TTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
UMNK88              GAAAAAAAA-CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
```

```
HSxxxx39            GAAAAAAAAACAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
BL21DE3             GAAAAAAAA-CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
REL606              GAAAAAAAA-CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
BL21_GoldDE3pLysS   GAAAAAAAA-CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
ATCCxx37            GAAAAAAAA-CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
O111H_              GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
O26H11              GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
UMN026              GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
042NC_0176261       GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
IAI39x23            GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
O7K1xx29            GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
SMS_3_5             GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
RM12579             GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
CB9615              GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
Xuzhou21            GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
TW14359             GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
EC4115              GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
EDL933              GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
Sakaix28            GAAAAAAG--CAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG
                    *******   ***** ************************************ *******

Prim.cons.          GAAAAAAGAACAGCTATTTCCAGTCACAGGTAGATAAAATCAGGAAGGAAGCGTATGCCG

                           850       860       870       880       890       900
                             |         |         |         |         |         |
MG1655              GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
MDS42x1             GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
W3110x2             GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
DH1NC_0176381       GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
ETECxx4             GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
P12bxx5             GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
BW2952              GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
DH10Bx7             GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
C321deltaA          GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
Wxxxxx20            GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
KO11FL              GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
LY180x19            GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
E24377A             GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
SE11xx14            GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
2009EL_2050         GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
2011C_3493          GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
55989x18            GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
IAI1xx13            GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
O103H2              GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
APECxx11            GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
UMNK88              GT------------GTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
HSxxxx39            GT------------GTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
BL21DE3             GT------------GTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
REL606              GT------------GTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
BL21_GoldDE3pLysS   GT------------GTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
ATCCxx37            GT------------GTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
O111H_              GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
O26H11              GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
UMN026              GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
042NC_0176261       GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
IAI39x23            GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGTTTAATCATTTCCTATTCTATTGCTG
O7K1xx29            GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGTTTAATCATTTCCTATTCTATTGCTG
SMS_3_5             GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGTTTAATCATTTCCTATTCTATTGCTG
RM12579             GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGTTTAATCATTTCCTATTCTATTGCTG
CB9615              GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGTTTAATCATTTCCTATTCTATTGCTG
Xuzhou21            GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGTTTAATCATTTCCTATTCTATTGCTG
TW14359             GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGTTTAATCATTTCCTATTCTATTGCTG
EC4115              GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGTTTAATCATTTCCTATTCTATTGCTG
EDL933              GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGTTTAATCATTTCCTATTCTATTGCTG
Sakaix28            GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGTTTAATCATTTCCTATTCTATTGCTG
                    **            ******************** *************************

Prim.cons.          GTGCCGCAGCCGGTGTCGTCGCCGGTCCATTTGGATTAATCATTTCCTATTCTATTGCTG
```

```
                           910       920       930       940       950       960
                             |         |         |         |         |         |
MG1655              CGGGCGTAGTTGAAGGAAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
MDS42x1             CGGGCGTAGTTGAAGGAAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
W3110x2             CGGGCGTAGTTGAAGGAAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
DH1NC_0176381       CGGGCGTAGTTGAAGGAAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
ETECxx4             CGGGCGTAGTTGAAGGAAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
P12bxx5             CGGGCGTAGTTGAAGGAAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
BW2952              CGGGCGTAGTTGAAGGAAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
DH10Bx7             CGGGCGTAGTTGAAGGAAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
C321deltaA          CGGGCGTAGTTGAAGGAAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
Wxxxxx20            CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
KO11FL              CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
LY180x19            CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
E24377A             CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
SE11xx14            CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
2009EL_2050         CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
2011C_3493          CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
55989x18            CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
IAI1xx13            CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
O103H2              CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
APECxx11            CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
UMNK88              CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
HSxxxx39            CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
BL21DE3             CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
REL606              CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
BL21_GoldDE3pLysS   CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
ATCCxx37            CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
O111H_              CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
O26H11              CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
UMN026              CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
042NC_0176261       CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAGTCTGTGCAGA
IAI39x23            CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
O7K1xx29            CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
SMS_3_5             CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
RM12579             CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
CB9615              CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
Xuzhou21            CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
TW14359             CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
EC4115              CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
EDL933              CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
Sakaix28            CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA
                    **************** ******************************** **********

Prim.cons.          CGGGCGTAGTTGAAGGGAAACTGATTCCAGAATTGAAGAACAAGTTAAAATCTGTGCAGA

                           970       980       990      1000      1010      1020
                             |         |         |         |         |         |
MG1655              ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
MDS42x1             ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
W3110x2             ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
DH1NC_0176381       ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
ETECxx4             ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
P12bxx5             ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
BW2952              ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
DH10Bx7             ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
C321deltaA          ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
Wxxxxx20            ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
KO11FL              ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
LY180x19            ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
E24377A             ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
SE11xx14            ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
2009EL_2050         ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
2011C_3493          ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
55989x18            ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
IAI1xx13            ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
O103H2              ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
APECxx11            ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
UMNK88              ATTTCTTTACCACCCTGTCAAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
```

```
HSxxxx39            ATTTCTTTACCACCCTGTCAAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
BL21DE3             ATTTCTTTACCACCCTGTCAAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
REL606              ATTTCTTTACCACCCTGTCAAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
BL21_GoldDE3pLysS   ATTTCTTTACCACCCTGTCAAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
ATCCxx37            ATTTCTTTACCACCCTGTCAAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
O111H_              ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
O26H11              ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
UMN026              GTTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
042NC_0176261       GTTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
IAI39x23            GTTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
O7K1xx29            GTTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
SMS_3_5             GTTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
RM12579             GTTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
CB9615              GTTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
Xuzhou21            GTTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
TW14359             GTTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
EC4115              GTTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
EDL933              GTTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
Sakaix28            GTTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA
                     ****************** ****************************************

Prim.cons.          ATTTCTTTACCACCCTGTCTAACACGGTTAAACAAGCGAATAAAGATATCGATGCCGCCA

                          1030      1040      1050      1060      1070      1080
                             |         |         |         |         |         |
MG1655              AATTGAAATTAACCACCGAAATAGCCGCCATCGGTGAGATAAAAACGGAAACTGAAACAA
MDS42x1             AATTGAAATTAACCACCGAAATAGCCGCCATCGGTGAGATAAAAACGGAAACTGAAACAA
W3110x2             AATTGAAATTAACCACCGAAATAGCCGCCATCGGTGAGATAAAAACGGAAACTGAAACAA
DH1NC_0176381       AATTGAAATTAACCACCGAAATAGCCGCCATCGGTGAGATAAAAACGGAAACTGAAACAA
ETECxx4             AATTGAAATTAACCACCGAAATAGCCGCCATCGGTGAGATAAAAACGGAAACTGAAACAA
P12bxx5             AATTGAAATTAACCACCGAAATAGCCGCCATCGGTGAGATAAAAACGGAAACTGAAACAA
BW2952              AATTGAAATTAACCACCGAAATAGCCGCCATCGGTGAGATAAAAACGGAAACTGAAACAA
DH10Bx7             AATTGAAATTAACCACCGAAATAGCCGCCATCGGTGAGATAAAAACGGAAACTGAAACAA
C321deltaA          AATTGAAATTAACCACCGAAATAGCCGCCATCGGTGAGATAAAAACGGAAACTGAAACAA
Wxxxxx20            AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
KO11FL              AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
LY180x19            AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
E24377A             AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
SE11xx14            AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
2009EL_2050         AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
2011C_3493          AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
55989x18            AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
IAI1xx13            AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
O103H2              AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
APECxx11            AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
UMNK88              AATTGAAATTAACCACCGAAATAGTCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
HSxxxx39            AATTGAAATTAACCACCGAAATAGTCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
BL21DE3             AATTGAAATTAACCACCGAAATAGTCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
REL606              AATTGAAATTAACCACCGAAATAGTCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
BL21_GoldDE3pLysS   AATTGAAATTAACCACCGAAATAGTCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
ATCCxx37            AATTGAAATTAACCACCGAAATAGTCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
O111H_              AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
O26H11              AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
UMN026              AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
042NC_0176261       AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
IAI39x23            AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
O7K1xx29            AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
SMS_3_5             AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
RM12579             AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
CB9615              AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
Xuzhou21            AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
TW14359             AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
EC4115              AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
EDL933              AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
Sakaix28            AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
                    ************************ ********* *************************

Prim.cons.          AATTGAAATTAACCACCGAAATAGCCGCCATCGGGGAGATAAAAACGGAAACTGAAACAA
```

```
                          1090      1100      1110      1120      1130      1140
                             |         |         |         |         |         |
MG1655              CCAGATTCTACGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
MDS42x1             CCAGATTCTACGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
W3110x2             CCAGATTCTACGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
DH1NC_0176381       CCAGATTCTACGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
ETECxx4             CCAGATTCTACGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
P12bxx5             CCAGATTCTACGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
BW2952              CCAGATTCTACGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
DH10Bx7             CCAGATTCTACGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
C321deltaA          CCAGATTCTACGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
Wxxxxx20            CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
KO11FL              CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
LY180x19            CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
E24377A             CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
SE11xx14            CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
2009EL_2050         CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
2011C_3493          CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
55989x18            CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
IAI1xx13            CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
O103H2              CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
APECxx11            CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
UMNK88              CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
HSxxxx39            CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
BL21DE3             CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
REL606              CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
BL21_GoldDE3pLysS   CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
ATCCxx37            CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
O111H_              CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
O26H11              CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
UMN026              CCAGATTCTACGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
042NC_0176261       CCAGATTCTACGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
IAI39x23            CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
O7K1xx29            CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA
SMS_3_5             CCAGATTCTACGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCAAAAA
RM12579             CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAATA
CB9615              CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAATA
Xuzhou21            CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAATA
TW14359             CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAATA
EC4115              CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAATA
EDL933              CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAATA
Sakaix28            CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAATA
                    ********** ******************************************** ** *

Prim.cons.          CCAGATTCTATGTTGATTATGATGATTTAATGCTTTCTTTGCTAAAAGAAGCGGCCAAAA

                          1150      1160      1170      1180      1190      1200
                             |         |         |         |         |         |
MG1655              AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
MDS42x1             AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
W3110x2             AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
DH1NC_0176381       AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
ETECxx4             AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
P12bxx5             AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
BW2952              AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
DH10Bx7             AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
C321deltaA          AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
Wxxxxx20            AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
KO11FL              AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
LY180x19            AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
E24377A             AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
SE11xx14            AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
2009EL_2050         AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
2011C_3493          AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
55989x18            AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
IAI1xx13            AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
O103H2              AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
APECxx11            AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
UMNK88              AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
```

```
HSxxxx39            AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
BL21DE3             AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
REL606              AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
BL21_GoldDE3pLysS   AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
ATCCxx37            AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
O111H_              AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
O26H11              AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG
UMN026              AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAGAAGACACTCTTTGAG
042NC_0176261       AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAGAAGACACTCTTTGAG
IAI39x23            AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAGAAGACACTCTTTGAG
O7K1xx29            AAAATGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAGAAGACACTCTTTGAG
SMS_3_5             AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAGAAGACACTCTTTGAG
RM12579             AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAGAAGACACTCTTTGAG
CB9615              AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAGAAGACACTCTTTGAG
Xuzhou21            AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAGAAGACACTCTTTGAG
TW14359             AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAGAAGACACTCTTTGAG
EC4115              AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAGAAGACACTCTTTGAG
EDL933              AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAGAAGACACTCTTTGAG
Sakaix28            AAA-TGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAGAAGACACTCTTTGAG
                    *** **************************************** **************

Prim.cons.          AAAATGATTAACACCTGTAATGAGTATCAGAAAAGACACGGTAAAAAGACACTCTTTGAG


                          1210
                             |
MG1655              GTACCTGAAGTCTGA   .... 1230694
MDS42x1             GTACCTGAAGTCTGA
W3110x2             GTACCTGAAGTCTGA
DH1NC_0176381       GTACCTGAAGTCTGA
ETECxx4             GTACCTGAAGTCTGA
P12bxx5             GTACCTGAAGTCTGA
BW2952              GTACCTGAAGTCTGA
DH10Bx7             GTACCTGAAGTCTGA
C321deltaA          GTACCTGAAGTCTGA
Wxxxxx20            GTACCTGAAGTCTGA
KO11FL              GTACCTGAAGTCTGA
LY180x19            GTACCTGAAGTCTGA
E24377A             GTACCTGAAGTCTGA
SE11xx14            GTACCTGAAGTCTGA
2009EL_2050         GTACCTGAAGTCTGA
2011C_3493          GTACCTGAAGTCTGA
55989x18            GTACCTGAAGTCTGA
IAI1xx13            GTACCTGAAGTCTGA
O103H2              GTACCTGAAGTCTGA
APECxx11            GTACCTGAAGTCTGA
UMNK88              GTACCTGAAGTCTGA
HSxxxx39            GTACCTGAAGTCTGA
BL21DE3             GTACCTGAAGTCTGA
REL606              GTACCTGAAGTCTGA
BL21_GoldDE3pLysS   GTACCTGAAGTCTGA
ATCCxx37            GTACCTGAAGTCTGA
O111H_              GTACCTGAAGTCTGA
O26H11              GTACCTGAAGTCTGA
UMN026              GTACCTGAAGTCTGA
042NC_0176261       GTACCTGAAGTCTGA
IAI39x23            GTACCTGAAGTCTGA
O7K1xx29            GTACCTGAAGTCTGA
SMS_3_5             GTACCTGAAGTCTGA
RM12579             GTACCTGAAGTCTGA
CB9615              GTACCTGAAGTCTGA
Xuzhou21            GTACCTGAAGTCTGA
TW14359             GTACCTGAAGTCTGA
EC4115              GTACCTGAAGTCTGA
EDL933              GTACCTGAAGTCTGA
Sakaix28            GTACCTGAAGTCTGA
                    ***************

Prim.cons.          GTACCTGAAGTCTGA
```

Figure S1:

The open access soft ware programs
BLAST: (http://blast.ncbi.nlm.nih.gov/Blast.cgi) to search for sequence and strains with similarities to the *clyA*/*hlyE* gene, and
ClustalW: (http://pbil.ibcp.fr/htm/index.php) were used for alignment of the sequences with the *clyA* gene sequences of *E. coli* strain MG1655 (accession number of NC_000913.3) as the reference sequence. It includes the 1.2 kb region between nucleotide coordinates 1229483 and 1230694 and represents the entire *clyA* coding sequence and 300 base pairs upstream of the ATG start codon. The sequence of *clyA* was compared with the corresponding sequences of *clyA* in other *E. coli* strains (both IPEC and ExPEC).
Black nucleotide lettering and dashes indicates position where there are differences in the otherwise red letter compilation.
The translational start sequences (ATG and ribosome binding motif) are marked in green.
The transcriptional start sequences -35 and -10 motifs and the initiating nucleotide are marked in blue.
The binding site for the CRP/FNR regulators is marked in grey.
The binding sequences for SlyA are underlined.