



rrrB T1 transcription termination sequence: bases 106-149  
 rrrB T2 transcription termination sequence: bases 281-308  
 attL1: bases 358-457 (complementary strand)  
 CBP tag: 489-566  
 SBP tag: 585-719  
 Multiple cloning site (MCS): bases 720-793  
 attL2: bases 793-892  
 Kanamycin resistance gene: bases  
 pUC origin: bases

Recommended *E.coli* strain for propagation: TOP10F'

\* Site is not unique

# Site present only in pENTR1A-NTAP A

## pENTR 1A NTAP-A MCS (w322-1)

*atfL1*

352 GGGCCCCAAA TAATGATTTT ATTTTGACTG ATAGTGACCT GTTCGTTGCA ACAAATTGAT  
 CCCGGGGTTT ATTACTAAAA TAAACTGAC TATCACTGGA CAAGCAACGT TGTTTAACTA

*DraI*

412 AAG CAA TGC TTT TTT ATA ATG CCA ACT TTGTAC AAA AAA GCA GGC TTT  
 TTC GTT ACG AAA AAA TAT TAC GGT TGA AACATG TTT TTT CGT CCG AAA

*NotI*      *Kpn I, Nco I*

460 AAA GGAACC CBP SBP  
 TTT CCT TGG

SBP tag (3' end)

P S G G C K L G | Kas I | BamHI | PstI\* | EcoRI |  
 CCC TCC GGC GGC TGC AAG CTG GGC GCC CGG GCG GAT CCC CCG GGC TGC AGG AAT TC...

EcoRV\* Hind III Cla I Acc I/Sal I Xho I EcoRV\* Xba I  
 .. .G ATA TCA AGC TTA TCG ATA CCG TCG ACC TCG AGA TAT CTA GA ...

CC CAG CTT TCT TGT ACAA  
 GG GTC GAAAGAACA TGT TT

*atfL2*

GTTGGCATT TAAGAAAGCA TTGCTTATCA ATTTGTTGCA ACGAACAGGT CACTATCAGT  
 CAACCGTAAT ATTCTTTCGT AACGAATAGT TAAACAACGT TGCTTGTCCA GTGATAGTCA

reverse primer binding site

CAAAATAAAA TCATTATTTG CCATCCAGCT GCAGCTCTGG CCCGTGTCTC AAAATCTCTG  
 GTTTTATTTT AGTAATAAAC GGTAGGTCGA CGTCGAGACC GGGCACAGAG TTTTAGAGAC

ATGTTACATT  
 TACAATGTAA

\* Site is not unique

## pENTR 1A NTAP-B MCS (w323-1)

352 *atfL1*  
GGGCCCCAAA TAATGATTTT ATTTTGACTG ATAGTGACCT GTTCGTTGCA ACAAATTGAT  
CCCGGGGTTT ATTACTAAAA TAAAACTGAC TATCACTGGA CAAGCAACGT TGTTTAACTA  
412 *DraI*  
AAG CAA TGC TTT TTT ATA ATG CCA ACT TTGTAC AAA AAA GCA GGC TTT  
TTC GTT ACG AAA AAA TAT TAC GGT TGA AACATG TTT TTT CGT CCG AAA  
460 *NotI* *Kpn I, Nco I*  
AAA GGAACC CBP SBP  
TTT CCT TGG

SBP tag (3' end)  
P S G G C K L G  
CCC TCC GGC GGC TGC AAG CTG GGC IGC CCG GGC GGA TCC CCC GGG CTG CAG GAA TTC..  
BamHI Pst I\* EcoR I  
.. .GAT ATC AAG CTT ATC GAT ACC GTC GAC CTC GAG ATA TCT AGA ...  
EcoR V\* Hind III Cla I Acc I/Sal I Xho I EcoR V\* Xba I

CC CAG CTT TCT TGT ACAA  
GG GTC GAAAGAACA TGT TT

*atfL2*  
GTTGGCATT TAAGAAAGCA TTGCTTATCA ATTTGTTGCA ACGAACAGGT CACTATCAGT  
CAACCGTAAT ATTCTTTCGT AACGAATAGT TAAACAACGT TGCTTGTCCA GTGATAGTCA  
CAAATAAAAA TCATTATTTG CCATCCAGCT GCAGCTCTGG CCCGTGTCTC AAAATCTCTG  
GTTTTATTTT AGTAATAAAC GGTAGGTCGA CGTCGAGACC GGGCACAGAG TTTTAGAGAC  
reverse primer binding site  
ATGTTACATT  
TACAATGTAA

\* Site is not unique

## pENTR 1A NTAP-C MCS (w324-1)

*atfL1*

352 GGGCCCCAAA TAATGATTTT ATTTTGACTG ATAGTGACCT GTTCGTTGCA ACAAATTGAT  
 CCCGGGGGTTT ATTACTAAAA TAAAACTGAC TATCACTGGA CAAGCAACGT TGTTTAACTA

*DraI*

412 AAG CAA TGC TTT TTT ATA ATG CCA ACT TTGTAC AAA AAA GCA GGC TTT  
 TTC GTT ACG AAA AAA TAT TAC GGT TGA AACATG TTT TTT CGT CCG AAA

*NotI*      *Kpn I, Nco I*

460 AAA GGAACC CBP SBP  
 TTT CCT TGG

SBP tag (3' end)

P S G G C K L G  
 CCC TCC GGC GGC TGC AAG CTG GGC IIG CCC GGG CGG ATC CCC CGG GCT GCA GGA ATT...

BamHI      Pst I\*      EcoRI

.. .CGA TAT CAA GCT TAT CGA TAC CGT CGA CCT CGA GAT ATC TAG A

EcoRV\*    Hind III      Cla I      Acc I/Sal I      Xho I      EcoRV\*    Xba I

CC CAG CTT TCT TGT ACAA  
 GG GTC GAAAGAACA TGT TT

*atfL2*

GTTGGCATT TAAGAAAGCA TTGCTTATCA ATTTGTTGCA ACGAACAGGT CACTATCAGT  
 CAACCGTAAT ATTCTTTCGT AACGAATAGT TAAACAACGT TGCTTGTCCA GTGATAGTCA

reverse primer binding site

CAAAATAAAA TCATTATTTG CCATCCAGCT GCAGCTCTGG CCCGTGTCTC AAAATCTCTG  
 GTTTTATTTT AGTAATAAAC GGTAGGTCGA CGTCGAGACC GGGCACAGAG TTTTAGAGAC

ATGTTACATT  
 TACAATGTAA

\* Site is not unique