



rrnB T1 transcription termination sequence: bases 106-149  
 rrnB T2 transcription termination sequence: bases 281-308  
 attL1: bases 358-457 (complementary strand)  
 multiple cloning site (MCS): bases  
 attL2: bases  
 Kanamycin resistance gene: bases  
 pUC origin: bases

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

\* Sites are not unique

# pENTR4 -V5 MCS

attL1

GGGCCCCAAA TAATGATTTT ATTTTGACTG ATAGTGACCT GTTCGTTGCA ACAAATTGAT  
 CCCGGGGTTT ATTACTAAAA TAAAACTGAC TATCACTGGA CAAGCAACGT TGTTTAACTA

AAG CAA TGC TTT TTT ATA ATG CCA ACT TTG TAC AAA AAA GCA GGC TCC  
 TTC GTT ACG AAA AAA TAT TAC GGT TGA AAC ATG TTT TTT CGT CCG AGG

Nco I\* V5 epitope

ACC ATG GAA GGT AAG CCT ATC CCT AAC CCT CTC CTC GGT CTC GAT TCT ACG  
 Met Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr

BamHI\* Nco I\* XmnI SalI HincII BamHI\* KpnI EcoRI NotI

GGA TCC ATG GGA ACC AAT TCA GTC GAC TGG ATC CGG TAC CGA ATT CGC GGC  
 Gly Ser Met Gly Thr Asn Ser Val Asp Trp Ile Arg Tyr Arg Ile Arg Gly

XhoI EcoRV XbaI

CGC ACT CGA GAT ATC TAG ACC AGC TTT CTT GTA CAA A  
 Arg Thr Arg Asp Ile \*

attL2

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

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

reverse primer binding site

ATGTTACATT  
 TACAATGTAA

\* Sites not unique