



rrrB T1 transcription termination sequence: bases 106-149
 rrrB 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'

* Site is not unique

pENTR4 -V5_2 Ubc9 MCS

atf1.1

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

EcoRV Xba I

GGA TCC ATG GGA ACC AAT TCA GTC GAG ATA TCT AGA GGT GGC TCT GGT GGC
Gly Ser Met Gly Thr Asn Ser Val Glu Ile Ser Arg Gly Gly Ser Gly Gly

Ubc9

Term

CTAGACCCAG CTTTCTTGTA CAAA
GATCTGGGTC GAAAGAACAT GTTT

atf1.2

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

reverse primer binding site

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

ATGTTACATT
TACAATGTAA

* Site not unique