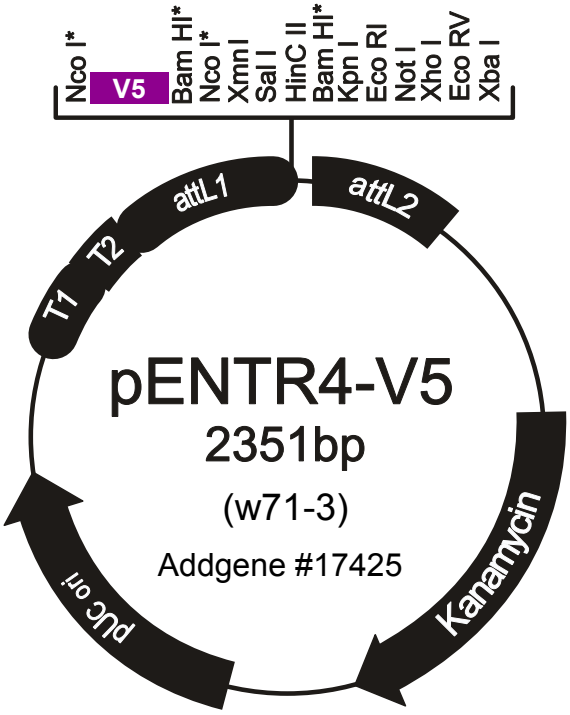


rrnBT1 transcription termination sequence: bases 106-149
rrnBT2 transcription termination sequence: bases 281-308
att L1: bases 358-457 (complementary strand)
V5 epitope: bases 469-510
Multiple cloning site (MCS): bases 511-579
att L2: bases 580-680
Kanamycin resistance gene: bases 802-1611
pUC origin: bases 1677-2348

V5 epitope

*Nco I**

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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

Bam HI* Nco I*          Xmn I        Sal I HinC II  Bam HI*        Kpn I EcoR I      Not I
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

     Xho I      Eco RV Xba I
CGC ACT CGA GAT ATC TAG ACC AGC TTT CTT GTA CAA A
Arg Thr Arg Asp Ile  *
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* Sites are not unique

Recommended *E.coli* strain for propagation: TOP10F' under kanamycin selection.

Eric Campeau January 2006