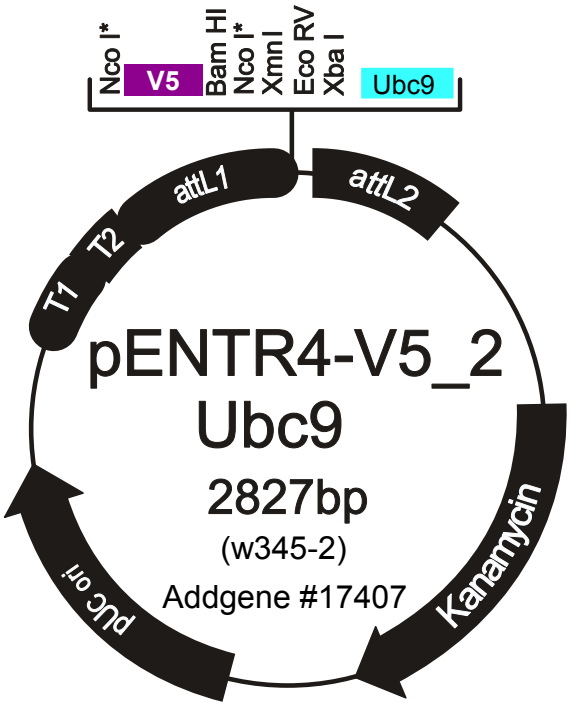


rrnB T1 transcription termination sequence: bases 106-149
rrnB T2 transcription termination sequence: bases 281-308
attL1: bases 358-457 (complementary strand)
V5 epitope: 463-510
Multiple cloning site (MCS): bases 511-546
Ubc9 cDNA: 563-1039
attL2: bases 1058-1158
Kanamycin resistance gene: bases 1280-2089
pUC origin: bases 2153-2824

*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** *Xmn I* *Eco RV* *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
```

* Site is not unique

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

NOTE: The position of the genetic element is approximative.

Eric Campeau May 2007