



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 461-512

3X nuclear localization signal (SV40): bases 514-585

myc tag: bases 598-627

stop codon: bases 640-642

att L2: bases 679-779

Kanamycin resistance gene: bases 900-1709

pUC origin: bases 1774-2446

*Nco I* *Pst I*\* *Sal I* *Xho*  
 ACC **ATG** GCC CAG GTG CAG CTG CAG GTC GAC CTC GAG ATC AAA CGG  
 Met Ala Gln Val Gln Leu Gln Val Asp Leu Glu Ile Lys Arg

*Not I* NLS #1 NLS #2  
 GCG GCC GCA GAT CCA AAA AAG AAG AGA AAG GTA GAT CCA AAA AAG AAG AGA AAG  
 Ala Ala Ala Asp Pro Lys Lys Lys Arg Lys Val Asp Pro Lys Lys Lys Arg Lys

NLS #3 myc epitope  
 GTA GAT CCA AAA AAG AAG AGA AAG GTA GAT ACG GCC GCA GAA CAA AAA CTC ATC TCA  
 Val Asp Pro Lys Lys Lys Arg Lys Val Asp Thr Ala Ala Glu Gln Lys Leu Ile Ser

*Xba I*\*\* *Bcl I* *Kpn I*  
 GAA GAG GAT CTG AAT GGG GCC GCA TAG TCTAGAAGCT CGCTGATCCGGTACCGAATT  
 Glu Glu Asp Leu Asn Gly Ala Ala \*\*\*

\*Site is not unique

\*\* Site is methylated in original vector (pCMV/myc/nuc)

The position of the genetic elements is approximative

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