



rrnB T1 transcription termination sequence: bases 106-149
 rrnB T2 transcription termination sequence: bases 281-308
 attL1:bases 358-457 (complementary strand)
 HA tag: bases 463-495
 PreScission cleavage site: bases 516-517
 Multiple cloning site (MCS): bases 523-581
 3X nuclear localization signal (SV40): bases 583-654
 myc tag: bases 667-696
 stop codon: bases 709-711
 att L2: bases 746-846
 Kanamycin resistance gene: bases 970-1779
 pUC origin: bases 1846-2516

HA epitope	PreScission site [†]	
<i>Eco 109 I, Apa I</i>		
ACC ATG GCC TAC CCC TAC GAC GTG CCC GAC TAT GCC AAA CTG GAA GTT CTG TTC CAG GGG	<i>Pci I*</i>	<i>Xcm I</i>
Met Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Lys Leu Glu Val Leu Phe Gln Gly	<i>Pst I*</i>	<i>Sal I</i>
CCC ACA TGT AAC ATG GCC CAG GTG CAG CTG CAG GTC GAC CTC GAG ATC AAA CGG	<i>Xho</i>	
Pro Thr Cys Asn Met Ala Gln Val Gln Leu Gln Val Asp Leu Glu Ile Lys Arg		
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<i>Not I</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 Arg Lys Val Asp Pro Lys Lys Lys Arg Lys		
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NLS #3		myc epitope
GTA GAT CCA AAA AAG AAG AGA AAG GTA GAT ACG GCC GCA GAA CAA AAA CTC ATC TCA	<i>Xba I**</i>	
Val Asp Pro Lys Lys Arg Lys Val Asp Thr Ala Ala Glu Gln Lys Leu Ile Ser		<i>Bcl I</i>
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GAA GAG GAT CTG AAT GGG GCC GCA TAG TCTAGAAGCT CGCTGATCCGGTACCGAATT		<i>Kpn I</i>
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'