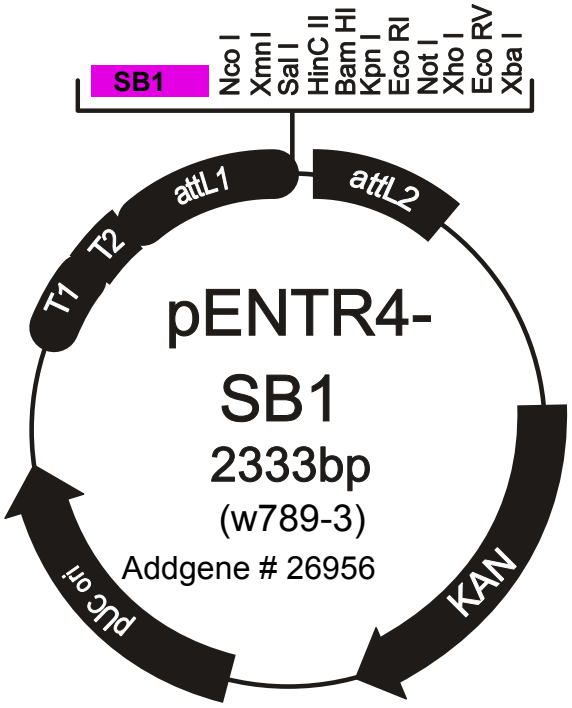


rrnBT1 transcription termination sequence: bases 106-149
rrnBT2 transcription termination sequence: bases 281-308
att L1: bases 358-457 (complementary strand)
SB1 epitope: bases 463-497
Multiple cloning site (MCS): bases 498-562
att L2: bases 562-662
Kanamycin resistance gene: bases 784-1593
pUC origin: bases 1659-2330

SB1 epitope — *Nco I*

ACC ATG CCA AGA CCA TCC AAC AAA CGC CTC CAG CAG TCC ATG
Met Pro Arg Pro Ser Asn Lys Arg Leu Gln Gln Ser Met

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

GGA ACC AAT TCA GTC GAC TGG ATC CGG TAC CGA ATT CGC GGC
Gly Thr Asn Ser Val Asp Trp Ile Arg Tyr Arg Ile Arg Gly

Xho I *Eco RV* *Xba I* Att L2

CGC ACT CGA GAT ATC TAG ACC AGC TTT CTT GTA CAA A
Arg Thr Arg Asp Ile *

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

NOTE: The SB1 epitope was characterized in Schaeffer et al. 2010 (NAR Apr;38(6):e91) as part of the SnAvi tag. The codon usage was slightly modified from the original article. The SB1 hybridoma cell line can be ordered from the DevelopmentalStudies Hybridoma bank (http://dshb.biology.uiowa.edu/synaptobrevin.) The tag works well for immunofluorescence with minimal background in HeLa cells where as it remains to be tested for other applications.

Eric Campeau November 2010