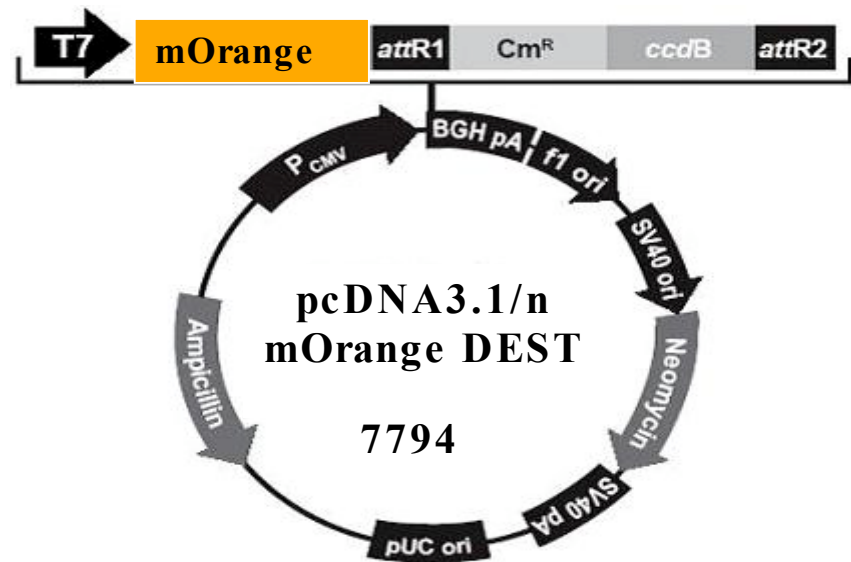


CMV promoter: bases 232-819
 T7 promoter/priming site: bases 863-882
 mOrange tag: bases 914-1625
 attR1 recombination site: bases 1665-1789
 Chloramphenicol resistance gene: bases 1898-2557
 ccdB gene: bases 2899-3204
 attR2 recombination site: bases 3245-3369
 BGH Reverse priming site: bases 3388-3405
 BGH polyadenylation region: bases 3391-3618
 f1 origin: bases 3664-4092
 SV40 early promoter and origin: bases 4119-4427
 Neomycin resistance gene (ORF): bases 4502-5296
 SV40 early polyadenylation region: bases 5470-5600
 pUC origin: bases 5983-6653
 Ampicillin resistance gene (ORF): bases 6798-7658 (complementary strand)



*pcDNA3.1/nV5 vector (Invitrogen) altered at SIDNET to create mOrange tag

Kozac (C inserted)

T7 promoter/priming site
 851 GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGT TAAGCTT **CACC**
 911 atg gtg agc aag ggc gag gag aat aac atg gcc atc atc aag gag ttc atg cgc ttc aag gtg cgc atg gag ggc tcc gtg
 aac ggc cac gag ttc gag atc gag ggc gag ggc gag ggc cgc ccc tac gag ggc ttt cag acc gct aag ctg aag gtg acc
 aag ggt ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc acc tac ggc tcc aag gcc tac gtg aag cac ccc
 gcc gac atc ccc gac tac ttc aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg aac ttc gag gac ggc ggc
 gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc
 tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc tcc tcc gag cgg atg tac ccc gag gac ggc gcc ctg
 aag ggc gag atc aag atg agg ctg aag ctg aag gac ggc gcc cac tac acc tcc gag gtc aag acc acc tac aag gcc aag
 aag ccc gtg cag ctg ccc ggc gcc tac atc gtc ggc atc aag ttg gac atc acc tcc cac aac gag gac tac acc atc gtg
 gaa cag tac gaa cgc gcc gag ggc cgc cac tcc acc ggc ggc atg gac gag ctg tac aag

1635 Gly Pro Asp Pro Ser Thr Asn Ser Ala Asp Ile
 GGC CCG GAT CCG TCG ACG AAT TCT GCA GAT ATC

1665 Thr Ser Leu Tyr Lys Lys Ala Gly
 ACA AGT TTG TAC AAA AAA GCA GGC TN- --- gene --- NACCCAGCTT TCTTG
 TGT TCA AAC ATG TTT TTT CGT CCG AN- --- gene --- NTGGGTCGAA AGAAC
 attB1 attB2

Ex Max ~ 548
Em Max ~ 562

BGH Reverse priming site
 3359 TACAAAGTGG TGATAAACCC GCTGATCAGC CTCGACTGTG CCTTCTAGTT GCCAGCCATC
 ATGTTTCACC ACTATTTCCC