



699 ^{enhancer region (3' end)}
 AATGGGAGTT TGTTTTGGCA CAAAATCAA CGGGACTTTC CAAAATGTCG TAACAACCTCC

759 ^{CAAT} ^{TATA} ^{3' end of hCMV}
 GCCCCATTGA CGCAAATGGG CGGTAGGCGT GTACGGTGGG AGGTCTATAT AAGCAGAGCT

819 ^{putative transcriptional start} ^{T7 promoter primer binding site}
 CTCTGGCTAA CTAGAGAACC CACTGCTTAC TGGCTTATCG AAATTAATAC GACTCACTAT

879 ^{Ig κ-chain leader sequence}
 AGGGAGACCC AAGCTGGCTA GCCACC **ATG** GAG ACA GAC ACA CTC CTG CTA TGG
 Met Glu Thr Asp Thr Leu Leu Leu Trp

932 ^{Sfi I}
 GTA CTG CTG CTC TGG GTT CCA GGT TCC ACT GGT GAC GCG GCC CAGCCG
 Val Leu Leu Leu Trp Val Pro Gly Ser Thr Gly Asp

980 ^{Asc I} ^{Hind III} ^{Asp718 I} ^{Kpn I} ^{BamH I} ^{Bst XI}
 GCCAGGCGC GCCG TACGAAG CTTGGTACCG AGCTCGGATC CACTCCAGTG TGGTGGAAAT

1040 ^{EcoR V} ^{BstX I} ^{Not I} ^{Xho I} ^{Dra II} ^{Apa I} ^{myc epitope}
 CTGCAGATAT CCAGCACAGT GGC GGCCGCT CGAGGAGGGC CC GAA CAA AAA CTC ATC
 Glu Gln Lys Leu Ile

1097 ^{Polyhistidine tag}
 TCA GAA GAG GAT CTG AAT AGC GCC GTC GAC CAT CAT CAT CAT CAT CAT TGA
 Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His His His ***

1148 ^{BGH reverse priming site}
 GTTTAAACCC GCTGATCAGC CTCGACTGTG CCTTCTAGTT GCCAGCCATC TGTTGTTTGC

1208 ^{BGH poly (A) addition site}
 CCCTCCCCCG TGCCTTCCTT GACCCTGGAA GGTGCCACTC CCACTGTCCT TTCCTAATAA

1268
 AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGT