

pcDNA3.1/Zeo (+)

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          |
          | enhancer region (3' end)
          |
          |
689  CATTGACGTC AATGGGAGTT TGTTTTGGCA CAAAATCAA CGGGACTTTC CAAAATGTCTG
          |
          |
          | CAAT
          |
749  TAACAACTCC GCCCCATTGA CGCAAATGGG CGGTAGGCGT GTACGGTGGG AGGTCTATAT
          |
          | 3' end of hCMV
          |
          | putative transcriptional start
          |
809  AAGCAGAGCT CTCTGGCTAA CTAGAGAACC CACTGCTTAC TGGCTTATCG AAATTAATAC
          |
          | T7 promoter priming site
          |
          | Nhe I
          |
          | Pme I Afl II Hind III Asp718 I Kpn I
869  GACTCACTAT AGGGAGACCC AAGCTGGCTA GCGTTTAAAC TTAAGCTTGG TACCGAGCTC
          |
          | BamH I
          |
          | BstX I EcoR I
          |
          | Pst I EcoR V
          |
          | BstX I Not I Xho I
929  GGATCCAATA GTCCAGTGTG GTGGAATTCT GCAGATATCC AGCACAGTGG CGGCCGCTCG
          |
          | Xba I
          |
          | Apa I Pme I
          |
          | BGH reverse priming site
989  AGTCTAGAGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT AGTTGCCAGC
          |
          |
1049 CATCTGTTGT TTGCCCTCC CCCGTGCCTT CCTTGACCCT GGAAGGTGCC ACTCCCCTG
          |
          | BGH poly (A) site
          |
1109 TCCTTTCCTA ATAAAATGAG GAAATTGCAT

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