



CATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTT  
 GTACTGGAATACCTGAAAGGATGAACCGTCATGTAGATGCATAATCAGTAGCGATAATGGTACCACTACGCCAA

375

CMV enhancer CMV promoter

TTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGGACTCACGGGGATTTCCAAGTCTCCACCCATTGACGTCAA  
 AACCGTCATGTAGTTACCCGCACCTATCGCCAAACTGAGTGCCCTAAAGTTTCAGAGGTGGGGTAACTGCAGTT

450

CMV promoter

TGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAAT  
 ACCCTCAAACAAAACCGTGTTTGTAGTTGCCCTGAAAGGTTTTACAGCATTGTTGAGGGCGGGGTAACTGCGTTTA

525

CMV promoter

GGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTGTAGTGAACCGTCAGATCCGCTAGCGCTA  
 CCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

600

CMV promoter

NheI

MCS

CCGGACTCAGATCTCGAGCTCAAGCTTCAATTCTGCAGTTCGACGGTACC GCGGGCCCGGGATCCACCGGTCGCC  
 GGCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGG

675

MCS

ACCATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAC  
 TGGTACCACTCGTTCCCGCTCCTCGACAAGTGCCCCACCACGGGTAGGACCAGCTCGACCTGCCGCTGCATTTG

750

1 Met Val Ser Lys Gly 5 Glu Glu Leu Phe Thr 10 Gly Val Val Pro Ile Leu Val Glu Leu Asp 20 Gly Asp Val Asn

EGFP

GGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGC  
CCGGTGTTC AAGTCGCACAGGCCGCTCCCGCTCCCGCTACGGTGGATGCCGTTTCGACTGGGACTTCAAGTAGACG

825

25 His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
EGFP

ACCACCGGCAAGCTGCCCGTGCCCTGGCCACCCCTCGTGACCACCTGACCTACGGCGTGCAGTGCTTCAGCCGC  
TGGTGGCCGTTTCGACGGGCACGGGACCGGGTGGGAGCACTGGTGGGACTGGATGCCGCACGTCACGAAGTCGGCG

900

50 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg  
EGFP

TACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATC  
ATGGGGCTGGTGTACTTCGTCGTGCTGAAGAAGTTCAGGCGGTACGGGCTTCCGATGCAGGTCCTCGCGTGGTAG

975

75 Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile  
EGFP

TTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCCTGGTGAACCGCATC  
AAGAAGTTCCTGCTGCCGTTGATGTTCTGGGCGCGGCTCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCGTAG

1050

100 Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
EGFP

GAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACAGCCAC  
CTCGACTTCCCGTAGCTGAAGTTCCTCCTGCCGTTGTAGGACCCCGTGTTCGACCTCATGTTGATGTTGTCGGTG

1125

125 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
EGFP

AACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGAC  
TTGCAGATATAGTACCGGCTGTTTCGTCTTCTTGCCGTAGTTCCACTTGAAGTTCAGGCGGTGTTGTAGCTCCTG

1200

150 Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp  
EGFP

GGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAAC  
CCGTGCGACGTCGAGCGGCTGGTGTATGGTCGTCTTGTGGGGTAGCCGCTGCCGGGGCACGACGACGGGCTGTTG

1275

175 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
EGFP

CACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTC  
GTGATGGACTCGTGGGTCAGGCGGGACTCGTTTTCTGGGGTTGCTCTTCGCGCTAGTGTACCAGGACGACCTCAAG

1350

200 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
EGFP

GTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAAGCGGCCGCGACTCTAGATCATAATCA  
CACTGGCGGGCCCTAGTGAGAGCCGTACCTGCTCGACATGTTTCATTTTCGCCGGCGCTGAGATCTAGTATTAGT

1425

225 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys \*  
EGFP