



5' ACGTTATCGACTGCACGGTGCACCAATGCTTCTGGCGTCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGG
 3' TGCAATAGCTGACGTGCCACGTGGTTACGAAGACCGCAGTCCGTCGGTAGCCTTCGACACCATAACCGACACGTCC

TCGTAAATCACTGCATAATTCGTGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTCGCGCCGACATCAT
 AGCATTTAGTGACGTATTAAGCACAGCGAGTTCGCGTGAGGGCAAGACCTATTACAAAAAACGCGGCTGTAGTA

AACGGTTCTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGAATTGTGAG
 TTGCCAAGACCGTTTATAAGACTTTACTCGACAACCTGTTAATTAGTAGCCGAGCATATTACACACCTTAACACTC

tac promoter

lac operator

CGGATAACAATTTACACAGGAAACAGTATTCATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGC
 GCCTATTGTTAAAGTGTGTCCTTTGTCATAAGTACAGGGGATATGATCCAATAACCTTTTAATTCCCGGAACAG

lac operator

1 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val
 GST

AACCCACTCGACTTCTTTTGGAAATATCTTGAAGAAAAATATGAAGAGCATTGTATGAGCGCGATGAAGGTGATA
 TTGGGTGAGCTGAAGAAAACCTTATAGAACTTCTTTTATACTTCTCGTAAACATACTCGCGCTACTTCCACTAT

15 Pro Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu His Leu Tyr Glu Arg Asp Glu Gly Asp
 GST

AATGGCGAAACAAAAGTTTGAATTGGGTTTGGAGTTTCCAATCTTCCTTATTATATTGATGGTGATGTTAAAT
 TTACCGCTTTGTTTTTCAAACCTTAACCCAAACCTCAAAGGGTTAGAAGGAATAATATAACTACCACTACAATTTA

40 Lys Trp Arg Asn Lys Lys Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 GST

75

150

225

300

375

450

TAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAACATGTTGGGTGGTTGTCCAAAAGAGCGTG
ATTGTGT CAGATACCGGTAGTATGCAATATATCGACTGTTTCGTGTTGTACAACCCACCAACAGGTTTTCTCGCAC
65 70 75 80 85
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg
GST

CAGAGATTTCAATGCTTGAAGGAGCGGTTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGTAAAGACT
GTCTCTAAAGTTACGAACTTCTCGCCAAAACCTATAATCTATGCCACAAAGCTCTTAACGTATATCATTCTGA
90 95 100 105 110
Ala Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser Lys Asp
GST

TTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTGGAAGATCGTTTTATGTCATA
AACTTTGAGAGTTTCAACTAAAAGAATCGTTTCGATGGACTTTACGACTTTTACAAGCTTCTAGCAAATACAGTAT
115 120 125 130 135
Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His
GST

AAACATATTTAAATGGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATAACA
TTTGTATAAATTTACCACTAGTACATTGGGTAGGACTGAAGTACAACATACTGCGAGAACTACAACAAAATATGT
140 145 150 155 160
Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr
GST

TGGACCCAATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTGTTTTAAAAACGTATTGAAGCTATCCCACAAATTG
ACCTGGGTTACACGGACCTACGCAAGGGTTTTAATCAAACAAAATTTTTTGCATAACTTCGATAGGGTGTGTTAAC
165 170 175 180 185
Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile
GST

ATAAGTACTTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACC
TATTCATGAACTTTAGGTCGTTTCATATATCGTACCGGAAACGTCCCAGCGTTTCGGTGCAAACCACCACCGCTGG
190 195 200 205 210
Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp
GST

ATCCTCCAAAATCGGATCTGGAAGTTCTGTTCCAGGGGCCCTGGGATCCCAGGAATTCCTGGGTGCGACTCGAG
TAGGAGGTTTTAGCCTAGACCTTCAAGACAAGGTCCCGGGGACCCCTAGGGGTCTTAAGGGCCCAGCTGAGCTC
215 1 5
His Pro Pro Lys Ser Asp Leu Glu Val Leu Phe Gln Gly Pro Leu Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg
GST HRV 3C site (in frame with HRV 3C site) MCS

NotI
CGGCCGCATCGTGACTGACTGACGATCTGCCTCGCGGTTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAG
GCCGGCGTAGCACTGACTGACTGCTAGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTC
Ala Ala Ala Ser *
MCS