



TAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAACATGTTGGGTGGTTGTCCAAAAGAGCGTG  
 ATTGTGTCAGATACCGGTAGTATGCAATATATCGACTGTTCTGTGTTGTACAACCCACCAACAGTTTTCTCGCAC  
 65 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  
 GTCTCTAAAGTTACGAACCTCCTCGCCAAAACCTATAATCTATGCCACAAAGCTCTTAACGTATATCATTCTGA  
 90 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

TTGAAACTCTCAAAGTTGATTTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTTGAAGATCGTTTTATGTCATA  
 AACTTTGAGAGTTTTCAACTAAAAGAATCGTTCGATGGACTTTACGACTTTTACAAGCTTCTAGCAAATACAGTAT  
 115 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

AAACATATTTAAATGGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATACA  
 TTTGTATAAATTTACCACTAGTACATTGGGTAGGACTGAAGTACAACATACTGCGGAGAACTACAACAAAATATGT  
 140 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

TGGACCCAATGTGCCTGGATGCGTTCCTCAAATAGTTTGTAAAAAACGTATTGAAGCTATCCCACAAATTG  
 ACCTGGGTACACGGACCTACGCAAGGGTTTTAATCAAACAAAATTTTTGCATAACTTCGATAGGGTGTTTAAC  
 165 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

ATAAGTACTTGAAATCCAGCAAGTATATAGCATGGCCTTTCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACC  
 TATTCATGAACTTTAGGTCGTTTCATATATCGTACCGGAAACGTCCCGACCGTTCGGTGCAAACCACCACCGCTGG  
 190 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

ATCCTCCAAAATCGGATCTGGAAGTTCTGTTCCAGGGGCCCTGGGATCCCCGGAATTCCTGGGTCGACTCGAGC  
 TAGGAGGTTTTAGCCTAGACCTTCAAGACAAGGTCCCCGGGACCCCTAGGGGCCTTAAGGGCCCAGCTGAGCTCG  
 215 His Pro Pro Lys Ser Asp Leu Glu Val Leu Phe Gln Gly Pro Leu Gly Ser Pro Glu Phe Pro Gly Arg Leu Glu  
 GST HRV 3C site (in frame with HRV 3C site) MCS

**NotI**  
 GGCCGCATCGTGAAGTACTGACTGACGATCTGCCTCGCGGTTTTGGTGTGATGACGGTGAACCTCTGACACATGCAGC  
 CCGGCGTAGCACTGACTGACTGCTAGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCG  
 Arg Pro His Arg Asp  
 MCS