



CGTTGAGCACC GCCGCGCAAGGAATGGTGCATGCAAGGAGATGGCGCCCAACAGTCCCCGGCCACGGGGCCTG  
 GCAACTCGTGGCGGCGGCGTTCCTTACCACGTACGTTCTCTACCGCGGGTTGTCTAGGGGGCCGGTGCCCCGGAC

4575

CCACCATACCCACGCCGAAACAAGCGCTCATGAGCCCGAAGTGGCGAGCCCGATCTTCCCCATCGGTGATGTCGG  
 GGTGGTATGGGTGCGGCTTTGTTTCGCGAGTACTCGGGCTTACCAGCTCGGGCTAGAAGGGGTAGCCACTACAGCC

4650

CGATATAGGCGCCAGCAACCGCACCTGTGGCGCCGGTGATGCCGGCCACGATGCGTCCGGCGTAGAGGATCGAGA  
 GCTATATCCGCGGTCTGTTGGCGTGGACACCGCGGCCACTACGGCCGGTGCTACGCAGGCCGCATCTCCTAGCTCT

4725

TCGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAA  
 AGCTAGAGCTAGGGCGCTTTAATTATGCTGAGTGATATCCCCTTAACACTCGCCTATTGTTAAGGGGAGATCTTT

4800



TAATTTTGTTTAACTTTAAGAAGGAGATATACATATGTCCCCTATACTAGGTTATTGGAAAATTAAGGCCTTGT  
ATTAAAACAAATTGAAATTCTTCCTCTATATGTATACAGGGGATATGATCCAATAACCTTTTAATTCCCGGAACA

4875

1 5 10  
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val  
GST

GCAACCCACTCGACTTCTTTTGGAAATATCTTGAAGAAAAATATGAAGAGCATTGTATGAGCGCGATGAAGGTGA  
CGTTGGGTGAGCTGAAGAAAACCTTATAGAACTTCTTTTATACTTCTCGTAAACATACTCGCGCTACTTCCACT

4950

15 20 25 30 35  
Gln Pro Thr Arg Leu Leu Glu Tyr Leu Glu Glu Tyr Glu His Leu Tyr Glu Arg Asp Glu Gly Asp  
GST

TAAATGGCGAAACAAAAAGTTTGAATTGGGTTTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAA  
ATTTACCGCTTTGTTTTTCAAACCTTAACCCAAACCTCAAAGGGTTAGAAGGAATAATATAACTACCACTACAATT

5025

40 45 50 55 60  
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

ATTAACACAGTCTATGGCCATCATACTGTTATATAGCTGACAAGCACAACATGTTGGGTGGTTGTCCAAAAGAGCG  
TAATTGTGTCAGATACCGGTAGTATGCAATATATCGACTGTTCTGTGTTGTACAACCCACCAACAGGTTTTTCTCGC

5100

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

TGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGTAAAGA  
ACGTCTCTAAAGTTACGAACCTTCTCGCCAAAACCTATAATCTATGCCACAAAGCTCTTAACGTATATCATTCT

5175

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

CTTTGAAACTCTCAAAGTTGATTTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTTGAAGATCGTTTATGTCA  
GAAACTTTGAGAGTTTCAACTAAAAGAATCGTTTCGATGGACTTTACGACTTTTACAAGCTTCTAGCAAATACGT

5250

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

TAAACATATTTAAATGGTGATCATGTAACCCATCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATA  
ATTTTGTATAAATTTACCACTAGTACATTGGGTAGGACTGAAGTACAACATACTGCGAGAACTACAACAAAATAT

5325

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

CATGGACCCAATGTGCCTGGATGCGTTCCCAAATAGTTTGTTTTAAAAAACGTATTGAAGCTATCCCACAAAT  
GTACCTGGGTTACACGGACCTACGCAAGGGTTTTAATCAAACAAAATTTTTTGCATAACTTCGATAGGGTGTTTA

5400

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

TGATAAGTACTTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGA 5475  
 ACTATTCATGAACTTTAGGTCGTTTCATATATCGTACCGGAAACGTCCCGACCGTTTCGGTGCAAACCACCACCGCT

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

CCATCCTCCAAAATCGGATGGTTCAACTAGTGGTTCTGGTCATCACCATCACCATCACTCCGCGGGTCTGGTGCC 5550  
 GGTAGGAGGTTTTAGCCTACCAAGTTGATCACCAAGACCAGTAGTGGTAGTGAGGCGCCAGACCACGG

215 His Pro Pro Lys Ser Asp Gly Ser Thr Ser Gly Ser Gly His His His His His His Ser Ala Gly Leu Val Pro  
 GST (in frame with GST) 6xHis thrombin site

ACGCGGTAGTACTGCAATTGGTATGAAAGAAACCGCTGCTGCTAAATTCGAACGCCAGCACATGGACAGCCAGA 5625  
 TGCGCCATCATGACGTTAACATACTTTCTTTGGCGACGACGATTTAAGCTTGCGGGTCGTGTACCTGTCGGGTCT

5 Arg Gly Ser Thr Ala Ile Gly Met Lys Glu Thr Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser Pro Asp  
 thrombin site S-Tag

PshAI NcoI EcoRV BamHI EcoRI

TCTGGGTACCGGTGGTGGCTCCGGTGATGACGACGACAAGAGTCCCATGGATATCGGGGATCCGAATTCTGTACA 5700  
 AGACCCATGGCCACCACCGAGGCCACTACTGCTGCTGTTCTCAGGGTACCTATAGCCCCTAGGCTTAAGACATGT

Leu Gly Thr Gly Gly Gly Ser Gly Asp Asp Asp Asp Lys Ser Pro Met Asp Ile Gly Asp Pro Asn Ser Val Gln  
 (in frame with S-Tag) enterokinase site (in frame with enterokinase site)  
 MCS

AscI PstI SacI SalI HindIII NotI XhoI

GGCCTTGGCGCGCCTGCAGGCGAGCTCCGTCGACAAGCTTGC GGCCGCACTCGAGCACCACCACCACCACCA 5775  
 CCGGAACCGCGCGGACGTCCGCTCGAGGCAGCTGTTCAACGCCGGCGTGAGCTCGTGGTGGTGGTGGTGGT

Ala Leu Ala Arg Leu Gln Ala Ser Ser Val Asp Lys Leu Ala Ala Ala Leu Glu His His His His His His His  
 (in frame with enterokinase site) 8xHis  
 MCS

CCACTAATTGATTAATACCTAGGCTGCTAAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGC 5850  
 GGTGATTAATAATTATGGATCCGACGATTTGTTTCGGGCTTTCTTCGACTCAACCGACGACGGTGGCGACTCG

His  
 8xHis

AATAACTAGCATAACCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGGAACCTATATCCG 5925  
 TTATTGATCGTATTGGGAACCCCGGAGATTTGCCCGAAGACTCCCCAAAAACGACTTTCCTCCTTGATATAGGC

T7 terminator

GAT 3'  
 ... 5928  
 CTA 5'