



5' TAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATCCCCTCTAGAAATAATTTTGTTTAACTTTAAGA 75
 3' ATTATGCTGAGTGATATCCCCTTAACACTCGCCTATTGTTAAGGGGAGATCTTTATTAACAACAATTGAAATTCT

T7 promoter lac operator

AGGAGATATACATATGTCTGGTTCTCATCATCATCATCATAGCAGCGGTATGTCCCCTATACTAGGTTATTG 150
 TCCTCTATATGTATACAGACCAAGAGTAGTAGTAGTAGTAGTATCGTCGCCATACAGGGGATATGATCCAATAAC



GAAAATTAAGGGCCTTGTGCAACCCACTCGACTTCTTTTGGAAATATCTTGAAGAAAAATATGAAGAGCATTGTA 225
 CTTTTAATCCCAGAACACGTTGGGTGAGCTGAAGAAAACCTTATAGAACTTCTTTTATACTTCTCGTAAACAT

Lys Ile Lys Gly Leu Val Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu Tyr

GST

TGAGCGGATGAAGGTGATAAATGGCGAAACAAAAGTTTGAATTGGGTTTGGAGTTTCCCAATCTTCTTATTA 300
 ACTCGCGCTACTTCCACTATTTACCGCTTTGTTTTTCAAACCTTAACCCAAACCTCAAAGGGTTAGAAGGAATAAT

Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Leu Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr

GST

TATTGATGGTGATGTTAAATTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAACATGTTGGG 375
 ATAACTACCACTACAATTTAATTGTGTCAGATACCGGTAGTAGTATGCAATATATCGACTGTTTCGTGTTGTACAACC

Ile Asp Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn Met Leu Gly

GST

TGTTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTGGATATTAGATACGGTGTTCGAG
ACCAACAGGTTTTCTCGCACGTCTCTAAAGTTACGAACCTCCTCGCCAAAACCTATAATCTATGCCACAAAGCTC
85 90 95 100 105
Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg
GST

450

AATTGCATATAGTAAAGACTTTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTT
TTAACGTATATCATTCTGAAACTTTGAGAGTTTCAACTAAAAGAATCGTTTCGATGGACTTTACGACTTTTACAA
110 115 120 125 130
Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe
GST

525

CGAAGATCGTTTATGTCATAAAACATATTTAAATGGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGC
GCTTCTAGCAAATACAGTATTTTGTATAAATTTACCACTAGTACATTGGGTAGGACTGAAGTACAACATACTGCG
135 140 145 150 155
Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala
GST

600

TCTTGATGTTGTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAATAGTTTTGTTTTAAAAACGTAT
AGAACTACAACAAAATATGTACCTGGGTTACACGGACCTACGCAAGGGTTTAATCAAACAAAATTTTTTGCATA
160 165 170 175 180
Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile
GST

675

TGAAGCTATCCCACAAATTGATAAGTACTTGAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGC
ACTTCGATAGGGTGTTTAACTATTCATGAACTTTAGGTCGTTTCATATATCGTACCGGAAACGTCCCGACCGTTCC
185 190 195 200 205
Glu Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
GST

750

CACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGGCCACACAGGCCATAGATCTGGTACCGACGACGA
GTGCAAACCACCACCGCTGGTAGGAGTTTTAGCCTAGACCCGGTGTGTCCGGTATCTAGACCATGGCTGCTGCT
210 215
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Gly His Thr Gly His Arg Ser Gly Thr Asp Asp Asp
GST (in frame with GST) enterokinase site
MCS

825

CGACAAGGCCATGGCTGATATCGGATCCGAATTCGAGCTCGTTCGACAAGCTTGCGGCCGCACTCGAGCACCACCA
GCTGTTCCGGTACCGACTATAGCCTAGGCTTAAGCTCGAGCAGCTGTTTCGAACGCCGGCGTGAGCTCGTGGTGGT
5 1
Asp Lys Ala Met Ala Asp Ile Gly Ser Glu Phe Glu Leu Val Asp Lys Leu Ala Ala Ala Leu Glu His His His
enterokinase site (in frame with enterokinase site) 6xHis
MCS

900

CCACCACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA
GGTGGTGGTGACTCTAGGCCGACGATTGTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGCGGACTCGTTAT
5
His His His *
6xHis

975

ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGGAACCTATATCCGGATT
TGATCGTATTGGGGAACCCCGGAGATTGCCCAGAACTCCCCAAAAACGACTTTCCTCCTTGATATAGGCCTAA
T7 terminator

1050