



5' ... AGCTTATCGACTGCACGGTGCACCAATGCTTCTGGCGTCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGG 75  
 3' TCGAATAGCTGACGTGCCACGTGGTTACGAAGACCGCAGTCCGTCGGTAGCCTTCGACACCATAACCGACACGTCC

TCGTAATCACTGCATAATTCGTGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCAT 150  
 AGCATTTAGTGACGTATTAAGCACAGCGAGTTCCGCGTGAGGGCAAGACCTATTACAAAAAACGCGGCTGTAGTA

AACGGTCTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGAATTGTGAG 225  
 TTGCCAAGACCGTTTATAAGACTTTACTCGACAACCTGTTAATTAGTAGCCGAGCATATTACACACCTTAACACTC

tac promoter

lac operator

CGGATAACAATTTACACAGGAAACAGTATTCATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGC 300  
 GCCTATTGTTAAAGTGTGTCCTTTGTCATAAGTACAGGGGATATGATCCAATAACCTTTTAATTCCCGGAACAG

lac operator

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

AACCCACTCGACTTCTTTTGGGAATATCTTGAAGAAAAATATGAAGAGCATTGTATGAGCGCGATGAAGGTGATA 375  
 TTGGGTGAGCTGAAGAAAACCTTATAGAACTTCTTTTATACTTCTCGTAAACATACTCGCGCTACTTCCACTAT

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

AATGGCGAAACAAAAAGTTTGAATTGGGTTTGGAGTTTCCAATCTTCCTTATTATATTGATGGTGATGTAAAT 450  
 TTACCGCTTTGTTTTTCAAACCTTAACCCAAACCTCAAAGGGTTAGAAGGAATAATATAACTACCACTACAATTTA

40 Lys Trp Arg Asn Lys 45 Lys Phe Glu Leu Gly 50 Leu Glu Phe Pro Asn 55 Leu Pro Tyr Tyr Ile 60 Asp Gly Asp Val Lys  
 GST

TAACACAGTCTATGGCCATCATACTTATATAGCTGACAAGCACAACATGTTGGGTGGTTGTCCAAAAGAGCGTG  
ATTGTGTCAGATACCGGTAGTATGCAATATATCGACTGTTTCGTGTTGTACAACCCACCAACAGGTTTTCTCGCAC  
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

525

CAGAGATTTCAATGCTTGAAGGAGCGGTTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGTAAAGACT  
GTCTCTAAAGTTACGAACTTCCTCGCCAAAACCTATAATCTATGCCACAAAGCTCTTAACGTATATCATTCTGA  
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

600

TTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTCTGAAGATCGTTTATGTCATA  
AACTTTGAGAGTTTCAACTAAAAGAATCGTTCGATGGACTTTACGACTTTTACAAGCTTCTAGCAAATACAGTAT  
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

675

AAACATATTTAAATGGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATACA  
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

750

TGGACCCAATGTGCCTGGATGCGTTCCCAAATAGTTTTGTTTTAAAAACGTATTGAAGCTATCCACAAATTG  
ACCTGGGTTACACGGACCTACGCAAGGGTTTTAATCAAACAAAATTTTTTGCATAACTTCGATAGGGTGTTTAAC  
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

825

ATAAGTACTTGAAATCCAGCAAGTATATAGCATGGCCTTTCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACC  
TATTCATGAACTTTAGGTCGTTTCATATATCGTACCGGAAACGTCCCGACCGTTTCGGTGCAAACCACCACCGCTGG  
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

900

ATCCTCCAAAATCGGATCTGATCGAAGGTCGTGGGATCCCCGAATTCCTGGGTGCGACTCGAGCGGCCGCATCGTG  
TAGGAGGTTTTAGCCTAGACTAGCTTCCAGCACCCCTAGGGGCTTAAGGGCCAGCTGAGCTCGCCGGCGTAGCAC  
215  
His Pro Pro Lys Ser Asp Leu 1 Ile Glu Gly Arg Gly Ile Pro Glu Phe Pro Gly Arg Leu Glu Arg Pro His Arg  
GST Factor Xa site (in frame with Factor Xa site) MCS

975

ACTGACTGACGATCTGCCTCGCGGTTTTCGGTGATGACGGTGAACCTCTGACACATGCAGCTCCCGGAGACGG  
TGACTGACTGCTAGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCGAGGGCCTCTGCC  
Asp

1050

TCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTG  
AGTGTGCAACAGACATTGCCTACGGCCCTCGTCTGTTTCGGGCAGTCCCGCGCAGTCGCCACAACCGCCACAG

1125

GGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATAATCTTGAAGACGAAAGGGCCTCGTGATAC  
CCCCGCGTCGGTACTGGGTCAGTGCATCGCTATCGCCTCACATATTAAGAACTTCTGCTTTCCCGGAGCACTATG

1200

GCCTATTTTTATAGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCCGGGAAATGTGC  
CGGATAAAAATATCCAATTACAGTACTATTATTACCAAAGAATCTGCAGTCCACCGTGAAAAGCCCCTTTACAG

1275