



TAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAACATGTTGGGTGGTTGTCCAAAAGAGCGTG  
ATTGTGTCAGATACCGGTAGTATGCAATATATCGACTGTTCTGTTGTACAACCCACCAACAGTTTTCTCGCAC  
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

TTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTGGAAGATCGTTTATGTCATA  
AACTTTGAGAGTTTTCAACTAAAAGAATCGTTCGATGGACTTTACGACTTTTACAAGCTTCTAGCAAATACAGTAT  
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  
TTTGTATAAATTTACCACTAGTACATTGGGTAGGACTGAAGTACAACATACTGCGGAGAACTACAACAAAATATGT  
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

TGGACCCAATGTGCCTGGATGCGTTCACAAAATTAGTTTGTAAAAAACGATTGAAGCTATCCCACAAATTG  
ACCTGGGTACACGGACCTACGCAAGGGTTTTAATCAAACAAAATTTTTTGCATAAECTTCGATAGGGTGTTTAAC  
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

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

900

ATCCTCCAAAATCGGATCTGGTTCCGCGTGGATCCCCAGGAATTCCCGGGTCGACTCGAGCGGCCGCATCGTGAC  
TAGGAGGTTTTAGCCTAGACCAAGGCGCACCTAGGGTCTTAAGGGCCAGCTGAGCTCGCCGGCGTAGCACTG  
215  
His Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser \*  
GST thrombin site (in frame with thrombin site) MCS

975

TGACTGACGATCTGCCTCGCGGTTTTCGGTGATGACGGTGAACCTCTGACACATGCAGCTCCCGGAGACGGTC  
ACTGACTGCTAGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCGAGGGCCTCTGCCAG

1050

ACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTCCG  
TGTCGAACAGACATTGCCTACGGCCCTCGTCTGTTTCGGGCAGTCCCGCGCAGTCGCCACAACCGCCACAGCC

1125

GGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATAATTCTTGAAGACGAAAGGGCCTCGTGATACGC  
CCGCGTCGGTACTGGGTCAAGTGCATCGCTATCGCCTCACATATTAAGAATTCTGCTTTCCCGGAGCACTATGCG

1200

CTATTTTTATAGTTAATGTCATGATAATAATGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGC  
GATAAAAATATCCAATTACAGTACTATTATTACCAAAGAATCTGCAGTCCACCGTGAAGGCCCTTTACACGCG

1275