



TAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAACATGTTGGGTGGTTGTCCAAAAGAGCGTG 525
ATTGTGTCAGATACCGGTAGTATGCAATATATCGACTGTTCTGTGTTGTACAACCCACCAACAGGTTTTCTCGCAC
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 600
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

TTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTTGAAGATCGTTTATGTCATA 675
AACTTTGAGAGTTTCAACTAAAAGAATCGTTCGATGGACTTTACGACTTTTACAAGCTTCTAGCAAATACAGTAT
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

AAACATATTTAAATGGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATAACA 750
TTTGTATAAATTTACCACTAGTACATTGGGTAGGACTGAAGTACAACATACTGCGAGAACTACAACAAAATATGT
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

TGGACCCAATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTTTAAAAACGTATTGAAGCTATCCCACAAATTG 825
ACCTGGGTTACACGGACCTACGCAAGGGTTTTAATCAAACAAAATTTTTTGCATAAATTTCGATAGGGTGTTTAAC
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

ATAAGTACTTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACC 900
TATTCATGAACTTTAGGTCGTTTCATATATCGTACCAGGAAACGTCCCGACCGTTTCGGTGCAAACCACCACCGCTGG
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

ATCCTCCAAAATCGGATCTGGTTCGCGTGGATCCCCGGAATTCCCGGGTCGACTCGAGCGGCCGCATCGTGACT 975
TAGGAGGTTTTAGCCTAGACCAAGGCGCACCTAGGGGCTTAAAGGGCCCAGCTGAGCTCGCCGGCGTAGCACTGA
215 His Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Pro Gly Arg Leu Glu Arg Pro His Arg Asp
GST thrombin site (in frame with thrombin site) MCS

GACTGACGATCTGCCTCGCGGTTTTGGTGTGATGACGGTAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCA 1050
CTGACTGCTAGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTGAGGGCCTCTGCCAGT
*

CAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTGGGG 1125
GTCGAACAGACATTCGCCTACGGCCCTCGTCTGTTTCGGGCAGTCCCGCGCAGTCGCCACAAACGCCACAGCCC

GCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGATAATTCTTGAAGACGAAAGGGCCTCGTGATACGCC 1200
CGCGTCGGTACTGGGTCAGTGCATCGCTATCGCCTACATATTAAGAACTTCTGCTTTCCCGGAGCACTATGCGG

TATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTGAGGTGGCACTTTTCGGGGAAATGTGCGCG 1275
ATAAAAATATCCAATTACAGTACTATTATTACCAAAGAATCTGCAGTCCACCGTGAAAAGCCCCTTACACGCGC