

151 GGTGATGCCG GCCACGATGC GTCCGGCGTA GAGGATCGAG ATCTCGATCC CGCGAAATTA ATACGACTCA CTATAGGGGA
T7 promoter/priming site
T7 promoter

231 ATTGTGAGCG GATAACAATT CCCCTCTAGA AATAATTTTG TTAACTTTA AGAAGGAGAT ATACATA **ATG** GGA TCT GAT
lac operator RBS
Met Gly Ser Asp

310 AAA ATT ATT CAT CTG ACT GAT GAT TCT TTT GAT ACT GAT GTA CTT AAG GCA GAT GGT GCA ATC CTG
His-patch (HP) thioredoxin
Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp Val Leu Lys Ala Asp Gly Ala Ile Leu

376 GTT GAT TTC TGG GCA CAC TGG TGC GGT CCG TGC AAA ATG ATC GCT CCG ATT CTG GAT GAA ATC GCT
Val Asp Phe Trp Ala His Trp Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala

442 GAC GAA TAT CAG GGC AAA CTG ACC GTT GCA AAA CTG AAC ATC GAT CAC AAC CCG GGC ACT GCG CCG
Asp Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp His Asn Pro Gly Thr Ala Pro

508 AAA TAT GGC ATC CGT GGT ATC CCG ACT CTG CTG CTG TTC AAA AAC GGT GAA GTG GCG GCA ACC AAA
Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys
TrxFus forward priming site

574 GTG GGT GCA CTG TCT AAA GGT CAG TTG AAA GAG TTC CTC GAC GCT AAC CTG GCC GGC TCT GGA TCC
Val Gly Ala Leu Ser Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly Ser
Enterokinase (EK) recognition site EK cleavage site Sac I Hind III

640 GGT GAT GAC GAT GAC AAG CTG GGA ATT GAT CCC TTC ACC AAG GGC GAG CTC AAG CTT GAA
Gly Asp Asp Asp Asp Lys Leu Gly Ile Asp Pro Phe Thr TTC CCG CTC
G TGG Lys Gly Glu Leu Lys Leu Glu

700 GGT AAG CCT ATC CCT AAC CCT CTC CTC GGT CTC GAT TCT ACG CGT ACC GGT CAT CAT CAC CAT CAC
Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly His His His His His
V5 epitope Age I Polyhistidine (6xHis) region

766 CAT TGA GTTTGATCC GGCTGCTAAC AAAGCCCGAA AGGAAGCTGA GTTGGCTGCT GCCACCGCTG AGCAATAACT AGCA
His ***
T7 reverse priming site