

191 ⁻³⁵ TGTTCACAAT TAATCATCCG ⁻¹⁰ GCTCGTATAA TGTGTGGAAT ^{lac operator (lacO)} TGTGAGCGGA TAACAATTTT ACACAGGAAA

261 ^{rrnB antitermination sequence} CAGCGCCGCT GAGAAAAAGC GAAGCGGCAC TGCTCTTTAA CAATTTATCA GACAATCTGT GTGGGCACTC

331 ^{gene 10 translational enhancer} GACCGGAATT ATCGATTAAC TTTATTATTA AAAATTTAAAG ^{RBS} AGGTATATAT TA ^{Minicistron} ATG TAT CGA TTA
Met Tyr Arg Leu

395 ^{RBS} AAT AAG GAG GAA TAA ACC ^{Nco I} ATG GGG GGT TCT CAT CAT CAT CAT CAT CAT GGT ATG
Asn Lys Glu Glu *** Met Gly Gly Ser His His His His His His Gly Met
^{HisG epitope}
^{6xHis tag}

449 ^{Nhe I} Xpress™ Forward priming site GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG ^{Xpress™ epitope} GAT CTG TAC GAC GAT GAC GAT
Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp
^{EK recognition sequence}

503 ^{Bam HI} AAG GAT CCA ACC CTT **PCR Product** ^{Eco RI} AAG GGCGAATTCA ^{Bst BI} ATTCGAAGCT ^{Hind III} TGGCTGTTTT
TTC CTA GGT TGG GAA TTC CCGCTTAAGT TAAGCTTCGA ACCGACAAAA
Lys Asp Pro Thr Leu >>>
^{EK cleavage site}

551 ^{pTrcHis Reverse priming site} GCGGATGAG AGAAGATTTT CAGCCTGATA CAGATTAAAT CAGAACGCAG AAGCGGTCTG ATAAAACAGA

621 ^{rrnB T₁ and T₂ transcription termination sequence} ATTTGCCTGG CGGCAGTAGC GCGGTGGTCC CACCTGACCC CATGCCGAAC TCAGAAGTGA AACGCCGTAG

691 CGCCGATGGT AGTGTGGGGT CTCCCCATGC GAGAGTAGGG AACTGCCAGG CATCAAATAA AACGAAAGGC

761 TCAGTCGAAA GACTGGGCTT TTCGTTTTAT CTGTTGTTTG TCGGTGAACG CTCTCCTGAG TAGGACAAAT