



GCAATTGACCAACAAGGACCATAGATTATGAAAAATAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACG  
 CGTTAACTGGTTGTTCTGGTATCTAATACTTTTATTTTTGTCCACGTGCGTAGGAGCGTAATAGGCGTAATTGC

1 5 10 15  
 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr  
 MBP

ACGATGATGTTTTCCGCCTCGGCTCTCGCCAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAA  
 TGCTACTACAAAAGGCGGAGCCGAGAGCGGTTTTAGCTTCTTCCATTTGACCATTAGACCTAATTGCCGCTATTT

20 25 30 35 40  
 Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys  
 MBP

GGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAAGATACCGGAATTAAGTCACCGTTGAGCATCCG  
 CCGATATTGCCAGAGCGACTTCAGCCATTCTTTAAGCTCTTTCTATGGCCTTAATTTTCAGTGGCAACTCGTAGGC

45 50 55 60 65  
 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Asp Thr Gly Ile Lys Val Thr Val Glu His Pro  
 MBP

GATAAACTGGAAGAGAAAATCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGAC  
 CTATTTGACCTTCTCTTTAAGGGTGTCCAACGCCGTTGACCGCTACCGGGACTGTAATAGAAGACCCGTGTGCTG

70 75 80 85 90  
 Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp  
 MBP

CGGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTG  
1950  
GGCAAATGGACCCTACGGCATGCAATGTTGCCGTTTCGACTAACGAATGGGCTAGCGACAACCTTCGCAATAGCGAC

120 125 130 135 140  
Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu  
MBP

ATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAAGCTGAAA  
2025  
TAAATATTGTTTCTAGACGACGGCTTGGGCGGTTTTTGGACCCTTCTCTAGGGCCGCGACCTATTTCTTGACTTT

145 150 155 160 165  
Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Lys Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys  
MBP

GCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGG  
2100  
CGCTTTCATTCTCGCGCGACTACAAGTTGGACGTTCTTGGCATGAAGTGGACCGGCGACTAACGACGACTGCC

170 175 180 185 190  
Ala Lys Gly Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly  
MBP

GGTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG  
2175  
CCAATACGCAAGTTCATACTTTGCCGTTTCATGCTGTAATTTCTGCACCCGCACCTATTGCGACCGCGCTTTCGC

195 200 205 210 215  
Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala  
MBP

GGTCTGACCTTCTGGTTGACCTGATTAATAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCT  
2250  
CCAGACTGGAAGGACCAACTGGACTAATTTTTGTTTGTGTAAGTTACGCTCTGTGGCTAATGAGGTAGCGTCTTCGA

220 225 230 235 240  
Gly Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu Ala  
MBP

GCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCGATGGTCCAACATCGACACCAGCAAAGTG  
2325  
CGGAAATTATTTCCGCTTTGTCGCTACTGGTAGTTGCCGGGCACCCGTACCAGTTGTAGCTGTGGTGGTTTTAC

245 250 255 260 265  
Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys Val  
MBP

AATTATGGTGTAAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTTCGTTGGCGTGTGAGCGCAGGT  
2400  
TTAATACCACATTGCCATGACGGCTGGAAGTTCCAGTTGGTAGGTTTGGCAAGCAACCGCACGACTCGCGTCCA

270 275 280 285 290  
Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser Ala Gly  
MBP

ATTAACGCCCGCCAGTCCGAACAAAGAGCTGGCAAAAAGAGTTTCTCGAAAACCTATCTGCTGACTGATGAAGGTCTG  
2475  
TAATTGCGGGCGTCAAGGCTTGTCTCGACCGTTTTCTCAAGGAGCTTTTGATAGACGACTGACTACTTCCAGAC

295 300 305 310 315  
Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu  
MBP

GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAAGTCTTACGAGGAAGAGTTGGTGAAAGATCCG  
2550  
CTTCGCCAATTATTTCTGTTTGGCGACCCACGGCATCGCGACTTCAGAATGCTCTTCTCAACCACTTTCTAGGC

320 325 330 335 340  
Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu Val Lys Asp Pro  
MBP

CGTATTGCCGCCACTATGGAAAACGCCCAGAAAGGTGAAATCATGCCGAACATCCCGCAGATGTCCGCTTTCTGG  
2625  
GCATAACGGCGGTGATACCTTTTGCGGGTCTTTCCACTTTAGTACGGCTTGTAGGGCGTCTACAGGCGAAAGACC

345 350 355 360 365  
Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp  
MBP

TATGCCGTGCGTACTGCGGTGATCAACGCCGCCAGCGGTCGTCAGACTGTTCGATGAAGCCCTGAAAGACGCGCAG  
ATACGGCACGCATGACGCCACTAGTTGCGGCGGTCGCCAGCAGTCTGACAGCTACTTCGGGACTTTCTGCGCGTC

2700

370 375 380 385 390  
Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln

MBP

KpnI NdeI

ACTAATTCGAGCTCGAACAACAACAATAACAATAACAACAACCTCGGGGATGACGATGACAAGGTACCGCAT  
TGATTAAGCTCGAGCTTGTGTTGTTGTTATTGTTATTGTTGTTGGAGCCCTACTGCTACTGTTCCATGGCGTA

2775

Thr Asn Ser Ser Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Leu Gly Asp Asp Asp Asp Lys Val Pro His  
MBP (in frame with MBP) enterokinase site

MCS

NcoI NotI EcoRV SalI BamHI EcoRI SbfI PstI HindIII  
ATGTCCATGGGCGGCCGCGATATCGTCGACGGATCCGAATTCCTGTCAGGTAATTAATAAGCTTCAAATAAAA  
TACAGGTACCCGCGCGCTATAGCAGCTGCCTAGGCTTAAGGGACGTCCATTAATTTATTCGAAGTTTATTTG  
Met Ser Met Gly Gly Arg Asp Ile Val Asp Gly Ser Glu Phe Pro Ala Gly Asn  
(in frame with enterokinase site) rrnB T1 terminator

2850

MCS

GAAAGGCTCAGTCGAAAGACTGGGCCTTTTCGTTTTATCTGTTGTTTGTTCGGTGAACGCTCTCCTGAGTAGGACAA  
CTTTCCGAGTCAGCTTTCTGACCCGAAAGCAAAATAGACAACAACAGCCACTTGCAGAGGACTCATCTGTT  
rrnB T1 terminator

2925

ATCCGCCGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCGCATAAACTG  
TAGGCGGCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCTCCACCGCCCGTCTGCGGGCGGTATTTGAC  
rrnB T1 terminator

3000