



GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCGTCAGGCAGCCATCGG  
 CGTGTTAAGAGTACAAACTGTCGAATAGTAGCTGACGTGCCACGTGGTTACGAAGACCGCAGTCCGTTCGGTAGCC

1275

AAGCTGTGGTATGGCTGTGCAGGTCGTAATCACTGCATAATTCGTGTCGCTCAAGGCGCACTCCCGTTCTGGAT  
 TTCGACACCATACCGACACGTCCAGCATTAGTGACGTATTAAGCACAGCGAGTTCGCGTGAGGGCAAGACCTA

1350

AATGTTTTTTGCGCCGACATCATAACGGTTCTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCT  
 TTACAAAAAACGCGGCTGTAGTATTGCCAAGACCGTTTATAAGACTTTACTCGACAACCTGTTAATTAGTAGCCGA

1425

tac promoter

CGTATAATGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTACGA  
 GCATATTACACACCTTAACACTCGCCTATTGTTAAAGTGTGTCCTTTGTTCGGTCAGGCAAATCCACAAAAGTGCT

1500

tac promoter

lac operator

GCAATTGACCAACAAGGACCATAGATTATGAAAATAAAAACAGGTGCACGCATCCTCGCATTATCCGCATTAACG  
 CGTAACTGGTTGTTTCTGGTATCTAATACTTTTATTTTTGTCCACGTGCGTAGGAGCGTAATAGGCGTAATTGC

1575

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

1650

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

1725

GATAAACTGGAAGAGAAATTCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGAC  
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

1800

CGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGACAAAGCGTTCAGGACAAGCTGTAT  
GCGAAACCACCGATGCGAGTTAGACCGGACAACCGACTTTAGTGGGGCCTGTTTTCGCAAGGTCCTGTTTCGACATA  
95 100 105 110 115  
Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr  
MBP

1875

CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCGATCGCTGTTGAAGCGTTATCGCTG  
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

1950

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

2025

GCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGG  
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

2100

GGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG  
CCAATACGCAAGTTCATACTTTTGGCGTTCATGCTGTAATTTCTGCACCCGCACCTATTGCGACCGCGCTTTTCG  
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

2175

GGTCTGACCTTCTGTTGACCTGATTA AAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCT  
CCAGACTGGAAGGACCAACTGGACTAATTTTTGTTTGTGTACTTACGTCTGTGGCTAATGAGGTAGCGTCTTCGA  
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

2250

GCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTG  
CGGAAATTATTTCCGCTTTGTCGCTACTGGTAGTTGCCGGGCACCCGTACCAGGTTGTAGCTGTGGTCGTTTCAC  
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

2325

AATTATGGTGTAAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTTCGTTGGCGTGCTGAGCGCAGGT  
TTAATACCACATTGCCATGACGGCTGGAAGTTCCAGTTGGTAGGTTTGGCAAGCAACCGCACGACTCGCGTCCA  
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

2400

ATTAACGCCGCCAGTCCGAACAAAGAGCTGGCAAAGAGTTCCTCGAAAACCTATCTGCTGACTGATGAAGGTCTG  
TAATTGCGGGCGGTGAGGCTTGTCTCGACCGTTTTCTCAAGGAGCTTTTGATAGACGACTGACTACTTCCAGAC  
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

2475

GAAAGCGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGTGAAAGATCCG  
CTTCGCCAATTATTTCTGTTTGGCGACCCACGGCATCGCGACTTCAGAATGCTCCTTCTCAACCACTTTCTAGGC  
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

2550

CGTATTGCCGCCACTATGGAAAACGCCAGAAAGGTGAAATCATGCCGAACATCCCGCAGATGTCCGCTTTCTGG  
GCATAACGGCGGTGATACCTTTTGGGGTCTTTCCACTTTAGTACGGCTTGTAGGGCGTCTACAGGCGAAAGACC  
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

2625

TATGCCGTGCGTACTGCGGTGATCAACGCCGCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAG  
ATACGGCACGCATGACGCCACTAGTTGCGGGCGGTCCGCAGCAGTCTGACAGCTACTTCGGGACTTTCTGCGCGTC  
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

2700

**SacI** **AvaI** **KpnI** **NdeI**  
ACTAATTCGAGCTCGAACAACAACAATAACAATAACAACAACCTCGGGGATGACGATGACAAGGTACCGCAT  
TGATTAAGCTCGAGCTTGTGTTGTTGTTATTGTTATTGTTGTTGGAGCCCCTACTGCTACTGTTCCATGGCGTA  
Thr Asn Ser Ser Ser 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

2775

**NcoI** **NotI** **EcoRV** **SalI** **BamHI** **EcoRI** **PstI** **HindIII**  
ATGTCCATGGGCGGCCGCGATATCGTCGACGGATCCGAATTCCTGCAGGTAATTAATAAGCTTCAAATAAAAC  
TACAGGTACCCGCCGGCGCTATAGCAGCTGCCTAGGCTTAAGGGACGTCATTAATTTATTCGAAGTTTATTTTG  
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  
MCS

2850

GAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTGCGGTGAACGCTCTCCTGAGTAGGACAA  
CTTTCCGAGTCAGCTTCTGACCCGGAAAGCAAATAGACAACAACAGCCACTTGCGAGAGGACTCATCCTGTT  
rrnB T1 terminator

2925