



GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCGTCAGGCAGCCATCGG
CGTGTTAAGAGTACAAACTGTCTGAATAGTAGCTGACGTGCCACGTGGTTACGAAGACCGCAGTCCGTTCGGTAGCC

1275

AAGCTGTGGTATGGCTGTGCAGGTCGTAATCACTGCATAATTCGTGTCGCTCAAGGCGCACTCCCGTTCTGGAT
TTCGACACCATACCGACAGTCCAGCATTAGTGACGTATTAAGCACAGCGAGTTCGCGTGAGGGCAAGACCTA

1350

AATGTTTTTTCGCGGACATCATAACGGTCTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCT
TTACAAAAACGCGGCTGTAGTATTGCCAAGACCGTTTATAAGACTTTACTCGACAACGTTAATTAGTAGCCGA

1425

tac promoter

CGTATAATGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTACGA
GCATATTACACACCTTAACACTCGCCTATTGTTAAAGTGTGTCCTTTGTTCGGTCAGGCAAATCCACAAAAGTGCT

1500

tac promoter

lac operator

GCAATTGACCAACAAGGACCATAGATTATGAAAATCGAAGAAGGTAACCTGGTAATCTGGATTAACGGCGATAAA
CGTTAACTGGTTGTTCTGTTATCTAATACTTTTAGCTTCTTCCATTTGACCATTAGACCTAATTGCCGCTATTT

1575

1 Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
MBP

GGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAGTCACCGTTGAGCATCCG
CCGATATTGCCAGAGCGACTTCAGCCATTCTTTAAGCTCTTTCTATGGCCTTAATTTTCAGTGGCAACTCGTAGGC

1650

Gly Tyr Asn Gly²⁰ Leu Ala Glu Val Gly²⁵ Lys Lys Phe Glu Lys³⁰ Asp Thr Gly Ile Lys³⁵ Val Thr Val Glu His⁴⁰ Pro
MBP

GATAAACTGGAAGAGAAATTCACACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGAC
CTATTTGACCTTCTCTTTAAGGGTGTCCAACGCCGTTGACCGCTACCGGGACTGTAATAGAAGACCCGTTGTGCTG

1725

Asp Lys Leu Glu⁴⁵ Glu Lys Phe Pro Gln Val Ala Ala Thr⁵⁵ Gly Asp Gly Pro Asp Ile⁶⁰ Ile Phe Trp Ala His⁶⁵ Asp
MBP

CGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT
GCGAAACCACCGATGCGAGTTAGACCGGACAACCGACTTTAGTGGGGCCTGTTTCGCAAGGTCTGTTTCGACATA

1800

Arg Phe Gly Gly⁷⁰ Tyr Ala Gln Ser Gly⁷⁵ Leu Leu Ala Glu Ile⁸⁰ Thr Pro Asp Lys Ala⁸⁵ Phe Gln Asp Lys Leu⁹⁰ Tyr
MBP

CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTG
GGCAAATGGACCCTACGGCATGCAATGTTGCCGTTGCGACTAACGAATGGGCTAGCGACAACCTTCGCAATAGCGAC

1875

Pro Phe Thr Trp⁹⁵ Asp Ala Val Arg Tyr¹⁰⁰ Asn Gly Lys Leu Ile¹⁰⁵ Ala Tyr Pro Ile Ala¹¹⁰ Val Glu Ala Leu Ser¹¹⁵ Leu
MBP

ATTTATAACAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAAGCTGAAA
TAAATATTGTTTCTAGACGACGGCTTGGGCGGTTTTTGGACCCCTCTCTAGGGCCGCGACCTATTTCTTGACTTT

1950

Ile Tyr Asn Lys¹²⁰ Asp Leu Leu Pro Asn¹²⁵ Pro Pro Lys Thr Trp¹³⁰ Glu Glu Ile Pro Ala¹³⁵ Leu Asp Lys Glu Leu¹⁴⁰ Lys
MBP

GCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGG
CGCTTTCCATTCTCGCGGACTACAAGTTGGACGTTCTTGGCATGAAGTGGACCGGCGACTAACGACGACTGCC

2025

Ala Lys Gly Lys¹⁴⁵ Ser Ala Leu Met Phe¹⁵⁰ Asn Leu Gln Glu Pro¹⁵⁵ Tyr Phe Thr Trp Pro¹⁶⁰ Leu Ile Ala Ala Asp¹⁶⁵ Gly
MBP

GGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG
CCAATACGCAAGTTCATACTTTTGGCGTTCATGCTGTAATTTCTGCACCCGCACCTATTGCGACCGCGCTTTTCGC

2100

Gly Tyr Ala Phe¹⁷⁰ Lys Tyr Glu Asn Gly¹⁷⁵ Lys Tyr Asp Ile Lys¹⁸⁰ Asp Val Gly Val Asp¹⁸⁵ Asn Ala Gly Ala Lys¹⁹⁰ Ala
MBP

GGTCTGACCTTCTGGTTGACCTGATTA AAAACAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCT
CCAGACTGGAAGGACCAACTGGACTAATTTTTGTTTGTGTA CTTACGTCTGTGGCTAATGAGGTAGCGTCTTCGA

2175

Gly Leu Thr Phe¹⁹⁵ Leu Val Asp Leu Ile²⁰⁰ Lys Asn Lys His Met²⁰⁵ Asn Ala Asp Thr Asp²¹⁰ Tyr Ser Ile Ala Glu²¹⁵ Ala
MBP

GCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTG
CGGAAATTATTTCCGCTTTGTCGCTACTGTTAGTTGCCGGGCACCCGTACCAGGTTGTAGCTGTGGTCTGTTTCAC

2250

Ala Phe Asn Lys²²⁰ Gly Glu Thr Ala Met²²⁵ Thr Ile Asn Gly Pro²³⁰ Trp Ala Trp Ser Asn²³⁵ Ile Asp Thr Ser Lys²⁴⁰ Val
MBP

AATTATGGTGTAAACGGTACTGCCGACCTTCAAGGGTCAACCATCAAACCGTTTCGTTGGCGTGCTGAGCGCAGGT
TTAATACCACATTGCCATGACGGCTGGAAGTTCCAGTTGGTAGGTTTGGCAAGCAACCGCACGACTCGCGTCCA

2325

Asn Tyr Gly Val²⁴⁵ Thr Val Leu Pro Thr²⁵⁰ Phe Lys Gly Gln Pro²⁵⁵ Ser Lys Pro Phe Val²⁶⁰ Gly Val Leu Ser Ala²⁶⁵ Gly
MBP

ATTAACGCCGCCAGTCCGAACAAGAGCTGGCAAAGAGTTCCTCGAAAACCTATCTGCTGACTGATGAAGGTCTG 2400
 TAATTGCGGCGGTCAGGCTTGTCTCGACCGTTTTCTCAAGGAGCTTTTGATAGACGACTGACTACTTCCAGAC

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

GAAGCGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGTGAAGATCCG 2475
 CTTCCGCAATTATTTCTGTTTGGCGACCCACGGCATCGCGACTTCAGAATGCTCCTTCTCAACCACTTTCTAGGC

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

CGTATTGCCGCCACTATGGAAAACGCCAGAAAGGTGAAATCATGCCGAACATCCCGCAGATGTCCGCTTTCTGG 2550
 GCATAACGGCGGTGATACCTTTTGGCGGCTTTCCACTTTAGTACGGCTTGTAGGGCGTCTACAGGCGAAAGACC

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

TATGCCGTGCGTACTGCGGTGATCAACGCCGCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAG 2625
 ATACGGCACGCATGACGCCACTAGTTGCGGCGGTGCGCCAGCAGTCTGACAGCTACTTTCGGGACTTTCTGCGCGTC

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

SacI **AvaI** **KpnI** **NdeI**
 ACTAATTCGAGCTCGAACAACAACAACAATAACAATAACAACAACCTCGGGGATGACGATGACAAGGTACCGCAT 2700
 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

NcoI **NotI** **EcoRV** **SalI** **BamHI** **EcoRI** **PstI**
 ATGTCCATGGGCGGCCGCGATATCGTCGACGGATCCGAATTCCTGCAGGTAATTAATAAGCTTCAAATAAAAC 2775
 TACAGGTACCCGCGGCGCTATAGCAGCTGCCTAGGCTTAAGGGACGTCCATTAATTTATTTCGAAGTTTATTTTG

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

GAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTGCGGTGAACGCTCTCCTGAGTAGGACAA 2850
 CTTTCCGAGTCAGCTTTCTGACCCGAAAGCAAATAGACAACAACAGCCACTTGCAGAGGACTCATCCTGTT

rrnB T1 terminator