



GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCGTCAGGCAGCCATCGG
 CGTGTTAAGAGTACAAACTGTCTGAATAGTAGCTGACGTGCCACGTGGTTACGAAGACCGCAGTCCGTCCGGTAGCC

1275

AAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCGTGTCGCTCAAGGCGCACTCCCGTTCTGGAT
 TTCGACACCATACCGACACGTCCAGCATTAGTGACGTATTAAGCACAGCGAGTTCCGCGTGAGGGCAAGACCTA

1350

AATGTTTTTTCGCGGACATCATAACGGTCTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCT
 TTACAAAAACGCGGCTGTAGTATTGCCAAGACCGTTTATAAGACTTTACTCGACAACCTGTTAATTAGTAGCCGA

1425

tac promoter

CGTATAATGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTACGA
 GCATATTACACACCTTAACACTCGCCTATTGTTAAAGTGTGTCCTTTGTGGTTCAGGCAAATCCACAAAAGTGCT

1500

tac promoter lac operator

GCAATTGACCAACAAGGACCATAGATTATGAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAA
 CGTTAACTGGTTGTTCTGGTATCTAATACTTTAGCTTCTTCATTTGACCATTAGACCTAATTGCCGCTATTT

1575

1 5 10 15
 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 Glu³⁰ Lys Asp Thr Gly Ile Lys³⁵ Val Thr Val Glu His⁴⁰ Pro
MBP

GATAAACTGGAAGAGAAATTCACACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGAC
CTATTTGACCTTCTCTTTAAGGGTGTCCAACGCCGTTGACCGCTACCGGGACTGTAATAGAAGACCCGTTGTGCTG
1725
Asp Lys Leu Glu⁴⁵ Glu Lys Phe Pro Gln⁵⁰ Val Ala Ala Thr⁵⁵ Gly Asp Gly Pro Asp Ile⁶⁰ Ile Phe Trp Ala His⁶⁵ Asp
MBP

CGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGACAAAGCGTTCCAGGACAAGCTGTAT
GCGAAACCACCGATGCGAGTTAGACCGGACAACCGACTTTAGTGGGGCTGTTTCGCAAGGTCCTGTTTCGACATA
1800
Arg Phe Gly Gly⁷⁰ Tyr Ala Gln Ser Gly⁷⁵ Leu Leu Ala Glu⁸⁰ Ile Thr Pro Asp Lys⁸⁵ Ala Phe Gln Asp Lys⁹⁰ Leu Tyr
MBP

CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTG
GGCAAATGGACCCTACGGCATGCAATGTTGCCGTTGACTAACGAATGGGCTAGCGACAACCTTCGCAATAGCGAC
1875
Pro Phe Thr Trp⁹⁵ Asp Ala Val Arg Tyr¹⁰⁰ Asn Gly Lys Leu¹⁰⁵ Ile Ala Tyr Pro Ile Ala¹¹⁰ Val Glu Ala Leu Ser¹¹⁵ Leu
MBP

ATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAACCTGGGAAGAGATCCCGGCGCTGGATAAAGAACTGAAA
TAAATATTGTTTCTAGACGACGGCTTGGGCGGTTTTTGGACCCTTCTCTAGGGCCGCGACCTATTTCTTGACTTT
1950
Ile Tyr Asn Lys¹²⁰ Asp Leu Leu Pro Asn¹²⁵ Pro Pro Lys Thr Trp¹³⁰ Glu Glu Ile Pro Ala¹³⁵ Leu Asp Lys Glu Leu Lys¹⁴⁰
MBP

GCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGG
CGCTTTCATTCTCGCGCGACTACAAGTTGGACGTTCTTGGCATGAAGTGGACCGGCGACTAACGACGACTGCC
2025
Ala Lys Gly Lys¹⁴⁵ Ser Ala Leu Met Phe¹⁵⁰ Asn Leu Gln Glu¹⁵⁵ Pro Tyr Phe Thr Trp¹⁶⁰ Pro Leu Ile Ala Ala¹⁶⁵ Asp Gly
MBP

GGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG
CCAATACGCAAGTTCATACTTTTGCCGTTTCATGCTGTAATTTCTGCACCCGCACCTATTGCGACCGCGCTTTTCGC
2100
Gly Tyr Ala Phe¹⁷⁰ Lys Tyr Glu Asn Gly¹⁷⁵ Lys Tyr Asp Ile¹⁸⁰ Lys Asp Val Gly Val Asp¹⁸⁵ Asn Ala Gly Ala Lys¹⁹⁰ Ala
MBP

GGTCTGACCTTCTGGTTGACCTGATTA AAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCT
CCAGACTGGAAGGACCAACTGGACTAATTTTTGTTTGTGTACTTACGCTGTGGCTAATGAGGTAGCGTCTTCGA
2175
Gly Leu Thr Phe¹⁹⁵ Leu Val Asp Leu Ile²⁰⁰ Lys Asn Lys His²⁰⁵ Met Asn Ala Asp Thr Asp²¹⁰ Tyr Ser Ile Ala Glu²¹⁵ Ala
MBP

GCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTG
CGGAAATTATTTCCGCTTTGTCGCTACTGTTAGTTGCCGGGCACCCGTACCAGGTTGTAGCTGTGGTCTTTTCAC
2250
Ala Phe Asn Lys²²⁰ Gly Glu Thr Ala Met²²⁵ Thr Ile Asn Gly²³⁰ Pro 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 Gln²⁵⁵ Pro Ser Lys Pro Phe Val²⁶⁰ Gly Val Leu Ser Ala²⁶⁵ Gly
MBP

ATTAACGCCGCCAGTCCGAACAAAGAGCTGGCAAAGAGTTCTCTCGAAAACCTATCTGCTGACTGATGAAGGTCTG
TAATTGCGGCGGTGTCAGGCTTGTCTCTCGACCGTTTTCTCAAGGAGCTTTTGATAGACGACTGACTACTTCCAGAC

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

270 275 280 285 290

MBP

2400

GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGTGAAAGATCCG
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

295 300 305 310 315

MBP

2475

CGTATTGCCGCCACTATGGAAAACGCCAGAAAGGTGAAATCATGCCGAACATCCCGCAGATGTCCGCTTTCTGG
GCATAACGGCGGTGATACCTTTTGGCGGCTTTTCCACTTTAGTACGGCTTGTAGGGCGTCTACAGGGCAAAGACC

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

320 325 330 335 340

MBP

2550

TATGCCGTGCGTACTGCGGTGATCAACGCCGCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAG
ATACGGCACGCATGACGCCACTAGTTGCGGGCGGTCGCCAGCAGTCTGACAGCTACTTCGGGACTTTCTGCGCGTC

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

345 350 355 360 365

MBP

2625

ACTAATTCGAGCTCGAACAAACAACAATAACAATAACAACAACCTCGGGATCGAGGGAAGGATTTACATATG
TGATTAAGCTCGAGCTTGTGTTGTTGTTATTGTTATTGTTGTTGGAGCCCTAGCTCCCTTCTAAAGTGTATAC

SacI AvaI NdeI

2700

Thr Asn Ser Ser Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Leu Gly Ile Glu Gly Arg Ile Ser His Met

MBP (in frame with MBP) Factor Xa site MCS

TCCATGGGCGGCCGCGATATCGTTCGACGGATCCGAATTCCTGCAGGTAATTAATAAGCTTCAAATAAACGAA
AGGTACCCGCCGCGCTATAGCAGCTGCCTAGGCTTAAGGGACGTCCATTAATTTATTTCGAAGTTTATTTTGCTT

NcoI NotI EcoRV SalI BamHI EcoRI PstI HindIII

Ser Met Gly Gly Arg Asp Ile Val Asp Gly Ser Glu Phe Pro Ala Gly Asn * rrnB T1 terminator

MCS

2775

AGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTGCGGTGAACGCTCTCCTGAGTAGGACAAATC
TCCGAGTCAGCTTTCTGACCCGGAAGCAAATAGACAACAACAGCCACTTGCGAGAGGACTCATCCTGTTTATG

rrnB T1 terminator

2850