

TTGTTTAACTTTAAGAAGGAGATATACATATGAGCGATAAAATTATTCACCTGACTGACGACAGTTTTTGACACGG  
AACAAATTGAAATTCCTCCTCTATATGTATACTCGCTATTTTAATAAGTGGACTGACTGCTGTCAAACCTGTGCC

5250

1 Met Ser Asp Lys Ile Ile His Leu Thr 10 Asp Asp Ser Phe Asp Thr 15  
TrxA

ATGTA CTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAATGATCGCCC  
TACATGAGTTTCGCCTGCCCGCTAGGAGCAGCTAAAGACCCGTCTCACCACGCCAGGCAGTTTTACTAGCGGG

5325

20 Asp Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp Cys Gly Pro Cys Lys Met Ile Ala 40  
TrxA

CGATTCTGGATGAAATCGCTGACGAATATCAGGGCAAACCTGACCGTTGCAAACCTGAACATCGATCAAACCCCTG  
GCTAAGACCTACTTTAGCGACTGCTTATAGTCCCCTTTGACTGGCAACGTTTTTGACTTGTAGCTAGTTTTGGGAC

5400

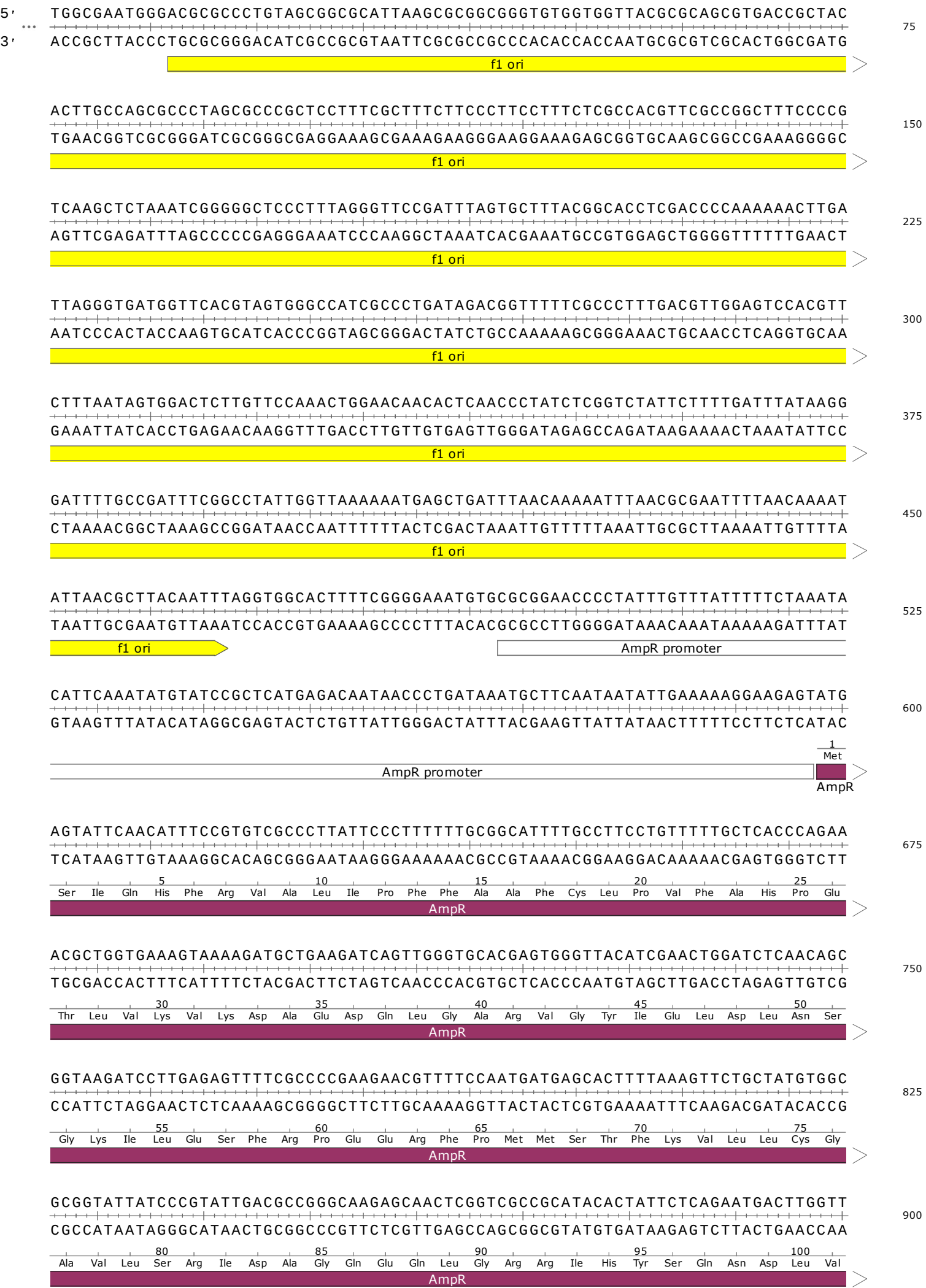
45 Pro Ile Leu Asp Glu Ile Ala Asp Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn Pro 65  
TrxA

GCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAACCGTGAAGTGGCGGCAACCA  
CGTGACGCGGCTTTATACCGTAGGCACCATAGGGCTGAGACGACGACAAGTTTTTGCCACTTCACCGCCGTTGGT

5475

70 Gly Thr Ala Pro Lys Tyr Gly Ile Arg 75 Gly Ile Pro Thr Leu 80 Leu Leu Phe Lys Asn 85 Gly Glu Val Ala Ala Thr 90  
TrxA





GAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACC  
CTCATGAGTGGTCAGTGTCTTTTTCGTAGAATGCCTACCCTACTGTCACTTCTCTTAATACGTCACGACGGTATTGG

975

105 110 115 120 125  
Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr

AmpR

ATGAGTGATAAACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCAC  
TACTCACTATTGTGACGCCGGTTGAATGAAGACTGTTGCTAGCCTCCTGGCTTCCTCGATTGGCGAAAAAACGTG

1050

130 135 140 145 150  
Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His

AmpR

AACATGGGGGATCATGTAACCTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGT  
TTGTACCCCTAGTACATTGAGCGGAACTAGCAACCCTTGGCCTCGACTTACTTCGGTATGTTTTGCTGCTCGCA

1125

155 160 165 170 175  
Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg

AmpR

GACACCACGATGCCTGCAGCAATGGCAACAACGTTGCGCAAACCTATTAACCTGGCGAACTACTTACTCTAGCTTCC  
CTGTGGTGCTACGGACGTCGTTACCGTTGTTGCAACGCGTTTGATAATTGACCGCTTGATGAATGAGATCGAAGG

1200

180 185 190 195 200  
Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser

AmpR

CGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGC  
GCCGTTGTTAATTATCTGACCTACCTCCGCCTATTTCAACGTCCTGGTGAAGACGCGAGCCGGGAAGGCCGACCG

1275

205 210 215 220 225  
Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly

AmpR

TGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGT  
ACCAAATAACGACTATTTAGACCTCGGCCACTCGCACCCAGAGCGCCATAGTAACGTCGTGACCCCGGTCTACCA

1350

230 235 240 245 250  
Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly

AmpR

AAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCT  
TTCGGGAGGGCATAGCATCAATAGATGTGCTGCCCTCAGTCCGTTGATACCTACTTTGCTTTATCTGTCTAGCGA

1425

255 260 265 270 275  
Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala

AmpR

GAGATAGGTGCCTCACTGATTAAGCATTGGTAACGTGTCAGACCAAGTTTACTCATATATACTTTAGATTGATTTA  
CTCTATCCACGGAGTGACTAATTCGTAACCATTGACAGTCTGGTTCAAATGAGTATATATGAAATCTAACTAAAT

1500

280 285  
Glu Ile Gly Ala Ser Leu Ile Lys His Trp

AmpR

AAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAATCCCTTAACGT  
TTTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCA

1575

GAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGC  
CTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTTCTAGAAGAACTCTAGGAAAAAAGACGCG

1650

ori

GTAATCTGCTGCTTGCAAACAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACT  
CATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAACGGCCTAGTTCTCGATGGTTGA

1725

ori

CTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGC  
GAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCG

1800

ori

CACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGT  
GTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCA

1875

ori

GGCGATAAGTCGTGTCTTACCGGGTTGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACG  
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1950

ori

GGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGA  
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2025

ori

GAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGC  
CTTTCGCGGTGCGAAGGGCTTCCCTCTTCCGCTGTCCATAGGCCATTGCGCGTCCCAGCCTTGTCTCTCGCG

2100

ori

ACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGT  
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2175

ori

CGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTG  
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2250

ori

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2325

TTTGAGTGAGCTGATACCGCTCGCCGACGCCGAACGACCGAGCGCAGCGAGTCAAGTGAAGGAGGAAGCGGAAGAG  
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2400

CGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCGCAATGGTGCCTCTCAGTACAATCT  
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2475

bom

GCTCTGATGCCGCATAGTTAAGCCAGTATACACTCCGCTATCGCTACGTGACTGGGTTCATGGCTGCGCCCGACA  
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2550

bom

CCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGT  
GGGCGGTTGTGGGCGACTGCGCGGGACTGCCCGAACAGACGAGGGCCGTAGGCGAATGTCTGTTTCGACACTGGCA

2625

CTCCGGGAGCTGCATGTGTAGAGGTTTTACCGTTCATACCGAAACGCGCGAGGCAGCTGCGGTAAGCTCATC  
GAGGCCCTCGACGTACACAGTCTCCAAAAGTGGCAGTAGTGCTTTGCGCGCTCCGTCGACGCCATTTTCGAGTAG

2700

\* Leu Asn Glu Gly Asp Asp Gly Phe Arg Ala Leu Cys Ser Arg Tyr Leu Glu Asp  
rop

AGCGTGGTTCGTGAAGCGATTACAGATGTCTGCCTGTTTCATCCGCGTCCAGCTCGTTGAGTTTCTCCAGAAGCGT  
TCGCACCAGCACTTCGCTAAGTGTCTACAGACGGACAAGTAGGCGCAGGTCGAGCAACTCAAAGAGGTCTTCGCA

2775

rop

Ala His Asp His Leu Ser Glu Cys Ile Asp Ala Gln Glu Asp Ala Asp Leu Glu Asn Leu Lys Glu Leu Leu Thr

TAATGTCTGGCTTCTGATAAAGCGGGCCATGTTAAGGGCGGTTTTTCTCTGTTTGGTCACTGATGCCTCCGTGTA  
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2850

20 15 10 5 1  
Leu Thr Gln Ser Arg Ile Phe Arg Ala Met Asn Leu Ala Thr Lys Glu Gln Lys Thr Met  
rop

AGGGGGATTTCTGTTCATGGGGGTAATGATACCGATGAAACGAGAGAGGATGCTCACGATACGGGTTACTGATGA  
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2925

TGAACATGCCCGGTTACTGGAACGTTGTGAGGGTAAACAACCTGGCGGTATGGATGCGGCGGGACCAGAGAAAAAT  
ACTTGTACGGGCCAATGACCTTGCAACACTCCCATTTGTTGACCGCCATACCTACGCCGCCCTGGTCTCTTTT

3000

CACTCAGGGTCAATGCCAGCGCTTCGTTAATACAGATGTAGGTGTTCCACAGGGTAGCCAGCAGCATCCTGCGAT  
GTGAGTCCCAGTTACGGTGCAGCAAGCAATTATGTCTACATCCACAAGGTGTCCCATCGGTGCTCGTAGGACGCTA

3075

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3150

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3225

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3300

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3375

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3450

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3525

GACGATAGTCATGCCCGCGCCACCAGGAGCTGACTGGGTTGAAGGCTCTCAAGGGCATCGGTGAGATCC  
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3600

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3675

360 355  
Gln Gly Ser Glu Leu Arg Ser Val Gln Arg  
lacI

GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCCAGGGTGGTTTTTC  
CACGGTCGACGTAATTACTTAGCCGGTTGCGCGCCCTCTCCGCCAAACGCATAACCCGCGGTCCACCAAAAAG

3750

350 345 340 335 330  
Ala Leu Gln Met Leu Ser Asp Ala Leu Ala Arg Pro Ser Ala Thr Gln Thr Asn Pro Ala Leu Thr Thr Lys Arg  
lacI

TTTTACCAGTGAGACGGGCAACAGCTGATTGCCCTTACCAGCCTGGCCCTGAGAGAGTTGCAGCAAGCGGTCCA  
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3825

325 320 315 310 305  
Lys Val Leu Ser Val Pro Leu Leu Gln Asn Gly Lys Val Ala Gln Gly Gln Ser Leu Gln Leu Leu Arg Asp Val  
lacI

CGCTGGTTTGCCCCAGCAGGCGAAAATCCTGTTTGTGGTGGTTAACGGCGGGATATAACATGAGCTGTCTTCGG  
GCGACCAAACGGGGTCTGTCGCTTTTAGGACAAACTACCACCAATTGCCGCCCTATATTGTAICTCGACAGAAGCC

3900

300 295 290 285 280  
Ser Thr Gln Gly Leu Leu Arg Phe Asp Gln Lys Ile Thr Thr Leu Pro Pro Ile Tyr Cys Ser Ser Asp Glu Thr  
lacI



GGTTCACCACGCGGGAAACGGTCTGATAAGAGACACCGGCATACTCTGCGACATCGTATAACGTTACTGGTTTCA  
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4725

25 Asn Val Val Arg Ser Val Thr Gln Tyr Ser Val Gly Ala Tyr Glu Ala Val Asp Tyr Leu Thr Val Pro Lys Met

lacI

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4800

lacI promoter

lacI

TGTCCGGGATCTCGACGCTCTCCCTTATGCGACTCCTGCATTAGGAAGCAGCCCAGTAGTAGGTTGAGGCCGTTG  
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4875

lacI promoter



