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375

Glu Ser Phe Arg Pro⁶⁰ Glu Glu Arg Phe⁶⁵ Pro Met Met Ser Thr⁷⁰ Phe Lys Val Leu Leu⁷⁵ Cys Gly Ala Val Leu Ser⁸⁰

AmpR

CCGTATTGACGCCGGGCAAGAGCAACTCGGTGCGCCGATACACTATTCTCAGAATGACTTGGTTGAGTACTCACC
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450

Arg Ile Asp Ala⁸⁵ Gly Gln Glu Gln Leu⁹⁰ Gly Arg Arg Ile His Tyr⁹⁵ Ser Gln Asn Asp¹⁰⁰ Leu Val Glu Tyr Ser¹⁰⁵ Pro

AmpR

AGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAA
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525

Val Thr Glu Lys His¹¹⁰ Leu Thr Asp Gly¹¹⁵ Met Thr Val Arg Glu Leu¹²⁰ Cys Ser Ala Ala¹²⁵ Ile Thr Met Ser Asp¹³⁰ Asn

AmpR

CACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCCTTTTTTGCACAACATGGGGGA
GTGACGCCGGTTGAATGAAGACTGTTGCTAGCCTCCTGGCTTCCTCGATTGGCGAAAAACGTGTTGTACCCCT

600

Thr Ala Ala Asn¹³⁵ Leu Leu Leu Thr Thr¹⁴⁰ Ile Gly Gly Pro Lys¹⁴⁵ Glu Leu Thr Ala Phe¹⁵⁰ Leu His Asn Met Gly¹⁵⁵ Asp

AmpR

TCATGTAECTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCAGAT
AGTACATTGAGCGGAAGTAGCAACCCTTGGCCTCGACTTACTTCGGTATGGTTTGCTGCTCGCACTGTGGTGCTA

675

His Val Thr Arg¹⁶⁰ Leu Asp Arg Trp Glu¹⁶⁵ Pro Glu Leu Asn Glu¹⁷⁰ Ala Ile Pro Asn Asp¹⁷⁵ Glu Arg Asp Thr Thr¹⁸⁰ Met

AmpR

GCCTGTAGCAATGGCAACAACGTTGCGCAAACATTAACCTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATT
CGGACATCGTTACCGTTGTTGCAACGCGTTTGATAATTGACCGCTTGATGAATGAGATCGAAGGGCCGTTGTTAA

750

Pro Val Ala Met¹⁸⁵ Ala Thr Thr Leu Arg¹⁹⁰ Lys Leu Leu Thr¹⁹⁵ Gly Glu Leu Leu Thr²⁰⁰ Leu Ala Ser Arg²⁰⁵ Gln Gln Leu

AmpR

AATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGC
TTATCTGACCTACCTCCGCCTATTTCAACGTCCTGGTGAAGACGCGGAGCCGGGAAGGCCGACCGACCAATAACG

825

Ile Asp Trp Met²¹⁰ Glu Ala Asp Lys Val²¹⁵ Ala Gly Pro Leu Leu Arg²²⁰ Ser Ala Leu Pro Ala²²⁵ Gly Trp Phe Ile²³⁰ Ala

AmpR

TGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCG
ACTATTTAGACCTCGGCCACTCGCACCCAGAGCGCCATAGTAACGTCGTGACCCCGGTCTACCATTCTGGGAGGGC

900

Asp Lys Ser Gly²³⁵ Ala Gly Glu Arg Gly²⁴⁰ Ser Arg Gly Ile Ile²⁴⁵ Ala Ala Leu Gly Pro Asp²⁵⁰ Gly Lys Pro Ser²⁵⁵ Arg

AmpR

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ATAGCATCAATAGATGTGCTGCCCTCAGTCCGTTGATACCTACTTGCTTTATCTGTCTAGCGACTCTATCCACG

975

Ile Val Val Ile²⁶⁰ Tyr Thr Thr Gly Ser²⁶⁵ Gln Ala Thr Met Asp²⁷⁰ Glu Arg Asn Arg²⁷⁵ Gln Ile Ala Glu Ile Gly²⁸⁰ Ala

AmpR

CTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACCTTCATTT
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1050

Ser Leu Ile Lys His²⁸⁵ Trp

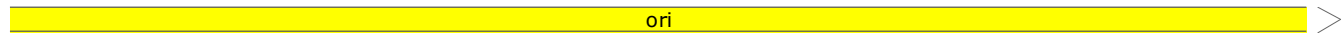
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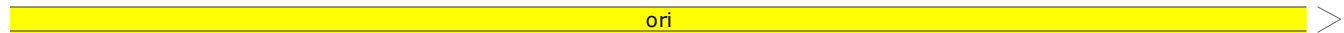
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EcoRV

GCCTTTTGCTCACATGTTCTTTCCGATATCATTGG 3' 1835
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