

5' HPRT vector Map.mpd (1 > 9912) Site and Sequence

Enzymes : 47 of 242 enzymes (Filtered)

Settings: Linear, Certain & Uncertain Sites, Standard Genetic Code



AATTCAAGATAATCAAGGAAAAATGAGAGGCAACTATTTTAGACTGATTACTTTTATAAAATAAATAAGCTCAGCTTAGCCAGATATAAGCAA
TTAAGTTCTATTAGTTCTTTTTACTCTCCGTTGATAAAATCTGACTAATGAAAAATTTTTATTTATTCGAGTCAATCGGTCTATATTCGTT

MUSTYR1 5'flank & promoter

Sspl

TATTCTGAGTTCTGAAGAAAAATTTTTGACAAAATGAGTTCTATAAATGTTATTGTCTACTTATGATCTCTAAATACAACAGGCTTGTATTCA
ATAAGACTCAAGACTTCTTTTTAAAACTGTTTTACTCAAGATATTTACAATAACAGATGAATACTAGAGATTTATGTTGTCCGAACATAAGT

MUSTYR1 5'flank & promoter

Xbal

GAATCTAGATGTTTCATGACCTTTATTCATAAGAGATGATGATTCTTGATACTACTTCTCATTTGCAAATTCGAATTATTATTAATTTTCATA
CTTAGATCTACAAAGTACTGGAAATAAGTATTCTCTACTACATAAGAACTATGATGAAGAGTAAACGTTTAAGGTTAATAATAATTAAGTAT

MUSTYR1 5'flank & promoter

TCAATTAGAATAATATATCTTCCCTTCAATTTAGTTACCTCACTATGGGCTATGTACAACTCCAAGAAAAGTTAGTCATGTGCTTTGCAGAA
AGTTAATCTTATTATATAGAAGGAAGTTAAATCAATGGAGTGATACCCGATACATGTTTGAGGTTCTTTTTCAATCAGTACACGAAACGTCTT

MUSTYR1 5'flank & promoter

HindIII

PciI

GATAAAAGCTTAGTGTA AACAGGCTGAGAGTATTTGATGTAAGAAGGGGAGTGGTTATATAGGCTTAGCCAAAACATGTGATAGTCACTCC
CTATTTTTCGAATCACATTTTGTCCGACTCTCATAAACTACATTTCTTCCCTCACCAATATATCCAGAATCGGTTTTGTACACTATCAGTGAGG

MUSTYR1 5'flank & promoter

■ MUSTYR1 ■

XmnI

AGGGGTTGCTGGAAAAGAAGTCTGTGACACTCATTAACTATTGGTGCAGATTTTGTATGATCTAAAGGAGAAAATGTTCTTGGCTGTTTTGT
TCCCAACGACCTTTTCTTCAGACACTGTGAGTAATTGGATAACCACGTCTAAAACATACTAGATTTCTCTTTTACAAGAACCAGACAAAACA

MUSTYR1 5'flank & promoter

M F L A V L
MUSTYR1 cDNA

MUSTYR1 5'UTR

BglII

MscI

XhoI

NcoI

ATTGCCTTCTGTGGAGTTTCCAGATCTCTGATGGCCATTTTCTCGAGCCTGTGCCTCCTCTAAGAACTTGTGGCAAAGAATGCTGCCAC
TAACGGAAGACACCTCAAAGGTCTAGAGACTACCGGTA AAAAGGAGCTCGGACACGGAGGAGATTCTTGAACAACCGTTTTCTTACGACGGGTG

Y C L L W S F Q I S D G H F P R A C A S S K N L L A K E C C P
MUSTYR1 cDNA

EcoRV

CATGGATGGGTGATGGGAGTCCCTGCGGCCAGCTTTCAGGCAGAGGTTCTGCCAGGATATCCTTCTGTCCAGTGCACCATCTGGACCTCAGT
GTACCTACCCACTACCTCAGGGACGCCGGTCGAAAGTCCGCTCCAAGGACGGTCTATAGGAAGACAGGTCACGTGGTAGACCTGGAGTCA

P W M G D G S P C G Q L S G R G S C Q D I L L S S A P S G P Q
MUSTYR1 cDNA

TCCCTTCAAAGGGTGGATGACCGTGAGTCTGGCCCTCTGTGTTTTATAATAGGACCTGCCAGTGCTCAGGCAACTTCATGGGTTTTCAACT 2511
AGGGGAAGTTTTCCCCACCTACTGGCACTCAGGACCGGGAGACACAAAATATTATCCTGGACGGTCACGAGTCCGTTGAAGTACCCAAAGTTGA

F P F K G V D D R E S W P S V F Y N R T C Q C S G N F M G F N
MUSTYR1 cDNA

PspOMI
ApaI

GCGGAAACTGTAAGTTTGGATTTGGGGGCCCAAATTGTACAGAGAAGCGAGTCTTGATTAGAAGAAACATTTTTGATTTGAGTGTCTCCGAAA 2604
CGCCTTTGACATTCAAACCTAAACCCCCGGGTTAACATGTCTCTTCGCTCAGAACTAATCTTCTTTGTAAAACTAAACTCACAGAGGCTTT

C G N C K F G F G G P N C T E K R V L I R R N I F D L S V S E
MUSTYR1 cDNA

XmnI MscI

AGAATAAGTTCTTTTCTTACCTCACTTTAGCAAAACATACTATCAGCTCAGTCTATGTCATCCCCACAGGCACCTATGGCCAAATGAACAATG 2697
TCTTATTCAAGAAAAGAATGGAGTGAAATCGTTTTGTATGATAGTCGAGTCAGATACAGTAGGGGTGTCCGTGGATACCGGTTTACTTGTTAC

K N K F F S Y L T L A K H T I S S V Y V I P T G T Y G Q M N N
MUSTYR1 cDNA

EcoRV NsiI

GGTCAACACCCATGTTTAAATGATATCAACATCTACGACCTCTTTGTATGGATGCATTACTATGTGTCAAGGGACACACTGCTTGGGGGCTCTG 2790
CCAGTTGTGGGTACAAATTACTATAGTTGTAGATGCTGGAGAAACATACCTACGTAATGATACACAGTTCCCTGTGTGACGAACCCCCGAGAC

G S T P M F N D I N I Y D L F V W M H Y Y V S R D T L L G G S
MUSTYR1 cDNA

AAATATGGAGGGACATTGATTTTGGCCATGAAGCACCAGGGTTTCTGCCCTGGCACAGACTTTTCTGTTATTGTGGGAACAAGAAATTCGAG 2883
TTTATACCTCCCTGTAACATAAACCGGTACTTTCGTGGTCCCAAAGACGGAACCGTGTCTGAAAAGAACAATAACACCCTTGTCTTTAAGCTC

E I W R D I D F A H E A P G F L P W H R L F L L L W E Q E I R
MUSTYR1 cDNA

Scal

AACTAACTGGGGATGAGAACTTCACTGTTCCATACTGGGATTGGAGAGATGCAGAAAACGTGACATTTGCACAGATGAGTACTTGGGAGGTC 2976
TTGATTGACCCCTACTCTTGAAGTGACAAGGTATGACCCTAACCTCTCTACGTCTTTTGACACTGTAACGTGTCTACTCATGAACCCTCCAG

E L T G D E N F T V P Y W D W R D A E N C D I C T D E Y L G G
MUSTYR1 cDNA

GTCACCCTGAAAATCCTAACTTACTCAGCCCAGCATCCTTCTTCTCCTCCTGGCAGATCATTGTAGCAGATCAGAAGAGTATAATAGCCATC 3069
CAGTGGGACTTTTAGGATTGAATGAGTCGGGTCTAGGAAGAAGAGGAGGACCGTCTAGTAAACATCGTCTAGTCTTCTCATATTATCGGTAG

R H P E N P N L L S P A S F F S S W Q I I C S R S E E Y N S H
MUSTYR1 cDNA

AGGTTTTATGCGATGGAACACCTGAGGGACCACTATTACGTAATCCTGGAAACCATGACAAAGCCAAAACCCCAAGGCTCCCATCTTCAGCAG 3162
TCCAAAATACGCTACCTTGTGGACTCCCTGGTGATAATGCATTAGGACCTTTGGTACTGTTTCGGTTTTGGGGTCCGAGGGTAGAAGTCGTC

Q V L C D G T P E G P L L R N P G N H D K A K T P R L P S S A
MUSTYR1 cDNA

ATGTGGAATTTTGTCTGAGTTTGACCCAGTATGAATCTGGATCAATGGATAGAAGTCCCAATTTTCAGCTTTAGAAACACACTGGAAGGATTTG 3255
TACACCTTAAAACAGACTCAAACCTGGGTCATACTTAGACCTAGTTACCTATCTTGACGGTTAAAGTCGAAATCTTTGTGTGACCTTCTAAAC

D V E F C L S L T Q Y E S G S M D R T A N F S F R N T L E G F
MUSTYR1 cDNA

SphI

CCAGTCCACTCACAGGGATAGCAGATCCTTCTCAAAGTAGCATGCACAATGCCTTACATATCTTTATGAATGGAACAATGTCCCAAGTACAGG
GGTCAGGTGAGTGTCCCTATCGTCTAGGAAGAGTTTCATCGTACGTGTTACGGAATGTATAGAAATACTTACCTTGTTACAGGGTTCATGTCC

3348

A S P L T G I A D P S Q S S M H N A L H I F M N G T M S Q V Q
MUSTYR1 cDNA

GATCGGCCAACGATCCCATTTTTCTTCTTACCATGCTTTTGTGGACAGTATTTTGAACAATGGCTGCGAAGGCACCGCCCTCTTTTGAAG
CTAGCCGGTTGCTAGGGTAAAAAGAAGAAGTGGTACGAAAACACCTGTCATAAAAACTTGTACCGACGCTTCCGTGGCGGGAGAAAACCTTC

3441

G S A N D P I F L L H H A F V D S I F E Q W L R R H R P L L E
MUSTYR1 cDNA

TTTACCCAGAAGCCAATGCACCTATCGGCCATAACAGAGACTCTTACATGGTTCCTTTCATACCGCTCTATAGAAATGGTGATTTCTTCATAA
AAATGGGTCTTCGGTTACGTGGATAGCCGGTATTGTCTCTGAGAATGTACCAAGGAAAGTATGGCGAGATATCTTTACCACTAAAGAAGTATT

3534

V Y P E A N A P I G H N R D S Y M V P F I P L Y R N G D F F I
MUSTYR1 cDNA

CATCCAAGGATCTGGGATATGACTACAGCTACCTCCAAGAGTCAGATCCAGGCTTTTACAGAAATTATATTGAGCCTTACTTGAACAAGCCA
GTAGGTTCTTAGACCCTATACTGATGTCGATGGAGTTCTCAGTCTAGGTCCGAAAATGTCTTTAATACTCGGAATGAACCTTGTTCCGT

3627

T S K D L G Y D Y S Y L Q E S D P G F Y R N Y I E P Y L E Q A
MUSTYR1 cDNA

MscI
NcoI

PstI

GTCGTATCTGGCCATGGCTTCTTGGGGCAGCACTGGTGGGAGCTGTTATTGCTGCAGCTCTCTCTGGGCTTAGCAGTAGGCTATGCCTTCAGA
CAGCATAGACCCGTACCGAAGAACCCCGTCGTGACCACCCTCGACAATAACGACGTCGAGAGAGACCCGAATCGTCATCCGATACGGAAGTCT

3720

S R I W P W L L G A A L V G A V I A A A L S G L S S R L C L Q
MUSTYR1 cDNA

AGAAGAAGAAGAAGAAGCAACCCAGGAGGAAAGGCAGCCACTCCTCATGGACAAAGACGACTACCACAGCTTGCTGTATCAGAGCCATCTGT
TCTTCTTCTTCTTCTTCTTGGGTCTCCTTTCCGTCCGTGAGGAGTACCTGTTTCTGCTGATGGTGTGCAACGACATAGTCTCGGTAGACA

3813

K K K K K K Q P Q E E R Q P L L M D K D D Y H S L L Y Q S H L
MUSTYR1 cDNA

AvrII

SpeI

GAACATCCTAGGAAACAGAGTGGGACTGAAAGGTTTTACCTCACTCGACCTATTTGTTGGTGTCTTACAAATTTAACTAGTATAAAACATA
CTTGATAGGATCCTTTGTCTCACCCCTGACTTTCCAAAATGGAGTGAGCTGGATAAACAACCACAAAGATGTTTAAATTTGATCATATTTTGTAT

3906

MUSTYR1 pA signal

GACCATAGCTGTTTGGCTTTTTTTCAGACCCATGTTTTTTCCTAAGTCTAGTTTCTAAGAAATGACTGGGATTTGCTAAAATATATATATAT
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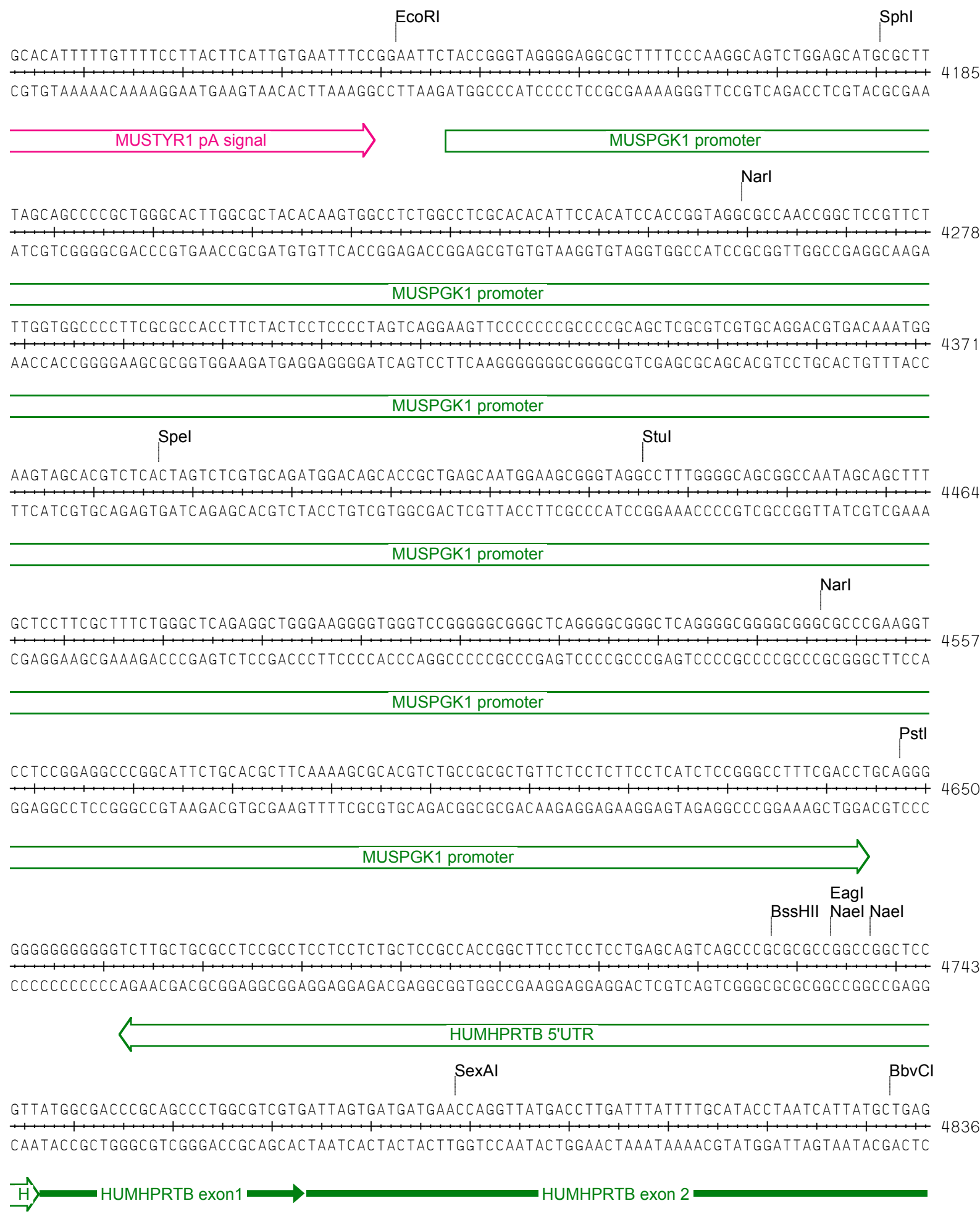
3999

MUSTYR1 pA signal

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TATTTATTATTGAATGATTATCGATTTATTTTAAAGGAGAATGTTGATTAACCTCGACCAAAAATACTTACACAGAATTAATAAATTTGAACCTC

4092

MUSTYR1 pA signal





AGGCGGTGCCCCAACGTCTCTGGGCCTCTCCACTAATAACGGCTACTTCCAATTGATTGGACGCGCCATCTTGCCTGCCTTATGCATATTCAG
TCCGCCACGGGGTTGCAGGACCCCGGAGAGGTGATTATTGCCGATGAAGGTTAACTAACCTGCGCGGTAGAACGGACGGAATACGTATAAGTC

Nsil

5766

MUSPOI1 promoter

CGGTGAACTGAATATTCATGAACGAGGCCCGTCCCGTCCCTCCCTCTTCCCCCACCCCGGAACCCGCTCCGGAGGACCCGAAGGGCCCCG
GCCACTTGACTTATAAGTACTTGCTCCGGGCAGGGCAGGGAGGGAGGAAGGGGGTGGGGCCTTGGGCGAGGCTCTGGGCTTCCCGGGGC

SspI

PspOMI
ApaI

5859

MUSPOI1 promoter

CCTTCATTACCGATGCGTAGGACAAACCATTTTCCCGATGTGTGTGGGGGATACTAATGAGAGACTTTAGCTGAAAATGAGCCTGAACTCCG
GGAAGTAATGGCTACGCATCTGTGGTAAAAGGGCTACACACACCCCCCTATGATTACTCTCTGAAATCGACTTTTACTCGGACTTGAGGC

5952

MUSPOI1 promoter

AAGCTGAGTAAAAATGGCCTAACTTTATCCTCCGTTCTGTAAGTCCTCGGTTTGAGTGCACGGGAAACCCGAAAGGAGGACGACAGGACCAGG
TTCGACTCATTTTTACCGGATTGAAATAGGAGGCAAGACATTCAGGAGCCAACTCACGTGCCCTTTGGGCTTCTCTCTGCTGTCTCTGGTCC

6045

MUSPOI1 promoter

AACATTCTCCTCCTCCTGTGCGTTCAGAAAGAACACCCAACCAGGGAGCCGGAGCCCTAGCGTCAACAACCTCCGCCGCGCGCTCCGTGTAG
TTGTAAGAGGAGGAGGACAGCGCAGTCTTTCTTGTGGGTGGTCCCTCGGCCTCGGGATCGCAGTTGTTGAGGCGGCGCGCGAGGCACATC

BssHII
BssHII

6138

MUSPOI1 promoter

GCCGGTGCGGGCGGCCCGTAGCGCAAGGGAGGGCGGAAAGGAAGGGGCGGGACACAAGGGCGAATCTATAAAGGGCGTCACTCAGCCAGTT
CGGCCACGCCC GCCGGGCATCGCGTTCCTCCCGCCCTTCTCTCCCGCCCTGTGTTCCCGCTTAGATATTTCCCGCAGTGAGTCGGTCAA

6231

MUSPOI1 promoter

CTCTCCTCAGAAGCGCCGAGAGCGCGACCCGGGACGGTTGGAGAAGAAGGTGGCTCCCGGAAGGGGAGAGACAACTGCCGTAACCTCTGCCG
GAGAGGAGTCTTCGCGGCTCTCGCGCTGGCCCTGCCAACCTCTTCTTCCACCGAGGGCCTTCCCCCTCTCTGTTTGACGGCATTGGAGACGGC

6324

MUSPOI1 promoter

TTCAGGATCATCGAATTCCTGCAGCCAATATGGGATCGGCCATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGC
AAGTCCTAGTAGCTTAAGGACGTGCGTTATACCCTAGCCGGTAACTTGTCTACCTAACGTGCGTCCAAGAGGCCGGCAACCCACCTCTCCG

EcoRI

PstI

EagI

6417



M G S A I E Q D G L H A G S P A A W V E R
neomycin phosphotransferase (neo)

NarI

TATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCCGGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGTTCTTTTTGTCA
ATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTTCGCGTCCCCGCGGGCCAAGAAAAACAGT

6510

L F G Y D W A Q Q T I G C S D A A V F R L S A Q G R P V L F V
neomycin phosphotransferase (neo)

PstI MscI PvuII

AGACCGACCTGTCCGGTGCCTGAATGAACTGCAGGACGAGGCAGCGGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTGC 6603
TCTGGCTGGACAGGCCACGGGACTTACTTGACGTCTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTTCGACACG

K T D L S G A L N E L Q D E A A R L S W L A T T G V P C A A V
neomycin phosphotransferase (neo)

TCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCTGTCACTCACCTTGCTCCTGCCGAGA 6696
AGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCTAGAGGACAGTAGAGTGAACGAGGACGGCTCT

L D V V T E A G R D W L L L G E V P G Q D L L S S H L A P A E
neomycin phosphotransferase (neo)

AAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATACGCTTGATCCGGCTACCTGCCATTGACCCACCAAGCGAAACATCGCATCGAGC 6789
TTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTGCTTTGTAGCGTAGCTCG

K V S I M A D A M R R L H T L D P A T C P F D H Q A K H R I E
neomycin phosphotransferase (neo)

GAGCACGTACTIONGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGC 6882
CTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTTCGGCTTGACAAGCGGTCCG

R A R T R M E A G L V D Q D D L D E E H Q G L A P A E L F A R
neomycin phosphotransferase (neo)

BssHII SphI NcoI

TCAAGGCGCGCATGCCCCGACGGCGATGATCTCGTCTGACCCATGGCGATGCTTGCTTGGCGAATATCATGGTGGAAAATGGCCGCTTTTCTG 6975
AGTTCCGCGCGTACGGGCTGCCGCTACTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGAC

L K A R M P D G D D L V V T H G D A C L P N I M V E N G R F S
neomycin phosphotransferase (neo)

NaeI RsrII

GATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAAT 7068
CTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACC GCCGCTTA

G F I D C G R L G V A D R Y Q D I A L A T R D I A E E L G G E
neomycin phosphotransferase (neo)

GGGCTGACCGCTTCTCTGCTTTACGGTATCGCCGCTCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGGGG 7161
CCCCACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAAGTCTCAAGAAGACTCCCC

W A D R F L V L Y G I A A P D S Q R I A F Y R L L D E F F
neomycin phosphotransferase (neo)

XbaI SacI BclI

ATCAATTCTCTAGAGCTCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGGCCCTCCCCCGTGCCTTCTTGACCC 7254
TAGTTAAGAGATCTCGAGCGACTAGTCGGAGCTGACACGGAAGATCAACGGTCGGTAGACAACAACGGGGAGGGGGCACGGAAGGAAGTGGG

BOVGHG H pA signal

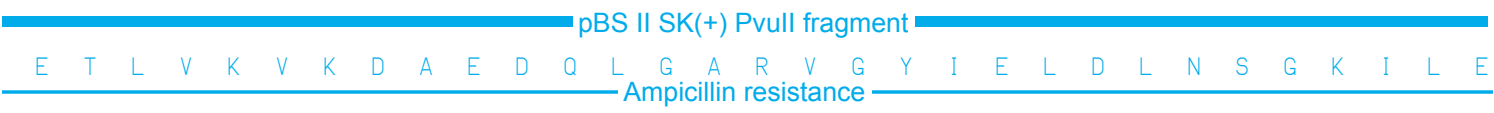
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ACCTTCCACGGTGAGGGTGACAGGAAAGGATTATTTTACTCCTTTAACGTAGCGTAACAGACTCATCCACAGTAAGATAAGACCCCCCACCCC

BOVGHG H pA signal



AGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGA
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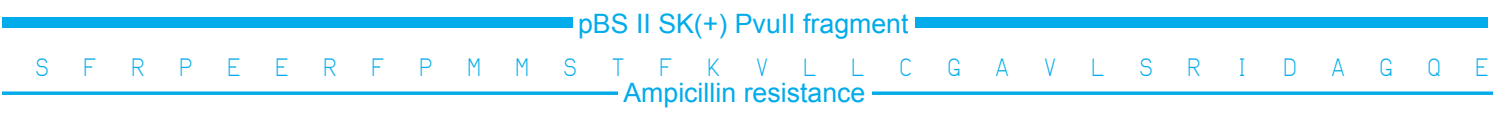
8277



XmnI

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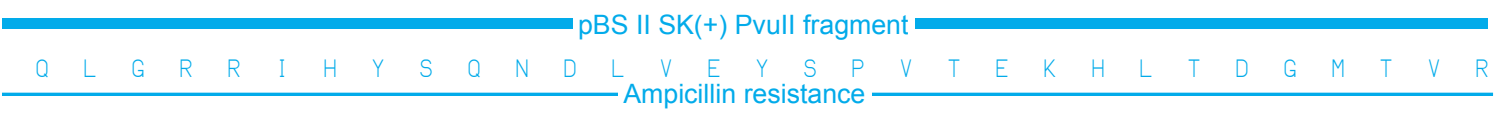
8370



Scal

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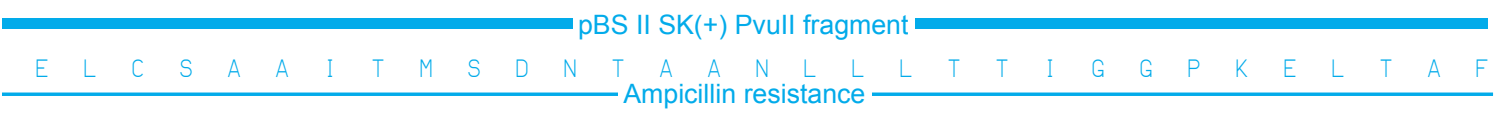
8463



PvuI

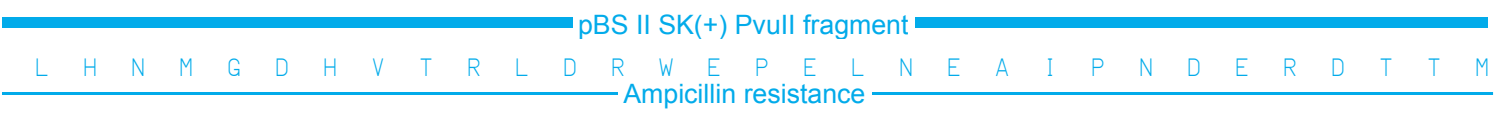
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8556



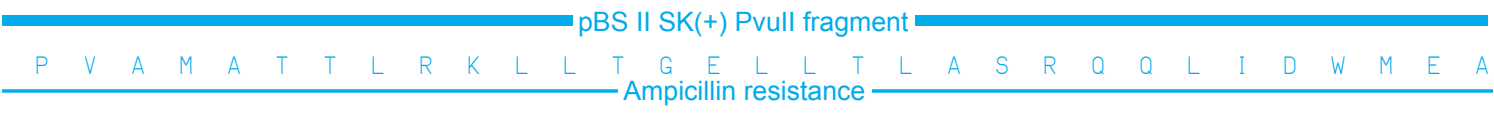
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8649



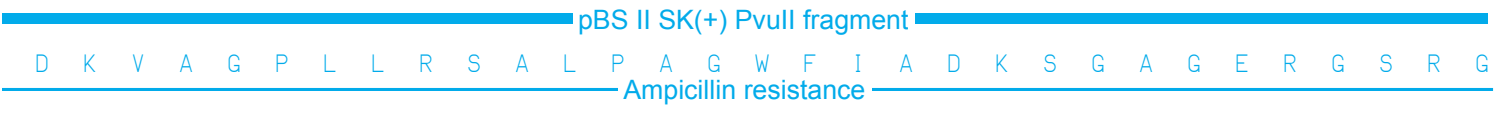
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8742



GGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGG
CCTATTTCAACGTCTCTGGTGAAGACGCGAGCCGGGAAGGCCGACCGACCAAATAACGACTATTTAGACCTCGGCCACTCGCACCCAGAGCGCC

8835



TATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAG
ATAGTAACGTCGTGACCCCGGTCTACCATTCGGGAGGGCATAGCATCAATAGATGTGCTGCCCTCAGTCCGTTGATACCTACTTGCTTTATC

8928

