

pBI101.3 TDNA Map (1 > 5352) Site and Sequence

Enzymes : 151 of 392 enzymes (Filtered)

Settings : Circular, Subrange Context, Certain & Uncertain Sites, Standard Genetic Code

Eco57 I
Bcl I
BspH I BsrB I

Dra I
Pme I

GTTTACCCGCCAATATATCCTGTCAAACACTGATAGTTTAAACTGAAGGCGGGAAACGACAATCTGATCATGAGCGGAGAATTAAGGGAG
 CAAATGGGCGGTTATATAGGACAGTTTGTGACTATCAAATTTGACTTCCGCCCTTTGCTGTTAGACTAGTACTCGCCTCTTAATTCCTC 90

Mlu113 I

TCACGTTATGACCCCGCCGATGACGCGGGACAAGCCGTTTTACGTTTGGAACTGACAGAACC GCAACGATTGAAGGAGCCACTCAGCCG
 AGTGCAATACTGGGGGCGGCTACTGCGCCCTGTTTCGGCAAATGCAAACCTTGACTGTCTTGGCGTTGCTAACTTCTCGGTGAGTCGGC 180

Uba1221 I
Uba1221 I
Bpm I

Nhe I
Ace II

Sac II

Bsu36 I

CGGGTTTCTGGAGTTTAATGAGCTAAGCACATACGTCAGAAACCATTATTGCGGTTCAAAGTCGCCTAAGGTCACTATCAGCTAGCAA
 GCCCAAAGACCTCAAATTACTCGATTCTGTGTATGCAGTCTTTGGTAATAACGCGCAAGTTTTTCAGCGGATTCCAGTGATAGTCGATCGTT 270

Ssp I

Bsp24 I

Bsg I
Bsp24 I'

ATATTTCTTGTCAAAAATGCTCCACTGACGTTCCATAAATTCCTTCGGTATCCAATTAGAGTCTCATATTCACTCTCAATCCAAATAAT
 TATAAAGAACAGTTTTTACGAGGTGACTGCAAGGTATTTAAGGGGAGCCATAGGTTAATCTCAGAGTATAAGTGAGAGTTAGGTTTATTA 360

BsaB I

BspM I

Taq II'
EagI
EagI
Eco52 I

CTGCACCGGATCTGGATCGTTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTA
 GACGTGGCCTAGACCTAGCAAAGCGTACTAACTTGTCTACCTAACGTGCGTCCAAGAGGCCGCGGAACCCACCTCTCCGATAAGCCGAT 450

neomycin

Kas I
Nar I
Ehe I
Bbe I

TGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTCCGGCTGTCAGCGCAGGGCGCCCGGTTCTTTTTGTCAAGACCGA
 ACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCGCGGGCCAAGAAAAACAGTTCTGGCT 540

neomycin

Drd I Taq II Pst I Msp20 I Bal I Msp20 I Fsp I Pvu II

CCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTGCTCGA
GGACAGGCCACGGGACTTACTTGACGTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTGCACACGAGCT

630

neomycin

Tth111 I Eco57 I

CGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAA
GCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTACAGGCCCGTCTAGAGGACAGTAGAGTGAACGAGGACGGCTCTT

720

neomycin

BsrD I BspM I EcoR124 II

AGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGA
TCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCCAACTAGGCCGATGGACGGGTAAGCTGGTGGTTTCGCTTTGTAGCGTAGCT

810

neomycin

Ear I Sap I Bce83 I

GCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACGTTCGC
CGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTTCGGCTTGACAAGCG

900

neomycin

BscE I BssH II BscE I Sph I Nco I

CAGGCTCAAGGCGCGCATGCCCGACGGCGAGGATCTCGTCTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCG
GTCCGAGTTCGCGCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGC

990

neomycin

Taq II' NgoM I Nae I Csp I Ear I Sap I

CTTTTCTGGATTATCGACTGTGGCCGGCTGGGTGTGGCGGACCCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCT
GAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCTGTATCGCAACCGATGGGCACATAACGACTTCTCGA

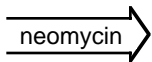
1080

neomycin

Eco57 I BssS I BsrB I
TGGCGGCGAATGGGCTGACCGCTTCTCGTGCTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTTGACGA
ACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCT 1170

neomycin

Bpl I BsrB I Bpl I Csp45 I Taq II BspM I BssS I
GTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCTTC
CAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGTCTAAAGCTAAGGTGGCGCGGAAG 1260



Bpm I NgoM I Nae I Bsp24 I' Bsp24 I EcoD XXI
TATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGTGGAGTTCTTCGCCAG
ATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCTAGAGTACGACCTCAAGAAGCGGGTC 1350

Bpm I EcoR124 I EcoR V EagI EagI Eco52 I Bpu10 I
GGATCTCTGCGGAACAGGCGGTTCGAAGGTGCCGATATCATTACGACAGCAACGGCCGACGAGCACAACGCCACGATCCTGAGCGACAATA
CCTAGAGACGCCTTGTCCGCCAGCTTCCACGGCTATAGTAATGCTGTCGTTGCCGGCTGCTCGTGTTCGGTGCTAGGACTCGCTGTTAT 1440

Bsp120 I Apa I Taq II EcoR V
TGATCGGGCCCGGCGTCCACATCAACGGCGTCCGGCGGCGACTGCCAGGCAAGACCGAGATGCACCGCGATATCTTGCTGCGTTCCGATA
ACTAGCCCGGGCCGAGGTGTAGTTGCCGAGCCGCGCTGACGGGTCCGTTCTGGCTCTACGTGGCGCTATAGAACGACGCAAGCCTAT 1530

Pvu I Bst98 I
TTTTCGTGGAGTTCGGCCACAGACCCGGATGATCCCCGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCG
AAAAGCACCTCAAGGGCGGTGCTCGGGCTACTAGGGGCTAGCAAAGTTTGTAAACGTTATTTCAAAGAATTCTAAGTTAGGACAACGGC 1620

BsaB I BspLU11 I Ppu10 I BfrB I Nsi I
GTCTTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGG
CAGAACGCTACTAATAGTATATTAAGACAACCTAATGCAATTCGTACATTATTAATTGTACATTACGTACTGCAATAAATACTCTACCC 1710

TTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGG
1800
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TGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGAGGCGGTTCCGGTGGTGGCTCTGGTCCGGTGATTTTGATTATGAAAAGATGGC
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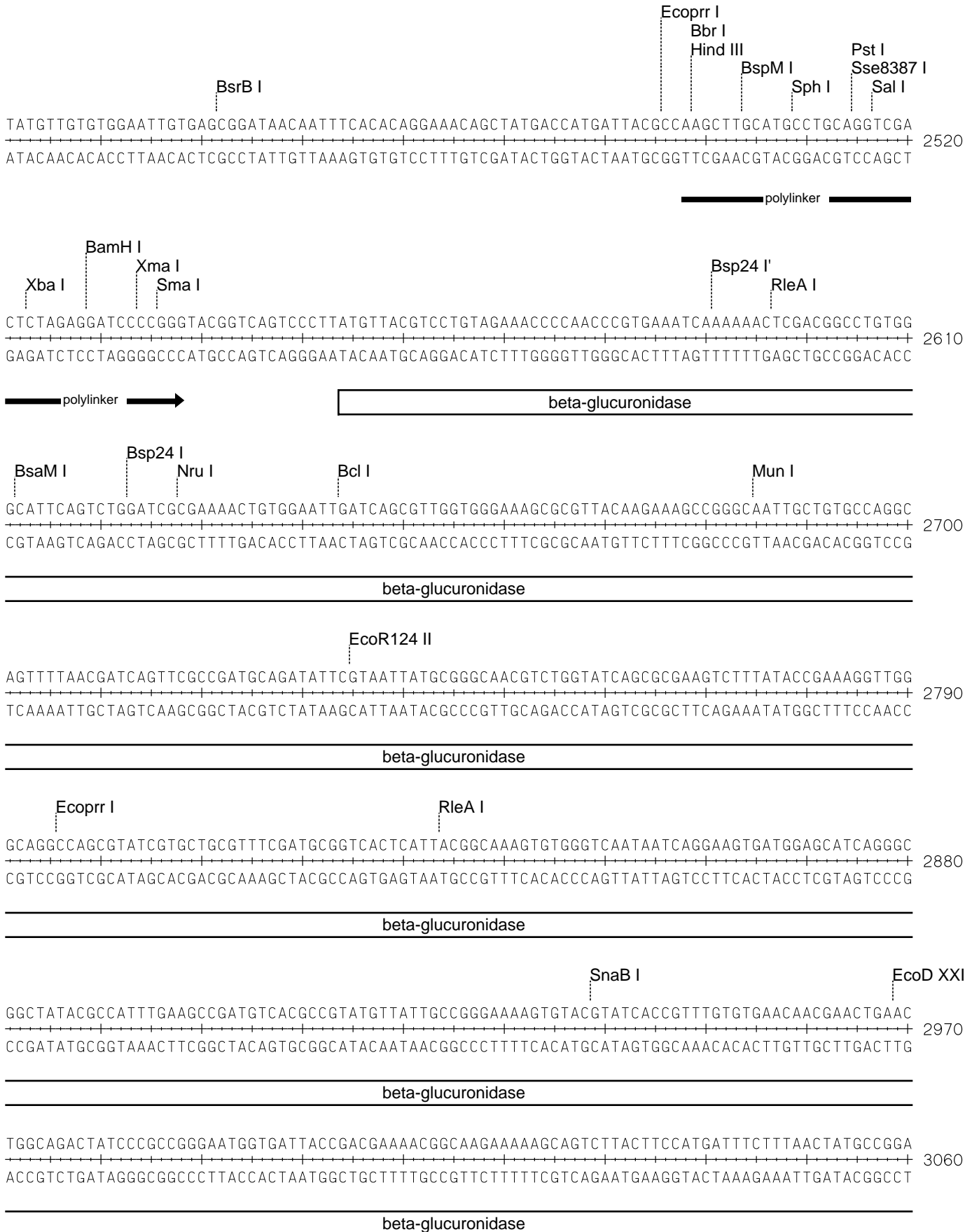
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2070
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2160
AATGCCACGACGATAGCTACCAAAGTAACCACTGCAAAGGCCGAACGATTACCATTACCACGATGACCACTAAAACGACCGAGATTAAG

CCAAATGGCTCAAGTCGGTGACGGTGATAATTCACCTTTAATGAATAATTTCCGTCAATATTTACCTTCCCTCCCTCAATCGGTTGAATG
2250
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TCGCCCTTTTGTCTTTGGCCCAATACGCAAACCGCCTCTCCCCGCGGTTGGCCGATTCATTAATGCAGCTGGCAGCAGAGGTTCCCGA
2340
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CTGGAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCAGGCTTTACACTTTATGCTTCCGGCTCG
2430
GACCTTTGCCCCGCTACTCGCGTTGCGTTAATTACACTCAATCGAGTGAGTAATCCGTGGGGTCCGAAATGTGAAATACGAAGCCGAGC



Taq II' EcoR V PshA I Mlu I
ATCCATCGCAGCGTAATGCTCTACACCACGCCGAACACCTGGGTGGACGATATCACCGTGGTGACGCATGTCGCGCAAGACTGTAACCAC 3150
TAGGTAGCGTCGCATTACGAGATGTGGTGCGGCTTGTGGACCCACCTGCTATAGTGGCACCACCTGCGTACAGCGCGTTCTGACATTGGTG

beta-glucuronidase

BspM I Msp20 I Bal I Msp20 I BsaB I
GCGTCTGTTGACTGGCAGGTGGTGGCCAATGGTGATGTCAGCGTTGAACTGCGTGATGCGGATCAACAGGTGGTTGCAACTGGACAAGGC 3240
CGCAGACAACCTGACCGTCCACCACCGGTTACCACTACAGTCGCAACTTGACGCACTACGCCTAGTTGTCCACCAACGTTGACCTGTTCCG

beta-glucuronidase

ACTAGCGGGACTTTGCAAGTGGTGAATCCGCACCTCTGGCAACCGGTGAAGGTTATCTCTATGAACTGTGCGTCACAGCCAAAAGCCAG 3330
TGATCGCCCTGAAACGTTACCACCTTAGGCGTGGAGACCGTTGGCCCACTTCCAATAGAGATACTTGACACGCAGTGTCGGTTTTCGGTC

beta-glucuronidase

EcoR V CfrA I AlwN I
ACAGAGTGTGATATCTACCCGCTTCGCGTCGGCATCCGGTCACTGGCAGTGAAGGGCCAACAGTTCCTGATTAACCACAAACCGTTCTAC 3420
TGCTCACACTATAGATGGGCGAAGCGCAGCCGTAGGCCAGTCACCGTCACTTCCCGGTTGTCAAGGACTAATTGGTGTGGCAAGATG

beta-glucuronidase

BspH I Bcg I' Bcg I EcoDR3 ApaL I Vsp I
TTTACTGGCTTTGGTTCGTCATGAAGATGCGGACTTACGTGGCAAAGGATTCGATAACGTGCTGATGGTGCACGACCACGCATTAATGGAC 3510
AAATGACCGAAACCAGCAGTACTTCTACGCCTGAATGCACCGTTTCTAAGCTATTGCACGACTACCACGTGCTGGTGCCTAATTACCTG

beta-glucuronidase

Ear I Eco57 I EcoR124 I EcoP15 I EcoP15 I
TGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCCTTACGCTGAAGAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATT 3600
ACCTAACCCCGTTGAGGATGGCATGGAGCGTAATGGGAATGCGACTTCTCTACGAGCTGACCCGTCTACTTGTACCGTAGCACCCTAA

beta-glucuronidase

Bcg I' Csp45 I Bcg I BsrG I Ear I
GATGAACTGCTGCTGTCGGCTTTAACCTCTCTTTAGGCATTGGTTTTCGAAGCGGGCAACAAGCCGAAAGAAGTGTACAGCGAAGAGGCCA 3690
CTACTTTGACGACGACAGCCGAAATTGGAGAGAAATCCGTAACCAAAGCTTCGCCCGTTGTTTCGGCTTTCTTGACATGTCGCTTCTCCGT

beta-glucuronidase

Ace III Taq II'

GTCAACGGGGAAACTCAGCAAGCGCACTTACAGCGATTAAAGAGCTGATAGCGGTGACAAAAACCACCCAAGCGTGGTGTGTGGAGT
CAGTTGCCCTTTGAGTCGTTCCGCGTGAATGTCCGCTAATTTCTCGACTATCGCGCACTGTTTTGGTGGGTTGCGACCACTACACCTCA

3780

beta-glucuronidase

ApaI I Ssp I Mlu I Mlu I

ATTGCCAACGAACCGGATACCCGTCCGCAAGTGCACGGGAATATTTCCGCACTGGCGGAAGCAACGCGTAACTCGACCCGACGCGTCCG
TAACGGTTGCTTGGCCTATGGGCAGGCGTTCACGTGCCCTTATAAAGCGGTGACCGCCTTCGTTGCGCATTTGAGCTGGGCTGCGCAGGC

3870

beta-glucuronidase

EcoD XXI
BspM I

ATCACCTGCGTCAATGTAATGTTCTGCGACGCTCACACCGATACCATCAGCGATCTCTTTGATGTGCTGTGCCTGAACCGTTATTACGGA
TAGTGGACGCAGTTACATTACAAGACGCTGCGAGTGTGGCTATGGTAGTCGCTAGAGAAACTACACGACACGGACTTGGCAATAATGCCT

3960

beta-glucuronidase

TGGTATGTCCAAAGCGGCGATTTGGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAACTGCATCAGCCGATT
ACCATACAGTTTTGCCGCTAAACCTTTGCCGTCTTTCCATGACCTTTTTCTTGAAGACCGGACCGTCTCTTTGACGTAGTCGGCTAA

4050

beta-glucuronidase

BsaB I Bsg I BsrG I BspLU11 I
Ear I

ATCATCACCGAATACGGCGTGGATACGTTAGCCGGGCTGCACTCAATGTACACCGACATGTGGAGTGAAGAGTATCAGTGTGCATGGCTG
TAGTAGTGGCTTATGCCGCACCTATGCAATCGGCCGACGTGAGTTACATGTGGCTGTACACCTCACTTCTCATAGTCACACGTACCGAC

4140

beta-glucuronidase

BsaB I

GATATGTATCACCGCGTCTTTGATCGCGTCAGCGCCGTCGTCGGTGAACAGGTATGGAATTTCCCGATTTTGGCACCCTCGCAAGGCATA
CTATACATAGTGGCGCAGAACTAGCGCAGTCGCGGCAGCAGCCACTTGTCCATACCTTAAAGCGGCTAAAACGCTGGAGCGTTCGCTAT

4230

beta-glucuronidase

Nru I
EcoP15 I Bcg I'

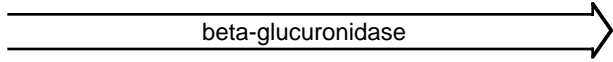
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4320

beta-glucuronidase

Bcg I Bcg I' EcoP15 I Bcg I

ATGAACTTCGGTGAAAAACCGCAGCAGGGAGGCAAACAATGAATCAACAACCTCTCTGGCGCACCATCGTCGGCTACAGCCTCGGGAATT 4410
TACTTGAAGCCACTTTTTGGCGTCGTCCCTCCGTTTGTTACTTAGTTGTTGAGAGGACCGCGTGGTAGCAGCCGATGTCGGAGCCCTTAA



EcoICR I Sac I Pvu I Bst98 I BsaB I

GCTACCGAGCTCGAATTTCCCGGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTAT 4500
CGATGGCTCGAGCTTAAAGGGGCTAGCAAGTTTGTAAACCGTTATTTCAAAGAATTCTAACTTAGGACAACGGCCAGAACGCTACTAATA

BspLU11 I Ppu10 I BfrB I Nsi I

CATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGT 4590
GTATATTAAGACAACCTAATGCAATTCGTACATTATTAATTGTACATTACGTACTGCAATAAATACTCTACCCAAAATACTAATCTCA

BscE I BssH II BscE I BscE I BssH II BscE I

CCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAAC TAGGATAAATTATCGCGCGGGTGT CATCTATGTTACT 4680
GGGCGTTAATATGTA AATTATGCGCTATCTTTTGT TTTATATCGCGCGTTTGATCTATTTAATAGCGCGGCCACAGTAGATACAATGA

EcoR I EcoDR2

AGATCGGGAATTC ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCC TGGCGTTACCCAACCTTAATCGCCTTGCAGCACATCCCC 4770
TCTAGCCCTTAAGTGACCGGCAGCAAAATGTTGCAGCACTGACCCTTTTGGGACCGCAATGGGTTGAATTAGCGGAACGTCGTGTAGGGG

Pvu II Ear I Pvu I Fsp I Bgl I Kas I Nar I Ehe I Bbe I BsrB I

CTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGCCCGCTCCTTTTCGT 4860
GAAAGCGGTCGACCGCATTATCGCTTCTCCGGGCGTGGCTAGCGGGAAGGGTTGTCAACGCGTCGGACTTACC GCGGGCGAGGAAAGCGA

NgoM I Nae I

TTCTTCCCTTCTTCTCGCCACGTTTCGCCGGCTTTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTA 4950
AAGAAGGGAAGGAAAGAGCGGTGCAAGCGGCCGAAAGGGGCAGTTTCGAGATTTAGCCCCGAGGGAAATCCCAAGGCTAAATCACGAAAT

