



PvuI (7)
SgfI (6)
MfeI (82)

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

Psp1406I (203)
PvuII (239)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCTCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **SphI (560)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTGAGCTGAGCCTTGGCACGGAAAGCCATGCAGAGAGCTTC

BstAPI (631) 1▶ M Q P W H G K A M Q R A S

601 CGAGGCCGAGCCACTGCCCAAGGTTCCGCACGGAATGCCAGGGGCGCCCGATGGATCCACCAGTCTCCGGTGCCTCCGAGGCCGCCCTGCCT

13▶ E A G A T A P K A S A R N A R G A P M D P T E S P A A P E A A L P

701 AAGGCGGAAAGTTCGGCCCCGAGGAAAGTCCGGATCCCGCAGAAAAGAGCGCCCCGACACCCAGGAGAGGCGCCCGTCCGCGCAACTGGGGCCC

47▶ K A G K F G P A R K S G S R Q K K S A P D T Q E R P P V R A T G A

NgoMIV (897)

801 GCGCAAAAAGGCCCTCAGCGCGCCAGGACACGAGCCGTCTGACGCCACGCGCCCTGGGGCAGAGGGCTGGAGCCTCTGCGGCTCGGAGGCC

80▶ R A K K A P Q R A Q D T Q P S D A T S A P G A E G L E P P A A R E P

XmaI (967)
SrfI (966)

901 GGCTCTTCCAGGGTGGTTCTTGC CGCAGAGGGGCGCGCTGCTCCACGAAGCCAAGACCTCCGCCGGCCCTGGGACGTGCCAGCCCCGGCCTG

113▶ A L S R A G S C R Q R G A R C S T K P R P P P G P W D V P S P G L

BsiWI (1020) **EcoRV (1093)**

1001 CCGGTCTCGCCCCATTCTCGTACGGAGGGATGCGGCGCTGGGCTCGAAGCTCCGGGCGGTTTTGGAGAAGTTGAAGCTCAGCCGCGATGATATCT

147▶ P V S A P I L V R R D A A P G A S K L R A V L E K L K L S R D D I

SacII (1193)

1101 CCACGGCGCGGGATGGTGAAGGGTTGTGGACCCTGCTGCTCAGACTGAAGTGC GACTCCGCGTTCAGAGGCGTGGGCTGCTGAACACC GCGGC

180▶ S T A A G M V K G V V D H L L L R L K C D S A F R G V G L L N T A A

BbrPI (1210) **PmeI (1248)**

1201 CTACTATGAGCACGTGAAGATTTCTGCACCTAATGAATTTGATGTCATGTTTAAACTGGAAGTCCCCAGAATCAACTAGAGAATATTCCAACACTCGT

213▶ Y Y E H V K I S A P N E F D V M F K L E V P R I Q L E E Y S N T R

1301 GCATATTACTTTGTGAAATTTAAAGAAATCCGAAAGAAATCCTCTGAGTCAGTTTTTGAAGGTGAAATATTATCAGCTTCTAAGATGCTGTCAAAGT

247▶ A Y Y F V K F K R N P K E N P L S Q F L E G E I L S A S K M L S K

BspHI (1451)

1401 TTAGGAAATCATTAAGGAAGAAATTAACGACATTAAGATACAGATGTCATCATGAAGAGGAAAAGAGGAGGCCCTGCTGTAACACTTCTTATTAG

280▶ F R K I I K E E I N D I K D T D V I M K R K R G G S P A V T L L I S

FspI (1574)

NheI (1555) **StuI (1569)**

1501 TGAATAATATCTGTGGATATAACCTGGCTTTGGAATCAAAAAGTAGCTGGCCTGTAGCACCAGAAAGGCTGCGCATTCAAACTGGCTTTCAGCA

313▶ E K I S V D I T L A L E S K S S W P A S T Q E G L R I Q N W L S A

SphI (1647)

1601 AAAGTTAGGAAGCAACTACGACTAAAGCCATTTTACCTGTACCCAAGCATGCAAAGGAAAGAAATGGTTTCCAAGAAGAAACATGGCGGCTATCCTTCT

347▶ K V R K Q L R L K P F Y L V P K H A K E G N G F Q E E T W R L S F

1701 CTCACATCGAAAAGGAAATTTGAACAATCATGAAAATCTAAAACGTGCTGTGAAAACAAAGAGAAATGTTGCAGGAAAGATTGTTTAAAACCTAAT

380▶ S H I E K E I L N N H G K S K T C C E N K E E K C C R K D C L K L M

PvuII (1816)

1801 GAAATACCTTTTAGAACAGCTGAAAGAAAGTTTAAAGACAAAAACATCTGGATAAATTCTTCTTATCATGTGAAAACCTGCCTTCTTTCACGTATGT

413▶ K Y L L E Q L K E R F K D K K H L D K F S S Y H V K T A F F H V C

1901 ACCCAGAACCCTCAAGACAGTCAAGTGGACCGCAAAGACTGGGCTCTGCTTTGATAACTGCGTGACATACTTTCTTCAAGTCCCTCAGGACAGAAAAAC

447▶ T Q N P Q D S Q W D R K D L G L C F D N C V T Y F L Q C L R T E K

2001 TTGAGAATTTTTATTCTGAATTCATCTATTCTAGCAACTAATTGACAAAAGAAAGAAATTTCTGACAAAGCAAATTGAATATGAAAGAAA

480▶ L E N Y F I P E F N L F S S N L I D K R S K E F L T K Q I E Y E R N

AvrII (2131) **MscI (2143)**

PshAI (2129)

2101 CAATGAGTTTCCAGTTTTTGTGAATTTGACCTAGGTCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAG

513▶ N E F P V F D E F •

HpaI (2275) **MfeI (2286)**

2201 TGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACACAACAATTGCATTCATT

2301 TTATGTTTCAGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTT

2401 TAACCTCCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCT

SapI (2553)

2501 CACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAC TAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCC

SwaI (2624)

2601 TTTTTAGTAAAATATT CAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATA

2701 TCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCGGTGTA CTCTGA

141 • N R T Y K L

SacI (2885)

2801 GGGGATGAGTTCCTCAATGGTGGTTTTGACCAGTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCGCAT

134 P I L E E I T T K V L K G N M E I L V F C D P A Y D S I L E R C M

BstXI (2914)

2901 GCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACA

101 G C P S V V R I S R D V E D S Y P H R V A V I T D F D K Q G N S V

StuI (3049)

3001 GCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGG

67 A S G I A I A E A C V T V R G I Y A E I H V A S I I E G T K T R I A

BspHI (3199)

BbsI (3195)

XmnI (3191)

3101 CCGCCCCGACATGGTGCTTGTGCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTT

34 A G V H H K N D E Y L M T I K E T A V E V L E L D Q Q S I N F T K

AseI (3257)

3201 CATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTG

1 M

SacI (3314)

3301 ACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTGGAAAG

SpeI (3412)

3401 TCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCATTTGATGT

SnaBI (3540)

3501 ACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCA

NdeI (3645)

3601 GCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACC

3701 CATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTATTATTGACGTCAATGGGCGGGGTCGTTGGCGGTGAGCCAGGCGGGC

PaeI (3831)

PstI (3824)

SdaI (3823)

BspLU11I (3841)

3801 CATTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCG

3901 TTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTC

4001 CCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCTGCCGTTACCGGATACTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAG

ApaLI (4155)

4101 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGT

4201 AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTA

4301 CAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGG

4401 TAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCT

EagI (4591)

Pacl (4571) SwaI (4580) **NotI (4590)**

4501 TTGATCTTTTCTACGGGCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCA

4601 TAAAAATCTTTATTTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAACAAAACGAAACAAAACAACTA

4701 GCAAATAGGCTGTCCCAGTCAAGTGACAGGTGCCAGAACATTTCTCTATCGAA