



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

MfeI (82)

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGCC

PvuII (239)

Bsu36I (291)

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)

AgeI (552) 501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGCAGACAATTTTTCGCTCCATGATGCGTTATCTGG

NcoI (560) 1 M A D N F S L H D A L S G

BstXI (645) 601 GTCTGAAACCCAAACCTCAAGGATGGCCTGGCGCATGGGGAAACAGCCTGCTGGGACAGGGGCTACCCAGGGGCTTCTATCCTGGGGCTACCCC

XmaI (697)

13 S G N P N P Q G W P G A W G N Q P A G A G G Y P G A S Y P G A Y P

701 GGGCAGCACCCCGGGGCTTATCCTGGACAGGCACCTCCAGGCGCTACCTGGAGCACCTGGAGCTTATCCCGGAGCACCTGCACCTGGAGTCTACC

47 G Q A P P G A Y P G Q A P G A Y P G A P G A Y P G A Y P G V Y

801 CAGGGCCACCCAGCGGCCCTGGGGCTACCCATCTTCTGGACAGCCAAGTGCACCGGAGCCTACCTGCCACTGGCCCTATGGCGCCCTGCTGGGCC

80 P G P P S G P G A Y P S S G Q P S A T G A Y P A T G P Y G A P A G P

SphI (947)

901 ACTGATTGTGCCTTATAACCTGCCTTTGCCTGGGGAGTGGTGCCTCGCATGCTGATAACAATTCTGGGCACGGTGAAGCCCAATGCAACAGAATTGCT

113 L I V P Y N L P L P G G V V P R M L I T I L G T V K P N A N R I A

1001 TTAGATTTCAAAGAGGAATGATGTTGCCTTCCACTTTAACCACGCTTCAATGAGAACAACAGGAGAGTCATTGTTGCAATACAAAGCTGGATAATA

147 L D F Q R G N D V A F H F N P R F N E N R R V I V C N T K L D N

XmnI (1146) 1101 ACTGGGAAGGGAAGAAAGACAGTCGGTTTTCCATTTGAAAGTGGGAAACATTCAAATACAAGTACTGGTTGAACCTGACCATTCAAGTTGCAGT

180 N W G R E E R Q S V F P F E S G K P F K I Q V L V E P D H F K V A V

1201 GAATGATGCTCACTTGTGACGTACAATCATCGGGTAAAAAACTCAATGAAATCAGCAAACCTGGAAATTTCTGGTGACATAGACCTCACCAGTGCTTCA

213 N D A H L L Q Y N H R V K K L N E I S K L G I S G D I D L T S A S

MscI (1334)

NheI (1328) 1301 TATACCATGATATAATCTGAAAGGGGCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAA

247 Y T M I •

HpaI (1466) 1401 TGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTC

MfeI (1477)

EcoRI (1562)

1501 AGGTTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCATAAATACAGCATAGCAAACTTTAACCTCCA

1601 AATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCGAGCTCACCTTCTT

SapI (1744)

1701 TCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTAGTA

SspI (1801) 1801 AAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGT

SwaI (1815)

1901 TTAGTAGTTGACTTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGA

141 N R T Y K L P I L

SacI (2076)

2001 GTTCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGG

131 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 G C P

BstXI (2105)

2101 GCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCA

98 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 A S G

StuI (2240)

2201 ATGGCAATGGCTTTCAGCAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGA

64 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 A G V

BbsI (2386)

XmnI (2382) 2301 CATGGTGCTTGTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTTCATGGTGGC

31 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 M

2401 **AseI (2448)**
CTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCAC

2501 **SacI (2505)**
TAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGA

2601 **SpeI (2603)**
TTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAA

2701 **SnaBI (2731)**
ACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCA

2801 **NdeI (2836)**
TTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGT

2901 CAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCG

3001 **PstI (3015)** **SdaI (3014)** **PacI (3022)** **BspLU11I (3032)**
TAAGTTATGTAACGCCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCAT

3101 AGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAACCAGGCGTTTCCCCTGGAA

3201 GCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGAAGCGTGGCGTTTCTCATAGCTCACGCTG

3301 **ApaLI (3346)**
TAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTAACTATCGT

3401 CTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCT

3501 TGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTG

3601 ATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTT

3701 **EagI (3782)** **PacI (3762)** **SwaI (3771)** **NotI (3781)**
TCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATC

3801 TTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAG

3901 GCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA