



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGCC
PvuII (239)
301 GCCATCCACGCCGGTTGAGTTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACC
Bsu36I (291)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspHI (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTATCATGACCAAGCCGGTAGCAAGGGCGGGAACCTCCGCGA
1► M T K A G S K G G N L R D
601 CAAGCTGGACGGCAATGAGTGGACCTGAGCCTCAGCGACCTGAAGTCCCCGTCAGGAGCTGGCTGCACCTCCAAGGCTACGGTATTGGATCTG
13► K L D G N E L D L S L S D L N E V P V K E L A A L P K A T V L D L

ScaI (715) 701 TCCTGCAATAAACTGAGTACTTCCGTCGGATTTCTGTGGCCTCACACACCTGGTAAAGCTGGACCTCAGCAAGAACAAGCTGCAGCAGCTACCCGCGAG
47► S C N K L S T L P S D F C G L T H L V K L D L S K N K L Q Q L P A
PstI (781)
801 ACTTTGGCCGCTGGTAACTTACAGTTCGATCTCCTCAACAACAGGCTGGTACCCTGCCTGTCAGCTTGGCCAGCTCAAGAATCTGAAGTGGCT
80► D F G R L V N L Q H L D L L N N R L V T L P V S F A Q L K N L K W L

Tth111I (922) **MscI (932)**
901 GGATCTGAAGACAATCCCTGGACCTGTCTGGCCAAGGTGGCAGTGTATTGCTTGGATGAGAAGCAATGTAAGCAGTGTGCAAAACAAGGTGTTACAG
113► D L K D N P L D P V L A K V A G D C L D E K Q C K Q C A N K V L Q

BsrBI (1033)
1001 CACATGAAGCCGTGCAGGCAGATCAGGAACGAGAGCGGCGCCGGCTGGAAGTGGAGCGAGAGGCAGAGAAGAAGCGTGAGGCCAAGCAGCAAGCTA
147► H M K A V Q A D Q E R E R Q R R L E V E R E A E K K R E A K Q Q A

SgrAI (1153)
1101 AGGAAGCGAAGGAGCGCGAGCTGCGGAAGCGGGAGAAGGCGGAGGAGAAGGAGCGCCGGCGGAAGGAGTATGACGCTCAGAAGCGTCCAAGCGGGAGCA
180► K E A K E R E L R K R E K A E E K E R R R K E Y D A Q K A S K R E Q
1201 AGAGAAGAAGCCTAAGAAAGAGGCAAAACAGGCCCCGAAATCGAAGTCTGGCTCTGCTCCTCGCAAGCCACCACCCCGAAAACACACTCGCTCCTGGGCT
213► E K K P K K E A N Q A P K S K S G S R P R K P P P R K H T R S W A
1301 GTGCTGAAGGTGTTGCTGTTGCTCCTGCTGTGTGTAGCAGGAGGGCTGGTGTATGCCGGGTGACAGGGCTGCACCAGCAGCCCTCTGCACCAGCG
247► V L K V L L L L L L L C V A G G L V V C R V T G L H Q Q P L C T S

MscI (1492)
1401 TGAACACCATCTACGACAATGCGGTCCAGGGCCTGCGTCATCATGAGATCCTCCAGTGGTCTGCAAACCGACTCCCAGCAGTGAGCTAGCTGGCCAGA
280► V N T I Y D N A V Q G L R H H E I L Q W V L Q T D S Q Q •
1501 CATGATAAGATACATTGATGAGTTTGGACAAACCACAACACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTGTA

HpaI (1624) **MfeI (1635)**
1601 ACCATTATAAGCTGCAATAAACCAAGTTAACAAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAA

EcoRI (1720)
1701 ACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAG
1801 GCATAGGCATCAGGGGCTGTTGCCAATGTCATTAGCTGTTTGACGCTCACCTTCTTCATGGAGTTAAGATATAGTGATTTTCCAAGGTTTGAAC

SapI (1902) 1901 TAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAAT
SspI (1959) **SwaI (1973)**
2001 AAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAA
2101 TTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAA
141◀ • N R T Y K L P I L E E I T T K V L K G N M E I

SacI (2234) **BstXI (2263)**
2201 TGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGTCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGG
117◀ L V F C D P A Y D S I L E R C M G C P S V V R I S R D V E D S Y P

StuI (2398)
2301 GTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAACAGACAGAGTACCCTGCCAATGTAG
84◀ H R V A V I T D F D K Q G N S V A S G I A I A E A C V T V R G I Y
2401 GCCTCAATGTGGACAGCAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTGTTGTCTCATAGAGCATGGTATCTTCTCAG
50◀ A E I H V A S I I E G T K T R I A A G V H H K N D E Y L M T I K E T

BbsI (2544)
XmnI (2540)

2501 TGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATG
17 A V E V L E L D Q Q S I N F T K M

AseI (2606) SacI (2663)

2601 CCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCT

SpeI (2761)

2701 ACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGICAAAACAACTCCCATTGACGTCAATGGGGTGG

SnaBI (2889)

2801 AGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGT

NdeI (2994)

2901 ACTGCCAAGTAGGAAAGTCCCATAAAGTCACTGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATG

3001 ATACACTTGATGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGCTC

PacI (3180)
PstI (3173)
SdaI (3172) BspLU11I (3190)

3101 ATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGC
CCTGCAGGTTAATTAAGAACATGTGAGC

3201 AAAAGGCCAGAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCA

3301 AGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGCTTACCG

3401 GATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGG

ApaLI (3504)

3501 CTGTGTGCACGAACCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATGCCACTGGCA

3601 GCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTAT

3701 TTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGT

3801 TTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAA

EagI (3940)
PacI (3920) SwaI (3929) NotI (3939)

3901 GGGATTTTGGTCATGGCTAGTTAATTAACATTTAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATC

4001 GTAACAAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTAT

4101 CGAA