



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC
PvuII (239)
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **SphI (560)** **Bsp120I (587)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTGAGTGGTGTCTCCTCCTGATCTGGGCCAGGGCT
M R W C L L L I W A Q G L
601 GAGGCAGGCTCCCTCGCCTCAGGAATGATGACAGGCACAATAGAAAACAGGGGAACATTTCTGCAGAGAAAGTGGCTCTATCATTTACAATGTCAC
13 R Q A P L A S G M M T G T I E T T G N I S A E K G G S I I L Q C H

PshAI (723) **MscI (758)**
701 CTCTCCTCCACCACGGCAAGTGACCCAGGTCAACTGGGAGCAGCAGGACCAGTCTTGGCCATTTGTAATGCTGACTTGGGGTGGCACATCTCCCAT
47 L S S T T A Q V T Q V N W E Q Q D Q L L A I C N A D L G W H I S P

ScaI (875)
801 CCTTCAAGGATCGAGTGGCCCCAGTCCCGCCTGGGCTCACCTCCAGTCGCTGACCGTGAACGATACAGGGGAGTACTTCTGCATCTATCACACCTA
80 S F K D R V A P G P G L G L T L Q S L T V N D T G E Y F C I Y H T Y

NcoI (995)
901 CCCTGATGGGACGTACTGAGGAAATCTTCTGGAGTCTTAGAAAGCTCAGTGGCTGAGCACGGTCCAGGTTCCAGATTCCATTGCTTGGAGCCATG
113 P D G T Y T G R I F L E V L E S S V A E H G A R F Q I P L L G A M

XmnI (1073) **BstEII (1090)**
1001 GCCCGACGCTGGTGGTATCTGCACAGCAGTATCGTGGTGGTGCCTGACTAGAAAAGAAAGCCCTCAGAATCCATTCTGTGGAAGGTGACCTCA
147 A A T L V V I C T A V I V V V A L T R K K K A L R I H S V E G D L

PvuII (1109) **BstAPI (1168)**
1101 GGAGAAAATCAGCTGGACAGGAGGAATGGAGCCCCAGTGTCCCTCACCCCCAGGAAGCTGTGTCCAGGCAGAAGCTGCACCTGCTGGGCTCTGTGGAGA
180 R R K S A G Q E E W S P S A P S P P G S C V Q A E A A P A G L C G E
1201 GCAGCGGGGAGAGGACTGTGCCAGTGCATGACTACTTCAATGTCCTGAGTTACAGAAGCCTGGGTAAGTGCAGTCTTTCACAGAGACTGGTTAGCAA
213 Q R G E D C A E L H D Y F N V L S Y R S L G N C S F F T E T G •

MscI (1325)
NheI (1319)
1301 CCAGAGGCATCTTCTGGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCAACTAGAATGCAGTGAAAAAATGCTTTATT

HpaI (1457) **MfeI (1468)**
1401 TGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTATTATGTTTCAGGTTCCAGG

EcoRI (1553)
1501 GGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCC
1601 TCTACTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGT

SapI (1735) **SspI (1792)**
1701 TTAAGATATAGTGTATTTTCCCAAGTTTGAAGTCTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAAATTTCA

SwaI (1806)
1801 GAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTT
1901 GGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAA
141 • N R T Y K L P I L E E I

SacI (2067) **BstXI (2096)**
2001 TGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCAC
128 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 S V V
2101 CCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCCTGCTCACAGCAGACCAATGGCAATG
95 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 I A I

StuI (2231)
2201 GCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGT
61 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 H H K

BbsI (2377) **XmnI (2373)**
2301 TGTTCCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATA
28 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 (2439)** **SacI (2496)**
GTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGC

2501 **SpeI (2594)**
TCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTTACTAGT

2601
CAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCA

2701 **SnaBI (2722)**
TCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGGGGCCATTTACCGTC

2801 **NdeI (2827)**
ATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAA

2901
GTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGCGGGTCTTGGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATG

3001 **PacI (3013)** **SdaI (3005)** **BspLU11I (3023)**
TAACGCCCTGCAGGTTAAITAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGC

3101
CCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCG

3201
TGCCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCT

3301 **ApaLI (3337)**
CAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC

3401
AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGT

3501
GGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA

3601
ACAAACCACCGCTGGTAGCGGTGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGG

3701 **EagI (3773)** **PacI (3753)** **Swal (3762)** **NotI (3772)**
TCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAAATATCTTTATTTTC

3801
ATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCC

3901
AGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA