



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCGCTACCTGAGGGCC

301 GCCATCCAGCGCGGTTGAGTCGCGTTTCTGCCGCCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGTCAAGTGCAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555)
AgeI (552) **MluI (591)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCATTGGCTTGGCTCCTGAGAGGGCAGCCCCACGCGTGTCT
1▶ M A L A P E R A A P R V L

BstAPI (629)
601 GTTCGGAGAGTGGCTCCTTGGAGAGATCAGCAGCGGCTGCTATGAGGGGTGTCAGTGGCTGGACGAGGCCCGCACCTGTTTCCGCGTGCCTGGAAGCAC
13▶ F G E W L L G E I S S G C Y E G L Q W L D E A R T C F R V P W K H

StuI (743)
701 TTCGCGCGCAAGGACCTGAGCGAGGCGGACGCGCATCTTCAAGGCTGGGCTGTGGCCCGCGCAGGTGGCCGCTAGCAGCAGGGGAGGTGGCCCGC
47▶ F A R K D L S E A D A R I F K A W A V A R G R W P P S S R G G G P

NgoMIV (826) **MluI (865)** **SandI**
801 CCCCCGAGGTGAGACTGCGGAGCGCGCGGCTGGAAAACCAACTTCCGCTGCGCACTGCGCAGCAGCGTCTGCTTCTGATGCTGCGAGATAACTCGGG
80▶ P P E A E T A E R A G W K T N F R C A L R S T R R F V M L R D N S G

EagI (905) **DraIII (916)**
901 GGACCCGGCCGACCCGACAAGGTGTACGCGCTCAGCCGGGAGCTGTGCTGGCGAGAAGGCCAGGCACGACCAGACTGAGGCAGAGGCCCGCGAGCT
113▶ D P A D P H K V Y A L S R E L C W R E G P G T D Q T E A E A P A A

DraIII (1010) **SfiI (1019)**
1001 GTCCACACCACAGGGTGGGCCCCAGGGCCATTCTGGCACACACATGCTGGACTCCAAGCCCCAGGCCCTCCCTGCCCCAGCTGGTGACAAGG
147▶ V P P P Q G G P P G P F L A H T H A G L Q A P G P L P A P A G D K

Tth111I (1152)
1101 GGGACCTCCTGCTCCAGGCAGTGAACAGAGCTGCCTGGCAGACCATCTGCTGACAGCGTCATGGGGGAGAGTCCAGTCCCAACCAAGGCTCCTGGAGA
180▶ G D L L L Q A V Q Q S C L A D H L L T A S W G A D P V P T K A P G E

XmaI (1297)
1201 GGGACAAGAAGGGCTTCCCTGACTGGGCGCTGTGCTGGAGGCCAGGGCTCCCTGCTGGGAGCTGTACGGGTGGGAGTAGAGACGCCCCAGCCCC
213▶ G Q E G L P L T G A C A G G P G L P A G E L Y G W A V E T T P S C C

1301 GGGCCCCAGCCCGGCGGACTAACGACAGGCGGCGGCCAGGATCCCCGACCCAGGCAGAGCCGTACCTGTCACCCTCCCAAGCGCTGCACCG
247▶ G P Q P A A L T T G E A A A P E S P H Q A E P Y L S P S P S A C T

BsrGI (1442)
1401 CGGTGCAAGAGCCAGCCAGGGGCGCTGGACGTGACCATATGATAAAGGCCGACCGTGTGCTGAGAAGGTGGTGGGACCCGAGCTGCACGTTCT
280▶ A V Q E P S P G A L D V T I M Y K G R T V L Q K V V G H P S C T F L

1501 ATACGGCCCCCAGACCCAGCTGTCCGGCCACAGACCCCGAGGAGTATCCCCAGCCCTGCCGAGCTCCCGGACCAGAAGCAGCTGCGCTACAG
313▶ Y G P P D P A V R A T D P Q Q V A F P S P A E L P D Q K Q L R Y T

BbrPI (1615)
1601 GAGAACTGCTGCGGCACGTGGCCCTGGGTTGCACTGGAGCTTCCGGGGCCACAGCTGTGGCCCGCGCATGGGCAAGTGAAGGTGACTGGGAGG
347▶ E E L L R H V A P G L H L E L R G P Q L W A R R M G K C K V Y W E

1701 TGGCGGACCCCGAGGCTCCGCCAGCCCTCCACCCAGCCTGCTGCTGCTCGGAAGTGTGACACCCCATCTTCCAGTTCAGAGTCTTCTTCAAGA
380▶ V G G P P G S A S P S T P A C L L P R N C D T P I F D F R V F F Q E

EcoRI (1807) **SapI (1896)**
1801 GCTGGTGAATTCCGGGACGCGCGCTGGCTCCCCACGCTATACCATCTACCTGGGCTTCCGGGACGACCTGTGAGTGGGAGGCCAAGGAGAAG
413▶ L V E F R A R Q R R G S P R Y T I Y L G F G Q D L S A G R P K E K

ApaLI (1939)
1901 AGCCTGGTCTGGTGAAGCTGGAACCTGGCTGTGCCGAGTGCACCTAGAGGGCAGCAGCGTGAGGGTGTGCTTCCCTGGATAGCAGCAGCCTCAGCC
447▶ S L V L V K L E P W L C R V H L E G T Q R E G V S S L D S S S L S

BamHI (2071)
2001 TCTGCCTGTCCAGCGCAACAGCCTCTATGACGACATCGAGTGTCTTCTTATGGAGCTGGAGCAGCCCGGATCCTATCCCTATGATGTGCCAGACTA
480▶ L C L S S A N S L Y D D I E C F L M E L E Q P A G S Y P Y D V P D Y

NdeI (2111) **NheI (2168)** **MscI (2174)**
2101 TGCTGGCTATCCATATGATGTTCTGATTATGCTGGATACCCTTATGATGTGCCAGACTATGCCTAAAGCTAGCTGGCCAGACATGATAAGATACATTGA
513▶ A G Y P Y D V P D Y A G Y P Y D V P D Y A •

2201 TGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAAT

HpaI (2306) **MfeI (2317)**
2301 AAACAAGTTAACAACAACATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTA

EcoRI (2402)
2401 TGGAAATCTAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTGAACTCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCT

SapI (2584)

2501 GTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTCTCTTCATTTCTTTA

SspI (2641) SwaI (2655)

2601 TGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGC

2701 AGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCG

2801 AGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAG

141 • N R T Y K L P I L E E I T T K V L K G N M E I L V F C D P

2901 GAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAAT

111 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 H R V A V I

StuI (3080)

3001 GGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCA

78 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 A E I H V A

3101 GAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCGACATGGTGGTGTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCT

44 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 A V E V L E

BspHI (3230)

AseI (3288)

3201 CCAGATCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAA

11 L D Q Q S I N F T K M

3301 AACAGCGTGGATGGCGTCTCCAGC TATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAA

SpeI (3443)

3401 TGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTGATTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCG

SnaBI (3571)

3500 TGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAG

NdeI (3676)

3600 TCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTACCCTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTG

3700 CCAAGTGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGG

SdaI (3854) PacI (3862) BspLU11I (3872)

3800 GCGGGGTCGTTGGGCGTCAAGCAGGCGGGCCATTTACCCTAAGTTATGTAACGCTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGCCAGCAAAA

3898 GGCCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGA

3998 AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCT

ApaLI (4186)

4098 TTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTCCAAGCTGGGCTGTGTGCACGAACC

4198 CCCCCTTACAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAC

4298 AGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTC

4398 TGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTGTGTTGAAGCAGCAGAT

4498 TACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATG

EagI (4622)

PacI (4602) SwaI (4611) NotI (4621)

4598 GCTAGTTAATTAACATTTAAATC AGCGGCCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACATAACATACGC

4698 TCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA