



125

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

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) **AgeI (552)** **BspHI (560)**
501 TCTGTTTGTCCGCGTTACAGATCCAAGCTGTGACCGGGCGCTA CCTGAGATCACCGGTATCATGAGGTTCCGCATCTACAAACGGAAGTGCTAATCCT

601 GACGCTCGTGGTGGCCGCTGCGGCTTCTGCTCTGGAGCAGCAATGGGCGACAAAGGAAGAACGAGGCCCTCGCCACCGTTGCTGGACGCCGAACCC
13▶ T L V V A A C G F V L W S S N G R Q R K N E A L A P P L L D A E P
1▶ M R F R I Y K R K V L I L

EagI (714)
NotI (713)
NgoMIV (709)
NaeI (709) **SacII (717)**
701 GCGCGGGTGGCGGGCGCGGTGGGACCACCCCTCTGTGGTGTGGGCATCCGAGGGTCTCCAACGTGTCGGCGGTTCCCTGGTCCCGCGGTCC
47▶ A R G A G G R G G D H P S V A V G I R R V S N V S A A S L V P A V

AgeI (833)
Acc65I (830) **Bsu36I (870)** **Bsp120I**
801 CCCAGCCGAGGGCGGACAACCTGACGCTGCGGTACCGGTCCCTGGTGTACCAGCTGAACCTTGTGATCAGACCCTGAGGAATGTAGATAAGGCTGGCACCTG
80▶ P Q P E A D N L T L R Y R S L V Y Q L N F D Q T L R N V D K A G T W

XmaI (905) **BstBI (974)** **Tth111I (994)**
901 GGCCCCCGGAGCTGGTGTGGTGTCCAGGTGCATAACCGCCGAATACCTCAGACTGCTGCTGGACTCACTTCGAAAAGCCAGGAATTGACAAC
113▶ A P R E L V L V V Q V H N R P E Y L R L L L D S L R K A Q G I D N

SalI (1029)
1001 GTCCTCGTCATCTTTAGCCATGACTTCTGGTCGACCGAGATCAATCAGCTGATCGCCGGGTGAATTTCTGTCCGGTTCTGCAGGTGTTCTTTCTTTCA
147▶ V L V I F S H D F W S T E I N Q L I A G V N F C P V L Q V F F P F
1101 GCATTTCAGTTGTACCCTAACGAGTTTCCAGGTAGTGACCTAGAGATTGTCCAGAGACCTGCCGAAGAAATGCCGCTTTGAAATTTGGGGTGCATCAATGC
180▶ S I Q L Y P N E F P G S D P R D C P R D L P K N A A L K L G C I N A
1201 TGAGTATCCCGACTCTTCGGCCATTATAGAGAGGCCAAATTTCCAGACCAAACATCACTGGTGGTGGAAAGCTGCATTTTGTGGGAAAGAGTGAAA
213▶ E Y P D S F G H Y R E A K F S Q T K H H W W W K L H F V W E R V K
1301 ATTCTTCGAGATTATGCTGGCCTTATACTTTTCTAGAAGAGGATCACTACTTAGCCCGAGACTTTTACCATGCTTCAAAAAGATGTGGAACTGAAGC
247▶ I L R D Y A G L I L F L E E D H Y L A P D F Y H V F K K M W K L K
1401 AGCAAGAGTGCCTGAATGTGATGTTCTCTCCCTGGGACCTATAGTGCCAGTGCAGTTTCTATGGCATGGTGACAAGGTAGATGTAAAACCTGGAA
280▶ Q Q E C P E C D V L S L G T Y S A S R S F Y G M A D K V D V K T W K

ApaLI (1560)
1501 ATCCACAGAGCACAATATGGGTCTAGCCTTGACCCGGAATGCCTATCAGAAGCTGATCGAGTGCACAGACACTTTCTGTACTTATGATGATTATAACTGG
313▶ S T E H N M G L A L T R N A Y Q K L I E C T D T F C T Y D D Y N W

BstXI (1636) **AvrII (1669)** **Ppu10I (1699)**
1601 GACTGGACTTTCAATACTTGACTGTATCTTGCTTCCAAAATCTGGAAAGTGTGGTTCCTCAAATTCCTAGGATCTTTCATGCTGGAGACTGTGGTA
347▶ D W T L Q Y L T V S C L P K F W K V L V P Q I P R I F H A G D C G

BspLU11I (1775)
1701 TGCATCACAAGAAAACCTGTAGACCATCCACTCAGAGTGCCAAAATTGAGTCACTCTTAAATAATAACAACAATACATGTTTCCAGAAAACCTAACTAT
380▶ M H H K K T C R P S T Q S A Q I E S L L N N N K Q Y M F P E T L T I
1801 CAGTAAAAGTTTACTGTGGTAGCCATTTCCACCTAGAAAAATGGAGGGTGGGAGATATTAGGGACCATGAACCTGTAAAAGTTATAGAAAGCTG
413▶ S E K F T V V A I S P P R K N G G W G D I R D H E L C K S Y R R L

MscI (1941)
NheI (1935)
1901 CAGTAAAATCACAGTTACAAAAGCAGCTCTTCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTG
447▶ Q •

HpaI (2073) **MfeI (2084)**
2001 AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACCTGATTGCTTTT

EcoRI (2169)
2101 ATGTTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTTCAAATAACAGCATAGCAAACTTTA

2201 ACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCA

2301 CCTCTTTTCATGGAGTTTAAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTGCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTT

SspI (2408) **SwaI (2422)**
2401 TTTAGTAAAATTTAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATC

2501 CCCAGTTTGTAGTTGGACTTAGGGAACAAAGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGG
141▶ • N R T Y K L

SacI (2683)

2601 GGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCATGC
133 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 G

BstXI (2712)

2701 CACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGC
100 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 A

StuI (2847)

2801 AGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCC
67 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 (2997)

XmnI (2989)

2901 GCCCCGACATGGTGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCA
33 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 M

AseI (3055)

3001 TGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGC T TATCTGAC
0

SacI (3112)

3101 GGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTGTACGACATTTTGGAAAGTC

SpeI (3210)

3201 CCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCAGCCATTGATGTA

SnaBI (3338)

3300 CTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCTACTGGGCATAATGCCAG

NdeI (3443)

3400 GCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACC

3500 ATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCC

SdaI (3621) PacI (3629) BspLU11I (3639)

3600 ATTTACCGTAAGTTATGTAACGCC T G C A G G T T A A T T A A G A A C A T G T G A G C A A A A G G C C A G C A A A A G G C C A G G A A C C G T A A A A A G G C C G T T G C T G G C

3698 GTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACGAGCGTTT

3798 CCCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCGACCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATA

ApaI (3953)

3898 GCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCTTATCCGG

3998 TAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCT

4098 ACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTG

4198 GTAGCTCTTGATCCGGCAACAAACACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCC

EagI (4389)

PacI (4369) SmaI (4378) NotI (4388)

4298 TTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCA

4398 ATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAACGAAACAAACAAACT

4498 AGCAAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTATCGAA