



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82)

101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCACTCTACGCTTTTGTTCGTTT

BspLU11I (560)
AgeI (552) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCAACATGTGGGAGGCTCAGTTCCTGGGCTTGTGTTTCTGCA

601 GCCGCTTTGGGTGGCTCCAGTGAAGCCTCTCCAGCCAGGGGCTGAGGTCCCGGTGGTGTGGGCCAGGAGGGGCTCCTGCCAGCTCCCTGCAGCCCC
13▶ P L W V A P V K P L Q P G A E V P V V W A Q E G A P A Q L P C S P

701 ACAATCCCCCTCCAGGATCTCAGCCTTCTGCAAGAGCAGGGGTCACTTGGCAGCATCAGCCAGACAGTGGCCCGCCGCTGCCGCCCGGCCATCCCC
47▶ T I P L Q D L S L L R R A G V T W Q H Q P D S G P P A A A P G H P

SapI (731) SandI (873) **FspI (887)**
801 TGGCCCCGGCCCTACCCGCGCGCCCTCCTCCTGGGGCCAGGCCCGCCGCTACACGGTGTGAGCGTGGGTCCCGGAGGCTCGCAGCGGGAG
80▶ L A P G P H P A A P S S W G P R P R R Y T V L S V G P G G L R S G R

EagI (936) **BssHII (981)** **SgrAI (990)**
901 GCTGCCCCGAGCCCCGCTCCAGCTGGATGAGCGCGCCGGCAGCGCGGGACTTCTCGTATGGCTGCGCCAGCCCGCGCGCGGACGCCGGCGAG
113▶ L P L Q P R V Q L D E R G R Q R G D F S L W L R P A R R A D A G E

ApaLI (1012) **SacII (1007)** Bsu36I (1017)
1001 TACCGCGCCGGTGCACCTCAGGGACCGGCCCTCTCCTGCCGCTCCGTCTGCGCCTGGGCCAGGCCCTCGATGACTGCCAGCCCCCAGGATCTCTCA
147▶ Y R A A V H L R D R A L S C R L R L R L G Q A S M T A S P P G S L

Tth11I (1108) **BspEI (1169)**
1101 GAGCCTCCGACTGGTCAATTTGAACTGCTCCTCAGCCGCCCTGACCGCCAGCCTCTGTGATTGGTTCGGAAACCGGGCCAGGCGGAGTCCCTGT
180▶ R A S D W V I L N C S F S R P D R P A S V H W F R N R G Q G R V P V

HindIII (1230) **NcoI (1259)**
1201 CCGGAGTCCCCCATCACCCTAGCGGAAAGCTTCTCTTCCGCAAGTCAAGCCATGGACTCTGGGCCCTGGGGCTGCATCCTCACCTACAGA
213▶ R E S P H H L A E S F L F L P Q V S P M D S G P W G C I L T Y R

1301 GATGGCTTCAACGCTCCATCATGTATAACCTCACTGTCTGGGTCTGGAGCCCCAAGTCCCTTGACAGTGTACGCTGGAGCAGGTTCCAGGGTGGGGC
247▶ D G F N V S I M Y N L T V L G L E P P T P L T V Y A G A G S R V G

Tth11I (1428) **SandI (1426)**
1401 TGCCTGCCGCTGCCTGCTGGTGTGGGACCCGGTCTTCTCACTGCCAAGTGGACTCCTCCTGGGGAGGCCCTGACCTCCTGGTACTGGAGACAA
280▶ L P C R L P A G V G T R S F L T A K W T P P G G G P D L L V T G D N

XcmI (1533) **XcmI (1592)**
1501 TGGCGACTTTACCCTTCGACTAGAGGATGTGAGCCAGGCCAGGCTGGGACTACACCTGCCATATCCATCTGCAGGAACAGCAGCTCAATGCCACTGTC
313▶ G D F T L R L E D V S Q A Q A G T Y T C H I H L Q E Q Q L N A T V

BamHI (1645) **BstEII (1637)**
1601 ACATTGGCAATCATCAGTACTCCAAATCCTTTGGGTACCTGGATCCCTGGGGAAGTGTCTTGTGAGGTGACTCCAGTATCTGGACAAGAACGCT
347▶ T L A I I T V T P K S F G S P G S L G K L L C E V T P V S G Q E R

1701 TTGTGTGGAGCTCTTGGACACCCATCCAGAGGAGTTTCTCAGGACTTGGCTGGAGGCACAGGAGCCAGCTCCTTTCCAGCCTTGGCAATGCCA
380▶ F V W S S L D T P S Q R S F S G P W L E A Q E A Q L L S Q P W Q C Q

BstXI (1866)
1801 GCTGTACCAGGGGAGAGGCTTCTTGGAGCAGCAGTGTACTTACAGAGCTGTCTAGCCAGGTGCCAACGCTCTGGGAGAGCCCCAGGTGCCCTCCA
413▶ L Y Q G E R L L G A A V Y F T E L S S P G A Q R S G R A P G A L P

BbsI (1985)
1901 GCAGGCCACCTCCTGCTGTTTCTACCCCTTGGTGTCTTCTCTGCTCCTTTGGTACTGGAGCCTTTGGCTTTCACCTTTGGAGAAGACAGTGGCGAC
447▶ A G H L L L F L T L G V L S L L L L V T G A F G F H L W R R Q W R

2001 CAAGACGATTTTCTGCCTTAGAGCAAGGATTACCCTCCGAGGCTCAGAGCAAGATAGAGGAGCTGGAGCAAGAACCAGGAGCCGGAGCCGGAGCCGGA
480▶ P R R F S A L E Q G I H P P Q A Q S K I E E L E Q E P E P E P E P E

MscI (2194) **BglII (2161)** **NheI (2188)**
2101 ACCGAGCCCGAGCCCGAGCCCGAGCCCGAGCAGCTCTGACCTGGAGCTGAGGCAGCCAGCAGATCTCAGCAGCCAGTCCAAATAAAGCTAGCTGGCCA
513▶ P E P E P E P E P E Q L •

2201 GACATGATAAGATACATTGATGAGTTTGACAAACCAACTAGAATGCAAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTG

HpaI (2326) MfeI (2337)
2301 TAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTA

EcoRI (2422)
2401 AAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATA

2501 AGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGTTTGA

SapI (2604) SspI (2661) SmaI (2675)

2601 ACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATTCCAGAAATAATTTAAATACATCATTGCAATGAAA

2701 ATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGA

2801 AATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTC
141 • N R T Y K L P I L E E I T T K V L K G N M E

BstXI (2965)

2901 AATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAG
118 I 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

3001 GGTGCCTGACAGCCACAATGGTGTCAAAGTCTTGCCTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGT
84 P 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

3101 AGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTGGTCTGATGGCCGCCGACATGGTGTCTGTGTCTCATAGAGCATGGTATCTTCTC
51 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

BbsI (3246) XmnI (3242)

3201 AGTGGCGACTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTA
18 T A V E V L E L D Q Q S I N F T K M

AseI (3308)

3301 TGCCGATGATTAATTGTCAAACACAGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGC

SpeI (3463)

3401 CTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGT

SnaBI (3591)

3501 GGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGAT

NdeI (3696)

3601 GTACTGCCAAGTAGGAAAGTCCATAAGTTCATGTAAGTGGGCATAATGCCAGGCGGGCCATTTACCGTATTGACGTCAATAGGGGGCGTACTTGGCATA

3701 TGATACACTTGATGTAAGTGGCAGTTTACCATAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACG

PacI (3882) SdaI (3874) BspLU11I (3892)

3801 TCATTATTGACGTCAATGGGCGGGGCTGTTGGGCGTTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGA
CCTGCAGGTTAATTAAGAACATGTGA

3901 GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCT

4001 CAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTCCGACCTGCCGCTTAC

4101 CGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTCCGCTCAAGCTG

ApaLI (4206)

4201 GGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGGTCCAACCCGTAAGACACGACTTATCGCCACTGG

4301 CAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGT

4401 ATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCACCGCTGGTAGCGGTGGTTTTTTT

4501 GTTTGAAGCAGCAGATTACGCGCAGAAAAAAGATCTCAAGAAGATCTTTGATCTTTTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTT

EagI (4642) PacI (4622) SmaI (4631) NotI (4641)

4601 AAGGGATTTTGGTATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAA

4701 TCGTAACATAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCT

4801 ATCGAA