



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGTCGTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGCC
PvuII (239)
Bsu36I (291)
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

BspEI (558)
501 TCTGTTCTGCCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGCTCCGACAAACATGTGGACCTTGGCACTGTGGGCATTCTCTTT
1▶ M W T L A L W A F S F
601 CCTCTGCAAATTCAGCCTGGCAGTCTGCCGACTAAGCCAGAGAACATTTCTGCGTCTTTACTTCGACAGAAATCTGACTTGCCTGGAGACCAGAG
11▶ L C K F S L A V L P T K P E N I S C V F Y F D R N L T C T W R P E
701 AAGGAAACCAATGATACCAGCTACATTGTGACTTTGACTTACTCCTATGGAAAAGCAATTATAGTGACAATGCTACAGAGGCTTCATATTCTTTCCCC
45▶ K E T N D T S Y I V T L T Y S Y G K S N Y S D N A T E A S Y S F P
801 GTTCTGTGCAATGCCCCAGACATCTGCAGTGTGAAGTACAAGCTCAAATGGAGATGGTAAAGTTAAATCTGACATCACATATTGGCATTAAATCTC
78▶ R S C A A M P P D I C S V E V Q A Q N G D G K V K S D I T Y W H L I S
901 CATAGAAAAACCGAACCACTATAATTTAAGTGTGAATCCAATTTGTAATAGAATGTTCCAGATACAATGGAAACCGCGTGGAAAGACTCGTGGTTT
111▶ I A K T E P P I I L S V N P I C N R M F Q I Q W K P R E K T R G F

SphI (1010)
NsiI (1008) 1001 CCTTTAGTATGCATGCTTCGGTTCAGAACTGTCAACAGTAGCCGCTGGACGGAAGTCAATTTTGAAAAGTGTAAACAGGTCTGCAACCTCACAGGACTTC
PshAI (1047)
145▶ P L V C M L R F R T V N S S R W T E V N F E N C K Q V C N L T G L
1101 AGGCTTTCACAGAATATGCTCGCTCAGATTGACTTCAATGACTCAAGATATTGGAGCAAGTGGAGCAAAGAAGAAACAGAGTACTATGGAGGA
178▶ Q A F T E Y V L A L R F R F N D S R Y W S K W S K E E T R V T M E E

EcoRI (1226)
1201 AGTTCACATGCTCGGACTGTGGAGAATTCTGGAACAGCAGACATGAACGGAGACAGGAAGGTGCGATTGCTGTGGAAGAAGGCAAGAGGAGCCCC
211▶ V P H V L D L W R I L E P A D M N G D R K V R L L W K K A R G A P

ScaI (1331)
1301 GTCTTGAGAAAAACATTTGGCTACCACATACAGTACTTTGCAGAGAACAGCACTAACCTCACAGAGATAAAACAACATCACCACCAGCAGTATGAACTGC
245▶ V L E K T F G Y H I Q Y F A E N S T N L T E I N N I T T Q Q Y E L

BamHI (1475)
DraIII (1417) 1401 TTCTGATGAGCCAGGCACACTCTGTGTCGGTACTTCTTTAATTCTTTGGCAAGTCCCAAGAGACCATCCTGAGGATCCCAGATGTCCATGAGAAGAC
Bsu36I (1470)
278▶ L L M S Q A H S V S V T S F N S L G K S Q E T I L R I P D V H E K T

SphI (1517)
1501 CTCCAGTACATTAAGAGCATGAGGCTACATAGCCGAGCCCTGTTGGTGGTGAAGTGGCAAAGCTCCATTCTGCGGTGGACACTTGGATAGTGGAG
311▶ F Q Y I K S M Q A Y I A E P L L V V N W Q S S I P A V D T W I V E
1601 TGGCTCCAGAAGCTGCCATGTCGAAGTTCCTGCCCTTCTGGGAATCTGTGTCTCAGGTCACGAACTGGACCATCGAGCAAGATAAACTAAAACCTT
345▶ W L P E A A M S K F P A L S W E S V S Q V T N W T I E Q D K L K P

HindIII (1766)
1701 TCACATGCTATAATATATCAGTGTATCCAGTGTGGGACACCAGTGGAGAGCCGATTCAATCCAAGCTTATGCCAAAGAAGGAACTCCATTAAGG
378▶ F T C Y N I S V Y P V L G H R V G E P Y S I Q A Y A K E G T P L K G
1801 TCCTGAGACCAGGTGGAGAACATCGGTCTGAGGACAGCCAGATCACATGGAAGGAGATTCTAAGAGTGTAGGAATGGATTTATCAACAATTACAT
411▶ P E T R V E N I G L R T A T I T W K E I P K S A R N G F I N N Y T

HpaI (1942)
1901 GTATTTTACCAAGCTGAAGGTGGAAAAGAACTCCAAGACTGTTAACTCTCATGCCCTGCAGTGTGACCTGGAGTCTCTGACACGAAGGACCTTTATA
445▶ V F Y Q A E G G K E L S K T V N S H A L Q C D L E S L T R R T S Y

Acc65I (2032) 2001 CTGTTTGGGTGATGGCCAGCACCAGAGCTGGAGGTACCAACGGGTGAGAATAAACTCAAGACATTTGCAATCAGTGTGTTGAAATGTCCTTCTAAC
Tth11I (2061)
478▶ T V W V M A S T R A G G T N G V R I N F K T L S I S V F E I V L L T

AgeI (2168)
2101 ATCTCTAGTTGGAGGAGCCTTCTTCTACTTAGCATAAAACAGTACTTTTGGCCTCAGAAAGCCAAACCGTTGACTCCCCTGTGTTGTCCTGATGTT
511▶ S L V G G G L L L L S I K T V T F G L R K P N R L T P L C C P D V

Tth11I (2293)
2201 CCAACCCTGCTGAAAGTAGTTTAGCCACATGGCTCGGAGATGGTTTCAAGAAGTCAAATATGAAGGAGACTGGAACTCTGGGACACAGAAGACGTGG
545▶ P N P A E S S L A T W L G D G F K K S N M K E T G N S G N T E D V

SacII (2321)
2301 TCCTAAAACCATGTCCTCCGCGGATCTCATTGACAAGCTGGTAGTGAACCTTTGAGAATTTCTGGAAGTAGTTTGGACAGGAAAGCTGGAAGGG
578▶ V L K P C P V P A D L I D K L V V N F E N F L E V V L T E E A G K G
2401 TCAGGCGAGCATTTTGGGAGGAGAAGCGAATGAGTATGTGACCTCCCGTCTAGGCCCGACGTTCCCCAGGGAAAAGTTTAAAGAGCCITCCATTTTA
611▶ Q A S I L G G E A N E Y V T S P S R P D G P P G K S F K E P S I L

BbrPI (2529)

2501 ACTGAGGTTGCTTCTGAAGACTCCCACAGCACGTGTTCCAGAATGGCGGACGAGGCGTACTCAGAATTGGCCAGGCAGCCTTCGTCTTCTGTCCAGAGTC
645▶ T E V A S E D S H S T C S R M A D E A Y S E L A R Q P S S S C Q S

2601 CAGGGCTATCGCCTCCCCGTGAAGACCAAGCTCAGAATCCGTATTTGAAAAATTCACTGACAACCCAGGGAATTTCTTGTGCATGAGAATATCCCAGAGCA
678▶ P G L S P P R E D Q A Q N P Y L K N S V T T R E F L V H E N I P E H

NheI (2719)

2701 CAGCAAAGGAGAAGTCTGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATT
711▶ S K G E V •

HpaI (2857) MfeI (2868)

2801 TGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAACACAACAATTGCATTCAATTTATGTTTCAGGTTTCAGG

EcoRI (2953)

2901 GGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCC

3001 TCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGT

SapI (3135) SspI (3192)

3101 TTAAGATATAGTGATTTTCCCAAGTTTGAAGTAGCTCTTCATTTCTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCA

SwaI (3206)

3201 GAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTT

3301 GGAAGTGGGAAACAAAGGAACCTTTAATAGAAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAA
141▶ • N R T Y K L P I L E E I

SacI (3467) BstXI (3496)

3401 TGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCCAC
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

3501 CCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATG
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

3601 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

3701 TGTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCAGCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATA
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

AseI (3839) SacI (3896)

3801 GTGAGTCGTATTATACTATGCGGATATACTATGCGGATGATTAATTGTCAAACACGCTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGC

SpeI (3994)

3901 TCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTTACTAGT

4001 CAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCTGAGTCAAACCGTATCCACGCCATTGATGACTGCCAAAACCGCATCA

SnaBI (4122)

4101 TCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCACTGACTGGGCATAATGCCAGGCGGGCCATTTACCGTC

NdeI (4227)

4201 ATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAA

4301 GTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGCTGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATG

PacI (4413) SdaI (4405)

4401 TAACGCCTGCAGGTTAAITAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGC

4501 CCCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTTCCCCTGGAAGCTCCCTCG

4601 TGGCTCTCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCT

ApaLI (4737)

4701 CAGTTCGGTGTAGTTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTTCCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCC

4801 AACCCGGTAAGACACGACTTATCGCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGT

4901 GGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA

5001 ACAAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACCGCGAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGG

EagI (5173) PacI (5153) SwaI (5162) NotI (5172)

5101 TCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAAATATCTTTATTTTC

5201 ATTACATCTGTGTGTTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCC

5301 AGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA