



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

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGGC
PvuII (239)
Bsu36I (291)
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspLU11I (560)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGTCAACATGTTGGATCTTCTCTTGAAAAACGTGGGTACGAC
1▶ M L D L L L E K R V G T T
BspHI [m] (660)
601 CTTGGCTGCCCAAGTCTAGCTCCGGTCCGTGAAGTTTCAAGACTGGCAGAGACTGGGATCATGAAAATGGACATGGAGGACGCTGATATGACTTTG
13▶ L A A P K S S S G S V K F Q G L A E T G I M K M D M E D A D M T L

BsrGI (727)
701 TGGACAGAGCGCGAGTTTGAAGAGAAGTGTACATACATAGTGAACGACCACCCTGGGATTCCGGCGTGACGGGGTACTTCTGTTCAAGCCGAGGCAT
47▶ W T E A E F E E K C T Y I V N D H P W D S G A D G G T S V Q A E A
801 CCTTACCAAGGAACCTGCTTTTCAAGTATGCTGCCAACACAGCAAAGAGTTATTGGCGTGGTAAGTAAGGAGTACATACCGAAGGGAACACGCTTTGG
80▶ S L P R N L L F K Y A A N N S K E V I G V V S K E Y I P K G T R F G

XcmI (993)
901 ACCCTCATCGGTGAAGTCTACACTAATGACACAGTCCCAAGAATGCCAACAGGAAGTATTTTTGGCGGATCTATCCAGAGAGGAGTTCCACCACTTC
113▶ P L I G E V Y T N D T V P K N A N R K Y F W R I Y S R E E F H H F

BsaBI (1095)
1001 ATTGATGGCTTAAATGAGGAGAAAAGCAACTGGATGCGCTACGTGAATCCAGCTCACTCTGCCGGGAGCAAAACCTGGTGCCTGTGAGAACGGGATGA
147▶ I D G F N E E K S N W M R Y V N P A H S A R E Q N L A A C Q N G M
1101 ACATCTACTTCTACACTATTAAGCCTATCCCTGCCAACAGGAACCTTGTGTGGTATTGTCGGGACTTTGCGGAGAGGCTCCACTACCTTATCCTGG
180▶ N I Y F Y T I K P I P A N Q E L L V W Y C R D F A E R L H Y P Y P G
1201 AGAGCTCACAGTGATAAATCTCACACAAACGGAAGCAACCAAGCAATACAGTAGTGAGAAAAATGAACTCTACCCAAAGAGTGTCCCAAGAGAGAG
213▶ E L T V I N L T Q T E S N P K Q Y S S E K N E L Y P K S V P K R E
1301 TACAGCGTGAAGAAATCTAAAACCTGACTCCAATCCCTCCAAAGGAAGGACATCACCCTTCAACATTTACCCCTTACTTTAGAAAAGGACATGG
247▶ Y S V K E I L K L D S N P S K R K D I Y R S N I S P F T L E K D M
1401 ATGGCTTTCGAAAAATGGGAGCCCCGACATGCCCTTCTACCTCGGGTGGTTATCCTATCCGGGCACCTCTGCCAGAAGACTTTTTGAAAGCGTCCT
280▶ D G F R K N G S P D M P F Y P R V V Y P I R A P L P E D F L K A S L
1501 GGCCTATGGGATGGAGAGACCCACCTACATAACTCACAGTCCCCTCCGTCTCCACAACCTCAAGTCCCCTGCGAGCAGCAGCCCGGAGCAGAGCCTT
313▶ A Y G M E R P T Y I T H S P L P S S T T P S P P A S S S P E Q S L

StuI (1653)
1601 AAGAGCTCCAGCCCCACAGCAGCCGGGAAACACGGTGTACCCCTGGCGCCAGGCTCCCAGAACACCGGACTCCTACTCCTACTTGAATGTTTCTT
347▶ K S S S P H S S P G N T V S P L A P G L P E H R D S Y S Y L N V S

EcoO109I (1709)
1701 ATGGTTCGAGGGCTGGGCTCCTACCCTGGCTATGCACCTGCCCCACCTCCCACAGCTTTCATTCTTCTTACAATGCTCACTACCCCAAGTTCCT
380▶ Y G S E G L G S Y P G Y A P A P H L P P A F I P S Y N A H Y P K F L

BsiWI (1808) **AvrII (1879)**
1801 GTTGCCACCGTACGGCATTAGTTCCAATGGCTTGGACCCATGAACAACATCAATGGTATCAACAACCTTACGCTCTTCCCTAGGTTGTATCCCGTCTAC
413▶ L P P Y G I S S N G L S T M N N I N G I N N F S L F P R L Y P V Y
1901 AGTAACCTCCTTAGTGGCAGCAGCCTGCCTCATCCATGCTCAATCCAGCTTCCCTACCGAGTTCCTGCTACCGATGGAGCCCGGAGGCTGCTCCAC
447▶ S N L L S G S S L P H P M L N P A S L P S S L P T D G A R R L L P
2001 CGGAGCACCCAAAGAGGTGCTTATCCAGCACCCACAGTGCCTTCTCCCTTACCGGGGCTGAGCCAGCATGAAGGACGAGAGTAGTCCCCCAGCGG
480▶ P E H P K E V L I P A P H S A F S L T G A A A S M K D E S S P P S G

BbrPI (2134)
2101 ATCTCCAACGGCGGAACTGCAGCCACGTGAGAACCAACCAAGCTACCTCATCAGTGATGGCGGCCCCAGCACTGACGGAGCCATGAAT
513▶ S P T A G T A A T S E H V V Q P K A T S S V M A A P S T D G A M N
2201 CTCAATAAAAAACAAACGAAACATGACTGGTTACAAGACTTCTTCCCTTACCCTCTGAAGAAACAGAATGGCAAGATCAAGTATGAGTGAATGTCTGTGCCA
547▶ L I K N K R N M T G Y K T L P Y P L K K Q N G K I K Y E C N V C A
2301 AGACGTTCCGTCAGCTCTCAACCTGAAGTCCACCTGAGAGTGCACAGTGGAGAACGGCCTTCAAGTGCCAGACCTGCAACAAGGGTTTTACTCAGCT
580▶ K T F G Q L S N L K V H L R V H S G E R P F K C Q T C N K G F T Q L
2401 CGCCACCTGCAGAAACACTACTTGGTACACACAGGAGAGAAGCCACATGAGTGCCAGGTCTGCCACAAGAGATTTAGCAGCACAAGCAATCTCAAGACC
613▶ A H L Q K H Y L V H T G E K P H E C Q V C H K R F S S T S N L K T

BstAPI (2562)
2501 CACCTTCGATTGCATTCTGGAGAAAAACCTTACCAATGTAAGGTGTGCCCTGCCAAGTTTACGCAATTTGTGCACCTGAAGCTGCACAAGCGACTGCATA
647▶ H L R L H S G E K P Y Q C K V C P A K F T Q F V H L K L H K R L H

PvuII (2696)

BsrBI (2605) **BspI20I (2691)**

2601 CCCGGGAGCGGCCTCACAAAGTGTGCCAGTGTCAAGAGCTACATCCATCTCTGCAGCCTCAAGGTCCACCTGAAGGGCAACTGCCCTGCGGGCCCAGC
680▶ T R E R P H K C A Q C H K S Y I H L C S L K V H L K G N C P A G P A

Tth11II (2794)

2701 TGCTGGGCTGCCTTTGGAGGATCTGACCCGAATCAATGAAGAAATTGAGAGTTTCGACATCAGCGACAATGCAGACCGTCTTGAGGACATGGAGGACAGT
713▶ A G L P L E D L T R I N E E I E R F D I S D N A D R L E D M E D S

NcoI (2813)

2801 GTCGATGTGACCTCCATGGTGGAGAAGGAGATTCTAGCTGTGGTCAGAAAAGAGAAAGAAACCAGTCTGAAAGTGTCTTTGCAAAGAAACATGGGGA
747▶ V D V T S M V E K E I L A V V R K E K E E T S L K V S L Q R N M G

Bsu36I (2912) **BspHI (2951)**

2901 ACGGCCTCCTCTCCTCAGGGTGCAGCCTCTATGAGTCATCGGACCTGTCCCTCATGAAGTTGCCTCACAGCAACCCACTACCTCTGGTGCCTGTAAGGT
780▶ N G L L S S G C S L Y E S S D L S L M K L P H S N P L P L V P V K V

MscI (3078)

BamHI (3024) **NheI (3072)**

3001 CAAACAAGAAACAGTTGAACCGATGGATCCTTAAGATTTTCAGAAAATAAGTGTTTCGTGTTGCTTCTTAGGGCTAGCTGGCCAGACATGATAAGATACA
813▶ K Q E T V E P M D P •

3101 TTGATGAGTTTGGACAAACCACTAGAATGCAGTGAAAAAATGCTTTATTGTGAAATTTGTGATGCTATTGCTTTATTGTAACCATTATAAGCTG

HpaI (3210) **MfeI (3221)**

3201 CAATAAACAAAGTTAAACAACAATTGCATTATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGT

EcoRI (3306)

3301 GGTATGGAATTTAAATAACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGG

SapI (3488)

3401 GGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTGCTTTCATTTCC

SspI (3545) **SwaI (3559)**

3501 TTTATGTTTTAAATGCACCTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATT

EcoO109I (3620)

3601 AGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAA

3701 AGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAG
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

BstXI (3849)

3801 TCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGTGACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCA
112◀ 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 P H R V A V

StuI (3984)

3901 CAATGGTGTCAAAGTCTTCTGCCCCTTGTCCAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGAC
79◀ 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 A E I H V

4001 AGCAGAGATGATCCCCAGTCTTGGTCTGATGGCCGCCGACATGGTGTCTTGTTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACC
46◀ 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 T A V E V

XmnI (4126) **AseI (4192)**

4101 AGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTG
12◀ L E L D Q Q S I N F T K M

4201 TCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTGGC

SpeI (4347)

4301 TCAATGGGGCGGAGTTGTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCC

SnaBI (4475)

4401 CCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGA

NdeI (4580)

4501 AAGTCCATAAGTTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTA

4601 CTGCCAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAA

PacI (4766)

SdaI (4758) **BspLU11I (4776)**

4701 TGGGCGGGGTCGTTGGGCGTCCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAA
4801 AGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGCTCCGCCCCCTGACGAGCATCACAAAAATCAGCGCTCAAGTCAGAGGTGGCG

4901 AAACCCGACAGGACTATAAAGATACCAGCGTTTTCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCC

5001 TTTCTCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTCCGCTCAAGCTGGGCTGTGTGCACGAA

5101 CCCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA
5201 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCCTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCT
5301 CTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTGCAAGCAGCAGA
5401 TTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTGGTCAT

EagI (5526)

Pacl (5506) SwaI (5515) **NotI (5525)**

5501 GGCTAGTTAATTAACATTTAAATCAGCGGCCGCATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACG
5601 CTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA