



PvuI (7)
SgfI (6)
1 GGATCTGGATCGCTCCGGTGCCTGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGGGGTAAGTGGAAAGTGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAGGGCC
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) **AgeI (552)** **SphI (560)** **BstEII (576)** **XmaI (582)**
501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTGACGATGCGGACGGCCGGGTGACCCCGGGCTGGCGGGGG
601 GCTACTCCTGCTGTTGCTGCGGTCCTTGGGCTTGTGGAGCCTTCTGAGAGCTCAGGTAATGATCCATTACCATCGTCCATGAAAACACTGGCAAGTGC
13▶ L L L L L L L R S F G L V E P S E S S G N D P F T I V H E N T G K C
701 ATCCAGCCGCTGCTGACTGGGTAGTGGCCAGGACTGTAGCGGAATAACAACATGTTGGAAGTGGGTGCCAGCACCGCTCTTTACCTGGAAT
47▶ I Q P L S D W V V A Q D C S G T N N M L W K W V S Q H R L F H L E
801 CCCAGAAGTGCCTCGGCCTCGATATTACAAAGCCAGGACAACCTGCGAATGTTGAGCTGTGACTCCACCGTCATGCTGTGGTGGAAATGTGAGCACCA
80▶ S Q K C L G L D I T K A T D N L R M F S C D S T V M L W W K C E H H
901 TTCGCTGTACACCGCTGCCAGTACAGGCTAGCTCTGAAAGATGGATATGCCGTAGCCAATACGAATACATCTGATGTCTGGAAGAAGGGAGGCTCCGAG
113▶ S L Y T A A Q Y R L A L K D G Y A V A N T N T S D V W K K G G S E

BsrGI (905) **NheI (927)**
1001 GAAAACCTTTGTGCCAGCCTTATCATGAGATATACACAGAGATGGGAATTCCTACGGGAGACCTTGTGAATCCCTTTCTTATTGGTGGAGACATGGT
147▶ E N L C A Q P Y H E I Y T R D G N S Y G R P C E F P F L I G E T W

BsaBI (1117)
1101 ACCATGACTGCATTATGATGAAGATCATAGTGGGCCATGGTGTGCCACTACCCTAAGTTATGAATATGATCAAAAGTGGGCATCTGCCTACTACCAGA
180▶ Y H D C I H D E D H S G P W C A T T L S Y E Y D Q K W G I C L L P E
1201 AAGTGGCTGTGAAGGTAAGTGGGAAAAGAAATGAGCAGATTGGAAGTTGCTACCAATTTAATAATCAGGAAATCTGTCTTGGAAAAGAGCTTATGTTTCC
213▶ S G C E G N W E K N E Q I G S C Y Q F N N Q E I L S W K E A Y V S
1301 TGTGAGAAACAAGGAGCTGACTTACTGAGCATCCACAGTGTGCCGAATTAGCCTACATTTACGGGAAAAGAGGACATTGCTAGACTTGTGGCTTGGAC
247▶ C Q N Q G A D L L S I H S A A E L A Y I T G K E D I A R L V W L G

BamHI (1467)
1401 TGAATCAGCTCTATTCTGCGAGAGGTTGGGAATGGTCAGACTTCAGGCCACTCAAATTTCTTAAGTGGGATCCAGGCACGCCGTTGCACCTGTGATTGG
280▶ L N Q L Y S A R G W E W S D F R P L K F L N W D P G T P V A P V I G
1501 TGGGTCAAGCTGTGCCAGAAATGGACACAGAGTCCGGGCTGTGGCAAAGTGTTCCTGTGAATCTCAGCAGCCTTACGCTGTGCAAGAAGCCACTGAACAAC
313▶ G S S C A R M D T E S G L W Q S V S C E S Q Q P Y V C K K P L N N
1601 ACGCTGGAGCTCCAGATGTTTGGACTTACACAGATACCAGTCCATGTGGGCTGGCTGCCAAATAATGGGTTTGTCTATCTGCTGGCGAATGAAAGTA
347▶ T L E L P D V W T Y T D T H C H V G W L P N N G F C Y L L A N E S

SphI (1754)
1701 GTTCTGGGATGCAGCACATTTGAAATGCAAAGCCTTCGGTGCAGACCTCATCAGCATGCACCTCTTAGCAGATGTGGAGGTGGTGTGCAGAAACTCCA
380▶ S S W D A A H L K C K A F G A D L I S M H S L A D V E V V V T K L H
1801 TAATGGGGATGTCAAAAAAGAAATATGGACAGGCCCTTAAAAACACAAACAGCCCTGCTTTGTTCCAGTGGTCCGACGGAACGGAAGTTACTCTAACGTAC
413▶ N G D V K K E I W T G L K N T N S P A L F Q W S D G T E V T L T Y
1901 TGGAAATGAGAATGAGCCGAGTGTTCCTTCAACAGACTCCCACTGTGTTTCTATTTAGGAAAGTGGTCAAGTGGAAAGTCCAGTCTGTGAGAAGA
447▶ W N E N E P S V P F N K T P N C V S Y L G K L G Q W K V Q S C E K
2001 AACTCAGATATGTATGCAAGAAAAGGGAGAAATAACTAAGGATGCAGAGTCCGATAAGCTGTGTCGCCAGACGAGGGCTGGAAGAGACATGGAGAAC
480▶ K L R Y V C K K K G E I T K D A E S D K L C P P D E G W K R H G E T
2101 CTGTTACAAGATTTATGAGAAAAGGGCCCTTTTGGAAACGAAGTCAACCTGACCATCACTAGCAGGTTCCGAGCAGGAATTTGAAATATATGATGAAG
513▶ C Y K I Y E K E A P F G T N C N L T I T S R F E Q E F L N Y M M K

ScaI (2222) **XhoI (2255)**
2201 AACTATGATAAGTCCCTTCGGAAGTACTTCTGGACTGGCTGAGAGACCTGACTCTCGAGGAGAATACAGTTGGGCCGTTGCTCAGGGAGTAAAGCAGG
547▶ N Y D K S L R K Y F W T G L R D P D S R G E Y S W A V A Q G V K Q
2301 CTGTGACCTTTTCCAAGTGGAAATTTCTTGAACCGCGCTCCAGCGGGTGGTGGCTATGTCTACTGGAAGACTCTTGGCAAGTGGGAAGTGAAGAA
580▶ A V T F S N W N F L E P A S P G G C V A M S T G K T L G K W E V K N

PshAI (2482)
2401 CTGCAAGAGCTTCCGTGCTTTTCAATATGCAAGAAAGTGAAGCAACCCAGGAGCCTGAAGAAGCAGCCCCAAGCCCAGCACCCTGTCTGTAAGGC
613▶ C R S F R A L S I C K K V S E P Q E P E E A A P K P D D P C P E G
2501 TGGCACACTTTCCCTCCAGCTTTCTGTTATAAGGTGTTCCATATAGAAAGAAATCGTAAGAAGAGGAACTGGGAAGAAAGCCGAAAGTTCTGCCAAG
647▶ W H T F P S S L S C Y K V F H I E R I V R K R N W E E A E R F Q C Q
2601 CCCTTGGAGCTCACCTACCAGCTTCAGTCGTAGAGAGAAATTAAGGACTTTGTGCATTTGTTAAAGGACCAGTTTCAGTGGGACGCTTGGTGTGGAT
680▶ A L G A H L P S F S R R E E I K D F V H L L K D Q F S G Q R W L W I
2701 TGGTCTGAATAAGAGAAGCCCTGATTTACAAGGTCCTGGCAGTGGAGTGACCGACACCAGTGTCTGCTGTGATGATGGAGCCGGAGTTTCAACAGGAT
713▶ G L N K R S P D L Q G S W Q W S D R P V S A V M M E P E F Q Q D
2801 TTTGACATCAGACTGTGCTGCATCAAGGTCCTTGTGATGACTTGGCGAAGAGTCTGGCATCTATGAGGACAAGGACTATGCTTACTGGAACCTT
747▶ F D I R D C A A I K V L D V P W R R V W H L Y E D K D Y A Y W K P

Bsp120I (2998)
2901 TTGCTTGTGATGCCAAGCTTGTGGTGTGCCAGATTCAAAAGGTAGCACTCCCGAGATGCCAGACTGGTATAATCCAGAGCGCACTGGAATTCATGG
780▶ F A C D A K L E W V C Q I P K G S T P Q M P D W Y N P E R T G I H G

3001 GCCCCAGTTATAATGAAGGAAGTGAATACTGGTTTTGTTGCTGATCCCCACTTAACTACGAAGAAGCCGTCTTATACTGTGCTAGCAATCACAGCTTT
813> P P V I I E G S E Y W F V A D P H L N Y E E A V L Y C A S N H S F
3101 CTTGCCACGATAACATCGTTTACAGGACTAAAAGCTATCAAAAACAAACTAGCAAATATTTTGGCGAGGAACAGAAGTGGTGGGTGAAAACGAGTGAGA
847> L A T I T S F T G L K A I K N K L A N I S G E E Q K W W V K T S E
3201 ATCCAATTGATCGTTACTTTCTAGGCTCGCGCCGCCCTGTGGCACCATTTCCCATGACGTTTGGAGATGAATGTTTGACATGTCAGCCAAGACGTG
880> N P I D R Y F L G S R R R L W H H F P M T F G D E C L H M S A K T W

BsrBI (3320)

3301 GCTTGTGACTTAAGTAAACGAGCGGACTGTAATGCCAAGTTGCCCTTTCATCTGTGAAAGATAACAATGTCTTTCATTAGAGAAATACAGCCCAGATCCT
913> L V D L S K R A D C N A K L P F I C E R Y N V S S L E K Y S P D P

ApaLI (3414)

Bsp120I (3469)

3401 GCAGCCAAAGTACAGTGCATGAGAAGTGGATTCTTTTCAAATAAGTGCTTCTAAAGGTCAACTCTGGGCCCGTTACGTTTTCTCAAGCAAGCGGCA
947> A A K V Q C T E K W I P F Q N K C F L K V N S G P V T F S Q A S G

3501 TTTGTCATTCTACGCGGCCACCCTTCTTCCGTGCTGAGCCGGGTGAACAAGATTTTATTATATCCTTGTCTTCTGAAATGGAAGCTAGTCTATGGAT
980> I C H S Y G G T L P S V L S R G E Q D F I I S L L P E M E A S L W I

3601 TGGTCTGCGCTGGACTGCCTACGAAAGGATAAAACAGATGGACAGACAACAGAGAGCTGACCTACAGCAACTTTTACCCACTGCTGGTCCGGTCCGAGGCTG
1013> G L R W T A Y E R I N R W T D N R E L T Y S N F H P L L V G R R L

3701 AGCATACCAACGAATTTCTTGTGATGAGTCCCACTTCCACTGCGCTTATTCTTAATCTCAAAAAGTCCCGCTTACTGGGAAATTTTACTT
1047> S I P T N T F F D D E S H F H C A L I L N L K K S P L T T G T W N F T

3801 CCTGTTCAGAACGACTCTCTGTCTCTGTCAAAAATACTCAGAGACTGAAGACGGACAGCCCTGGGAGAACAATTTCAAAAACAGTGAAGTATCTAAA
1080> S C S E R H S L S L C Q K Y S E T E D G Q P W E N T S K T V K Y L N

3901 TAACCTATACAAAATCATCTCGAAGCCCTGACGTGGCAGCGGCTCTGAAGGAGTGCATGAAAGAGAAGATGAGGTTGGTGAGCATCACAGACCCTTAC
1113> N L Y K I I S K P L T W H G A L K E C M K E K M R L V S I T D P Y

FspI (4031)

4001 CAGCAGGCCCTTCTCGCAGTGCAGGCCACCCTGCGCAACAGCTCCTTCTGGATCGGACTCTCCAGTCAAGATGATGAACCTCAACTTTGGTTGGTCAGATG
1147> Q Q A F L A V Q A T L R N S S F W I G L S S Q D D E L N F G W S D

4101 GAAAACGTCTTCAATTTAGTAACTGGGCTGGAAGCAATGAGCAACTTGTGACTGCGTGATATTAGACACAGATGGATTCTGGAAAACAGTACTGCTGA
1180> G K R L Q F S N W A G S N E Q L D D C V I L D T D G F W K T A D C D

KasI (4213)

BsrGI (4290)

4201 TGATAACACAGCCTGGCGCATTGCTACTATCCAGGAAATGAGACTGAGGAGGAGTCCAGAGCTGGACACTGCTAAATGCCCGTCTCTGTACAGAGC
1213> D N Q P G A I C Y Y P G N E T E E E V R A L D T A K C P S P V Q S

BbrPI (4389)

4301 ACCCATGGATACCATTCCAGAACTCCTGCTACAATTTTATGATTACCAACAACAGGCATAAGACAGTACACCCGGAGGAAGTGCAGTCCACGTGCGAGA
1247> T P W I P F Q N S C Y N F M I T N N R H K T V T P E E V Q S T C E

BstBI (4407)

4401 AGCTGCATTGAAAGCACACAGTCTGAGCATTCCGAATGAGGAGGAGAATAACCTTTGTTGGAACAGCTTCTGTACTTCAATTATATTGCCATCGGTT
1280> K L H S K A H S L S I R N E E E N T F V V E Q L L Y F N Y I A S W V

4501 CATGTTAGGAATAACCTATGAAAACAATTTTGTGATGTGGTTTGATAAACTGCATTGTCTACACACTGGAGAACGGGAAGCAACTGTGAAAAT
1313> M L G I T Y E N N S L M W F D K T A L S Y T H W R T G R P T V K N

ScaI (4621)

4601 GGCAAATTTTTGGCTGGTCTAAGTACTGATGGATTCTGGGATATTGAGTCTTTCAATGTTATTGAAGAAACACTTCAATTTTACCAGCACAGTATTTCTG
1347> G K F L A G L S T D G F W D I Q S F N V I E E T L H F Y Q H S I S

4701 CTTGTAATTTGAAATGGTTGACTATGAGGACAAACACAATGGCACCTGCCACAGTTCATCCATATAAGGACGGGCTACAGCGTTATTGAGAAGAA
1380> A C K I E M V D Y E D K H N G T L P Q F I P Y K D G V Y S V I Q K K

MluI (4823)

MscI (4850)

4801 GGTGACGTGGTATGAAGCATTGAACGCTGCTCTCAAAGTGGGGAGAGTTGGCAGTGTTCAACAACCAATGGGAAGCTCTTTCTGGAAGACATTGTG
1413> V T W Y E A L N A C S Q S G G E L A S V H N P N G K L F L E D I V

BstBI (4960)

4901 AACCGTGACGGATTCCCTCTCTGGGTTGGGCTCTCAAGTCATGATGGAAGCGAATCGAGTTTCAATGGTCCGATGGCAGAGCATTGACTATGTCCCAT
1447> N R D G F P L W V G L S S H D G S E S F E W S D G R A F D Y V P

5001 GGCAGAGCCTACAATCTCCCGGAGACTGTGCTGCTTATATCCAAAAGAAATTTGGAGACGTGAAAAATGCCTGTCTGTTAAGGATGGTGTATTGTTA
1480> W Q S L Q S P G D C V V L Y P K G I W R R E K C L S V K D G A I C Y

5101 CAAGCCTACAAAAGATAAAAAGCTGATCTTTTATGATAAATCATAAAATGTCCAGTGGCAAAGAGGGATGGTCCCAGTGGGTCAGTATGGGGGCCAC
1513> K P T K D K K L I F H V K S S K C P V A K R D G P Q W V Q Y G G H

5201 TGTTACGTTCCGACCAGTACTGCACAGCTTCTCAGAGGCCAAACAAGTGTGCAAGAGCTTGTGATCATTCCGCAACTGTTGTACCATAGCAGATGAAA
1547> C Y A S D Q V L H S F S E A K Q V C Q E L D H S A T V V T I A D E

5301 ATGAGAATAAGTTTGTGAGCAGACTGATGAGGGAGAATAAATACTATGAGAGTTTGGCTTGGCCTGTCTCAGCATTCACTCGATCAGTCTTGGAG
1580> N E N K F V S R L M R E N Y N I T M R V W L G L S Q H S L D Q S W S

PshAI (5421)

5401 TTGGCTCGATGGATTAGATGTGACATTTGTCAAATGGGAAAAATAAACTAAGGATGGTGTAGGGAAATGTAGCATTTTAAATAGCTTCAAATGAAACCTGG
1613> W L D G L D V T F V K W E N K T K D G D G K C S I L I A S N E T W

BbrPI (5516)

5501 AGAAAAGTCCATTGCTACAGTGGCTATGCAAGAGCTGTCTGCAAAATTCCTCTGAGCCCGGACTACACAGGCATAGCCATCCTGTTTGGCGTGTGTGCC
1647> R K V H C S R G Y A R A V C K I P L S P D Y T G I A I L F A V L C

5601 TCTTAGGGCTCATCAGTTGGCATTGTTCTCTTGAACGATCCCAATCCGCTGGACCGCTTCTCCTCGTTCCGGTATGAAATGGAACCAACGA
1680> L L G L I S L A C I W F L L Q R S H I R W T G F S S V R Y E H G T N E

AvrII (5734)

MscI (5746)

5701 AGACGAGGTGATGCTCCCTTCTTCCACGACTAACCTAGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACAGAAATG
1713> D E V M L P S F H D

HpaI (5878)

5801 CAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACAACATTCATTC

5901 ATTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTCAAAAATACAGCATAGCAAAA

6001 CTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAG

6101 CCTCACCTTCTTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATT

SapI (6156)

6201 CCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATA

Swal (6227)

6301 ATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACT

6401 TGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCA

6501 CATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTC

6601 ACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGCA

6701 TGGCCGCCCGACATGGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGT

AseI (6860)

6801 CTTATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTAT

6901 CTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGA

SpeI (7015)

7001 AAGTCCCCTGATTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAAATCCCCTGAGTCAAACCGCTATCCACGCCATTGA

SnaBI (7143)

7101 TGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATCGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATG

NdeI (7248)

7201 CCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGCGTACTTGGCATATGATACACTTGTGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCC

7301 ACCCATTGACGTCAATGAAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCTTGGGCGGTCAGCCAGGCG

PacI (7434)

SdaI (7426)

7401 GGCCATTTACCGTAAGTTATGTAACGCCCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTG

7501 CGCTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACAGGCGT

7601 TTCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGGACCTGCCGCTTACCGGATACTGTCCGCCTTCTCCCTTCGGAAAGCGTGGCGCTTCTCA

ApaLI (7758)

7701 TAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCCTTATCC

7801 GGTAACATATCGTCTTGTAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTG

7901 CTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGT

8001 TGGTAGCTCTTGATCCGGCAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGAT

EagI (8194)

8101 CTTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCG

PacI (8174)

Swal (8183)

NotI (8193)

8201 CAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAAAACAAAACAAA

8301 CTAGCAAAATAGGCTGTCCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA