



PvuI (7)
SgfI (6)
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

BstEII (555) **AgeI (552)** **NcoI (560)**
501 TCTGTTTGTCCGGCTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCCCATGGCTCAGTGAACCAGCTGCAGCAGCTGGACACAGG

13▶ M A Q W N Q L Q Q L D T R

BsrGI (623) **NcoI (641)** **NdeI (692)**
601 CTACCTGGAGCAGCTGCACCAGCTGTACAGCGACAGCTTCCCATGGAGCTGCGGCAGTTCCTGGCACCTGGATTGAGAGTCAAGACTGGGCATATGCA

13▶ Y L E Q L H Q L Y S D S F P M E L R Q F L A P W I E S Q D W A Y A

701 GCCAGCAAAGAGTCACATGCCACGTTGGTGTTCATAATCTCTGGGTGAAATTGACCAGCAATATAGCCGATTCTGCAAGAGTCCAATGCTCTATC

47▶ A S K E S H A T L V F H N L L G E I D Q Q Y S R F L Q E S N V L Y

BstBI (809) **BstAPI (822)**
801 AGCACAACTTTCGAAGAATCAAGCAGTTTCTGCAGAGCAGGTATCTTGAGAAGCCAATGAAAATTGCCGGATCGTGGCCGATGCCTGTGGGAAGAGTC

80▶ Q H N L R R I K Q F L Q S R Y L E K P M E I A R I V A R C L W E E S

901 TCGCTCTCCAGACGGCAGCCACGGCAGCCAGCAAGGGGGCAGGCCAACCCCAACAGCCGCTAGTGACAGAGAAGCAGCAGATGTTGGAGCAG

113▶ R L L Q T A A T A A Q Q G G Q A N H P T A A V V T E K Q Q M L E Q

BspEI (1013) **XbaI (1032)**
1001 CATCTTCAGGATGTCCGGAAGCGAGTGCAGGATCTAGAACAGAAAATGAAGGTGGTGGAGAACCTCCAGGACGACTTTGATTTCAACTACAAAACCTCA

147▶ H L Q D V R K R V Q D L E Q K M K V V E N L Q D D F D F N Y K T L

1101 AGAGCCAAGGAGACATGCAGGATCTGAATGAAACAACAGTCTGTGACCAGACAGAAGTGCAGCAGCTGGAACAGATGCTCACAGCCCTGGACCAGAT

180▶ K S Q G D M Q D L N G N N Q S V T R Q K M Q Q L E Q M L T A L D Q M

SapI (1273)
1201 GCGGAGAAGCATTGTGAGTGTGAGCTGGCGGGCTCTTGTGAGCAATGGAGTACGTGCAGAAGACACTGACTGATGAAGAGCTGGCTGACTGGAAGAGGCGG

213▶ R R S I V S E L A G L L S A M E Y V Q K T L T D E E L A D W K R R

1301 CAGCAGATCGCGTGCATCGGAGGCCCTCCCAACATCTGCCTGGACCGTCTGAAAACCTGGATAACTTCATTAGCAGAATCTCAACTTCAGACCCGCAAC

247▶ Q Q I A C I G G P P N I C L D R L E N W I T S L A E S Q T C T R Q

1401 AAATTAAGAACTGGAGGAGCTGCAGCAGAAAGTGTCTACAAGGGGACCCCTATCGTGCAGCACCGCCCATGCTGGAGGAGGATCGTGGAGCTGTT

280▶ Q I K K L E E L Q Q K V S Y K G D P I V Q H R P M L E E R I V E L F

SphI (1544) **RsrII (1559)** **PshAI (1581)**
1501 CAGAACTTAATGAAGAGTGCCTTCGTGGTGGAGCGGCAGCCCTGCATGCCATGCACCCGGACCGGCCCTTAGTCATCAAGACTGGTGTCCAGTTTACC

313▶ R N L M K S A F V V E R Q P C M P M H P D R P L V I K T G V Q F T

1601 ACGAAAGTCAGTTGCTGGTCAAATTTCTGAGTTGAATTATCAGCTTAAAATTAAGTGTGCATTGATAAAGACTCTGGGATGTTGCTGCCCTCAGAG

347▶ T K V R L L V K F P E L N Y Q L K I K V C I D K D S G D V A A L R

Bsu36I (1797)
1701 GGTCTCGGAAATTTAACATTCTGGGCACGAACAAAAAGTATGAACATGGAGGAGTCTAACAACGGCAGCCTGTCTGCAGAGTTCAAGCACCTGACCCT

380▶ G S R K F N I L G T N T K V M N M E E S N N G S L S A E F K H L T L

1801 TAGGGAGCAGAGATGTGGGAATGGAGGCCGTGCCAATTGTGATGCCTCCTTGTGACTGAGGAGCTGCACCTGATCACCTTCGAGACTGAGGTGTAC

413▶ R E Q R C G N G G R A N C D A S L I V T E E L H L I T F E T E V Y

StuI (1905)
1901 CACCAAGGCCTCAAGATTGACCTAGAGACCCACTCCTTGCCAGTTGTGGTGTCTCCAACATCTGTCAGATGCCAAATGCTTGGGCATCAATCCTGTGGT

447▶ H Q G L K I D L E T H S L P V V V I S N I C Q M P N A W A S I L W

XmnI (2031)
2001 ATAACATGCTGACCAATAACCCCAAGAAGCTGAACTTCTTCACTAAGCCGCCAATTGGAACCTGGGACCAAGTGGCCGAGGTGCTCAGCTGGCAGTTCTC

480▶ Y N M L T N N P K N V N F F T K P P I G T W D Q V A E V L S W Q F S

AvrII (2157)
2101 GTCCACCACCAAGCGGGGCTGAGCATCGAGCAGCTGACAACGCTGGCTGAGAAGCTCCTAGGGCCTGGTGTGAACTACTCAGGGTGTGAGTACATGAG

513▶ S T T K R G L S I E Q L T T L A E K L L G P G V N Y S G C Q I T W

2201 GCTAAATCTGCAAGAAAACATGGCTGGCAAGGGCTTCTCCTTCTGGGTCTGGTGTAGACAATATCATCGACCTGTGAAAAAGTATATCTTGGCCCTTT

547▶ A K F C K E N M A G K G F S F W V W L D N I I D L V K K Y I L A L

XmaI (2367)
2301 GGAATGAAGGTTACATCATGGTTCATCAGCAAGGAGCGGGAGCGGGCCATCCTAAGCACAAAGCCCGGGCACCTTCTACTGCGCTTCAGCGAGAG

580▶ W N E G Y I M G F I S K E R E R A I L S T K P P G T F L L R F S E S

2401 CAGCAAAGAAGGAGGGTCACTTTCAGTGGGTGAAAAGGACATCAGTGGCAAGACCCAGATCCAGTCTGTAGAGCCATACCAAGCAGCAGCTGAAC

613▶ S K E G G V T F T W V E K D I S G K T Q I Q S V E P Y T K Q Q L N

BspLU11I (2501)
2501 AACATGTCATTTGCTGAAATCATCATGGGCTATAAGATCATGGATGCGACCAACATCCTGGTGTCTCCAATTGCTACCTCTACCCCGACATTCCTCAAGG

647▶ N M S F A E I I M G Y K I M D A T N I L V S P L V Y L Y P D I P K

ScaI (2615)

2601 AGGAGGCATTTGGAAAGTACTGTAGGCCGAGAGCCAGGAGCACCCCGAAGCCGACCCAGGTAGTGCTGCCCGTACCTGAAGACCAAGTTCATCTGTGT
680▶ E E A F G K Y C R P E S Q E H P E A D P G S A A P Y L K T K F I C V
2701 GACACCAACGACCTGCAGCAATACCATTGACCTGCCGATGTCCCCCGCATTAGATTGATGACAGTTTGGAAATAACGGTGAAGGTGCTGAGCCC
713▶ T P T T C S N T I D L P M S P R T L D S L M Q F G N N G E G A E P

NheI (2894)

2801 TCAGCAGGAGGGCAGTTTGTAGTCGCTCACGTTTGCATGGATCTGACCTCGGAGTGTCTACCTCCCCATGTGAGGAGCTGAAACCAGAAGCTGCTAGC
747▶ S A G G Q F E S L T F D M D L T S E C A T S P M •

MscI (2900)

2901 TGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTT

HpaI (3032)

3001 TATTTGTAACCATTATAAGCTGCAATAAACCAAGTTAACAAACAATTCATTGCTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAG

EcoRI (3128)

3101 CAAGTAAACCTCTACAAATGTGGTATGGAATTCATAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGA

3201 TGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTCTTTCATGGAGTTTAAAGATATAGTGTATTTCCCAAG

SapI (3310)

SspI (3367)

SwaI (3381)

3301 GTTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCA

3401 ATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTT

3501 AATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCGTGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATT

141◀ • N R T Y K L P I L E E I T T K V L K G N

SacI (3642)

3601 CATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCA

120◀ 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 R I S R D V E D

3701 GAGTAGGGGTGCCTGACAGCCCAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGC

86◀ 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 A E A C V T V R G

StuI (3806)

3801 CAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGTCCTCATAGAGCATGGTGAT

53◀ 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 N D E Y L M T I

XmnI (3948)

3901 CTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAAGTCTATTATACTATGCCGAT

20◀ K E T A V E V L E L D Q Q S I N F T K M

AseI (4014)

SacI (4071)

4001 ATACTATGCCGATGATTAATTGTCAAACACGGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATAGACCTCCACCCT

SpeI (4169)

4101 ACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAA

SnaBI (4297)

4201 TGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATAC

4301 GTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTGATGACTGGGCATAATGCCAGGCGGGCCATTACCCTGATTGACGTCAATAGGGGGCGTACTT

NdeI (4402)

4401 GGCATATGATACACTTGATGACTGCCAAGTGGCAGTTTACCCTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAA

PacI (4588)

SdaI (4580)

BspLU11I

4501 CATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGTCAAGCAGGCGGGCCATTTACCCTAAGTTATGTAACGCCTGCAGGTTAAITAAAGAAC

4601 ATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATC

4701 GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCC

4801 GCTTACCGGATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCC

ApaLI (4912)

4901 AAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAG

5001 CACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAG

5101 AACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCTGTTAGCGGTGGT

5201 TTTTTTGTTCGAAGCAGCAGATTACCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACT

EagI (5348)

PacI (5328) SwaI (5337) NotI (5347)

5301 CACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTG
5401 TGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACAT
5501 TTCTCTATCGAA