



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

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTATGTGCTGACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACCGCCCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCGCTTGCTGCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552)
BspHI (560)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTATCATGAGACCCAGATCCTGCTGCTCCTGGCCCTGCTGAC

1 ▶ M R P Q I L L L L A L L T

AvrII (600)

601 CCTAGGCTGGTGCACAACACCAAGACAAAGTGCCCTGTAAGATGGTGGACAAGAAGGTCTCGTGCCAGGTTCTGGGCTGCTCCAGGTCCCTCGGTG

13▶ L G L A A Q H Q D K V P C K M V D K K V S C Q V L G L L Q V P S V

701 CTCCGCCAGACACTGAGACCCTTGATCTATCTGGAAACAGCTGCGGAGTATCCTGGCTCACCCCTGGGCTTCTACACGGCACTTCGTCACCTGGACC

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

801 TGAGCACAATGAGATCAGCTTCTCCAGCCAGGAGCCTCCAGGCCCTGACCCACCTGGAGCACCTCAGCCTGGCTCACAACCGGTGGCGATGGCCAC

80▶ L S T N E I S F L Q P G A F Q A L T H L E H L S L A H N R L A M A T

Bsp120I (921)
MluI (933)
BsrGI (968)
BsrBI (985)

901 TGCCTGAGTGTGGTGGCCTGGGCCCTGCCACGCTGACCTCCCTGGACCTGTCTGGAAACAGCTGTACAGCGGCTGCTGGAGCGGCTGTGGGG

113▶ A L S A G G L G P L P R V T S L D L S G N S L Y S G L L E R L L G

1001 GAGGCACCCAGCTGCATACCCTCTACTGGCGGAGAACAGTCTGACTCGCCTCACCCGCCACACCTCCGGGACATGCTGCGCTGGAGCAGCTTGACC

147▶ E A P S L H T L S L A E N S L T R L T R H T F R D M P A L E Q L D

BsaBI (1116)
EcoRI (1179)

1101 TGCATAGCAACGTGCTGATGGACATCGAGGATGGCGCCTTCGAGGGTCTGCCCGCCTGACCCATCTCAACCTCTCCAGGAATCCCTCACCTGCATCTC

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

1201 CGACTTCAGCCTCCAGCAGCTGCGGGTCTAGACCTGAGCTGCAACAGCATCGAGGCTTTTCAGACGGCCTCCAGCCAGGCTGAGTTCAGCTCACC

213▶ D F S L Q Q L R V L D L S C N S I E A F Q T A S Q P Q A E F Q L T

1301 TGGCTGACCTGCGGGAGAACAACCTGCTCCATTTCCCGACCTGGCCGCGCTCCCGAGACTCATCTACCTGAACTGTCCAACAACCTCATCGGCTCC

247▶ W L D L R E N K L L H F P D L A A L P R L I Y L N L S N N L I R L

EagI (1491)

NotI (1490)

1401 CCACAGGGCCACCCAGGACAGCAAGGGCATCCACGCACCTTCCGAGGGTGGTCCAGCCTGCCCTCTCAGCCCCAGCGGGAATGCCAGCGGCCGCC

280▶ P T G P P Q D S K G I H A P S E G W S A L P L S A P S G N A S G R P

1501 CCTTTCCAGCTCTTGAATCTGGATTTGAGCTACAATGAGATTGAGCTCATCCCCGACAGCTTTCTTGAGCACCTGACCTCCCTGTGCTTCTGACCTC

313▶ L S Q L L N L D L S Y N E I E L I P D S F L E H L T S L C F L N L

BstAPI (1601)

1601 AGCAGAACTGCTTGCAGCCTTTGAGGCCCGCGCTTAGGCTCCCTGCCCTGCTGATGCTCCTGACTTAAGCCACAATGCCCTGGAGACTGGAAC

347▶ S R N C L R T F E A R R L G S L P C L M L L D L S H N A L E T L E

BstXI (1706)

1701 TGGGCGCCAGAGCCCTGGGGTCTCTGCGGACGCTGCTCCTACAGGGCAATGCCCTGCGGGACCTGCCCCATACACCTTTGCCAATCTGGCCAGCCTGCA

380▶ L G A R A L G S L R T L L L Q G N A L R D L P P Y T F A N L A S L Q

1801 GCGGCTCAACCTGAGGGGAACCGAGTCAAGCCCTGTGGGGGCGCAGATGAGCCTGGCCCTCCGGCTGTGTGGCCTTCTCCGGCATCACCTCCCTCCGC

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

1901 AGCCTGAGCCTGGTGGATAATGAGATAGAGTGTCTCAGGGCAGGGCCTTCTCCACACCCCACTGACTGAGCTGGACCTTTCTTCAATCTGGGCTGG

447▶ S L S L V D N E I E L L R A G A F L H T P L T E L D L S S N P G L

SfiI (2004)

2001 AGTGGCCACGGGGCCTTGGGAGGCTGGAGGCTCCTTGGAGGTCTGGCACTGCAGGGCAACGGGCTGATGGTCTGCAGGTGGACCTGCCCTGCTT

480▶ E V A T G A L G G L E A S L E V L A L Q G N G L M V L Q V D L P C F

2101 CATCTGCCTCAAGCGGCTCAATCTTGCCGAGAACCCTGAGCCACCTTCCCGCTGGACACAGGCTGTGCTACTGGAGGTGCTGGACCTGCGAAACAC

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

NotI (2225)

2201 AGCTTACGCTCCTGCCAGGAGTGCATGGGTGGCTGGAGACCAGCCTCCGGCGCCTTACCTGCAGGGGAATCCACTCAGCTGCTGCGGCAATGGCT

547▶ S F S L L P G S A M G G L E T S L R R L Y L Q G N P L S C C G N G

BbrPI (2395)

2301 GGCTGGCAGCCAGCTGCACCAGGGCCGTGTGGACGTGGACGCCACCCAGGACCTGATCTGCCGCTTACGCTCCAGGAGGAGGTGTCCCTGAGCCACGT

580▶ W L A A Q L H Q G R V D V D A T Q D L I C R F S S Q E E V S L S H V

2401 GCGTCCGAGGACTGTGAGAAGGGGGGACTGAAGAATCAACCTCATCATCTCACCTTCACTGGTCTGTCATCTCCTCACCACGCTGGCC

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

NgoMIV (2516)

NheI (2588)

2501 GCCTGCTGCTGCTGCGCCGGCAGAGTTTAAACCAACAGTATAAAGCCTAAAGAAGCCGGGAGACACTTAGTGCAGTGGGGAGCCTGCTAGCTGGCCA

647▶ A C C C V R R Q K F N Q Q Y K A •

2601 GACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTG

HpaI (2726) MfeI (2737)

2701 TAACCATTATAAGCTGCAATAAAACAAGTTAACAAACAACATTGCATTCATTTTATGTTTCAGGTTCCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTA

EcoRI (2822)

2801 AAACCTCTACAAATGTGGTATGGAAATCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATA

2901 AGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAGATATAGTGTATTTTCCAAGGTTTGA

SapI (3004) SspI (3061) SwaI (3075)

3001 ACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAA

3101 ATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGA

3201 AATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATCTC

BstXI (3365)

3301 AATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAG

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

3401 GGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGT

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

3501 AGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCGACATGGTGTCTGTTGTCCTCATAGAGCATGGTGTCTTCTC

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 (3646) XmnI (3642)

3601 AGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTA

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

AseI (3708)

3701 TGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGC

SpeI (3863)

3801 CTACCGCCATTTGCGTCAATGGGGCGGAGTTGTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGT

SnaBI (3991)

3901 GGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCGCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGAT

NdeI (4096)

4001 GTAAGTCCCAAGTAGGAAAGTCCATAAGGTCATGTAAGTCCGCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGAT

4101 TGATACACTTGATGTAAGTCCCAAGTGGGCGGAGTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACG

PacI (4282) BspLU11I (4292)

4201 TCATTATTGACGTCAATGGGGCGGGTCTGTTGGGCGGTGAGCCAGGCGGGCCATTACCGTAAAGTTATGTAACGCTGCAGGTTAAATAAGAACATGTGA

4301 GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCT

4401 CAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGCTTAC

4501 CGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGTTGAGGTGCTTCCGCTCAAGCTG

ApaLI (4606)

4601 GGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTGAGTCAACCCGGTAAGACACGACTTATGCCACTGG

4701 CAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGTACACTAGAAGAACAGT

4801 ATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCAGCTGGTAGCGGTGGTTTTTTT

4901 GTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCTTTGATCTTTTACGGGGTCTGACGCTCAGTGAACGAAACTCACGTT

EagI (5042) PacI (5022) SmaI (5031) NotI (5041)

5001 AAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAA

5101 TCGTAACTAACATACGCTCTCCATCAAAACAAACGAAACAAACAACTAGCAAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCT

5201 ATCGAA