



PvuI (7)
SgfI (6)
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555) **AgeI (552)** **NcoI (560)** **BsrGI (578)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTACCATTGGAGAACGGAGCGGTGTACAGCCCCACTACGGAGGA
1▶ M E N G A V Y S P T T E E

Bsp120I (606) **XmaI (603)** **NgoMIV (656)** **BstAPI (693)**
601 GGACCCGGGCCCCGCCAGAGGCCCGGAGCGGCTCGCTGCCTACTTTTTTCATGGGCGGCTCCATTGCTCCGGCGGTTCTCAAGGGCTTGCAGCTG
13▶ D P G P A R G P R S G L A A Y F F M G R L P L L R R V L K G L Q L

PstI (786)
701 TTGCTGTCTGTGCTGGCCTTCATCTGTGAAGAAGTTGTATCACAATGACTTTATGTGGAGGACTTTATTTTTTTGAGTTTGAAGCTGCAGTGCCTTTC
47▶ L L S L L A F I C E E V V S Q C T L C G G L Y F F E F V S C S A F

801 TTCTGAGTCTCCTTATACTGATTGTGATTGCACTCCATTTTATGAGAGAGTTGATACCACAAAAGTAAAATCATCGGATTTTATATTACTTTGGGAAC
80▶ L L S L L I L I V Y C T P F Y E R V D T T K V K S S D F Y I T L G T

901 AGGATGTGTGTTTTGTTGGCATCCATCATTTTTGTTCCACACATGACAGGACTTACGTGAGATTGCTGCAATTGTGTTGGATTATAGCAAGTTTT
113▶ G C V F L L A S I I F V S T H D R T S A E I A A I V F G F I A S F

PshAI (1040)
1001 ATGTTCTACTTGACTTTATCACTATGCTGTATGAAAAACGACAGGAGTCCAGCTGAGAAAACTGAAAATACCACTAGGGCTGAAGCCCTCACTGAGC
147▶ M F L L D F I T M L Y E K R Q E S Q L R K P E N T T R A E A L T E

MscI (1146) **NheI (1140)**
1101 CACTTAATGCCTAAAGACTCTGGGAGCAGATGTTACCTAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATG
180▶ P L N A •

HpaI (1278)
1201 CAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTC

EcoRI (1374)
1301 ATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAA
1401 CTTAACTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAG

SapI (1556)
1501 CCTCACCTCTTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATT

SspI (1613) **SwaI (1627)**
1601 CCCTTTTGTAGTAAATATTGAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATA
1701 ATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACT
141▶ • N R T Y K

SacI (1888)
1801 TGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCA
135▶ L P I L E E I 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

BstXI (1917)
1901 CATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTC
102▶ M G C P S V V 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

StuI (2052)
2001 ACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTCTGA
68▶ V A S G I A I 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

BbsI (2198) **XmnI (2194)**
2101 TGGCCGCCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGT
35▶ A A G V H H K 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

AseI (2260)
2201 CTTCACTGGTGGCCCTCTATAGTGTGATCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTAT
2▶ K M

2301 CTGACGGTTCACATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGA
SacI (2317)

2401 AAGTCCCCTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGA
SpeI (2415)

2501 TGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATG
SnaBI (2543)

2601 CCAGGCGGGCCATTACCCTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACTTGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCC
NdeI (2648)

2701 ACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCTGTTGGGCGGTGAGCCAGGCG
PacI (2834)

2801 GGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTG
PstI (2827) SdaI (2826) BspLUII (2844)

2901 GCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGT
BspLUII (2844)

3001 TTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA
BspLUII (2844)

3101 TAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCC
ApaLI (3158)

3201 GGTAAGTATCGTCTTGTAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTG
ApaLI (3158)

3301 CTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGT
ApaLI (3158)

3401 TGGTAGCTCTTGATCCGGCAAAACACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGAT
ApaLI (3158)

3501 CCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCG
EagI (3594) PacI (3574) SmaI (3583) NotI (3593)

3601 CAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAA
EagI (3594)

3701 CTAGCAAAATAGGCTGTCCCGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA
EagI (3594)