



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

1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

Psp1406I (203)
PvuII (239)
Bsu36I (291)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)

AgeI (552) **NcoI (560)**
FspI (581)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGCGTCACGCATAGGGTTGCGCATGCAGCTCATGCG

▶

▶ M A S R I G L R M Q L M R

NsiI (652)

601 GGAGCAGGCGCAGCAGGAGGAGCAGCGGGAGCGCATGCAGCAACAGGCTGTATGCATTACATGCAGCAGCAGCAGCAGCAACAGCAGCAGCTCGGA

13▶ E Q A Q Q E E Q R E R M Q Q Q A V M H Y M Q Q Q Q Q Q Q Q L G

701 GGGCGCCACCCCGCCATCAATACCCCGTCCACTTCCAGTCGCCACCACCTGTGCTGGGAGGTGTTGAAGGTGCAGTCCTACCTGGAGAATCCCA

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

PstI (811)

801 CATCTACCATCTGCAGCAGTCGCAGCATCAGAAGGTGCGGGAGTACCTGTCCGAGACCTATGGGAACAAGTTTGTGCCACATCAGCCAGCCAGCCAGGG

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

BbrPI (946)
XcmI (980)
NcoI (989)

901 CTCTCCGAAACCCACCCAGCCGCTCCCGAGGGTGCAGCTGGACACGTGTCTCCTCCGCTGGCAACAGTGTCCCAATAGCCCATGGCCATG

113▶ S P K P P P A A S P G V R A G H V L S S S A G N S A P N S P M A M

Tth111I (1063)

1001 CTGCACATTGGCTCAACCCGTAGAGGGAGTTGGATGATGTCATTGACAACATTATGCGTCTGGACGATGTCCTTGGCTACATCAATCCTGAAATGCAGA

147▶ L H I G S N P E R E L D D V I D N I M R L D D V L G Y I N P E M Q

BsrGI (1139)

1101 TGCCCAACACGCTACCCCTGTCCAGCAGCCACCTGAATGTGTACAGCAGCAGCCACCCAGGTCACAGCCTCCCTGGTGGGCGTCACCAGCAGCTCCTGCC

180▶ M P N T L P L S S S H L N V Y S S D P Q V T A S L V G V T S S S C P

Bsp120I (1244)
BsrBI (1258)

1201 TGCGGACCTGACCAGAAGCGAGAGCTCACAGATGCTGAGAGCAGGGCCCTGGCCAAGGAGCGGCAGAAAGAAACAATCACAACTTAATTGAAAGGAGA

213▶ A D L T Q K R E L T D A E S R A L A K E R Q K K D N H N L I E R R

1301 CGAAGTTCAACATCAATGACCCATCAAGGAGTTGGGAATGCTGATCCCAAGGCAATGACCTGGACGTGCGCTGGAACAAGGGCACCATCCTCAAGG

247▶ R R F N I N D R I K E L G M L I P K A N D L D V R W N K G T I L K

BspEI (1415)

1401 CCTCTGTGGATTACATCCGGAGGATGCAGAAGGACCTGCAAAAGTCCAGGGAGCTGGAGAACCACTCTCGCCGCTGGAGATGACCAACAAGCAGCTCTG

280▶ A S V D Y I R R M Q K D L Q K S R E L E N H S R R L E M T N K Q L W

ApaLI (1534)

XhoI (1529)

1501 GCTCCGTATCCAGGAGCTGGAGATGCAGGCTCGAGTGACGGCTCCCTACCACCTCCCCGTCGGCATGAACATGGCTGAGCTGGCCAGCAGGTGGTG

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

Bsp120I (1623)

1601 AAGCAGGAGCTGCTAGCGAAGAGGGCCAGGGAGGCTGTGCTGGGGGCTGAGTCCCTGACCTGAGCCACTGCCAGCTCTGCCCCGCAAGCCC

347▶ K Q E L P S E E G P G E A L M L G A E V P D P E P L P A L P P Q A

SanDI (1785)

PshAI (1780)
XmaI (1791)

1701 CGCTGCCCTGCCACCCAGCCACCGTCCCATTCATCACCTGGACTTCAGCCACAGCCTGAGCTTTGGGGGAGGGAGGACGAGGGTCCCCGGGCTA

380▶ P L P L P T Q P P S P F H H L D F S H S L S F G G R E D E G P P G Y

XcmI (1847)

1801 CCCCAGCCCTGGCAGCGGGGATGGCTCCCATTCAGCCTGTCCAAGAAGGATCTGGACCTCATGCTCCTGGACGACTCACTGCTACCCTGGCC

413▶ P E P L A P G H G S P F P S L S K K D L D L M L L D D S L L P L A

SfiI (1932)

1901 TCTGATCCAATTCTGTCCACCATGTCCCGGAGGCTCCAAGGCCAGCAGCCGCCGAGCAGCTTCAGCATGGAGGAGGGCGATGTGCTGTGACCCTGGC

447▶ S D P L L S T M S P E A S K A S S R R S S F S M E E G D V L •

NheI (2001)

2001 TGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCT

HpaI (2139)
MfeI (2150)

2101 ATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTT

2201 **EcoRI (2235)**
TTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTACTGAATCCTTTTC

2301 TGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATT

2401 **SapI (2417)** **SspI (2474)** **SwaI (2488)**
TCCAAGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACAT

2501 CATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGG

2601 AACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCT

2701 TGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGCCAC
122 G N 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

2801 CTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTG
89 E D 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

2901 ACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGCTCATAGAGCA
55 V R G 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

BbsI (3059)
3001 TGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGATTATACTA
22 T I K E T A V E V L E L D Q Q S I N F T K M

XmnI (3055)

3101 **AseI (3121)**
TGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGACCTC

3201 **SpeI (3276)**
CCACCGTACAGCCTACCGCCATTGCGTCAATGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTG

3301 ACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATGGAATAGCGATGA

SnaBI (3404)
3401 CTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGACTGGGCATAATGCCAGGCGGGCCATTACCGTCATTGACGTCAATAGGGGG

NdeI (3509)
3501 CGTACTTGGCATATGATACACTGATGACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACT

PacI (3695)
3601 ATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGTCCAGCCAGGCGGGCCATTACCGTAAGTTATGTAACGCTGCAGGTTAAT
PstI (3688)
SdaI (3687)

BspLU11I (3705)
3701 TAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAGGCCGCTTCTGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAC
3801 AAAAAATCAGCGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGA
3901 CCCTGCCGCTTACCGGATACCTGTCGCTTTCTCCCTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGATAGGTATCTCAGTTCGGTGTAGGTCGT

ApaLI (4019)
4001 TCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCAACCCGGTAAGACACGAC
4101 TTATCGCCACTGGCAGCAGCCACTGTTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGATTCTTGAAGTGGTGGCCTAACTACGGCTACA
4201 CTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTATCGGCAAAACAAACCAGCTGGTAG
4301 CGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGTCTGACGCTCAGTGGAAC

EagI (4455)
4401 **PacI (4435)** **SwaI (4444)** **NotI (4454)**
GAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGG
4501 TTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGAAGTGCAGGTGCC
4601 AGAACATTTCTCTATCGAA