



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

MfeI (82)

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGTTGAGTCGGCTTTCGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

Bsp120I (577)
501 TCTGTTTGTCCGCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTCAGCATGCCGCCACCGCCGGCCCGCCGCGCCCTGGGCAC

AgeI (552) **SphI (560)** **SrfI (573)**
1▶ M P P P P G P A A A L G T

DraIII (637) **BstAPI (669)**
601 TGCCTTCTGCTGCTCCTGCTGGCTTCCGAGTCTTCTCACACTGTGCTTGGCGGCGGTGAGGCGGCGCAGTTTCTGCGGCCAGGCGCGCCGCC

13▶ A L L L L L L L A S E S S H T V L L R A R E A A Q F L R P R Q R R A

701 TACCAAGTCTTCGAGGAGGCCAAGCAGGGCCACTGGAACGGGAGTGCCTGGAGGAGTGTGACAGCAAAGAGGAGGCCAGAGAGGTGTTCGAGAACGACC

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

801 CCGAGACGGAGTATTTCTATCCACGATATCAAGAGTGCATGAGAAAAATGCGAGGCCCTGAAGAAAAAACCAGATTTCCGCAAAATGTGTTCCAGAACTT

80▶ P E T E Y F Y P R Y Q E C M R K Y G R P E E K N P D F A K C V Q N L

901 GCCTGACCAGTGACCCCAAACCTTGTGATAAGAAGGTAAGTACTCATATCTGCCAAGACCTCATGGGCAACTTCTTCTGCTGTGCACAGATGGCTGGGGA

113▶ P D Q C T P N P C D K K G T H I C Q D L M G N F F C V C T D G W G

NgoMIV (1001) **HindIII (1080)**
1001 GGCCGGCTCTGTGACAAAGATGTCAATGAGTGTGCCAGAAGTGGGGGCTGCAGCCAGGTCTGCCACAACAAACCAGGAAGCTTCCAATGTGCCTGCC

147▶ G R L C D K D V N E C V Q K N G G C S Q V C H N K P G S F Q C A C

ClaI (1144)
1101 ATAGTGGCTTCTCGTTGCATCAGACGGCCAGACTGCCAAGATATCGATGAATGCACAGACTCAGACACCTGTGGGGACGCGCATGCAAGAAGCTTGCC

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

PshAI (1299)
1201 AGGCTCCTACTCTTGCCCTGCGATGAGGGATACATACAGCTCCAAGGAGAAGACCTGCCAAGATGTGGACGAGTGCCAGCAGGATCGCTGTGAGCAG

213▶ G S Y S C L C D E G Y T Y S S K E K T C Q D V D E C Q Q D R C E Q

1301 ACCTGTGTAACCTCCCAAGCAGCTATACCTGCCACTGTGATGGGCGAGGGGGCTAAAACCTATCCCAGACATGGATACTTGTGAGGACATCTTACCAT

247▶ T C V N S P G S Y T C H C D G R G G L K L S P D M D T C E D I L P

MscI (1415) **SandI (1459)**
1401 GTGTGCCCTTCAGCATGGCAAGAGCGTGAAGTCTTGTACCTGGGCCGATGTTGAGCGGGACCCCCGTGATTAGACTACGTTCAAGAGGCTTCAGCC

280▶ C V P F S M A K S V K S L Y L G R M F S G T P V I R L R F K R L Q P

1501 TACCAGGCTGCTGGCTGAATTTGACTTCCGCACTTTTGACCCTGAAGGAGTCTCTTCTCGCTGGAGGCCGTTTCCAGACAGCAGCTGGATTGCTGCGGC

313▶ T R L L A E F D F R T F D P E G V L F F A G G R S D S T W I V L G

1601 CTAAGAGCTGGGCGGCTTGTAGCTGCAGCTTCGTTAATGGGCTTGGCGCATCACCAGCAGCGGGCAACCATCAACCACGGCATGTGGCAACTATCT

347▶ L R A G R L E L Q L R Y N G V G R I T S S G P T I N H G M W Q T I

SapI (1705)
1701 CCGTGAAGAGCTGGAACGTAACCTTGTATCAAGGTCAACAAAGATGCTGTAATGAAGATCGCGGTAGCTGGGGAGCTGTTTCACTGAGAGGGGCGCT

380▶ S V E E L E R N L V I K V N K D A V M K I A V A G E L F Q L E R G L

1801 CTATCACCTGAATCTCACCGTGGGCGGCACTTCCCTCAAGGAGAGTGAAGTCTGTCAGCCGATTAACCTCGCTGGATGGGTGCATGAGGAGTTGGAAC

413▶ Y H L N L T V G G I P F K E S E L V Q P I N P R L D G C M R S W N

1901 TGGCTGAACGGGGAAGACAGCGCCATCCAGGAGACAGTCAAGGCAAACAAAAATGCAGTCTTCTGTGACAGAAAGGGCTCCTTCTCCCGGGGA

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

BamHI (2087)
2001 ATGGATTTGCTACCTACAGGCTCAACTACACCCGAACATCGTGGATGTCGGCACGGAAACCCTGGGAAGTTAAAGTTGTGGCTCGGATCCGCCCTGC

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

Tth111I (2137) **SalI (2167)**
2101 CACGGACACGGGGTGTGCTGGCGCTGGTGGGGGACGACGATGTCGTCACCCATCTCTGTGGCCCTAGTTCGACTACCACTCTACAAAGAAGCTCAAGAAG

513▶ T D T G V L L A L V G D D D V V P I S V A L V D Y H S T K K L K K

BsaBI (2241)
2201 CAGTTGGTGGTCTGGCAGTGGAGGATGTTGCCCTGGCACTGATGAAATCAAGGTGTGCGACAGCCAGGAACACACGGTCACTGTCTCCTGCGGGAGG

547▶ Q L V V L A V E D V A L A L M E I K V C D S Q E H T V T V S L R E

XcmI (2306)
2301 GTGAGGCCACCTAGAAAGTGGATGGCACAAGGGCCAGAGTGAAGTGAAGTGCAGTGCAGGAGCGACTGGACACACTTAAGACACATCTGCAAGG

580▶ G E A T L E V D G T K G Q S E V S T A Q L Q E R L D T L K T H L Q G

NsiI (2475) **SacII (2469)**
2401 CTCTGTGCACACCTATGTTGAGGCCTGCCAGAAGTATCGGTGATTTCTGCACCCGCTACTGCGTTCTACCGGGATGCATGACTCTGAGGTAACGGG

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

SphI (2571)

2501 AAAATCCTGGACCTGGATACGGCCTCGTACAAGCACAGTGACATCACCTCCCCTCTGCCCCCTGTGGAGCATGCCACCCCTAGACCGAGCTGCAAG
647▶ K I L D L D T A S Y K H S D I T S H S C P P V E H A T P •

MscI (2623)

NheI (2617)

2601 AGGGCTCCACACCTAAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTGG

HpaI (2755) MfeI (2766)

2701 TGAAATTTGTGATGCTATTGCTTTATTGTAACCATTATAAGCTGCAATAAACAGTTAAACAACAACAAATTGCATTATTTTATGTTTCAGGTTTCAGGGG

EcoRI (2851)

2801 GAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTTAACCTCCAAATCAAGCCTC
2901 TACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTT

SapI (3033) SspI (3090)

3001 AAGATATAGTGATTTTCCCAAGTTTGAACCTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATCCCTTTTATGAAAAATTTCCAGA

SwaI (3104)

3101 AATAATTTAAATACATCATTGCAATGAAAATAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGG

3201 ACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGGATGAGTTCCTCAATG
3301 GTGGTTTTGACCAGCTTGCCATTTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCC
127▶ 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 M G C P S V R
3401 TGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCAGCAGACCCAATGGCAATGGC
94▶ 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 V A S G I A I A
3501 TTCAGCACAGACAGTACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCGACATGGTGCTG
61▶ 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 A A G V H H K

XmnI (3671)

3601 TTGCCTCATAGAGCATGGTATCTTCTCAGTGGCAGCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGT
27▶ 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 K M

AseI (3737)

3701 GAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGTTCACTAAACGAGCTC

SpeI (3892)

3801 TGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTGGAAAGTCCCGTTGATTTACTAGTCA
3901 AAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATC

SnaBI (4020)

4001 ATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGTGCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCAT

NdeI (4125)

4101 TGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAAGT
4201 CCCTATTGGCGTTACTATGGAAACATACGTCATTATTGACGTCAATGGGCGGGGCTGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTA

PacI (4311)

SdaI (4303) BspLU11I (4321)

4301 ACGCCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGGAAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCC
4401 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGTCCCTCGTG
4501 CGCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCA
4601 GTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA
4701 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGG
4801 CCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAC
4901 AAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTC

EagI (5071)

PacI (5051) SwaI (5060) NotI (5070)

5001 TGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTCAT

5101 TACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCCTCATAAAAAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAG
5201 TGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA