



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

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTTCGAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGGCTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
Bsp120I (583)
AgeI (552)
NcoI (560)
SrfI (579)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGCCCTTCGCTCTCGCCCGGGCCGCCCTGCG

1▶ M A P S L S P G P A A L R

SacII (632)

601 CGCGCGCCGCGAGCTGCTGCTGCTGCTGCTGGCCGCGGAGTGC GCGCTTGCCGCGCTGTTGCCGGCGCGAGGCCACGCAGTTCCTGCGGCCAGGCAG

13▶ R A P Q L L L L L L A A E C A L A A L L P A R E A T Q F L R P R Q

701 CGCCGCGCCTTTAGGCTTCGAGGAGGCAAGCAGGGCCACCTGGAGAGGGAGTGCCTGGAGGAGCTGTGCAGCCGCGAGGAGGCGGGAGGTGTTCCG

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

801 AGAACGACCCCGAGACGGATTATTTTTACCCAAGATACTAGACTGCATCAACAAGTATGGGTCTCCGTACACAAAACTCAGGCTTCGCCACCTGCGT

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

ApaLI (918)
SandI (946)

901 GCAAACTCGCTGACCAAGTGCACGCCAACCCCTGCGATAGGAAGGGACCAAGCCTGCCAGGACCTCATGGGCAACTTCTTGCCTGTGTAAGCT

113▶ Q N L P D Q C T P N P C D R K G T Q A C Q D L M G N F F C L C K A

BglIII (1067)

1001 GGCTGGGGGGCCGGCTCTGCGACAAAGATGTCAACGAATGCAGCCAGGAGAACGGGGGCTGCCTCCAGATCTGCCACAACAAGCCGGGTAGCTTCCACT

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

FspI (1162)
StuI (1175)

1101 GTTCTGCCACAGCGGCTTCGAGCTCCTCTGATGGCAGGACCTGCCAAGACATAGACGAGTGCAGACTCGGAGGCTCGGGGAGGCGCGCTGCAA

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

PshAI (1279)

1201 GAACCTGCCCCGCTCCTACTCCTGCCTCTGTGACGAGGGCTTTGCGTACAGCTCCCAGGAGAAGGCTTGCCGAGATGTGGACGAGTGTCTGCAGGGCCGC

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

1301 TGTGAGCAGGTCTGCGTAACTCCCAAGGAGCTACACCTGCCACTGTGACGGGCGTGGGGCCCTCAAGCTGTCCAGGACATGGACACCTGTGAGGACA

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

MscI (1424)
SandI (1468)

1401 TCTTGCCGTGCGTGCCCTTCAGCGTGGCCAAGAGTGTGAAGTCTTGTACCTGGCCGGATGTTGAGTGGACCCCGTGATCCGACTGCGCTTCAAGAG

280▶ I L P C V P F S V 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

BstXI (1508)
BspEI (1535)

1501 GCTGCAGCCCACAGGCTGGTAGCTGAGTTTGACTTCCGGACCTTTGACCCCGAGGGCATCCTCCTTTTCCGGAGGCCACCAGGACAGCACCTGGATC

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

NcoI (1686)

1601 GTGCTGGCCCTGAGAGCCGCGCGGCTGGAGCTGCAGCTGCGTACAACGGTGTGCGCCGTGTACCAGCAGCGGCCCGGTCATCAACCATGGCATGTGGC

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

BspHI (1760)

1701 AGACAATCTCTGTTGAGGAGCTGGCGCGGAATCTGGTTCATCAAGTCAACAGGGATGCTGTGATGAAAATCGCGGTGGCCGGGACTTGTCCAACCGGA

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

1801 GCGAGGACTGTATCATCTAACCTGACCGTGGGAGGTATCCCTTCCATGAGAAGGACCTCGTGCAGCCTATAAACCTCGTGGATGGCTGCATGAGG

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

1901 AGCTGGAAGTGGTGAACGGAGAAGACACCACCATCCAGGAAACGGTGAAGTGAACACGAGGATGCAGTGTCTCGGTGACGGAGAGAGGCTCTTTCT

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

BsrBI (2007)

2001 ACCCCGGGAGCGGCTTCGCTTCTACAGCCTGGACTACATGCGGACCCCTCTGGACGTGCGGACTGAATCAACCTGGGAAGTAGAAGTCGTGGCTCACAT

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

Bsp120I (2138)

2101 CCGCCAGCCGACAGACAGGCGTGTGTTGCGCTCTGGCCCGCCGACCTCCGTGCCGTGCCTCTCTGTGGCACTGGTAGACTATCACTCCACGAAG

513▶ R P A A D T G V L F A L W A P D L R A V P L S V A L V D Y H S T K

BstEII (2289)

BbrPI (2284)

2201 AAACCAAGAAGCAGCTGGTGGTCTGGCCGTGGAGCATAACGGCTTGGCCCTAATGGAGATCAAGGTCGACGGCCAAGAGCAGTGGTACCGTCT

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

XcmI (2318)
XhoI (2392)

2301 CGCTGAGGACGGTGAAGCCACCTGGAGGTGGACGGCACCAGGGCCAGAGCGAGGTGAGCACCAGGCGAGCTGCAGGAGAGGCTGGCCGTGCTCGAGAG

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

2401 GCACCTGCGGAGCCCCGTGCTCACCTTTGCTGGCGCCTGCCAGATGTGCCGGTGACTTCAGCGCCAGTCACCGGTTCTACCGCGGCTGCATGACACTG
613▶ H L R S P V L T F A G G L P D V P V T S A P V T A F Y R G C M T L

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

MseI (2618)
NheI (2612)
2601 CCCCCACGGGACGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAA

HpaI (2750) MfeI (2761)
2701 TTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAACACAACAATTGCATTCTTTTATGTTTCAGGTTCCAGGGGAGGT

EcoRI (2846)
2801 GTGGGAGGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTT
2901 GAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTTCATGGAGTTAAGAT

SapI (3028) SspI (3085) SwaI (3099)
3001 ATAGTGTATTTTCCCAAGTTTGAACAGTCTTTCATTTCTTTATGTTTTAAATGCAGTACCTCCACATCCCTTTTTAGTAAAATATTCAGAAATAA
3101 TTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTA
3201 GGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGT
141◀ • N R T Y K L P I L E E I T T

BstXI (3389)
3301 TTTGACCAGTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATG
126◀ 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 V R I
3401 GATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCAGAGACCAATGGCAATGGCTTCAG
92◀ 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 E A

StuI (3524)
3501 CACAGACAGTGACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCACTTGGTCTGATGGCCGCCGACATGGTGTCTGTTGTC
59◀ 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 N D

XmnI (3666)
3601 CTCATAGAGCATGGTGTCTTCTCAGTGGCAGCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTTCATGGTGGCCCTCTATAGTGAGTC
26◀ 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 (3732)
3701 GTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTT

SpeI (3887)
3801 ATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACA
3901 AACTCCCATTGACGTCAATGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAACCGCATCATCATGGT

SnaBI (4015)
4001 AATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTAAGTGGGCATAATGCCAGGCGGGCCATTTACCGTATTGACG

NdeI (4120)
4101 TCAATAGGGGGCTACTTGGCATATGATACACTTGATGTAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTA

SdaI (4298)
4201 TTGGCGTTACTATGGAAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCC

PacI (4306) BspLU11I (4316)
4301 TGCAAGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTG
4401 ACGAGCATCAGAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGGCTC
4501 TCCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCG

ApaLI (4630)
4601 GTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGG
4701 TAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAA
4801 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAAC
4901 ACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGTCTGACG

PacI (5046) SmaI (5055) NotI (5065)

5001 CTCAGTGAACGAAAACACGTTAAGGGATTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACAT

5101 CTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAA

5201 GTGCAGGTGCCAGAACATTTCTCTATCGAA