



PvuI (7)
SgfI (6) MfeI (82)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) HindIII (245) Bsu36I (291)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) BspHI (560) SacII (578)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTTCATCATGACCGCGCGGGGCGCCGCGGGGCGCTGCCTTCTTC
1▶ M T A R G A A G R C P S S

BspHI (638)
601 GACATGGCTGGGCTCCCGCTGCTGCTGGTCTGTCTCCTCATGAGCAGGAGTATTGCCAAGGAGGTGTGAGAACACTGTAGCCACATGATTGGGAATGGA
13▶ T W L G S R L L L V C L L M S R S I A K E V S E H C S H M I G N G

PstI (712)
701 CACCTGAAGGTCTGCAGCAGTTGATCGACAGTCAAATGGAGACTTCATGCCAGATTGCCTTTGAATTTGTAGACCAGGAACAGCTGGATGATCCTGTTT
47▶ H L K V L Q Q L I D S Q M E T S C Q I A F E F V D Q E Q L D D P V
801 GCTACCTAAAGAAGGCTTTTTCTGGTACAAGACATAATAGATGAGACCATCGCTTTAAAGACAACACCCCAATGCTAACGCCACCGAGGCTCCA
80▶ C Y L K K A F F L V Q D I I D E T M R F K D N T P N A N A T E R L Q
901 GAAACTCTCAATAAAGCTGAACAGCTGCTTACCAAGGACTATGAGGAGCAGAACAAGGCTGTGTCCGAACCTTCCATGAGACTCCTCTCCAGCTGCTG
113▶ E L S N N L N S C F T K D Y E E Q N K A C V R T F H E T P L Q L L
1001 GAGAAGATCAAGAAGCTTTTAAATGAAACAAAGAAATCTCCTTGAAAAGGACTGGAACATTTTTACCAAGAAGTCAACAACAGCTTTGCTAAGTGCTCTA
147▶ E K I K N F F N E T K N L L E K D W N I F T K N C N N S F A K C S

BstEII (1110)
1101 GCCGAGATGTGGTGACCAAGCCTGATTGCAACTGCCTGTACCTAAAGCCACCCCTAGCAGTGACCCGGCCTCTGCCTCCCCTCACCAGCCCCCGCCCC
180▶ S R D V V T K P D C N C L Y P K A T P S S D P A S A S P H Q P P A P

XcmI (1202) NcoI (1202)
1201 CTCATGGCCCTCTGGCTGGCTTGGCTTGGGATGATTCTCAGAGGACAGAGGGCAGCTCCCTCTTGCCAGTGAGCTTCCCCTTCGCATAGAGGACCA
213▶ S M A P L A G L A W D D S Q R T E G S S L L P S E L P L R I E D P

XhoI (1342) NcoI (1365)
1301 GGCAGTGCCAAGCAGCGACCACCCAGGAGTACCTGCCAGACCTCGATCAACAGAGCAACCAACCATGGGGACAGACTCACTGAGGACTCACAACTC
247▶ G S A K Q R P P R S T C Q T L E S T E Q P N H G D R L T E D S Q P

Bsp120I (1414) HindIII (1478)
1401 ATCCTTCTGCGGGGGGGCCCGTCCCTGGGGTGAAGACATTCTGAATCTTACTGGGCACTAACTGGTCCCTAGAAGAAGCTTCTGGAGAGGCTAGTGA
280▶ H P S A G G P V P G V E D I L E S S L G T N W V L E E A S G E A S E

Bsp120I (1580)
1501 GGGATTTTTGACCAGGAAGCAAAGTTTTCCCTCCACGCTGTAGGGGACAGATCCAGGCAGAGACTGACAGACCCAGGCCCCTCAGCATCTCCA
313▶ G F L T Q E A K F S P S T P V G G S I Q A E T D R P R A L S A S P

MscI (1680)
1601 TTCCTAAATCAACAGAGGACAAAAGCCAGTGGATATAACAGACAGGCCGTTGACAGAGGTGAACCTATGAGACCCATTGGCCAGACACAGAATAATA
347▶ F P K S T E D Q K P V D I T D R P L T E V N P M R P I G Q T Q N N
1701 CTCCTGAGAAGACTGATGGTACATCCACGCTGCGTGAAGACCACAGGAGCCAGGCTCTCCCATATTGCGACACCGAATCCCAACGAGTCAGCAACTC
380▶ T P E K T D G T S T L R E D H Q E P G S P H I A T P N P Q R V S N S
1801 AGCCACCCCGTTGCTCAGTTACTGCTTCCAAAAGCCACTCTGGGGCATTGTGCTGCCCTTGGGGAGCTTGAGGGCAAGAGAAGTACCAGGGATCGA
413▶ A T P V A Q L L L P K S H S W G I V L P L G E L E G K R S T R D R
1901 AGGAGCCCGCAGAGCTGGAAGGAGGATCAGCAAGTGAAGGGGAGCCAGGCTGTGGCCGTTTTAATTCATTCTTTGACTGACACAGGCATGTGG
447▶ R S P A E L E G G S A S E G A A R P V A R F N S I P L T D T G H V

BamHI (2011)
2001 AGCAGCATGAGGGATCTCTGACCCCGATCCCTGAGTCTGTCTTCCACCTGCTGGTGGCGGCATCATCTAGTCTTGTGACTGTTGGGGCCTCCT
480▶ E Q H E G S S D P Q I P E S V F H L L V P G I I L V L L T V G G L L
2101 GTTCTACAAGTGAAGTGGAGGACCATCGAGACCCTCAGACATTGGATTCTTCTGTGGGGGACCCAGGACAGCTCCCTGACCCAGGATGAGGACAGA
513▶ F Y K W K W R S H R D P Q T L D S S V G R P E D S S L T Q D E D R

NdeI (2269)
2201 CAGGTGGAAGTCCAGTATAGAAAGGATTCTATGCTGGGCACACAGGACTATCTCTTTATGGAAGGAGACATATGGGAACATCCACCACTACCCTCTCCT
547▶ Q V E L P V •

MscI (2362) NheI (2356)
2301 ACCATCTTCTGGGAATGTGGCCTACCACTACCAGAGCTCCTGCCTACCAAGACTGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACA

HpaI (2494)
2401 ACCACAAGTGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAC

MfeI (2505) EcoRI (2590)
 2501 AACACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAA
 2601 ATACAGCATAGCAAACCTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTG

SapI (2772)

2701 CATTAGCTGTTTGAGCCTCACCTTCTTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTAAATGC

SspI (2829) SmaI (2843)

2801 ACTGACCTCCACATTCCCTTTTGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATG
 2901 CTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTT

141

3001 TAGTTCCTGGTGTACTTGAGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAG
 140 • N R T Y K 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
 3101 AGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGCCACCTCATCAGAGTAGGGGCTGCAGCCACAATGGTGTCAAAGTC
 107 I L E R C 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
 3201 CTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTGCACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCC
 74 K Q G N S 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 E
 3301 CCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCT
 40 G T K T R I 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

AseI (3476)

3401 GAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGAT
 7 S I N F T K M
 3501 GCGCTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTT

SpeI (3631)

3601 GTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCCG

SnaBI (3759)

3701 TATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAAGTCA

NdeI (3864)

3801 TGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGT
 3901 TTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTG

PacI (4050)

PstI (4043) SdaI (4042) BspLU11I (4060)

4001 GGCGGTACAGCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAA
 4101 AAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAAGGTTGGCGAAACCCGACAGGACTA
 4201 TAAAGATACCAGCGTTTTCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAA

ApaLI (4374)

4301 GCGTGGCGTTTTCTCATAGCTCACGCTGAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGA
 4401 CCGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCCAAACCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCG
 4501 AGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA
 4601 CCTTCGGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAGCAGATTACCGCGAGAAAAAA

PacI (4790) SmaI (4799)

4701 AGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACA

EagI (4810) NotI (4809)

4801 TTTAAATCAGCGCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAA
 4901 AACGAAACAAACAACTAGCAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA