



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTTCGAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCGCCCGCCCTACCTGAGGCC

HindIII (245) 301 GCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

Bsu36I (291)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

NgoMIV (441)

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTACCATTGGCTGGACCTGCCACCCAGAGCCCCATGAAGCTGAT

BstEII (555) 1▶ M A G P A T Q S P M K L M
AgeI (552) **NcoI (560)** **XcmI (587)**

601 GGCCTGCAGCTGCTGTGGCACAGTGCACCTCTGGACAGTGCAGGAAGCCACCCCTGGCCCTGCCAGTCCCTGCCCCAGAGCTTCTGCTCAAG

BstAPI (606) 13▶ A L Q L L L W H S A L W T V Q E A T P L G P A S S L P Q S F L L K
ApaLI (626) **Bsp120I (660)**

701 TGCTTAGAGCAAGTGAAGAAGTCCAGGGCGATGGCGCAGCGCTCCAGGAGAAGCTGTGTCCACCTACAAGCTGTGCCACCCGAGGAGCTGGTGCTGC

47▶ C L E Q V R K I Q G D G A A L Q E K L C A T Y K L C H P E E L V L
Eco47III (738)

801 TCGGACACTCTCTGGCATCCCTGGGCTCCCTGAGCAGCTGCCACAGCCAGCCCTGCAGCTGGCAGGCTGCTTGAAGCAACTCCATAGCGGCTTTT

80▶ L G H S L G I P W A P L S S C P S Q A L Q L A G C L S Q L H S G L F

901 CCTCTACCAGGGCTCCTGCAGGCCCTGGAAGGGATCTCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCACTTTGCCACCAC

SdaI (915) 113▶ L Y Q G L L Q A L E G I S P E L G P T L D T L Q L D V A D F A T T
SandI (948)

1001 ATCTGGCAGCAGATGGAAGAAGTGGAAATGGCCCTGCCTGCAGCCACCCAGGGTCCATGCCGCTTCCGCTTCTGTTTCCAGCGCCGGCAGGAG

NgoMIV (1062) 147▶ I W Q Q M E E L G M A P A L Q P T Q G A M P A F A S A F Q R R A G
 1101 GGGTCTAGTTGCCTCCATCTGCAGAGCTTCTGGAGGTGTCTACCGCTTCTACGCCACTTGGCCAGCCCTGAGCCAAGCCCTCCCATCCATGT

180▶ G V L V A S H L Q S F L E V S Y R V L R H L A Q P •

1201 ATTTATCTCTATTTAATTTATGTCTATTTAAGCCTCATATTTAAAGACAGGGAAGAGCAGAACGCTAGCTGGCCAGACATGATAAGATACATTGATGA

SspI (1214) **SapI (1253)** **NheI (1265)** **MscI (1271)**

1301 GTTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAA

1401 CAAGTTAAACAACA AATTGCATTCA TTTTATGTTTCAGGTT CAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGG

HpaI (1403) **MfeI (1414)** **EcoRI (1499)**

1501 AATTCTAAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTT

1601 GCCAATGTGATTAGCTGTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGGTTTGAAGTACTGCTCTTCATTTCTTTATGT

SapI (1681)

1701 TTTAAATGCACTGACCTCCACATTCCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGA

SspI (1738) **SwaI (1752)**

1801 ATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTGTAGTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGC

1901 TTCTAGCTTGTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAG

141▶ • 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

2001 CATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGT

SacI (2013) 110▶ Y D S 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

2101 GTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAATGGCAATGGCTTTCAGCACAGACAGTACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAG

77▶ D F D 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
StuI (2177)

2201 ATGATCTCCCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCA

43▶ I I E 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

2301 GATCTGCTGAGAGATGTTGAAGGCTTCATGGTGGCCCTCTATAGTGTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAC

XmnI (2319) 10▶ D Q Q S I N F T K M
AseI (2385)

2401 AGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGG

SacI (2442)

2501 GGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGAGACTTGAAATCCCCGTGAG

SpeI (2540)

2601 TCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCC

SnaBI (2668)

2701 ATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTACCCTGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAA

NdeI (2773)

2801 GTGGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTATTATTGACGTCAATGGGCGG

2901 GGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTACCCTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAG

SdaI (2951) PacI (2959) BspLU11I (2969)

3001 GAACCGTAAAAAGGCCGCTTGTGCGCTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCG

3101 ACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCC

3201 CTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGT

ApaLI (3283)

3301 TCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT

3401 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGA

3501 AGCCAGTTACCTTCGAAAAAGATTGGTAGCTCTTGATCCGGCAAACAACACCGCTGGTAGCGGTGGTTTTTTTGTTCGCAAGCAGCAGATTACCGG

3601 CAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGTAGT

PacI (3699)

EagI (3719)

Swal (3708) NotI (3718)

3701 TAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCA

3801 TCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA