



PvuI (7)
SgfI (6)
 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGGCC
 301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **SphI (560)**
 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTGAGCATGCAGAGTAATAAACTTTTAACTTGAGAGAAGCAAAA
 601 CCATACTCCAAGAAAGCATCATCAACATCACCACCAGCAGCAGCACCACCAGCAGCAACAGCAGCAGCCGCCACCACCAGCAATACCTGCAAATGGGCAA
 13▶ H T P R K H H Q H H H Q Q Q H H Q Q Q Q Q P P P P P I P A N G Q Q
 701 CAGGCCAGCAGCAAAATGAAGCTTACTATTGACCTGAAGAATTTAGAAAACCAGGAGAGAAGACCTTACCCAAACGAAGCCGCTTTTTGTGGGAA
 47▶ Q A S S Q N E G L T I D L K N F R K P G E K T F T Q R S R L F V G
 801 ATCTTCTCCGACATCACTGAGGAAGAAATGAGGAACTATTTGAGAAATATGAAAAGGCAGGCGAAGTCTTATTATAAGGATAAAGGATTTGGCTT
 80▶ N L P P D I T E E E M R K L F E K Y G K A G E V F I H K D K G F G F

DraIII (959)
 901 TATCCGCTTGAAAACCCGAACCTAGCGGAGATTGCCAAAGTGGAGCTGGACAATATGCCACTCCGTGGAAAGCAGCTGCGTGTGCGCTTTGCTGCCAT
 113▶ I R L E T R T L A E I A K V E L D N M P L R G K Q L R V R F A C H

BstBI (1016) **MscI (1074)**
 1001 AGTGCATCCCTTACAGTTCGAAACCTTCTCAGTATGTGTCCAACGAAGTCTGGAAGAAGCCTTTTCTGTGTTTGGCCAGGTAGAGAGGGCTGTAGTCA
 147▶ S A S L T V R N L P Q Y V S N E L L E E A F S V F G Q V E R A V V

Bsu36I (1121)
 1101 TTGTGGATGATCGAGGAAGGCCCTCAGGAAAAGCATTGTTGAGTTCCTCAGGGAAGCCAGCTGCTCGGAAAGCTCTGGACAGATGCAGTGAAGGCTCCTT
 180▶ I V D D R G R P S G K G I V E F S G K P A A R K A L D R C S E G S F

NcoI (1238)
 1201 CCTGTAACCACATTTCTCGTCTGTGACTGTGGAGCCATGGACCAGTTAGATGATGAAGAGGGACTTCCAGAGAAGCTGGTTATAAAAAACAGCAA
 213▶ L L T T F P R P V T V E P M D Q L D D E E G L P E K L V I K N Q Q
 1301 TTTACAAGGAACGAGAGCAGCCACCCAGATTTGCACAGCCTGGCTCCTTTGAGTATGAATATGCCATGCGCTGGAAGGCACTCATTGAGATGGAGAAGC
 247▶ F H K E R E Q P P R F A Q P G S F E Y E Y A M R W K A L I E M E K
 1401 AGCAGCAGGACCAAGTGGACCGCAACATCAAGGAGGCTCGTGAAGACTGGAGATGGAGATGGAAGCTGCACGCCATGAGCACCAGGTATGCTAATGAG
 280▶ Q Q Q D Q V D R N I K E A R E K L E M E M E A A R H E H Q V M L M R
 1501 ACAGGATTTGATGAGGCGCAAGAAGAACTTCGAGGATGGAAGAGCTGCACAACCAAGAGGTGCAAAAACGAAAGCAACTGGAGCTCAGGCAGGAGGAA
 313▶ Q D L M R R Q E E L R R M E E L H N Q E V Q K R K Q L E L R Q E E
 1601 GAGCGCAGGCGCGTGAAGAAGAGATGCGGCGCAGCAAGAAGAAATGATGCGGCGACAGCAGGAAGGATTCAAGGGAACCTTCCCTGATGCGAGAGAGC
 347▶ E R R R R E E E M R R Q Q E E M M R R Q Q E G F K G T F P D A R E

Acc65I (1786)
 1701 AGGAGATTCGGATGGTCCAGATGGCTATGGGAGTGTATGGGCATAAACAACAGAGTGCCATGCCCTGCTCCTGTGCCAGTGGTACCCAGCTCC
 380▶ Q E I R M G Q M A M G G A M G I N N R G A M P P A P V P A G T P A P
 1801 TCCAGGACCTGCCACTATGATGCCGGATGGAACCTTTGGGATTGACCCACCAACAACCTGAACGCTTTGGTCAGGCTGTACAATGGAAGGAATTTGGGCA
 413▶ P G P A T M M P D G T L G L T P P T T E R F G Q A A T M E G I G A
 1901 ATTGGTGAACCTCCTCCTGCATTCAACCGTGCAGCTCCTGGAGCTGAATTTGCCCAACAACCGTCCGATATAAAGTGCAGTGTCTAGTTTCT
 447▶ I G G T P P A F N R A A P G A E F A P N K R R R Y •

MscI (2015)
NheI (2009)
 2001 CAAAACCTGTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTT

HpaI (2147)
 2101 GTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTCATTCTTTATGTTTCAGGTTACAGGGGAGGTGTG

EcoRI (2243)
 2201 GGAGGTTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAAATCTAATAACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAA
 2301 TCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATA

SspI (2482) **SwaI (2496)**
 2401 GTGTATTTTCCAAGGTTTGAAGTACTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGAAAATATTCAGAAATAATTT
 2501 AAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGG
 2601 AACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTT

141 • N R T Y K L P I L E E I T T K

BstXI (2786)

2701 GACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGAT
125 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 S
2801 CTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCAC
91 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 C

StuI (2921)

2901 AGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGTCCTC
58 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 E
3001 ATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTA
25 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 (3129)

3101 TTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAACGAGCTCTGCTTATA

SpeI (3284)

3201 TAGACCTCCCACCGTACACGCCTACCGCCATTTCGTCATATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAAC

3301 TCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAAT

SnaBI (3412)

3401 AGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGTTCATGTACTGGGCATAATGCCAGGCGGGCCATTACCCTGATTGACGTCA

NdeI (3517)

3501 ATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCCTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTG

PstI (3696)

SdaI (3695)

3601 GCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGTCCAGCCAGGCGGGCCATTACCCTAAGTTATGTAACGCTGC

PacI (3703) **BspLU11I (3713)**

3701 AGGTTAAITTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACG

3801 AGCATCACA AAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCC

3901 TGTTCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTG

ApaLI (4027)

4001 TAGGTCGTTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAA

4101 GACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTA

4201 CGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACC

4301 GCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTC

EagI (4463)

PacI (4443) **Swal (4452)** **NotI (4462)**

4401 AGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAATCAGCGGCCAATAAAAATATCTTTATTTTCATTACATCTG

4501 TGTGTTGGTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAACAAAACGAAACAAAACAAAACAGCAAAAATAGGCTGTCCCAGTGCAAGTG

4601 CAGGTGCCAGAACATTTCTCTATCGAA