



PvuI (7) **SgfI (6)** **MfeI (82)**
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGGAAAGTATGTCGTGTACTGGCTCCGCCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)**
201 GTGAACGTTCTTTTTGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCGCCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMI (441) **NaeI (441)**
401 GGGCCTTTGTCCGGCGCTCCCTTGAGGCTACCTAGACTCAGCCGGCTCCACGCTTTCCTGACCTGCTTGTCAACTCTACGCTTTTGTTTCGTTT

SphI (560) **AgeI (552)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTACGATGCAGCCTTGGCACGGAAAGGCCATGCAGAGAGCTTC
1 M Q P W H G K A M Q R A S

BamHI (657)
601 CGAGGCCGAGCCACTGCCCCAAGGCTCCGCACGGAATGCCAGGGGCGCCCGATGGATCCACCGAGTCCGGTGCCTCCCGAGGCCCGCTGCCT
13 E A G A T A P K A S A R N A R G A P M D P T E S P A A P E A A L P

BamHI (733) **Bsp120I (794)**
701 AAGGCGGAAAGTTCCGCCCCGCGAGGATCGGGATCCCGCAGAAAAGAGCGCCCGGACACCAGAGAGCGCCCGTCCGCGCAACTGGGGCC
47 K A G K F G P A R K S G S R Q K K S A P D T Q E R P P V R A T G A

NgoMI (897) **NaeI (897)**
801 GCGCCAAAAGGCCCTCAGCGGCCAGGACACGAGCCGCTGACGCCACGAGCCCTGGGGCAGAGGGCTGGAGCCTCCTCGCGCTCGGGAGCC
80 R A K K A P Q R A Q D T Q P S D A T S A P G A E G L E P P A A R E P

Bsp120I (970) **SmaI (967)** **SrfI (966)**
901 GGCTCTTCCAGGGCTGGTCTTGCCGCCAGAGGGGCGCGCTGCTCCACGAAGCCAAAGACCTCCGCCGGCCCTGGGACGTGCCAGCCCCGGCCTG
113 A L S R A G S C R Q R G A R C S T K P R P P P G P W D V P S P G L

BsiWI (1020) **EcoRV (1093)**
1001 CCGGTCTCGGCCCATCTCTGACGAGGGATCGCGCGCTGGGCCCTCGAAGTCCGGCGGTTTTGGAGAAGTTGAAGCTCAGCCGCGATGATATCT
147 P V S A P I L V R R D A A P G A S K L R A V L E K L K L S R D D I
1101 CCACGCGCGGGGATGGTAAAGGGGTTGTGGACCCTGCTGCTCAGACTGAAGTGCAGCTCCGCGTTCAGAGGCGTCCGGTCTGAACACCGGGAG
180 S T A A G M V K G V V D H L L L R L K C D S A F R G V G L L N T G S

BbrPI (1210) **PmeI (1248)**
1201 CTACTAGCAGCTGAAGATTTCTGCACCTAATGAATTTGATGTCATGTTAACTGGAAGTCCCAGAATCAACTAGAAGAATATCCAACACTCGT
213 Y Y E H V K I S A P N E F D V M F K L E V P R I Q L E E Y S N T R
1301 GCATATTACTTTGAAATTTAAAGAAATCCGAAAGAAATCCTCTGAGTCAGTTTTTAGAAGTGAATATTATCAGCTTAAAGTGTCAAAGT
247 A Y Y F V K F K R N P K E N P L S Q F L E G E I L S A S K M L S K

BspHI (1451)
1401 TTAGGAAAATCATTAAAGAGAAATTAACGACATTAAGATACAGATGTCATGAAGAGAAAAGAGGAGGCCCTGCTGTAACACTTCTTATTAG
280 F R K I I K E E I N D I K D T D V I M K R K R G G S P A V T L L I S

FspI (1574) **NheI (1555)** **StuI (1569)**
1501 TGAAAAATATCTGTGGATATAACCCCTGGCTTTGGAATCAAAAAGTAGCTGGCTGTAGCACCAAGAAGCCCTGCGCATTCAAACTGGCTTTCAGCA
313 E K I S V D I T L A L E S K S S W P A S T Q E G L R I Q N W L S A

SphI (1647)
1601 AAAGTTAGGAAGCAACTACGACTAAAGCCATTTTACCTTGTACCCAAGCATGCAAGGAAGGAAATGGTTTTCCAAGAAGAAACATGGCGGCTATCCTTCT
347 K V R K Q L R L K P F Y L V P K H A K E G N G F Q E E T W R L S F
1701 CTCACATCGAAAAGGAAATTTGAACAATCATGGAATAATCAAAACGTGTGTGAAAACAAAAGAGAAATGTTGAGGAAAGATGTTTAAACATAAT
380 S H I E K E I L N N H G K S K T C C E N K E E K C C R K D C L K L M

PvuII (1816)
1801 GAAATACCTTTTGAACAGCTGAAAGAAAGGTTTAAAGCAAAAAACATCTGGATAAATCTCTTCTTATCATGTGAAAAGTGCCTTCTTTCACGTATGT
413 K Y L L E Q L K E R F K D K K H L D K F S S Y H V K T A F F H V C
1901 ACCCAGAACCCTCAAGACAGTCAGTGGGACCGCAAAGACCTGGGCCCTGCTTTGATAAAGTGCAGTACACTTCTTTCAGTGCCTCAGGACAGAAAAAC
447 T Q N P Q D S Q W D R K D L G L C F D N C V T Y F L Q C L R T E K
2001 TTGAGAATTTTATTCTGAAATCAATCTATTCTAGCAACTTAATTGACAAAAGAAAGTAAAGAAATTTCTGACAAAAGCAAAATGAATATGAAAGAAA
480 L E N Y F I P E F N L F S S N L I D K R S K E F L T K Q I E Y E R N

BamHI (2128) **NdeI (2168)**
2101 CAATGAGTTTCCAGTTTTGATGAATTTGGATCCTATCCCTATGATGTGCCAGACTATGCTGGCTATCCATATGATGTTCTGATTATGCTGGATACCC
513 N E F P V F D E F G S Y P Y D V P D Y A G Y P Y D V P D Y A G Y P

MscI (2231) **NheI (2225)**
2201 TATGATGTCCAGACTATGCTCAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCAACAAGTGCAGTGAATAAATGC
547 Y D V P D Y A •

HpaI (2363) **MfeI (2374)**
2301 TTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTAAGCTGCAATAAACAAGTTAAACAACAATTCGATTCATTTATGTTTCAGG
2401 TTCAGGGGGAGGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTTAAAATACAGCATAGCAAACTTTAACCTCCAAAT
2501 CAAGCCTCTACTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCA
2601 TGGAGTTAAGATATAGTATTTTCCCAAGTTTGAAGTCTCTCATTTCTTATGTTTTAAATGCACTGACCTCCACATCCCTTTTATAGTAAA

2701 ^{SwaI (2712)} TATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTA

2801 GTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTT
 141 • N R T Y K L P I L E
 SacI (2973)
 Ecl136II (2973)

2901 CCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCGACATGCCACAGGGCT
 130 E I 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
 BstXI (3002)

3001 GACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGCCCAATG
 97 V V R 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
 StuI (3137)

3101 GCAATGGCTTCAGCAGACAGTACCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGCCGCCCGGACAT
 63 A I A 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
 BspHI (3287)
 BpuAI (3283)
 BbsI (3283)
 XmnI (3279)

3201 GGTGCTTGTTCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGCCCT
 30 H K 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 ←

3301 CCTATAGTGAGTCGTATTATACTACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCTGGATGGCGTCTCCAGCTTATCTGACGGTCTACTAA
 AseI (3345)

3401 ^{SacI (3402)}
^{Ecl136II (3402)} ACGAGCTCTGTTATATAGACCTCCACCGTACACGCCATCCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTT

3501 ^{SpeI (3500)} ACTAGTCAAACAACCTCCATTGACGTCAATGGGTGGAGACTTGGAAATCCCGTGGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACC

3601 ^{SnaBI (3628)} GCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGCCATTT

3701 ^{NdeI (3733)} ACCGTCATTGACGTCAATAGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAA

3801 TGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTATTATTGACGTCAATGGGCGGGGTCGTTGGCGGTGAGCCAGGCGGCCATTTACCGTAA

3901 ^{PacI (3919)}
^{PstI (3912)}
^{SdaI (3911)}
^{SbfI (3911)} GTTATGTAACGCCTGCAGTTAATTAAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCCGGTTGCTGGCGTTTTTCCATAGG
^{PciI (3929)}
^{BspLUIII (3929)}

4001 CTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTTCCCTGGAAGCT

4101 CCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAG

4201 ^{ApaLI (4243)} GTATCTCAGTTCGGTGTAGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTT

4301 GAGTCAAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGA

4401 AGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATC

4501 CGGCAAAACAAACCCGCTGGTAGCGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT

4601 ^{EagI (4679)}
^{PacI (4659)} ^{Swal (4668)} ^{NotI (4678)} ACGGGGCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCGCCGAATAAAATATCTTT

4701 ATTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTT

4801 GTCACAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA