



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**

101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAACACAGTGAAGCTTCGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGCC **HindIII (245)**

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGTCAAGTGCAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT **NgoMIV (441)**

501 TCTGTTTGTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCCATGGTAGGGCTGGGAGCTGCACCCTGACTGGAGTTAC **KasI (535)** **BstEII (555)** **AgeI (552)**
1 M V G L G A C T L T G V T

601 CCTGATCTTCTTGTACTCCCAGAAGTCTGGAGAGCTGTGGACACATCGAGATTTACCCCTGTTGTCCGCTGGGGACCTGTCCTGGCCTCTTGC **BglIII (740)** **BstAPI (789)**
13 L I F L L L P R S L E S C G H I E I S P P V V R L G D P V L A S C

701 ACCATCAGCCAAACTGCAGCAACTGGACCAACAGGCAAAGATCTTATGGAGACTGCAAGATGAGCCATCCAACCTGGGGACAGACAGCATCATCTGC **BstAPI (789)**
47 T I S P N C S K L D Q Q A K I L W R L Q D E P I Q P G D R Q H H L

801 CTGATGGGACCAAGAGTCCCTCATCACTCTGCCTCACTTGAAGTACACCCAGGCCTTCTCTTGTGTTAGTGCCATGGGAAGACAGCGTCCAACCTCCT **BstAPI (789)**
80 P D G T Q E S L I T L P H L N Y T Q A F L F C L V P W E D S V Q L L

901 GGATCAAGCTGAGCTTACGCGAGGTATCCCCCTGACCCCTCAAACCTATCTGCCTCATGCACCTACCACCAACAGCCTGGTCTGCCAGTGGGAG **BstAPI (789)**
113 D Q A E L H A G Y P P A S P S N L S C L M H L T T N S L V C Q W E

1001 CCAGTCTGAGACCCACCTGCCACCAGCTTTCATCTAAAGAGCTTCCAGGAGCCGCGCCGACTGTGAGTACCAAGGGGACACCATCCCGATTGTGTGG **BstAPI (789)**
147 P G P E T H L P T S F I L K S F R S R A D C Q Y Q G D T I P D C V

1101 CAAAGAAGAGGAGCAACAAGTCTCCATCCCCGAAAAAATTGCTCCTGTACAGTATATGGCCATCTGGGTGCAAGCAGAGAATATGCTAGGGTCCAG **BstAPI (789)**
180 A K K R Q N N C S I P R K N L L L Y Q Y M A I W V Q A E N M L G S S

1201 CGAGTCCCCAAAGCTGTGCTCGACCCCATGGATGTTGTGAAATTGGAGCCTCCATGTGCAGGCCCTGGACATTGGCCCTGATGTAGTCTCTCACCAG **BstAPI (789)**
213 E S P K L C L D P M D V V K L E P P M L Q A L D I G P D V V S H Q

1301 CCTGGCTGCTGTGGCTGAGCTGGAAGCCATGGAAGCCAGTGAAGTACATGGAACAGGAGTGTGAAGTTCGCTACCAGCCACAGCTCAAAGGAGCCAACT **BstAPI (789)**
247 P G C L W L S W K P W K P S E Y M E Q E C E L R Y Q P Q L K G A N

1401 GGACTCTGGTGTCCACCTGCCTTCCAGCAAGGACCAGTTTGAAGTCTGCGGGCTCCATCAGGCCCCAGTCTACACCTACAGATGCGATTGCATTGCCTC **NsiI (1488)**
280 W T L V F H L P S S K D Q F E L C G L H Q A P V Y T L Q M R C I R S

1501 ATCTCTGCCTGGATTCTGGAGCCCTGGAGCCCGGCCTGCAGCTGAGGCCTACCATGAAGGCCCCACCATCAGACTGGACACGTTGGTGCAGAGAAG **DraIII (1581)** **BbrPI (1581)**
313 S L P G F W S P W S P G L Q L R P T M K A P T I R L D T W C Q K K

1601 CAACTAGATCCAGGGACAGTGTGAGCTGTTCTGGAAGCCACCGCCCTGCAGGAAGACAGTGGACAGATCCAGGGCTACCTGCTGTCCTGGAATT **SdaI (1650)**
347 Q L D P G T V S V Q L F W K P T P L Q E D S G Q I Q G Y L L S W N

1701 CCCAGATCATCAAGGGCAGGACATACACCTTTGCAACACCACGAGCTCAGCTGTATCTTCTCCTGCCCTCAGAGGCCAGAACGTGACCCTGTGGC **SdaI (1650)**
380 S P D H Q G Q D I H L C N T T Q L S C I F L L P S E A Q N V T L V A

1801 CTACAACAAGCAGGGACCTTTCACCTACTACAGTGGTTTTCTGGAGAACGAAGTCCAGCTGTGACTGGACTCCATGCCATGGCCCAAGACCTTAAC **SdaI (1650)**
413 Y N K A G T S S P T T V V F L E N E G P A V T G L H A M A A Q D L N

1901 ACCATCTGGGTAGACTGGGAAGCCCGCCCTTCTGCCTCAGGCTATCTCATTGAGTGGGAATGAGTCTCCAGCTACAATAACAGCTATAAGTCCCT **SdaI (1650)**
447 T I W V D W E A P S L L P Q G Y L I E W E M S S P S Y N N S Y K S

2001 GGATGATAGAACCTAACGGGAACATCACTGGAATTCTGTTAAAGGACAACATAAATCCCTTTCAGCTCTACAGAATTACAGTGGCTCCCTGTACCCAGG **SdaI (1650)**
480 W M I E P N G N I T G I L L K D N I N P F Q L Y R I T V A P L Y P G

2101 CATCGTGGGACCCCTGTAATGTCTACACCTTCTGCTGGAGAGAGCTCCTCCTCATGCTCCAGCGCTGCATCTAAAGCATGTTGGCACAACCTGGGCA **Eco47III (2163)**
513 I V G P P V N V Y T F A G E R A P P H A P A L H L K H V G T T W A

2201 CAGCTGGAGTGGGTACCTGAGGCCCTAGGCTGGGGATGATACCCCTACCCACTACACCATCTTCTGGGCCGATGCTGGGGACCACTCCTTCTCCGTCA **Acc65I (2211)** **AvrII (2224)**
547 Q L E W V P E A P R L G M I P L T H Y T I F W A D A G D H S F S V

2301 CCCTAAACATCTCCCTCCATGACTTTGTCTGAAGCACCTGGAGCCCGCCAGTTTGTATCATGTCTACCTCATGGCCACCACTGAGCAGGGTCCACCAA **Acc65I (2211)** **AvrII (2224)**
580 T L N I S L H D F V L K H L E P A S L Y H V Y L M A T S R A G S T N

2401 TAGTACAGGCCTTACCCTGAGGACCCTAGATCCATCTGACTTAAACATTTTCTGGGCATACTTTGCTTGTACTCTTGTCCACTACCTGTGTAGTGACC **BstAPI (2456)** **ScaI (2469)**
613 S T G L T L R T L D P S D L N I F L G I L C L V L L S T T C V V T

2501 TGGCTCTGCTGCAACCGCAGAGGAAAGACTTCTTCTGGTGTGATGTGCCAGACCCAGCCACAGTAGCCTGAGCTCCTGGTTGCCACCATCATGACAG **XmnI (2522)** **BspHI (2591)**
647 W L C C C K R R G K T S F W S D V P D P A H S S L S S W L P T I M T

2601 AGGAAACCTTCCAGTACCAGCTTCTGGGACTCCAGCGTGCATCAATCACCAAGTCACTGAAGTGGAGGAAGCAAGAAACCGCACCACTGGGATTC **BspHI (2591)**
680 E E T F Q L P S F W D S S V P S I T K I T E L E E D K K P T H W D S

2701 CGAAAGCTCTGGGAATGGTAGCCTTCCAGCCCTGGTTCAGGCCTATGTCTCAAGGAGATCCAAGAGAAATTTCAACCACTCCAGCCTCCCTCTCGC **BspHI (2591)**
713 E S S G N G S L P A L V Q A Y V L Q G D P R E I S N Q S Q P P S R

2801 ACTGGTGACCAGTCTCTATGGTCAAGTCTTGGAGCCCCACCCAGGAGTAATGCAGTACATTCGCTCTGACTCCACTCAGCCCTCTTGGGGG **BstEII (2803)** **Bsp120I**
747 T G D Q V L Y G Q V L E S P T S P G V M Q Y I R S D S T Q P L L G

2901 GCCCCACCCCTAGCCTAAATCTTATGAAAACATCTGGTTCATTCAAGACCCAGGAGACCTTTGTGCCCAACCTCCAACCAGGAAGATGACTGTGT
780▶ G P T P S P K S Y E N I W F H S R P Q E T F V P Q P P N Q E D D C V

3001 CTTTGGGCCTCCATTTGATTTTCCCTCTTTCAGGGGCTCCAGGTCCATGGAGTTGAAGAACAAGGGGTTTCTAGAACTTTGGGCTAGCTGGCCAGAC
813▶ F G P P F D F P L F Q G L Q V H G V E E Q G G F •

3101 ATGATAAGATACATTGATGAGTTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAA

HpaI (3223) MfeI (3234)

3201 CCATTATAAGCTGCAATAAAACAAGTTAAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAAA

3301 CCTCTACAAATGTGGTATGGAATTCTAAAAACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGG

3401 CATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTTCCCAAGGTTTGAAC

SapI (3501) SspI (3558) SmaI (3572)

3501 AGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATTCAGAAAAATTTAAATACATCATTGCAATGAAAAATA

3601 AATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAAT

3701 TGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCTCAAT

3801 GAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGTATGGATCTGTCCACCTCATCAGAGTAGGGG

3901 TGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGG

4001 CCTCAATGTGGACAGCAGAGATGATCTCCACAGTCTGGTCTGATGGCCGCCCGACATGGTCTTGTGTCCTCATAGAGCATGGTATCTTCTCAGT

4101 GGCGACTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGC

4201 CGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTA

XmnI (4139)

4301 CCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTTGACGTCAATGGGGTGGGA

SpeI (4360)

4401 GACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA

SnaBI (4488)

4501 CTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGA

NdeI (4593)

4601 TACACTTGATGTACTGCCAAGTGGGCGAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCA

SdaI (4771) PacI (4779) BspLU111 (4789)

4701 TTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAATAAGAACATGTGAGCA

4801 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAA

4901 GTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGG

5001 ATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTTCGCTCCAAGCTGGGC

ApaI (5103)

5101 TGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACAGACTTATGCCACTGGCAG

5201 CAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATT

5301 TGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGT

5401 TGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAG

EagI (5539)

5501 GGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCG

PacI (5519) SmaI (5528) NotI (5538)

5601 TAACTAACATACGCTCTCCATCAAAACAAACGAAACAAACAAACTAGCAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATC

5701 GAA