



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

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTAGGAGGGCACCATGGATAACCCAGGGCCTTCGCTCCGTGGTG **AgeI (552)** **NcoI (567)**
1► M D N P G P S L R G

601 CCTTTGGCATTCTAGGTGCCTTGAAAGGGACAGGCTGACCCACCTGAAACACAAGCTGGGGAGTCTGTGTTACGGCAGCCAGGAGTCAAAGCTTCTCCA **HindIII (689)**
11► A F G I L G A L E R D R L T H L K H K L G S L C S G S Q E S K L L H

701 TGCCATGGTACTCCTGGCTCTGGCCAGGACACGGAGGCCAGGCTCTCTGAGTCTTGAAGTGAACACAGTAGCCAGCTGGTAGCCACCAAGTGG **NcoI (702)**
44► A M V L L A L G Q D T E A R V S L E S L K M N T V A Q L V A H Q W

801 GCAGACATGGAGACCACAGAGGGCCTGAGGAGCTCCAGACTTGTCTGGACGGTGGCTCGCCTGTACCACCTGCTGGCTGAGGAGAACCCTGTGTCCGG **StuI (984)**
78► A D M E T T E G P E E P P D L S W T V A R L Y H L L A E E N L C P

901 CCTCCACAAGGGACATGGCTTACCAGGTGGCCCTTCGTGACTTTGCTCCAGGGTGACCACCAGCTGGGCCAACTCCAGAATGAGGCCTGGGATCGGTG **SmaI (1017)**
111► A S T R D M A Y Q V A L R D F A S Q G D H Q L G Q L Q N E A W D R C

1001 CAGTTCAGATATCAAGGGGACCCCAAGTGGTTTCCAGCCACTCCATTCTCATCAGGGTCCCTGCAGCCACCTTCAGCATCCCTGCAGTGACCAAGAAGC **EcoRV (1007)** **BstAPI (1076)**
144► S S D I K G D P S G F Q P L H S H Q G S L Q P P S A S P A V T R S

1101 CAGCCTCGTCCCATTGACACACCAGACTGGAGTTGGGGACATACGTTACTCCACCAACAGCACTGCCTCACTGGCCAGCCACTAGAGATCAGCCAGT **MscI (1173)**
178► Q P R P I D T P D W S W G H T L H S T N S T A S L A S H L E I S Q

1201 CACCACTCTTGCCTTTCTCTTCCACACCATGGAACCATGGGCCAGCAAGCTATGTAACACACCGCTGGACACTCAGGAGCCTCAGCTTGTCCCTGA **NcoI (1228)** **NcoI (1237)**
211► S P T L A F L S S H H G T H G P S K L C N T P L D T Q E P Q L V P E

1301 AGGCTGCCAAGAACCTGAGGAGATAAGCTGGCCTCCATCAGTGGAGACCAAGTCTCCTTAGGGTTACCACACGAAATTAGCGTTCCAGAGGTGTCTCCA **PshAI (1345)**
244► G C Q E P E E I S W P P S V E T S V S L G L P H E I S V P E V S P

1401 GAGGAGGCTTCGCCATCCTCCCTGACGCCCTGGCTGCTCCAGACACAAGTGTCCACTGTCCATTGAATGCACAGAGTTGTCTACAACTCCAGGTCTC **NcoI (1228)** **NcoI (1237)**
278► E E A S P I L P D A L A A P D T S V H C P I E C T E L S T N S R S

1501 CCCTGACGTCCACCACAGAAAGTGTGGAAAGCAGTGGCCTATTACAAGTCAAGGTCACCTCAGGTTCTGTAGGAGATGATTCTCTGCAGAACCACC **NcoI (1228)** **NcoI (1237)**
311► P L T S T T E S V G K Q W P I T S Q R S P Q V P V G D D S L Q N T T

1601 GTCATCCAGCCCTCTGCCAGCCACCATCCCTCCAAGCTCCCTAAGTGCCTCCTCCCTCTGTCTCTGCTTCTCCCGAGCAGCTACCCTGCT **NcoI (1228)** **NcoI (1237)**
344► S S S P P A Q P P S L Q A S P K L P P S P L S S A S S P S S Y P A

1701 CCTCCAACCTCCACATCCCTGTTTGGACCACTCAGAAACATCTGATCAGAAATTCTATAACTTTGTGGTTATCCATGCCAGGGCTGATGAACAGGTGG **NcoI (1228)** **NcoI (1237)**
378► P P T S T S P V L D H S E T S D Q K F Y N F V V I H A R A D E Q V

1801 CCCTACGTATTCGGGAGAAGCTGGAGACCTCGGGGTACTGACGGGGCCACCTTCTGTGAGGAATTTAGGTGCCCGGGCGTGGTGAGCTGCACCTGTCT **SnaBI (1803)** **Acc65I (1834)** **SrfI (1873)**
411► A L R I R E K L E T L G V P D G A T F C E E F Q V P G R G E L H C L

1901 CCAAGATGCCATCGATCACTCGGGTTCACGATCCTGCTCCTGACTGTAGCTTTGATTGACGCTGAGCCTGCATCAAATCAACCATGCTCTCATGAAC **ClaI (1910)** **NheI (1946)** **BspHI (1992)**
444► Q D A I D H S G F T I L L L T A S F D C S L S L H Q I N H A L M N

2001 AGCCTTACACAGTCTGGGAGGACGACTGTGTGATCCCTCCTCCACTTGAAGTGTCTCAGGCCAGCTCAGCCCAGATACAACCAGACTGCTCCACA **BspHI (1992)**
478► S L T Q S G R Q D C V I P L L P L E C S Q A Q L S P D T T R L L H

2101 GCATTGTGTGGCTGGATGAACACTCCCCAATCTTCCGAGAAAGTGGCAACACCTTCAAGACACAGAAGCTCCAGGCACAGCGGTACGCTGGAAGAA **BstXI (2136)**
511► S I V W L D E H S P I F A R K V A N T F K T Q K L Q A Q R V R W K K

2201 AGCGCAGGAGGCCAGAACCCTCAAGGAGCAGAGCATAAGCTGGAGGACAGAGCGGCAAAACCTGGCAGCCATATCTGCTGCCTACACAGCCTATGTCCAT **BsrBI (2249)**
544► A Q E A R T L K E Q S I Q L E A E R Q N V A A I S A A Y T A Y V H

2301 AGCTATAGGCCTGGCAAGCAGAGATGAACAAACTTGGGGTGGCTTTTGGGAAGAACTTGTCACTGGGACTCCAACACCCAGCTGGCCCGGATGTCCAC **BsrBI (2249)**
578► S Y R A W Q A E M N K L G V A F G K N L S L G T P T P S W P G C P

2401 AGCCAATACCTTCTACTCCTCAGGTTGTTACTCCAGTTCCTCCCTATCCCCACAGCCTCCATCCTCCCTCAGCCTCCATGCTTCCCTCAGCCTCCATC **BsrBI (2249)**
611► Q P I P S H P Q G G T P V F P Y S S P Q P P S F P Q P P C F P Q P P S

2501 CTTCCCTCAGCCTCCATCCTTCCACTGCCTCCAGTCTCTTCCACAGTCCCAATCCTTCCATCAGCCTCCTCCAGCCACAGACTCCAGGACCT **BsrBI (2249)**
644► F P Q P P S F P L P P V S S P Q S Q S F P S A S S P A P Q T P G P

2601 CAGCCTCATTATTCCACATGCCAGATGGTTACAGTGGGTGTCAACAATCACATGTGGGCCACACAGGGCCAGTCACTGATGACAAGACTGAGT **BspLU11I (2652)**
678► Q P L I I H H A Q M V Q L G V N N H M W G H T G A Q S S D D K T E

NheI (2774)

2701 GTTCCGGAAACCCCTGTATGGGCCCTCTGACTGATCAGGGCGAACCCCTTCTTGAGACTCCAGAGTGAGAATTCGCTAGCTCGACATGATAAGATAACATT
711▶ C S E N P C M G P L T D Q G E P L L E T P E •

2801 GATGAGTTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTGAAATTTGTGATGCTAT

HpaI (2937) MfeI (2948)

2901 TGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACA AATTGCATTCTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTT

EcoRI (3033)

3001 TAAAGCAAGTAAACCTCTACAAATGTGGTATGGAAATCTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTG
3101 AGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAGATATAGTGTATTTTC

SapI (3215) SspI (3272) SmaI (3286)

3201 CCAAGGTTTGAAC TAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCA
3301 TTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAA
3401 CCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTG
141 • N R T Y K L P I L E E I T T K V L K

SacI (3547) BstXI (3576)

3501 CCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTTCGCACATGCCACAGGGGCTGACCCCTGATGGATCTGTCCACCT
121▶ 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 R D V E
3601 CATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGAC
88▶ 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 V T V

StuI (3711)

3701 CCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTGTCTCATAGAGCATG
55▶ 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 Y L M

BbsI (3857) XmnI (3853)

3801 GTGATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATG
21▶ T I K E T A V E V L E L D Q Q S I N F T K M

AseI (3919) SacI (3976)

3901 CCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAACGAGCTCTGCTTATATAGACCTCCC

SpeI (4074)

4001 ACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGAC
4101 GTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTA CTGCCAAAACCGCATCATCATGGTAATAGCGATGACT

SnaBI (4202)

4201 AATACGTAGATGTA CTGCAAGTAGGAAAGTCCATAAGGTCACTGTA CTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTC AATAGGGGGCG

NdeI (4307)

4301 TACTTGGCATATGATACACTTGATGTA CTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTC AATGGAAAGTCCCTATTGGCGTTACTAT

PacI (4493) SdaI (4485)

4401 GGGAACATACGTCATTATTGACGTC AATGGGCGGGGTCGTTGGGCGGT CAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAATTA

BspLU1II (4503)

4501 AGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAA
4601 AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTTCCCTGGAAAGCTCCCTCGTGCCTCTCTGTCCGACC
4701 CTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCC

ApaLI (4817)

4801 GCTCCAAGCTGGGCTGTGTGCACGAACCCCGTT CAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTT
4901 ATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCCTAACTACGGCTACACT
5001 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA AAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCCGCTGGTAGCG
5101 GTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGA

EagI (5253) PacI (5233) SmaI (5242) NotI (5252)

5201 AAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCTATTACATCTGTGTGGTGGTT
5301 TTTTGTGTAATCGTAACATAACGCTCTCCATCAAAAACAAAACGAAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAG
5401 AACATTTCTCTATCGAA