



PvuI (7)
SgfI (6) **EcoNI (96)**
1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **EcoNI (287)**
201 GTGAACGTTCTTTTTTCGAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspLU11I (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAACATGTCCCATCAACCTCTCAGCTGCCTCACTGAAAAGGA

601 GGACAGCCCCAGTGAAGCACAGGAAATGGACCCCCACCTGGCCACCCAAACCTGGACACGCTTTACCCCGGAGGAGCTGTCAGCAGATGAAAAGAG
13▶ D S P S E S T G N G P P H L A H P N L D T F T P E E L L Q Q M K E
701 CTCCTGACCGAGAACCACAGCTGAAAGAAGCCATGAAGCTAAATAATCAAGCCATGAAAGGGAGATTTGAGGAGCTTTGGCCTGGACAGAGAAACAGA
47▶ L L T E N H Q L K E A M K L N N Q A M K G R F E E L S A W T E K Q

BspHI (864) **SapI (886)**
801 AGGAAGAACGCCAGTTTTTTGAGATACAGAGCAAGAAGCAAAAGAGCGTCTAATGGCCTTGAGTCATGAGAATGAGAAATGAAGGAAGAGCTTGGAAA
80▶ K E E R Q F F E I Q S K E A K E R L M A L S H E N E K L K E E L G K
901 ACTAAAAGGGAAATCAGAAAGTTCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAAGCGGAGCAGGAAAAGACCAGCTCAGGACCCAG
113▶ L K G K S E R S S E D P T D D S R L P R A E A E Q E K D Q L R T Q
1001 GTGGTGAGGCTACAAGCAGAGAAGGCAGACCTGTTGGGCATCGTGTCTGAACTGCAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAGATTCTTTGTTG
147▶ V V R L Q A E K A D L L G I V S E L Q L K L N S S G S S E D S F V

Bsp120I (1159)
1101 AAATTAGGATGGCTGAAGGAGAAGCAGAAGGGTCACTAAAAGAAATCAAGCATAGTCTGGGCCACGAGAACAGTCTCCACTGGCACGGCATTGTCTAA
180▶ E I R M A E G E A E G S V K E I K H S P G P T R T V S T G T A L S K

BstBI (1237)
Bsp119I (1237)
BglII (1210) **XmnI (1230)** **HpaI (1251)**
1201 ATATAGGAGCAGATCTGCAGATGGGGCCAAGAATTACTTCAACATGAGGAGTTAACTGTGAGCCAGCTCCTGCTGTGCCTAAGGGAAGGGAATCAGAAG
213▶ Y R S R S A D G A K N Y F E H E E L T V S Q L L L C L R E G N Q K
1301 GTGGAGACTTGAAGTTGCATCAAGGAGGCCAAAGAAAGATTTTCAGATTTTAAAAAGAAAACAAGTAATCGTTCTGAGATTGAAACCCAGACAGAGG
247▶ V E R L E V A L K E A K E R V S D F E K K T S N R S E I E T Q T E
1401 GGAGCACAGAGAAAAGAGAATGATGAAGAGAAAGGCCCGGAGACTGTTGGAAGCGAAGTGAAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGGACT
280▶ G S T E K E N D E E K G P E T V G S E V E A L N L Q V T S L F K E L
1501 TCAAGAGGCTCATACAAAACCTCAGCGAAGCTGAGCTAATGAAGAAGAGACTTCAAGAAAAGTGTGAGCCCTTAAAAGGAAAATTCTGCAATTCATCA
313▶ Q E A H T K L S E A E L M K K R L Q E K C Q A L E R K N S A I P S

SphI (1661)
1601 GAGTTGAATGAAAAGCAAGAGCTTGTTTATACTAACA AAAAGTTAGAGCTACAAGTGGAAAGCATGCTATCAGAAAATCAAAAATGGAACAGGCTAAAACAG
347▶ E L N E K Q E L V Y T N K K L E L Q V E S M L S E I K M E Q A K T

HindIII (1744) **NsiI (1766)**
1701 AGGATGAAAAGTCCAATTAACCTGTGCTACAGATGACACACAACAAGCTTCTCAAGAACATAATAATGCATTGAAAACAATTGAGGAACTAACAAGAAA
380▶ E D E K S K L T V L Q M T H N K L L Q E H N N A L K T I E E L T R K
1801 AGAGTCAGAAAAAGTGGACAGGGCAGTCTGAAAGAACTGAGTGA AAAACTGGAAGTGGCAGAGAAGGCTCTGGCTTCCAAACAGCTCAAAATGGATGAA
413▶ E S E K V D R A V L K E L S E K L E L A E K A L A S K Q L Q M D E
1901 ATGAAGCAAACATTGCCAAGCAGGAAGAGGACCTGAAAACCATGACCATCCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTTCATGCTGAAAGAG
447▶ M K Q T I A K Q E E D L E T M T I L R A Q M E V Y C S D F H A E R

BbsI (2080)
BstBI (2077)
Bsp119I (2077)
2001 CAGCGAGAGAGAAAATTCATGAGGAAAAGGAGCAACTGGCATTGCAGCTGGCAGTTCTGCTGAAAGAGAATGATGCTTTTCAAAGAGCAGGAGGCGAGTC
480▶ A A R E K I H E E K E Q L A L Q L A V L L K E N D A F E D G G R Q S
2101 CTTGATGGAGATCAGAGTCGTATGGGGCAGAAACAAGTACTCTGACCAGCAGGCTTACCTTGTCAAAGAGGAGCTGAGGACAGGACTGGCGGCAA
513▶ L M E M Q S R H G A R T S D S D Q Q A Y L V Q R G A E D R D W R Q

SspI (2206) **BbrPI (2272)**
2201 CAGCGGAATATCCGATTCACTCTGCCCAAGTGTGGAGAGTTCTGCTGACATAGACACGTTACAGATTACGTTGATGGATTGCATCATTAAAGTGT
547▶ Q R N I P I H S C P K C G E V L P D I D T L Q I H V M D C I I •

MscI (2310)
NheI (2304)
2301 TGATGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACAACCTAGAATGCAGTGA AAAAATGCTTTATTTGTGAAATTTGTGAT

HpaI (2442)
2401 GCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACAATTGCATTCATTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGG

2501 **EcoRI (2538)**
TTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCATAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTT

2601 TTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGA

2701 **SapI (2720)** **SspI (2777)** **SwaI (2791)**
TTTTCCAAGTTTGAAGTAGCTCTTCAATTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTAGAAATAATTTAAATA

2801 CATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAA

2901 AGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCA
141 • N R T Y K L P I L E E I T T K V L

3001 **BstXI (3081)**
GCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTG
123 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 R D

3101 CACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACA
90 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 V

3201 **StuI (3216)**
GTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTGTCTCATAGA
56 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 Y L

3301 **BbsI (3362)** **XmnI (3358)**
GCATGGTATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATA
23 M T I K E T A V E V L E L D Q Q S I N F T K M

3401 **AseI (3424)**
CTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGAC

3501 **SpeI (3579)**
CTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCCA

3601 TTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGA

3701 **SnaBI (3707)**
TGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGTTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGG

3801 **NdeI (3812)**
GGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCGAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTT

3901 **PacI (3998)** **SdaI (3990)**
ACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGTCCAGCCAGCGGGCCATTTACCCTAAGTTATGTAACGCCGTCAGGTT

4001 **BspLU11I (4008)**
AATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCAT

4101 CACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTC

4201 CGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGT

4301 **ApaLI (4322)**
CGTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCAACCCGGTAAGACAC

4401 GACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCT

4501 AACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCCGCTGG

4601 TAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGG

4701 **EagI (4758)** **PacI (4738)** **SwaI (4747)** **NotI (4757)**
AACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAAATATCTTTATTTTTCATTACATCTGTGTGT

4801 TGGTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAGTGCAGGT

4901 GCCAGAACATTTCTATCGAA