



PvuI (7) **SgfI (6)** **MfeI (82)** **EcoNI (96)**
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)** **EcoNI (287)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCGCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCCTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

KasI (535) **BstEII (555)** **AgeI (552)** **NcoI (560)**
501 TCTGTTCTGGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTACCATTGGTGCCTGTGTTACTAATTCTTGTGGAGCTTTGGC
601 AACACTGCAAGCTGACTTACTTAATCACAAAAAGTTTTACTTCTACCACCTGTCAATTTTACCATTAAAGCCACTGGATTAGCTCAAGTTCTTTTACAC
13▶ T L Q A D L L N H K K F L L L P P V N F T I K A T G L A Q V L L H

SmaI (701) **EcoO109I (701)** **XbaI (738)** **BbrPI (748)** **BbsI (772)**
701 TGGGACCCAAATCCTGACCAAGAGCAAAGGCATGTTGATCTAGAGTATCACGTGAAAAATAATGCCCCACAAGAGACGAATATGATACCAGAAAGACTG
47▶ W D P N P D Q E Q R H V D L E Y H V K I N A P Q E D E Y D T R K T

BspHI (822) **NheI (838)** **MscI (878)**
801 AAAGCAATGTGTGACCCCTTTCATGAAGCTTTGCAGCTAGCGTGAGGACCATTCTGAAGAGCAGCCATACAACCTGCGCCAGCAGTTGGGTTTCTGC
80▶ E S K C V T P L H E G F A A S V R T I L K S S H T T L A S S W V S A
901 TGAAGTCAAAGCTCCACCAGGATCTCCTGGAACCTCGGTTACGAATTTAACTTGTACCACACACTGTTGTAAGTAGCCACCCACTTAAGGCCATAC
113▶ E L K A P P G S P G T S V T N L T C T T H T V V S S H T H L R P Y

Bsu36I (1042)
1001 CAAGTGTCCCTTCGTTGCACCTGGCTTGTGGGAAGGATGCCCTGAGGACACACAGTATTTCTATACTACAGGTTTGGTGTTTTACTGAAAAATGCC
147▶ Q V S L R C T W L V G K D A P E D T Q Y F L Y Y R F G V L T E K C

SphI (1135) **ApaLI (1189)** **AseI (1195)**
1101 AAGAATACAGCAGAGATGCACTGAACAGAAATACTGCATGCTGGTTTCCAGGACATTTATCAACAGCAAAGGGTTTGGAGCAGCTTGTGTCACATTAA
180▶ Q E Y S R D A L N R N T A C W F P R T F I N S K G F E Q L A V H I N
1201 TGGCTCAAGCAAGCGTGTGCAATCAAGCCCTTTGATCAGCTGTTCCAGTCCATTGCCATTGACCAAGTGAATCCTCAAGGAATGTCACAGTGGAAATT
213▶ G S S K R A A I K P F D Q L F S P L A I D Q V N P P R N V T V E I
1301 GAAAGCAATTCTCTATATACAGTGGGAGAAACCACTTTCTGCCTTTCCAGATCATTGCTTTAACTATGAGCTGAAAAATTTACAACCAAAAAATGGTC
247▶ E S N S L Y I Q W E K P L S A F P D H C F N Y E L K I Y N T K N G
1401 ACATTGAAAGGAAAAACTGATCGCAATAAGTTCATCTCAAAAATTGATGATGTTTCTACATATTCCATTCAAGTGAAGAGCAGCTGTGAGCTCACCTTG
280▶ H I Q K E K L I A N K F I S K I D D V S T Y S I Q V R A A V S S P C

BstXI (1507)
1501 CAGAATGCCAGGAAGTGGGGGAGTGGAGTCAACCTATTTATGTGGGAAAGGAAAGGAGTCCCTGGTAGAATGGCATCTCATTGTGCTCCCAACAGCC
313▶ R M P G R W G E W S Q P I Y V G K E R K S L V E W H L I V L P T A

PstI (1632) **AgeI (1668)** **BglII (1698)**
1601 GCCTGCTTCGTCTTGTAAATCTTCTCACTCATCTGCAGAGTGTGCATCTATGGACCAGGTTGTTTCCACCGGTTCCGGCCCCAAAGAGTAACATCAAAG
347▶ A C F V L L I F S L I C R V C H L W T R L F P P V P A P K S N I K

BstBI (1731) **BsrGI (1755)**
1701 ATCTCCCTGTGGTACTGAATATGAGAAACCTTGAATGAAACAAAATTGAAGTTGTACATTGTGTGGAAGAGGTTGGATTTGAAGTATGGGAAATTC
380▶ D L P V V T E Y E K P S N E T K I E V V H C V E E V G F E V M G N S

AvrII (1837) **MscI (1849)**
1801 CACGTTTTGATGGCATTGTCATTCTGAAATGAACCTCTAGGACTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGA
413▶ T F •

HpaI (1981) **MfeI (1992)**
1901 ATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTAAACAACAACATTGCA

EcoRI (2077)
2001 TTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCA
2101 AAACTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTG
2201 CAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCCAAGGTTTGAAGTACTCTTCTTTTATGTTTAAATGCACTGACCTCCAC

SspI (2316) **SwaI (2330)** **EcoO109I (2391)**
2301 ATTCCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTC
2401 ATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTAAATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGT
141▶ • N R T Y

BstXI (2620)
2501 ACTTGAGGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCT
136▶ K L P I L E 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
2601 GCACATGCCACAGGGGCTGACCACCTGATGGATCTGCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTG
103▶ C M G C P S 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

2701 **StuI (2755)**
CTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCC
69 S V A S G I 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

2801 **XmnI (2897)**
TGATGGCCGCCCCGACATGGTGTCTTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAA
36 I A A G V H 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

2901 **BspHI (2905)** **BbsI (2901)** **AseI (2963)**
GGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGC T
3 T K M

3001 TATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTT

3101 **SpeI (3118)**
GGAAAGTCCC GTT GATTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCTGAGTCAAACCGCTATCCACGCCCA

3200 **SnaBI (3246)**
TTGATGTA CTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA CTGCCAAGTAGGAAAGTCCCATAAGGTCATGTA CTGGGCAT

3300 **NdeI (3351)**
AATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGCCATATGATACACTTGATGTA CTGCCAAGTGGGCAGTTTACCGTAAATA

3400 CTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCA

3500 **PstI (3530)** **SdaI (3529)** **PacI (3537)** **BspLU111 (3547)**
GGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAA TTAAGAACATGTGAGCAAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAGGCCGCG

3598 TTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACT

3698 AGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCT

3798 **ApaLI (3861)**
TTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCC

3898 TTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAG

3998 GCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAA

4098 AAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAA

4198 **PacI (4277)** **SwaI (4286)** **NotI (4296)**
GAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AG

4298 **EagI (4297)**
CGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAA

4398 AACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA