



PvuI (7)
SgfI (6) EcoNI (96)
1 GGATCTGCGATCCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGTCTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTCAGTAGTCGCC

HindIII (245) **Bsu36I (291)**
Psp1406I (203) **PvuII (239)** **EcoNI (287)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441) **NaeI (441)**
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

NcoI (560) **BstEII (555)** **AgeI (552)** **PvuII (580)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGTACCATGGCTCCGCTTCTGTTGCAGCTGGCGGTGCTCGGCGC
1 M A P L L L Q L A V L G A

EagI (608) **NotI (607)** **BsaBI (627)** **XmnI (690)**
601 GCGCTGGCGGCGCAGCCCTCGTACTGATTTCCATCGTTGCATTTACAAGTCTACAAAAATGCCAGCACTCCATCGACATGAAGAAGAGAAATCTCTC
13 A L A A A A L V L I S I V A F T T A T K M P A L H R H E E E K F F

NdeI (735)
701 TTAAATGCCAAAGCCAGAAAGAACTTTACCAGCATATGGGACTCACCTACCAAACAACCTTCTGTGTTGTGCCTTCATACAATGAAGAAAAACGGT
47 L N A K G Q K E T L P S I W D S P T K Q L S V V V P S Y N E E K R

XbaI (831)
801 TGCCTGTGATGATGGATGAAGCTCTGAGCTATCTAGAGAAGAGACAGAAACGAGATCCTGCGTTCACTTATGAAGTGATAGTGTGATGATGGCAGTAA
80 L P V M M D E A L S Y L E K R Q K R D P A F T Y E V I V V D D G S K

SspI (926) **BstXI (933)**
901 AGATCAGACCTCAAAGGTAGCTTTTAAATATTGCCAGAAATATGGAAGTGACAAAGTACGTGTGATAACCTGGTGAAGAATCGTGGAAAAGGTGGAGCG
113 D Q T S K V A F K Y C Q K Y G S D K V R V I T L V K N R G K G G A

1001 ATTAGAATGGGTATATTCAGTTCTCGAGGAGAAAAGATCCTTATGGCAGATGCTGATGGAGCCACAAAAGTTCCAGATGTTGAGAAATTAGAAAAGGGGC
147 I R M G I F S S R G E K I L M A D A D G A T K F P D V E K L E K G

1101 TAAATGATCTACAGCCTTGGCCTAATCAAATGGCTATAGCATGTGGATCTCGAGCTCATTAGAAAAAGAATCAATTGCTCAGCGTTCTTACTTCCGTAC
180 L N D L Q P W P N Q M A I A C G S R A H L E K E S I A Q R S Y F R T

DraIII (1262) **DraIII (1260)**
1201 TCTTCTCATGTATGGGTTCCACTTTCTGGTGTGGTTCCTTTGTGTCAAAGGAATCAGGGACACACAGTGTGGGTTCAAATTATTTACTCGAGAAGCAGCT
213 L L M Y G F H F L V W F L C V K G I R D T Q C G F K L F T R E A A

BsrGI (1355)
1301 TCACGGACGTTTTTCATCTCTACACGTTGAACGATGGGCATTTGATGTAGAACTACTGTACATAGCACAGTTCCTTTAAAATTCCAATAGCAGAAATTGCTG
247 S R T F S S L H V E R W A F D V E L L Y I A Q F F K I P I A E I A

XcmI (1435)
1401 TCAACTGGACAGAAATTGAAGTTCTAAATTAGTTCATTCTGGAGCTGGCTACAAATGGGTAAGACCTACTTTTTATACGACTTCGATATTTGACTGG
280 V N W T E I E G S K L V P F W S W L Q M G K D L L F I R L R Y L T G

MscI (1566) **BbsI (1547)** **NheI (1560)**
1501 TGCCTGGAGGCTTGAAGCAACTCGGAAAATGAATTAGGTTGTTTGCAGTCTTCAGTTGTGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTG
313 A W R L E Q T R K M N •

HpaI (1698)
1601 GACAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGT

EcoRI (1794)
1701 TAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTC
1801 TAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAA
1901 TGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTCTTCATTTCTTTATGTTTAA

SspI (2033) **Swal (2047)**
2001 ATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCA

EcoO109I (2108)
2101 GATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTA
2201 GCTTAGTTCCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAG
141 N R T Y 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

BstXI (2337)
2301 TCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAA
108 D S I L E R 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

StuI (2472)

2401 AGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGAT
75 D K Q G N 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
2501 CTCCCAGTCTTGGTCCTGATGGCCGCCCGACATGGTCTTGTTCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCC
42 E G T K T R 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

BspHI (2622)

BbsI (2618)
XmnI (2614) **AseI (2680)**

2601 TGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGT
8 Q Q S I N F T K M ←

2701 GGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGG

SpeI (2835)

2801 AGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAA

SnaBI (2963)

2900 ACCGCTATCCAGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAA

NdeI (3068)

3000 GGTCATGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCCAAGTGG
3100 GCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGT

PstI (3247)
SdaI (3246) **PacI (3254)** **BspLU11I (3264)**

3200 CGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCC T G C A G G T T A A T T A A G A A C A T G T G A G C A A A A G G C C A G A A A A G G C C A G G A
←

3298 ACCGTA AAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATC A C A A A A A T C G A C G C T C A A G T C A G A G G T G G C G A A A C C C G A C
3398 AGGACTATAAAGATACCAGGCGTTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCT

ApaLI (3578)

3498 TCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTT
3598 AGCCCGACCCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAG
3698 CAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAG
3798 CCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGGAAGCAGCAGATTACGCGCA

PacI (3994)

3898 GAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACACGTTAAGGGATTTTGGTCATGGCTAGTTA

EagI (4014)
SwaI (4003) **NotI (4013)**

3998 ATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTTGTGGAATCGTAACTAACATACGCTCTCCATC
4098 AAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGAAGTGACGGTGCCAGAACATTTCTCTATCGAA