



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

101 GAGAAGGTGGCGCGGGTAAACTGGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTCGCGTTCGCCGCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMI (441) **NaeI (441)**
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

NcoI (560) **BstEII (555)** **KasI (535)** **AgeI (552)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTACCCATGGCTGTCTCAAGGGCTCCAGCACCCGACTCCGCCTG
1 M A V S R A P A P D S A C

601 TCAGAGGATGGTCTGGCTCTTCCACTTGTCTTCTGCCTCGGCTCAGGGAGTGAAGTTTACAGAGCAGCTCAGACCCAGCTAATGAATGGCGTTCTA
13 Q R M V W L F P L V F C L G S G S E V S Q S S S D P Q L M N G V L **XcmI (678)**

SdaI (730) **HindIII (724)**
701 GGAGAGTCTGCAGTCTTCTCTAAAGCTTCTGCAGGGAAGATAGCCAATATCATCATCTGGAATTATGAATGGGAAGCGTCAAGTCACTGCCCTCG
47 G E S A V L P L K L P A G K I A N I I I W N Y E W E A S Q V T A L

BspHI (833)
801 TTATCAACCTAAGTAATCTGAAAGTCCACAAATCATGAACACTGATGTAAGAAGAGACTGAACATCACCCAGTCTACTCCCTGCAAAATCAGCAACCT
80 V I N L S N P E S P Q I M N T D V K K R L N I T Q S Y S L Q I S N L

NcoI (902) **FspI (927)**
901 TACATGGCAGACAGGATCATACTGCGCAGATAACCACAAAGGACTCTGAAGTATCACCTTCAAATATATTCTGAGGGTCTTTGAACGATTGGGT
113 T M A D T G S Y T A Q I T T K D S E V I T F K Y I L R V F E R L G

1001 AACCTAGAAACTACCAACTATACTCTCTGCTAGAGAATGGGACTGCCAGATACACCTGGCCTGTGTTTGAAGAATCAAAGTCAAAGTGTCTCAGTTG
147 N L E T T N Y T L L L E N G T C Q I H L A C V L K N Q S Q T V S V

EcoRI (1164) **PshAI (1179)** **SandI (1154)** **BstEII (1171)**
1101 AGTGGCAAGCCACAGGAAACATCTCTTTAGGAGGACCAATGTCACTATCTTTTGGACCCGAGGAATTCTGGTGACCAGACTTACGTCTGCAGAGCCAA
180 E W Q A T G N I S L G G P N V T I F W D P R N S G D Q T Y V C R A K

1201 GAATGCTGTGAGCAATTTGTCAGTCTCTGTTTGCACCCAGAGTCTCTGCAAAGGGGTTCTAATAATCCACCTGGAATGCAGTATGGTTTATGACTACA
213 N A V S N L S V S V S T Q S L C K G V L T N P P W N A V W F M T T

BspLU11I (1347) **XmnI (1361)**
1301 ATTTCAATAATCAGTGCAGTCACTACTCTTTGTGTGCTGGAGCATACATGTTTGGAAAGAGAGGTTCTTCTCTTTGACTAGCCAAATCCAGAGT
247 I S I I S A V I L I F V C W S I H V W K R R G S L P L T S Q H P E

XcmI (1404)
1401 CCTCCAGAGCACAGATGGCCAGGCTCTCCAGGGAACACTGTGATGCACAAGTCACTCGTCCAATGCAGGAAATGAAAATCCCAAACCTATCAAAAA
280 S S Q S T D G P G S P G N T V Y A Q V T R P M Q E M K I P K P I K N

HpaI (1588)
1501 TGACTCCATGACAATTTACTCCATAGTTAATCATTCCAGAGAGGAAACAGTGGCTTTAACCGGTATAACCAACCCATTACCCTGAAGGTTAACTTTA
313 D S M T I Y S I V N H S R E E T V A L T G Y N Q P I T L K V N T L

MscI (1639) **NheI (1633)**
1601 ATCAACTATAACTCTGAAGGAAGAGCACTGCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCCAACTAGAATGCAGTGAA
347 I N Y N S •

HpaI (1771) **MfeI (1782)**
1701 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACAACTAATGCATTCATTTTAT

EcoRI (1867)
1801 GTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTTAAAATACAGCATAGCAAACCTTTAAC
1901 CTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCCTCACC

2001 TTCTTTCATGAGGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTTCTTATTTGTTTAAATGCAGTGCCTCCACATTCCTTTT

SspI (2106) **SwaI (2120)**
2101 TAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCC

2201 CCAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTAAATAGAAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTACTTGAGGGG
141 • N R T Y K L P **SacI (2381)**

2301 GATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCA
133 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 C M G

BstXI (2410)
2401 CAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAG
99 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 S V A S

StuI (2545)
Eco147I (2545)
2501 ACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGC
66 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 I A A

BspHI (2695)
XmnI (2687)
2601 CCCGACATGGTGTGCTTGTTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATG
33 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 T K M

VspI (2753)
AseI (2753)
2701 ATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGG
←

SacI (2810)
2801 TTCCTAAACGAGCTCTGTTATATAGACCTCCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCC
←

SpeI (2908)
2901 GTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGACT
←

SnaBI (3036)
Eco105I (3036)
3000 GCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGC
←

NdeI (3141)
3100 GGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCAT
←

3200 TGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGCGGGGGTCTTGGGCGGTGAGCCAGGCGGGCCAT
←

SdaI (3319) **PaeI (3327)** **BspLU11I (3337)**
3300 TTACCGTAAGTTATGTAACGCTGCAGTTAA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCTTGTGGCGT
←

3398 TTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCC
←

3498 CCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGC
←

ApaLI (3651)
3598 TCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTA
←

3698 ACTATCGTCTTGTGCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTAC
←

3798 AGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGT
←

3898 AGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTT
←

EagI (4087)
PaeI (4067) **SwaI (4076)** **NotI (4086)**
3998 TGATCTTTTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAAT
←

4098 AAAATATCTTTATTTTATTACATCTGTGTGTTGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAG
4198 CAAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA