



PvuI (7)
SgfI (6)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGTGAAGCTTCGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGGCC

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

BspLU11I (560)
AgeI (552)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAACATGTCTCAGTGGTACGAACTTACGAGCTTGACTCAA

1 M S Q W Y E L Q Q L D S K

NcoI (641)
601 ATTCCTGGAGCAGGTTACCAGCTTTATGATGACAGTTTTCCATGGAATACGAGCAGTACCTGGCACAGTGGTTAGAAAAGCAAGACTGGGAGCAGCGCT

13 F L E Q V H Q L Y D D S F P M E I R Q Y L A Q W L E K Q D W E H A

BspHI (732)
701 GCCAATGATGTTTCATTTGCCACCATCCGTTTTATGACCTCCTGTACAGCTGGATGATCAATATAGTCGTTTTCTTTGGAGAATAACTTCTTGCTAC

47 A N D V S F A T I R F H D L L S Q L D D Q Y S R F S L E N N F L L

801 AGCATAACATAAGGAAAAGCAAGCGTAATCTTCAGGATAATTTTCAGGAAGCCCAATCCAGATGTCTATGATCATTACAGCTGTCTGAAGGAAAGAAAG

80 Q H N I R K S K R N L Q D N F Q E D P I Q M S M I I Y S C L K E E R

901 GAAAATTCGAAAACGCCAGAGATTTAATCAGGCTCAGTCGGGAATATTAGAGCACAGTGTAGACAAACAGAAAAGAGCTTACAGTAAAGTC

113 K I L E N A Q R F N Q A Q S G N I Q S T V M L D K Q K E L D S K V

1001 AGAAAATGTGAAGGACAAGTTATGTGTATAGAGCATGAAATCAAGAGCCTGGAAGATTTACAAGATGAATAGACTTCAAATGCAAAAACCTTGCAGAACA

147 R N V K D K V M C I E H E I K S L E D L Q D E Y D F K C K T L Q N

1101 GAGAACACGAGACCAATGGTGTGGCAAAGAGTGATCAGAAAACAAGAACAGCTGTACTCAAGAAAGATGATTTAATGCTTACAATAAGAGAAAAGGAAGT

180 R E H E T N G V T A K S D Q K Q E Q L L L K K M Y L M L D N K R K E V

AseI (1255) **SpeI (1266)**
1201 AGTTCACAAAATAATAGAGTTGCTGAATGTCACTGAACCTACCCAGAATGCCCTGATTAATGATGAACCTAGTGGAGTGGAAAGCGGAGACAGCAGAGCGCC

213 V H K I I E L L N V T E L T Q N A L I N D E L V E W K R R Q Q S A

1301 TGTATTGGGGGGCGCCCAATGCTTGCTTGATCAGCTGCAGAACTGGTACTACTAGTTGCGGAGAGTCTGCAGCAAGTTCCGGCAGCAGCTTAAAAAGT

247 C I G G P P N A C L D Q L Q N W F T I V A E S L Q Q V R Q Q L K K

1401 TGGAGGAATTGGAACAGAAATACACCTACGAACATGACCTATCAGAAAACAAACAAGTGTATGGGACCGCACCTTCACTCTTTCCAGCAGCTCAT

280 L E E L E Q K Y T Y E H D P I T K N K Q V L W D R T F S L F Q Q L I

SphI (1532) **PshAI (1569)**
1501 TCAGAGCTCGTTTGTGGTGGAAAGACAGCCCTGCATGCCAACGCACCCTCAGAGGCCGCTGGTCTTGAAGACAGGGGTCCAGTTCAGTGTGAAGTTGAGA

313 Q S S F V V E R Q P C M P T H P Q R P L V L K T G V Q F T V K L R

1601 CTGTTGGTGAATGCAAGAGCTGAATTAATTTGAAAGTCAAAGTCTTATTTGATAAAGATGTGAATGAGAGAAATACAGTAAAAGGATTTAGGAAGT

347 L L V K L Q E L N Y N L K V K V L F D K D V N E R N T V K G F R K

1701 TCAACATTTTGGGCACGCACAAAAAGTGAACATGGAGGATCCACCAATGGCAGTCTGGCGGCTGAATTTCCGCACCTGCAATTTGAAAGAACAGAA

380 F N I L G T H T K V M N M E E S T N G S L A A E F R H L Q L K E Q K

SapI (1843)
1801 AAATGCTGGCACCAGAACGAATGAGGGTCTCTCATCGTTACTGAAGAGCTTCACTCCCTTAGTTTTGAAACCAATTTGTCAGCCTGGTTTGGTAATT

413 N A G T R T N E G P L I V T E E L H S L S F E T Q L C Q P G L V I

XhoI (1903) **BsrBI (1956)**
1901 GACCTCGAGACGACCTCTCTGCCGTTGTGGTGTCTCCAACGTGACGAGCTCCCGAGCGGTTGGGCTCCATCCTTTGGTACAACATGCTGGTGGCGG

447 D L E T T S L P V V V I S N V S Q L P S G W A S I L W Y N M L V A

ApaLI (2036)
DraIII (2030)
2001 AACCCAGGAATCTGCTCTTCTCCTGACTCCACCATGTGCACAGTGGGCTCAGCTTTCAGAAGTGTGAGTTGGCAGTCTTCTTCTGTACCAAAAAGAGG

480 E P R N L S F F L T P P C A R W A Q L S E V L S W Q F S S V T K R G

BspLU11I (2120) **HindIII (2134)**
2101 TCTCAATGTGGACCAGCTGAACATGTTGGGAGAGAAGCTTCTTGGTCTTAACGCCAGCCCGATGGTCTCATTCCGTGGACGAGTTTTGTAAGGAAAT

513 L N V D Q L N M L G E K L L G P N A S P D G L I P W T R F C K E N

2201 ATAAATGATAAAAATTTCCCTTCTGGCTTTGGATTGAAAGCATCTAGAACTCATTAAAAAACCTGCTCCCTCTCTGGAATGATGGGTGCATCATGG

547 I N D K N F P F W L W I E S I L E L I K K H L L P L W N D G C I M

XmaI (2381)
2301 GCTTCATCAGCAAGGAGCGAGAGCGTCCCTGTTGAAGGACCAGCAGCCGGGACCTTCTGCTGCGGTTGAGAGCTCCCGGGAAGGGCCATCAC

580 G F I S K E R E R A L L K D Q Q P G T F L L R F S E S S R E G A I T

BsrBI (2413)
2401 ATTCACATGGGTGGAGCGGTCACAGAACGGAGCGAACCTGACTTCCATGCGGTTGAACCCCTACACGAAGAAAGAACTTTCTGCTGTTACTTTCCCTGAC

613 F T W V E R S Q N G G E P D F H A V E P Y T K K E L S A V T F P D

2501 ATCATTGCAATTAACAAAGTCATGGCTGCTGAGAATATCTGAGAACTCCCTGAAAGTATCTGTATCCAAATATTGACAAAGACCATCTTTGGAAAGT

647 I I R N Y K V M A E N I P E N P L K Y L Y P N I D K D H A F G K

2601 ATTACTCCAGGCCAAAGGAGCACCAGACCAATGGAACCTGATGGCCCTAAAGGAACTGGATATATCAAGACTGAGTTGATTTCTGTGTCTGAAGTTCA

680 Y Y S R P K E A P E P M E L D G P K G T G Y I K T E L I S V S E V H

XbaI (2704) **Bsu36I (2743)** **EcoRI (2785)**
2701 CCCTTCTAGACTTCAGACCAAGACAACCTGCTCCCATGTCTCCTGAGGAGTTTTCAGAGGTTGCTCGGATAGTGGGCTCTGTAGAATTCGACAGTATG

713 P S R L Q T T D N L L P M S P E E F D E V S R I V G S V E F D S M

NheI (2825)

2801 ATGAACACAGTATAGAGCATGAATTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGC
747▶ M N T V •

BstAPI (2816) MscI (2831)

HpaI (2963)

2901 TTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAATTGCATTCATTTTATGTTTCAGG

EcoRI (3059)

3001 TTCAGGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAAT

3101 CAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCA

SapI (3241)

3201 TGGAGTTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATAGTAAA

SwaI (3312)

3301 TATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTA

3401 GTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTT

StuI (3737)

3501 CCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGTCACATGCCACAGGGGCT
130▶ 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 C P S

3601 GACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATG
97▶ 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 G I

3701 GCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGCAGCAGAGATGATCTCCCAAGTCTTGGTCTGTAGGCCGCCCCGCAT
63▶ 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 G V H

3801 GGTGCTTGTTCCTCATAGAGCATGGTATCTTCTCAGTGGCAGCTCCACAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCT
30▶ 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

AseI (3945)

3901 CCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAA

4001 ACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTT

SpeI (4100)

4101 ACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACC

SnaBI (4228)

4201 GCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATT

NdeI (4333)

4301 ACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAA

4401 TGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTGTTGGCGGTGAGCCAGGCGGGCCATTTACCGTAA

PacI (4519)

SdaI (4511) BspLU11I (4529)

4501 GTTATGTAACGCCTGCAGGTTAAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAAAGGCCGCTTGGCTGGCGTTTTTCCATAGG

4601 CTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCT

4701 CCCTCGTGGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAG

ApaLI (4843)

4801 GTATCTCAGTTCCGGTGTAGTGTCTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTT

4901 GAGTCCAACCCGGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGA

5001 AGTGGTGGCCTAACTACGGCTACACTAGAAGAAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATC

5101 CGGCAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT

EagI (5279)

PacI (5259) SwaI (5268) NotI (5278)

5201 ACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTT

5301 ATTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCT

5401 GTCCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA