



PvuI (7) SgfI (6) MfeI (82)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGGGGTAAGTGGAAAGTGATGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) Bsu36I (291)
201 GTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGGCC
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

KasI (535) BspEI (558)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACTGAGATCACCGGCTCCGGACATGACGGATCCCGAGGTATTCTGTTTCATCAC
601 CAAGATCTGTGCGCTCACGGGGCCGCATGACCTGGAGAACTGCTGGGTGAGATCAGCCTCCCGAAGCGCAACTCTACGAGCTGCTGAAGGCAGCA
11▶ K I L C A H G G R M T L E E L L G E I S L P E A Q L Y E L L K A A

PvuI (705) Bsp120I (700) XhoI (770) ScaI (794)
701 GGGCCGATCGCTTTGTGCTATTGGAGACTGGAGACCAGGCGGGATCACTCGGTCGGTGGTGGCTACTACTCGAGCCCGCTGCGCGTCGCAAGTACT
45▶ G P D R F V L L E T G D Q A G I T R S V V A T T R A R V C R R K Y

EagI (846) SspI (887)
801 GCCAGAGACCTGCGACAGCCTGCACCTTTGCAAGCTTAATCTGCTGGCGGTGCCACTATGCACAGTCCCAGCGGAACCTCTGCAATATTCTCACGA
78▶ C Q R P C D S L H L C K L N L L G R C H Y A Q S Q R N L C K Y S H D
901 TGTTCTCTCGAACAGAACTTCCAGTCTGAAGAATCATGAGCTCTCCGGGTTAACCAAGAGGAGCTGGCGGTCTCTGTTCCAAAGCGACCTTTCT
111▶ V L S E Q N F Q V L K N H E L S G L N Q E E L A V L L V Q S D P F

BglII (1046)
1001 TTCATGCCTGAGATATGCAAGAGTTACAAAGGAGAGGGCCGCAACAGATCTGCGGGCAGCCGAGCCCTGCGAGAGACTCCACATCTGTGAGCACTTCA
145▶ F M P E I C K S Y K G E G R K Q I C G Q P Q P C E R L H I C E H F

XmaI (1100)
1101 CCCGGGCAACTGCGATTTACCTCAACTGTCTCAGTCTCATAACTGATGGACAGGAAGTGTGGCCATCATGAGGGAGCATGGGCTGAGTTCTGATGT
178▶ T R G N C S Y L N C L R S H N L M D R K V L A I M R E H G L S S D V

EcoRV (1216)
1201 GGTCCAGAACATCCAGGATATCTGCAACAACAACACACTCGGAGGAACCCCTAGCATGAGAGCTCCCACCCACATCGCAGAGGGGGGCACACAGG
211▶ V Q N I Q D I C N N K H T R R N P P S M R A P H P H R R G G A H R

XbaI (1338)
1301 GACAGAAGCAAAGCAGAGACCGTTCATCACAACAGTCTAGAGTCTCAACGGTCTCACCTCTGGGATCTGGTCCCCCTAGCCAGATGTCACCG
245▶ D R S K S R D R F H H N S L E V L S T V S P L G S G P P S P D V T

ApaI (1472)
1401 GCTGTAAGGATCCCTGGAGGATGTGCTGTCAGATGTACCCAGAAGTTCAAGTACCTGGGACTCAGACCGTGCACAGCTTCTCCTCGTCTCATCTAA
278▶ G C K D P L E D V S A D V T Q K F K Y L G T Q D R A Q L S S V S S K

Tth111I (1517) BsaBI (1555)
1501 GGCCGCTGGTGTCCGAGGACCCAGTCAAATGAGAGCAAGCCAGGAGTTTTGGAGGATGGGGATCCAGATGGCTTGTCTTAGGAATCGTTCTGATTCCG
311▶ A A G V R G P S Q M R A S Q E F L E D G D P D G L F S R N R S D S

SphI (1676)
1601 TCCACAAGTCGAACCTCTGCTGCTGGCTTCTCTCGTTGCGGCACAAAGAAATGAAGCTGGGGCCATGAAAATGGGCATGCCTTCAGGACACCAGCTCG
345▶ S T S R T S A A G F P L V A A Q R N E A G A M K M G M P S G H H V

EcoRI (1790)
1701 AGGTCAAGGGCAAGAACGAGGACATTGATCGCGTCCCGTTTTTAAATAGTTATATTGATGGGGTAAACAATGGAAGAAGCAACAGTCTCAGGAATTCTAGG
378▶ E V K G K N E D I D R V P F L N S Y I D G V T M E E A T V S G I L G

PshAI (1813)
1801 TAAAAGGGCCACAGACAACCGGCTGGAAGAAATGATACTATCTAGCAACCATCAGAAGAGTGTGGCTAAGACCCAGGATCCCCAGACCCTGGCAGAATC
411▶ K R A T D N G L E E M I L S S N H Q K S V A K T Q D P Q T A G R I
1901 ACTGACAGTGGCCAGACACGGCATTCTGCATAGTAAATATGAAGAAAACCCAGCGTGGCCAGGTACATCTACCCATAACGGCCAAATGGCTTTAGTC
445▶ T D S G Q D T A F L H S K Y E E N P A W P G T S T H N G P N G F S
2001 AAATTATGGATGAAACGCCTAATGTCTCAAAAGTAGTCCCACTGGTTTTGGCATAAAATCAGCAGTCACTGGAGAAAAGAAGCAGTCTATTCTGGAGT
478▶ Q I M D E T P N V S K S S P T G F G I K S A V T G G K E A V Y S G V

BsrGI (2151)
2101 TCAGAGTCTGAGAAGCCATGTCCTGGCTATGCCTGGGAGACCACTACTCCTGTACAGGGCAGCAATAGGCTGCCTCCGTCACCTCTGTCTTCTTCCACA
511▶ Q S L R S H V L A M P G E T T T P V Q G S N R L P P S P L S S S T

XhoI (2274)
2201 AGCCACAGAGTTGCAGCCTCTGGGAGCCCTGGCAAGAGCTCCACCCATGCCTCTGTGAGCCCAGCCAGTGAAGGAAATCTGTCTGGATCATCTGTACAGGGG
545▶ S H R V A A S G S P G K S S T H A S V S P A S E P S R M M M M M S

AvrII (2344) BsrGI (2390)
2301 ACCCTGCTGAGTATTCCTATGCTACATCGTAAATCCTGTATCTCCTAGGATGGATGATCATGGCCTGAAGGAAATCTGTCTGGATCATCTGTACAGGGG
578▶ D P A E Y S L C Y I V N P V S P R M D D H G L K E I C L D H L Y R G

XmnI (2424) AgeI (2444)
2401 CTGTCAGCAGGTCAACTGCAACAAGAACCCTCCATCTGCCCTACCGGTGGCAGCTGTTTCATATTGCCCACTTGGATGGACTTTTCAGGACATGGAGTAT
611▶ C Q Q V N C N K N H F H L P Y R W Q L F I L P T W M D F Q D M E Y

BsrBI (2503)
2501 ATCGAGCGGGCTATTGTGATCCCAAAATTGAAATCATTGTGATAGAAAAACATCGGATCAATTTCAAGAAAATGACTTGTGATTCTACCCCATCCGTC
645▶ I E R A Y C D P Q I E I I V I E K H R I N F K K M T C D S Y P I R

DraIII (2649)

2601 GCCTCTCCACTCCTTCATTTGTCGAAAAACACTTAATTCTGTCTTACCACCAAGTGGCTTTGGTATTGGAGGAATGAATTGAATGAATATACTCAGTA
678▶ R L S T P S F V E K T L N S V F T T K W L W Y W R N E L N E Y T Q Y

AseI (2734)

2701 TGGGCATGAGAGCCCAAGCCATACCAGCTCCGAAATTAATTCTGCATACCTGGAGTCTTTCTTCCACTCCTGTCCAGGGGAGTTTTGCAGTTCACGCT
711▶ G H E S P S H T S S E I N S A Y L E S F F H S C P R G V L Q F H A

BstBI (2898)

2801 GGTTACAGAAATACGAGTTAAGCTTTCAAGGGATGATTCAGACGAATATAGCTTCCAAGACTCAAAGGCATGTTGTGAGAAGCCAGTTTTTTGTTCTT
745▶ G S Q N Y E L S F Q G M I Q T N I A S K T Q R H V V R R P V F V S

NheI (2961)

2901 CGAAGGATGTGGAGCAGAAGAGAAGAGTCCAGAGTAAGTGTTCAGCAGCTGTTAGCTCAGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTT
778▶ S K D V E Q K R R G P E •

HpaI (3099)

3001 GGACAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAG

MfeI (3110) EcoRI (3195)

3101 TTAAACAACAACAAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATT

3201 CTAAAATACAGCATAGCAAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCA

3301 ATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTAGCTCTTCATTTCTTTATGTTTTA

SspI (3434) SwaI (3448)

3401 AATGACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCC

3501 AGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCT

3601 AGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATA
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

3701 GTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCA
109▶ 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

StuI (3873)

3801 AAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGA
75▶ F 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

3901 TCTCCCCAGTCTTGGTCTGATGGCCGCCACATGGTGCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATC
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

XmnI (4015) AseI (4081)

4001 CTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGGC
9▶ Q Q S I N F T K M

4101 TGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCCATTTGCGTCAATGGGGC

SpeI (4236)

4200 GGAGTTGTTACGACATTTTGGAAAGTCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTC

SnaBI (4364)

4299 AAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCCAT

NdeI (4469)

4399 AAGTTCATGTAAGTGGCATAATGCCAGGCGGGCATTACCCTGATTGACGTCAATAGGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGT

4499 GGGCGATTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGAAACATACGTCATTATTGACGTCAATGGGCGGGG

SdaI (4647) PaeI (4655) BspLU11I (4665)

4599 GTCGTTGGGCGTACGCCAGGCGGGCATTACCCTAAGTTATGTAACGCTG C A G G T T A A T T A A G A A C A T G T G A C A A A A G G C C A G A A A G G C C A G

4697 GAACCGTAAAAAGGCCGCTTGTGCGCTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCGG

4797 ACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCC

ApaLI (4979)

4897 CTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGTTGAGTGTAGTTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCCGT

4997 TCAGCCCCAGCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT

5097 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAAGTATTTGGTATCTGCGCTCTGCTGA

5197 AGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTCCGCAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGGC

PaeI (5395)

5297 CAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGT

EagI (5415) NotI (5414)

SwaI (5404)

5397 TAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCA

5497 TCAAAAACAAAACGAAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA