



PvuI (7) SgfI (6) MfeI (82)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) HindIII (245) Bsu36I (291)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGCC
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCCTCCCGCTGTGGTGCCTCCTGAAGTCGCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (560) BstEII (555) EagI (567) BssHII (587)
AgeI (552) NgoMIV (565) Bsp120I (578)
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTACCATTGGCCGGCGGTGCGGGGCCGTGGCGCGTGTGCC
1 M A G R C G A R G A L S P

BamHI (650) BsrBI (673)
601 ACAGTTGCTGCTTTCGACTGCGCCCGCACTGCTGGGAGAGCTTTGCGGGATCCTGGACAGTGCATGGCCCGCTCGGCTGGCGGGCCTGGCGGAG
13 Q L L L F D L P P A L L G E L C G I L D S C D G P L G W R G L A E

SnaBI (742)
701 CGACTTTCAAACAGCTGGCTGGATGTTCTGCATATTGAAAAGTACGTAAACCAAGGTAAGTGAACAAGAGAATTGCTCTGGTCTGGGCACAGAAAA
47 R L S N S W L D V R H I E K Y V N Q G K S G T R E L L W S W A Q K

PvuI (806)
801 ACAAGACGATCGCGACCTTTAGAGGTTCTCCAGGACATGGGGCATCAACGAGCTATCCACTTAATCATCAACTATGGAGTAAGCTGGACTCCTTCAGT
80 N K T I G D L L E V L Q D M G H Q R A I H L I I N Y G V S W T P S V

Bsu36I (937) SphI (948)
901 GCAGACGATCAGAGCTTCCATCCCCAGCTTCCCACCTGAGGTGAAGCATGCGTGCAGAGAAAACGACCTGGACCTCTGGAACCAGCCAATGTCACA
113 Q T H H E L P F P S F P P E V K H A C R E N D P G P L E P A N V T
1001 GTGGATAATGTTCTTCTTCTGAACATAATGAAAAGAACACTGCAGAAAACCCCTATCAGTTCAGAGTATCCTAGAAGGAACCAAAACATTTCCACA
147 V D N V L V P E H N E K G T L Q K T P I S F Q S I L E G T K H F H

Bst1107I (1135) NdeI (1163) PmeI (1179)
1101 AAGACTTCTGATTGGAGAAGGGGAGATATTCGAAGTATACAGAGTGACATTCGAAACCAAGCATATGCTGTTAAATTTTAAACAGGAGAAAAAAT
180 K D F L I G E G E I F E V Y R V D I R N Q A Y A V K L F K Q E K K M

BsaBI (1223)
1201 GCACTAAAGAAGCACTGGAAGAGATTTTATCAGAAGTGAAGTCTACTCCTGTTCCGTCACCCCCACATACTAGAGCTGGCTGCATATTTACGGAG
213 Q L K K H W K R F L S E L E V L L L F R H P H I L E L A A Y F T E

ApaLI (1362)
1301 ACTGAGAACTTTGTCTGGTTTATCCCTATATGAGCAACGGGACGCTTTTCGACAGATTACAGTGCACAAATGGCACAACCCCGCTTCTGGCAGCTTC
247 T E K L C L V Y P Y M S N G T L F D R L Q C T N G T T P L S W H V

Psp1406I (1477)
1401 GAATCAGCGTATTGATAGGAATAGCCAAAGCCATCCAATACTTGCAACACTCAGCCGTGCGCCGTATCTGTGGCAACGTTTCCAGTGCAACATACT
280 R I S V L I G I A K A I Q Y L H N T Q P C A V I C G N V S S A N I L

XbaI (1560)
1501 CTTGGATGACCAGCTCCAACCCAACTAACGGATTTTGTCTGCAGCGCACTTCCGACCAATCTAGAGCAGCAGAGTTCTACCATAAATATGACCGGGCGT
313 L D D Q L Q P K L T D F A A A H F R P N L E Q Q S S T I N M T G G
1601 GGCAGGAAACATCTGTGGTACATGCCAGAAGAATACATCAGACAGGGAAGACTTTCCGTTAAACTGATGTCTACAGCTTCCGAATCGTGATCATGGAGG
347 G R K H L W Y M P E E Y I R Q G R L S V K T D V Y S F G I V I M E

StuI (1782)
1701 TTCTAACGGGCTGCAAAGTGGTGTCTGGATGACCCGAAACACGTTTCTGCTGCGGGACCTCCTCATGGAAGTGTGGAGAAAAGGGCTAGACTCCTGCCT
380 V L T G C K V V L D D P K H V Q L R D L L M E L M E K R L G L D S C L
1801 GTCCTTCTAGACAGGAAGATACCCTGTCTCGGAACTTCTCTGCAAAGCTTCTCTCTGCGGGCCGGTGTGTGGCAACGAAGGCCAAGTTAAGA
413 S F L D R K I P P C P R N F S A K L F S L A G R C V A T K A K L R

Tth111I (1909)
1901 CCCACGATGGACGAAGTCTCTCTGGAGAGCACCAGCCTAGCTTGTATTTTGAGAAGACCCTCCACGTCCTTGAAGTCTTCAAGGTGCCTT
447 P T M D E V L S S L E S T Q P S L Y F A E D P P T S L K S F R C P
2001 CTCCACTGTTCTTGGATAATGTCCCAAGTATTCCAGTAGAAGATGATGAAAACCAAGAATAACCATTCAGTACCTCCCAAGGAAGTTTGGGGACAGATAG
480 S P L F L D N V P S I P V E D D E N Q N N H S V P P K E V L G T D R

BstEII (2139)
2101 AGTGACTCAGAAAACCCCTTTGAATGCAGCCAGTCTGAGGTACCTTTCTAGGCTTGGACCGAAACAGAGGGAACAGGGGAAGTGAAGCGGATTGCAAC
513 V T Q K T P F E C S Q S E V T F L G L D R N R G N R G S E A D C N

BspHI (2214) PshAI (2257)
2201 GTGCCAGTCTTCTCATGAGGAATGCTGGTCCCAGAGCTTGTGGCGCCATCCCAGGACTTAAGTCTACTGTGATCAGTTTGGGCTCGTCTTGGGAAG
547 V P S S S H E E C W S P E L V A P S Q D L S P T V I S L G S S W E

BstXI (2307) MscI (2398) NheI (2392)
2301 TACCAGGCCATTTTATGGGAGCAAGCCAAATGGAGAAGAGGTGTTCTCTGGGCTCTTTTGCAAGTGCAGTGAACAGTCCAAAAAGCAGTGCAGTCTAGCTG
580 V P G H S Y G S K P M E K R C S S G L F C S E H E Q S K K Q •
2401 GCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTA

HpaI (2530) MfeI (2541)
2501 TTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTCATTCTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGTTTTTTAAAGCA

2601 **EcoRI (2626)**
 AGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATG
 2701 AATAAGGCATAGGCATCAGGGGCTGTTGCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTTAAGATATAGTGATTTTCCCAAGGT

2801 **SspI (2865)** **SwaI (2879)**
 TTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAAT
 2901 GAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAA

3001 TAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCA
 141 • N R T Y K L P I L E E I T T K V L K G N M
SacI (3140) **BstXI (3169)**
 3101 TCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTTCGCATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGA
 119 E I L V F C D P A Y D S I L E R C M G C P S V V R I S R D V E D S
 3201 GTAGGGGTGCCTGACAGCCAAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCTGCCA
 86 Y P H R V A V I T D F D K Q G N S V A S G I A I A E A C V T V R G

StuI (3304)
 3301 ATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTGTCTCATAGAGCATGGTGATCT
 52 I Y A E I H V A S I I E G T K T R I A A G V H H K N D E Y L M T I K
 3401 TCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATAT
 19 E T A V E V L E L D Q Q S I N F T K M

AseI (3512) **SacI (3569)**
 3501 ACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTAC

SpeI (3667)
 3601 ACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATG

SnaBI (3795)
 3701 GGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGT
 3801 AGATGTA CTGCAAGTAGGAAAGTCCCAT AAGGTCATGTACTGGCATAATGCCAGGCGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGG

NdeI (3900)
 3901 CATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACA

PacI (4086) **SdaI (4078)** **BspLU11I**
 4001 TACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGCGGTACAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTGCAGGTTAATTAAGAACAT
 4101 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGA
 4201 CGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGC
 4301 TTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTCCGCTCAA

ApaLI (4410)
 4401 GCTGGGCTGTGTGCACGAACCCCGTTTCAGCCCAGCCGCTGCGCCTTATCCGGTAACTATCGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAA
 4501 CTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAA
 4601 CAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA AAAAGAGTTGGTAGCTTGTATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTT
 4701 TTTTGTGGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCA

EagI (4846) **PacI (4826)** **SwaI (4835)** **NotI (4845)**
 4801 CGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTG
 4901 TGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGCAAGTGCAGGTGCCAGAACATTT
 5001 CTCTATCGAA