



**PvuI (7)**  
**SgfI (6)**  
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA  
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)** **HindIII (245)**  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMI (441)**  
**NaeI (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTGTTTCGTTT

**NcoI (560)**  
**BstEII (555)**  
**AgeI (552)** **BspHI (590)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTCACCATTGGACGAACAGGAGGCATTGAAGTCAATCATGAACGA  
1 M D E Q E A L N S I M N D

**PshAI (664)**  
601 TCTGGTGGCCCTCCAGATGAACCGACGTCACCGGATGCCTGGATATGAGACCATGAAGAACAAAGACACAGGTCACCTCAATAGGCAGAGTGACGTCAGA  
13 L V A L Q M N R R H R M P G Y E T M K N K D T G H S N R Q S D V R

**NgoMI (743)**  
**NaeI (743)** **DraIII (772)**  
701 ATCAAGTTCGAGCACAACGGGAGAGGGGAATTATAGCGTTACGCGGCTGTGAAATATGAAGATGTGGAGCACAAGGTGACACAGTATTTGGACAAC  
47 I K F E H N G E R R I I A F S R P V K Y E D V E H K V T T V F G Q  
801 CTCTTGATCTACATTACATGAACAATGAGCTCTCCATCCTGCTGAAAAACCAAGATGATCTTGATAAAGCAATTGACATTTTAGATAGAGCTCAAGCAT  
80 P L D L H Y M N N E L S I L L K N Q D D L D K A I D I L D R S S S M  
901 GAAAAGCCTTAGGATATTGCTGTTGTCCAGGACAGAAACATAACAGTCTCTCCCACTCTGGGGTGTCCAGACAGGTGCGGATCAAGGCTCCCG  
113 K S L R I L L L S Q D R N H N S S S P H S G V S R Q V R I K A S Q  
1001 TCCGACGGGATATAAATACTATCTACCAGCCCCGAGCCAGAACGAGGCACCTCTGTGACGCTCCAGAACCTGGCCGAGCTCACCTCCCCCTG  
147 S A G D I N T I Y Q P P E P R S R H L S V S S Q N P G R S S P P P

**BsrBI (1111)** **EcoO109I (1138)** **SphI (1196)**  
1101 GCTATGTTCTGAGCGGACGACGACATTGCCCGCAGGGGTCCTACACCAGCATCAACAGTGAAGGGGATTCATCCAGAGACCAGCGAGCAGTGCAT  
180 G Y V P E R Q Q H I A R Q G S Y T S I N S E G E F I P E T S E Q C M

**BamHI (1203)** **BspEI (1280)**  
1201 GCTGGATCCCTGAGCAGTGCAGAAAATTCCTTGTCTGGAAGCTGCCAATCCTTGACAGGTCAGCAGACAGCCATCCTCCGAAATCACGAATGTCC  
213 L D P L S S A E N S L S G S C Q S L D R S A D S P S F R K S R M S

**BbrPI (1399)**  
1301 CGTGCCAGAGCTTCCCTGACAACAGACAGGAATACTCAGATCGGAAACTCAGCTTTATGACAAAGGGTCAAAGTGAACCTACCCCGGCGCTACC  
247 R A Q S F P D N R Q E Y S D R E T Q L Y D K G V K G G T Y P R R Y

**ApaLI (1408)** **BsrBI (1497)**  
1401 ACGTGTCTGTGCACCACAAGGACTACAGTGATGGCAGAAGAACATTTCCCGAATACGCGCTCATCAAGGCAACTTGTTCACCCTGGTCCCTCCAGCCG  
280 H V S V H H K D Y S D G R R T F P R I R R H Q G N L F T L V P S S R  
1501 CTCCCTGAGCACAATGGCGAGAACATGGGTCTGGCTGTGCAATACCTGGACCCCGTGGGCGCTGCGGAGTGGGACAGCGAGAATGCCCTCTCTGTG  
313 S L S T N G E N M G L A V Q Y L D P R G R L R S A D S E N A L S V  
1601 CAGGAGAGGAATGTCCAACCAAGTCTCCAGTGCCTCCATCAACTGGCGCCGGGAAAGTCTCTGGCCAGGGTGCCTCGGAGGGTCTATTTGTGCT  
347 Q E R N V P T K S P S A P I N W R R G K L L G Q G A F G R V Y L C  
1701 ATGACGTGGACACGGGACGTGAACCTGCTTCCAAGCAGGTCGAATTTGATCCAGACAGTCTGAGACAAGCAAGGAGGTGAGTGTCTGGAGTGCAGAT  
380 Y D V D T G R E L A S K Q V Q F D P D S P E T S K E V S A L E C E I

**ScaI (1838)**  
1801 CCAGTTGCTAAAGAAGTTCAGCATGAGCGCATCGTGCAGTACTATGGCTGTCTGCGGGACCGGCTGAGAAGACCTGACCATCTTCATGGAGTACATG  
413 Q L L K N L Q H E R I V Q Y Y G C L R D R A E K T L T I F M E Y M  
1901 CCAGGGGCTCGGTGAAAGACAGTTGAAGGCTTACGGTGTCTGACAGAGAGCGTGACCCGAAAGTACACGCGGAGATCCTGGAGGGCATGCTCCTACC  
447 P G G S V K D Q L K A Y G A L T E S V T R K Y T R Q I L E G M S Y  
2001 TGCACAGCAACATGATTGTTACCGGGACATTAAGGGAGCCAACATCCTCCGAGACTCTGCTGGGAATGTAAGCTGGGGGACTTTGGGGCCAGCAAACG  
480 L H S N M I V H R D I K G A N I L R D S A G N V K L G D F G A S K R

**PstI (2101)** **SphI (2129)**  
2101 CCTGCAGACGATCTGTATGTCGGGGACGGGATGCGCTCCGCTACTGGACACCCCTACTGGATGAGCCCTGAGGTGATCAGCGCGAGGGCTATGGAAGG  
513 L Q T I C M S G T G M R S V T G T P Y W M S P E V I S G E G Y G R  
2201 AAAGCAGACGTGTGGAGCCTGGGCTGCACTGTGGTGGAGATGCTGACAGAGAACCACCGTGGGAGAGTATGAAGCTATGGCCGCACTCTCAAGATTG  
547 K A D V W S L G C T V V E M L T E K P W A E Y E A M A A I F T K I  
2301 CCACCCAGCCCAACCTCCTCAGCTGCCCTCCACATCTCTGAACATGGCCGGGACTTCTGAGGCGCATTTTTGTGGAGGCTCGCCAGAGACCTTCAGC  
580 A T Q P T N P Q L P S H I S E H G R D F L R R I F V E A R Q R P S A

**MscI (2466)**  
**NheI (2460)**  
2401 TGAGGAGTGTCTCACACACCACTTTGCACAGCTCATGTACTGAGCTCTCACGGCCACACAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTG  
613 E E L L T H H F A Q L M Y •

**HpaI (2598)**  
2501 GACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGT

**EcoRI (2694)**  
2601 TAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTC

2701 TAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAA  
 2801 TGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTAA

SspI (2933) SwaI (2947)

2901 ATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCA

EcoO109I (3008)

3001 GATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTA

3101 GCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCACTCAATGAGCACAAGCAGTCAGGAGCATAG  
 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  
 3201 TCAGAGATGAGCTCTCTGCACATGCCACAGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAA  
 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 (3372)

3301 AGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGAT  
 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  
 3401 CTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGTCCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACCAGCTCCAGATCC  
 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 (3522) XmnI (3514) AseI (3580)

3501 TGCTGAGAGATGTTGAAGGCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGT  
 8 Q Q S I N F T K M

3601 GGATGGCGTCTCCAGCTTATCTGACGGTTCACAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCTACCGCCATTGCGTCAATGGGGCGG

SpeI (3735)

3701 AGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAA

SnaBI (3863)

3800 ACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAA

NdeI (3968)

3900 GGTCATGTACTGGGCATAATGCCAGGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGG  
 4000 GCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGT

PstI (4147) SdaI (4146) PacI (4154) BspLU11I (4164)

4100 CGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCC 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 C A A A A G G C C A G G A  
 4198 ACCGTAAAAAGGCCGCTTGTGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGAC  
 4298 AGGACTATAAAGATACCAGCGTTTTCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCT

ApaLI (4478)

4398 TCGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGCTTC  
 4498 AGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAG  
 4598 CAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAG  
 4698 CCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGGAAGCAGCAGATTACGGCA

PacI (4894)

4798 GAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTA

EagI (4914) SwaI (4903) NotI (4913)

4898 ATTAACATTTAAATC AGCGGCCGAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATC  
 4998 AAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA