



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCGCCGCCCTACCTGAGGCC  
**HindIII (245)**  
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT  
**NgoMIV (441)**  
501 TCTGTTTGTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAACATGTCTGTGGGGTCTGGTCTCCAAGATGCCCCAGA  
**AgeI (552)** 1 M S L W G L V S K M P P E  
**BspLU11I (560)**

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**SalI (619)** 601 AAAAGTGCAGCGGCTCTATGTGCACTTTCCCAACACCTGCGGCATCTTCTGGGTGACTGGCTGGAGAGCCAGCCCTGGGAGTTCCTGGTCCGCTCCGAC  
13 K V Q R L Y V D F P Q H L R H L L G D W L E S Q P W E F L V G S D  
**Tth11I (736)**  
701 GCCTTCTGCTGCAACTTGGCTAGTGCCTACTTTCCAGACACTGTCAGCACCTTCAGGCTCGGTGGGAGAGCAGGGGAGGGGAGCACCATCTTGAAC  
47 A F C C N L A S A L L S D T V Q H L Q A S V G E Q G E G S T I L Q  
**SandI (830)**  
801 ACATCAGCACCTTGAGAGCATATATCAGAGGGACCCCTGAAGCTGGTGCCACTTTTCCAGACAAATACTTCAAGGAGAGAAAAAGCTGTTATGGAACA  
80 H I S T L E S I Y Q R D P L K L V A T F R Q I L Q G E K K A V M E Q  
901 GTTCCGCCACTTGCCAATGCCTTTCCACTGGAAGCAGGAAGAAGTCAAGTTAAGACAGGCTTCCGGAGGCTGCAGCACCAGTGGGGAGATCCACCTT  
113 F R H L P M P F H W K Q E E L K F K T G L R R L Q H R V G E I H L  
1001 CTCCGAGAAGCCCTGCAGAAGGGGGCTGAGGCTGGCCAAGTGTCTGTCACAGCTTGTAGAAACTCTGTAATGGGACTGGCCAAGTGGGCCCTGG  
147 L R E A L Q K G A E A G Q V S L H S L I E T P A N G T G P S E A L  
**BamHI (1160)**  
1101 CCATGCTACTGCAGGAGACCCTGGAGAGCTAGAGGCAGCCAAAGCCCTAGTGTGAAGAGGATCCAGATTTGAAACGGCAGCAGCAGCTGGCAGGGAA  
180 A M L L Q E T T G E L E A A K A L V L K R I Q I W K R Q Q Q L A G N  
1201 TGGCGCACGTTTGGAGAGCTGGCCCACTCCAGGAGGTTGAAAGCCTGGTGGACATTTATCCAGCTACAGCAGGAGGTAGGGGGCGGTGGT  
213 G A P F E E S L A P L Q E R C E S L V D I Y S Q L Q Q E V G A A G

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**XmaI (1319)** 1301 GGGGAGCTTGAGCCCAAGACCCGGGCATCGCTGACTGGCCGGCTGGATGAAGTCTGAGAACCCTCGTACCAGTTGCTTCTGGTGGAGAAGCAGCCCC  
247 G E L E P K T R A S L T G R L D E V L R T L V T S C F L V E K Q P  
**NgoMIV (1337)**  
1401 CCCAGGTAAGACTCAGACCAAGTTCAGGCTGGAGTTCGATTCTGTTGGGCTTGGAGTTCCTGGGGGGCCAGCCAAGCTCCGCTGGTCAGGGC  
280 P Q V L K T Q T K F Q A G V R F L L G L R F L G A P A K P P L V R A  
1501 CGACATGGTGACAGAGAAGCAGGCGCGGAGCTGAGTGTGCCTCAGGGTCTGGGGCTGGAGCAGAAAGCACTGGAGAAATCATCAACAACACTGTGCC  
313 D M V T E K Q A R E L S V P Q G P G A G A E S T G E I I N N T V P  
**Bsp120I (1469)**  
1601 TTGGAGAACAGCATTCTGGAACTGCTGCTGCTGCCCTGTTCAAGAACCTGCTTCTCAAGAAGATCAAGCGGTGTGAGCGGAAGGGCACTGAGTCTGTCA  
347 L E N S I P G N C C S A L F K N L L L K K I K R C E R K G T E S V  
**BsrBI (1675)**  
1701 CAGAGGAGAAGTGCCTGCTTCTGCCAGCTTACACTTGGCCCCGCAAACCTCCCATCCAGCTCCAGGCCCTGCTCTGCCCTGGTGGTGCAT  
380 T E E K C A V L F S A S F T L G P G K L P I Q L Q A L S L P L V V I  
**BsrBI (1891)**  
1801 CGTCCATGGCAACCAAGACAACAATGCCAAAGCCACTATCCTGTGGACAATGCCTTCTGTGAGATGGACCGCTGCCCTTTGTGGTGGCTGAGCGGGT  
413 V H G N Q D N N A K A T I L W D N A F S E M D R V P F V V A E R V  
**XmnI (1998)**  
1901 CCCTGGGAGAAGATGTGTGAAACTCTGAACCTGAAGTTATGCTGAGGTGGGGACCAACCGGGGGCTGCTCCAGAGCACTTCTTCTTCCGCCCAGA  
447 P W E K M C E T L N L K F M A E V G T N R G L L P E H F L F L A Q  
**BglIII (2000)**  
2001 AGATCTTCAATGACAACAGCCTCAGTATGGAGGCTTCCAGCACCGTTCGTGTCTGCTGCTGCGAGTTCAACAAGGAGATCCTGCTGGCCGTGGCTTAC  
480 K I F N D N S L S M E A F Q H R S V S W S Q F N K E I L L G R G F T  
**BspEI (2147)**  
2101 CTTTTGGCAGTGGTTTGTGGTGTCTGGACCTCACCAACGCTGTCTCCGGAGCTACTGGTCTGACCGCTGATCATTGGCTTCATCAGCAAACAGTAC  
513 F W Q W F D G V L D L T K R C L R S Y W S D R L I I G F I S K Q Y  
2201 GTTACTAGCTTCTCTCAATGAGCCGACGGAACCTTCTCCTCGCTTCCAGCAGTACAGAGATTGGGGCATTACCATTGCCATGTCATCCGGGGCC  
547 V T S L L L N E P D G T F L L R F S D S E I G G I T I A H V I R G  
2301 AGGATGGCTCTCCACAGATAGAGAACATCCAGCATTCTGTGCCAAAGACCTGTCATTGCTACTGGGGGACCGAATCCGGATCTTGTCTCAGCTCAA  
580 Q D G S P Q I E N I Q P F S A K D L S I R S L G D R I R D L A Q L K  
**BspEI (2435)**  
2401 AAATCTCTATCCCAAGAAGCCCAAGGATGAGGCTTCCGGAGCCACTACAAGCCTGAACAGATGGGTAAGGATGGCAGGGGTTATGTCCAGCTACCATC  
613 N L Y P K K P K D E A F R S H Y K P E Q M G K D G R G Y V P A T I  
2501 AAGATGACCGTGGAAAGGACCAACCACTTCTACCCAGAGCTCCAGATGCCTACCATGGTGCCTTCTATGACCTTGAATGGCCCTGATTCCTCCA  
647 K M T V E R D Q P L P T P E L Q M P T M V P S Y D L G M A P D S S  
**SphI (2603)**  
2601 TGAGCATGCAGCTTGGCCAGATATGGTCCCCAGGTGTACCCACCACACTCTCACTCCATCCCCCGTATCAAGGCCTCTCCCAGAAGAATCAGTCAA  
680 M S M Q L G P D M V P Q V Y P P H S H S I P P Y Q G L S P E E S V N

2701 CGTGTGTGACGCTTCCAGGAGCCTCACCTGCAGATGCCCCAGCCTGGCCAGATGAGCCTGCCCTTTGACCAGCCTACCCCCAGGGCCTGCTGCCG  
 713▶ V L S A F Q E P H L Q M P P S L G Q M S L P F D Q P H P Q G L L P

2801 TGCCAGCCTCAGGAGCATGCTGTGTCCAGCCCTGACCCCTGCTCTGCTCAGATGTACCATGGTGAAGACAGCTGCCCTGAGCCAGCCAGTGACAGCGT  
 747▶ C Q P Q E H A V S S P D P L L C S D V T M V E D S C L S Q P V T A

HindIII (2971)

2901 TTCCTCAGGGCACTTGGATTGGTGAAGACATATTCCTCTGCTGCCCTCCACTGAACAGGACCTCACTAAGCTTCTCCTGGAGGGCAAGGGGAGTC  
 780▶ F P Q G T W I G E D I F P P L L P P T E Q D L T K L L L E G Q G E S  
 3001 GGGGGAGGGTCTTGGGGCAGCAGCCCTCCTGCAGCCCTCCACTATGGGCAATCTGGGATCTCAATGTCCACATGACCTAAGGGCCAAACCCAGT  
 813▶ G G G S L G A Q P L L Q P S H Y G Q S G I S M S H M D L R A N P S

NheI (3125)

3101 TGGTGATCCCAGCTGGAGGGAGAACGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGC  
 847▶ W •

HpaI (3263) MfeI (3274)

3201 TTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAACAAACAACAATTGCATTCAATTTATGTTTCAGG

EcoRI (3359)

3301 TTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAAT  
 3401 CAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCA

SapI (3541) SspI (3598)

3501 TGGAGTTTAAGATATAGTGATTTTCCCAAGTTTGAAGTACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATAGTAAAA

SwaI (3612)

3601 TATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTA  
 3701 GTAGTTGGACTTAGGGAACAAAGGAACCTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTT  
 3801 CCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCT  
 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

BstXI (3902)

3901 GACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATG  
 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  
 4001 GCAATGGCTTCAACAGACAGTACCCCTGCCAATGTAGGCCTCAATGTGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGGACAT  
 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

XmnI (4179)

4101 GGTGCTTGTGCTCATAGAGCATGGTATCTTCTAGTGGCAGCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCT  
 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 (4245)

4201 CCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTIATCTGACGGTCACTAA  
 4301 ACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTT

SpeI (4400)

4401 ACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACC

SnaBI (4528)

4501 GCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATT

NdeI (4633)

4601 ACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCTCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAA  
 4701 TGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGCGGGTCTGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAA

PacI (4819) SdaI (4811) BspLU11I (4829)

4801 GTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGGTGGCGTTTTTCCATAGG  
 4901 CTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCAAAACCCGACAGGACTATAAAGATACCAGGCTTTCCCTGGAAGCT  
 5001 CCCTCGTGGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAG

ApaLI (5143)

5101 GTATCTCAGTTCCGTTGATGCTGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTT  
 5201 GAGTCAACCCGGTAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGA  
 5301 AGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATC  
 5401 CGGCAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT

EagI (5579) NotI (5578)

5501 ACGGGTCTGACGCTCAGTGAACGAAAACTCACGTAAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTT  
 5601 ATTTTCATTACATCTGTGTGTTGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAACGAAACAAACAACTAGCAAAATAGGCT  
 5701 GTCCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA