



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 **MfeI (82)** **EcoNI (96)**

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)**
**EcoNI (287)**  
 201 GTGAACGTTCTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
 401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

**BspHI (560)**  
**AgeI (552)**
**SacII (566)**
**BstAPI (579)**  
 501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTATCATGACCGCGGCAGCGGAGAATCTGCAAGCATTGAG
   
1▶ M T A A Q R Q N L Q A F R

**XhoI (658)**  
 601 AGACTATATCAAGAAGATTCTGGACCCACCTACATCCTCAGCTACATGAGTTCCTGGCTCGAGGATGAGGAGGTGCAGTACATTGAGGCTGAGAAGAAC
   
 13▶ D Y I K K I L D P T Y I L S Y M S S W L E D E E V Q Y I Q A E K N

**Bsp120I (705)**
**StuI (773)**  
 701 AACAAAGGCCAATGGAAGTGCCTCACTTCTCCTCCAGTACCTGTTGAAGTGCAGTGCAGAGGGCTGGTCCAGGCCCTTTTGGATGCCTGTACCATG
   
 47▶ N K G P M E A A S L F L Q Y L L K L Q S E G W F Q A F L D A L Y H
   
 801 CAGTTACTGTGGACTTTGTGAAGCCATCGAAAGTTGGACTTTCAAAAAATTGAAAAGTTAGAGGAACACAGATTACTTTTAAAGCCTTTAGAACCAGA
   
 80▶ A G Y C G L C E A I E S W D F Q K I E K L E E H R L L L R R L E P E

**EcoRV (925)**
**AseI (955)**  
 901 ATTTAAGGCCACAGTTGATCCAAATGATATCCTTCTGAAGTATCCGAATGTTTGATTAATCAGGAATGTGAAGAAATCAGACAGATCCGAGACACTAAA
   
 113▶ F K A T V D P N D I L S E L S E C L I N Q E C E E I R Q I R D T K

**MseI (1060)**  
 1001 GGGAGAATGCAGGTGCGGAGAAGTGGCCGAATGTCTTATCAGATCCGACAAGGAAAACCTGGCCAAAGGCTTTCGCAACTTGCTTTGGAGAAAGACAACA
   
 147▶ G R M A G A E K M A E C L I R S D K E N W P K V L Q L A L E K D N

**BsrBI (1172)**  
 1101 GCAAGTTTAGTGAATTGTGGATTGTTGATAAAGGTTTCAAAGGGCTGAAAGCAAGGCTGATGAGGATGATGGAGCGGAGCGTCCAGCATCCAGATTTT
   
 180▶ S K F S E L W I V D K G F K R A E S K A D E D D G A E A S S I Q I F

**XmaI (1240)**  
 1201 CATTGAGGAGAGCCAGAGTGTGAGAATCTCAGTCAAGTCCCGGGCCTCCTTCAAGAGCGTCTTCTAATAATTTACACAGCCATTGAAACCAAGAAT
   
 213▶ I Q E E P E C Q N L S Q N P G P P S E A S S N N L H S P L K P R N
   
 1301 TACCAACTGGAGCTTGCCTGCCTGCCAAGAAAGGAAATAAATAATATGCCCCACTGGTGTGGAAAAACCTTTGTGCTTCTTATATGTG
   
 247▶ Y Q L E L A L P A K K G K N T I I C A P T G C G K T F V S L L I C
   
 1401 AACACCACTTAAAAAATCCCATGTGGACAAAAAGGAAAGTGGTCTTCTCGCTAACCAAAATCCTGTCTATGAGCAGCAGGCAACTGTGTTCTCAGC
   
 280▶ E H H L K K F P C G Q K G K V V F F A N Q I P V Y E Q Q A T V F S R

**EcoRV (1588)**  
 1501 ATATTTGAAAGACTTGGGTACAACATTGCGAGCATTCTGGGCAACATCTGATAGCGTCTCAGTGCAGCACATCATTGAAGACAATGATATCATCATC
   
 313▶ Y F E R L G Y N I A S I S G A T S D S V S V Q H I I E D N D I I I
   
 1601 CTGACACCCAGATTCTTGTGAACAATCTCAACAACGGAGCCATCCCCTCGTTGTCTGTCTTCACTCTGATGATTTGATGAGTGCATAACACTAGCA
   
 347▶ L T P Q I L V N N L N N G A I P S L S V F T L M I F D E C H N T S

**SmaI (1760)**  
 1701 AAAACCACCATACAATCAGATCATGTTTTCAGATACCTAGACCACAAACTGGAGATCACGGGACCCACTGCCTCAGGCTGTTGGGCTGACTGCCTCCGT
   
 380▶ K N H P Y N Q I M F R Y L D H K L G E S R D P L P Q V V G L T A S V

**SacII (1820)**
**Psp1406I (1897)**  
 1801 CGGCGTTGGAGATGCTAAGACCGGAGGAAGCCATGCAACATATCTGTAAGTCTGTGCCGCTGGATGCCTCCGTGATTGCCACAGTCAGAGACAAC
   
 413▶ G V G D A K T A E E A M Q H I C K L C A A L D A S V I A T V R D N

**BstBI (1965)**  
**Bsp119I (1965)**
**NsiI (1980)**  
 1901 GTTGCAAGTGGAAACAGGTCGTTTATAAGCCCGAGAAAATTTCCAGGAAAGTGGCAATCCCGGACTTCGAACAGGTTTAAATGCATCATCTCTCAGCTGA
   
 447▶ V A E L E Q V V Y K P Q K I S R K V A S R T S N T F K C I I S Q L

**NheI (2016)**
**EcoRI (2071)**  
 2001 TGAAGGAGACAGAGAAGCTAGCCAAGGATGTCTCCGAGGAACTGGAAAGCTTTTCAAATTCAAAACAGAGAATTCGGCACCCAGAAAATATGAACAGTG
   
 480▶ M K E T E K L A K D V S E E L G K L F Q I Q N R E F G T Q K Y E Q W

**BsrGI (2183)**  
 2101 GATTGTCGGCGTCCACAAAGCGTGTGCTCAGTGTTCAGATGGCAGACAAAGAGGAGAGCGGGTCTGCAAAGCGTCTTCTGTACACATCATTG
   
 513▶ I V G V H K A C S V F Q M A D K E E E S R V C K A L F L Y T S H L
   
 2201 CGGAAATACAACGATGCACTCATCATCAGTGGAGATGCACAGATGACAGACGCTCTAAATTACCTCAAAGCCTTCTCCACGATGTCGAGAGCAGCAT
   
 547▶ R K Y N D A L I I S E D A Q M T D A L N Y L K A F F H D V R E A A

**BamHI (2370)**  
 2301 TCGATGAGACCGAGCGAGGCTTACTCGGAGGTTTGAAGAAAACTAGAGGAATTAGAAAAAGTTTCCAGGATCCCGCAATGAGAATCCTAAACTAAG
   
 580▶ F D E T E R E L T R R F E E K L E E L E K V S R D P S N E N P K L R

**XcmI (2471)**  
 2401 AGACCTCTACTTGGTCTTACAAGAAGAGTACCCTTAAAGCCAGAGACCAAGACCATTCTCTTGTGAAGACAGAGCACTCGTGGATGCTCTGAAGAAA
   
 613▶ D L Y L V L Q E E Y H L K P E T K T I L F V K T R A L V D A L K K
   
 2501 TGGATTGAAGAAAATCCTGCACTAAGCTTTCTAAAGCCTGGCATACTGACTGGGCGTGGCAGAACAAACCGGGCAACAGAAATGACGCTCCCGCACAGA
   
 647▶ W I E E N P A L S F L K P G I L T G R G R T N R A T G M T L P A Q

SspI (2638)

2601 AGTGTGTGCTGGAGGCATTGAGCCAGCGGAGATAACAATATTCTGATTGCTACCTCGGTGCGTGATGAAGGCATTGACATTGCTGAGTGAATCTCGT  
680▶ K C V L E A F R A S G D N N I L I A T S V A D E G I D I A E C N L V  
2701 CATTCTCTATGAGTACGTGGGCAACGTCATCAAGATGATCCAAACAGAGGCCGAGGAAGAGCACGAGATAGCAAGTGTTCCTCCTGACCAGCAGCGCT  
713▶ I L Y E Y V G N V I K M I Q T R G R G R A R D S K C F L L T S S A  
2801 GACGTGATTGAAAAAGAAAAGGGCAACATGATCAAGGAAAAAATAATGAATGAATCCATCTTAAGACTGCAGACATGGGATGAAATGAAATTTGGAAAGA  
747▶ D V I E K E K A N M I K E K I M N E S I L R L Q T W D E M K F G K  
2901 CGGTTCCACGCATACAGGTGAATGAAAACTCCTCAGAGACAGT CAGCACAAACCACAACCTGTTCTGACAAAAGAAAACAAGAACTGCTGTGTGGAAA  
780▶ T V H R I Q V N E K L L R D S Q H K P Q P V P D K E N K K L L C G K  
3001 GTGCAAGAATTTTGCCTGCTACACAGCTGACATTGAGTGTGTTGAGACGTCCCACTACTGTCTTGGAGACGCTTTTAAGGAGCGCTTTGTGTGTAAG  
813▶ C K N F A C Y T A D I R V V E T S H Y T V L G D A F K E R F V C K

BglII (3116)

3101 CCACACCCTAAACCAAGATCTATGACAATTTTGAAGAAGAAAGCAAAGATATTCTGCGCCAAACAGAAGTGTAGCCACGACTGGGGAATTTTGTGAGAT  
847▶ P H P K P K I Y D N F E K K A K I F C A K Q N C S H D W G I F V R

BsrBI (3258)

3201 ACAAGACGTTTCGAGATTCAGTCATAAAAATTGAAAGTTTCGTCGTGGAAGATATTGTGAGCGGAGTTT CAGAACC GGCACTCAAAGTGGAAAGACTTTCA  
880▶ Y K T F E I P V I K I E S F V V E D I V S G V Q N R H S K W K D F H

XbaI (3363) MscI (3375)

3301 TTTTGAAGGATACAGTTTCGATCCTGCAGAAATGTCCGTATGACCTCAGGCTTCTCCGCTCCTAGACCTAGCTGGCCAGACATGATAAGATACATTG  
913▶ F E R I Q F D P A E M S V •

3401 ATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAA

---

HpaI (3507) MfeI (3518)

3501 TAAACAAGTTAACACAACAATTCATTTCATTTATGTTTCAGGTTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCTCTACAATGTGGT

---

EcoRI (3603)

3601 ATGGAATTTCTAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGC  
▶ ◀

3701 TGGTGCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTGCTTTCATTCTTT

---

SspI (3842) SmaI (3856)

3801 ATGTTTTAAATGCACTGACCTCCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGG  
▶ ◀

3901 CAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGC  
▶ ◀

4001 GAGCTTCTAGCTTTAGTTCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGTTGCCATTCTCAATGAGCACAAAGCAGTCA  
144◀ • 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

SacI (4117)

4101 GGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAA  
111◀ 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 Y P H R V A V I

StuI (4281)

4201 TGGTGCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGC  
78◀ 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 I Y A E I H V A

4301 AGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCGACATGGTGTCTTGTTCCTCATAGAGCATGGTGTATCTTCTCAGTGGCGACCTCCACCAGC  
45◀ 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 E T A V E V L

XmnI (4423) AseI (4489)

4401 TCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCA  
11◀ E L D Q Q S I N F T K M ◀

SacI (4546)

4501 AAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCA  
▶ ◀

SpeI (4644)

4601 ATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGTGGAGACTTGAAATCCCCG  
▶ ◀

SnaBI (4772)

4701 TGAGTCAAACCGTATCCACGCCATTGATGTAAGTCCGCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAG  
▶ ◀

NdeI (4877)

4801 TCCATAAGGTCATGTAAGTGGGCATAATGCCAGGCGGGCCATTTACCGTATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTAAGT  
▶ ◀

4901 CCAAGTGGGAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATATTGACGTCAATGG  
▶ ◀

PaeI (5063) SdaI (5055) BspLU11I (5073)

5001 GCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCCTAAGTTATGTAAGCCTGCGAGGTTAAATAAGAATCATGTGAGCAAAAGGCCAGCAAAGG  
▶ ◀

5101 CCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCAGCGCTCAAGTCAAGGTGGCGAAA  
▶ ◀

5201 CCCGACAGGACTATAAAGATACCAGCGTTTTCCCTGGAAGTCCCTCGTGGCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTT  
▶ ◀

ApaLI (5387)

5301 CTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTACGCTGATGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCC  
▶ ◀

5401 CCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCACTGGCAGCAGCCACTGGTAACAG  
▶ ◀

5501 GATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTG  
5601 CTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGGTTGCAAGCAGCAGATTA  
5701 CGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGC

**EagI (5823)**

PacI (5803)    SmaI (5812)

**NotI (5822)**

5801 TAGTTAATTAACATTTAAATC AGCGGCCCAATAAAATATCTTTATTTTCATTACATCTGTGTGGTTTTTTTGTGTAATCGTAACTAACATACGCTC  
5901 TCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCGAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA