



**PvuI (7)**  
**SgfI (6)**  
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

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101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

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301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

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**KasI (535)** **AgeI (552)** **BspHI (560)**  
501 TCTGTTTGTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTAAGCTGAGATCACCGGTATCATGAGCGCCCTACTACCGCAGCGGGTTGCTGTTCCCT

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601 GGGGATGCTTCAAGCCTTCCCAACGGATCGACCACTCAAGACCACCTGTGCCGGAGACCTCAGCCACTACCCAGGGGAGGCTGCCAGGAAGTGTCTGTTAC

13> G M L Q A F P T D R P L K T T C A G D L S H Y P G E A A R N C C Y

1> M S A L L T A A G L L F L

**PstI (753)** **BbsI (790)**  
701 CAGTGCCCTCAGGGTTGTCTCCGACACAGCCATGCCACGGGGTCTGCCCACTGCAGGAAGCAGTGTGCACCTGACTACTACGTCAATGAAGACGGGA

47> Q C P S G L S P T Q P C P R G P A H C R K Q C A P D Y Y V N E D G

**BstAPI (803)** **SphI (890)** **BstAPI (890)**  
801 AGTGCACAGCCTCGTGACCTGTTTCCAGGCCTGTGGAGAAGGCTCCGTGTTCCGGAACTCTCCTCGAATCTGTGAGTGTGACCGCTGGCATGCACTG

80> K C T A C V T C L P G L V E K A P C S G N S P R I C E C Q P G M H C

901 CTGCACACCAGCAGTCAATTCCTGCGCCCGCTGCAAACTCCACTGTTCTGGAGAGGAGTTGTCAAGTCTCCAGGCACAGCAAAGAAGGACACTATCTGT

113> C T P A V N S C A R C K L H C S G E E V V K S P G T A K K D T I C

**BstEII (1042)** **XbaI (1092)**  
1001 GAGCTGCCTTCTCGGGATCTGGTCCCAATTGCTCCAATCCGGGTGACCGCAAGACACTACTAGCCATGCCACTCCTCAGGCCATGCCACTACTCTAGAAT

147> E L P S S G S G P N C S N P G D R K T L T S H A T P Q A M P T L E

1101 CCCAGCCAATGACAGTGAAGGAGCTTGTGCCAATCGGTGTACCAACCTTGTGCAGGAAGATGCTACTGAGTTGGTGAAGTTCCAGAATCTTCCTC

180> S P A N D S A R S L L P M R V T N L V Q E D A T E L V K V P E S S S

1201 GTCCAAGCAAGGAGCCAGTCCAGTCCAGTAAATGCAGAGAAGAATGACCTTGGAGCTTCCATCTCCAGGGACACTCCCTGACATCAGCAGCTCA

213> S K A R E P S P D P G N A E K N M T L E L P S P G T L P D I S T S

1301 GAAAACAGCAAGGAGCCTGCAAGTACCGCCTCCACCCTAAGCCTTGTGGTAGATGCCTGGACCAGCAGCAGGATGCAGCCACCTCTCCATTGTCACGG

247> E N S K E P A S T A S T L S L V V D A W T S S R M Q P T S P L S T

**Bsp120I (1420)** **NcoI (1442)**  
1401 GAACACCATTTCTGGATCCAGGGCCCGTCTTCTGGGTGGCCATGGTGGTCTACTGGTTGGCTCCGGCTCCTTTCTCCTGTGTTACTGGAAGGCCTG

280> G T P F L D P G P V L F W V A M V V L L V G S G S F L L C Y W K A C

1501 TAGGAGGCGGTTCCAGCAGAAGTTTACCTGGACTACCTAGTGCAGACCTTCCAGCCCAAGATGGAGCAGACAGATTCTGTCTACTGAAAAGCTAACC

313> R R R F Q Q K F H L D Y L V Q T F Q P K M E Q T D S C P T E K L T

1601 CAGCCACAGAGAAGCGGTCCGTGACAGATCCAGCAGCAGGACACAAGTTGAGCCAGTGAAGCCCTCCTCAGCTGTAGAGACTTGTGCCAGTGTGGG

347> Q P Q R S G S V T D P S T G H K L S P V S P P P A V E T C A S V G

**XmaI (1778)**  
1701 CCACCTACTGGAGAACCTGCCGCTGCTGGATGACAGCCAGCTGGGAATCCTTTTCTCCAGGGAACTCCAGAGCCCGGGTATCCACGGAACACAC

380> A T Y L E N L P L L D D S P A G N P F S P R E P P E P R V S T E H T

**BspHI (1826)**  
1801 CAATAACAGGATTGAGAAAATCTACATCATGAAGGCCGACACAGTGTCTGGGCTCTGTA AAAACTGAAGTCCCTGAGGGCCGGCTCCAGCAGGGTCT

413> N N R I E K I Y I M K A D T V I V G S V K T E V P E G R A P A G S

1901 ACAGAGTCTGAGTTGGAAGCTGAAGTGGACATGCCCCCATACCCGGAGCAGGAGACAGAACCACCTCTGGGCAGCTGCACTGAGGTCATGT

447> T E S E L E A E L E V D H A P H Y P E Q E T E P P L G S C T E V M

**Bsp120I (2032)** **MscI (2077)**  
2001 TCTCGGTGGAGGAAGGAGGAAAAGAGGACCATGGGCCACGACTGTCTCTGAGAAGTGACAACCATTTAGCTAGCTGGCCAGACATGATAAGATACAT

480> F S V E E G G K E D H G P T T V S E K •

2101 TGATGAGTTTGGACAAACCACAACCTAGAACTGAGTGA AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGC

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**HpaI (2209)**  
2201 AATAACAAGTTAAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTG

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**EcoRI (2305)**  
2301 GTATGGAATCTAAAATACAGCATGACAAAACCTTAACCTCCAATCAAGCCTCTACTGAACTCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGG

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**SapI (2487)**  
2401 GCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTGCTTCTCATTTCT

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**SspI (2544)** **Swal (2558)**  
2501 TTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTA

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2601 GGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAA

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2701 GCGAGCTTCTAGCTTTAGTTCTGGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGT  
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

2801 CAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCAC  
112 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

2901 AATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACA  
79 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 I Y A E I H V

3001 GCAGAGATGATCTCCCAGTCTTGGTCTGTATGGCCGCCCGACATGGTGCTTGTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCA  
45 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 E T A V E V L

BbsI (3129)  
XmnI (3125) AseI (3191)

3101 GCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGT  
12 E L D Q Q S I N F T K M

SacI (3248)

3201 CAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTGCGT

SpeI (3346)

3301 CAATGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCC

SnaBI (3474)

3401 CGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAA

NdeI (3579)

3501 AGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTAC

3601 TGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAAT

PacI (3765)  
PstI (3758)  
SdaI (3757) BspLU11I (3775)

3701 GGGCGGGGTCGTTGGCGGTGACCCAGCGGGCCATTTACCGTAAGTTATGTAAACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAAAGGCCAGCAAAA  
GGCCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGA

3801 GGCCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGA

3901 AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCT

4001 TTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTCCGCTCAAGCTGGGCTGTGTGCACGAACC

4101 CCCCCTTCAGCCGACCGCTGCGCTTATCCGTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAC

4201 AGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTC

4301 TGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTGTGTTGAAGCAGCAGAT

4401 TACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATG

EagI (4525)  
PacI (4505) SwaI (4514) NotI (4524)

4501 GCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAATATCTTTATTTTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACATAACATACGC

4601 TCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA