



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC **HindIII (245)** **Bsu36I (291)**

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTCGCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTACCATTGGGAGCCCGAGCTGGCAGCCTTGTCTCTGTCTCT **NcoI (560)** **BstEII (555)** **AgeI (552)** 1 M G S P R L A A L L L S L

601 CCCGCTACTGCTCATCGCCTCGTGTGTCTGCTCGGGTTGCCTGCCCTGCCTGCGGAGTTGGACCAGCCACTGTCTCTGGCTACCGTGTGGATAAA **Psp1406I (698)**  
13 P L L L I G L A V S A R V A C P C L R S W T S H C L L A Y R V D K

701 CGTTTTGTGGCCTTCAGTGGGGCTGGTCCCTCTCTGGTGAGGAAATCTAAAAGTCCCTCTAAATTTGAAGACTATTGGAGGCACAGGACACCAGCAT  
47 R F A G L Q W G W F P L L V R K S K S P P K F E D Y W R H R T P A

801 CCTCCAGAGGAAGCTGTAGGCAGCCCTTCCCTGTCTGAGGAAAGCCATCGAATTTCCATCCCTCCTCAGCCATCTCCACAGAGGCCAACGCACCAA  
80 S F Q R K L L G S P S L S E E S H R I S I P S S A I S H R G Q R T K

**Bsp120I (902)**  
901 AAGGCCCCAGCCTTCAGTGCAGAAGGAAGAGAACATCTCCCTGAAGCAGGGTACAAAAGTGTGGAGACCTGAATTCCTTTGATTTGCTGCCCGAG  
113 R A Q P S A A E G R E H L P E A G S Q K C G G P E F S F D L L P E

**SdaI (1024)**  
1001 GTGCAAGCTGTTCCGGGTGACTATTCTGCAGGCCCAAGGCCAGTGTGCGCCTTTGTTATCAGTGGGCACTGGAATGTGAAGACTTGAAGTACCCCTTTTG  
147 V Q A V R V T I P A G P K A S V R L C Y Q W A L E C E D L S S P F

1101 ATACCCAGAAAATTTGTGTCTGGAGGCCACACTGTAGACTGCCTTATGAATTCCTTCTGCCCTGCATGTGCATAGAGGCCCTCCTACCTGCAAGAGGACAC  
180 D T Q K I V S G G H T V D L P Y E F L L P C M C I E A S Y L Q E D T

**HindIII (1238)**  
1201 TGTGAGGCGCAAAAAGTGTCCCTCCAGAGCTGGCCTGAAGCTTATGGCTCAGACTTCTGGCAGTCAATACGCTTCACTGACTACAGCCAGCACAATCAG  
213 V R R K K C P F Q S W P E A Y G S D F W Q S I R F T D Y S Q H N Q

1301 ATGGTCATGGCTCTGACACTCCGCTGCCACTGAAACTGGAGGCTCCCTCTGCTGGAGGCGAGACCCACTCACACCTGCGAAAACCTTCCCAACGCCA  
247 M V M A L A T L R C P L K L E A S L C W R Q D P L T P C E T L P N A

1401 CAGCACAGGAGTCAAGGATGATATCCTGGAGAATGTGACTTGCACCCAGCTGTCTTAAGTTCTCATTGAAAACAGCAGCCAGCTTGAATG  
280 T A Q E S E G W Y I L E N V D L H P Q L C F K F S F E N S S H V E C

**NdeI (1586)**  
1501 TCCCCACAGAGTGGCTCTCTCCCATCCTGGACTGTGAGCATGGATACCCAGGCCAGCAGCTGACGCTTCACTTTTCTCGAGGACATATGCCACCTTC  
313 P H Q S G S L P S W T V S M D T Q A Q L T L H F S S R T Y A T F

**BsrGI (1652)**  
1601 AGTGTGCTGGAGTGACCCAGGTTTGGGCGCGGATACCCCATGCCTCCTGTGTACAGCATCAGCCAGACCCAGGGCTCAGTCCCAGTGACGCTAGACC  
347 S A A W S D P G L G P D T P M P P V Y S I S Q T Q G S V P V T L D

**Bsu36I (1713)**  
1701 TCATCATCCCCTTCTGAGGCGAGGAATTCATCCTGGTGTGGAGTGTGATGTCATTTTGCCTGGAAGCAGCTTGTGTCTGATGTCCTCCATAG  
380 L I I P F L R Q E N C I L V W R S D V H F A W K H V L C P D V S H R

**BsrBI (1838)** **NgoMIV (1871)**  
1801 ACACCTCGGGCTCTTGATCCTGGCACTGCTGGCTCTACCCGCTCTAGTGGGTGTAGTTCTGGTCTCCTCGGCGCGGCTACTGCCAGGCTCCGGTTCGA  
413 H L G L L I L A L L A L T A L V G V V L L V L L G R R L L P G S G R

1901 ACAAGGCCAGTTTTACTCCTACATGCAGCGGACTCAGAGGCACAGCAGCCTGGTGGGAGCTTTGGCCGAAGTGTGCGGACGCGCTGGGAGGTGGAC  
447 T R P V L L L H A A D S E A Q R R L V G A L A E L L R T A L G G G

2001 GCGACGTGATCGTGATCTCTGGGAAGGGACGCACGTAGCAGCATTGGACCCTGCCGTGGCTTTGGGAGCGCGGGAGCGCTGGCGGGGAGCAGGG  
480 R D V I V D L W E G T H V A R I G P L P W L W A A R E R V A R E Q G

**BstAPI (2135)**  
2101 CACAGTGTGCTCCTGTGGAAGTGTGCGGGTCCAGCACCCTGCAGCGGTGACCCGAGGCTGCGTCCCTTCGCACCTTGTGTGCGCTGCTCCACGT  
513 T V L L L W N C A G P S T A C S G D P Q A A S L R T L L C A A P R

**SmaI (2127)** **BstEII (2149)**  
2201 CCGTGTGCTCGCTACTTCACTGCTGCTGCGCCAAAGGTGACATCCCGCGCGCTGCGCCTGTCGCACGCTACCGCTGCTTCTGACCTGCCGC  
547 P L L L A Y F S R L C A K G D I P R P L R A L P R Y R L L R D L P

**BssHII (2259)**  
2301 GCCTGTGAGAGCACTGGATGCTCAGCCTGCCACCCTAGCCTCCAGCTGGAGTCACTTGGGGCTAAGCGGTGCTTGA AAAACCGTCTGGAGCAGTGTCA  
580 R L L R A L D A Q P A T L A S S W S H L G A K R C L K N R L E Q C H

**BstAPI (2311)** **MscI (2487)** **NheI (2481)**  
2401 CCTGTGGAAGTGGAGTGGCAAGATGACTACCAAGGCTCAACCAATAGTCCCTGTGGTTTCAAGTGTCTGTAGCCTCAGCTAGCTGGCCAGACATGA  
613 L L E L E A A K D D Y Q G S T N S P C G F S C L •

2501 TAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGA AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTGTAACCAT

**HpaI (2619)** MfeI (2630)  
 2601 TATAAGCTGCAATAAACAAAGTTAAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCTC  
 2701 TACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATA  
**SapI (2897)**  
 2801 GGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTTAAAGATATAGTGATTTTTCCCAAGGTTTGAAC TAGCT  
**SspI (2954)** SwaI (2968)  
 2901 CTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTGAGAAATAATTTAAATACATCATTGCAATGAAAATAAATG  
 3001 TTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGA  
 3101 CAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCGGTGACTTTGAGGGGATGAGTTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCACTCAATGAGC  
 1+1 • N R T Y K L P I L E E I T T K V L K G N M E I L  
**SacI (3229)**  
 3201 ACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCC  
 115 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 Y P H R  
 3301 TGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTC  
 82 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 I Y A E  
 3401 AATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCCGACATGGTGCTTGTGTCTCATAGAGCATGGTGATCTTCTCAGTGCCG  
 49 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 E T A  
 3501 ACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGAT  
 15 V E V L E L D Q Q S I N F T K M  
**AseI (3601)** **SacI (3658)**  
 3601 GATTAATTGTCAAACAGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGC  
**SpeI (3756)**  
 3701 CCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACT  
**SnaBI (3884)**  
 3801 TGGAAATCCCCGTGAGTCAAACCGTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGGATGACTAATACGTAGTAGTACTGC  
**NdeI (3989)**  
 3901 CAAGTAGGAAAGTCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACA  
 4001 CTTGATGACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTAT  
**SdaI (4167)** **PacI (4175)** **BspLU11I (4185)**  
 4101 TGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCCCTGCAGGTTAATTAAGAACATGTGAGCAAAG  
 4201 GCCAGCAAAGGCCAGGAACCGTAAAAAGCGCGTGGTGGCCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCA  
 4301 GAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGTTACCGGATAC  
**ApaLI**  
 4401 CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCTGCTCCAAGCTGGGCTGTG  
 4501 TGCACGAACCCCGTTACGCCCAGCCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCGGTAAGACACGACTTATCGCCACTGGCAGCAGC  
 4601 CACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT  
 4701 ATCTGCGCTCTGTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAACAAACACCGCTGGTAGCGGTGTTTTTTTGTGTTGCA  
 4801 AGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGAT  
**PacI (4915)** **SwaI (4924)** **NotI (4934)**  
 4901 TTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGTTTTTTGTGTAATCGTAAC  
 5001 TAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA