



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

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC **PvuII (239)** **Bsu36I (291)**

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGTTGCTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATGGCTAGACTCTGTGCTTTCCTCGTGATGCTGATAGT **NcoI (560)** **BstEII (555)**  
1 M A R L C A F L V M L I V

601 GATGAGCTACTGGTCAATCTGTTCTCTAGGATGCGATCTGCCTCACACTTATAACCTCAGGAACAAGAGGGCCTTGAAGGTCTGGCACAGATGAGGAGG **Bsu36I (654)**  
13 M S Y W S I C S L G C D L P H T Y N L R N K R A L K V L A Q M R R  
701 CTCCTTCTCTCTGCTGAGGACAGGACGACTTTGGATTCCCCCTGGAGAAGGTGGATAACCAGCAGATCCAGAAGGCTCAAGCCATCCCTGTGC  
47 L P F L S C L K D R Q D F G F P L E K V D N Q Q I Q K A Q A I P V

801 TGGGAGATCTTACTCAGCAGACCTTGAACCTCTTACATCAAAGGCTTCACTGCTGCTTGAATGCAACCTCTAGACTCATTCTGCAATGACCTCCA **BglIII (804)**  
80 L R D L T Q Q T L N L F T S K A S S A A W N A T L L D S F C N D L H

901 CCAGCAGCTCAATGACCTGCAAACCTGTCTGATGCAGCAGGTGGGGTG CAGGAACCTCTGACCCAGGAAGACGCCCTGCTGGCTGTGAGGAAATAT **SspI (995)**  
113 Q Q L N D L Q T C L M Q Q V G V Q E P P L T Q E D A L L A V R K Y  
1001 TTCCACAGGATCACTGTACTCTGAGAGAGAAGAAACACAGCCCTGTGCTGGGAGGTGGTCAGAGCAGAAGTCTGGAGAGCCCTGTCTTCTCAGTCA  
147 F H R I T V Y L R E K K H S P C A W E V V R A E V W R A L S S S V

1101 ACTTGCTGCCAAGACTGAGTGAAGAGAAGGAGTGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTG **MscI (1141)** **NheI (1135)**  
180 N L L P R L S E E K E •

1201 AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCATTTT **HpaI (1273)** **MfeI (1284)**

1301 ATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGGTATGGAATTCTAAAATACAGCATAGCAAACTTTA **EcoRI (1369)**

1401 ACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCA

1501 CCTCTTTTATGAGTTTAAAGATATAGTATTTTCCCAAGGTTTGAAGTCTTCTTCTTTATGTTTTAAATGCAGTACCTCCACATTCCCTT

1601 TTTAGTAAATATTTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATC **SspI (1608)** **SwaI (1622)**

1701 CCCAGTTTATGATTTGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGCTGACTTGGAGG **SacI (1883)**  
141 N R T Y K L

1801 GGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGC **BstXI (1912)**  
133 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 D S I L E R C M G

1901 CACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGC **StuI (2047)**  
100 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 D K Q G N S V A

2001 AGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCC **AseI (2255)**  
67 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 E G T K T R I A  
2101 GCCCGACATGGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCAGCTCCACAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCA  
33 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 Q Q S I N F T K M

2201 TGGTGGCCCTCTATAGTGAAGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGAC **SacI (2312)**  
0

2301 GGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTC

2401 CCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAC **SpeI (2410)**

2501 TGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAGGTCATGACTGGGCATAATGCCAGG **SnaBI (2538)**

**NdeI (2643)**

2601 CGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCTCAAGTGGGCGAGTTTACCGTAAATACTCCACCCA  
2701 TTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGCGGGGGTCTGTTGGCGGTCAGCCAGCGGGCCA

**PacI (2829)**

**PstI (2822)**

**SdaI (2821)**

**BspLU11I (2839)**

2801 TTTACCGTAAGTTATGTAACGCTGCAGGTTAA**TTAAGAACAT**GTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTT  
2901 TTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCC  
3001 CCTGGAAGCTCCCTCGTGCCTCTCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCT

**ApaLI (3153)**

3101 CACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAA  
3201 CTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACA  
3301 GAGTTCCTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTA  
3401 GCTCTTGATCCGGCAAACAACACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTT

**EagI (3589)**

**PacI (3569)**

**Swal (3578)**

**NotI (3588)**

3501 GATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATA  
3601 AAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGC  
3701 AAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAATTTCTCTATCGAA