



**PvuI (7)**  
**SgfI (6)**  
 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**  
**Psp1406I (203)** **PvuII (239)** **Bsu36I (291)**  
 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC  
 301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**  
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

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**BstEII (555)** **AgeI (552)** **NcoI (560)** **Bsp120I (581)**  
 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGGGATGCCACTGCCCTGGGCCCTCAGCCTCTTGT  
 601 GGCTCTCTGCTCAGACCTGGGCTCAGAGACCCGCCCCACTGATGTATCATCTCACGGTGTGTCAAACCCATCTACGGGGCTTCCCTCTTCTGG  
 13▶ V L L P Q T W G S E T R P P L M Y H L T A V S N P S T G L P S F W  
 701 GCACAGGCTGGTGGTCTCAGCAGTATCTGACCTACAACAGCCTGCGGCAGGAAGCTGACCCTGTGGGGCTGGATGTGGGAAATCAGGTGTCTT  
 47▶ A T G W L G P Q Q Y L T Y N S L R Q E A D P C G A W M W E N Q V S

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**XemI (701)** **SapI (843)** **PstI (898)**  
 801 GGTATTGGGAGAAGGAGACCACAGACCTCAAAGCAAAGAACAGCTCTTCTGGAGGCCCTCAAGACCCTGGAGAAGATTAATGGACCTACACACT  
 80▶ W Y W E K E T T D L K S K E Q L F L E A L K T L E K I L N G T Y T L  
 901 GCAGGGCTGTGGCTGTGAACTGGCCTCGGATAATCTCAGTGCCACGGCTGTGTTGCCCTCAATGGTGAAGAGTTTATGAAATCAACCAAGA  
 113▶ Q G L L G C E L A S D N S S V P T A V F A L N G E E F M K F N P R  
 1001 ATCGGCAATTGGACTGGGAGTGGCCTGAGACGGAAATCGTTGCTAATCTGTGGATGAAGCAGCCTGATGCGGCAAGGAAGGAGAGCGAGTTCTGCTAA  
 147▶ I G N W T G E W P E T E I V A N L W M K Q P D A A R K E S E F L L

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**BstAPI (900)** **BspEI (1107)**  
 1101 ACTCTTGTCCGGAGCGACTGCTAGGCCACCTGGAGAGGGCCGACGGAACCTGGAGTGAAGGAGCCCGCTCTATGCGCCTGAAGGCCCGTCTGGCAA  
 180▶ N S C P E R L L G H L E R G R R N L E W K E P P S M R L K A R P G N

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**Bsu36I (1283)** **NheI (1278)**  
 1201 CTCTGGCTCCTCCGTGCTGACCTGTGCTGCTTCTCCTTCTACCCACCGAGCTCAAGTTCGATTCTCGGCAATGGGCTAGCCTCAGGCTCCGGGAAT  
 213▶ S G S S V L T C A A F S F Y P P E L K F R F L R N G L A S G S G N  
 1301 TGCAGCACTGGTCCCAATGGAGATGGCTCTTCCACGCATGGTCATTGCTGGAGGTCAAACGTGGAGATGAGCACCATTATCAATGTCAAGTGAGGACATG  
 247▶ C S T G P N G D G S F H A W S L L E V K R G D E H H Y Q C Q V E H

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**BglIII (1444)** **MscI (1496)**  
 1401 AGGGGCTGGCACAGCCTCTCACTGTGGACCTAGATTATCAGCCAGATCTTCTGTGCCTGTGGTGGAAATCGTTCTTGGTTTATTGCTGGTGGTAGTGGC  
 280▶ E G L A Q P L T V D L D S S A R S S V P V V G I V L G L L L V V V A

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**NcoI (1552)** **BstEII (1582)**  
 1501 CATCGCAGCGGTGTGCTGTGTTGGGCGAGGATGCGCAGCGGTCTGCCAGCCCATGGCTTCTCTCAGCGCGATGACTCTGGTACCTGTTGCCTGGT  
 313▶ I A G G V L L W G R M R S G L P A P W L S L S G D D S G D L L P G

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**NheI (1679)** **EcoRI (1673)**  
 1601 GGGAACTTCCCCAGAAGTGAACCTCAAGGTGCAAATGCCTTCCAGCCACTTCTGATGCAGACTCGGGCGAATTCGCTAGCTCGACATGATAAGAT  
 347▶ G N L P P E A E P Q G A N A F P A T S •  
 1701 ACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTGAAATTTGTGAT

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**HpaI (1842)**  
 1801 GCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGG

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**EcoRI (1938)**  
 1901 TTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTT  
 2001 TTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATAGTGA

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**SapI (2120)** **SspI (2177)** **SwaI (2191)**  
 2101 TTTTCCAAGGTTTGAACCTAGCTCTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATA  
 2201 CATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAA  
 2301 AGGAACCTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGGGGGATGAGTTCTCAATGGTGGTTTTGACCA  
 141▶ • N R T Y K L P I L E E I T T K V L

2401 GCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTC  
123 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 V V R I S R D  
2501 CACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGCAAAAGTCTTTCTGCCGTTGTCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACA  
90 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 A I A E A C V

**StuI (2616)**

2601 GTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGTCTCATAGA  
56 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 H K N D E Y L

**BbsI (2762)**  
**XmnI (2758)**

2701 GCATGGTGATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCTCATGGTGGCCCTCTATAGTGAGTCGTATTATA  
23 M T I K E T A V E V L E L D Q Q S I N F T K M

**AseI (2824)**

2801 CTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGAC

**SpeI (2979)**

2901 CTCCCACGCTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTTACTAGTCAAAACAAACTCCCA  
3001 TTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGA

**SnaBI (3107)**

3101 TGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTGATGACTGGGCATAATGCCAGGCGGGCCATTTACCCTCATTGACGTCAATAGG

**NdeI (3212)**

3201 GGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCCTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTT

**PacI (3398)**  
**PstI (3391)**  
**SdaI (3390)**

3301 ACTATGGGAACATACGTCATTATTGACGTCAATGGGGCGGGGTGCTTGGGCGGTGACGCCAGCGGGCCATTTACCCTAAGTTATGTAACGCTGCAGGTT

**BspLU11I (3408)**

3401 AATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCAT  
3501 CACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGACTATAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGTCTCTGTTC  
3601 CGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGGTGTAGGT

**ApaLI (3722)**

3701 CGTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACAC  
3801 GACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCT  
3901 AACTAGAGAAGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGG  
4001 TAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGG

**EagI (4158)**

**PacI (4138) SwaI (4147) NotI (4157)**

4101 AACGAAAACCTCACGTAAAGGATTTTGGTCATGGCTAGTAAATTAACATTTAAATCAGCGGCCGAATAAAAATATCTTTATTTTACATTACATCTGTGTG  
4201 TGGTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGAAGTGCAGGT  
4301 GCCAGAACATTTCTATCGAA