



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

101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGGCCCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGGTTCGCGCCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)** 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

EagI (565)  
**AgeI (552)** SphI (560)  
501 TCTGTTTGTCCGGCTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCCGGCCGGAGGGCGGGGAATGGAGCTCGGAGGGCGG

601 CGAGGAGCGCCTGCCTGAGGAGAGCAGGAGGGAGCACTGGCAGTTGCTGGTAATTTGAAGACGACGGTGGAGGGTTTGGTATCAACCAACAGCCCCAAC  
13> E E R L P E E S R R E H W Q L L G N L K T T V E G L V S T N S P N  
701 GTCTGGTCTAAGTATGGTGGCTTGAGCGGCTTTCAGGGACATGCAGAGCATCCTCTATCACGGCTTATCCGTGACCAGGCGTCCGCCCGCAGACGG  
47> V W S K Y G G L E R L C R D M Q S I L Y H G L I R D Q A C R R Q T

BbrPI (853) ApaLI (874)  
801 ATTACTGGCAGTTCGTGAAAGACATCCGGTGGCTCAGTCCCCACTCAGCCCTTACGTTGGAGAAGTTCATCAGCGTGCACGAGAACGACCAGAGCAGTGC  
80> D Y W Q F V K D I R W L S P H S A L H V E K F I S V H E N D Q S S A

BstAPI (942)  
901 TGATGGTGCCAGTGAACGTGCTGTTGCCGAGCTGTGGTGCAGCACAGCCTGCAGTACCAGTCCCTCTCAGCCAGCTCCGGCCCTGCTCGGGGATAGA  
113> D G A S E R A V A E L W L Q H S L Q Y H C L S A Q L R P L L G D R  
1001 CAGTATATCAGAAAATTCTACACAGATGCTGCCTTCTGCTAAGTACGCTCATGTACGGCCATGCTGAGTGCCTGGAAGCAGTGGAAACAGAAACCC  
147> Q Y I R K F Y T D A A F L L S D A H V T A M L Q C L E A V E Q N N

**ClaI (1117)**  
1101 CCCGCTCCTGGCTCAGATCGATGCTCCATGTTTCCAGAAAAGCACGAGAGCCGCTCCTGGTGACAAAAGCCAGAGCCTGACAGCCCTGCCAGTTC  
180> P R L L A Q I D A S M F A R K H E S P L L V T K S Q S L T A L P S S

BglII (1294)  
1201 CACATACACCCCTCAACACAGTATGCTCAGCATTCTACTTTGGGTCTTCTAGCCTCCACCAATCCGTGCCAACAATGGCTCAGAGAGAAGATCT  
213> T Y T P P N S Y A Q H S Y F G S F S S L H Q S V P N N G S E R R S  
1301 ACTTCTTTCCACTCTGCGCCTCCCGGAAACCTCAAGAAAGCAGAGGGCAGCTCACCAGCAGAGGATCAAACCTCAAGCCCCCAGTTTCCAG  
247> T S F P L S G P P R K P Q E A S R G H V S P A E D Q T I Q A C P P V S  
1401 TCTCTGCACTAGCCAGGATTCCCTTTGACCCCAAATGAAATGAGCTCCAGTACTCTGACCAGCCCATAGAGGCATCCTGGGTGAGCAGCCAGAATGA  
280> V S A L A R D S P L T P N E M S S S T L T S P I E A S W V S S Q N D  
1501 TTCCCAGGTGATGCCAGTGGGGCCCTGAGTACCTGGCCATTGGCACTTGGACCCCGAGGCGGACTGCCAGTGTGAGTGCAGAGTGCAGCAGCAATGCC  
313> S P G D A S E G P E Y L A I G N L D P R G R T A S C Q S H S S N A  
1601 GAGAGCAGCAGTTCGAATTTGTTCTCCTCCAGCAGCTCCAGAAGCCAGATTCGCTGCTCCTTCTAGGGGACCAGGAAGGAGGTGGGGAGAGCCAGC  
347> E S S S N L F S S S S Q K P D S A A S S L G D Q E G G G E S Q  
1701 TGCCAGTGTCTCCGAGTCCAGCTTCTCAGAGGGGAGCAGTACTGTACCAGTGGGGCAAAGAAAAGCCACATTCGCTCCATCCGATCCGATACCAG  
380> L S S V L R R S S F S E G Q T L T V T S G A K K S H I R S H S D T S  
1801 CATTGCCTCCAGGGAGCTCCAGAATCTGCAATGATAAGGCGAAGTTGAGAGGCCCTTTGCCCTACTCTGGTCAAAGCAGTGAAGTGCAGCACCCAGC  
413> I A S R G A P E S C N D K A K L R G P L P Y S G Q S S E V S T P S

**BsrGI (1904)** **Acc65I (1928)**  
1901 TCTCTGTACATGGAATATGAAGTGGTCCGTACCTGTGCTCAGGGGAAGGCATGTTCCGAAGACCATCAGAAGGACAGTCCCTCATCAGCTACCTCTCTG  
447> S L Y M E Y E G G R Y L C S G E G M F R R P S E G Q S L I S Y L S  
2001 AGCAAGACTTCGGCAGCTGTGCCGACCTGAAAAGGAGAATGCCACTTCAGCATCTCAGAGTCCCTAATTGCTGCCATCGAGCTAATGAAGTGAACAT  
480> E Q D F G S C A D L E K E N A H F S I S E S L I A A I E L M K C N M  
2101 GATGAGCCAGTGCCTAGAGGAGGAGGAAGTGAAGAGGAAGACAGTGTAGAGAGATCCAGGAGTGAAGCAGAAGATCCGCTTCCGCGCCAGCAAATC  
513> M S Q C L E E E E V E E E D S D R E I Q E L K Q K I R L R R Q Q I

**BstEII (2253)**  
2201 CGCACCAAGAACCTGCTCCCATGTACCAGGAGCTGAGCACGGGAAGCTTTCGGGTACCTCCAGCAGTCCAGTTCAGCTACGTGATTCCGGCACAGC  
547> R T K N L L P M Y Q E A E H G S F F R V T S S S S Q F S S R D S A Q  
2301 TCTCTGACTCTGGCTCTGCTGATGAGGTTGATGAATTTGAAATCCTAAGATGCTGACATCAGAAGAACACAGCCTCAAGCAGCAAATCCTTCTGTTTCTC  
580> L S D S G S A D E V D E F E I Q D A D I R R N T A S S S K S F V S S

**NcoI (2450)**  
2401 CCAGTCTTCTCCACTGCTTCTGCACTCCACGTCTGCTGAGGCGGTGGCCATGGGGTCTCTGAAGCAGTTTGGGGGATGCAGCTTCCAGCCGCTCG  
613> Q S F S H C F L H S T S A E A V A M G L L K Q F E G M Q L P A A S  
2501 GAGCTGGAGTGGCTTGTCCGGAGCATGATGCCCTCAGAAGCTCTGCCATTCTGACTACTGCCATCTCAGGATGACGGGAGCAGCAGCTGACA  
647> E L E W L V P E H D A P Q K L L P I P D S L P I S P D D G Q H A D  
2601 TCTACAAGCTGCGGATTCGTGTTCTGTTGCAACTTGGAGTGGGCCCCGCCCGCTCAGATAATTTTAAATGTTTCATCCAGCCCAACGAGGAAAATTC  
680> I Y K L R I R V R G N L E W A P P R P Q I I F N V H P A P T R K I A

**BspEI (2738)**

2701 CGTGGCCAAGCAGAATTACCGCTGTGCAGGATGTGGCATCCGGACTGACCCTGATTACATCAAGCGACTGCGGTACTGTGAGTACCTGGGCAAGTACTTC  
713▶ V A K Q N Y R C A G C G I R T D P D Y I K R L R Y C E Y L G K Y F

**BsaBI (2826) FspI (2849)**

2801 TGCCAGTGTGCCACGAGAATGCCAGATGGCCATCCCCAGCCGGTTCTGCGCAAGTGGGACTTCAGCAAGTACTACGTGACCAACTTCTCCAAGGACC  
747▶ C Q C C H E N A Q M A I P S R V L R K W D F S K Y Y V S N F S K D

**BglIII (2909)**

2901 TGCTCATTAAGATCTGGAATGATCCTCTCTTCAACGTGCGAGGACATAAACAGTGCCCTCTATAGGAAGGTCAAGCTGCTCAATCAAGTCCGGCTGCTGCG  
780▶ L L I K I W N D P L F N V Q D I N S A L Y R K V K L L N Q V R L L R

**BspLU11I (3023) XmnI (3021) Tth111I (3070)**

3001 GGTCCAGCTGTGTACATGAAGAACATGTTCAAGACTTGCCGACTGGCCAAGGAGCTTCTGGATTCTTTGACACAGTCCCAGGCCACCTGACAGAGGAC  
813▶ V Q L C H M K N M F K T C R L A K E L L D S F D T V P G H L T E D  
3101 CTCACCTGTACTCACTGAATGACCTGACTGCGACCAGGAAGGGGAGCTGGGGCCCCGGCTTGTGAGCTCACCAGGCGAGGGGCTACCCATGTGGAGA  
847▶ L H L Y S L N D L T A T R K G E L G P R L A E L T R A G A T H V E

**SphI (3203) BstAPI (3203) NsiI (3201)**

3201 GATGCATGCTCTGCCAAGCCAAAGGCTTCATCTGTGAGTTCGTGAGAATGAGGATGACATCATCTTTCCCTTTGAGCTCCATAAGTGCCGGACCTGTGA  
880▶ R C M L C Q A K G F I C E F C Q N E D D I I F P F E L H K C R T C E  
3301 AGAGTGTAAAGCGTGTACCATAAAGCCTGCTTCAAGTCTGGAAGCTGTCGCGCTGCGAGCGGCTGCAGGCCGGCGGGAGGCACTGCCAGGCAGAGC  
913▶ E C K A C Y H K A C F K S G S C P R C E R L Q A R R E A L A R Q S

**Eco47III (3441) SacII (3434) NheI (3481)**

3401 CTGGAGTCTTACCTGTGACTACGAGGAGGAGCCCGCGGAAGCGCTGGCCCTGGAAGCCGCGCTCTGGAGGCCACTGAGCTAGCTGGCCAGACATGA  
947▶ L E S Y L S D Y E E E P A E A L A L E A A V L E A T •  
3501 TAAGATACATTGATGAGTTTGGACAAACCACAACACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCAT

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**HpaI (3619) MfeI (3630)**

3601 TATAAGCTGCAATAAACCAAGTTAACCAACAACATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTC

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**EcoRI (3715)**

3701 TACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATA

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**SapI (3897)**

3801 GGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTGTCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGGTTTGAAGTACTAGCT

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**SspI (3954) SwaI (3968)**

3901 CTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATG  
4001 TTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGA  
4101 CAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTATCTCAATGAGC  
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

**BstXI (4258)**

4201 ACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCC  
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

**StuI (4393)**

4301 TGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCTGCCAATGTAGGCCTC  
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  
4401 AATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGCTCATAGAGCATGGTGATCTTCTAGTGGC  
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

**XmnI (4535)**

4501 ACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGAT  
15▶ V E V L E L D Q Q S I N F T K M

**AseI (4601)**

4601 GATTAATTGTCAAACACAGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCCG

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**SpeI (4756)**

4701 CCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATGACGTCAATGGGGTGGAGACT

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**SnaBI (4884)**

4801 TGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGC

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**NdeI (4989)**

4901 CAAGTAGGAAAGTCCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACA

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5001 CTTGATGTACTGCCAAGTGGGCGTTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTAT

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PacI (5175)

**SdaI (5167)**

BspLU11I (5185)

5101 TGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAG  
 5201 GCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCA  
 5301 GAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATAC

ApaLI (5499)

5401 CTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTG  
 5501 TGCACGAACCCCCGTTACGCCGACCCTGCGCCTTATCCGGTAACTATCGTCTTGAAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGC  
 5601 CACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT  
 5701 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCA  
 5801 AGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGAT

EagI (5935)

PacI (5915) SwaI (5924) **NotI (5934)**

5901 TTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAAC  
 6001 TAACATACGCTCTCCATCAAAACAAACGAAACAAACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA