



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)**  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCGCCGCCCTACCTGAGGCC  
**HindIII (245)**  
**Bsu36I (291)**  
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

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**BstEII (555)**  
**AgeI (552)** 501 TCTGTTTGTCCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGAAGGTGCCGATGCCTGCAGGAGCAATGGGGCCAG  
**NcoI (560)** 1▶ M E G A D A C R S N G A S

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**SmaI (630)**  
601 CCCGGAAGCCAGGACACCCGACGCCACCGGGTCCCAGCGGCAGCCTAGAGAATGGCACTAAAGCAGACAGTAAGGACACCAAGACAACCAACGGGCAC  
13▶ P E A R D T R S P P G P S G S L E N G T K A D S K D T K T T N G H

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**StuI (790)**  
701 AGTGGGGAGGTGACAGAGGGCAAGACCCTGGGAGTGCCTGAAGTCAGGGGAGGGGAAGAGTGGCCTATTTCCAGCAATGAGTGGCGCAGGCTATCA  
47▶ S G E V T E G K T L G S A L K S G E G K S G L F S S N E W R R P I

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**SalI (817)**  
801 TCCAGTTTGTGGAGTCTGTGACGACAAAGGCTCCAGTTACTTCAATGATGAGCTCTGCGGAAGGCAGGAGTCCCCTTATGCGGGGCTCCAGTTGGGGG  
80▶ I Q F V E S V D D K G S S Y F S M D S A E G R R S P Y A G L Q L G A

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**BstEII (978)** 901 TTCCAAGAACTCCTGTGACCTTTGCTGAGAAGGGGAGCTGCGAAAGTCCATTTTCTCCGAGCCCCGAAACCCACGGTACCATCGTGGAGCCCCGG  
**XmaI (994)** 113▶ S K K P P V T F A E K G E L R K S I F S E P R K P T V T I V E P G

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**BstXI (1034)**  
1001 GAAGTCCGAGGAATAGCTACCCAGGGGCTGACTCCAGCCTCTGGCGGGCAAAGTCCGGGCTCCGAGGAGGTGCTGTGCGACTCCTGCATCGGCAACA  
147▶ E V R R N S Y P R A D S S L L A R A K S G S E E V L C D S C I G N  
1101 AGCAGAAGGCCGTCAGTCTGCTGCTGGTGTGCCAGGCTTCCTTCTGTGAGCTGCATCTGAAGCCCCACCTGGAGGGCCTGCCTTCCGGGACCACAGCT  
180▶ K Q K A V K S C L V C Q A S F C E L H L K P H L E G A A F R D H Q L

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**XhoI (1201)** 1201 GCTCGAGCCCATCCGAGACTTCGAGGCCGAAAATGTCCCTTGACCGCAAGACTATGAGGCTCTTCTGTGACACCGACAGACTGCATCTGTTATCTC  
213▶ L E P I R D F E A R K C P L H G K T M E L F C Q T D Q T C I C Y L  
1301 TGCATGTTCCAGGAGCACAAGAACCACAGCACCGTGCAGGTGGAGGAGCCAAAGCAGAGAAGGAGACCGAGCTGTACTGCAAAAAGGAACAGCTGCAAC  
247▶ C M F Q E H K N H S T V T V E E A K A E K E T E L S L Q K E Q L Q  
1401 TGAAGATCATTGAGATTGAAGATGATGTTGAGAAGTGGCAAAAGGAGAAGACCGGATCAAGAGCTTTACCACCAACGAGAAGGCGATCCTGGAGCAGAA  
280▶ L K I I E I E D D V E K W Q K E K D R I K S F T T N E K A I L E Q N  
1501 CTTGAGGACCTGGTGGAGGAGTGGAGAAGCAGAAGGAGGAAGTACGGGCTGCACTGGAGCAGCGGGAGCAGGATGCTGTGGACCAAGTGAAGGTGATC  
313▶ F R D L V R E L E K Q K E E V R A A L E Q R E Q D A V D Q V K V I

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**SapI (1260)**  
1601 GTGGATGCTCTGATGAGAGGGCCAAGGTGCTGCAIGAGGACAAGCAGACCCGAGAGCAGCTGCACAACATCAGTGACTCGGTGCTGTTCTGCAGGAAT  
347▶ V D A L D E R A K V L H E D K Q T R E Q L H N I S D S V L F L Q E  
1701 TTGGTGCATTGATGAGCAATTACTCTCCCTCCACCTCTGCCACCTACCATGTCCTGCTGGAGGGAGAGGGGCTGGGACAGTCTCTTGGCAACTGCAA  
380▶ F G A L M S N Y S L P P P L P T Y H V L L E G E G L G Q S L G N C K

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**XbaI (1608)**  
1801 GGATGACCTGCTCAATGTGTGCATGCGTCATGTTGAGAAGATGTGCAAGGCCGATTTGAGCCGCAACTTCATTGAGAGGAACCATATGAAAAATGGTGGG  
413▶ D D L L N V C M R H V E K M C K A D L S R N F I E R N H M E N G G  
1901 GACCATCGCTACATGAACAGCTACACCAGCAGCTATGGGAACGAGTGGAGCACGCTGACACCATGAAAAGATACTCCATGTACTCAGCCCAAGGGTG  
447▶ D H R Y M N S Y T S S Y G N E W S T P D T M K R Y S M Y L T P K G  
2001 GGGGCCGACATCCTACCAGCCATCCTCGCTAGCCGCTCTCAAGGAGACCAACAGAAGAATTTAAACATCTGTATGGCAGAAAAGGCAACTATAC  
480▶ G G R T S Y Q P S S P S R L S K E T N Q K N F N N L Y G T K G N Y T  
2101 CTCCAGGCTCGGGAGTACACATCCACGGTTGAGAACTCTGAGGACATGCCACGVTGCAAGGCAACTCCTCCTTCTCCCTGAAAGGCTTTCCCTCCTC  
513▶ S R V W E Y T S T V Q N S E D M P T V Q G N S S F S L K G F P S L

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**BspEI (2201)** 2201 CTCCGAGCCAAGTTCCCAAGGCCAGCCTCAGACTTGAAAATCTGGCAAGCAGACTCTGCTGTCTACTACCGCCATTCTAGTCAACAAGGGCAGCG  
547▶ L R S Q V P K A Q P Q T W K S G K Q T L L S H Y R P F Y V N K G S

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**BstAPI (2250)**  
**MscI (2356)**  
2301 GCATCGGATCCAACGAGGCGCCCTGAGTTCAGGATGGAGGAAGCTGCACTGCTAGTGGCCGACATGATAAGATACATTGATGAGTTGGACAAACCA  
580▶ G I G S N E A P •

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**BamHI (2305)** 2401 AACTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATATAAGCTGCAATAAACAAGTTAAACAACAC  
**HpaI (2488)** **MfeI (2499)**

2501 AATTGCATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAG  
EcoRI (2584)  
2601 CATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAG

2701 CTGTTTGAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTTCCAAGGTTTGAAGTACTCTTCATTCTTTATGTTTTAAATGCAGTCAAG  
SapI (2766)

2801 CTCCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAG  
SspI (2823) SwaI (2837)

2901 GCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTC  
141 • N

3001 CTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGA  
138 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 P A Y D S I L

3101 GCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTG  
105 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 I T D F D K Q  
BstXI (3127)

3201 CCCGTTGCTCACAGCAGACCCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAGTC  
72 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 A S I I E G T  
3301 TTGTCTGATGGCCGCCGACATGGTGCTTGTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGA  
38 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 E L D Q Q S I  
StuI (3262)

3401 TGTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTC  
5 N F T K M  
3501 TCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTCAATGGGGCGGAGTTGTTACG  
AseI (3470)

3601 ACATTTTGAAAGTCCCCTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCTGAGTCAAACCGCTATCCA  
SpeI (3625)

3701 CGCCATTGATGTACTGCCAAAACCGCATCATCATGGAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACT  
SnaBI (3753)

3801 GGGCATAATGCCAGGCGGGCATTACCCTGATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCGAGTTTACCG  
NdeI (3858)

3901 TAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGT

4001 CAGCCAGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGC  
PacI (4044) BspLUIII (4054)

4101 CGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGA

4201 TACCAGCGTTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGG

4301 CGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGTTGTTAGTGTCTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCCACCGCTG  
ApaLI (4368)

4401 CGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT

4501 GTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG

4601 GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATC

4701 TCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAA  
PacI (4784) SwaI (4793)

4801 TCAGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAA  
EagI (4804)

4901 ACAAACAAACTAGCAAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA  
NotI (4803)