



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

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**HindIII (245)**  
**Psp1406I (203)** **PvuII (239)**  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCCGCCGCCCTACCTGAGGCC  
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTGTTTCGTTT

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**KasI (535)** **AgeI (552)** **BspHI (560)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTCATCATGAACCTGGAGGGCGGGCCGAGGCGGAGAGTTCGG  
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1▶ M N L E G G G R G G E F G

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**XmaI (673)**  
601 CATGAGCGGGTGAAGCTGCGGCAACGGGAAGCTCCGCCAGTGGCTGATCGACCAGATCGACAGCGGCAAGTACCCGGGCTGGTGGGAGAACGAGGAG  
13▶ M S A V S C G N G K L R Q W L I D Q I D S G K Y P G L V W E N E E  
701 AAGAGCATCTCCGCATCCCTGGAAGCAGCGGGCAAGCAGGACTACAACCGCAGGAGGACGCCGCTCTTCAAGCTTGGGACTGTTTAAAGGAA  
47▶ K S I F R I P W K H A G K Q D Y N R E E D A A L F K A W A L F K G

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**BbsI (840)** **BsrBI (895)**  
801 AGTCCGAGAAGGCATCGACAAGCCGACCTCCACCTGGAAGACGCGCTGCGGTGCGCTTTGAACAAGAGCAATGACTTTGAGGAACTGGTTGAGCG  
80▶ K F R E G I D K P D P P T W K T R L R C A L N K S N D F E E L V E R

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**PvuII (904)** **BsrGI (932)**  
901 GAGCCAGCTGGACATCTCAGACCCGTACAAGTGTACAGGATTGTTCTGAGGGAGCCAAAAAGGAGCCAAGCAGCTCACCTGGAGGACCCGAGATG  
113▶ S Q L D I S D P Y K V Y R I V P E G A K K G A K Q L T L E D P Q M  
1001 TCCATGAGCCACCCCTACCCATGACAACGCCTTACCTTCGCTCCAGCCAG GTTCACAACACTACATGATGCCACCCCTCGACCGAAGCTGGAGGGACT  
147▶ S M S H P Y T M T T P Y P S L P A Q V H N Y M M P P L D R S W R D

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**SacII (1158)**  
1101 ACGTCCCGGATCAGCCACACCCGAAATCCCGTACCAATGTCCCATGACGTTTGGACCCCGGCCACCACTGGCAAGGCCAGCTTGTGAAAATGGTTG  
180▶ Y V P D Q P H P E I P Y Q C P M T F G P R G H H W Q G P A C E N G C  
1201 CCAGGTGACAGGAACTTTTATGCTTGTGCCACCTGAGTCCAGGCTCCCGGAGTCCACAGAGCCAAGCATAAGGTCTGCCGAAGCCTTGGCGTTC  
213▶ Q V T G T F Y A C A P P E S Q A P G V P T E P S I R S A E A L A F

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**NgoMIV (1307)** **SnaBI (1398)**  
1301 TCAGACTGCCGGCTGCACATCTGCCTGTACTACCGGAAATCCTCGTGAAGGAGCTGACCACGTCCAGCCCGAGGGCTGCCGATCTCCATGGACATA  
247▶ S D C R L H I C L Y Y R E I L V K E L T T S S P E G C R I S H G H

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**MscI (1452)**  
1401 CGTATGACGCCAGCAACCTGGACCAGGTCTGTCCCTACCCAGAGGACAATGGCCAGAGGAAAAACATTGAGAAGCTGCTGAGCCACCTGGAGAGGGG  
280▶ T Y D A S N L D Q V L F P Y P E D N G Q R K N I E K L L S H L E R G

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**Bsp120I (1570)**  
1501 CGTGGTCTCTGGATGGCCCCGACGGGCTCTATGCGAAAAGACTGTGCCAGAGCAGGATCTACTGGGACGGGCCCTGGCGTGTGCAACGACCGGCC  
313▶ V V L W M A P D G L Y A K R L C Q S R I Y W D G P L A L C N D R P

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**BsrBI (1683)**  
1601 AACAACTGGAGAGAGACAGACCTGCAAGCTCTTTGACACACAGCAGTCTTGTGACAGCTGCAAGCGTTTGTCCACACGGCCGCTCCCTGCCAAGAT  
347▶ N K L E R D Q T C K L F D T Q Q F L S E L Q A F A H H G R S L P R

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**NheI (1782)**  
1701 TCCAGGTGACTCTATGCTTTGGAGAGGAGTTTCCAGACCTCAGAGGCAAGAAAGCTCATCACAGCTCACGTAGAACCTCTGCTAGCCAGACAATA  
380▶ F Q V T L C F G E E F P D P Q R Q R K L I T A H V E P L L A R Q L Y

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**BglII (1882)**  
1801 TTATTTGCTCAACAAAACAGTGGACATTTCTGAGGGGTACGATTTACCAGAACACATCAGCAATCCAGAAGATTACCACAGATCTATCCGCCATTCC  
413▶ Y F A Q Q N S G H F L R G Y D L P E H I S N P E D Y H R S I R H S

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**NheI (1952)**  
1901 TCTATTCAAGAATGAAAAATGTCAAGATGAGTGGTTTTCTTTTTCCGAATTCGCTAGCTCGCATGATAAGATACATTGATGAGTTTGGACAACCCAAA  
447▶ S I Q E •

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2001 CTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCAATTATA

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**HpaI (2115)** **MfeI (2126)**  
2101 AGCTGCAATAAACAGTTAAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACA

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**EcoRI (2211)**  
2201 AATGTGGTATGGAATCTAAAAACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCA  
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2301 TCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTAGCTCTTC

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**SspI (2450)** **SwaI (2464)**  
2401 ATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTT  
2501 TTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATGGACAGC

2601 AAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAA  
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 V F  
SacI (2725)

2701 AGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGAC  
114 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 V  
StuI (2889)

2801 AGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTACAGACAGACAGTACCCTGCCAATGTAGGCCTCAATG  
81 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 I  
2901 TGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGCTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCT  
47 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 V E  
BspHI (3039)  
BbsI (3035)

3001 CCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATT  
14 V L E L D Q Q S I N F T K M ← AseI (3097)

3101 AATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCCAT  
SacI (3154)

3201 TTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAA  
SpeI (3252)

3301 AATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAG  
SnaBI (3380)

3401 TAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTG  
NdeI (3485)

3501 ATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGAC

3601 GTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCA  
PacI (3671)  
PstI (3664)  
SdaI (3663)  
BspLU11I (3681)

3701 GCAAAAGGCCAGGAACCGTAAAAAGGCCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGG  
3801 TGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGT

3901 CCGCCTTTCTCCCTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCA  
ApaLI (3995)

4001 CGAACCCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACT  
4101 GGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCT  
4201 GCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGATTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCA  
4301 GCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGGATTTTG  
PacI (4411) SwaI (4420) NotI (4430)

4401 GTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAAC  
4501 ATACGCTCTCCATCAAACAAACGAAACAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA