



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGCC  
**HindIII (245)**  
301 GCCATCCACGCCGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT  
**NgoMIV (441)**

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501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACAGCATGCAGACTTTTCAAAATGGTTCTAGAAGAAATCTGGAC  
**KasI (535)** **AgeI (552)** **SphI (560)** **XbaI (582)**  
1 M Q T F T M V L E E I W T  
**MscI (656)**

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601 AAGTCTTTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGTCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCCTCTGTACTCTCAACC  
13 S L F M W F F Y A L I P C L L T D E V A I L P A P Q N L S V L S T  
**BsrGI (791)**

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701 AACATGAAGCATCTTTGATGTGGAGCCAGTGATCGCGCTGGAGAAACAGTGTACTATTCTGTGAATACCAGGGGAGTACGAGAGCCTGTACACGA  
47 N M K H L L M W S P V I A P G E T V Y Y S V E Y Q G E Y E S L Y T  
**BstAPI (818)**

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801 GCCACATCTGGATCCCCAGCAGCTGGTGTCTCACTCACTGAAGGTCTGAGTGTGATGTCAGTGTGATGACATCACGGCCACTGTGCCATACAACCTTCGTGT  
80 S H I W I P S S W C S L T E G P E C D V T D D I T A T V P Y N L R V  
**BamHI (809)**

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901 CAGGGCCACATTGGGCTCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGATCACC  
113 R A T L G S Q T S A W S I L K H P F N R N S T I L T R P G M E I T  
**BsaBI (987)**

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1001 AAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCAAGTTTGTGTTCTTGTGGCCTACTGGAGGAGGGAGCCTGGTCCCGAGGAACATG  
147 K D G F H L V I E L E D L G P Q F E F L V A Y W R R E P G A E E H  
**Bsp120I (1039)** **BspLU11I (1095)**

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1101 TCAAATGGTGAGGAGTGGGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATCTGTGTGAAGGCCAGACATTCGTGAAGGCCATTGG  
180 V K M V R S G G I P V H L E T M E P G A A Y C V K A Q T F V K A I G  
**ApaLI (1129)** **NcoI (1142)**

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1201 GAGGTACAGCGCCTTCCAGCCAGACAGAATGTGTGGAGGTGCAAGGAGAGGCCATTCCCTGGTACTGGCCTGTTTGCCTTTGTTGGCTTCATGCTGATC  
213 R Y S A F S Q T E C V E V Q G E A I P L V L A L F A F V G F M L I  
**BstXI (1250)**

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1301 CTTGTGGTCTGCCACTGTTCTGCTGAAAAATGGGCCGCTGCTCCAGTACTCCTGTTGCCCGTGGTGGTCTCCAGACACCTTAAAAATAACCAATT  
247 L V V V P L F V W K M G R L L Q Y S C C P V V V L P D T L K I T N  
**XemI (1312)** **NgoMIV (1334)** **ScaI (1346)**

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1401 CACCCAGAAGTTAATCAGTGCAGAAAGGAGGAGGTGGATGCTGTGCCAGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGATCTCATAGGT  
280 S P Q K L I S C R R E E V D A C A T A V M S P E E L L R A W I S •  
**PstI (1419)**

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1501 TTGCGGAAGGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAACAGATAAGTGAAGGAAATGCTTTATTTGTGAAATT  
**NheI (1510)**

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1601 TGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTCATTATTTATGTTTCAGGTTCCAGGGGAGGTGT  
**HpaI (1648)** **MfeI (1659)**

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1701 GGGAGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTAACTCCAAATCAAGCCTCTACTTGA  
**EcoRI (1744)**  
1801 ATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGATTAGCTGTTTGCAGCCTCACCTTCTTTATGGAGTTTAAAGATAT

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1901 AGTGTATTTTCCAAGGTTTGAAGTACTGCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATAGTAAATATTCAGAAATAATT  
**SapI (1926)** **SspI (1983)** **SwaI (1997)**

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2001 TAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTGTAGTTGGACTTAGG  
**Bsp120I (1039)**

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2101 GAACAAAGGAACCTTAAATGAAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTT  
141 • N R T Y K L P I L E E I T T K  
**SacI (2258)** **BstXI (2287)**

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2201 TGACCAGCTTCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGA  
125 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 C P S V V R I S  
2301 TCTGTCCACTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTGGCTCACAGCAGACCAATGGCAATGGCTTCAGCA  
92 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 S G I A I A E A  
**StuI (2422)**

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2401 CAGACAGTACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGCTCT  
58 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 A G V H H K N D E

BbsI (2568)  
XmnI (2564)

2501 CATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCCTATAGTGAGTCGT  
 25 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

AseI (2630) SacI (2687)

2601 ATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTAT

SpeI (2785)

2701 ATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAAA

2801 CTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCCAAACCGCATCATCATGGTAA

SnaBI (2913)

2901 TAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGGGGCCATTTACCGTCATTGACGTC

NdeI (3018)

3001 AATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCTGCAAGTGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCTATT

PstI (3197)  
SdaI (3196)

3101 GCGGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCCTG

PacI (3204) BspLU11I (3214)

3201 CAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGAC

3301 GAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCGTGAAGCTCCCTCGTGGCTCTC

3401 CTGTTCCGACCCTGCCGTTACCGGATACTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGT

ApaLI (3528)

3501 GTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA

3601 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACT

3701 ACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTTTGATCCGGCAAACAAACCAC

3801 CGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTACGGGGTCTGACGCT

EagI (3964)  
NotI (3963)

PacI (3944) SmaI (3953)

3901 CAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCGCAATAAAATATCTTTATTTTCATTACATCT

4001 GTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCAAGTGAAGT

4101 GCAGGTGCCAGAACATTTCTATCGAA