



**PvuI (7)**  
**SgfI (6)**
**MfeI (82)** **EcoNI (96)**

1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)**
**HindIII (245)** **Bsu36I (291)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC  
 301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)** **NaeI (441)**

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

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**NcoI (560)**

**KasI (535)**
**BstEII (555)** **AgeI (552)** **NdeI (581)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCATTGGACGCAGCCACTTTGACATATGATACTCTCCGGTT  
 601 TGCTGAATTTGAAGATTTCCCTGAGACCTCAGAGCCTGTTTGGATTCTGGGCAGAAAATACAGCATTTCACAGAGAAGGACGAAATCTTGTCTGATGTT  
 13▶ A E F E D F P E T S E P V W I L G R K Y S I F T E K D E I L S D V  
 701 GCATCCAGACTTTGGTTTACATACAGGAGAAAATTTCCAGCTATTGGGGAACTGGCCCTACTTCAGACACAGGCTGGGGTTGCATGCTTCGGTGTGGAC  
 47▶ A S R L W F T Y R R N F P A I G G T G P T S D T G W G C M L R C G

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**SphI (782)**

801 AGATGATCTTTGCCAGGCCCTGGTATGCCGCACTTAGTGCAGATTGGAGGTGGACTCAGCGGAAGAGGCAGCCTGACAGCTACTTTAATGTCCTCAA  
 80▶ Q M I F A Q A L V C R H L G R D W R W T Q R K R Q P D S Y F N V L N  
 901 TGCTTTCTCGACAGGAAGGACAGCTACTATCCATCCATCAGATAGCGCAAATGGGAGTTGGCGAAGGCAAGTCTATAGGCCAGTGGTACGGGCCGAAC  
 113▶ A F L D R K D S Y Y S I H Q I A Q M G V G E G K S I G Q W Y G P N  
 1001 ACTGTTGCCAGGTCCTCAAGAACTTGTCTGATTTCGACACATGGAGTTCCTTGGCTGTTTACATAGCAATGGACAACACTGTGGTATGGAGGAAATCA  
 147▶ T V A Q V L K K L A V F D T W S S L A V H I A M D N T V V M E E I  
 1101 GAAGGTTATGCAGGGCCAACCTTCCCTGTGCTGGGGCGGCTGCCTTCTACTGATTACAGAGGCACTGTAATGGGTTCCCTGCTGGAGCTGAAGTCAAC  
 180▶ R R L C R A N L P C A G A A A L P T D S E R H C N G F P A G A E V T

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**NgoMIV (827)** **NaeI (827)**

1201 CAACAGGCCATCGGCTTGGAGACCACTAGTGTCTCCTCCTCCGCTGGGACTGACAGACATCAATGAGGCCTATGTGGAGACGCTGAAGCACTGT  
 213▶ N R P S A W R P L V L L I P L R L G L T D I N E A Y V E T L K H C

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**BspHI (1301)**
**XcmI (1350)**

1301 TTCATGATGCCCCAGTCCCTGGGTGTTATTGGAGGGAAGCCCAACAGTGCCACTACTTTATTGGCTATGTTGGGGAGGAGCTCATCTATCTGGACCCCC  
 247▶ F M M P Q S L G V I G G K P N S A H Y F I G Y V G E E L I Y L D P

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**PstI (1412)**
**PvuII (1431)**

1401 AACTACACAGCCTGCAGTGGAGCTGACTGACAGCTGCTTCATCCCGACGAGAGCTTCCACTGCCAGCACCCCTCCTAGGATGGGCATTGGAGAGCT  
 280▶ H T T Q P A V E L T D S C F I P D E S F H C Q H P P S R M G I G E L

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**PshAI (1552)**

1501 TGACCCGTCATTGCTGTGGGGTTTTCTGTAAGAAAGGAGGAAGACTTTAACGACTGGTGTGACGCAAGTCAAAAAGCTATCCCAGCTTGGAGGTGCCCTG  
 313▶ D P S I A V G F F C K K E E D F N D W C Q Q V K K L S Q L G G A L

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**XcmI (1601)**

1601 CCCATGTTGAGCTGGTGAACAGCAGCCTTCCATCTGGCCTGCCAGGATGCTCTGAACTGCTCCTAGACTCTTCTGATGTAGAGAGACTGGAGAGGT  
 347▶ P M F E L V E Q Q P S H L A C Q D V L N L S L D S S D V E R L E R

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**MscI (1763)**

**NheI (1757)**

1701 TTTTGTACTGAGGATGAAGACTTTGAAATCTTATCCCTCTGAAAATCCTGGGGTGTCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGAC  
 380▶ F F D S E D E D F E I L S L •

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**HpaI (1895)**

1801 AAACCACAAC TAGAATGCAGTGA AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAA

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**MfeI (1906)**
**EcoRI (1991)**

1901 CAACAACAATTGCATTCA TTTTATGTTTCAGGTT CAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAA  
 2001 AATACAGCATAGCAAAC TTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGT  
 2101 GCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAAGTACTGCTTCTATTCTTTATGTTTTAAATG

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**SspI (2230)**
**SwaI (2244)**

2201 CACTGACCTCCACATTCCTTTT TAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAAGATCCAGAT  
 2301 GCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTCTAGCT

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2401 TTAGTTCCTGGTGTACTT GAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCA  
 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 C D P A Y D  
 2501 GAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGT  
 107▶ 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 A V I T D F D

StuI (2669)

2601 CCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTC  
74 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 H V A S I I E  
2701 CCCAGTCTTGGTCCTGATGGCCGCCCGACATGGTGTGTTGCTCCTATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGC  
41 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 V L E L D Q

BspHI (2819)

XmnI (2811) AseI (2877)

2801 TGAGAGATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGA  
7 Q S I N F T K M ←

2901 TGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAG

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SpeI (3032)

3000 TTGTTACGACATTTTGAAAAGTCCCCTGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAAATCCCCTGAGTCAAAC  
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SnaBI (3160)

3099 CGCTATCCACGCCATTGATGTACTGCCAAAACGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGG

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NdeI (3265)

3199 TCATGTAAGTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGC  
3299 AGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTGC

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PstI (3444) SdaI (3443) PacI (3451) BspLU11I (3461)

3399 TTGGGCGTCAAGCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCCTGCAGGTTAA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAAC  
←

3497 CGTAAAAGGCCCGTGTGCTGGCGTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAG  
3597 GACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCGCTTTTCTCCCTTC

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ApaLI (3775)

3697 GGGAAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAG  
3797 CCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCA  
3897 GAGCGAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCC  
3997 AGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGA

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PacI (4191)

4097 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAAT

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EagI (4211) NotI (4210)

SwaI (4200)

4197 TAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAA  
4297 AACAAAACGAAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGCAAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA