



PvuI (7) MfeI (82)  
 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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Psp1406I (203) HindIII (245)  
 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGTGAAGCTTCGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGCC  
 301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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NgoMIV (441)  
 401 GGGCCTTTGTCCGGGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

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NcoI (560) BstEII (555)  
 501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATTGGACGAAGTGTCCCCCTCATCTCCGGCAGAGCC  
 1 M D E L F P L I F P A E P

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SphI (653) SacII (686)  
 601 AGCCAGGCTCTGGCCCTATGTGGAGATCATTGAGCAGCCCAAGCAGCGGGCATGCGCTTCCGCTACAAGTGCAGGGCGCTCCGCGGGCAGCATC  
 13 A Q A S G P Y V E I I E Q P K Q R G M R F R Y K C E G R S A G S I

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FspI (776) BstEII (789)  
 701 CCAGGCGAGAGGAGCACAGATACCACCAAGACCCACCCACCATCAAGATCAATGGCTACACAGGACCAGGGACAGTGCGCATCTCCCTGGTACCAAGG  
 47 P G E R S T D T T K T H P T I K I N G Y T G P G T V R I S L V T K

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RsrII (878)  
 801 ACCCTCTCACCGGCTCACCCACGAGCTTGTAGGAAAGGACTGCCGGATGGCTTCTATGAGGCTGAGCTCTGCCGGACCCTGCATCCACAGTTT  
 80 D P P H R P H P H E L V G K D C R D G F Y E A E L C P D R C I H S F  
 901 CCAGAACCTGGGAATCCAGTGTGTGAAGAAGCGGGACCTGGAGCAGGCTATCAGTCAGCGCATCCAGACCAACAACACCCCTTCAAGTTCCTATAGAA  
 113 Q N L G I Q C V K K R D L E Q A I S Q R I Q T N N N P F Q V P I E

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SmaI (1058)  
 1001 GAGCAGCGTGGGACTACGACCTGAATGCTGTGCGGCTCTGCTCCAGGTGACAGTGCGGGACCATCAGGCAGGCCCTCCGCTGCCGCTGTCTTT  
 147 E Q R G D Y D L N A V R L C F Q V T V R D P S G R P L R L P P V L

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BglII (1145) BglII (1193)  
 1101 CTCATCCCATCTTTGACAATCGTGCCCAACTGCGGAGCTCAAGATCTGCCGAGTGAACCGAACTCTGGCAGCTGCCTCGGTGGGATGAGATCTT  
 180 S H P I F D N R A P N T A E L K I C R V N R N S G S C L G G D E I F

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ApaLI (1291)  
 1201 CCTACTGTGTGACAAGGTGCAGAAAGAGGACATTGAGGTGATTTTACCGGACCAGGCTGGGAGGCCGAGGCTCCTTTTCGCAAGCTGATGTGCACCGA  
 213 L L C D K V Q K E D I E V Y F T G P G W E A R G S F S Q A D V H R

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MscI (1304) BspEI (1316) SdaI (1344)  
 1301 CAAGTGGCATTGTGTTCCGACCCCTCCCTACGACACCCAGCCTGCAGGCTCCTGTGCGTGTCTCCATGCAGCTGCGGGCGCCTCCGACCGGGAGC  
 247 Q V A I V F R T P P Y A D P S L Q A P V R V S M Q L R R P S D R E

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EcoRI (1414) PvuI (1440) NdeI (1475) BspHI (1496)  
 1401 TCAGTGGCCATGGAATCCAGTACCTGCCAGATACAGACGATCGTACCAGGATTGAGGAGAAACGTAAGGACATATGAGACCTTCAAGAGCATCAT  
 280 L S E P M E F Q Y L P D T D D R H R I E E K R K R T Y E T F K S I M  
 1501 GAAGAAGAGTCTTTTCAGCGGACCCACCGACCCCGGCTCCACCTCGACGATTGCTGTGCCTTCCCGCAGCTCAGCTTCTGTCCCAAGCCAGCACCC  
 313 K K S P F S G P T D P R P P P R R I A V P S R S S A S V P K P A P

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NcoI (1655)  
 1601 CAGCCATCCCTTTACGTCATCCCTGAGCACCATCAACTATGATGAGTTTCCACCATGGTGTTCCTTCTGGGAGATCAGCCAGGCTCGGCTTGG  
 347 Q P Y P F T S S L S T I N Y D E F P T M V F P S G Q I S Q A S A L

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NcoI (1754)  
 1701 CCCCAGCCCTCCCAAGTCTGCCAGGCTCCAGCCCTGCCCTGCTCCAGCATGGTATCAGCTCTGGCCAGGCCAGCCCTGTCCAGTCCCT  
 380 A P A P P Q V L P Q A P A P A P A P A M V S A L A Q A P A P V P V L  
 1801 AGCCAGGCTCTCAGGCTGTGGCCACCTGCCCAAGCCACCCAGGCTGGGAAGGACGCTGTGAGGCGCTGTGAGGCTGTGAGGCTGTGAGTGTGAT  
 413 A P G P P Q A V A P P A P K P T Q A G E G T L S E A L L Q L Q F D

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SalI (1966)  
 1901 GATGAAGACCTGGGGCCTTGTGGCAACAGCACAGACCCAGCTGTGTTACAGACCTGGCATCCGTCGACAACTCCGAGTTTCAGCAGCTGTGAACC  
 447 D E D L G A L L G N S T D P A V F T D L A S V D N S E F Q Q L L N

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Bsp120I (2078)  
 2001 AGGCATACCTGTGGCCCCACACAACACTGAGCCATGCTGATGGAGTACCCTGAGGCTATAACTCGCCTAGTGACAGGGGCCAGAGGCCCCCGACCC  
 480 Q G I P V A P H T T E P M L M E Y P E A I T R L V T G A Q R P P D P

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XmaI (2121) Bsp120I (2117) XcmI (2168)  
 2101 AGCTCCTGCTCACTGGGGCCCGGGCTCCCAATGGCCTCCTTTCAGGAGATGAAGACTTCTCCTCCATTGCGGACATGGACTTCTCAGCCCTGCTG  
 513 A P A P L G A P G L P N G L L S G D E D F S S I A D M D F S A L L

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MscI (2237) NheI (2231)  
 2201 AGTCAGATCAGCTCCTAAGGGGTGACGCTCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAA  
 547 S Q I S S •

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HpaI (2369) MfeI (2380)  
 2301 AAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACATTGCATTCTTTATGT

2401 TTCAGGTTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCT  
 EcoRI (2465)

2501 CCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTCATTAGCTGTTTGCAGCCTCACCTT

2601 CTTTCATGGAGTTTAAAGATATAGTGATTTTCCCAAGGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTAA

2701 GTAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCC  
 SspI (2704) SwaI (2718)

2801 AGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGA  
 141 • N R T Y K L P I

2901 TGAGTTCTCAATGGTGGTTTTGACCAGCTTGCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACACATGCCACA  
 132 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 E R C M G C

3001 GGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGAC  
 99 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 G N S V A S

3101 CCAATGGCAATGGCTTACGACAGACAGTGACCCTGCCAATGTAGGCCTAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCC  
 65 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 K T R I A G  
 BspHI (3293)

3201 CGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGAT  
 32 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 N F T K M  
 XmnI (3285)

3301 GGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGTT  
 AseI (3351)

3400 TCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAATGGGGCGGAGTTGTACGACATTTTGAAAGTCCCG

3500 TTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTG  
 SpeI (3506)

3599 CAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAAGTCATGTACTGGGCATAATGCCAGGCG  
 SnaBI (3634)

3699 GGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGATTACCGTAAATACTCCACCCATT  
 NdeI (3739)

3799 GACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATT

3899 TACCGTAAGTTATGTAACGCCTG C A G G T T A A T T A A G A A C A T G T G A G C A A A A G G C C A G A A A G G C C A G G A A C C G T A A A A G G C C G T T G C T G G C G T T  
 SdaI (3917) PacI (3925) BspLU11I (3935)

3997 TTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCC

4097 CCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCT

4197 CACGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAA  
 ApaLI (4249)

4297 CTATCGTCTTGTAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACA

4397 GAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTA

4497 GCTCTTGATCCGGCAAACAAACCACCGTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTT

4597 GATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATA  
 PacI (4665) SwaI (4674) EagI (4685) NotI (4684)

4697 AAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGC

4797 AAAATAGGCTGTCCCAAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA