



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACC GTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCGCCCTACCTGAGGCC
PvuII (239)
Bsu36I (291)
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCGCCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGCTCAACTCTACGCTTTTGTTCGTTT

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTATCATGAATAATCAAGATGCCGTGGCTTCGATACTGCATGA
AgeI (552) **BspHI (560)**
601 GTGCAAGGAAGTCTGGATCGTCTCTTGTGGAAACGCGAGATGTGTCTACAGAGGACAAGAGTGGAGACCAGCGGTGCAGAGCTTCACTCCCAGCGAG
13▶ C K E V L D R L L L E T P D V S T E D K S E D Q R C R A S L P S E
701 TTAAGGACCTGATCCAGGAGGAGGAAATGAAGTGGCCCTTCGTGCTGAAAAGTGGCAATACAAACAAGCCATGAGCCAGAGGACAAAACAAACC
47▶ L R T L I Q E A E E M K W P F V P E K W Q Y K Q A M S P E D K T N
801 TGCAAGATGTGATTGGCGCCGGCTGCAGCAGTTACTGGCGCCTTGCAGCCTCCATCCTTGTCCAGGACTGCGTCCGCTCCGCTATTGCTTCTT
80▶ L Q D V I G A G L Q Q L L A A L R A S I L V Q D C A A A S A I V F L

901 GATGGACCGGTTCTGTATGGACTTGACGTCTCCGAAAACCTCTGCAGGTCGCCAAAGGCTTGCACAAGCTGAAGCCTGCAACGCCATCGCCCCGAG
AgeI (905) **BspEI (931)** **SdaI (942)**
113▶ M D R F L Y G L D V S G K L L Q V A K G L H K L K P A T P I A P Q

1001 GTGGTCATCCGACAAGCCGAGTCTCCGTCAACTCAGGAAAAGTGTGAAGGCAGAATACATCCTGAGCAGCCTGATAAGCAACAACGGAGCAACCGGTA
147▶ V V I R Q A R V S V N S G K L L K A E Y I L S S L I S N N G A T G

1101 CCTGGCTGTATAGGAATGAGAGTGACAAAGTCTGGTACAATCGGTCTGCATACAGATCAGAGGGCAGATTCTGCAGAAGCTAGGCATGTGGTATGAAGC
180▶ T W L Y R N E S D K V L V Q S V C I Q I R G Q I L Q K L G M W Y E A

1201 GGCAGAATTGATATGGGCTCCGTCATAGGATATCTGACACTCCCTCAGCCAGATAAGAAGGGCATTTCACATCACTGGGCATACTGGCAGACATCTTT
213▶ A E L I W A S V I G Y L T L P Q P D K K G I S T S L G I L A D I F

1301 GTTCCATGAGCAAAACCGATTATGAAAAGTTAAGAAGGCCAAAGGTTAACTTGGCCCTGCTCAAGGAGTTTGACCACATTTGTGTGTCAGCCGCGG
247▶ V S M S K T D Y E K F K K S P K V N L A L L K E F D H H L L S A A

1401 AAGCTGCAAGCTGGCAGCTGCCTTCAGTGCCTACACACCCCTCTTTGTGCTCAGGGCTGTGAATATCCGTGGCAGATGTTTGTGTCATATAGCTGTTC
280▶ E A C K L A A A F S A Y T P L F V L R A V N I R G T C L L S Y S C S
1501 TGCTGACTGCCCTCCGGGAATGAAAAGTGTGCATCTGTGTGAAGCCAAAGAAGCTTTTGTGATTGGCCTCCTGACCAAGAAAGATGGCGAGCTGGTTAGT
313▶ A D C P P G M K S V H L C E A K E A F E I G L L T K K D G E L V S

1601 GGCAAGCAGGAGCTGCACAGCTTCATCAAAGCTGCTTTCGGCCTCACCACGGTGCACCTCAGACTCCATGGGGAGACAGATGCAGTTCCGCGCAGCAAGGC
347▶ G K Q E L H S F I K A A F G L T T V H S R L H G E T D A V R A A R
1701 AGCTATGCAGTGAAGCTGTGGGCAAGCTCTACACCTTCAGCACTTCCCCACAAGCCAGGACAGAGAAGGCCTGTCTCAGGAAATCATGTCTCTCATCAG
380▶ Q L C S E A V G K L Y T F S T S P T S Q D R E G L S Q E I M S L I S
1801 CCAGGTGAAGGGACATCTACGAGTTCAAAGTTCCTCAAATTTAGATGTTTGTCTTATGTCCAGAGAGTTTCAAGTGTGGTTTAGATCGACTCATCTTG
413▶ Q V K G H L R V Q S F P N L D V C S Y V P E S F K C G L D R L I L

1901 CATGGACACGTGGATTTCCAACAAATTCTTGAACCTATTCCAGCACCATACTTCAGTGTGTGAGGTATTTGAAAGCACTTGTGGGAACAGCAAAAGCA
447▶ H G H V D F Q Q I L E T Y S Q H H T S V C E V F E S T C G N S K S

2001 ACCAGAGAGACACAAAATCGGAGTCTGTATTACCACTCTGAAGACAGAAACAAACACCTGCAGATACTATGGTTGCTACTCTAGAGAGGGTGAGTTCCCA
480▶ N Q R D T K S E V C I T T L K T E T N T A D T M V A T L E R V S S Q
2101 AGACAGCAGGAGTACAGCTTCTTCAAATGTCTAAGAAAGATCAAGGGAAGCTCAAAGAGAAAGGGGAGAAGCTGGACCCGTTCAAAGGCATTCCGA
513▶ D S R S T A S S K M S K K D Q G K L Q R E R G R S W T R S K A F R

2201 GTCTCCCTGGATCTAGATATGGAGACTGAGACTGAGCCACCAATCACAGCAATGGAGGGACAGATGTTTTCAACAAGTCTCTGAGAGACAACTCTAGCT
547▶ V S L D L D M E T E T E P P N H S N G G T D V F N K S L R D N S S
2301 CCTGTTCTTGGGCGAGACTGTACAGGCTCAGCTTCCACAAGCTGGGAGGAAGTGAAGTGCCTGTTGAGGATGTAGTAAGGAAAGGGTCTGGCCAAGA
580▶ S C S W G R L S G L S S S T S W E E V N C A V Q D V V R K G S G Q E
2401 AAGCCTCTGTGGAGGCGCAAAGCTCTGAGGCAGTGTCTGAGGACCCAGAGGAAACAGAAAGCAGCAGCTGTGTGTTTGTCTTCAAAGCTCCGTGGT
613▶ K H P V E A Q S S E A V V S E E P K R N R S S R A V F L S S K L R G
2501 GTCTCTCTCAGCAACTGGAGATGACAACCTTAGAGTCTTACCAAGTCAGTTACACAATCACACATCCATCCTTCTTCAATGCAAAAGATACTTGT
647▶ V S L Q T T G D D N L E S S P S Q L H N H T S I L P F N A K D T C
2601 TGGCCTCGGGTGCAGGACTGGTAGAAACCGTGAAGGATCTAACAATACTTCTTTCAGTCCAGTCATTGCTGTGGTCTGATTCTGGTCTTGTCTAG
680▶ L A S G A G L V E T A E G S N N T S L Q S S H S C G S D S W S L S S

L A S G A G L V E T A E G S N N T S L Q S S H S C G S D S W S L S S
2701 TTCAGACAGGTTACAGATGTGACCACGAATCCTTCAGTTCAGGAAGAAGAACCCTCTGGAATAATGGGTGATGTCCAGAATCCAAGTATGACTITAAA
713▶ S D R F T D V T T N P S V Q E E E P S G I M G D V P E S K Y D F K
2801 GACTGGCACGGAGAAAAGAAATGGGGAAACACTCACTGAAATATGCACAGGGCCTGAATTAACATITGCCCCCTCTTCGGTCGACCCAGAAGGAGAAAACAG
747▶ D W H G E K N G G T L T E I C T G P E L T F A P S S V D P E G E T
AvrII (2940) MluI (2974) BspEI (2991)
2901 CAGAAAGCACAGACGATGGACTATCACCTCTCAGGTAGCCCTAGGATGTTTAGAAGGCAGCCATTCAATGTCTACGCGTAGGACTTCTTTCCGGATGG
780▶ A E S T D D G L S P S Q V A L G C L E G S H S M S T R R T F F P D G
3001 GTCGGTTCAAACGCTGACTCAGCAAAGACTGGCTGCTCAGTCAGAGACCAGACTGTCGACCTGATGCCTCAACGGTGGATGAGGAGGGCCAAATGCTT
813▶ S V Q N A D S A K T G C S V R D Q T V D P D A S T V D E E G Q M L
BbrPI (3146)
3101 GACAGCACAGAGTCTGCTCCATTGGCCAGGATGGCGCTCACAGACCAGTCTTTGAGGTCCGGTCAGAGTCCGGAGGGGCCAAAGTCTTTGTAATG
847▶ D S T E V C S I G Q D G A H R P R A L R S G Q S A E G P K S F V N
SphI (3266)
3201 GCTCCAGACCTTCCCCTATCTTCGATGAGGACTTCAGCACCACAGAGGAAGGAGAGGAGCTTGGGAGCATGTGAAGAGCAGCCAAAACCTCCAGITCATA
880▶ G S R P S P I F D E D F S T T E E G E E L G S M L K S S Q N S S S Y
NcoI (3304)
3301 CTCACCATGGTGGITAAAATCACCAGCCTTTTCCCGCAGTTCGTGATGGGAAAGCTCCTGGTCTCTGCTGAACCTCAAGCAGAAGTTCCTTCGCCTCG
913▶ S P W W L K S P A F S R S S S D G E S S W S L L N S S R S S F A S
XmnI (3460)
3401 CTGGCAGGACAGACCAGTCAAGAGATCCTTGAGGCTCGAACCTACAGCCTGATGACCTTGA AAAACTTCTGGCGGGCGTGAGGCATGATTGGCTGCTTC
947▶ L A G Q T S Q E I L E A R T L Q P D D L E K L L A G V R H D W L L
3501 AGAGACTGGAGAATACTGGCGTTTTGAAGTCCAATCAACTCCAACAAGCCACAGTGCCTTCTGCTAAAATATCCAAAAAGTCTGAGTTGTGGACAGC
980▶ Q R L E N T G V L K S N Q L Q Q A H S A L L L K Y S K K S E L W T A
3601 GCAGGAAACTGTGGTGTATCTGGGAGACTACCTGAAAGTGAAGAAGAAGGGCAAGCAGAGAAATGCATTTGGGTCCACTATCTCCATCAAGAGGAAACC
1013▶ Q E T V V Y L G D Y L K V K K K G K Q R N A F W V H Y L H Q E E T
BsrBI (3766) DraIII (3787)
3701 CTGGGAGATACGTTGGGAAAGAATAACAAGAGAGGAAGGGCTCCGGCACCCTTCACTGATGTGGAGCGCAGATGACAGCACAGCACTACGTGACAG
1047▶ L G R Y V G K E Y K E R K G L R H H F T D V E R Q M T A Q H Y V T
3801 AGTTTAAACAGAGACTCTACGAGCAAAAGATCCGACTCAGATATTCTACGCTCCCTCTACAATATTACTGATTTTGAAGACAGGACTATAAAGGGATG
1080▶ E F N K R L Y E Q K I P T Q I F Y V P S T I L L I L E D R T I K G C
EcoRI (3928)
3901 CATCAGTGTGGAGCCTTACATCCTGGGGAAATTCGTCAAGTTATCCAATAACACCAAAGTAGTCAAAAATGAGTACAAGCTACAGAATATGGCTTGCC
1113▶ I S V E P Y I L G E F V K L S N N T K V V K N E Y K A T E Y G L A
BamHI (4098)
4001 TATGGCCATTTTTCTTATGAGTTTTCTAACCATAGAGATGTGGTGGTTGATTTACAAGTTGGGTGACTGGTAATGGAAAAGCCTGATCTATCTCACGG
1147▶ Y G H F S Y E F S N H R D V V V D L Q G W V T G N G K G L I Y L T
4101 ATCCTCAGATTCACTCTGTAGACCAGAAAGATGCTACTACAACTTTGAAAGCGGGGAATATTTACTTCTTAAATAACCAACATGCAAGCTGTAATGA
1180▶ D P Q I H S V D Q K D V T T N F G K R G I F Y F F N N Q H A S C N E
NheI (4272)
4201 AATATGCCATCGTCTTTCTCTGACTAGACCTTCACTAGAGCAAAACAAGTAAGGTATAGCCTGTGGTTGGAGCTAGCTGGCCAGACATGATAAGATACA
1213▶ I C H R L S L T R P S L E Q T S K V •
4301 TTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGA AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTG

HpaI (4410) MfeI (4421)
4401 CAATAAACAAAGTTAAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGT

EcoRI (4506)
4501 GGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGG
4601 GGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAACACTGCTTTCATTTCC

SwaI (4759)
4701 TTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATT
4801 AGGCAGATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAA
4901 AGCGAGCTTCTAGCTTTAGTTCTGCTGACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAG
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

SacI (5020) BstXI (5049)
5001 TCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCA
112▶ 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 A V
5101 CAATGGTGTCAAAGTCTTCTGCCGTTGCTCAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGAC
79▶ 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 H V
5201 AGCAGAGATGATCTCCCACTTGGTCTGATGGCCGCCGACATGGTGTGTTGTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACC
46▶ 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 V
XmnI (5326) AseI (5392)
5301 AGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGTGATTATACTATGCCGATATACTATGCCGATGATTAATTG
12▶ L E L D Q Q S I N F T K M

5401 TCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACGCCATTGCG
SacI (5449)

5501 TCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCC
SpeI (5547)

5601 CCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGA
SnaBI (5675)

5701 AAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTA
NdeI (5780)

5801 CTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAA

5901 TGGGCGGGGTGCTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAITTAAGAACATGTGAGCAAAGGCCAGCAA
SdaI (5958) PaeI (5966) BspLU11I (5976)

6001 AGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG
PaeI (6006) SmaI (6015) NotI (6025)

6101 AAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCTGGAAGTCCCTCGTGGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGC

6201 TTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGACGAA
ApaLI (6290)

6301 CCCCCTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA

6401 CAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCT

6501 CTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCGCTGGTAGCGGTGGTTTTTTGTTGCAAGCAGCAGA

6601 TTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCAT

6701 GGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAATATCTTTATTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACG
EagI (6726)

6801 CTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA