



PvuI (7)
SgfI (6)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGACAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCCTTACGCGCCCGCCGCTACCTGAGGCC
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGCTCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) **AgeI (552)** **NcoI (568)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTAGGAGGGCCACCATGGTGTGTTTCGATGTGGACACGGAAGAGA
601 CAAATTTTGTCTTTTTAAATATGCTCTTAGTTTCTAGAGTCTTTGGTTTCGATGGTTTCTAAAACCTACCTTGTGAAGTTAAAGTAAATATCCCAG
701 AGGCCCATGTGATCGTGGACTGCACAGACAAGCATTGACAGAAATCCCTGAGGGCATTCCCACTAACACCACCAATCTTACCCTTACCATCAACCACAT
801 ACCAAGCATCTCTCCAGATTCTTCCGTAGGCTGAACCATCTGGAAGAAATCGATTTAAGATGCAATTGTGTACCTGTTCTACTGGGGTCCAAAGCCAAT
901 GTGTGTACCAAGAGGCTGCAGATTAGACCTGGAAGCTTAGTGGACTCTGACTTAAAAGCCCTTACTGGATGGAACCAACTTCTGGAGATACCAC
1001 AGGATCTGCCATCCAGCTTACATCTTCTGAGCCTTGAGGCTAACCAACATCTTCCATCACGAAGGAGAATCTAACAGAACTGGTCAACATTGAAACACT
1101 CTACCTGGGTCAAACCTGTTATTATCGAAATCCTTGAATGTTTCTATTCTATTGAAAAAGATGCTTCTAGTTATGAGAAATTTGAAGTTCTCTCA
1201 CTAAGATAACAATGTACAGCTGTCCCAACCACTTTGCCACCTAATTTACTAGAGCTCTATCTTTATAACAATATCATTAGAAAAATCCAAGAAAATG
1301 ATTTAATAACCTCAATGAGTTGCAAGTCTTGACCTAAGTGAAATTCGCCATATCCGTGACACCGTGTGAAATAATTC
1401 CCCCTTACAGATCCATGACAATGCTTTCAATTCATTGACAGAATTAAGTTTACGTTTACACAGTAATTTCTTTCAGCATGTGCCCAACATGGTTT
1501 AAAAAATGAGAACTCCAGGAAGTACCTTCCCAAACTACTTGGCCAGAGAAATTTGAGGAGGCCAAATTTTGCATTTTCTCCCAACCTTGTG
1601 AGTTGGATTTTCTTTCAATTATGAGCTGCAGGCTACCATGCATCTATAACTTTACCACATTCCTCTTTCATTGGAAAACCTGAAAATTTCTGCGTGT
1701 CAAGGGGTATGTCTTTAAAGAGCTGAAAACCTCCAGTCTTTCTGTATTGCACAAGCTTCCAGGCTGGAAGTTCTTGACCTTGGCACTAACTTATAAAA
1801 ATTGCTGACCTCAACATATTCAACATTTTAAAACCTCAAACCTCATAGACCTTTTCAAGTGAATAAGATATCTCCTTCAGAAGAGTCAAGAGAAGTTGGCT
1901 TTTGCTCTAATGCTCAAACCTTCTGTAGACCGTATGGGCCAGGCTTCTGAGGCTTACACTATTTCCGATACGATGAATATGCACGGAGCTGCAGGTT
2001 CAAAAACAAAGAGCCACCTTCTTTCTGCTTTGAATGCAGACTGCCACATATATGGGACAGCTTAGACTTAAAGTAGAAATAACATATTTTTTATTA
2101 CCTTCTGATTTTTCAGCATCTTTTCAATTCCTCAAATGCTCAACTTATCAGGAAACACCATTTGGCCAAACTCTTAATGGCAGTGAAGTCTGGCCGTTGAGAG
2201 AGTTGCGGTACTTAGACTTCTCCAACAACCGGCTTACTTACTCAACAGCCTTTGAGAGCTCCAGAGTCTTGAAGTTCTGGATCTAAGTAGTAA
2301 CAGCCACTATTTTCAAGCAGAAGGAATTACTCACATGCTAACTTTACCAAGAAATTACGGCTTCTGGACAACTCATGATGAATGATAATGACATCTCT
2401 ACTTCGGCCAGCAGGACCATGGAAGTACTCTCTTGAATTCGGAGTTTCAGAGGCAACCATTTAGATGTTCTATGGAGAGCCGGTGATAACAGATACT
2501 TGGACTTCTTCAAGAATTTGTTCAATTTAGAGGTATTAGATATCTCCAGAAATTCCTGAATTCCTTGCCTCCTGAGGTTTTTGGAGGTATGCCGCAAA
2601 TCTAAAGAATCTCTCCTTGGCCAAAATGGGCTCAAATCTTTCTTTGGGACAGACTCCAGTTACTGAAGCATTTGAAATTTGGACCTCAGCCATAAC
2701 CAGCTGACAAAAGTACCTGAGAGATTGGCCAACTGTTCCAAAAGTCTCACAACACTGATTCTTAAGCATAATCAAATCAGGCAATTGACAAAATTTTTC
2801 Q L T K V P E R L A N C S K S L T T L I L K H N Q I R Q L T K Y F

BbsI (2861)
2801 TAGAAGATGCTTTGCAATTGCGCTATCTAGACATCAGTTCAAATAAAAATCCAGGTCATTGAGAAAGACTAGCTTCCCAGAAAATGCTCTCAACAATCTGGA
744▶L E D A L Q L R Y L D I S S N K I Q V I Q K T S F P E N V L N N L E

HpaI (2964)
2901 GATGTTGGTTTTACATCACAAATCGCTTTCTTTGCAACTGTGATGCTGTGGTTGTCTGGTGGGTTAACCATACAGATGTTACTATTCCATACTGGCC
777▶ M L V L H H N R F L C N C D A V W F V W W V N H T D V T I P Y L A

Bst1107I (3062) BglII (3077)
3001 ACTGATGTGACTTGTGTAGTCCAGGAGCACACAAAGGTCAAAGTGCATATCCCTTGATCTGTATACGTGTGAGTTAGATCTCACAAAACCTGATTCTGT
811▶ T D V T C V G P G A H K G Q S V I S L D L Y T C E L D L T N L I L

3101 TCTCAGTTTCCATATCATCAGTCTCTTTCTTATGGTAGTTATGACAACAAAGTCACTCTTTTTCTGGGATATGGTACATTTATTATTTTTGGAAAGC
844▶ F S V S I S S V L F L M V V M T T S H L F F W D M W Y I Y Y F W K A

NcoI (3229)
3201 AAAGATAAAGGGGTATCAGCATCTGCAATCCATGGAGTCTTGTATGATGCTTTTATTGTGTATGACACTAAAAACTCAGCTGTGACAGAATGGGTTTTG
877▶ K I K G Y Q H L Q S M E S C Y D A F I V Y D T K N S A V T E W V L

3301 CAGGAGCTGGTGGCAAAATGGAAGATCCAAGAGAAAAACACTTCAATTTGTGTCTAGAAGAAAGAGACTGGCTACCAGGACAGCCAGTTCTAGAAAACC
911▶ Q E L V A K L E D P R E K H F N L C L E E R D W L P G Q P V L E N

3401 TTTCCCAGAGCATACAGCTCAGCAAAAAGACAGTGTGTGATGACACAGAAATATGCTAAGACTGAGAGTTTTAAGATGGCATTTTATTTGTCTCATCA
944▶ L S Q S I Q L S K K T V F V M T Q K Y A K T E S F K M A F Y L S H Q

3501 GAGGCTCTGGATGAAAAAGTGGATGTGATTATCTTGATATTCTTGGAAAAGCCTCTCAGAAGTCTAAGTTTCTCAGCTCAGGAAGAGACTCTGCAGG
977▶ R L L D E K V D V I I L I F L E K P L Q K S K F L Q L R K R L C R

3601 AGCTCTGTCTTGGAGTGGCTGCAATCCACAGGCTCACCCATACTTCTGGCAGTGCCTGAAAAATGCCTGACCACAGACAATCATGTGGCTTATAGTC
1011▶ S S V L E W P A N P Q A H P Y F W Q C L K N A L T T D N H V A Y S

AvrII (3743) NheI (3757)
3701 AAATGTTCAAGGAAACAGTCTAGCTCTCTGAAGAATGCCACCTAGGACATGCCTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGAC
1044▶ Q M F K E T V •

HpaI (3895)
3801 AAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAA
3901 CAACAACAATTGCATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAA
4001 AATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGT

SapI (4173)
4101 GCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATG

SspI (4230) SmaI (4244)
4201 CACTGACCTCCCACATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGAT
4301 GCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTCTAGCT

4401 TTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCA
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

4501 GAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGT
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 (4669)
4601 CCTCTGCCCGTTGCTCACAGCAGACCCAAATGGCAATGGCTTACGACAGACAGTGCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTC
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

4701 CCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGC
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

BbsI (4815) XmnI (4811) AseI (4877)
4801 TGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGGA
74▶ Q S I N F T K M

4901 TGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTGCGTCAATGGGGCGGAGT

SpeI (5032)
5001 TGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCG

SnaBI (5160)
5101 CTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAAGGTC

NdeI (5265)
5201 ATGTACTGGGCATAATGCCAGGCGGGCCATTTACCCTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAG
5301 TTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTT

PacI (5451) SdaI (5443) BspLU11I (5461)
5401 GGGCGTCCAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCCTGCAGGTTAAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTA
5501 AAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT
5601 AATAAGATACCAGCGTTTTCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGA

ApaI (5775)

5701 AGCGTGGCGCTTTTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCG

5801 ACCGCTGCGCCTTATCCGTAACATATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC

5901 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT

6001 ACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGGTTTGAAGCAGCAGATTACGCGCAGAAAAA

PacI (6191)

6101 AAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAAC

EagI (6211)

SwaI (6200)

NotI (6210)

6201 ATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACA

6301 AAACGAAACAAAACAACTAGCAAATAGGCTGTCGCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA