



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

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

KasI (535) **AgeI (552)** **SphI (560)**
501 TCTGTTCTGGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCAGCATGCTCCTGCCTGGGCCACCTTGCCCCGGCCTGGC
1▶ M L L P W A T S A P G L A

NdeI (665) **SdaI (686)**
601 CTGGGGCCTCTGGTGTGGCCTCTTGGGCTCTGGCAGCATCGCAGCCCCAGGCGGTGCCTCATATGCGTCGGAGAACCAGACCTGCAGGGACCAG
13▶ W G P L V L G L F G L L A A S Q P Q A V P P Y A S E N Q T C R D Q
701 GAAAAGGAATACTATGAGCCCCAGCACCAGCATGCTGCTGCCGCTGCCGCCAGGCACCTATGTCTCAGCTAAATGTAGCCGCATCCGGGACACAGTTT
47▶ E K E Y Y E P Q H R I C C S R C P P G T Y V S A K C S R I R D T V

BspLU11I (805) **EcoRI (816)** **PvuII (856)** **XhoI (889)**
801 GTGCCACATGTGCCGAGAATTCCTACAACGAGCACTGGAACCTACCTGACCATCTGCCAGCTGTGCCGCCCTGTGACCCAGTGTGGCCCTCGAGGAGAT
80▶ C A T C A E N S Y N E H W N Y L T I C Q L C R P C D P V M G L E E I

XhoI (970) **Bsp120I (965)** **BsrGI (976)**
901 TGCCCCCTGCACAAGCAAACGGAAGACCCAGTGCCTGCCAGCCGGGAATGTTCTGTGCTGCCTGGCCCTCGGGCCCTCGAGTGTACACACTGCGAGCTACTTTCT
113▶ A P C T S K R K T Q C R C Q P G M F C A A W A L E C T H C E L L S
1001 GACTGCCCGCCTGGCACTGAAGCCGAGCTCAAAGATGAAGTTGGGAAGGTAACAACCACTGCGTCCCTGCAAGGCAGGGCACTTCCAGAATACCTCCT
147▶ D C P P G T E A E L K D E V G K G N N H C V P C K A G H F Q N T S

DraIII (1125)
1101 CCCCCAGCGCCCGTCCAGCCCCACACAGGTGTGAGAACAAGTCTGGTGGAGGCAGCTCCAGGCACTGCCAGTCCGACACAACCTGCAAAAATCC
180▶ S P S A R C Q P H T R C E N Q G L V E A A P G T A Q S D T T C K N P
1201 ATTAGAGCACTGCCCCAGAGATGTCAGGAACATGCTGATGCTGGCGTCTGCTGCCACTGGCCTTTCTTCTGCTCCTTGCACCGTCTTCTCCTGC
213▶ L E P L P P E M S G T M L M L A V L L P L A F F L L L A T V F S C

SandI (1368)
1301 ATCTGGAAGGCCACCCTTCTCTGCAAGAACTGGGATCGTGTCTCAAGAGCGTCCGAGGGAGGGACCAACTCTGTAGCTGGAAGCTGGGAGC
247▶ I W K S H P S L C R K L G S L L K R R P Q G E G P N P V A G S W E
1401 CTCCGAAGGCCATCCATACTTCCCTGACTTGGTACAGCCACTGTACCCATTCTGGAGATGTTCCCAAGTATCCACTGGGCTCCCGCAGCCCCAGT
280▶ P P K A H P Y F P D L V Q P L L P I S G D V S P V S T G L P A A P V

XmaI (1564) **Acc65I (1591)**
1501 TTTGGAGGCAGGGGTGCCGAACAGCAGAGTCTCTGGACCTGACCAGGGAGCCGAGTTGGAACCCGGGGAGCAGAGCCAGTGGCCACGGTACCAAT
313▶ L E A G V P Q Q Q S P L D L T R E P Q L E P G E Q S Q V A H G T N

SgrAI (1611) **ScaI (1662)**
1601 GGCATTATGTCACCGCGGGTCTATGACTATCACTGGCAACATCTACATCTACAATGGACCAGTACTGGGGGACCACCGGGTCTGGAGACCTCCAG
347▶ G I H V T G G S M T I T G N I Y I Y N G P V L G G P P G P G D L P

SandI (1736) **XmaI (1750)** **BstXI (1770)**
1701 CTACCCCGAACCTCCATACCCATTCCCGAAGAGGGGACCTGGCCCTCCCGGGCTCTCTACACCCACCAGGAAGATGGCAAGGCTTGGACCTAGC
380▶ A T P E P P Y P I P E E G D P G P P G L S T P H Q E D G K A W H L A

Bsp120I (1836) **Tth111I (1868)** **NheI (1889)** **MscI (1895)**
1801 GGAGACAGAGCACTGTGGTGCCACACCTCTAACAGGGGCCAAAGGAACCAATTTATCACCCATGACTGACGGAGTCTGAGAAAAGGCAGCTAGCTGGCC
413▶ E T E H C G A T P S N R G P R N Q F I T H D •
1901 AGACATGATAAGATACATTGATGAGTTTGGACAACCACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTT

HpaI (2027) **MfeI (2038)**
2001 GTAACCATTATAAGTGAATAAACAAGTTAAACAACAATTGCATTATTTATGTTTCAGGTTTCAGGGGAGGTGTGGAGGTTTTTAAAGCAAGT

EcoRI (2123)
2101 AAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAAT
2201 AAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAGATATAGTGTATTTTCCCAAGGTTTG

SspI (2362) **SwaI (2376)**
2301 AACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAA
2401 AATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAG
2501 AAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTGATTCTGGTGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGTTCATTTCATCT
141▶ • N R T Y K L P I L E E I T T K V L K G N M E

2601 CAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTA
118 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 R D V E D S Y
2701 GGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATG
85 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 C V T V R G I
StuI (2801)
2801 TAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCACATGGTGCTTGTGCTCATAGAGCATGGTGATCTTCT
51 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 Y L M T I K E
BspHI (2951)
XmnI (2943)
2901 CAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACT
18 T A V E V L E L D Q Q S I N F T K M
AseI (3009)
3001 ATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCCTACAC
SpeI (3164)
3100 GCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGG
SnaBI (3292)
3199 GGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTA
NdeI (3397)
3299 GATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGGGGCCATTTACCCTGTCATTGACGTCAATAGGGGGCGTACTTGGC
3399 ATATGATACACTTGATGTACTGCCAAGTGGGAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACAT
SdaI (3575) PacI (3583) BspLU11I (3593)
3499 ACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGACCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCC T G C A G G T T A A T T A A G A A C A
3597 TGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCG
3697 ACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCG
3797 CTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCA
ApaLI (3907)
3897 AGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCC
3997 ACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGA
4097 ACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTT
4197 TTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTACGGGGTCTGACGCTCAGTGAACGAAAACTC
EagI (4343)
Pacl (4323) SwaI (4332) NotI (4342)
4297 ACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTGT
4397 GTGAATCGTAACTAACATACGCTCTCCATCAAACAAACGAAACAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATT
4497 TCTCTATCGAA