



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

1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
Bsu36I (291)

HindIII (245) **EcoNI (287)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCCGCCCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTTCTTTGTTTCGTTT

NcoI (560)

BstEII (555)
AgeI (552)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATTGGCGCCGTCGCCGTCTGGCGCCGCTGGCCGTCCG
1▶ M A P V A V W A A L A V G

601 ACTGGAGCTCTGGGCTGCGGCGCACGCCTTGCCCGCCAGGTGGCATTACACCTACGCCCGGAGCCGGGAGCACATGCCGGCTCAGAGAATACTAT
 13▶ L E L W A A A H A L P A Q V A F T P Y A P E P G S T C R L R E Y Y

BbsI (754)
DraIII (777)

701 GACCAGACAGCTCAGATGTGCTGCAGCAATGCTCGCCGGCCAAATGCAAAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTACTCCTGTGAGG
 47▶ D Q T A Q M C C S K C S P G Q H A K V F C T K T S D T V C D S C E
 801 ACAGCACATACCCAGCTCTGAACTGGGTTCCCGAGTGTGAGCTGTGGCTCCCGCTGTAGCTCTGACCAGGTGAAACTCAAGCTGCACTCGGGA
 80▶ D S T Y T Q L W N W V P E C L S C G S R C S S D Q V E T Q A C T R E

SdaI (917)
FspI (980) **SrfI (992)**

901 ACAGAACCGCATCTGCACCTGCAGGCCCGGCTGGTACTGCGCGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAGTCCGCCCGGGC
 113▶ Q N R I C T C R P G W Y C A L S K Q E G C R L C A P L R K C R P G
 1001 TTCGGCGTGGCCAGACCAGGAATGAAACATCAGACGTGGTGTGCAAGCCCTGTGCCCGGGGACGTTCTCCAACACGACTTCATCCACGGATATTTGCA
 147▶ F G V A R P G T E T S D V V C K P C A P G T F S N T T S S T D I C

BglIII (1109) **XcmI (1175)**

1101 GGCCCCACAGATCTGTAACGTGGTGGCCATCCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCACCCGGAGTATGGCCCCAGGGGC
 180▶ R P H Q I C N V V A I P G N A S M D A V C T S T S P T R S M A P G A

Bsp120I (1296)

1201 AGTACACTTACCCAGCCAGTGTCCACACGATCCCAACACAGCAGCCAACTCCAGAACCAGCACTGCTCCAAGCACCTCCTTCTGCTCCCAATGGGC
 213▶ V H L P Q P V S T R S Q H T Q P T P E P S T A P S T S F L L P M G

SapI (1336)

1301 CCCAGCCCCCAGCTGAAGGGAGCACTGGCGACTTCGCTCTCCAGTTGGACTGATTGTGGGTGTGACAGCCTTGGGTCTACTAATAATAGGAGTGGTGA
 247▶ P S P P A E G S T G D F A L P V G L I V G V T A L G L L I I G V V

BspHI (1409) **Bsp120I (1497)**

1401 ACTGTGTCATCATGACCCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGAGAGAAGCAAGTGCCTCACTTGCCTGCCGATAAGCCCCGGGTACACAGGG
 280▶ N C V I M T Q V K K K P L C L Q R E A K V P H L P A D K A R G T Q G

BstXI (1565)

1501 CCCCAGCAGCAGCACCTGCTGATCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGAGAGCTCGGCCAGTGCCTTGGACAGAAGGGCGCCCACTCGGAAC
 313▶ P E Q Q H L L I T A P S S S S S S L E S S A S A L D R R A P T R N

PshAI (1689)
SanI (1687)

SrfI (1642) **NcoI (1683)**

1601 CAGCCACAGGCACCAGGCGTGGAGGCCAGTGGGGCCGGGAGGCCCGCCAGCACCGGGAGCTCAGATTCTTCCCCTGGTGGCCATGGGACCCAGGTCA
 347▶ Q P Q A P G V E A S G A G E A R A S T G S S D S S P G G H G T Q V

XcmI (1763)

1701 ATGTCACCTGCATCGTGAACGTCTGTAGCAGCTGTGACACAGCTCACAGTGTCTCCTCCAAGCCAGCTCCACAATGGGAGACACAGATTCCAGCCCCCTC
 380▶ N V T C I V N V C S S S D H S S Q C S S Q A S S T M G D T D S S P S
 1801 GGAGTCCCGAAGGACGAGCAGGTCCCTTCTCCAAGGAGGAATGTGCTTTTCGGTCCAGCTGGAGACGCCAGAGACCTGCTGGGAGCACCGAAGAG
 413▶ E S P K D E Q V P F S K E E C A F R S Q L E T P E T L L G S T E E

HpaI (1943) **NheI (1955)**

1901 AAGCCCCTGCCCTTGGAGTGCCTGATGCTGGGATGAAGCCAGTTAACCAGCCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAA
 447▶ K P L P L G V P D A G M K P S •

HpaI (2093)

2001 ACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAGTTAACA

MfeI (2104) **EcoRI (2189)**

2101 ACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATCTAAAA
▶

2201 TACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGC

SapI (2371)

2301 ATTAGCTGTTTGACGCTCACCTTCTTTTCATGGAGTTTAAAGATATAGTATTTTCCCAAGGTTTGAAGTGTCTTTCATTTCTTTATGTTTTAAATGCA

SspI (2428) **SwaI (2442)**

2401 CTGACCTCCACATTCCCTTTTTAGTAAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAGGCAGAATCCAGATGC

2501 TCAAGGCCCTTCATAATATCCCCAGTTTGTAGTGTGGACTTAGGGAACAAAGGAACCTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTT

2601 AGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGA
140 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 S

BstXI (2732)

2701 GATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCC
107 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 (2867)

2801 TTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTACGACACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCC
73 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 G

2901 CAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTG
40 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 Q

BbsI (3013)

XmnI (3009) AseI (3075)

3001 AGAGATGTTGAAGGCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATG
7 S I N F T K M

3101 GCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTCAATGGGGCGGAGTTG

SpeI (3230)

3201 TTACGACATTTTGAAAGTCCCCTGTTGATTTACTAGTCAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCT

SnaBI (3358)

3301 ATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATCGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCAT

NdeI (3463)

3401 GTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGCGTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTT

3501 TACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGG

SdaI (3641) PacI (3649) BspLU111 (3659)

3601 GCGGTCAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCCTGCAGGTTAATTAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAA
AAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCAAACCCGACAGGACTAT

3701 AAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCAAACCCGACAGGACTAT

3801 AAAGATACAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAG

ApaLI (3973)

3901 CGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGAC

4001 CGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGA

4101 GGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC

4201 CTTGGA AAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAA

PacI (4389) SmaI (4398)

4301 GGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACAT

EagI (4409)
NotI (4408)

4401 TTAATC AGCGGCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAA
4501 ACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA