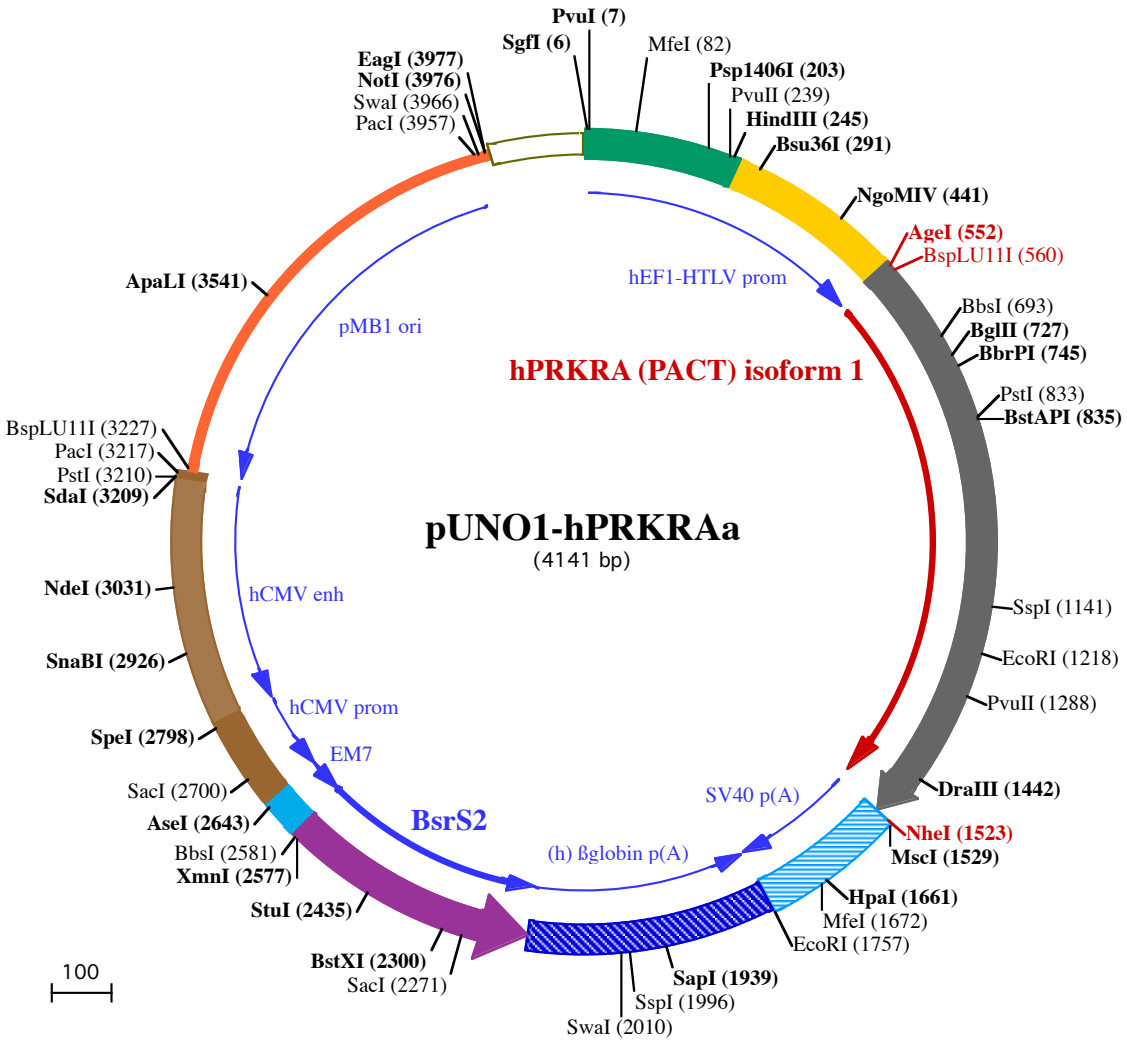
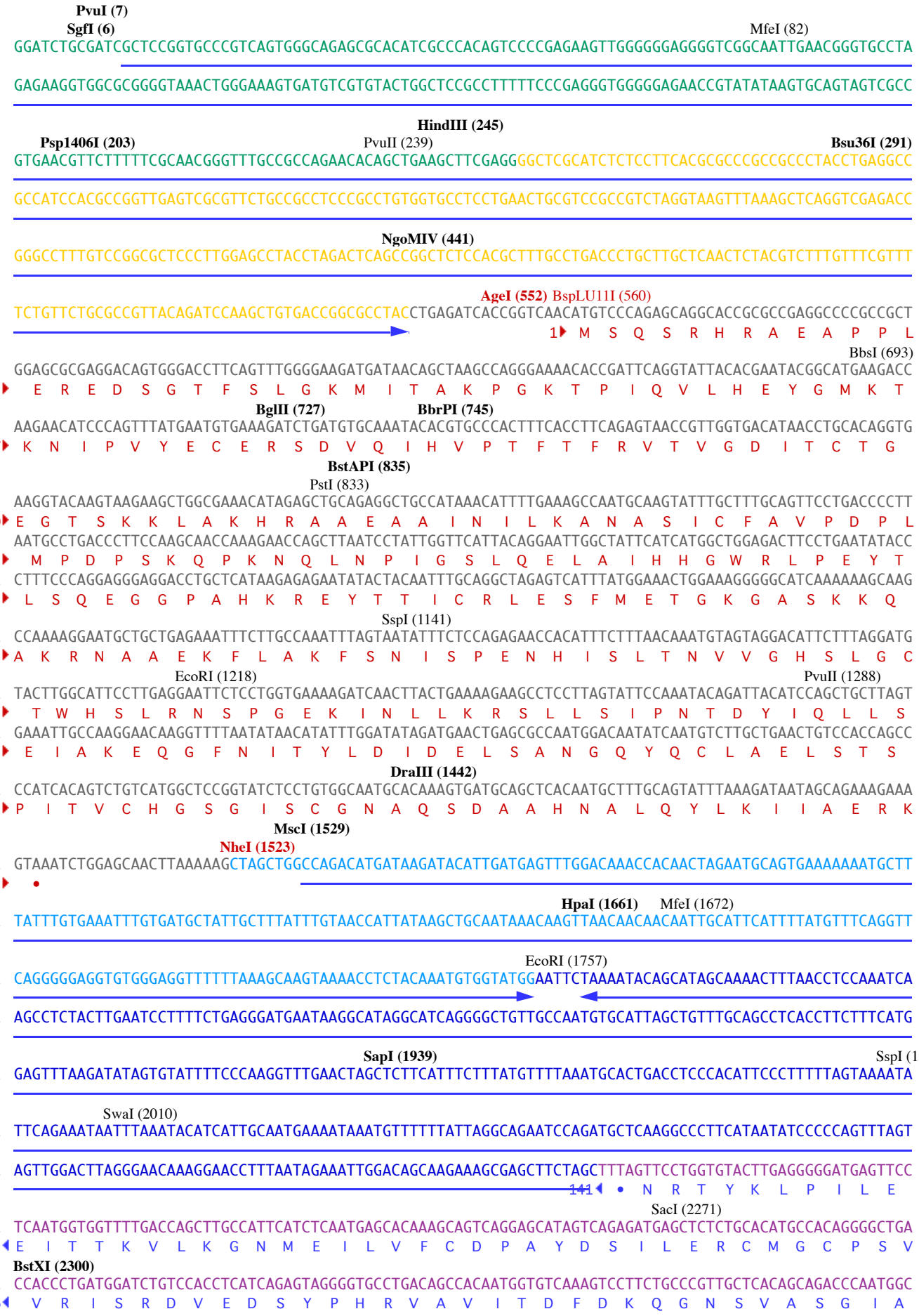
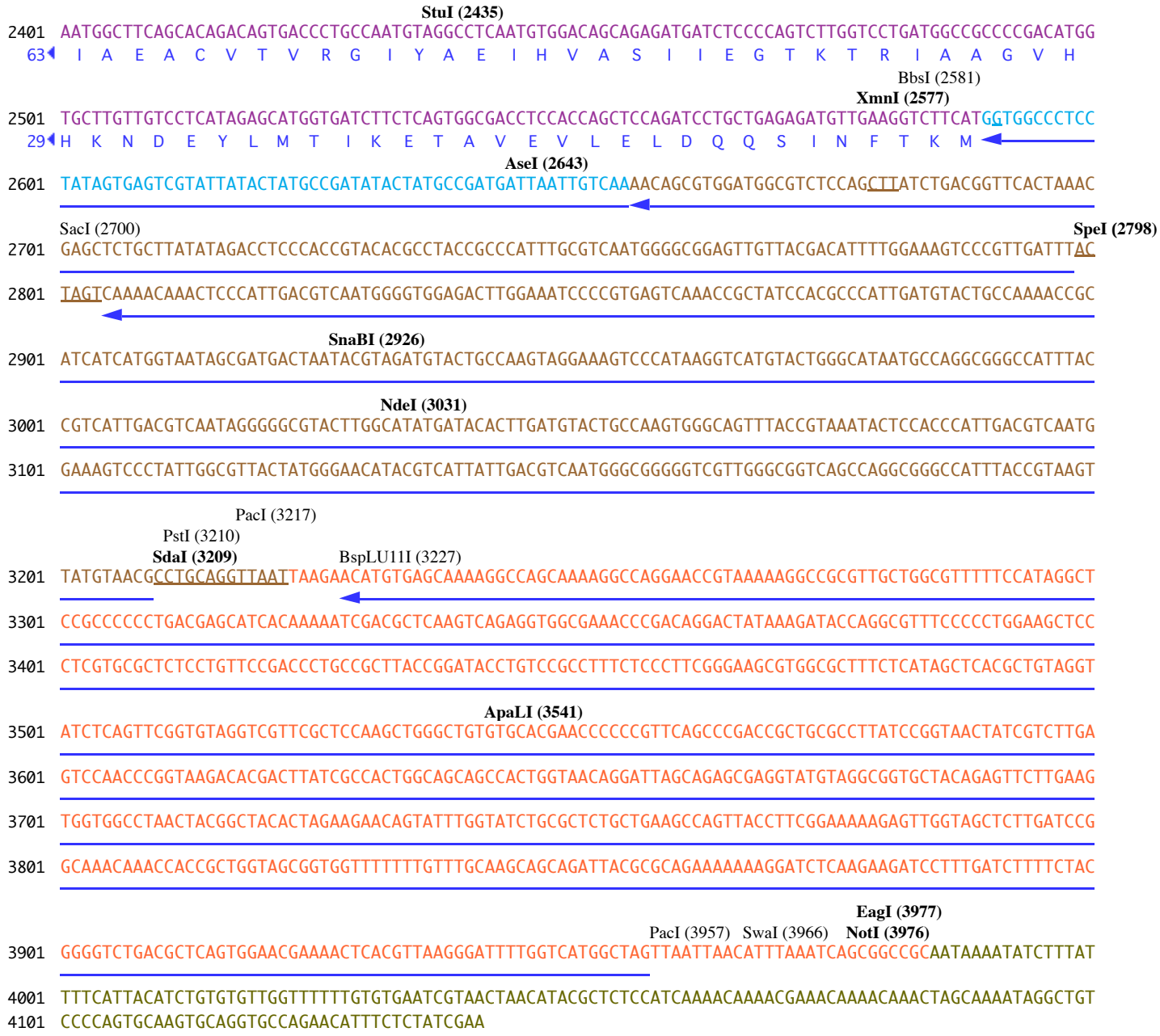

pUNO1-hPRKRAa
(4141 bp)
hPRKRA (PACT) isoform 1
PvuI (7)
SgfI (6)
MfeI (82)
Psp1406I (203)
PvuII (239)
HindIII (245)
Bsu36I (291)
NgoMIV (441)
AgeI (552)
BspLU11I (560)
BbsI (693)
BglII (727)
BbrPI (745)
PstI (833)
BstAPI (835)
SspI (1141)
EcoRI (1218)
PvuII (1288)
DraIII (1442)
NheI (1523)
MscI (1529)
HpaI (1661)
MfeI (1672)
EcoRI (1757)
SapI (1939)
SspI (1996)
SwaI (2010)
BstXI (2300)
SacI (2271)
StuI (2435)
BbsI (2581)
XmnI (2577)
AseI (2643)
SacI (2700)
SpeI (2798)
SnaBI (2926)
NdeI (3031)
BspLU11I (3227)
PacI (3217)
PstI (3210)
SdaI (3209)
ApaLI (3541)
EagI (3977)
NotI (3976)
SwaI (3966)
PacI (3957)
hEF1-HTLV prom
pMB1 ori
hCMV enh
hCMV prom
EM7
BsrS2
SV40 p(A)
(h) ßglobin p(A)
100


PvuI (7)
SgfI (6)
MfeI (82)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
HindIII (245)
Psp1406I (203)
PvuII (239)
Bsu36I (291)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTT
AgeI (552) BspLU11I (560)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAACATGTCCCAGAGCAGGCACCGCGCCGAGGCCCCGCCGCT
1 M S Q S R H R A E A P P L
BbsI (693)
601 GGAGCGCGAGGACAGTGGGACCTTCAGTTTGGGGAAGATGATAACAGCTAAGCCAGGGAAAACACCGATTCAGGTATTACACGAATACGGCATGAAGACC
13 E R E D S G T F S L G K M I T A K P G K T P I Q V L H E Y G M K T
BglII (727)
BbrPI (745)
701 AAGAACATCCCAGTTTATGAATGTGAAAGATCTGATGTGCAAATACACGTGCCCACTTTCACCTTCAGAGTAACCGTTGGTGACATAACCTGCACAGGTG
47 K N I P V Y E C E R S D V Q I H V P T F T F R V T V G D I T C T G
BstAPI (835)
PstI (833)
801 AAGGTACAAGTAAGAAGCTGGCGAAACATAGAGCTGCAGAGGCTGCCATAAACATTTTGAAAGCCAATGCAAGTATTTGCTTTGCAGTTCCTGACCCCTT
80 E G T S K K L A K H R A A E A A I N I L K A N A S I C F A V P D P L
901 AATGCCTGACCCTTCCAAGCAACCAAAGAACCAGCTTAATCCTATTGGTTCATTACAGGAATTGGCTATTCATCATGGCTGGAGACTTCCTGAATATACC
113 M P D P S K Q P K N Q L N P I G S L Q E L A I H H G W R L P E Y T
1001 CTTTCCCAGGAGGGAGGACCTGCTCATAAGAGAGAATATACTACAATTTGCAGGCTAGAGTCATTTATGGAAACTGGAAAGGGGGCATCAAAAAAGCAAG
147 L S Q E G G P A H K R E Y T T I C R L E S F M E T G K G A S K K Q
SspI (1141)
1101 CCAAAAGGAATGCTGCTGAGAAATTTCTTGCCAAATTTAGTAATATTTCTCCAGAGAACCACATTTCTTTAACAAATGTAGTAGGACATTCTTTAGGATG
180 A K R N A A E K F L A K F S N I S P E N H I S L T N V V G H S L G C
EcoRI (1218)
PvuII (1288)
1201 TACTTGGCATTCCTTGAGGAATTCTCCTGGTGAAAAGATCAACTTACTGAAAAGAAGCCTCCTTAGTATTCCAAATACAGATTACATCCAGCTGCTTAGT
213 T W H S L R N S P G E K I N L L K R S L L S I P N T D Y I Q L L S
1301 GAAATTGCCAAGGAACAAGGTTTTAATATAACATATTTGGATATAGATGAACTGAGCGCCAATGGACAATATCAATGTCTTGCTGAACTGTCCACCAGCC
247 E I A K E Q G F N I T Y L D I D E L S A N G Q Y Q C L A E L S T S
DraIII (1442)
1401 CCATCACAGTCTGTCATGGCTCCGGTATCTCCTGTGGCAATGCACAAAGTGATGCAGCTCACAATGCTTTGCAGTATTTAAAGATAATAGCAGAAAGAAA
280 P I T V C H G S G I S C G N A Q S D A A H N A L Q Y L K I I A E R K
MscI (1529)
NheI (1523)
1501 GTAAATCTGGAGCAACTTAAAAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAAAAAAATGCTT
313 •
HpaI (1661)
MfeI (1672)
1601 TATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTT
EcoRI (1757)
1701 CAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAACTTTAACCTCCAAATCA
1801 AGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATG
SapI (1939)
SspI (1996)
1901 GAGTTTAAGATATAGTGTATTTTCCCAAGGTTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTTAGTAAAATA
SwaI (2010)
2001 TTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCCAGTTTAGT
2101 AGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCC
141 • N R T Y K L P I L E
SacI (2271)
2201 TCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGA
129 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 P S V
BstXI (2300)
2301 CCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAATGGC
96 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 G I A


StuI (2435)
2401 AATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCCCGACATGG
63 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 A G V H
BbsI (2581)
XmnI (2577)
2501 TGCTTGTTGTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCC
29 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
AseI (2643)
2601 TATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAAC
SacI (2700)
SpeI (2798)
2701 GAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTAC
2801 TAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCATTGATGTACTGCCAAAACCGC
SnaBI (2926)
2901 ATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTAC
NdeI (3031)
3001 CGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATG
3101 GAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGT
PacI (3217)
PstI (3210)
SdaI (3209)
BspLU11I (3227)
3201 TATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCT
3301 CCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCC
3401 CTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGT
ApaLI (3541)
3501 ATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGA
3601 GTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAG
3701 TGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCG
3801 GCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC
EagI (3977)
PacI (3957)
SwaI (3966)
NotI (3976)
3901 GGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTAT
4001 TTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAAATAGGCTGT
4101 CCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA