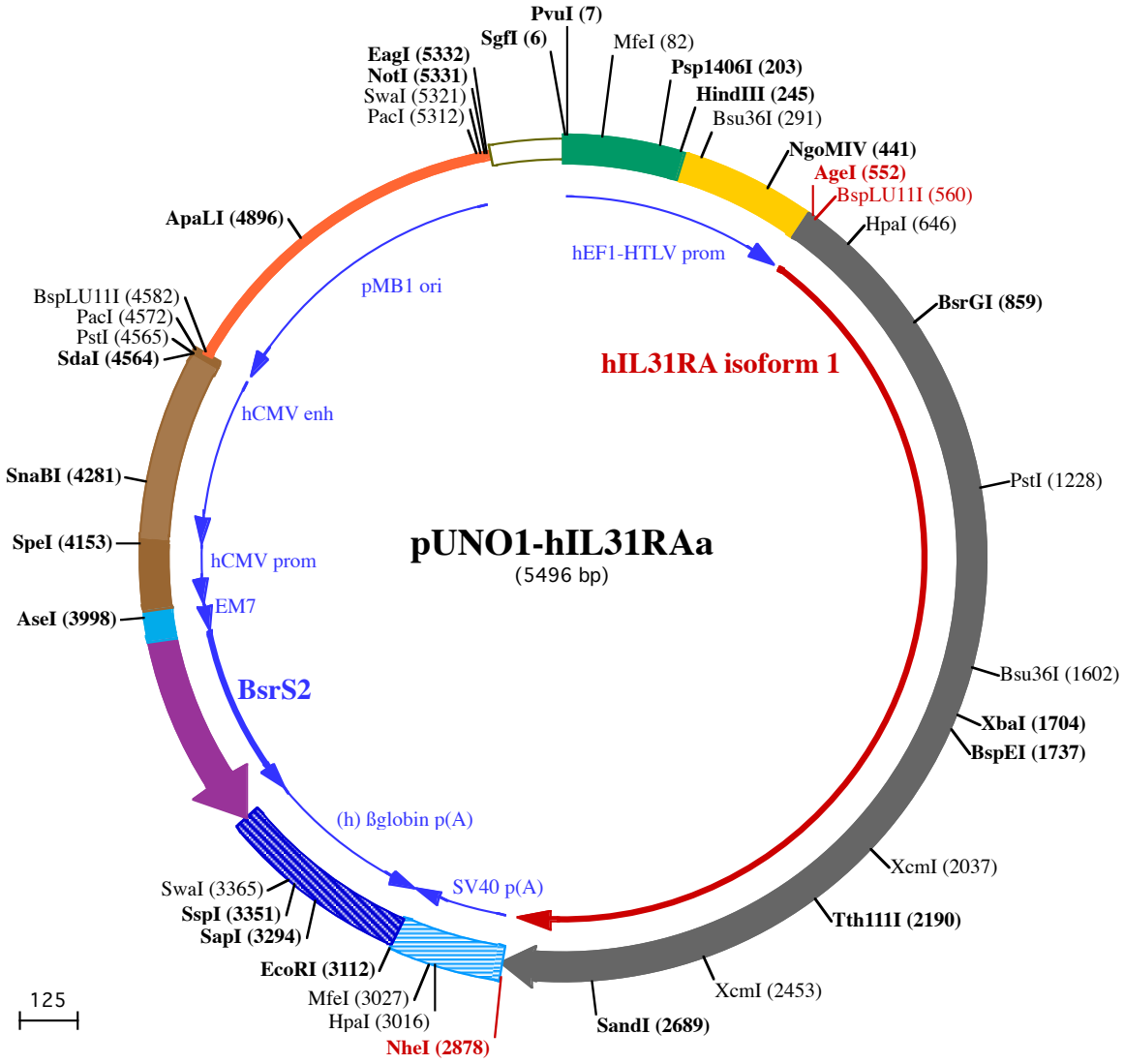
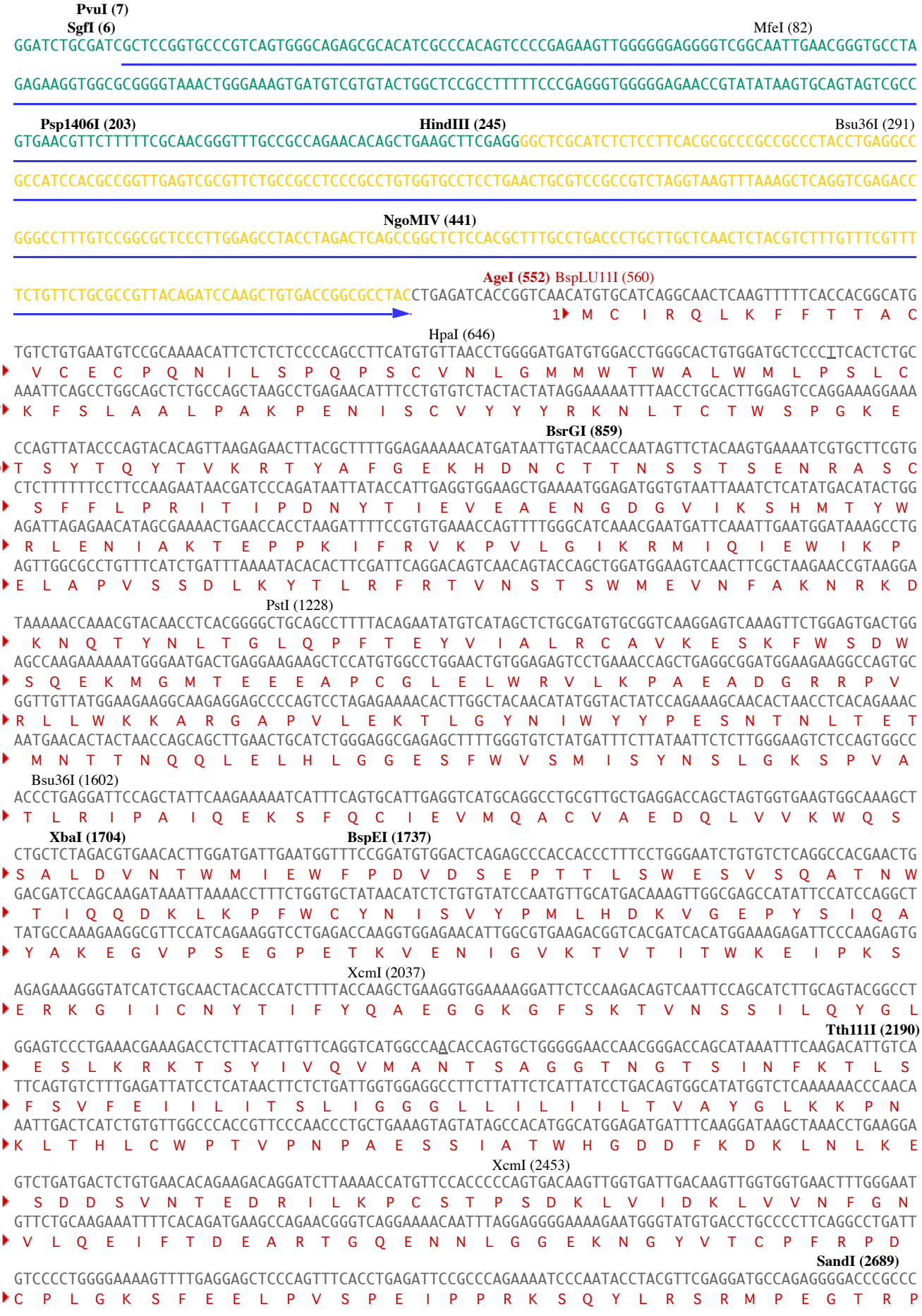
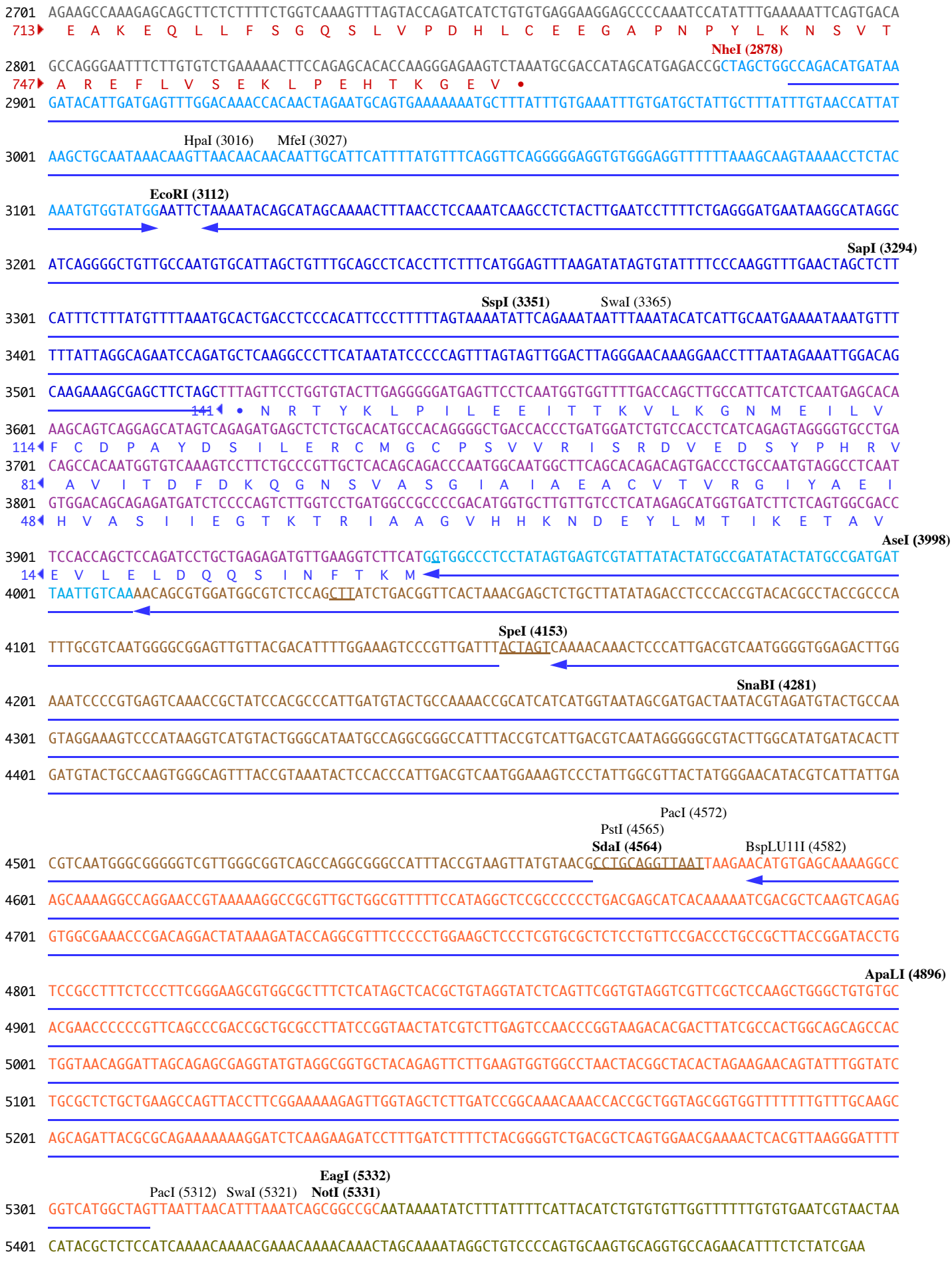

pUNO1-hIL31RAa
(5496 bp)
hIL31RA isoform 1
hEF1-HTLV prom
pMB1 ori
hCMV enh
hCMV prom
EM7
BsrS2
(h) ßglobin p(A)
SV40 p(A)
PvuI (7)
SgfI (6)
MfeI (82)
Psp1406I (203)
HindIII (245)
Bsu36I (291)
NgoMIV (441)
AgeI (552)
BspLU11I (560)
HpaI (646)
BsrGI (859)
PstI (1228)
Bsu36I (1602)
XbaI (1704)
BspEI (1737)
XcmI (2037)
Tth111I (2190)
XcmI (2453)
SandI (2689)
NheI (2878)
MfeI (3027)
HpaI (3016)
EcoRI (3112)
SwaI (3365)
SspI (3351)
SapI (3294)
AseI (3998)
SnaBI (4281)
SpeI (4153)
ApaLI (4896)
EagI (5332)
NotI (5331)
SwaI (5321)
PacI (5312)
BspLU11I (4582)
PacI (4572)
PstI (4565)
SdaI (4564)
125


PvuI (7)
SgfI (6)
MfeI (82)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
Psp1406I (203)
HindIII (245)
Bsu36I (291)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTT
AgeI (552) BspLU11I (560)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAACATGTGCATCAGGCAACTCAAGTTTTTCACCACGGCATG
1 M C I R Q L K F F T T A C
HpaI (646)
601 TGTCTGTGAATGTCCGCAAAACATTCTCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACCTGGGCACTGTGGATGCTCCCTTCACTCTGC
13 V C E C P Q N I L S P Q P S C V N L G M M W T W A L W M L P S L C
701 AAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGAACATTTCCTGTGTCTACTACTATAGGAAAAATTTAACCTGCACTTGGAGTCCAGGAAAGGAAA
47 K F S L A A L P A K P E N I S C V Y Y Y R K N L T C T W S P G K E
BsrGI (859)
801 CCAGTTATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAATTGTACAACCAATAGTTCTACAAGTGAAAATCGTGCTTCGTG
80 T S Y T Q Y T V K R T Y A F G E K H D N C T T N S S T S E N R A S C
901 CTCTTTTTTCCTTCCAAGAATAACGATCCCAGATAATTATACCATTGAGGTGGAAGCTGAAAATGGAGATGGTGTAATTAAATCTCATATGACATACTGG
113 S F F L P R I T I P D N Y T I E V E A E N G D G V I K S H M T Y W
1001 AGATTAGAGAACATAGCGAAAACTGAACCACCTAAGATTTTCCGTGTGAAACCAGTTTTGGGCATCAAACGAATGATTCAAATTGAATGGATAAAGCCTG
147 R L E N I A K T E P P K I F R V K P V L G I K R M I Q I E W I K P
1101 AGTTGGCGCCTGTTTCATCTGATTTAAAATACACACTTCGATTCAGGACAGTCAACAGTACCAGCTGGATGGAAGTCAACTTCGCTAAGAACCGTAAGGA
180 E L A P V S S D L K Y T L R F R T V N S T S W M E V N F A K N R K D
PstI (1228)
1201 TAAAAACCAAACGTACAACCTCACGGGGCTGCAGCCTTTTACAGAATATGTCATAGCTCTGCGATGTGCGGTCAAGGAGTCAAAGTTCTGGAGTGACTGG
213 K N Q T Y N L T G L Q P F T E Y V I A L R C A V K E S K F W S D W
1301 AGCCAAGAAAAAATGGGAATGACTGAGGAAGAAGCTCCATGTGGCCTGGAACTGTGGAGAGTCCTGAAACCAGCTGAGGCGGATGGAAGAAGGCCAGTGC
247 S Q E K M G M T E E E A P C G L E L W R V L K P A E A D G R R P V
1401 GGTTGTTATGGAAGAAGGCAAGAGGAGCCCCAGTCCTAGAGAAAACACTTGGCTACAACATATGGTACTATCCAGAAAGCAACACTAACCTCACAGAAAC
280 R L L W K K A R G A P V L E K T L G Y N I W Y Y P E S N T N L T E T
1501 AATGAACACTACTAACCAGCAGCTTGAACTGCATCTGGGAGGCGAGAGCTTTTGGGTGTCTATGATTTCTTATAATTCTCTTGGGAAGTCTCCAGTGGCC
313 M N T T N Q Q L E L H L G G E S F W V S M I S Y N S L G K S P V A
Bsu36I (1602)
1601 ACCCTGAGGATTCCAGCTATTCAAGAAAAATCATTTCAGTGCATTGAGGTCATGCAGGCCTGCGTTGCTGAGGACCAGCTAGTGGTGAAGTGGCAAAGCT
347 T L R I P A I Q E K S F Q C I E V M Q A C V A E D Q L V V K W Q S
XbaI (1704)
BspEI (1737)
1701 CTGCTCTAGACGTGAACACTTGGATGATTGAATGGTTTCCGGATGTGGACTCAGAGCCCACCACCCTTTCCTGGGAATCTGTGTCTCAGGCCACGAACTG
380 S A L D V N T W M I E W F P D V D S E P T T L S W E S V S Q A T N W
1801 GACGATCCAGCAAGATAAATTAAAACCTTTCTGGTGCTATAACATCTCTGTGTATCCAATGTTGCATGACAAAGTTGGCGAGCCATATTCCATCCAGGCT
413 T I Q Q D K L K P F W C Y N I S V Y P M L H D K V G E P Y S I Q A
1901 TATGCCAAAGAAGGCGTTCCATCAGAAGGTCCTGAGACCAAGGTGGAGAACATTGGCGTGAAGACGGTCACGATCACATGGAAAGAGATTCCCAAGAGTG
447 Y A K E G V P S E G P E T K V E N I G V K T V T I T W K E I P K S
XcmI (2037)
2001 AGAGAAAGGGTATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTGGAAAAGGATTCTCCAAGACAGTCAATTCCAGCATCTTGCAGTACGGCCT
480 E R K G I I C N Y T I F Y Q A E G G K G F S K T V N S S I L Q Y G L
Tth111I (2190)
2101 GGAGTCCCTGAAACGAAAGACCTCTTACATTGTTCAGGTCATGGCCAACACCAGTGCTGGGGGAACCAACGGGACCAGCATAAATTTCAAGACATTGTCA
513 E S L K R K T S Y I V Q V M A N T S A G G T N G T S I N F K T L S
2201 TTCAGTGTCTTTGAGATTATCCTCATAACTTCTCTGATTGGTGGAGGCCTTCTTATTCTCATTATCCTGACAGTGGCATATGGTCTCAAAAAACCCAACA
547 F S V F E I I L I T S L I G G G L L I L I I L T V A Y G L K K P N
2301 AATTGACTCATCTGTGTTGGCCCACCGTTCCCAACCCTGCTGAAAGTAGTATAGCCACATGGCATGGAGATGATTTCAAGGATAAGCTAAACCTGAAGGA
580 K L T H L C W P T V P N P A E S S I A T W H G D D F K D K L N L K E
XcmI (2453)
2401 GTCTGATGACTCTGTGAACACAGAAGACAGGATCTTAAAACCATGTTCCACCCCCAGTGACAAGTTGGTGATTGACAAGTTGGTGGTGAACTTTGGGAAT
613 S D D S V N T E D R I L K P C S T P S D K L V I D K L V V N F G N
2501 GTTCTGCAAGAAATTTTCACAGATGAAGCCAGAACGGGTCAGGAAAACAATTTAGGAGGGGAAAAGAATGGGTATGTGACCTGCCCCTTCAGGCCTGATT
647 V L Q E I F T D E A R T G Q E N N L G G E K N G Y V T C P F R P D
SandI (2689)
2601 GTCCCCTGGGGAAAAGTTTTGAGGAGCTCCCAGTTTCACCTGAGATTCCGCCCAGAAAATCCCAATACCTACGTTCGAGGATGCCAGAGGGGACCCGCCC
680 C P L G K S F E E L P V S P E I P P R K S Q Y L R S R M P E G T R P


NheI (2878)
HpaI (3016)
MfeI (3027)
EcoRI (3112)
SapI (3294)
SspI (3351)
SwaI (3365)
AseI (3998)
SpeI (4153)
SnaBI (4281)
PacI (4572)
PstI (4565)
SdaI (4564)
BspLU11I (4582)
ApaLI (4896)
EagI (5332)
PacI (5312)
SwaI (5321)
NotI (5331)