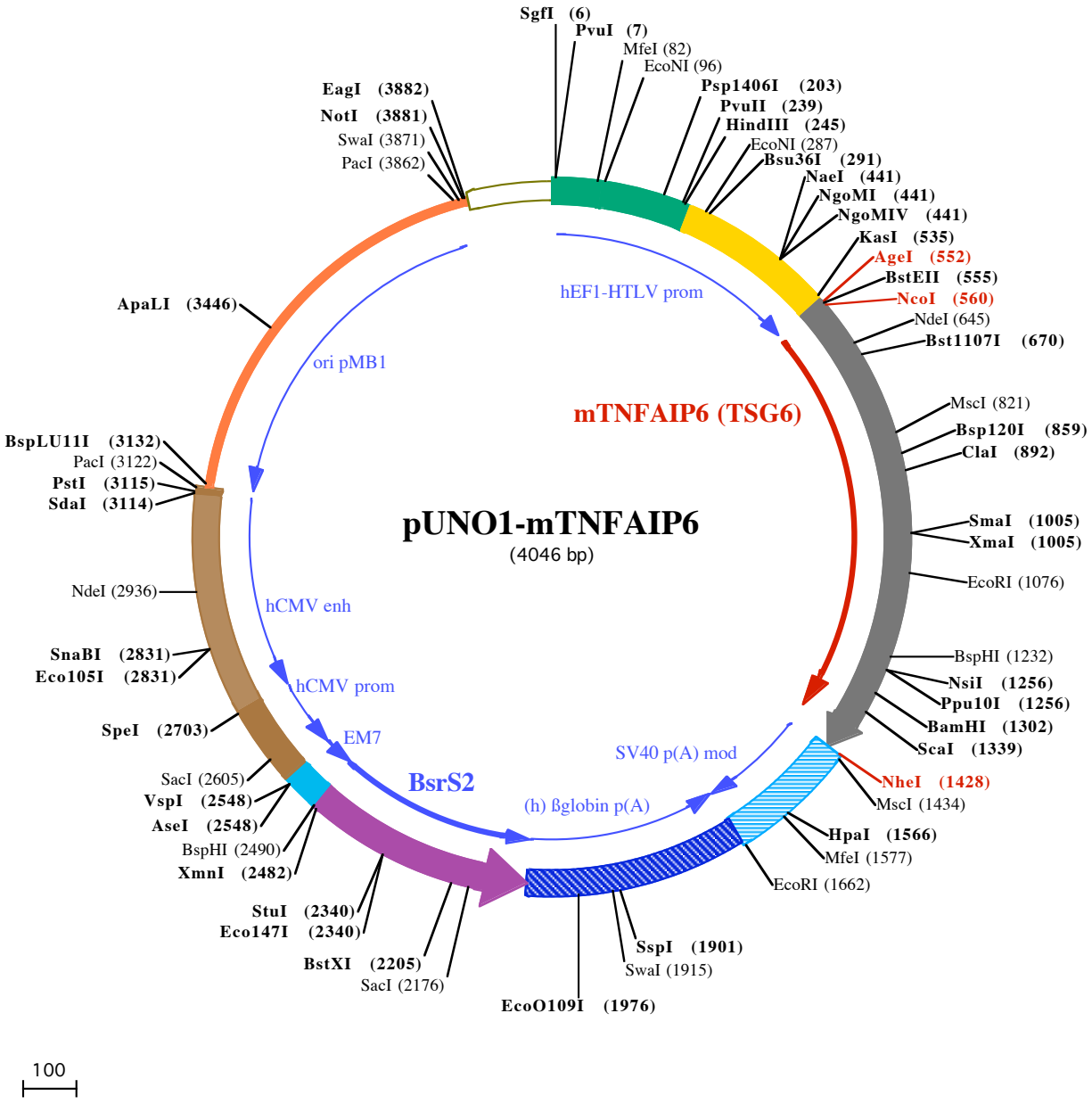
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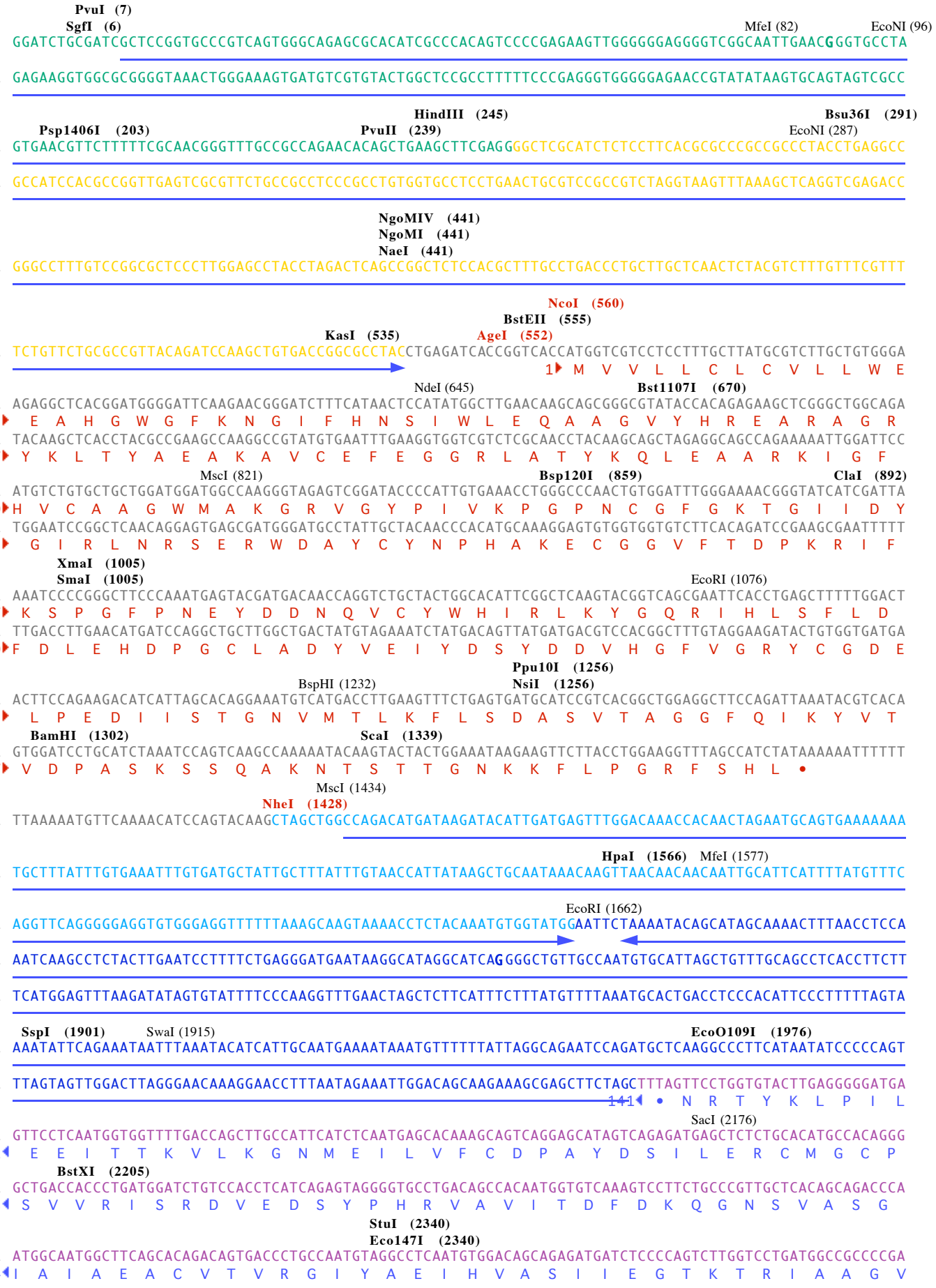
(4046 bp)
mTNFAIP6 (TSG6)
hEF1-HTLV prom
ori pMB1
hCMV enh
hCMV prom
EM7
BsrS2
SV40 p(A) mod
(h) ßglobin p(A)
SgfI (6)
PvuI (7)
MfeI (82)
EcoNI (96)
Psp1406I (203)
PvuII (239)
HindIII (245)
EcoNI (287)
Bsu36I (291)
NaeI (441)
NgoMI (441)
NgoMIV (441)
KasI (535)
AgeI (552)
BstEII (555)
NcoI (560)
NdeI (645)
Bst1107I (670)
MscI (821)
Bsp120I (859)
ClaI (892)
SmaI (1005)
XmaI (1005)
EcoRI (1076)
BspHI (1232)
NsiI (1256)
Ppu10I (1256)
BamHI (1302)
ScaI (1339)
NheI (1428)
MscI (1434)
HpaI (1566)
MfeI (1577)
EcoRI (1662)
SspI (1901)
SwaI (1915)
EcoO109I (1976)
BstXI (2205)
SacI (2176)
StuI (2340)
Eco147I (2340)
XmnI (2482)
BspHI (2490)
AseI (2548)
VspI (2548)
SacI (2605)
SpeI (2703)
Eco105I (2831)
SnaBI (2831)
NdeI (2936)
SdaI (3114)
PstI (3115)
PacI (3122)
BspLU11I (3132)
ApaLI (3446)
PacI (3862)
NotI (3881)
EagI (3882)
SwaI (3871)
100

InvivoGen


PvuI (7)
SgfI (6)
MfeI (82)
EcoNI (96)
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101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
HindIII (245)
Bsu36I (291)
Psp1406I (203)
PvuII (239)
EcoNI (287)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
NgoMIV (441)
NgoMI (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTT
NcoI (560)
BstEII (555)
KasI (535)
AgeI (552)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCACCATGGTCGTCCTCCTTTGCTTATGCGTCTTGCTGTGGGA
1 M V V L L C L C V L L W E
NdeI (645)
Bst1107I (670)
601 AGAGGCTCACGGATGGGGATTCAAGAACGGGATCTTTCATAACTCCATATGGCTTGAACAAGCAGCGGGCGTATACCACAGAGAAGCTCGGGCTGGCAGA
13 E A H G W G F K N G I F H N S I W L E Q A A G V Y H R E A R A G R
701 TACAAGCTCACCTACGCCGAAGCCAAGGCCGTATGTGAATTTGAAGGTGGTCGTCTCGCAACCTACAAGCAGCTAGAGGCAGCCAGAAAAATTGGATTCC
47 Y K L T Y A E A K A V C E F E G G R L A T Y K Q L E A A R K I G F
MscI (821)
Bsp120I (859)
ClaI (892)
801 ATGTCTGTGCTGCTGGATGGATGGCCAAGGGTAGAGTCGGATACCCCATTGTGAAACCTGGGCCCAACTGTGGATTTGGGAAAACGGGTATCATCGATTA
80 H V C A A G W M A K G R V G Y P I V K P G P N C G F G K T G I I D Y
901 TGGAATCCGGCTCAACAGGAGTGAGCGATGGGATGCCTATTGCTACAACCCACATGCAAAGGAGTGTGGTGGTGTCTTCACAGATCCGAAGCGAATTTTT
113 G I R L N R S E R W D A Y C Y N P H A K E C G G V F T D P K R I F
XmaI (1005)
SmaI (1005)
EcoRI (1076)
1001 AAATCCCCGGGCTTCCCAAATGAGTACGATGACAACCAGGTCTGCTACTGGCACATTCGGCTCAAGTACGGTCAGCGAATTCACCTGAGCTTTTTGGACT
147 K S P G F P N E Y D D N Q V C Y W H I R L K Y G Q R I H L S F L D
1101 TTGACCTTGAACATGATCCAGGCTGCTTGGCTGACTATGTAGAAATCTATGACAGTTATGATGACGTCCACGGCTTTGTAGGAAGATACTGTGGTGATGA
180 F D L E H D P G C L A D Y V E I Y D S Y D D V H G F V G R Y C G D E
Ppu10I (1256)
BspHI (1232)
NsiI (1256)
1201 ACTTCCAGAAGACATCATTAGCACAGGAAATGTCATGACCTTGAAGTTTCTGAGTGATGCATCCGTCACGGCTGGAGGCTTCCAGATTAAATACGTCACA
213 L P E D I I S T G N V M T L K F L S D A S V T A G G F Q I K Y V T
BamHI (1302)
ScaI (1339)
1301 GTGGATCCTGCATCTAAATCCAGTCAAGCCAAAAATACAAGTACTACTGGAAATAAGAAGTTCTTACCTGGAAGGTTTAGCCATCTATAAAAAATTTTTT
247 V D P A S K S S Q A K N T S T T G N K K F L P G R F S H L •
MscI (1434)
NheI (1428)
1401 TTAAAAATGTTCAAAACATCCAGTACAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAAAAAAA
HpaI (1566)
MfeI (1577)
1501 TGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTC
EcoRI (1662)
1601 AGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAACTTTAACCTCCA
1701 AATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTT
1801 TCATGGAGTTTAAGATATAGTGTATTTTCCCAAGGTTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTTAGTA
SspI (1901)
SwaI (1915)
EcoO109I (1976)
1901 AAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCCAGT
2001 TTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGA
1411 • N R T Y K L P I L
SacI (2176)
2101 GTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGG
131 E 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
BstXI (2205)
2201 GCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCA
98 S V 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
StuI (2340)
Eco147I (2340)
2301 ATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCCCGA
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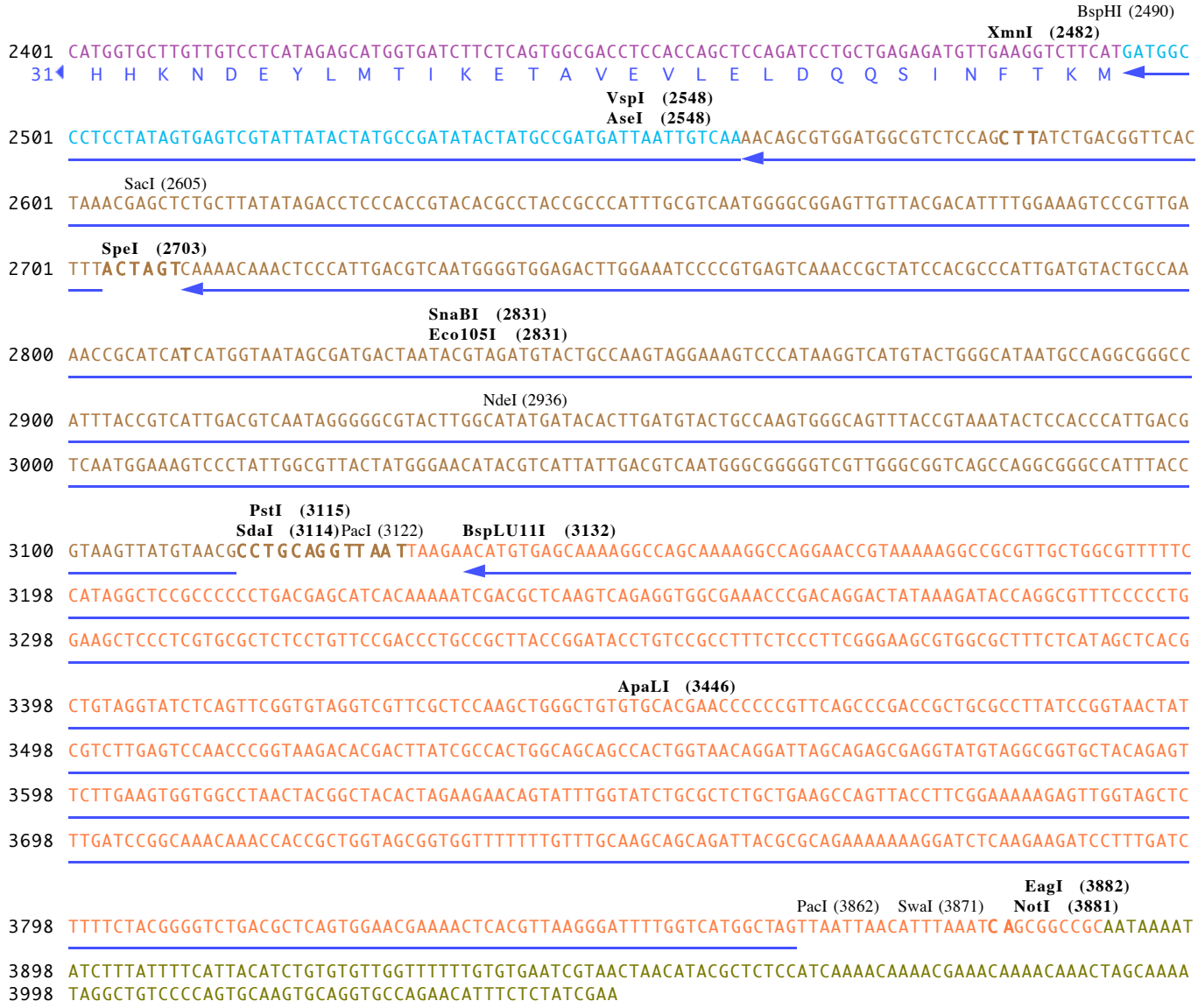
BspHI (2490)
XmnI (2482)
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31 H H K N D E Y L M T I K E T A V E V L E L D Q Q S I N F T K M
VspI (2548)
AseI (2548)
2501 CCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAACAGCGTGGATGGCGTCTCCAGCTTTATCTGACGGTTCAC
SacI (2605)
2601 TAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGA
SpeI (2703)
2701 TTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCATTGATGTACTGCCAA
SnaBI (2831)
Eco105I (2831)
2800 AACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCC
NdeI (2936)
2900 ATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACG
3000 TCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACC
PstI (3115)
SdaI (3114)
PacI (3122)
BspLU11I (3132)
3100 GTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTC
3198 CATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTG
3298 GAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACG
ApaLI (3446)
3398 CTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTAT
3498 CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGT
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3698 TTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATC
EagI (3882)
PacI (3862)
SwaI (3871)
NotI (3881)
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3898 ATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAAA
3998 TAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA