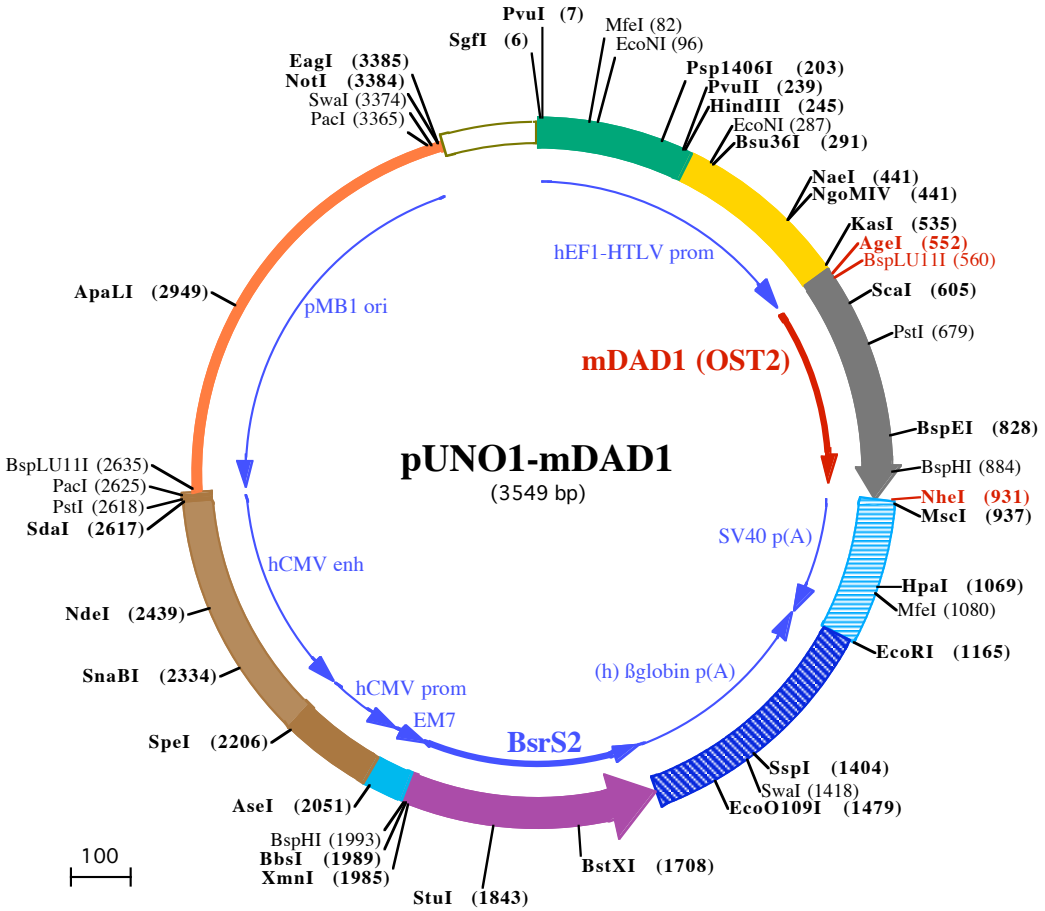
pUNO1-mDAD1
(3549 bp)
mDAD1 (OST2)
BsrS2
hEF1-HTLV prom
pMB1 ori
hCMV enh
hCMV prom
EM7
SV40 p(A)
(h) ßglobin p(A)
PvuI (7)
SgfI (6)
MfeI (82)
EcoNI (96)
Psp1406I (203)
PvuII (239)
HindIII (245)
EcoNI (287)
Bsu36I (291)
NaeI (441)
NgoMIV (441)
KasI (535)
AgeI (552)
BspLU11I (560)
ScaI (605)
PstI (679)
BspEI (828)
BspHI (884)
NheI (931)
MscI (937)
HpaI (1069)
MfeI (1080)
EcoRI (1165)
SspI (1404)
SwaI (1418)
EcoO109I (1479)
BstXI (1708)
StuI (1843)
BspHI (1993)
BbsI (1989)
XmnI (1985)
AseI (2051)
SpeI (2206)
SnaBI (2334)
NdeI (2439)
BspLU11I (2635)
PacI (2625)
PstI (2618)
SdaI (2617)
ApaLI (2949)
EagI (3385)
NotI (3384)
SwaI (3374)
PacI (3365)
100

InvivoGen

PvuI (7)
SgfI (6) MfeI (82) EcoNI (96)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

HindIII (245) Bsu36I (291)
Psp1406I (203) PvuII (239) EcoNI (287)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTT

BspLU11I (560)
KasI (535) AgeI (552)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAACATGTCGGCGTCTGTGGTGTCCGTCATCTCCCGGTTCCT
1 M S A S V V S V I S R F L

ScaI (605) PstI (679)
601 GGAGGAGTACTTGAGCTCCACTCCGCAGCGGCTGAAGTTGCTGGACGCCTATCTCCTTTATATACTGCTGACCGGGGCGCTGCAGTTCGGCTACTGTCTC
13 E E Y L S S T P Q R L K L L D A Y L L Y I L L T G A L Q F G Y C L
701 CTCGTGGGCACCTTCCCCTTCAACTCGTTCCTCTCTGGCTTCATCTCTTGTGTGGGCAGCTTCATCCTAGCGGTTTGCCTGAGAATACAGATCAACCCCC
47 L V G T F P F N S F L S G F I S C V G S F I L A V C L R I Q I N P

BspEI (828) BspHI (884)
801 AGAACAAGGCGGACTTCCAAGGCATCTCTCCGGAGCGAGCCTTTGCTGACTTCCTCTTTGCCAGCACGATCCTGCACCTTGTCGTCATGAACTTCGTTGG
80 Q N K A D F Q G I S P E R A F A D F L F A S T I L H L V V M N F V G

MscI (937)
NheI (931)
901 CTGAACTCCGTTTCCTTACCGTGGAGTTGGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAAAA
113 •

HpaI (1069) MfeI (1080)
1001 AAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGT

EcoRI (1165)
1101 TTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAACTTTAACCT

1201 CCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTT

1301 CTTTCATGGAGTTTAAGATATAGTGTATTTTCCCAAGGTTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTTA

SspI (1404) SwaI (1418) EcoO109I (1479)
1401 GTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCC

1501 AGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGA
141 • N R T Y K L P I
1601 TGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACA
132 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 I L E R C M G C

BstXI (1708)
1701 GGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGAC
99 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 K Q G N S V A S

StuI (1843)
1801 CCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCC
65 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 T K T R I A A G

BspHI (1993)
BbsI (1989)
XmnI (1985)
1901 CGACATGGTGCTTGTTGTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGAT
32 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 S I N F T K M

AseI (2051)
2001 GGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTT

2101 CACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGT

SpeI (2206)
2201 TGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCATTGATGTACTGC

SnaBI (2334)
2300 CAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGG

NdeI (2439)
2400 GCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTG

2500 ACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTT

PstI (2618)
SdaI (2617) PacI (2625) BspLU11I (2635)

2600 ACCGTAAGTTATGTAACG**CCTGCAGGTTAA**TTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTT

2698 TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCC

2798 CTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTC

ApaLI (2949)

2898 ACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAAC

2998 TATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAG

3098 AGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG

3198 CTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG

EagI (3385)
PacI (3365) SwaI (3374) **NotI (3384)**

3298 ATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAA

3398 AATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCA
3498 AAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA