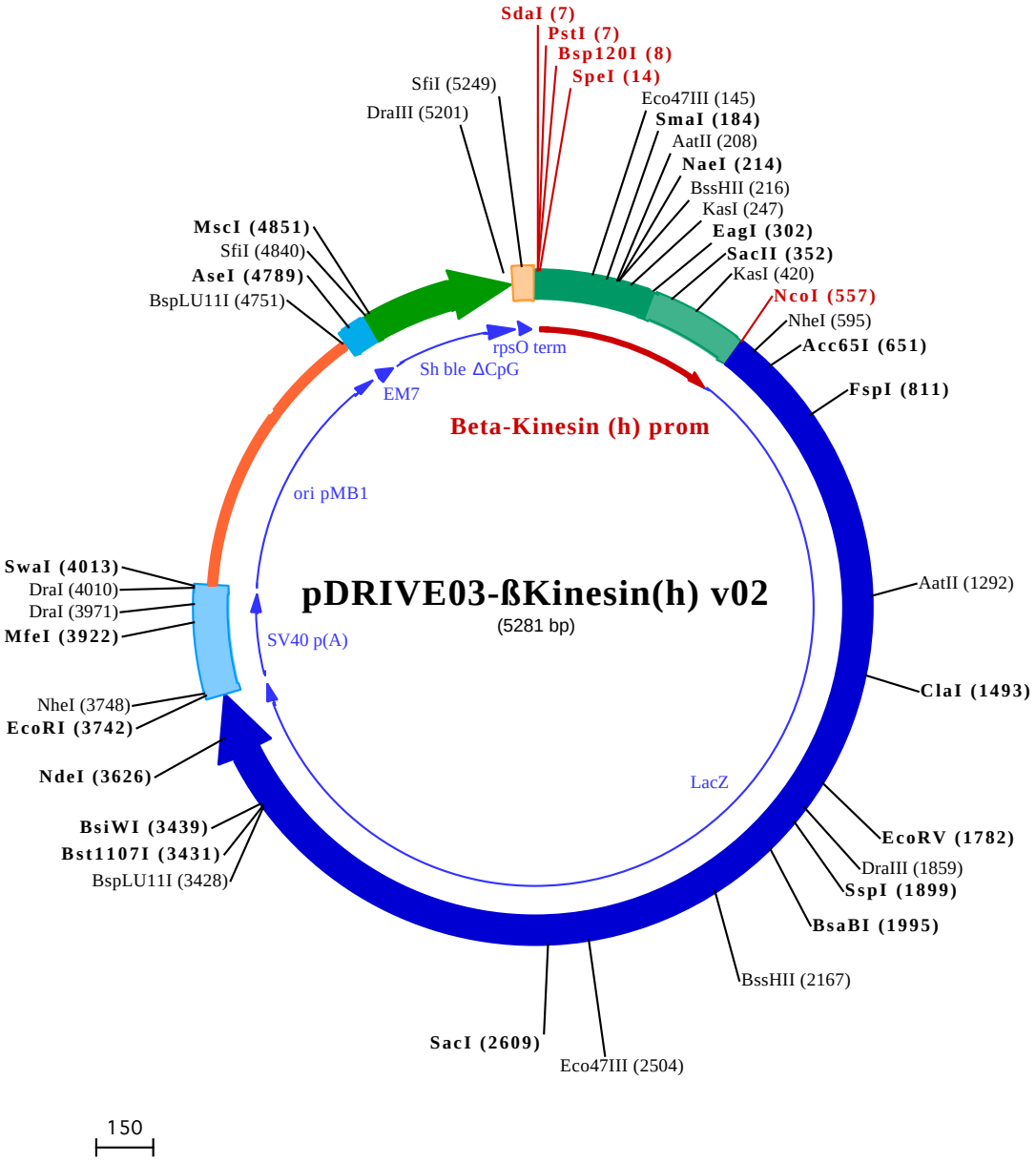
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KasI (420)
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rpsO term
Sh ble ΔCpG
EM7
Beta-Kinesin (h) prom
ori pMB1
pDRIVE03-ßKinesin(h) v02
(5281 bp)
SV40 p(A)
SwaI (4013)
DraI (4010)
DraI (3971)
MfeI (3922)
NheI (3748)
EcoRI (3742)
NdeI (3626)
BsiWI (3439)
Bst1107I (3431)
BspLU11I (3428)
AatII (1292)
ClaI (1493)
LacZ
EcoRV (1782)
DraIII (1859)
SspI (1899)
BsaBI (1995)
BssHII (2167)
SacI (2609)
Eco47III (2504)
150


Bsp120I (8)
PstI (7)
SdaI (7)
SpeI (14)
Eco47III (145)
SmaI (184)
BssHII (216)
AatII (208)
NaeI (214)
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EagI (302)
SacII (352)
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NcoI (557)
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AatII (1292)
ClaI (1493)
EcoRV (1782)
DraIII (1859)
SspI (1899)
BsaBI (1995)

BssHII (2167)

2101 GCCCGGTGCAGTATGAAGGCGGCGGAGCCGACACCACGGCCACCGATATTATTTGCCCGATGTACGCGCGCGTGGATGAAGACCAGCCCTTCCCGGCTGT

515 rgProValGlnTyrGluGlyGlyGlyAlaAspThrThrAlaThrAspI leI leCysProMetTyrAlaArgValAspGluAspGlnProPheProAlaVa
2201 GCCGAAATGGTCCATCAAAAAATGGCTTTCGCTACCTGGAGAGACGCGCCCGCTGATCCTTTGCGAATACGCCCACGCGATGGGTAACAGTCTTGGCGGT

548 lProLysTrpSerI leLysLysTrpLeuSerLeuProGlyGluThrArgProLeuI leLeuCysGluTyrAlaHisAlaMetGlyAsnSerLeuGlyGly
2301 TTCGCTAAATACTGGCAGGCGTTTCGTCAGTATCCCCGTTTACAGGGCGGCTTCGTCTGGGACTGGGTGGATCAGTCGCTGATTAAATATGATGAAAACG

582 PheAlaLysTyrTrpGlnAlaPheArgGlnTyrProArgLeuGlnGlyGlyPheValTrpAspTrpValAspGlnSerLeuI leLysTyrAspGluAsnG
2401 GCAACCCGTGGTCGGCTTACGGCGGTGATTTTGGCGATACGCCGAACGATCGCCAGTTCTGTATGAACGGTCTGGTCTTTGCCGACCGCACGCCGCATCC

615 lyAsnProTrpSerAlaTyrGlyGlyAspPheGlyAspThrProAsnAspArgGlnPheCysMetAsnGlyLeuValPheAlaAspArgThrProHisPr
Eco47III (2504)
2501 AGCGCTGACGGAAGCAAAACACCAGCAGCAGTTTTTCCAGTTCCGTTTATCCGGGCAAACCATCGAAGTGACCAGCGAATACCTGTTCCGTCATAGCGAT

648 oAlaLeuThrGluAlaLysHisGlnGlnGlnPhePheGlnPheArgLeuSerGlyGlnThrI leGluValThrSerGluTyrLeuPheArgHisSerAsp
SacI (2609)
2601 AACGAGCTCCTGCACTGGATGGTGGCGCTGGATGGTAAGCCGCTGGCAAGCGGTGAAGTGCCTCTGGATGTCGCTCCACAAGGTAAACAGTTGATTGAAC

682 AsnGluLeuLeuHisTrpMetValAlaLeuAspGlyLysProLeuAlaSerGlyGluValProLeuAspValAlaProGlnGlyLysGlnLeuI leGluL
2701 TGCCTGAACTACCGCAGCCGGAGAGCGCCGGGCAACTCTGGCTCACAGTACGCGTAGTGCAACCGAACGCGACCGCATGGTCAGAAGCCGGGCACATCAG

715 euProGluLeuProGlnProGluSerAlaGlyGlnLeuTrpLeuThrValArgValValGlnProAsnAlaThrAlaTrpSerGluAlaGlyHisI leSe
2801 CGCCTGGCAGCAGTGGCGTCTGGCGGAAAACCTCAGTGTGACGCTCCCCGCCGCGTCCCACGCCATCCCGCATCTGACCACCAGCGAAATGGATTTTTGC

748 rAlaTrpGlnGlnTrpArgLeuAlaGluAsnLeuSerValThrLeuProAlaAlaSerHisAlaI leProHisLeuThrThrSerGluMetAspPheCys
2901 ATCGAGCTGGGTAATAAGCGTTGGCAATTTAACCGCCAGTCAGGCTTTCTTTCACAGATGTGGATTGGCGATAAAAAACAACTGCTGACGCCGCTGCGCG

782 I leGluLeuGlyAsnLysArgTrpGlnPheAsnArgGlnSerGlyPheLeuSerGlnMetTrpI leGlyAspLysLysGlnLeuLeuThrProLeuArgA
3001 ATCAGTTCACCCGTGCACCGCTGGATAACGACATTGGCGTAAGTGAAGCGACCCGCATTGACCCTAACGCCTGGGTCGAACGCTGGAAGGCGGCGGGCCA

815 spGlnPheThrArgAlaProLeuAspAsnAspI leGlyValSerGluAlaThrArgI leAspProAsnAlaTrpValGluArgTrpLysAlaAlaGlyHi
3101 TTACCAGGCCGAAGCAGCGTTGTTGCAGTGCACGGCAGATACACTTGCTGATGCGGTGCTGATTACGACCGCTCACGCGTGGCAGCATCAGGGGAAAACC

848 sTyrGlnAlaGluAlaAlaLeuLeuGlnCysThrAlaAspThrLeuAlaAspAlaValLeuI leThrThrAlaHisAlaTrpGlnHisGlnGlyLysThr
3201 TTATTTATCAGCCGGAAAACCTACCGGATTGATGGTAGTGGTCAAATGGCGATTACCGTTGATGTTGAAGTGGCGAGCGATACACCGCATCCGGCGCGGA

882 LeuPheI leSerArgLysThrTyrArgI leAspGlySerGlyGlnMetAlaI leThrValAspValGluValAlaSerAspThrProHisProAlaArgI
3301 TTGGCCTGAACTGCCAGCTGGCGCAGGTAGCAGAGCGGGTAAACTGGCTCGGATTAGGGCCGCAAGAAAACTATCCCGACCGCCTTACTGCCGCCTGTTT

915 leGlyLeuAsnCysGlnLeuAlaGlnValAlaGluArgValAsnTrpLeuGlyLeuGlyProGlnGluAsnTyrProAspArgLeuThrAlaAlaCysPh
Bst1107I (3431)
BspLU11I (3428) **BsiWI (3439)**
3401 TGACCGCTGGGATCTGCCATTGTCAGACATGTATACCCCGTACGTCTTCCCGAGCGAAAACGGTCTGCGCTGCGGGACGCGCGAATTGAATTATGGCCCA

948 eAspArgTrpAspLeuProLeuSerAspMetTyrThrProTyrValPheProSerGluAsnGlyLeuArgCysGlyThrArgGluLeuAsnTyrGlyPro
3501 CACCAGTGGCGCGGCGACTTCCAGTTCAACATCAGCCGCTACAGTCAACAGCAACTGATGGAAACCAGCCATCGCCATCTGCTGCACGCGGAAGAAGGCA

982 HisGlnTrpArgGlyAspPheGlnPheAsnI leSerArgTyrSerGlnGlnGlnLeuMetGluThrSerHisArgHisLeuLeuHisAlaGluGluGlyT
NdeI (3626)
3601 CATGGCTGAATATCGACGGTTTCCATATGGGGATTGGTGGCGACGACTCCTGGAGCCCGTCAGTATCGGCGGAATTACAGCTGAGCGCCGGTCGCTACCA

1015 hrTrpLeuAsnI leAspGlyPheHisMetGlyI leGlyGlyAspAspSerTrpSerProSerValSerAlaGluLeuGlnLeuSerAlaGlyArgTyrHi
NheI (3748)
EcoRI (3742)
3701 TTACCAGTTGGTCTGGTGTCAAAAATAATAATCTAGTCGAGAATTCGCTAGCTCGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAA

1048 sTyrGlnLeuValTrpCysGlnLys•••
3801 TGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGC

MfeI (3922) DraI (3971)
3901 AATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTG

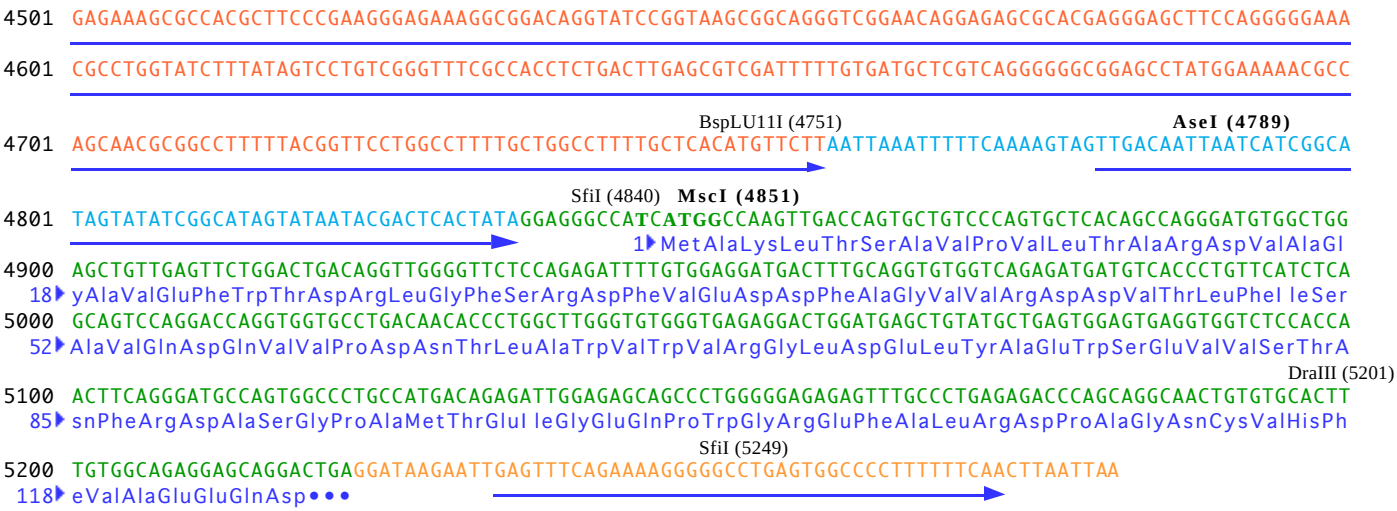
DraI (4010)
SwaI (4013)
4001 GTAGATCCATTTAAATGTTAATTAACTAGCCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGA

4101 TCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAA

4201 CTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC

4301 ACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCG

4401 GATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTAT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4601 CGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCC
BspLU11I (4751)
AseI (4789)
4701 AGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTAATTAAATTTTTCAAAAGTAGTTGACAATTAATCATCGGCA
SfiI (4840)
MscI (4851)
4801 TAGTATATCGGCATAGTATAATACGACTCACTATAGGAGGGCCATCATGGCCAAGTTGACCAGTGCTGTCCCAGTGCTCACAGCCAGGGATGTGGCTGG
1 MetAlaLysLeuThrSerAlaValProValLeuThrAlaArgAspValAlaGl
4900 AGCTGTTGAGTTCTGGACTGACAGGTTGGGGTTCTCCAGAGATTTTGTGGAGGATGACTTTGCAGGTGTGGTCAGAGATGATGTCACCCTGTTCATCTCA
18 yAlaValGluPheTrpThrAspArgLeuGlyPheSerArgAspPheValGluAspAspPheAlaGlyValValArgAspAspValThrLeuPheI leSer
5000 GCAGTCCAGGACCAGGTGGTGCCTGACAACACCCTGGCTTGGGTGTGGGTGAGAGGACTGGATGAGCTGTATGCTGAGTGGAGTGAGGTGGTCTCCACCA
52 AlaValGlnAspGlnValValProAspAsnThrLeuAlaTrpValTrpValArgGlyLeuAspGluLeuTyrAlaGluTrpSerGluValValSerThrA
DraIII (5201)
5100 ACTTCAGGGATGCCAGTGGCCCTGCCATGACAGAGATTGGAGAGCAGCCCTGGGGGAGAGAGTTTGCCCTGAGAGACCCAGCAGGCAACTGTGTGCACTT
85 snPheArgAspAlaSerGlyProAlaMetThrGlul leGlyGluGlnProTrpGlyArgGluPheAlaLeuArgAspProAlaGlyAsnCysValHisPh
SfiI (5249)
5200 TGTGGCAGAGGAGCAGGACTGAGGATAAGAATTGAGTTTCAGAAAAGGGGGCCTGAGTGGCCCCTTTTTTCAACTTAATTAA
118 eValAlaGluGluGlnAsp•••