



Posi.: pGL3 Control Vector  
(SV40 promoter)

Nega.: Empty Vector

APAF1: pGL4-phAPAF1 (RDB# 7316)

GADD45A: pGL4-phGADD45A (RDB# 7320)

**MKI67**: pGL4-phMKI67 (**RDB# 7323**)

TP53: pGL4-phTP53 (RDB#7330)

[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.02

1st Nucleotide Sequence

File Name : Reference Seq.gnu  
Sequence Size : 5661

2nd Nucleotide Sequence

File Name : RDB7323F.fasta  
Sequence Size : 527

Unit Size to Compare = 1  
Pick up Location = 1

[99.803% / 507 bp] INT/OPT.Score : < 1732/ 2012 >

```
1'          GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA
          *****
1" AGGTGCCAGA ACATTCTCT GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA

41' TAAAAGCGTG TTTAGGCTCC ATTCACTTCA CCCAGGTGG CCTACTGAGC CCACATGGCC
          *****
61" TAAAAGCGTG TTTAGGCTCC ATTCACTTCA CCCAGGTGG CCTACTGAGC CCACATGGCC

101' ACCAGCGCAA CTGAAGCAGA CCCCGATAGA ATCCTGTGTA GAATTATTTT AGGATTCACC
          *****
121" ACCAGCGCAA CTGAAGCAGA CCCCGATAGA ATCCTGTGTA GAATTATTTT AGGATTCACC

161' CATCTTGGCA TGCACAAGCC ATTTCAATTG AAGAATGTTT TCTAATAACA AACATTGTA
          *****
181" CATCTTGGCA TGCACAAGCC ATTTCAATTG AAGAATGTTT TCTAATAACA AACATTGTA

221' AACCTAAGTA TGTGGCAATA GTAATGATTA AGTAAATTAT GGTTTCCCGA AGCCCAGTGC
          *****
241" AACCTAAGTA TGTGGCAATA GTAATGATTA AGTAAATTAT GGTTTCCCGA AGCCCAGTGC
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281' TCTGCAGCCA TCAGAGAGTA AAAGCGAGAA TGTGTTTCAGT GGAGATAGCC TCAGGATATT
*****
301" TCTGCAGCCA TCAGAGAGTA AAAGCGAGAA TGTGTTTCAGT GGAGATAGCC TCAGGATATT

341' TAAAAGCAGA GAGCACAAAG TATAGAATCG TGTTGTGTAT GTTATGACCT TTTTTTCTGT
*****
361" TAAAAGCAGA GAGCACAAAG TATAGAATCG TGTTGTGTAT GTTATGACCT TTTTTTCTGT

401' GCTTTTAAAA AAGAGAATAC ACGTATAGC- AGGAAAAGAC ACACCAAACCT ACTTTATATA
*****
421" GCTTTTAAAA AAGAGAATAC ACGTATAGCA AGGAAAAGAC ACACCAAACCT ACTTTATATA

460' ATTGGTTGTT TTTGTGTTTG GTAAGATGTA TGCACTGAAG AGGAAGGTTT CGATTTTTTTT
*****
481" ATTGGTTGTT TTTGTGTTTG GTAAGATGTA TGCACTGAAG AGGAAGG

```

1st Nucleotide Sequence

File Name : Reference Seq. gnu  
Sequence Size : 5661

2nd Nucleotide Sequence

File Name : RDB7323R. fasta (Complementary)  
Sequence Size : 718

Unit Size to Compare = 1

Pick up Location = 1

[97.510% / 723 bp] INT/OPT. Score : < 2274/ 2687 >

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781' GGGATTACCG GCGTGAGCCA CCGCGTCCCG CCTGTTTTTA ATTTTATAGCA GTTTTAAATC
*** * * * *
1" CCCT GTTTATTTTA GAGTTTATC

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1441' GACTTTGGGT GCGACTTGAC ATCAAGATCT GGCCTCGGCG GCCAAGCTTG GCAATCCGGT  
\*\*\*\*\* \*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
616" GACTTTGGGT GCGACTT-AC ATCAAGATCT GGCCTCGGCG GCCAAGCTTG GCAATCCGGT

1501' ACTGTTGGTA AAGCCACCAT GGAAGATGCC AAAAACATTA AGAAGGGCCC AGCGCCATTC  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*  
675" ACTGTTGGTA AAGCCACCAT GGAAGATGCC AAAAACATTA AGAA