



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

XPC: pGL4-phXPC (RDB# 7351)

RELA: pGL4-phRELA (RDB# 7366)

DUSP1: pGL4-phDUSP1 (RDB# 7368)

EGR1: pGL4-phEGR1 (RDB#7369)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.06.04

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5407

2nd Nucleotide Sequence

File Name : RDB7368F.fasta
Sequence Size : 400

Unit Size to Compare = 1
Pick up Location = 1

[98.489% / 397 bp] INT/OPT. Score : < 782/ 1515 >

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1' GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA TTTTGCTTTC GGCCTATAAC
                                     ***** *****
64"                                     TTTTGCTTTC GGCCTATAAC

61' GGCCGCGACG ACAGGGAGCG AGGGTTGTGG CCGGCTT-CT GTTCCGGGTT GGAGGCCCC
   ***** ***** ***** ***** ** ***** *****
83" GGCCGCGACG ACAGGGAGCG AGGGTTGTGG CCGGCTTACT GTTCCGGGTT GGAGGCCCC

120' AGCCAGCGC TTAGTGGGCG CTCACTGTGT AACTGCCTA TTTGTATAAT AAAGAAAGG
   ***** ***** ***** ***** * ***** *****
143" AGCCAGCGC TTAGTGGGCG CTCACTGTGT AACTGCCTA TATGTATAAT AAAGAAAGG

180' ATGGAAGAGC TCAGTCTGGA GCCAAGGTGA CAGAAACGTG TCGGGCGGCC CCTGGGGGGC
   ***** ***** ***** ***** ***** *****
203" ATGGAAGAGC TCAGTCTGGA GCCAAGGTGA CAGAAACGTG TCGGGCGGCC CCTGGGGGGC

240' GCCGTCGAGT CGCGCTGCGG GTCGCCCTC ACCCTCAA ACGCAAACC CT-GGAATCC
   ***** ***** ***** ***** ***** ** *****
263" GCCGTCGAGT CGCGCTGCGG GTCGCCCTC ACCCTCAA ACGCAAACC CTGGGAATCC
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299' ACTGCGGGGC CTTGCGACCC CTCACGGGA TTTCAGCCCC CTGACCTGCC TCCCTT-GGC
*****
323" ACTGCGGGGC CTTGCGACCC CTCACGGGA TTTCAGCCCC CTGACCTGCC TCCCTTGGGC

358' TCCAAGTCTT CCGGGGGCCA CAAGACTAGG AATAGCATT TTTCCCGGTG GGAGTTTGCT
*****
383" TCCAAGTCTT CCGGGGGCCA CAAGACTAGG AATAGCATT TTTCCCGGTG GGAGTTTGCT

418' TGCTCACACT TT-CATGGCA AATGTAGATA TTTTAAAGCC ACCTTAAAGA AAAGTCTGGG
*****.*** ** *****
443" TGCTCNCAC TACATGGGC A

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Date : 2009.06.08

1st Nucleotide Sequence

File Name : Reference Seq. gnu
Sequence Size : 5407

2nd Nucleotide Sequence

File Name : RDB7368R. fasta (Complementary)
Sequence Size : 115

Unit Size to Compare = 1
Pick up Location = 1

[94.690% / 113 bp] INT/OPT. Score : < 344/ 402 >

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1081' TGATCACCAT TCAAACAAC A-CCCCCCT CCCCTGCGC GCGGGTCTGG CCGCCCCGT
**.* * *****
115" CCCANNC ACCCCCCCT CCCCTGCGC GCGGGTCTGG CCGCCCCGT

1140' CCCCAGAGG CCGCATATAA ACGCGCTCCC CGGGCCAGGC TCGTGCGAA G-GACATTTG
***** * *****

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162" CCCCAGAGG CCGCATATTA ACGCGCTCCC CGGGCCAGGC TCGCTGCGTA GTGACATTTG

1199' GGCTGTGTAT CAAGATCTGG CCTCGGCGGC CAAGCTTGGC AATCCGGTAC TGTGGTAAA

222" GGCTGTGT