



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

ANTXR1: pGL4-phANTXR1 (RDB# 7333)

BCL2L1: pGL4-phBCL2L1 (RDB# 7335)

CASP1: pGL4-phCASP1 (RDB# 7338)

DKK1: pGL4-phDKK1 (RDB#7341)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.03.02

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5411

2nd Nucleotide Sequence

File Name : RDB7338F.fasta
Sequence Size : 664

Unit Size to Compare = 1
Pick up Location = 1

[99.844% / 643 bp] INT/OPT. Score : < 2566/ 2566 >

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1'          GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA
          *****
1" GGTGCCAGAA CATGTACTCT GGCCTAACTG GCCGGTACCT GAGCTCGCTA GCCTCGAGGA

41' TAGATGCACT GCTTGAGGAT TCTAACAAAA GATAAACTTA GCTAAATAAT CTGCAAATAA
          *****
61" TAGATGCACT GCTTGAGGAT TCTAACAAAA GATAAACTTA GCTAAATAAT CTGCAAATAA

101' TCATCCTGA TTATTTTCT AACCTTAAAC ATTTGTATTA ATTATAATAA TATCACTCAT
          *****
121" TCATCCTGA TTATTTTCT AACCTTAAAC ATTTGTATTA ATTATAATAA TATCACTCAT

161' TATTTGCTTA CCATTTGCCA GGCTATGTTT CATGCATTTT CCACATTTTC TCTCACTTAA
          *****
181" TATTTGCTTA CCATTTGCCA GGCTATGTTT CATGCATTTT CCACATTTTC TCTCACTTAA

221' TGCTCAAAC TGTGTAGGTA CATACTATTA ATAAAATTAT TTCACATACA GAGGAACCAA
          *****
241" TGCTCAAAC TGTGTAGGTA CATACTATTA ATAAAATTAT TTCACATACA GAGGAACCAA
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281' TGCATAGGGA AGTTCATTAT CTTGCCAAGG AAGGGAAGTT TAAAATGCTA AGTTCGACAT
*****
301" TGCATAGGGA AGTTCATTAT CTTGCCAAGG AAGGGAAGTT TAAAATGCTA AGTTCACAT

341' TCTCATTCCA GAGCCTATGC TCTGGGCTC TACAATGCAA TTTCCCTCAA AAATAAACCC
*****
361" TCTCATTCCA GAGCCTATGC TCTGGGCTC TACAATGCAA TTTCCCTCAA AAATAAACCC

401' TCCAGGATGG GTGGGTGGCT CATGCCTGTA ATCCTAGCAA TTTGGGAGAC CAAGGTGGGC
*****
421" TCCAGGATGG GTGGGTGGCT CATGCCTGTA ATCCTAGCAA TTTGGGAGAC CAAGGTGGGC

461' ACATTGCTTG AGCCTGGGAG CTGAAGACAA GCCTAGGAAA CACAAGGAGA CCCTGTCTTT
*****
481" ACATTGCTTG AGCCTGGGAG CTGAAGACAA GCCTAGGAAA CACAAGGAGA CCCTGTCTTT

521' ACAAGAGATA CAAATATTAG CTGGCCATGG TGGCATGTGC CAGTAATTGC AGCTACTCGG
*****
541" ACAAGAGATA CAAATATTAG CTGGCCATGG TGGCATGTGC CAGTAATTGC AGCTACTCGG

581' GAGGCTGAGT TGGAAGAATC ATCTGAGCCT GGGAAGTGA GGCTGCAGTG AGCCAAGGTC
*****
601" GAGGCTGAGT TGGAAGAATC ATCTGAGCCT GGGAAGTGA GGCTGCAGTG AGCCAAGGTC

641' AAATAACTGC ATTCCGGCCT GCACGACAGA ATGATACCCT GTATCAGAAA AAAAAAAAAA
***
661" AAAA

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1st Nucleotide Sequence

File Name : Reference Seq. gnu
Sequence Size : 5411

2nd Nucleotide Sequence

File Name : RDB7338R. fasta (Complementary)
Sequence Size : 710



Unit Size to Compare = 1

Pick up Location = 1

[96.897% / 709 bp] INT/OPT. Score : < 2424/ 2626 >

601' ATCTGAGCCT -GGGAAGTGG AGGCTGCAGT GAGCCAAGG- TCAAATAACT GCATTCCGG-

***** **

1" AGAGCCT GGGGAGGTGG AGGCTGCAGT GAGCCCAGGT TCAAATAACT GCATTCCGGC

658' CCTGCACGAC AGAATGATA- CCCTGTATCA G----- ----AAA AAAAAAAAAAC

***** * ****

58" CCTGCACGAC AGAATGATAC CCCTGTATCA GAAAAAAAA AAAAAAAAA AAAAAAAAAAC

702' AGAAAGAAAA AAGCAATGTG AAAAGAAGGA CATTAAATAA GAAAAGCTTT AATTCTGGTG

***** *

118" AGAAAGAAAA AAGCAATGTG AAAAGAAGAA CATTAAATAA GAAAAGCTTT AATTCTGGTG

762' AAAAATGTTT CTATTTCTTA AAGCAAAAAT GTTTCACAGG GACATACATT ACCCACAAC

178" AAAAATGTTT CTATTTCTTA AAGCAAAAAT GTTTCACAGG GACATACATT ACCCACAAC

822' TTCCAAGAG CTATGAGGTG GGGTCAGGGG AACAGTGGT CACATACTCC AAAGTTGTG

238" TTCCAAGAG CTATGAGGTG GGGTCAGGGG AACAGTGGT CACATACTCC AAAGTTGTG

882' TTACTTTTCT CCGTCAAGCT TTCTAATGAT TGAGAACTC TTCACTGTGT GAATTTAATT

298" TTACTTTTCT CCGTCAAGCT TTCTAATGAT TGAGAACTC TTCACTGTGT GAATTTAATT

942' GTACACATAC TTTTCAATC CTGTCTTACT CTCCAAGCCC CATTCCCCTC CTACCCTGAT

358" GTACACATAC TTTTCAATC CTGTCTTACT CTCCAAGCCC CATTCCCCTC CTACCCTGAT

1002' CTATCCAAGG GCTGGTGAAG AAAATTTCCC ATGGATACAC TACCTGATGC AGGCTACAGT

418" CTATCCAAGG GCTGGTGAAG AAAATTTCCC ATGGATACAC TACCTGATGC AGGCTACAGT



1062' TCTGATTCTT TAATGGGAAG AAAAATAAAG ACATGCATAT GCATGCACAG TGAGTATTTT

 478" TCTGATTCTT TAATGGGAAG AAAAATAAAG ACATGCATAT GCATGCACAG TGAGTATTTT

1122' CCAATACATG TACAGGCCCT GCCAAAAAGG AAGGCGAAGC ATACTTTCAG TTTCAGTCAC

 538" CCAATACATG TACAGGCCCT GCCAAAAAGG AAGGCGAAGC ATACTTTCAG TTTCAGTCAC

1182' ACAAGAAGGG AGGAGAGAAA AGCCATGGCA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG

 598" ACAAGAAGGG AGGAGAGAAA AGCCATGGCA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG

1242' CAATCCGGTA CTGTTGGTAA AGCCACCATG GAAGATGCCA AAAACATTAA GAAGGCCCA

 658" CAATCCGGTA CTGTTGGTAA AGCCACCATG GAAGATGCCA AAAACATTAA GAA