



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 : 5456

2nd Nucleotide Sequence

File Name : RDB7335F.fasta
Sequence Size : 501

Unit Size to Compare = 1
Pick up Location = 1

[100.000% / 478 bp] INT/OPT.Score : < 1912/ 1912 >

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1'          GGCCTAA CTGGCCGGTA CCTGAGCTCG CTAGCCTCGA
          *****
1" TGCAGGTGCC AGAACATTTT TCTGGCCTAA CTGGCCGGTA CCTGAGCTCG CTAGCCTCGA

38' GGATTCCTGA TGCCAGTCAC TCAAGGCGCG CACTCCCTTT GCGTCTCGGG CTCGCGCGCG
          *****
61" GGATTCCTGA TGCCAGTCAC TCAAGGCGCG CACTCCCTTT GCGTCTCGGG CTCGCGCGCG

98' TTGCCGCGGC ACCGGAAGTG ACTGAGCTTG CAAGTTCCCC TGTCTTTCA GGGGAACTG
          *****
121" TTGCCGCGGC ACCGGAAGTG ACTGAGCTTG CAAGTTCCCC TGTCTTTCA GGGGAACTG

158' AGGCCGGCTT GTTCGGGAGA GACGGCGCGA GCAGTCAGCC AGGTAGGCCG GCAGCCAGGT
          *****
181" AGGCCGGCTT GTTCGGGAGA GACGGCGCGA GCAGTCAGCC AGGTAGGCCG GCAGCCAGGT

218' AGGCCGGCCC GGGTCCGCGG CGCGGAACTC GGCCGCGAAG AGCTCTTGCG TCTGGAAGCT
          *****
241" AGGCCGGCCC GGGTCCGCGG CGCGGAACTC GGCCGCGAAG AGCTCTTGCG TCTGGAAGCT
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278' ACCGGGCCGA TGAAGGGGA TGTGGCCCC CACGGCTCGC GGGGCTCGCA GGTGAGAGCG
*****
301" ACCGGGCCGA TGAAGGGGA TGTGGCCCC CACGGCTCGC GGGGCTCGCA GGTGAGAGCG

338' CCGCCTCCCC TGTGCGTGAC AGCCGTTGCG CCCAATAGGA GCCTTCGCCG TCCCGCTTCC
*****
361" CCGCCTCCCC TGTGCGTGAC AGCCGTTGCG CCCAATAGGA GCCTTCGCCG TCCCGCTTCC

398' GTGCCGGCTG GGCTCGCTGA TTGGCTGCGC TGGGGCGGAC CGCCGGGGGC GAGGCCCTC
*****
421" GTGCCGGCTG GGCTCGCTGA TTGGCTGCGC TGGGGCGGAC CGCCGGGGGC GAGGCCCTC

458' CTCTCAGGAA GGTCTAGGGG GCGCCCCCGG GGGAGGGCGG TTGCCTAGCA ACGGGGCGGT
*****
481" CTCTCAGGAA GGTCTAGGGG G

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1st Nucleotide Sequence

File Name : Reference Seq. gnu
Sequence Size : 5456

2nd Nucleotide Sequence

File Name : RDB7335R. fasta (Complementary)
Sequence Size : 447

Unit Size to Compare = 1

Pick up Location = 1

[100.000% / 447 bp] INT/OPT. Score : < 1788/ 1788 >

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841' AGAGCAAACC AGCGGCATTT GTTGGGGGTC TCCGGCCTTC AACATCACAG ACAGGCCTGG
*****
1" GGCCTGG

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901' GGGTGGCCTT CCCAAAGTCA GATTGCAGAT CTGAGGCAGT TTCCCCTCC CTGGTCCCT

 8" GGGTGGCCTT CCCAAAGTCA GATTGCAGAT CTGAGGCAGT TTCCCCTCC CTGGTCCCT

961' CACTGAAACC TTGAACCCCA TTGAGAAGTC CCTTTAGGGT TTCGGACGCC TCCACCTCAC

 68" CACTGAAACC TTGAACCCCA TTGAGAAGTC CCTTTAGGGT TTCGGACGCC TCCACCTCAC

1021' CCTGGGCTGG TGCTTAAATA GAAAAAAGAA AAACAAAAC CAACTAAATC CATACCAGCC

 128" CCTGGGCTGG TGCTTAAATA GAAAAAAGAA AAACAAAAC CAACTAAATC CATACCAGCC

1081' ACCTCCGGGA GAGTACTCCT GGCTCCAGT AGGAGGCGGA GAGCCAAGGG GCGTGCAAGA

 188" ACCTCCGGGA GAGTACTCCT GGCTCCAGT AGGAGGCGGA GAGCCAAGGG GCGTGCAAGA

1141' GAGAGGGGGC TGGGCTCCCG GGTGGCAGGA GGCCGCGGCT GCGGAGCGGC CGCCCTCGAT

 248" GAGAGGGGGC TGGGCTCCCG GGTGGCAGGA GGCCGCGGCT GCGGAGCGGC CGCCCTCGAT

1201' CCGGGCGATG GAGGAGGAAG CAAGCGAGGG GGCTGGTTC TGAGCTTCGC AATTCATCAA

 308" CCGGGCGATG GAGGAGGAAG CAAGCGAGGG GGCTGGTTC TGAGCTTCGC AATTCATCAA

1261' GATCTGGCCT CGGCGGCCAA GCTTGGCAAT CCGGTACTGT TGGTAAAGCC ACCATGGAAG

 368" GATCTGGCCT CGGCGGCCAA GCTTGGCAAT CCGGTACTGT TGGTAAAGCC ACCATGGAAG

1321' ATGCCAAAA CATTAGAAG GGCCAGCGC CATTCTACC ACTCGAAGAC GGGACCGCG

 428" ATGCCAAAA CATTAGAAG