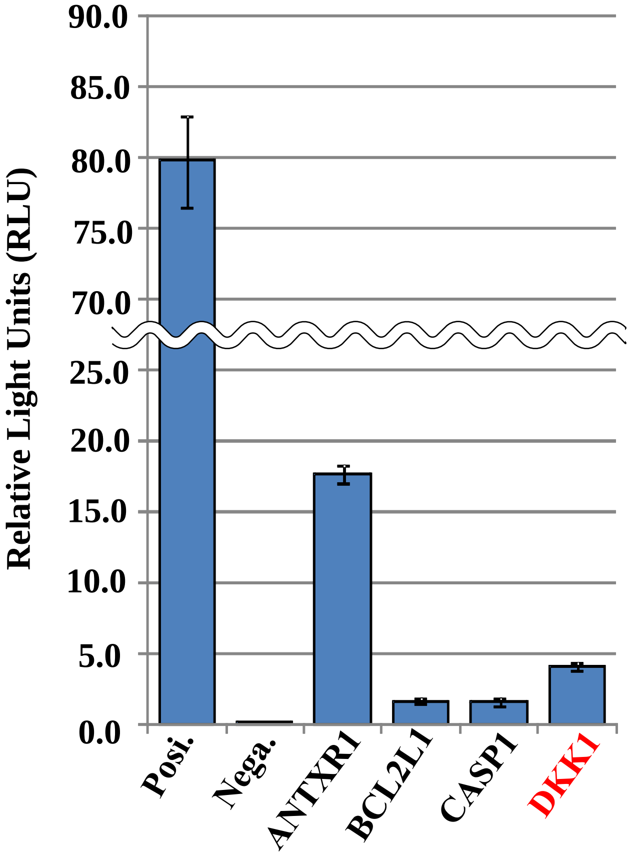
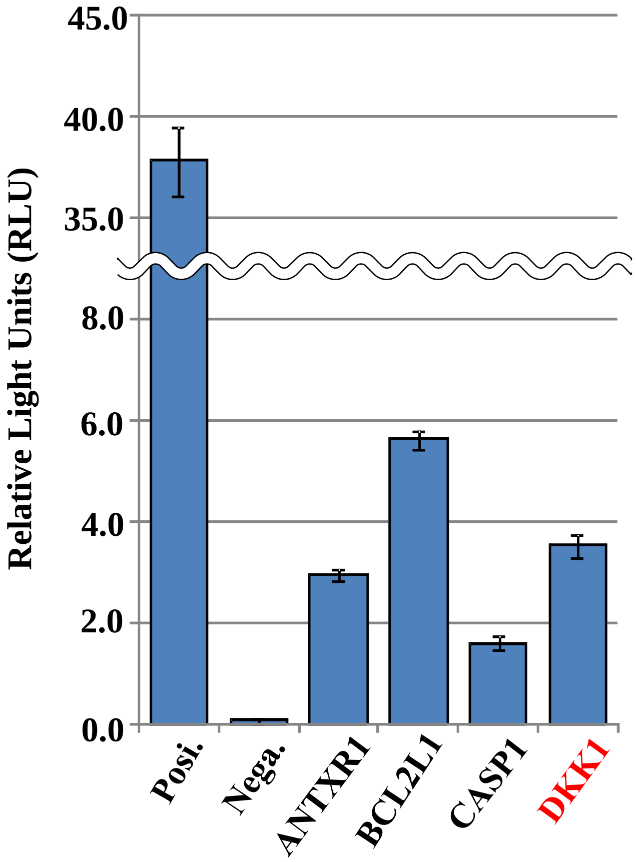
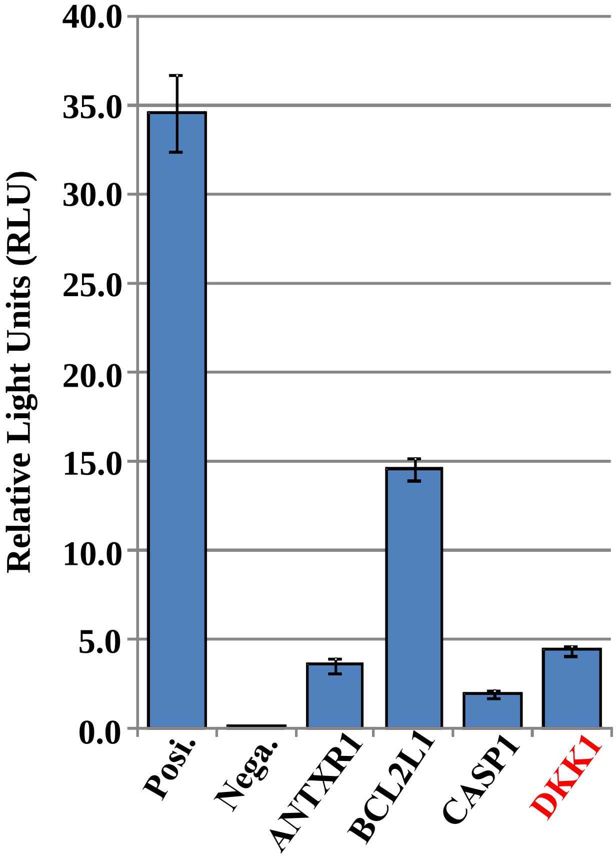
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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)

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.02

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5408

2nd Nucleotide Sequence
  File Name        : RDB7341F.fasta
  Sequence Size    : 532

  Unit Size to Compare = 1
  Pick up Location     = 1



[100.000% / 514 bp]     INT/OPT.Score : <   2056/  2056 >

     1’                    GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC
                           ** ********** ********** ********** **********
     1″ GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATC

    43’ ACACACCAAT TTCAATGACG TCAAATTCAC TTTCTAATTC ACTTTCAGCT CTTCTTCTCC
        ********** ********** ********** ********** ********** **********
    61″ ACACACCAAT TTCAATGACG TCAAATTCAC TTTCTAATTC ACTTTCAGCT CTTCTTCTCC

   103’ TCAAGGTTGT TTCTTTTCTC CCTAGAAAGG GTATTGCGTG GTCCCGTGCA AGGTAAGACT
        ********** ********** ********** ********** ********** **********
   121″ TCAAGGTTGT TTCTTTTCTC CCTAGAAAGG GTATTGCGTG GTCCCGTGCA AGGTAAGACT

   163’ TGGGAGCAAA CCCTGCATTC GGAAGCGTTG CGATGTGATA TACTAATGAG GAAGTCAGGC
        ********** ********** ********** ********** ********** **********
   181″ TGGGAGCAAA CCCTGCATTC GGAAGCGTTG CGATGTGATA TACTAATGAG GAAGTCAGGC

   223’ GCTAAGCCCT AAGGGTTTCT TATTTCTCCA CATTAGCCCA CCACTGAGAA GGGAGAACCG
        ********** ********** ********** ********** ********** **********
   241″ GCTAAGCCCT AAGGGTTTCT TATTTCTCCA CATTAGCCCA CCACTGAGAA GGGAGAACCG
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283’ GGGAAAGGCG ACTGACCTGG CACGTTGGAC CCTGTCCGCT TTGGTCCCGG CCACTTTGAT
     ********** ********** ********** ********** ********** **********
301″ GGGAAAGGCG ACTGACCTGG CACGTTGGAC CCTGTCCGCT TTGGTCCCGG CCACTTTGAT

343’ CTCACGCGTC TGCCTAATCA AGTTCATCTA CCGCCGCGAT TGCCCTGATT CAAAGAACAA
     ********** ********** ********** ********** ********** **********
361″ CTCACGCGTC TGCCTAATCA AGTTCATCTA CCGCCGCGAT TGCCCTGATT CAAAGAACAA

403’ CATTAAATGG TTTGATTATC GGATGGTCAT TTCCCTCTTC CCTCCACCCC TGATCTAATT
     ********** ********** ********** ********** ********** **********
421″ CATTAAATGG TTTGATTATC GGATGGTCAT TTCCCTCTTC CCTCCACCCC TGATCTAATT

463’ TCTAAACGCC AGTCTCTCGC CTCCCTCTCT AAACTTCCCA TCAAAAGAGA ATTAGCTCTT
     ********** ********** ********** ********** ********** **
481″ TCTAAACGCC AGTCTCTCGC CTCCCTCTCT AAACTTCCCA TCAAAAGAGA AT




1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5408

2nd Nucleotide Sequence
  File Name        : RDB7341R.fasta (Complementary)
  Sequence Size    : 671

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.209% / 670 bp]     INT/OPT.Score : <   2184/  2514 >

601’ GAGGAGGGCA ACTGAAGGAC CTCAAAGCCG GGGA-TCT-A ACTCAGATCT GC-AAACTGC
                                   *** **** *** * ******.*** ** *******
  1″                              CCCG GGGATTCTAA ACTCAGNTCT GCAAAACTGC
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 658’ G-AC-TCTAA A-GGGTTAAT GAGCAACTT- GCA-CCCG-C CACCTGGCCC TCTCAGAGGC
      * ** ***** * ****.*** *********  *** **** * ********** **********
  35″ GAACTTCTAA AGGGGTNAAT GAGCAACTTG GCACCCCGCC CACCTGGCCC TCTCAGAGGC

 712’ GTCTTGCTAG AGCCATTGAA TTACAGACCG G-TTTGTATT TAATACTGAA TATGACTTGT
      ********** ********** ********** * ******** ********** **********
  95″ GTCTTGCTAG AGCCATTGAA TTACAGACCG GTTTTGTATT TAATACTGAA TATGACTTGT

 771’ GTGCACAGTC AGCGAGTATT GGCATAAAGG AGAGGGGCAA AAAGTGCTTT TGCAGAGCCT
      ********** ********** ********** ********** ********** **********
 155″ GTGCACAGTC AGCGAGTATT GGCATAAAGG AGAGGGGCAA AAAGTGCTTT TGCAGAGCCT

 831’ ATCACCCCTC GGCTCTGTAA AGTATTTCAG ATCCGGATAA TTCAACCCTT ACTGCCAGGC
      ********** ********** ********** ********** ********** **********
 215″ ATCACCCCTC GGCTCTGTAA AGTATTTCAG ATCCGGATAA TTCAACCCTT ACTGCCAGGC

 891’ AAGGGCACCC AAGTTCCCAG AGTTCCTGCT GCCGCCTGCA TTTATTAAAG TCGTCTGCTA
      ********** ********** ********** ********** ********** **********
 275″ AAGGGCACCC AAGTTCCCAG AGTTCCTGCT GCCGCCTGCA TTTATTAAAG TCGTCTGCTA

 951’ TAACGCTCGC TGGTAGCCTT CACCCCGAAG GTGAGCCGGG CCAGCCGAGC GACTAAGCAA
      ********** ********** ********** ********** ********** **********
 335″ TAACGCTCGC TGGTAGCCTT CACCCCGAAG GTGAGCCGGG CCAGCCGAGC GACTAAGCAA

1011’ GGGAGGGGCG GGGTGAAGAG TGTCAAAGGC CCCCCTTCAT GTACACAAAC ACACCCCCTC
      ********** ********** ********** ********** ********** **********
 395″ GGGAGGGGCG GGGTGAAGAG TGTCAAAGGC CCCCCTTCAT GTACACAAAC ACACCCCCTC

1071’ CCAGCCCCTC CCAGCGCTTT GAAATCCCAT CCCGGCTTTG TTGTCTCCCT CCCAAGGGGC
      ********** ********** ********** ********** ********** **********
 455″ CCAGCCCCTC CCAGCGCTTT GAAATCCCAT CCCGGCTTTG TTGTCTCCCT CCCAAGGGGC

1131’ CGGAATGCTC CGGGCCCGCG GTATAAAGGC AGCCGCGGTG GCGGTGGCGG CGCAGAGCTC
      ********** ********** ********** ********** ********** **********
 515″ CGGAATGCTC CGGGCCCGCG GTATAAAGGC AGCCGCGGTG GCGGTGGCGG CGCAGAGCTC

1191’ TGTGCTCCCT GCAGTCAATC AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGGTACT
      ********** ********** ********** ********** ********** **********
 575″ TGTGCTCCCT GCAGTCAATC AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGGTACT
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1251’ GTTGGTAAAG CCACCATGGA AGATGCCAAA AACATTAAGA AGGGCCCAGC GCCATTCTAC
      ********** ********** ********** *******
 635″ GTTGGTAAAG CCACCATGGA AGATGCCAAA AACATTA
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