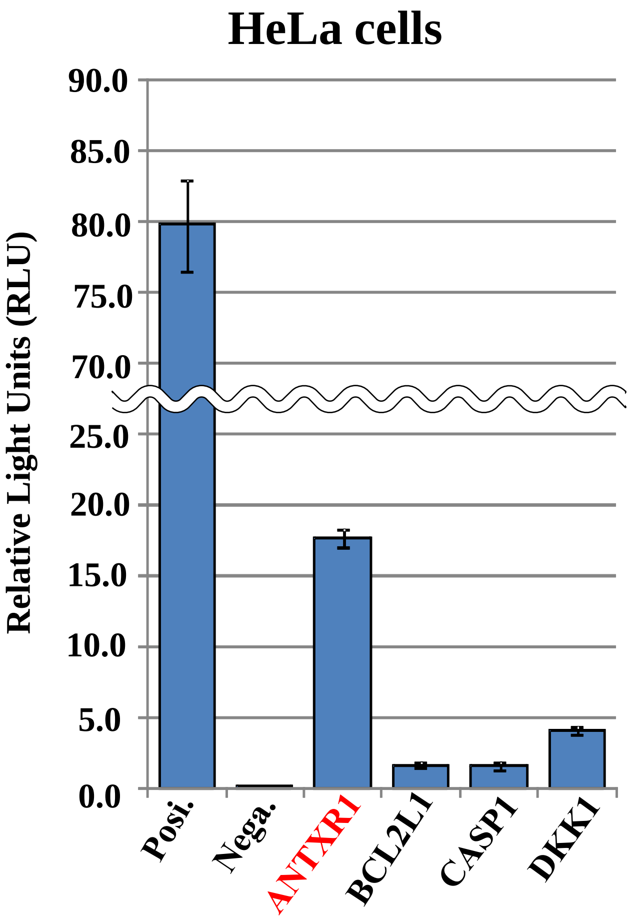
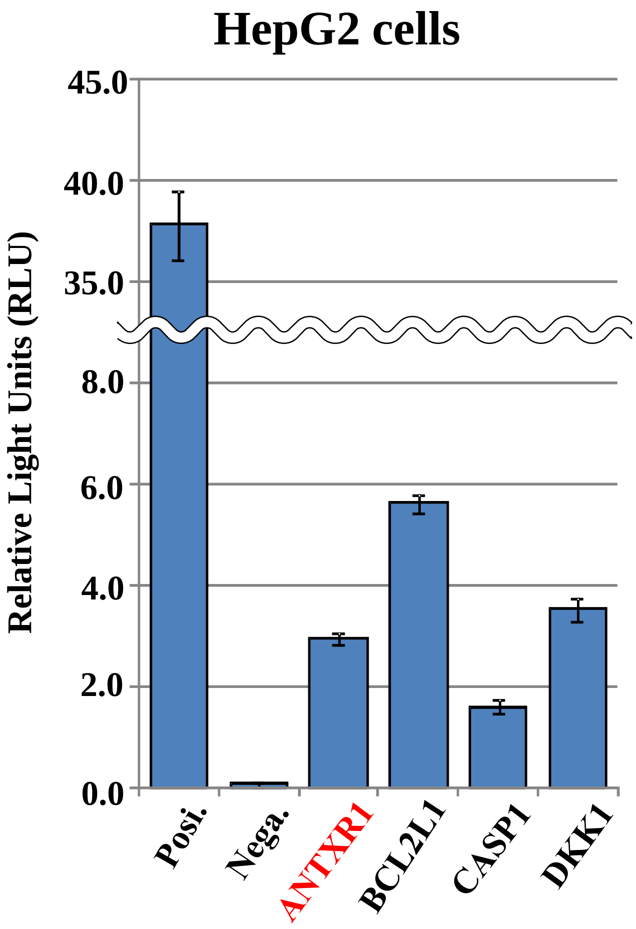
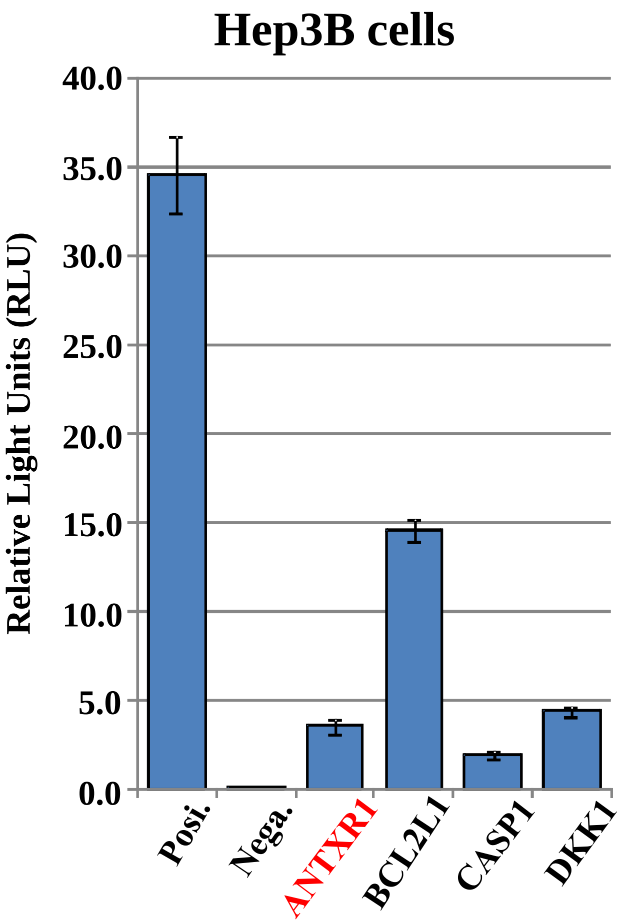
The Promoter Activities of Reporter Constructs


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)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.02

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5431

2nd Nucleotide Sequence
  File Name        : RDB7333F.fasta
  Sequence Size    : 703

  Unit Size to Compare = 1
  Pick up Location     = 1



[100.000% / 684 bp]     INT/OPT.Score : <   2736/  2736 >

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

    43’ GAGGAAGAAT CCTGGGAAAA CAGTACATGC ATATGCACTG AGGGCTCCCA GAGCGGAAGA
        ********** ********** ********** ********** ********** **********
    61″ GAGGAAGAAT CCTGGGAAAA CAGTACATGC ATATGCACTG AGGGCTCCCA GAGCGGAAGA

   103’ CAATAGGAAG CTAGAACTGG GGTACCACTC GGAACTGGGG CTCAGAGGCT GATTCTCCAA
        ********** ********** ********** ********** ********** **********
   121″ CAATAGGAAG CTAGAACTGG GGTACCACTC GGAACTGGGG CTCAGAGGCT GATTCTCCAA

   163’ TTTAGAGAGG CTAGCACGGA ACTTCCCTGC CAATTCCAAA CTGCTTGGAG CGTCTCTACT
        ********** ********** ********** ********** ********** **********
   181″ TTTAGAGAGG CTAGCACGGA ACTTCCCTGC CAATTCCAAA CTGCTTGGAG CGTCTCTACT

   223’ CTTGTAAGCT GTTTACTTCC TCCATCCTAA ATCAAAGATA GAGAGAAAAT GTCAAAGTTC
        ********** ********** ********** ********** ********** **********
   241″ CTTGTAAGCT GTTTACTTCC TCCATCCTAA ATCAAAGATA GAGAGAAAAT GTCAAAGTTC
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283’ ACAGGCTGAA AAGAAGAACT ATTATCATAG AATCCCTAAA AGATGGAGAT GGTGGCCATC
     ********** ********** ********** ********** ********** **********
301″ ACAGGCTGAA AAGAAGAACT ATTATCATAG AATCCCTAAA AGATGGAGAT GGTGGCCATC

343’ TAGAAGGCTC AGCTGTTCCA TGCCGGGAGC AGCCCTAAGT ACCACACTCT GTGGGGTTGT
     ********** ********** ********** ********** ********** **********
361″ TAGAAGGCTC AGCTGTTCCA TGCCGGGAGC AGCCCTAAGT ACCACACTCT GTGGGGTTGT

403’ TTGTGATGGT TTCAGACCGG ACCCCAACAG TCTCTTTTAT GGTCCAGACA GACTAAGACC
     ********** ********** ********** ********** ********** **********
421″ TTGTGATGGT TTCAGACCGG ACCCCAACAG TCTCTTTTAT GGTCCAGACA GACTAAGACC

463’ ATGTAAGGTC ACTCTGATGA CTCATACCAC AAAGGTCCCG TTTTTCCCCT ACTTCATCTG
     ********** ********** ********** ********** ********** **********
481″ ATGTAAGGTC ACTCTGATGA CTCATACCAC AAAGGTCCCG TTTTTCCCCT ACTTCATCTG

523’ CACAATGGTT TGTTTGCAAA GGTCCTAGCC TGGGGAGCCG GAGTCACCGT GGTTGGAGGA
     ********** ********** ********** ********** ********** **********
541″ CACAATGGTT TGTTTGCAAA GGTCCTAGCC TGGGGAGCCG GAGTCACCGT GGTTGGAGGA

583’ AACAAATTCT CATCCAATGT TTAGTGACCT TATCAAAAGA TGCAGGATAG GGAAGGAAAA
     ********** ********** ********** ********** ********** **********
601″ AACAAATTCT CATCCAATGT TTAGTGACCT TATCAAAAGA TGCAGGATAG GGAAGGAAAA

643’ GAAGGAATAG AAGGACTACA GAGAATGGAG AGGCGGTCAC GGAAAAAGAA AGGGAAAGTG
     ********** ********** ********** ********** **
661″ GAAGGAATAG AAGGACTACA GAGAATGGAG AGGCGGTCAC GGG
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1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5431

2nd Nucleotide Sequence
  File Name        : RDB7333R.fasta (Complementary)
  Sequence Size    : 642
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  Unit Size to Compare = 1
  Pick up Location     = 1



[99.378% / 643 bp]     INT/OPT.Score : <   1326/  2526 >

    661' CAGAGAATGG AGAGGCGGTC ACGGAAAAAG AAAGGGAAAG TGCGTGGGAA GAAGGAAGGA
                       ******* ********** ****** *** ********** **********
      1″              GGGCGGTC ACGGAAAAAG AAAGGGGAAG TGCGTGGGAA GAAGGAAGGA

    721' GTAAGAAAAC ACGCACAGCT CACATGAGAA TGGTAAGGAC AAGGAAATTT ATACGCGAAG
         ********** ********** ********** ********** ********** **********
     49″ GTAAGAAAAC ACGCACAGCT CACATGAGAA TGGTAAGGAC AAGGAAATTT ATACGCGAAG

    781' CCTGGAAGCG CCCCCGCCCC CGACGCACTC CCGCGGGTCC CACGCGTGCT TTCGCCGCCT
         ********** ********** ********** ********** ********** **********
    109″ CCTGGAAGCG CCCCCGCCCC CGACGCACTC CCGCGGGTCC CACGCGTGCT TTCGCCGCCT

    841' TTGTCCACAA GGTGGCAGCC TTTGAACTTT CTTCCCCGTA AGAACGCGAA AGGGGGGCAG
         ********** ********** ********** ********** ********** **********
    169″ TTGTCCACAA GGTGGCAGCC TTTGAACTTT CTTCCCCGTA AGAACGCGAA AGGGGGGCAG

    901' AGAGGAAGGA GAGAAGGCAA AGCACTGCCC CCACCAAGAA CAATTTGAAA CCCCCCCCCC
         ********** ********** ********** ********** **********   ********
    229″ AGAGGAAGGA GAGAAGGCAA AGCACTGCCC CCACCAAGAA CAATTTGAAA --CCCCCCCC

    961' CCCCCATCAT ATTTAAAATC TGGGACAAAG AACCGTCGGG ACGGAACTCC TTCCATTGCA
         ********** ********** ********** ********** ********** **********
    287″ CCCCCATCAT ATTTAAAATC TGGGACAAAG AACCGTCGGG ACGGAACTCC TTCCATTGCA

   1021' AAAGCTCGGC GCGGCCTCGG GAGCTGCCCG GCGGCCCCGG ACCGAGGCAG CCCTCCCCTT
         ********** ********** ********** ********** ********** **********
    347″ AAAGCTCGGC GCGGCCTCGG GAGCTGCCCG GCGGCCCCGG ACCGAGGCAG CCCTCCCCTT

   1081' TAAAAGAAGC GGAGGACAGG ATTGGGATCC TTGAAACCCG AAACCCAGAA ACAGCATCGG
         ********** ********** ********** ********** ********** **********
    407″ TAAAAGAAGC GGAGGACAGG ATTGGGATCC TTGAAACCCG AAACCCAGAA ACAGCATCGG
```

```
1141' AGCGGAAACC AGAGGGGAAA CCTTGAACTC CTCCAGACAA TTGCTTCCGG GGAGTTGCGA
      ********** ********** ********** ********** ********** **********
 467″ AGCGGAAACC AGAGGGGAAA CCTTGAACTC CTCCAGACAA TTGCTTCCGG GGAGTTGCGA

1201' GGGAGCGAGG GGGAATAAAG GACCCGCGAG ATCAAGATCT GGCCTCGGCG GCCAAGCTTG
      ********** ********** ********** ********** ********** **********
 527″ GGGAGCGAGG GGGAATAAAG GACCCGCGAG ATCAAGATCT GGCCTCGGCG GCCAAGCTTG

1261' GCAATCCGGT ACTGTTGGTA AAG-CCACCA TGGAAGATGC CAAAAACATT AAGAAGGGCC
      ********** ********** *** ****** ********** ********** ******
 587″ GCAATCCGGT ACTGTTGGTA AAGACCACCA TGGAAGATGC CAAAAACATT AAGAAG
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