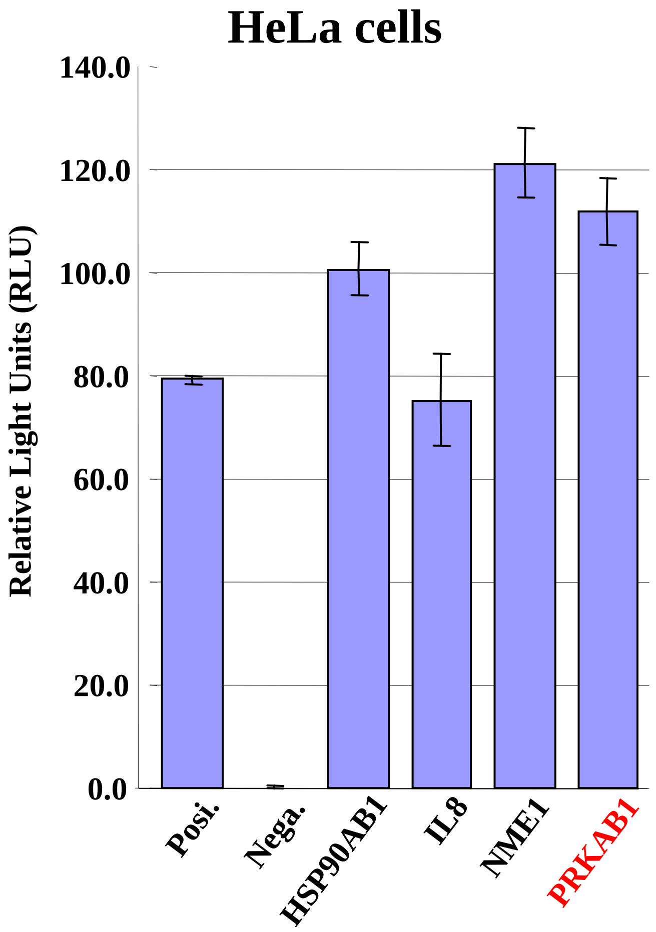
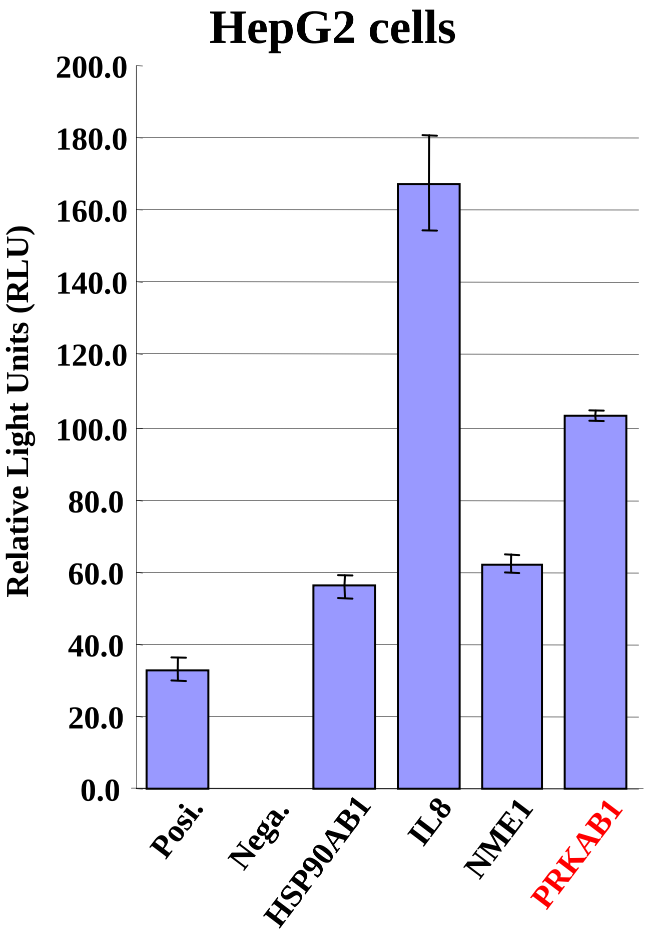
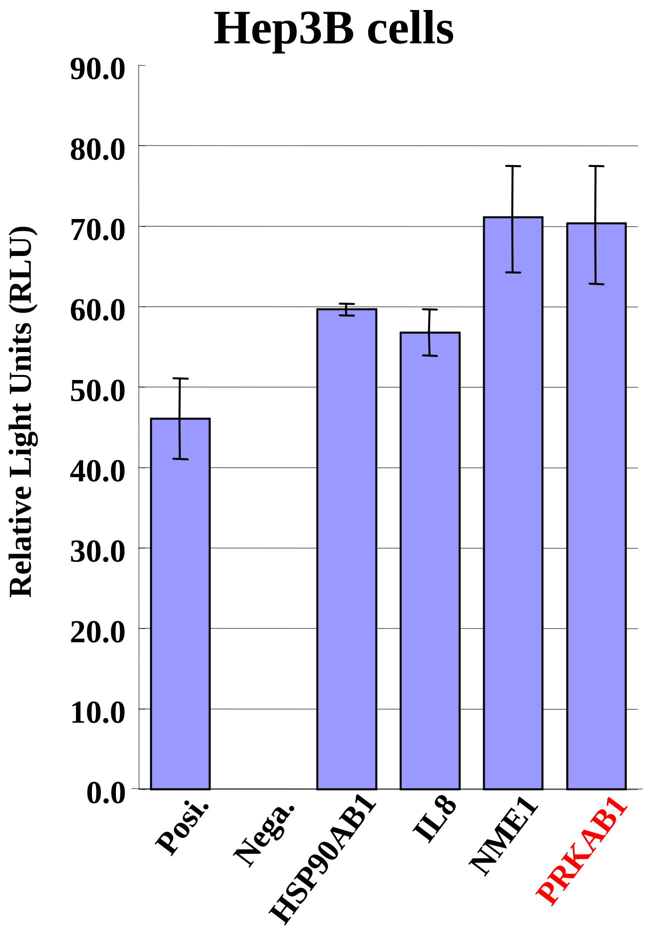
The Promoter Activities of Reporter Constructs







Posi.: pGL3 Control Vector
(SV40 promoter)
Nega.: Empty Vector

HSP90AB1: pGL4-phHSP90AB1 (RDB# 7321)
IL8: pGL4-phIL8 (RDB# 7322)
NME1: pGL4-phNME1 (RDB# 7326)
PRKAB1: pGL4-phPRKAB1 (RDB#7328)

2009, DNA Bank, RIKEN BioResource Center

```
[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.02

1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5415

2nd Nucleotide Sequence
  File Name        : RDB7328F.fasta
  Sequence Size    : 707

  Unit Size to Compare = 1
  Pick up Location     = 1



[98.113% / 689 bp]     INT/OPT.Score : <   2274/  2598 >

      1’                     G GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT
                             * ********** ********** ********** **********
      1″ GGTGCCAGAA CATTTCTCTG GCCTAACTGG CCGGTACCTG AGCTCGCTAG CCTCGAGGAT

     42’ TAAAATATAT GGGGGCATGG GGGGTGACAA GTGCATCTTA GAATATATTT TTGCATGTAA
         ********** ********** ********** ******** * ********** **********
     61″ TAAAATATAT GGGGGCATGG GGGGTGACAA GTGCATCTAA GAATATATTT TTGCATGTAA

    102’ ATATTTTGTA GATAATGCTT GTAAATAATT TTCATGTGTG TATTTCTGCA CAAGTTTCCT
         ********** ********** ********** ********** ********** **********
    121″ ATATTTTGTA GATAATGCTT GTAAATAATT TTCATGTGTG TATTTCTGCA CAAGTTTCCT

    162’ AGGAGTAAAA TTGTGTGTCA AAATGAAGGT GCATTTTTAA ATTTTGATGC ATACTGCTGA
         ********** ********** ********** ********** ********** **********
    181″ AGGAGTAAAA TTGTGTGTCA AAATGAAGGT GCATTTTTAA ATTTTGATGC ATACTGCTGA

    222’ ATTCCCCCCA GGAAACCTTA TCTTAGTCAT CTTGTGTTCC TCATTTCCTT AGCACAATGT
         ********** ********** ********** ********** ********** **********
    241″ ATTCCCCCCA GGAAACCTTA TCTTAGTCAT CTTGTGTTCC TCATTTCCTT AGCACAATGT
```

```
282’ CTGGTACTTT TTTAGGTACT AAATAAATGT TCAGTGGGTG AAATGCATGA CCTGACCCGG
     ********** ********** ********** ********** ********** **********
301″ CTGGTACTTT TTTAGGTACT AAATAAATGT TCAGTGGGTG AAATGCATGA CCTGACCCGG

342’ CAAATGCAAA GTATTTTGAG ATATTCACAC ACCAAAAAAC CCACAAAATA TGACAATGAC
     ********** ********** ********** ********** ********** **********
361″ CAAATGCAAA GTATTTTGAG ATATTCACAC ACCAAAAAAC CCACAAAATA TGACAATGAC

402’ TGACAATGAG AAGATGAGAA TATTTTACTA CCGTATTTGT ATGCACTTCT TGTTGAAGCA
     ********** ********** ********** ********** ********** **********
421″ TGACAATGAG AAGATGAGAA TATTTTACTA CCGTATTTGT ATGCACTTCT TGTTGAAGCA

462’ CTGACCAGAG TAAATGACAA ACGCTAATGC ATCTTATGCA GAAGGATGTT TCCGAAGTGA
     ********** ********** ********** ********** ********** **********
481″ CTGACCAGAG TAAATGACAA ACGCTAATGC ATCTTATGCA GAAGGATGTT TCCGAAGTGA

522’ TTACAAGATA TCTTGCAAAA TTACCTATCA AAAGATTGCA CACTCAATAA AAATACACGA
     ********** *** ****** * ******** ********** ******** * **********
541″ TTACAAGATA TCTAGCAAAA TAACCTATCA AAAGATTGCA CACTCAAT-A AAATACACGA

582’ ATAACTCCAG CATTTTACAA CCCCCAACCT ACTAGACATA AGAAATTTCC AGAGATCTTA
     ****** *** ******** * ***** **** ********** ******** * ******** *
600″ ATAACT-CAG CATTTTAC-A CCCCC-ACCT ACTAGACATA AGAAATTT-C AGAGATCTAA

642’ TGGTCTGCCA TTTTTTCAAA TA-CCTGC-A AGACTG-CCT GCACCCCCGA CCCTAATCTG
     ********** *********  ** ***** * ****** *** ********
656″ TGGTCTGCCA TTTTTTCAAT TACCCTGCAA AGACTGCCCT GCACCCCCCG AA
```

1st Nucleotide Sequence
File Name : Reference Seq.gnu
Sequence Size : 5415

2nd Nucleotide Sequence
File Name : RDB7328R.fasta (Complementary)
Sequence Size : 753

```
Unit Size to Compare = 1
Pick up Location     = 1



[98.141% / 753 bp]     INT/OPT.Score : <   2795/  2879 >

541' ATTACCTATC AAAAGATT-G CAC-ACTC-- AATAAAAATA CACG-AATAA CTCCA-GCAT
                *** **** * *** ****   * ******** **** ***** ***** ****
  1″            AAAGGATTGG CACAACTCAA ATTAAAAATA CACGAAATAA CTCCAGGCAT

595' TTTACAACCC CCAACCTACT AGACATAAGA AATTTCCAGA GATCTTATGG TCTGCCATTT
     ********** ** ****.** ****** **  ********** ********** *****  ***
 51″ TTTACAACCC CCCACCTNCT AGACATTAGG AATTTCCAGA GATCTTATGG TCTGCATTTT

655' TTTCAAATAC CTGCAAGACT GCCTGCACCC CCGACCCTAA TCTGTAGAAA TCATGATTCT
     ********** ********** ********** ********** ********** **********
111″ TTTCAAATAC CTGCAAGACT GCCTGCACCC CCGACCCTAA TCTGTAGAAA TCATGATTCT

715' GCAGGTCTGC AGTGGGGGAT GCATTTAACA AGCGCTCCAG GTTAACCTAA TGCACTGTAA
     ********** ********** ********** ********** ********** **********
171″ GCAGGTCTGC AGTGGGGGAT GCATTTAACA AGCGCTCCAG GTTAACCTAA TGCACTGTAA

775' AGCGTGAGAA CACGTGCATT AAAAGGGCTT TAAGAAGTGG AGTTTCTGAA TCAGATTTGC
     ********** ********** ********** ********** ********** **********
231″ AGCGTGAGAA CACGTGCATT AAAAGGGCTT TAAGAAGTGG AGTTTCTGAA TCAGATTTGC

835' ATTTTAGAAA GATCCCTCTG GCTGCAGAGT GTAGAATCAA CTATAAGTGA GCAAAGATAG
     ********** ********** ********** ********** ********** **********
291″ ATTTTAGAAA GATCCCTCTG GCTGCAGAGT GTAGAATCAA CTATAAGTGA GCAAAGATAG

895' CTAAATGGCA TTATTCAGCC CAGCGCATGA ACGGCTCAGA TTGCCCGCGC GCTGGGGTGC
     ********** ********** ********** ********** ********** **********
351″ CTAAATGGCA TTATTCAGCC CAGCGCATGA ACGGCTCAGA TTGCCCGCGC GCTGGGGTGC

955' CCCCTGCCGG CCCTCGGCAG CGCCTCGTCC TGGGCCTGGC CCTGGGCGGC CGGCTGCTGA
     ********** ********** ********** ********** ********** **********
411″ CCCCTGCCGG CCCTCGGCAG CGCCTCGTCC TGGGCCTGGC CCTGGGCGGC CGGCTGCTGA
```

```
1015' CTGCGACTGC GCGCTCCGAG GCCTGCAGAG ACGGCCCGGG GCACCTGTTA CCGCACCGCT
      ********** ********** ********** ********** ********** **********
 471″ CTGCGACTGC GCGCTCCGAG GCCTGCAGAG ACGGCCCGGG GCACCTGTTA CCGCACCGCT

1075' CAAGACCGGA AGCGGAAATG GAATCGAGAT AGCCTCGCGC GTTTAGCTGG CCGCCGCCAC
      ********** ********** ********** ********** ********** **********
 531″ CAAGACCGGA AGCGGAAATG GAATCGAGAT AGCCTCGCGC GTTTAGCTGG CCGCCGCCAC

1135' CTCCACGCCC TAGGCCGGGC CGACTTACGG AGTCGCCGGA AGCGGAAGTC GCTGAGGGGT
      ********** ********** ********** ********** ********** **********
 591″ CTCCACGCCC TAGGCCGGGC CGACTTACGG AGTCGCCGGA AGCGGAAGTC GCTGAGGGGT

1195' GGTGAAGCGG TTGGGAAAGT ATCAAGATCT GGCCTCGGCG GCCAAGCTTG GCAATCCGGT
      ********** ********** ********** ********** ********** **********
 651″ GGTGAAGCGG TTGGGAAAGT ATCAAGATCT GGCCTCGGCG GCCAAGCTTG GCAATCCGGT

1255' ACTGTTGGTA AAGCCACCAT GGAAGATGCC AAAAACATTA AGAAGGGCCC AGCGCCATTC
      ********** ********** ********** ********** ***
 711″ ACTGTTGGTA AAGCCACCAT GGAAGATGCC AAAAACATTA AGA
```