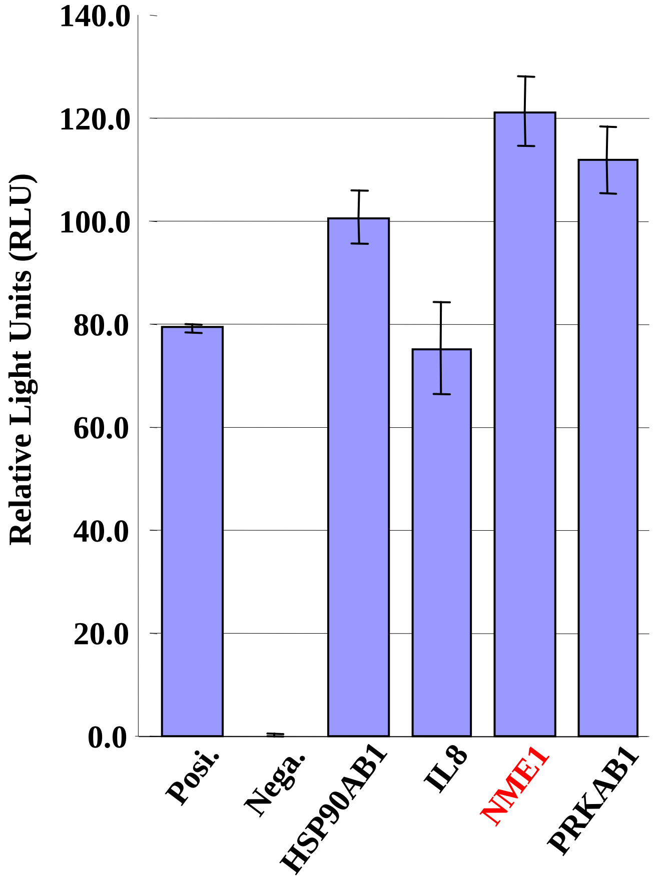
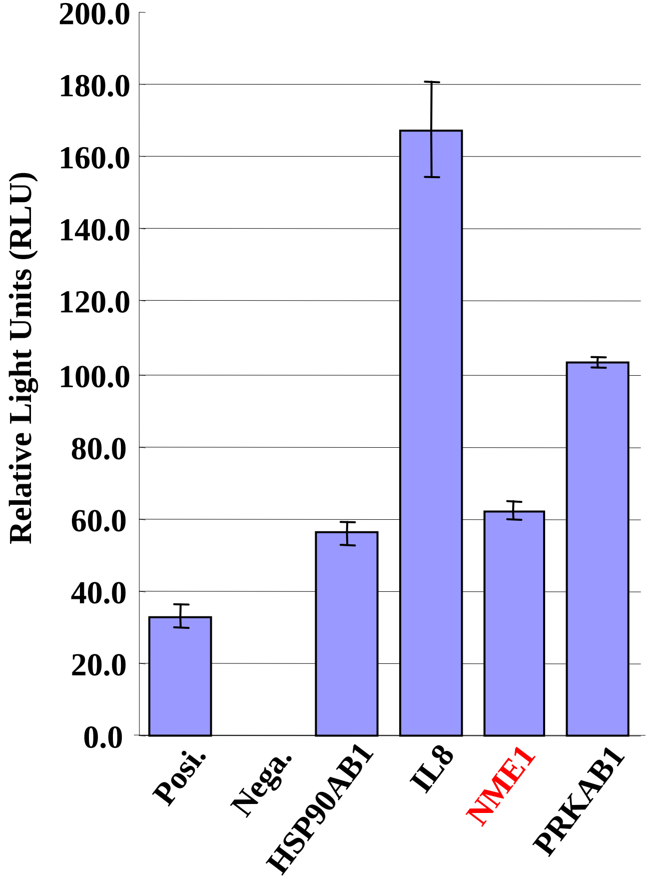
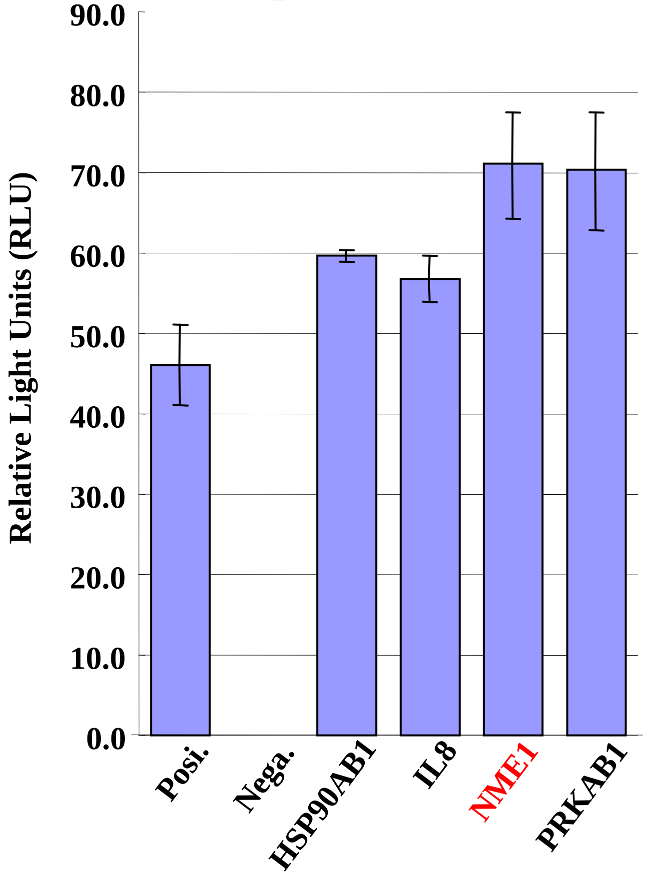
The Promoter Activities of Reporter Constructs



HeLa cells



HepG2 cells



Hep3B cells

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

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.02

1st Nucleotide Sequence
  File Name          : Reference Seq.gnu
  Sequence Size      : 5485

2nd Nucleotide Sequence
  File Name          : RDB7326F.fasta
  Sequence Size      : 661

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.068% / 644 bp]     INT/OPT.Score : <    1910/   2510 >

    1’                   GGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATCC
                         *** ********** ********** ********** **********
    1″ TGCCAGAACA TTTCTCTGGC CTAACTGGCC GGTACCTGAG CTCGCTAGCC TCGAGGATCC

   44’ CGGCTCATTT TTGTATGTTT AGTAGAGACG GGGTTTCACT ATGTTGCCCG GGCTGGTCTC
       ********** ********** ********** ********** ********** **********
   61″ CGGCTCATTT TTGTATGTTT AGTAGAGACG GGGTTTCACT ATGTTGCCCG GGCTGGTCTC

  104’ GAATTCCTGA GCTCAAGTGA TCCTCCCGCC GCTGCTTTCC AGCGTGCTGG GATTACAGGC
       ********** ********** ********** ********** ********** **********
  121″ GAATTCCTGA GCTCAAGTGA TCCTCCCGCC GCTGCTTTCC AGCGTGCTGG GATTACAGGC

  164’ GTGAGCCACC GCGCTCGGCC AAAAGTTTTA AATTTCAGTA AGTTCCAATT TATCAACTTT
       ********** ********** ********** ********** ********** **********
  181″ GTGAGCCACC GCGCTCGGCC AAAAGTTTTA AATTTCAGTA AGTTCCAATT TATCAACTTT

  224’ TTCCCTGTAT AGATTGGTCT TTTGGTGTCG TCTAAAAACT ATTTGCCTGG CCCTAGGTCC
       ********** ********** ********** ********** ********** **********
  241″ TTCCCTGTAT AGATTGGTCT TTTGGTGTCG TCTAAAAACT ATTTGCCTGG CCCTAGGTCC
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284' TGAGGATTTT TTTTAACTTT TTTTTTCCCC ATAAGTGATT TATTGTTTTA CATTTAAATC
     ********** ********** ********** ********** ********** **********
301″ TGAGGATTTT TTTTAACTTT TTTTTTCCCC ATAAGTGATT TATTGTTTTA CATTTAAATC

344' TATGATTCAT TTTGAGTAAA TTTTGTATAA GGTGAGAGGT TTAGGTTGAG GTTCTTTGGG
     ********** ********** ********** ********** ********** **********
361″ TATGATTCAT TTTGAGTAAA TTTTGTATAA GGTGAGAGGT TTAGGTTGAG GTTCTTTGGG

404' TCTATATTCG TCCAATTGCT CCAGCATCAT TTGTTGAAAC GGCTCCTGAT TCCATTTTTG
     ********** ********** ********** ********** ********** **********
421″ TCTATATTCG TCCAATTGCT CCAGCATCAT TTGTTGAAAC GGCTCCTGAT TCCATTTTTG

464' TACCTTTCCC CCGTTCATTT CCCCTTAGAG CAGTGGGAAT GTTTTTTTGT TAGTGATGAT
     ******* ** ********** ********** ********** ********** **********
481″ TACCTTT-CC CCGTTCATTT CCCCTTAGAG CAGTGGGAAT GTTTTTTTGT TAGTGATGAT

524' GTCATGCCTT GTGCAAAATC TGTATTAGCA TCTCACAACA TAAGATTTGG CTCTATTCTA
     ********** ********** ********** ********** ******* ** **********
540″ GTCATGCCTT GTGCAAAATC TGTATTAGCA TCTCACAACA TAAGATTCGG CTCTATTCTA

584' ACGGCATTTT CCACCACTCG ATGTCCA-CC GTAATACTTG GCTCTCG-AA GAATCACTGG
     ********** ********** ******* ** ********** ******* ** *******  *
600″ ACGGCATTTT CCACCACTCG ATGTCCACCC GTAATACTTG GCTCTCGAAA GAATCACCTG

642' GCTGGCTCCC TCACTTCATG CAGGTCTATT CTATTATCAC TTACTCAGAG ATTTCTCTGG
     *
660″ GG
```

1st Nucleotide Sequence
  File Name   : Reference Seq.gnu
  Sequence Size   : 5485

2nd Nucleotide Sequence
  File Name   : RDB7326R.fasta (Complementary)
  Sequence Size   : 694

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Unit Size to Compare = 1
Pick up Location     = 1



[98.844% / 692 bp]     INT/OPT.Score : <   2720/  2720 >

  661’ GCAGGTCTAT TCTATTATCA CTTACTCAGA GATTTCTCTG GCCTTTTCTT CACAGCACTT
                        **** * ******** ** ******* ********** **********
    1″                AAATCA CCTACTCAGA GAATTCTCTG GCCTTTTCTT CACAGCACTT

  721’ ACAAAATGCG ATCTATTACA TATTAATTTG CTTATTTGCT TCTTGTTTTC CTATACTCCC
       ******** * ********** **** ***** *** ****** *** ****** **********
   47″ ACAAAATGGG ATCTATTACA TATTTATTTG CTTTTTTGCT TCTGGTTTTC CTATACTCCC

  781’ ATCCCTCCCA GAAGCTCCAA GAGAGCATAC TGTTTTATCC CTAGGGCCTA GAATAATGCG
       ********** ********** ********** **** ***** ********** * ********
  107″ ATCCCTCCCA GAAGCTCCAA GAGAGCATAC TGTTGTATCC CTAGGGCCTA GGATAATGCG

  841’ TCCACGTAGT AGGTACTCAA AATTTTTTGC TTGACAGGCT AGAAAAGGTG AATAAACACA
       ********** ********** ********** ********** ********** **********
  167″ TCCACGTAGT AGGTACTCAA AATTTTTTGC TTGACAGGCT AGAAAAGGTG AATAAACACA

  901’ AAGCGGGAGC GAAAAGTCTA CTTCTAGGTC AGGCACTCTT TGGACTTCAC GCAACGTGTG
       ********** ********** ********** ********** ********** **********
  227″ AAGCGGGAGC GAAAAGTCTA CTTCTAGGTC AGGCACTCTT TGGACTTCAC GCAACGTGTG

  961’ AGCGCCACCT CTCGGGAAGC CAATTTGCTC GCGAACGAAG GAAGTGAGTC AGAGAACCCG
       ********** ********** ********** ********** ********** **********
  287″ AGCGCCACCT CTCGGGAAGC CAATTTGCTC GCGAACGAAG GAAGTGAGTC AGAGAACCCG

 1021’ GGGGTGGAGA GAAGAAAGCA AGCAGCTAAC CGGAAAGGTC TGAAAAAGCT AGCGCCGGAA
       ********** ********** ********** ********** ********** **********
  347″ GGGGTGGAGA GAAGAAAGCA AGCAGCTAAC CGGAAAGGTC TGAAAAAGCT AGCGCCGGAA

 1081’ GTTAAACTGC AGAAAGTTGT TCCCTAGAAT GACTGCCTAC TCCCAAGAGG AAGCGTGGGC
       ********** ********** ********** ********** ********** **********
  407″ GTTAAACTGC AGAAAGTTGT TCCCTAGAAT GACTGCCTAC TCCCAAGAGG AAGCGTGGGC
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1141’ GAGCGGTGTT CTGCAAAATG GGCTCTCCGG CAGCGGATCT GCGCAGAAGC GTTCCGTGCG
      ********** ********** ********** ********** ********** **********
 467″ GAGCGGTGTT CTGCAAAATG GGCTCTCCGG CAGCGGATCT GCGCAGAAGC GTTCCGTGCG

1201’ TGCAAGTGCT GCGAACCACG TGGGTCCCGG GCGCGTTTCG GGTGCTGGCG GCTGCAGCCG
      ********** ********** ********** ********** ********** **********
 527″ TGCAAGTGCT GCGAACCACG TGGGTCCCGG GCGCGTTTCG GGTGCTGGCG GCTGCAGCCG

1261’ GAGTTCAAAC CTAAGCAGCT GGAAATCAAG ATCTGGCCTC GGCGGCCAAG CTTGGCAATC
      ********** ********** ********** ********** ********** **********
 587″ GAGTTCAAAC CTAAGCAGCT GGAAATCAAG ATCTGGCCTC GGCGGCCAAG CTTGGCAATC

1321’ CGGTACTGTT GGTAAAGCCA CCATGGAAGA TGCCAAAAAC ATTAAGAAGG GCCCAGCGCC
      ********** ********** ********** ********** ********
 647″ CGGTACTGTT GGTAAAGCCA CCATGGAAGA TGCCAAAAAC ATTAAGAA
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