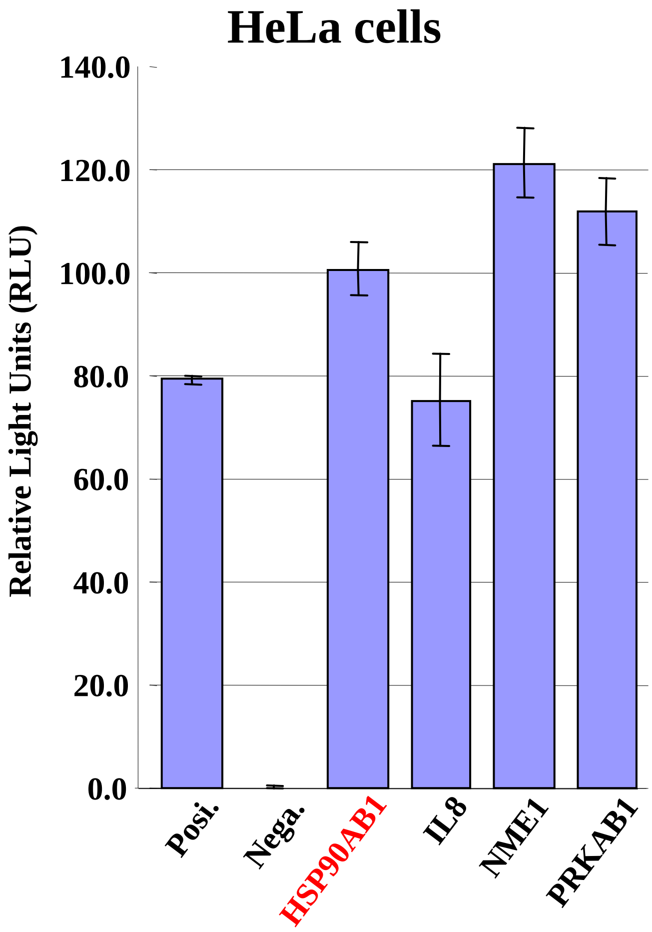
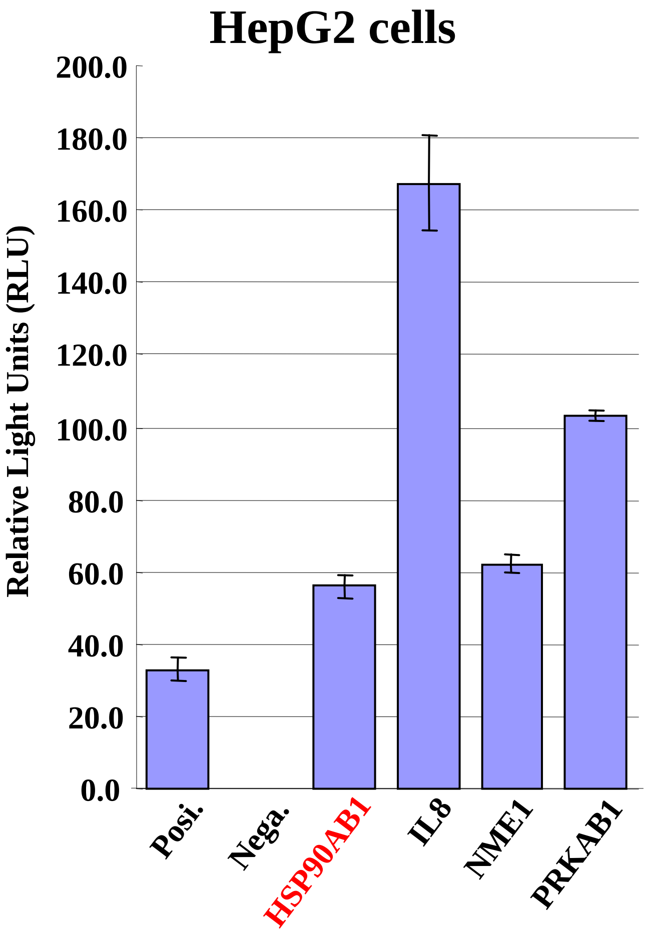
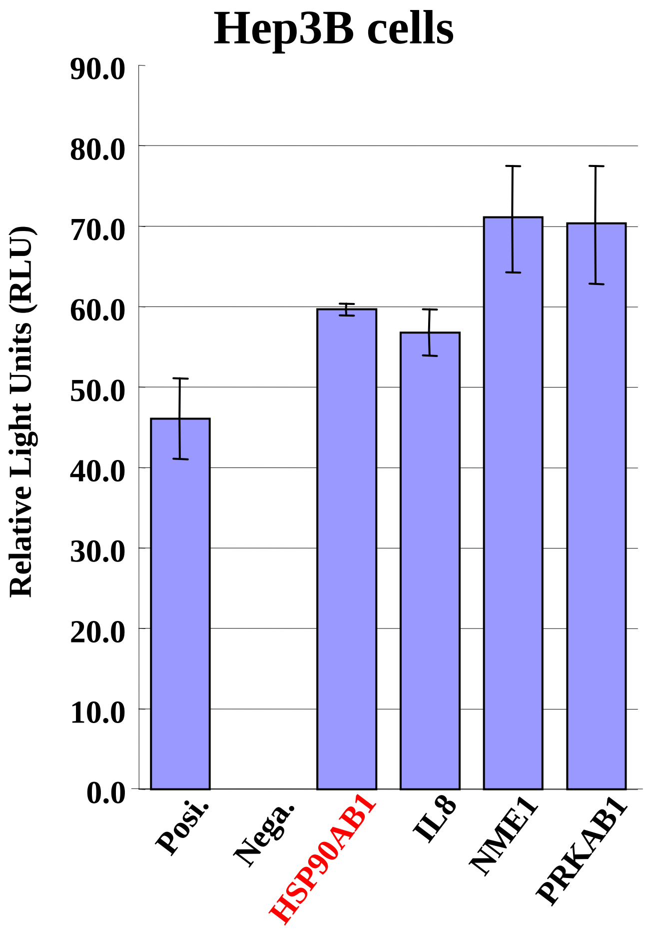
The Promoter Activities of Reporter Constructs







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

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.01

1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5458

2nd Nucleotide Sequence
  File Name         : RDB7321F.fasta
  Sequence Size     : 517

  Unit Size to Compare = 1
  Pick up Location     = 1



[100.000% / 498 bp]     INT/OPT.Score : <   1992/  1992 >

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

    42' AGGCTGAAGG GGAACAACTT GGCCAGCCGC TCTGTGGCCG GCATCGTCAC GCGGCCTCCA
        ********** ********** ********** ********** ********** **********
    61″ AGGCTGAAGG GGAACAACTT GGCCAGCCGC TCTGTGGCCG GCATCGTCAC GCGGCCTCCA

   102' AGAGCTCCGG CTGCCCTGCA CTGGTTCCCA GAGACTCCCT CCTTCCCAGG TCCAAATGGC
        ********** ********** ********** ********** ********** **********
   121″ AGAGCTCCGG CTGCCCTGCA CTGGTTCCCA GAGACTCCCT CCTTCCCAGG TCCAAATGGC

   162' TGCAGGAGCG AAGTGGGCGG AAAAAAAGCG AACCAGCTTG AGAAAGGGCT TGACGTGCCT
        ********** ********** ********** ********** ********** **********
   181″ TGCAGGAGCG AAGTGGGCGG AAAAAAAGCG AACCAGCTTG AGAAAGGGCT TGACGTGCCT

   222' GCGTAGGGAG GGCGCATGTC CCCGTGCTCC GTGTACGTGG CGGCCGCAGG GGCTAGAGGG
        ********** ********** ********** ********** ********** **********
   241″ GCGTAGGGAG GGCGCATGTC CCCGTGCTCC GTGTACGTGG CGGCCGCAGG GGCTAGAGGG
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    282' GGGTCCCCCC CGCAGGTACT CCACTCTCAG TCTGCAAAAG TGTACGCCCG CAGAGCCGCC
         ********** ********** ********** ********** ********** **********
    301″ GGGTCCCCCC CGCAGGTACT CCACTCTCAG TCTGCAAAAG TGTACGCCCG CAGAGCCGCC

    342' CCAGGTGCCT GGGTGTTGTG TGATTGACGC GGGGAAGGAG GGGTCAGCCG ATCCCTCCCC
         ********** ********** ********** ********** ********** **********
    361″ CCAGGTGCCT GGGTGTTGTG TGATTGACGC GGGGAAGGAG GGGTCAGCCG ATCCCTCCCC

    402' AACCCTCCAT CCCATCCCTG AGGATTGGGC TGGTACCCGC GTCTCTCGGA CAGGTCAGAG
         ********** ********** ********** ********** ********** **********
    421″ AACCCTCCAT CCCATCCCTG AGGATTGGGC TGGTACCCGC GTCTCTCGGA CAGGTCAGAG

    462' CGGGTCGCCG GGTGGGGTCG CTGCAAAAAC CCTGCCCCGG CCGCAGCCGG AGAGGCGGAG
         ********** ********** ********** *******
    481″ CGGGTCGCCG GGTGGGGTCG CTGCAAAAAC CCTGCCC




1st Nucleotide Sequence
  File Name        : Reference Seq.gnu
  Sequence Size    : 5458

2nd Nucleotide Sequence
  File Name        : RDB7321R.fasta (Complementary)
  Sequence Size    : 512

  Unit Size to Compare = 1
  Pick up Location     = 1



[99.609% / 512 bp]     INT/OPT.Score : <   2036/  2036 >

    781' ATGCTAGGAA GAAGATTGGG TCTGGGAGCG GTGGTCCGCG TGGTTAGCTG CCTCCGCTCT
                                                                 *********
      1″                                                         CTCCGCTCT
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 841’ TTTTCGGTGT CCCCCCCAGT CCCGCCCTTG GGTGTGGGGA CGCCTGCCCC ACAAGTGTTT
      ********** ********** ********** ********** ********** **********
  10″ TTTTCGGTGT CCCCCCCAGT CCCGCCCTTG GGTGTGGGGA CGCCTGCCCC ACAAGTGTTT

 901’ AGGGAGGTCA GTGGGTTCCT CGCCCGTAGA GACACCGTTT ATGCCAAATG AGCACTCCTC
      ********** ********** ********** ********** ********** **********
  70″ AGGGAGGTCA GTGGGTTCCT CGCCCGTAGA GACACCGTTT ATGCCAAATG AGCACTCCTC

 961’ ATCCCCGCTC TTGATGGAGT CATGTCCTAG ACGTGAAACT ATGGGGCTGT GATCACAAGC
      ********** ********** ********** ********** ********** **********
 130″ ATCCCCGCTC TTGATGGAGT CATGTCCTAG ACGTGAAACT ATGGGGCTGT GATCACAAGC

1021’ AAATGTGTGG GCGGATCCGT TGCTTGGGTT CTTCCCCGCC CCCTCTTTTT TTCGGACCAT
      ********** ********** ********** ********** ***** **** **********
 190″ AAATGTGTGG GCGGATCCGT TGCTTGGGTT CTTCCCCGCC CCCTCCTTTT TTCGGACCAT

1081’ GACGTCAAGG TGGGCTGGTG GCGGCAGGTG CGGGGTTGAC AATCATACTC CTTTAAGGCG
      ********** ********** ********** ********** ********** **********
 250″ GACGTCAAGG TGGGCTGGTG GCGGCAGGTG CGGGGTTGAC AATCATACTC CTTTAAGGCG

1141’ GAGGGATCTA CAGGAGGGCG GCTGTACTGT GCTTCGCCTT ATATAGGGCG ACTTGGGGCA
      ********** ********** ********** ********** ********** **********
 310″ GAGGGATCTA CAGGAGGGCG GCTGTACTGT GCTTCGCCTT ATATAGGGCG ACTTGGGGCA

1201’ CGCAGTAGCT CTCTCGAGTC ACTCCGGCGC AGTGTTGGGA CTGTCTGGGT ATCGGAAATC
      ********** ********** **********  ********* ********** **********
 370″ CGCAGTAGCT CTCTCGAGTC ACTCCGGCGC GGTGTTGGGA CTGTCTGGGT ATCGGAAATC

1261’ AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA
      ********** ********** ********** ********** ********** **********
 430″ AAGATCTGGC CTCGGCGGCC AAGCTTGGCA ATCCGGTACT GTTGGTAAAG CCACCATGGA

1321’ AGATGCCAAA AACATTAAGA AGGGCCCAGC GCCATTCTAC CCACTCGAAG ACGGGACCGC
      ********** ********** ***
 490″ AGATGCCAAA AACATTAAGA AGG
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