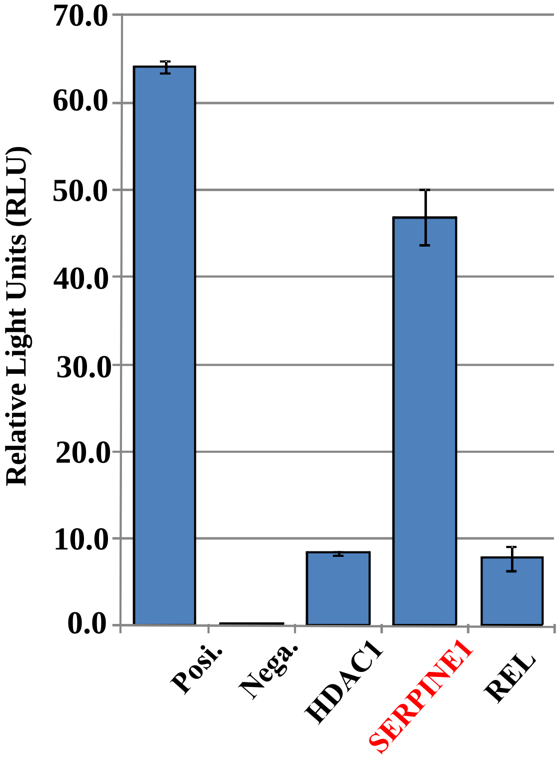
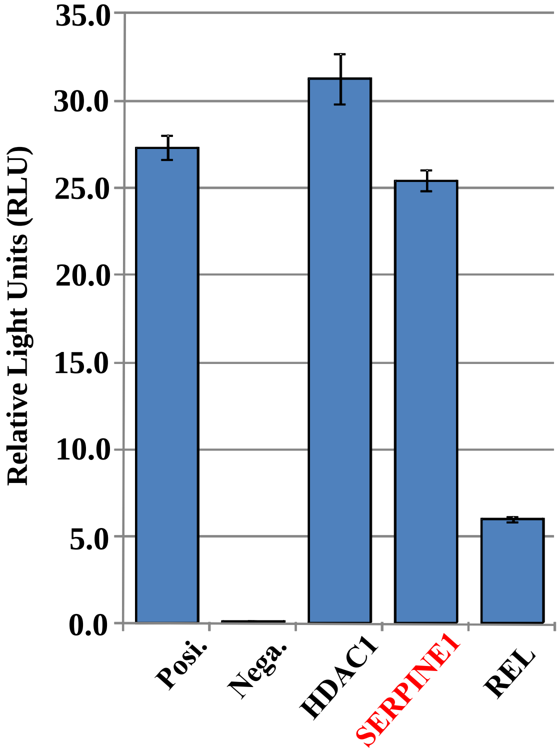
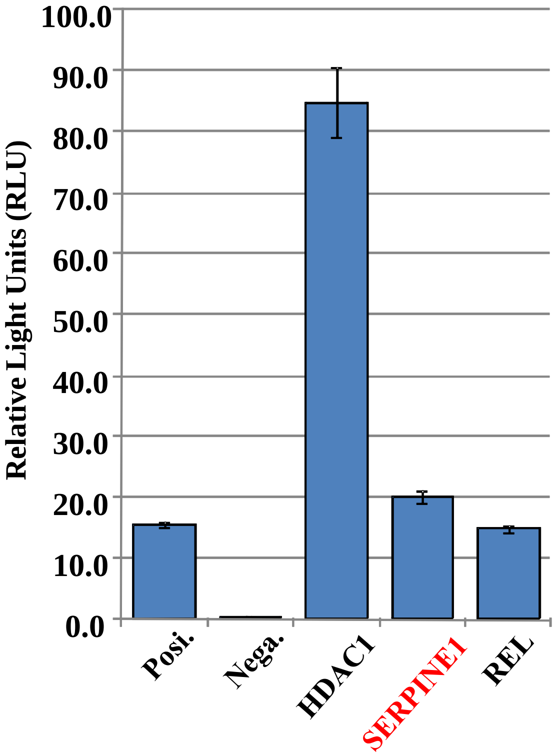
The Promoter Activities of Reporter Constructs


HeLa cells


HepG2 cells


Hep3B cells

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

HDAC1: pGL4-phHDAC1 (RDB# 7484)
SERPINE1: pGL4-phSERPINE1 (RDB# 7461)
REL: pGL4-phREL (RDB# 7481)

2010, DNA Bank, RIKEN BioResource Center

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[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.01.25

1st Nucleotide Sequence
  File Name         : Reference Seq 1.gnu
  Sequence Size     : 5720

2nd Nucleotide Sequence
  File Name         : RDB7461F.fasta
  Sequence Size     : 543

  Unit Size to Compare = 1
  Pick up Location     = 1



[97.561% / 533 bp]     INT/OPT.Score : <    287/  1957 >

   1'                     GG CCTAACTGGC CGGTACCTGA GCTCGCTAG- CCTCGAGGAT
                          ** ********** ********** *********  **********
   1" GGTGCCAGAA CTTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGA CCTCGAGGAT

  42' GCCACTCCTC ATCACTCGCA TTACCACNCA GAGCTCCACT CCCTGTCAGA TCAGCGGCGG
      ********** ********** ******* ** ********** ********** **********
  61" GCCACTCCTC ATCACTCGCA TTACCAC-CA GAGCTCCACT CCCTGTCAGA TCAGCGGCGG

 102' CATTAGATTC TCATAGGANG CTCGAACCCT ATTCTAAACT GTTCATGTGA GGGATCTAGG
      ********** ******** * ********** ********** ********** **********
 120" CATTAGATTC TCATAGGA-G CTCGAACCCT ATTCTAAACT GTTCATGTGA GGGATCTAGG

 162' TTGCAAGCTN CCCTATGAGA ATCTAATGCC TGATGATCTG TCACGGTCTC CCATCACCCC
      *********  ********** ********** ********** ********** **********
 179" TTGCAAGCT- CCCTATGAGA ATCTAATGCC TGATGATCTG TCACGGTCTC CCATCACCCC

 222' NTAGATGGGA CCATCTAGTT GCAGGAAAAC AAGCTCAGGG CTCCCACTGA TNTCTACACG
       ********* ********** ********** ********** ********** * ********
 238" -TAGATGGGA CCATCTAGTT GCAGGAAAAC AAGCTCAGGG CTCCCACTGA T-TCTACACG
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    282’ ATGGTGAATT GTGGAATTAT TTCATTATAT ATATTACAAT GTNAATAATA ATAGAAATAA
         ********** ********** ********** ********** ** ******* **********
    296″ ATGGTGAATT GTGGAATTAT TTCATTATAT ATATTACAAT GT-AATAATA ATAGAAATAA

    342’ AGCACACAAT AAATGTAATG TGCTTGAATC ATCNCCGAAA CCATCCCACC CTGGTCTGTG
         ********** ********** ********** *** ****** ********** **********
    355″ AGCACACAAT AAATGTAATG TGCTTGAATC ATC-CCGAAA CCATCCCACC CTGGTCTGTG

    402’ AAAAAATTGT CTTCCATGAA ACCANGTCCC TGGTGCCAAA AACGTTGAGG ACCACTGCTC
         ********** ********** **** ***** ********** ********** **********
    414″ AAAAAATTGT CTTCCATGAA ACCA-GTCCC TGGTGCCAAA AACGTTGAGG ACCACTGCTC

    462’ CACAGAATCT ATCGGNTCAC TCTTCCTCCC CTCACCCCCT TGCCCTAAAA GCACACCCTG
         ********** ***** **** ********** ********** ********** **********
    473″ CACAGAATCT ATCGG-TCAC TCTTCCTCCC CTCACCCCCT TGCCCTAAAA GCACACCCTG

    522’ CAAACCNTGC CATGAATTGA CACTCTGTTT CTATCCCTTT TCCCCTTGTG TCTGTGTNCT
         ******.  * *
    532″ CAAACCTGCC CC




1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5720

2nd Nucleotide Sequence
  File Name         : RDB7461R.fasta (Complementary)
  Sequence Size     : 455

  Unit Size to Compare = 1
  Pick up Location     = 1


[97.831% / 461 bp]     INT/OPT.Score : <    323/  1694 >
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1141' GGGGTCCTAG GCTTTTTGGG TCACCCGGCA TGGCAGACAG TCAACCTGGC NAGGACATCC
               * ********** ********** ********** **********  *********
   1″         GG GCTTTTTGGG TCACCCGGCA TGGCAGACAG TCAACCTGGC -AGGACATCC

1201' GGGAGAGACA GACACAGGCA GAGGGCAGAA AGGTCAAGGG ANGGTTCTCA GGCCAAGGCT
      ********** ********** ********** ********** * ******** **********
  52″ GGGAGAGACA GACACAGGCA GAGGGCAGAA AGGTCAAGGG A-GGTTCTCA GGCCAAGGCT

1261' ATTGGGGTTT GCTCAATTGT TCCTGAATGC TCNTTACACA CGTACACACA CAGAGCAGCA
      ********** ********** ********** ** ******* ********** **********
 111″ ATTGGGGTTT GCTCAATTGT TCCTGAATGC TC-TTACACA CGTACACACA CAGAGCAGCA

1321' CACACACACA CACACACATG CCTNCAGCAA GTCCCAGAGA GGGAGGTGTC GAGGGGGACC
      ********** ********** *** ****** ********** ********** **********
 170″ CACACACACA CACACACATG CCT-CAGCAA GTCCCAGAGA GGGAGGTGTC GAGGGGGACC

1381' CGCTGGCTGT TCAGNACGGA CTCCCAGAGC CAGTGAGTGG GTGGGGCTGG AACATGAGTT
      ********** **** ***** ********** ********** ********** **********
 229″ CGCTGGCTGT TCAG-ACGGA CTCCCAGAGC CAGTGAGTGG GTGGGGCTGG AACATGAGTT

1441' CATCTNATTT CCTGCCCACA TCTGGTATAA AAGGAGGCAG TGGCCCACAG AGGAGCNACA
      ***** **** ********** ********** ********** ********** ****** ***
 288″ CATCT-ATTT CCTGCCCACA TCTGGTATAA AAGGAGGCAG TGGCCCACAG AGGAGC-ACA

1501' GCTGTGTTTG GCTGCAGGGA TCAAGATCTG GCCTCGGCGG CCAAG-CTTG GCAATCCGGT
      ********** ********** ********** ********** ***** **** **********
 346″ GCTGTGTTTG GCTGCAGGGA TCAAGATCTG GCCTCGGCGG CCAAGTCTTG GCAATCCGGT

1560' ACTGTTGGTA AAGCCACCAT GG-AAGATGC CAAAAACATT AAGAAGGGCC CAGCGCCATT
      ********** ********** ** ******* **** ***** **********
 406″ ACTGTTGGTA AAGCCACCAT GGTAAGATGC CAAACACATT AAGAAGGGCC
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