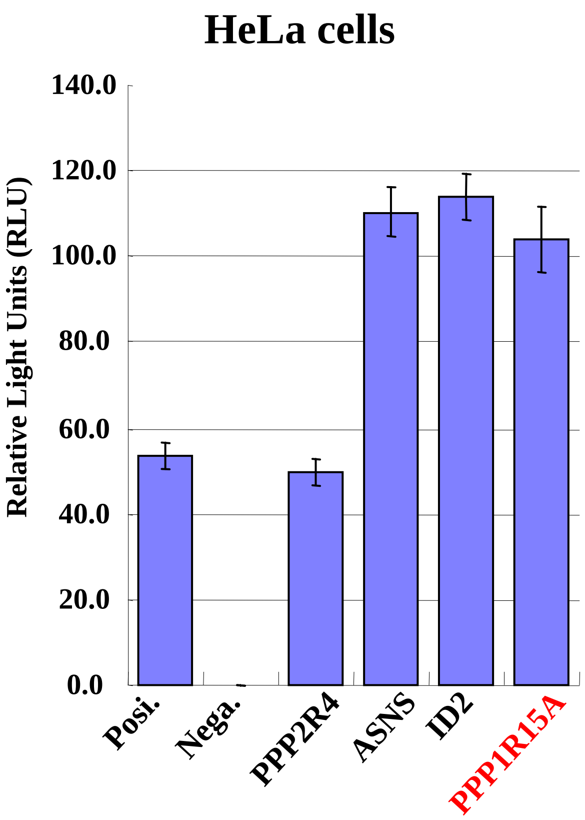
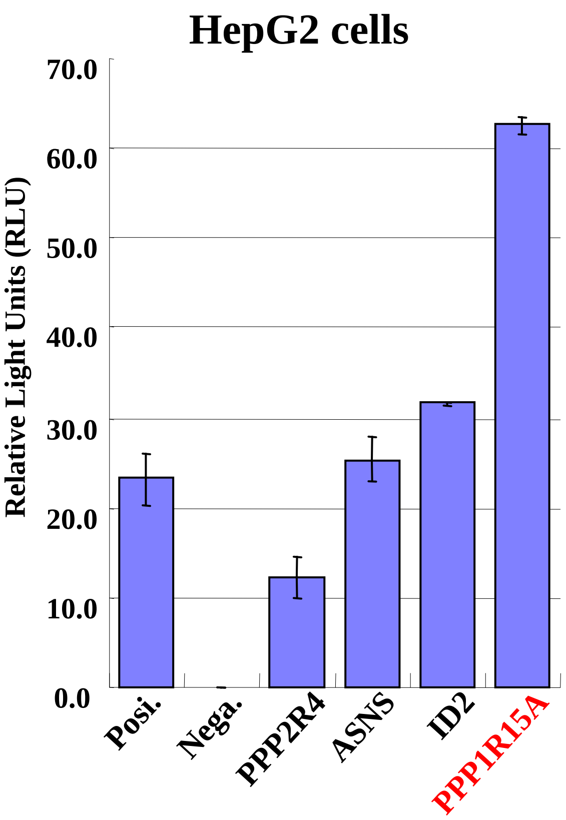
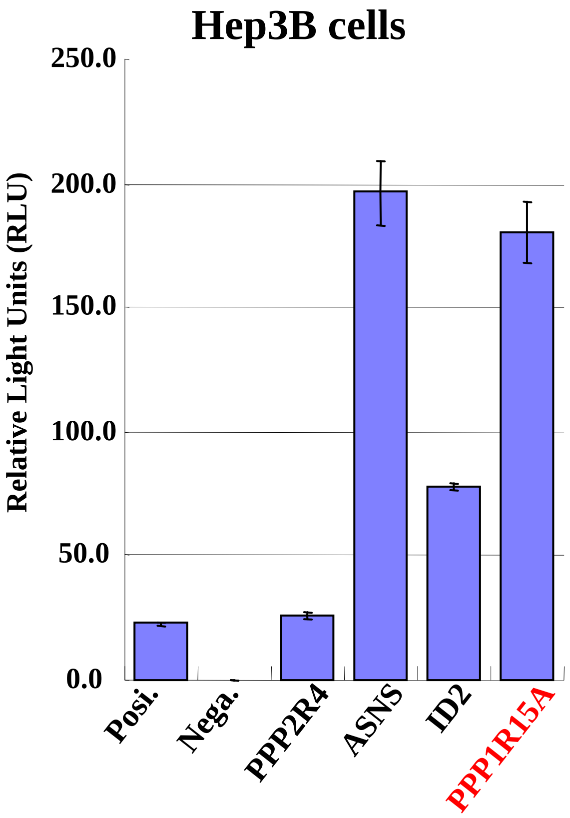
The Promoter Activities of Reporter Constructs







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

PPP2R4: pGL4-phPPP2R4 (RDB#7294)
ASNS: pGL4-phASNS(RDB#7305)
ID2:pGL4-phID2 (RDB#7306)
PPP1R15A: pGL4-phPPP1R15A (RDB#7307)

2009, 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.gnu
  Sequence Size      : 5488

2nd Nucleotide Sequence
  File Name          : RDB7307F.fasta
  Sequence Size      : 636

  Unit Size to Compare = 1
  Pick up Location     = 1



[72.562% / 605 bp]     INT/OPT.Score : <    179/  1020 >

      1’                                GG CCTAACTGGC CGGTACCTGA GC-TCGCTAG
                                        ** * ***** **      *** *  * * ***
      1″ CATTATAAAG ACAGCCGATC AAACAANCGG CTTAACT-GC GATCGCCTAA CCATAGCTCC

     32’ CCTCGAGGAT CAGAGTGAGA CGCCTACTCA AAAAATAAAN TAGGCTGGGT GCA-GTAG-C
            *   *    * *  ****    * *     ******** . * *   **** * * **** *
     60″ AACCACAGTA AACATCGAGA GCACCATCAC AAAAATAATT TTGATCGGGT GAACGTAGAC

     90’ TCACGCCTAT AAT-CCT-AA CACTTTGGGA AGCCNGAGGC AGG-CAGACT GCCTGAG-CT
          *** ** ** *** *** ** ********** ** *.  * * *** **** * ******* **
    120″ ACACACC-AT AATACCTAAA CACTTTGGGA AGACCAGGAC AGGACAGATT GCCTGAGACT

    146’ CAGGAGTTCG AG-AACAGCC TGGG-CAACN ATGG-CGAAA C-ACTGTCTC T-ACT-AAAA
         ********** ** ******* **** *** . **** ***** * ******** * *** ****
    179″ CAGGAGTTCG AGAAACAGCC TGGGACAAAC ATGGACGAAA CAACTGTCTC TAACTAAAAA

    200’ ATACAAAAAA TTAGCTGAGT GTGGNTAGTG CGTG-CCTGT AATCCCAG-C TACTCGGAGG
         *********  *   ****** **** ***** **** ***** ******** * **********
    239″ ATACAAAAAT TAGACTGAGT GTGG-TAGTG CGTGACCTGT AATCCCAGAC TACTCGGAGG
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258' -CTGAAGAGG GAGAATCGNC TTGAACCCGG AAGATGGAGG TTGCAGTGAG -CCGAGAT--
      ********* ********.  *  ******* ********** **********  *******
298" ACTGAAGAGG GAGAATCGCT TGAAACCCGG AAGATGGAGG TTGCAGTGAG ACCGAGATAC

314' CACG-CCATT GCANCTCCAG -CCTCGGTGA C-AGAG-CGA G-ACTCCATC TCAAAAAAAA
      *** ***** **********  ********* * **** *** * ******** **********
358" AACGACCATT GCANCTCCAG ACCTCGGTGA CAAGAGACGA GAACTCCATC TCAAAAAAAA

369' ATAAAAAANA TAAAAAATAA CAAA------ --TAAATAAA TAGG--CCTG GAGTGGTGGC
     ********.   * *******  ***         ******** ****  **** **********
418" ATAAAAAAAT AACAAAATAA TAAATAACCN AATAAATAAA TAGGACCCTG GAGTGGTGGC

419' TC-ACG--CC TGNCAATCCC AG--CACTTT -GGGA--GGC CAA--GGCA- GGCAGAACAC
     ** ***  ** **. *  *** **   *****  ****  * * ***  * **  ***** * **
478" TCAACGACCC TGCAATCCCC AGCCAACTTT GGGGAGGGAC CAAGGGACAG GGCAGGAAAC

468' CTGAGGTCAG GNAGTTCGAG ACCAGCC-TA GCAAACATGG TGAAATCCCG TCTCAGAAAA
          *  ** *.     *** *  * **  *  ** ** * *   ***   *  *    * ***
538" AACCTG-AAG GTTCAGGGAG ATAAACCGAA ACAGACCTAG CCAAA---CA TGGGTG-AAA

527' ATANAATAAT GAATAAATAA ATAAATAAAT AGGCCGGGCG CGGTGACTCA CGCCNTGTAA
     ** .  *  *  *  *** **  **..*****  **
593" ATCCCGT-CT CAGAAAAAAA TTANNTAAAT TGGGAAATTA TCTTT
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1st Nucleotide Sequence
  File Name         : Reference Seq.gnu
  Sequence Size     : 5488

2nd Nucleotide Sequence
  File Name         : RDB7307R.fasta (Complementary)
  Sequence Size     : 725

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

```
[84.311% / 733 bp]     INT/OPT.Score : <    436/  1987 >

 601' GAGGCCAAGG CGGGAGGATC CCCTGACGTC GNGGAGTTCC AGACCAGCCT GACCAACATG
                                                                   * *
   1″                                                             CCGTT

 661' GAGAAACTAC GTCTCTACTA AANCAAATAC AAAATTAGCC GGGCGTGGCG GCACATGCCT
       ***** **   * .  * ** **. **  *   ****  *** * *** **    * ** ****
   6″ CAGAAAATAA ATANGGA-TA AATAAATAAA TAAATAGGCC GTGCGCGG-T ACTCACGCCT

 721' GCAATCCCAG CACNTTTGGG AGGCCAAGGC GGGAGGA-TC CCCTGACGTC GGGA-GTTCC
      * .******* *** ****** ****** *** ******* ** **********  *** ** **
  64″ G-NATCCCAG CAC-TTTGGG AGGCCAGGGC GGGAGGATTC CCCTGACGTC TGGAGGTGCC

 779' AGACCANGCC TGACCAACA- TGGAGAAACT ACGTCTCTAC TAAACAAATA CAAAATTANG
      ****** *** *********  ********** ********** ********** ***.****.*
 122″ AGACCA-GCC TGACCAACAT TGGAGAAACT ACGTCTCTAC TAAACAAATA CAANATTAGG

 838' CCGGGCGTGG CGGCACATGC CTGCAATCCC AGATACTCGG GATGCTGAGN GCAGGAGAAT
      *** ****** ********** ********** ********** *********  **********
 181″ CCGTGCGTGG CGGCACATGC CTGCAATCCC AGATACTCGG GATGCTGAG- GCAGGAGAAT

 898' C-GCTTGAAC CCCGAA-GGC GGAGGTTGCG GTGAGCCGAG ATNCGCCCC- TTTGCATTCC
      * ******** ****** *** ********** ********** **. *****  **********
 240″ CTGCTTGAAC CCCGAAGGGC GGAGGTTGCG GTGAGCCGAG ATCTGCCCCT TTTGCATTCC

 955' AGCC-TGAGC AACAAGAGCA AAACTCCGCC TCAAANATAA CTAACTAAAT AAATAAATAA
      **** ***** ********** ********** ***** **** ********** **********
 300″ AGCCTTGAGC AACAAGAGCA AAACTCCGCC TCAAA-ATAA CTAACTAAAT AAATAAATAA

1014' ATTGGGGTGG GAAGGCATTG ACCCTGNAGC TGAGAGAGAA CTGGCTCGCT GTTGAAGCAG
      ********** ********** ****** *** ********** ********** **********
 359″ ATTGGGGTGG GAAGGCATTG ACCCTG-AGC TGAGAGAGAA CTGGCTCGCT GTTGAAGCAG

1074' GGCCACGCAT TTGATTGNAC AGTTCGTTTG TTGGAGGGGC GTGGTCACGC TCGGAAACTC
      ********** ******* ** ********** ********** ********** **********
 418″ GGCCACGCAT TTGATTG-AC AGTTCGTTTG TTGGAGGGGC GTGGTCACGC TCGGAAACTC
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1134’ CGCCGTGANC GTTGCAAAAG CTGGAATCTC CGCGAGAAGT CCTGTCTTAC TTCCACTTCN
      ******** * ********** ********** ********** ********** *********
 477″ CGCCGTGA-C GTTGCAAAAG CTGGAATCTC CGCGAGAAGT CCTGTCTTAC TTCCACTTC-

1194’ CCACCCTTCG GGTTGCGGTC TCGAAACCCC GCCTCTCTTC GTGACGTCAG NCACGCCGGG
      ********** ********** ********** *********  ***  **  *  ** ** **
 535″ CCACCCTTCG GGTTGCGGTC TCGAAACCCC GCCTCTCTT- GTGTAGTTCG -CA-GCGGGT

1254’ CGCGGTAGG- CTATAAAAG- CCTAGTGGCC ATTGTGATCA AGATCTGGCC TCGGCGGCCA
      *****. **  *********  *** ** * *   ****       ***  * ** * *  * **
 592″ CGCGGNTGGT CTATAAAAGT CCTGGTAGAC CATGTGTATC GGAT-GGTCC TGGTGGTCCG

1312’ AGCTTGGCAA -TCCGGTACT GTTGGTAAAG CCACCATGGA AGATGCCAAA AACATTAAGA
      *  *   ***  * **    * *  * *  **   ** *  **  * *    *  * * ****
 651″ ACGTGTTCAA NTGCGCCTAT GGGGTTTTAG TAACTACCGA GGGT----AG ACCTTTAAAC

1371’ AG-GGCCCAG CGCCATTCTA CCCACTCGAA GACGGGACCG CCGGCGAGCA GCTGCACAAA
      ** ******
 707″ AGAGGCCCAA ACTNTAATT
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