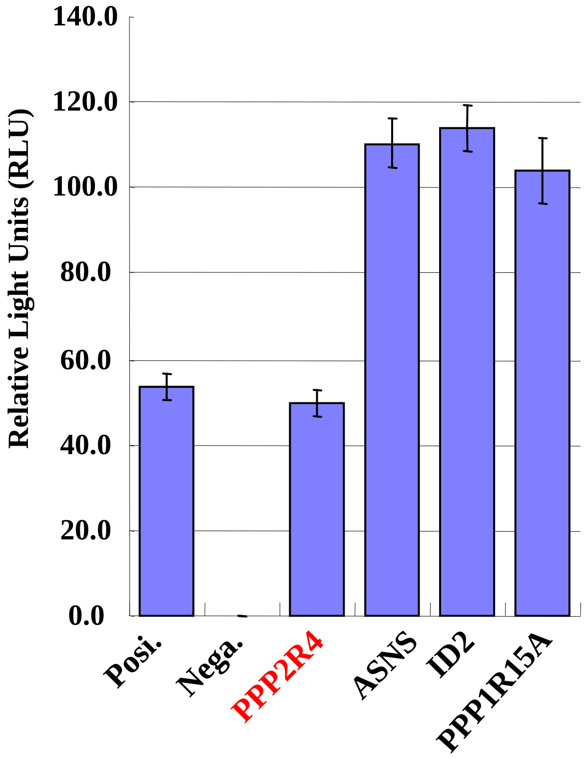
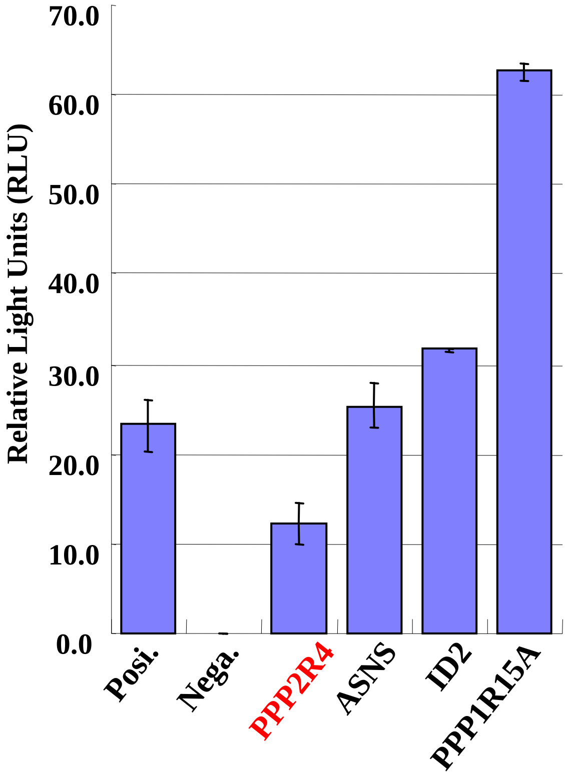
The Promoter Activities of Reporter Constructs

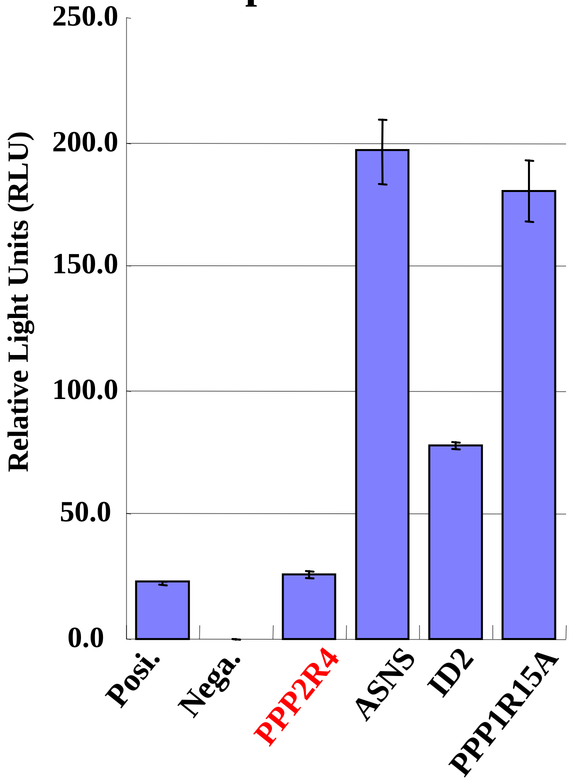
HeLa cells



HepG2 cells



Hep3B cells



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     : 5483

2nd Nucleotide Sequence
  File Name         : RDB7294F.fasta
  Sequence Size     : 661

  Unit Size to Compare = 1
  Pick up Location     = 1



[84.170% / 657 bp]     INT/OPT.Score : <    252/  1648 >

  1'                                     GGCCTAA CTGGCC-GGT ACCTGAGCTC
                                         ******* ****** *** **********
  1″ AGNTGCAATT CGCTGGTGCC AGAACATTTC TCTGGCCTAA CTGGCCTGGT ACCTGAGCTC

 27' GCTAGCCTCG AGGATCTTGG ATCAGGGACG GAAGGGACTG AAATTAGGCN TAGCATCCGG
     ********** ********** ********** ********** *********  **********
 61″ GCTAGCCTCG AGGATCTTGG ATCAGGGACG GAAGGGACTG AAATTAGGC- TAGCATCCGG

 87' GCTGCTCACC GGGGAGGACT GAGGGGTAGA TATAGCCAGG NGTGGGGAAG GGGGCTAGAG
     ********** ********** ********** **********  ********* **********
120″ GCTGCTCACC GGGGAGGACT GAGGGGTAGA TATAGCCAGG -GTGGGGAAG GGGGCTAGAG

147' GGGAGGATAT AGCCAGGGTG GGGAAGGGGG CNTGGAGGGA AGGATACAGC CAGGGTGGGG
     ********** ********** ********** * ******** ********** **********
179″ GGGAGGATAT AGCCAGGGTG GGGAAGGGGG C-TGGAGGGA AGGATACAGC CAGGGTGGGG

207' AAGGGGGCTG GAGGGGAGGG AGNACCATGG GGCTGCCACC TGCCAGTTCT GAGGCCTTTC
     ********** ******* ** ** ******* ********** ********** **********
238″ AAGGGGGCTG GAGGGGAAGG AG-ACCATGG GGCTGCCACC TGCCAGTTCT GAGGCCTTTC
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267’ TAGCTTGATG CCTNCCGCGT GTTTCTCTGG CCACACACAA TTCCCCAGGG ACCGTCTGAT
     **** ***** ***.** *** ********** ********** ********** **********
297″ TAGCCTGATG CCTCCC-CGT GTTTCTCTGG CCACACACAA TTCCCCAGGG ACCGTCTGAT

327’ AAACNCAAAG GAGTGTGACC AACTGGACAG GGTCGGAGGA GTGGCTCTGG CCTAANGCGT
      ***.****  **********  *** ****      **  ** *  *******  **  .***
356″ -AACCCAAA- GAGTGTGACC -ACT-GACA- ----GGTTGA GATGCTCTGG -CT--AGCG-

387’ GCGACGGGTG TGTCAATCGG AGAATAACTG GGAGAGTGAG CTAGGGNTCT GGATGCTCCT
     ****  **** **** ***     ***  *** ********** ***  *.*** * ********
403″ GCGA--GGTG TGTC-ATC-- -GAAATACT- GGAGAGTGAG CTA--GGTCT GAATGCTCCT

447’ GGTCTCTC-T CCCCT-ACCG GCCT-GTCTC -TGGG--TCT AAGNGG---T GGGGGTGC-T
     *** **** * *** * **** **** ** **  ****   ** ***.**     **** * * *
454″ GGTTTCTCTT CCCTTAACCG GCCTCGTTTC TTGGGTTCCT AAGGGGTTGG GGGGTTCCTT

497’ A-ACTGAA-- ---GCCGGGG TCCCCCTT-- GTCTTTCC-T GGGTCGTNTG GAACTG-AAT
     *  *****       *  ***  ********    * ***** * *******. *  ***** ***
514″ ACCCTGAAGC CCCGGGGGGT TCCCCCTTGG TTTTTTCCTT GGGTCGTTGG AAACTGAAAT

547’ GCTCCAGGAC GTGGGTTTAA TCCCGCTTCT GACCTTGCGN CCCCAATCTC CTGCTCTGCC
     *** *** **  **** **** * ** * *** *  ******  *******  *  ***   ***
574″ GCTTCAGAAC CTGGG-TTAA TTCCCCCTCT GGACTTGCG- CCCCAATTCC TTGCCTGGCC

607’ AAACCT-GGG ACGCCCGCCT GACCCCACCC CNATCAGCTG GAGGCCGGGT CGAACAGCGG
      ***** *** *   *** *  ** *** * *
632″ CAACCTGGGG AACGCCGGCG GAACCCCCAC
```

1st Nucleotide Sequence
  File Name : Reference Seq.gnu
  Sequence Size : 5483

2nd Nucleotide Sequence
  File Name : RDB7294R.fasta (Complementary)
  Sequence Size : 777

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Unit Size to Compare = 1
Pick up Location     = 1


[94.843% / 795 bp]     INT/OPT.Score : <    397/  2705 >

541' CTGAATGCTC CAGGACGTGG GTTTAATCCC GCTTCTGACC TTGCGNCCCC AATCTCCTGC
                                                   **** *** ******
  1″                                               CCCC AATTTCCTGC

601' TCTGCCAAAC CTGGGACGCC CGCCTGACCC CACCCCNATC AGCTGGAGGC CGGGTCGAAC
      *** ***** ** ******* ********** ****** *** ******* ** **********
 15″ -CTG-CAAAC CT-GGACGCC CGCCTGACCC CACCCC-ATC AGCTGGA-GC CGGGTCGAAC

661' AGCGGCCGCA GGACGCGGTC TCCGTTCNCC GGACGCAACC GCACGGCCCG CCCAGGCCGT
     ********** * ******** ******* ** * ******** ********** ***** ****
 70″ AGCGGCCGCA GAACGCGGTC TCCGTTC-CC GAACGCAACC GCACGGCCCG CCCAGCCCGT

721' CCAGGGCCCT CAGGCCCGNG GATCCGCCGC ACTCACCACG GTCCTGGCAG CGAAGGCTAA
     *** ****** ******** * ********** ********** ********** **********
129″ CCA-GGCCCT CAGGCCCG-G GATCCGCCGC ACTCACCACG GTCCTGGCAG CGAAGGCTAA

781' CATCTTCGCN TGCCCGTCCG CGGACACGCA GTCCGCTCCG CCCCACACAC CGGGCAAAGT
     *********  ********** ********** ********** ********** **********
187″ CATCTTCGC- TGCCCGTCCG CGGACACGCA GTCCGCTCCG CCCCACACAC CGGGCAAAGT

841' NCCGCGCCGC CGCCGCCGCG GCTGGGGTCG GTGGGTCCTT GCTAGAGCCT TNCGGGCCAA
      ********* ********** ********** ********** ********** * ********
246″ -CCGCGCCGC CGCCGCCGCG GCTGGGGTCG GTGGGTCCTT GCTAGAGCCT T-CGGGCCAA

901' GGTCGCTGAG TTACAGCCGC CAGCCGGTAG AGGCAGCCCC GCNGCCCACC CTCTGGGCCG
     ********** ********** ********** ********** ** ******* **********
304″ GGTCGCTGAG TTACAGCCGC CAGCCGGTAG AGGCAGCCCC GC-GCCCACC CTCTGGGCCG

961' AGCGGGCTGC GGGAAGGCAC CCGGGGAGGA GGANCTCGCG AGGCGGGGCC TGGGCCGGTA
     ********** *** ****** ********** *** ****** ********** **********
363″ AGCGGGCTGC GGGCAGGCAC CCGGGGAGGA GGA-CTCGCG AGGCGGGGCC TGGGCCGGTA
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1021’ GCGGGCCCCG GGCGGGCAAC GGTGNCCCGG GAGGTTGGCT GTGGGGCGGG GACGGGGCAT
      ********** ********** **** ***** ********** ********** * ********
 422″ GCGGGCCCCG GGCGGGCAAC GGTG-CCCGG GAGGTTGGCT GTGGGGCGGG GGCGGGGCAT

1081’ CGATGGGGCG GAGTCNTCCT TGAGGAGGGA CAGGAGGGGC GGGGACGGAG GGGCGGGGCG
      ********** ***** **** ********** ********** ********** **********
 481″ CGATGGGGCG GAGTC-TCCT TGAGGAGGGA CAGGAGGGGC GGGGACGGAG GGGCGGGGCG

1141’ TCGCCCNGGT AGCGGGTCGC AGTAGGCTGG CTGCGAGTCG GGGGCGGGAC CACGGCGNGG
      ****** *** ********** ********** ********** ********** ******* **
 540″ TCGCCC-GGT AGCGGGTCGC AGTAGGCTGG CTGCGAGTCG GGGGCGGGAC CACGGCG-GG

1201’ CGGGGACAGA GGGGCAGGGC CGAGGGCGAG TCATTGAGAC CTGTGGAGNG AGGAAGGAGG
      ********** ********** ***** **** ********** ******** * **********
 598″ CGGGGACAGA GGGGCAGGGC CGAGGACGAG TCATTGAGAC CTGTGGAG-G AGGAAGGAGG

1261’ AGGTCAC-CG TCCAGCTGTC TCTATCAAGA TCTGGCCTCG GCGGCCAAGC TTGGCAATCC
      ******* ** ********** ********** ********** **********  *********
 657″ AGGTCACACG TCCAGCTGTC TCTATCAAGA TCTGGCCTCG GCGGCCAAGC -TGGCAATCC

1320’ GGT-ACTGTT GG--TAAAGC CACCATGGAA G-ATGCCAAA AACATTAAGA AGGGCCCAGC
      *** ****** **   ***** ********** * ********  **** *  * * * * * **
 716″ GGTGACTGTT GGCTAAAAGC CACCATGGAA GTATGCCAAA CACATAAGCA AAGCCTCTGC

1376’ GCCATTCTAC CCACTCGAAG ACGGGACCGC CGGCGAGCAG CTGCACAAAG CCATGAAGCG
      .
 776″ NA
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