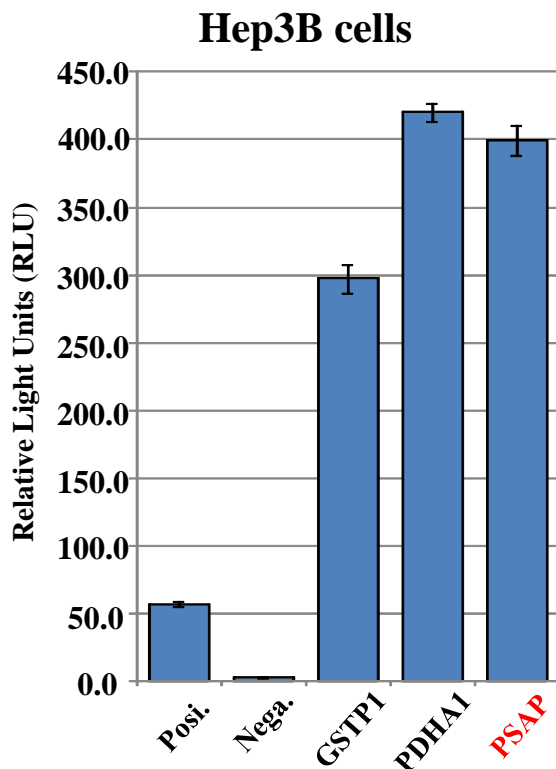
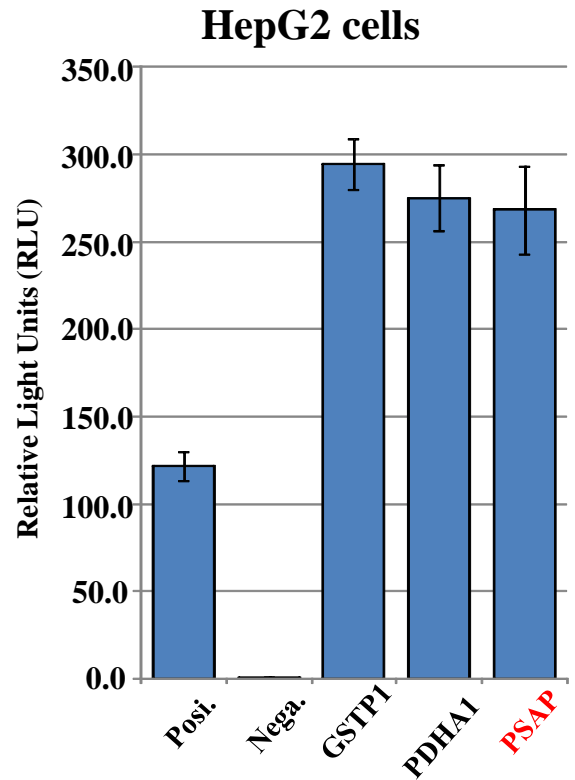
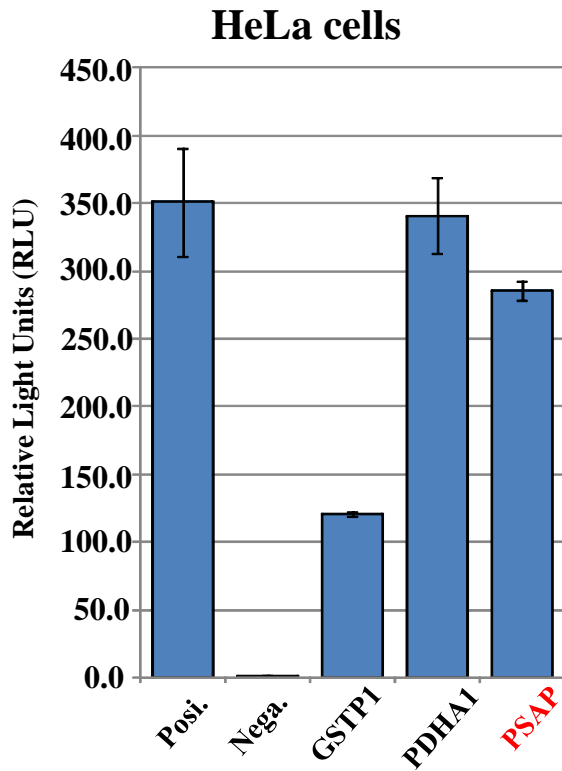


# The Promoter Activities of Reporter Constructs



**Posi.:** pGL3 Control Vector  
(SV40 promoter)

**Nega.:** Empty Vector

**GSTP1:** pGL4-phGSTP1 (RDB# 7477)

**PDHA1:** pGL4-phPDHA1 (RDB# 7514)

**PSAP:** pGL4-phPSAP (RDB# 7515)

[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2009.09.30

1st Nucleotide Sequence

File Name : Reference Seq.gnu  
Sequence Size : 5660

2nd Nucleotide Sequence

File Name : RDB7515F.fasta  
Sequence Size : 704

Unit Size to Compare = 1  
Pick up Location = 1

[99.710% / 690 bp] INT/OPT.Score : < 2438/ 2728 >

```
1'          GGCCTA ACTGGCCGGT ACCTGAGCTC GCTAGCCTCG AGGATGGGGG
          *****
1" CAGAACATGT CTCTGGCCTA ACTGGCCGGT ACCTGAGCTC GCTAGCCTCG AGGATGGGGG

47' CACTTAGGGA GA-TTGCAGG GGAGCAGAAC TGAA-GGTTG TGAGGCCTTA GTCCTGGGG
          ***** ** *****
61" CACTTAGGGA GATTGCAGG GGAGCAGAAC TGAAGGGTTC TGAGGCCTTA GTCCTGGGG

105' TTGTTCTCCA GAGCGGATTG CAGATTGGAG GAAGTTGGAG GAACTGTAGG TTTGCCCTTC
          *****
121" TTGTTCTCCA GAGCGGATTG CAGATTGGAG GAAGTTGGAG GAACTGTAGG TTTGCCCTTC

165' CTGGGTCAGG AAACCTGGCT TCGGGCCAGG TTCTATCTCT ACCTGTTGTG TGACCTTGA
          *****
181" CTGGGTCAGG AAACCTGGCT TCGGGCCAGG TTCTATCTCT ACCTGTTGTG TGACCTTGA

225' TAAACGTCTT GCCCTCTCCT AGGCTCAATG TCCCTACAGG TAAATGACCT CTAAGTGCCT
          *****
241" TAAACGTCTT GCCCTCTCCT AGGCTCAATG TCCCTACAGG TAAATGACCT CTAAGTGCCT
```

```

285' GCCCTAAGGG GCTAAGATTC CCCTCCTTTC CCTGCCTTGC GGTGGCAGG TTCTTATCCT
*****
301" GCCCTAAGGG GCTAAGATTC CCCTCCTTTC CCTGCCTTGC GGTGGCAGG TTCTTATCCT

345' TCTGGAGAGG GTCATCATCA TTCTCTGTTC AGGTCCTGGC AGGGGCAGCC ACAGGCAGAG
*****
361" TCTGGAGAGG GTCATCATCA TTCTCTGTTC AGGTCCTGGC AGGGGCAGCC ACAGGCAGAG

405' GGTCTTTGGG TCTTAATTTT TGAAGGCTTC CATGTCACAT AAAACGTTGA TTACATAAAT
*****
421" GGTCTTTGGG TCTTAATTTT TGAAGGCTTC CATGTCACAT AAAACGTTGA TTACATAAAT

465' TTGTTATGCT TTTCTCTTAA GCTGTCTCGT TACAGGAGTG TTGGTTGTGA CTCTTATGAT
*****
481" TTGTTATGCT TTTCTCTTAA GCTGTCTCGT TACAGGAGTG TTGGTTGTGA CTCTTATGAT

525' CTCTTATGAT GGGTGAGGAA TGGTATTACA TCTTTAACGG TACCACAATG TGAGGCTTAA
*****
541" CTCTTATGAT GGGTGAGGAA TGGTATTACA TCTTTAACGG TACCACAATG TGAGGCTTAA

585' AAGTTTTTTG TTTTTTTTTT TTTGGTGATG GGAATCTCTC TCGCTCTGTG GTCCAGGCTG
*****
601" AAGTTTTTTG TTTTTTTTTT TTTGGTGATG GGAATCTCTC TCGCTCTGTG GTCCAGGCTG

645' CAGTGCAGTA GTGCGATCTT GACTCACGGC AACCTCCACC TCCGGGTTT AAGCAATTTT
*****
661" CAGTGCAGTA GTGCGATCTT GACTCACGGC AACCTCCACC TCCC

```

1st Nucleotide Sequence

File Name : Reference Seq. gnu  
Sequence Size : 5660

2nd Nucleotide Sequence

File Name : RDB7515R. fasta (Complementary)  
Sequence Size : 303



Unit Size to Compare = 1  
Pick up Location = 1

[93.729% / 303 bp] INT/OPT. Score : < 1110/ 1122 >

```
1201' CTCTGACCTA TTCAATTAGT AGGGCTTTTC TTTTATGACC TTTCCCTTCC CTTTCTCCAA
                                     ..... * * ****
1" NNNNNNNNAA CCTCCTCCT

1261' GTTCTTCCTC ACTCCTCCCC ATAGCCCTTC CTTTCGCCCC TCCCATTGCC CCCTCCTATT
      *****
21" CCGTTTCCTC ACTCCTCCCC ATAGCCCTTC CTTTCGCCCC TCCCATTGCC CCCTCCTATT

1321' GGCCTCCCCT TCGCGCAGGC GCCCTCAGAG GCGCTGAGTC AGGGCGCTGT TGAGCTCGGG
      *****
81" GGCCTCCCCT TCGCGCAGGC GCCCTCAGAG GCGCTGAGTC AGGGCGCTGT TGAGCTCGGG

1381' CAGGCCCGGA TGGGGCGGGG TTAGCGCCTG CGCTCTGGAC GGCTTTGGGG CAGGGCAGAT
      *****
141" CAGGCCCGGA TGGGGCGGGG TTAGCGCCTG CGCTCTGGAC GGCTTTGGGG CAGGGCAGAT

1441' TTATATCTGC GGGGGATCAA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG CAATCCGGTA
      *****
201" TTATATCTGC GGGGGATCAA TCAAGATCTG GCCTCGGCGG CCAAGCTTGG CAATCCGGTA

1501' CTGTTGGTAA AGCCACCATG GAAGATGCCA AAAACATTAA GAAGGGCCCA GCGCCATTCT
      ***** ** ***** ***
261" CTGTTGGTAA AGCCACCATG GAAGATGCCA AACACATTAA GAA
```

