



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

MMP2: pGL4-phMMP2 (RDB#7314)

IFNG: pGL4-phIFNG (RDB#7297)

INS: pGL4-phINS (RDB#7387)

PLAUR: pGL4-phPLAUR (RDB#7312)

PLAT: pGL4-phPLAT (RDB#7295)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.01.25

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5425

2nd Nucleotide Sequence

File Name : RDB7314F.fasta
Sequence Size : 735

Unit Size to Compare = 1
Pick up Location = 1

[93.333% / 690 bp] INT/OPT.Score : < 354/ 2310 >

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1' GGCCTAACT GGCCGGTACC
*
1" AAATGGGAAA GCCCTGACAT AATCAACACT CGATCTTTGC GAGAAACGCN TAAAACCCCA

20' TGAGCTCGCT AGCCTCGAGG ATTCCTCAG AGACGGTTGT CACAGGGAGA ACTNTCAAAA
*** ** * ** * * **.* **.* **.* **.* **.* **.* **.* **.* **.* **.*
61" TGACGTCACA GTCCACAGGT ATNTCCACAG AGACGTTGTA CACAGGGAGA ACTTTCAAAA

80' TTGGGATTGG ACCTGAGAGG CCACATGGAT TCTTGGCTTG GCGCNAGGAA AGGATTCAAG
***** ***** ***** ***** ***** ***** ***** *****
121" TTGGGATTGG ACCTGAGAGG CCACATGGAT TCTTGGCTTG GCGC-AGGAA AGGATTCAAG

140' AGTGAGTGGG GAATTCGTGG AACTGAGGGC TCCTCNCCT TTTAGACCA TATAGGGTAA
***** ***** ***** ***** ***** ***** ***** *****
180" AGTGAGTGGG GAATTCGTGG AACTGAGGGC TCCTC-CCCT TTTAGACCA TATAGGGTAA

200' ACCTCCCCAC ATTGCCATGG CATTANTAA ACTGCCATGG CACTGGTGGG TGCTTCCTTT
***** ***** ***** ** ***** ***** ***** *****
239" ACCTCCCCAC ATTGCCATGG CATTTA-TAC ACTGCCATGG CACTGGTGGG TGCTTCCTTT
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260' AACATGCTAA TGCATTANTA ATTAGCGTAA AATGAGCAGT GAGGATGACC AGAGGTCGCT
 ***** ** *****
 298" AACATGCTAA TGCATTA-TA ATTAGCGTAA AATGAGCAGT GAGGATGACC AGAGGTCGCT

 320' TTCTTTGCNC ATCTTGTTTT TGGCTGGCTT CTTCACTGCA TACTGTTTTA TCAGTGGGN
 ***** * *****
 357" TTCTTTGC-C ATCTTGTTTT TGGCTGGCTT CTTCACTGCA TACTGTTTTA TCAGTGGG-

 380' TCTTTGTGAC CTCTATCTTA TAAACCAGT CTTG-CCCAA TTTCTATCTC ANTCCTGTGA
 ***** ***** ***** **** ***** * *****
 415" TCTTTGTGAC CTCTATCTTA TAAACCAGT CTTGCCCAA TTTCTATCTC A-TCCTGTGA

 439' CCGAGAATGC GGACCCTCCT GGGAGTGCAG CCCAGCAGGT CTNCAGCCTC ATTTTACCCA
 ***** ***** ***** ***** ** *****
 474" CCGAGAATGC GGACCCTCCT GGGAGTGCAG CCCAGCAGGT CT-CAGCCTC ATTTTACCCA

 499' GCCCCTGTT CAAGATGGAG TCGCTCTGGT TCCNAACGTC TCTAACGCGG GGCCCTGAC
 ***** ***** ***** *** ***** ** *****
 533" GCCCCTGTT CAAGATGGAG TCGCTCTGGT TCC-AACGTC TCTAACGCGG GGCCCTGAC

 559' TGCTCTATTT CCCAAGGTGT ATCTNAGCAT CTCGCACTAT ACGAGGCCAA GTTAAGGCTT
 ***** ** *** ***** ***** ***** ***** ** *****
 592" TGCTCTA-TT CCCAAGGTGT ATCT-AGCAT CTCGCACTAT ACGAGG-CAA GTTAAGGCTA

 619' ACACATTTGC AGAAGNGAAA GAGGTAAGGA AGCAACCTGG GACCTTCCAC TGTCTCTGTT
 ***** ***** ***** ***** ***** ***** *****
 649" ACACATTTGC AGAAG-GAAA GAGGT-AGGA AGCAACCTGG GACC-TCCAC TGTCTCTGTT

 679' TCCATCNTCT CTCTTCCAT CTCTGTTTCCAT CCCAGAATCT CTCTGTCCCT ATCCCTANAA
 * **** ** ***** ** * *
 706" T-CATC-TCT CTCTTCCCTC CTGTTCTCCA GA

1st Nucleotide Sequence

File Name : Reference Seq. gnu
 Sequence Size : 5425



2nd Nucleotide Sequence

File Name : RDB7314R.fasta (Complementary)

Sequence Size : 185

Unit Size to Compare = 1

Pick up Location = 1

[91.979% / 187 bp] INT/OPT. Score : < 330/ 661 >

1081' GTAGGGGGGT GGNGGCAGAG AGGGGCGGGC CCGAGTGCGC CCCCCGCCCC CAGCCCCGCT
1" ** *****
NN NNNNNNNNCC CAGCCCCGCT

1141' CTGNCCAGCT CCCTCCAGC CCAGCCGGCT ACATCTGGCG GCTGCCCTCC CTTGNTTCC
*** ***** ***** ***** ***** ***** ***** *****
23" CTG-CCAGCT CCCTCCAGC CCAGCCGGCT ACATCTGGCG GCTGCCCTCC CTTG-TTCC

1201' GCTGCATCCA GACTTCCTCA GCGGATCAAG ATCTGGCCTC GGCGGCAAG CTTGGCAATC
***** ***** ***** ***** ***** ***** *****
81" GCTGCATCCA GACTTCCTCA GCGGATCAAG ATCTGGCCTC GGCGGCAAG CTTGGCAATC

1261' CGGTACTGTT GGTAAAGCCA CCATGGAAGA TGCCAAAAC ATTAAGAAGG GCCCAGCGCC
***** ***, * *** ***** ***** *****
141" CGGTACTGTT GGTNGA-CCA CCATGGAAGA TGCCAAAAC ATTA

