



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

TH: pGL4-phTH (RDB#7301)

GH2: pGL4-phGH2(RDB#7309)

TNF: pGL4-phTNF (RDB#7310)

IL6: pGL4-phIL6 (RDB#7313)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2009.06.25

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5422

2nd Nucleotide Sequence

File Name : RDB7301F.fasta
Sequence Size : 531

Unit Size to Compare = 1
Pick up Location = 1

[96.724% / 519 bp] INT/OPT. Score : < 544/ 1857 >

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1'          GG CCTAACTGGC CGGTACCTGA G-CTCGCTAG CCTCGAGGAT
          ** *****
1'' GTGCCAGAAC ATGTCTCTGG CCTAACTGGC CGGTACCTGA GACTCGCTAG CCTCGAGGAT

42' -TCTGGCCAT CTCTGCTGAC CCCAGAGGGN ATGGGGAGGC CTCCCCTTCC ACCAGAAGGG
          *****
61'' GTCTGGCCAT CTCTGCTGAC CCCAGAGTG- ATGGGGAGGC CTCCCCTTCC ACCAGAAGGG

101' CCAGAAGCCA CCCT-GGGCA GNGGGCATCA CTCTCCCTGG GTGGGGCAGC GGCTGGGAGC
          *****
120'' CCAGAAGCCA CCCTGGGGCA GGGGCAGTCA CTCTCCCTGG GTGGGGCAGC GGCTGGGAGC

160' AGGAGGTGCC AGNTGGGCGT GGGCTGGATG CGGG-TGCCT GCGGGGCGGA CATGGAACTT
          *****
180'' AGGAGGTGCC AG-TGGGCGT GGGCTGGATG CGGGTTGCCT GCGGGGCGGA CATGGAACTT

219' GGGGNGAGGC TCTAGGCTGG GGTGTCTC AAGGGAGTTC TCAGGTCACC CCAGNGTCA
          *****
239'' GGGG-GAGGC TCTAGGCTGG GGTGTCTC AAGGGAGTTC TCAGGTCACC CCAGG-GTCA
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279' CCCTCAACCC GGGGCCTGGT GGGGTAGAGG AGAAACTGCA AAGGTCNTCT CCAAGGGGAA
*****
297" CCCTCAACCC GGGGCCTGGT GGGGTAGAGG AGAAACTGCA AAGGTC-TCT CCAAGGGGAA

339' GGCATCAGGG CCCTCAGCAC TGAGGGACGT GCGTGCTNCT TTAAAGAAGG GGCCACAGGA
*****
356" GGCATCAGGG CCCTCAGCAC TGAGGGACGT GCGTGCT-CT TTAAAGAAGG GGCCACAGGA

399' CCCCGAGGGA AGCCAGGAGC TAGCAGTGNG GCCATAGAGG GGCTGAGTGG GGTGGGTGGA
*****
415" CCCCGAGGGA AGCCAGGAGC TAGCAGTG-G GCCATAGAGG GGCTGAGTGG GGTGGGTGGA

459' AGCCGTCCTT GGCCTGGTN CGCCCTGGCA ACCCTGGTGG GGACTGTGAT GCAGGAGGTG
*****
474" AGCCGTCCTT GGCCTGGT- CGCCCTGGCA ACCCTGGTGG GGACTGTGAT GCAGGAGTGT

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1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5422

2nd Nucleotide Sequence

File Name : RDB7301R.fasta (Complementary)
Sequence Size : 549

Unit Size to Compare = 1

Pick up Location = 1

[96.057% / 558 bp] INT/OPT. Score : < 396/ 1898 >

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721' ACACGGCCTG GANATCTTCT GGAGAAGCAA ACAAATTGCC TCCTGACATC TGAGGCTGGA
** *****
1" CC TCCTGACATC TGAGGCTGGA

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781' GGCNTGGATT CCCCGTCTTG GGGCTTTCTG GGTCGGTCTG CCACGAGGTT CTGGNTGTTC
 *** *****
 23" GGC-TGGATT CCCCGTCTTG GGGCTTTCTG GGTCGGTCTG CCACGAGGTT CTGG-TGTTC

 841' ATTTAAAGTG TGCCCCTGGG CTGCCAGAAA GCCCCTCCCT GTGTGNCTCT CTTGAGGGCT

 81" ATTTAAAGTG TGCCCCTGGG CTGCCAGAAA GCCCCTCCCT GTGTG-CTCT CTTGAGGGCT

 901' GTGGGGCCAA GGGGACCCTG GCTGTCTCAG CCCCCNGCA GAGCACGAGC CCCTGGTCCC

 140" GTGGGGCCAA GGGGACCCTG GCTGTCTCAG CCCCC-GCA GAGCACGAGC CCCTGGTCCC

 961' CGCAAGCCCG CGGGCTGAGG ATGATTCNAG ACAGGGCTGG GGAGTGAAGG CAATTAGATT

 199" CGCAAGCCCG CGGGCTGAGG ATGATTC-AG ACAGGGCTGG GGAGTGAAGG CAATTAGATT

 1021' CCACGGACGA GCCCTTTCNT CCTGCGCCTC CCTCCTTCCT CACCCACCCC CGCCTCCATC

 258" CCACGGACGA GCCCTTTC-T CCTGCGCCTC CCTCCTTCCT CACCCACCCC CGCCTCCATC

 1081' AGGCACAGCN AGGCAGGGGT GGGGA-TGT AAGGAGGGGA AGGTGGGGGA CCCAGAGGGG

 317" AGGCACAGC- AGGCAGGGGT GGGGACTGT AAGGAGGGGA AGGTGGGGGA CCCAGAGGGG

 1140' GNCTTTGACG TCAGCTCAGC TT--ATAAGA GGCTGCTGGG CCAGGGCTGT GGAGNACGGA
 * *****
 376" G-CTTTGACG TCAGCTCAGC TTACATAAGA GGCTGCTGGG CCAGGGCTGT GGAG-ACGGA

 1198' GCCCGG-ACC TCCACACTGA G-CCATATCA AG-ATCTGGC CTCGGCGGCC AAGCTTGGA

 434" GCCCGGACC TCCACACTGA GCCCATATCA AGAATCTGGC CTCGGCGGCC AAGCTTGGA

 1255' -ATCCGGT-A CTGTTGGTAA AGCCA-CCAT GGAA-GATG- CCAA-AACA TTAAGAAGGG
 ***** *
 494" CATCCGGTAA CTGTTGGTAA AGCCACCCAT GGAACGATGC CCAAACAACA TTAATA