



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

STAT4: pGL4-phSTAT4 (RDB# 7711)

AGT: pGL4-phAGT(RDB# 7683)

IL1A: pGL4-phIL1A (RDB# 7682)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.01.21

1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5736

2nd Nucleotide Sequence

File Name : RDB7682F.fasta
Sequence Size : 667

Unit Size to Compare = 1
Pick up Location = 1

[100.000% / 636 bp] INT/OPT. Score : < 2544/ 2544 >

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1' GGCCTAACT GGCCGGTACC TGAGCTCGCT
*****
1" ATGCAATGTG CAGGTGCCAG AACATTTCTC TGGCCTAACT GGCCGGTACC TGAGCTCGCT

30' AGCCTCGAGG ATTGGCATAG GATAAGTGCA CAATAATTTT TTTTCCTAA ATGATTTAGA
*****
61" AGCCTCGAGG ATTGGCATAG GATAAGTGCA CAATAATTTT TTTTCCTAA ATGATTTAGA

90' TGACAGTGAC TCATTAAGGG TTCCTGAGG CCTCCTCAGA GTCGAGAGGT GGGTGCCTGA
*****
121" TGACAGTGAC TCATTAAGGG TTCCTGAGG CCTCCTCAGA GTCGAGAGGT GGGTGCCTGA

150' AGCCACCCAA AGTCCCTGTC ACAGGATGGC TCCCAACGCA CACACCACAG GCCTGCCAG
*****
181" AGCCACCCAA AGTCCCTGTC ACAGGATGGC TCCCAACGCA CACACCACAG GCCTGCCAG

210' TATGTTCCAC TATCTACCCA GTAGAGCCCT GCCCAGTAGG TTCCACTGTC CCTTCCTAG
*****
241" TATGTTCCAC TATCTACCCA GTAGAGCCCT GCCCAGTAGG TTCCACTGTC CCTTCCTAG
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270' AAGAGGTGAC TGTTGTTGAC AGTCCCAGAA AAGCGGGCTC CCCAAAACAA TGCAAGGACC
*****
301" AAGAGGTGAC TGTTGTTGAC AGTCCCAGAA AAGCGGGCTC CCCAAAACAA TGCAAGGACC

330' CACCTCTCTC TGAACCTCAC CCACCCTAGT TTTCTTTAA AAATCAATTT ACAAGAAGAT
*****
361" CACCTCTCTC TGAACCTCAC CCACCCTAGT TTTCTTTAA AAATCAATTT ACAAGAAGAT

390' CATGTGAAGG AAAAGGTTGG GTGATATTCT AACCCAAGTT AGCTGTTTCT CAACCAAGTT
*****
421" CATGTGAAGG AAAAGGTTGG GTGATATTCT AACCCAAGTT AGCTGTTTCT CAACCAAGTT

450' CTCTTTGAAA AATTCAACAA CCACCTTTGG GGAATTATTT ACAACAGAGG AGTGAGGATG
*****
481" CTCTTTGAAA AATTCAACAA CCACCTTTGG GGAATTATTT ACAACAGAGG AGTGAGGATG

510' GGACCAGGAT AGGTATTGCC TATGTTGGTG GAACCAGGGT TTTTTCCTG GATTACCAAA
*****
541" GGACCAGGAT AGGTATTGCC TATGTTGGTG GAACCAGGGT TTTTTCCTG GATTACCAAA

570' GAGATGGTAT GCATTGCTCC CAGAAGCTAA ATATCTTCAG GCTTTCAATG GTGGCCTTCA
*****
601" GAGATGGTAT GCATTGCTCC CAGAAGCTAA ATATCTTCAG GCTTTCAATG GTGGCCTTCA

630' CCTGAAAATG TTATCCCTGT TGAAGCTTTC AAGCCAGTAT TTTATAAGA ACTATATTTT
*****
661" CCTGAAA

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1st Nucleotide Sequence

File Name : Reference Seq. GNU
Sequence Size : 5736

2nd Nucleotide Sequence

File Name : RDB7682R.fasta (Complementary)
Sequence Size : 679



Unit Size to Compare = 1
Pick up Location = 1

[100.000% / 671 bp] INT/OPT. Score : < 2684/ 2684 >

901' GAACCAAGGT AAGCAGAAAT GTAGCCAGTT GGCTGGCATC ACTGTTGCTT CAGGATTCAT

1" CAGGATTCAT

961' CCTTAGACAC CCAAGCTTCT ACCCTAGTCT GGTGCTACAC TTACATTGCT TACATCCAAG

11" CCTTAGACAC CCAAGCTTCT ACCCTAGTCT GGTGCTACAC TTACATTGCT TACATCCAAG

1021' TGTGGTTATT TCTGTGGCTC CTGTTATAAC TATTATAGCA CCAGGTCTAT GACCAGGAGA

71" TGTGGTTATT TCTGTGGCTC CTGTTATAAC TATTATAGCA CCAGGTCTAT GACCAGGAGA

1081' ATTAGACTGG CATTAAATCA GAATAAGAGA TTTTGCACCT GCAATAGACC TTATGACACC

131" ATTAGACTGG CATTAAATCA GAATAAGAGA TTTTGCACCT GCAATAGACC TTATGACACC

1141' TAACCAACCC CATTATTTAC AATTAACAG GAACAGAGGG AATACTTTAT CCAACTCACA

191" TAACCAACCC CATTATTTAC AATTAACAG GAACAGAGGG AATACTTTAT CCAACTCACA

1201' CAAGCTGCTT TCCTCCAGA TCCATGCTTT TTTGCGTTA TTATTTTTTA GAGATGGGGG

251" CAAGCTGCTT TCCTCCAGA TCCATGCTTT TTTGCGTTA TTATTTTTTA GAGATGGGGG

1261' CTTCACTATG TTGCCACAC TGGACTAAA CTCTGGCCT CAAGTGATTG TCCTGCCTCA

311" CTTCACTATG TTGCCACAC TGGACTAAA CTCTGGCCT CAAGTGATTG TCCTGCCTCA

1321' GCCTCCTGAA TAGCTGGGAC TACAGGGGCA TGCCATCACA CCTAGTTCAT TTCCTCTATT

371" GCCTCCTGAA TAGCTGGGAC TACAGGGGCA TGCCATCACA CCTAGTTCAT TTCCTCTATT



1381' TAAATATAC ATGGCTTAAA CTCCAAGTGG GAACCCAAAA CATTCAATTG CTAAGAGTCT

 431" TAAATATAC ATGGCTTAAA CTCCAAGTGG GAACCCAAAA CATTCAATTG CTAAGAGTCT

1441' GGTGTTCTAC CACCTGAACT AGGCTGGCCA CAGGAATTAT AAAAGCTGAG AAATTCTTTA

 491" GGTGTTCTAC CACCTGAACT AGGCTGGCCA CAGGAATTAT AAAAGCTGAG AAATTCTTTA

1501' ATAATAGTAA CCAGGCAACA CCATTGAAGG CTCATATCAA GATCTGGCCT CGGCGGCCAA

 551" ATAATAGTAA CCAGGCAACA CCATTGAAGG CTCATATCAA GATCTGGCCT CGGCGGCCAA

1561' GCTTGGCAAT CCGTACTGT TGGTAAAGCC ACCATGGAAG ATGCCAAAAA CATTGAAGAAG

 611" GCTTGGCAAT CCGTACTGT TGGTAAAGCC ACCATGGAAG ATGCCAAAAA CATTGAAGAAG

1621' GGCCAGCGC CATTCTACCC ACTCGAAGAC GGGACCGCCG GCGAGCAGCT GCACAAAGCC
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 671" GAACACGTC