



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

HSP90AB1: pGL4-phHSP90AB1 (RDB# 7321)

IL8: pGL4-ph**IL8** (RDB# 7322)

NME1: pGL4-phNME1 (RDB# 7326)

PRKAB1: pGL4-phPRKAB1 (RDB#7328)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.03.02

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5505

2nd Nucleotide Sequence

File Name : RDB7322F.fasta
Sequence Size : 658

Unit Size to Compare = 1
Pick up Location = 1

[99.687% / 639 bp] INT/OPT.Score : < 2398/ 2534 >

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1'          GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATA
          ** *****
1" GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAGGATA

43' CCCTTCCTTG GTGCTCTTTA TCTACAGAAT CCAAGACCTT TCAAGAAAGG TCTTGGATTC
          *****
61" CCCTTCCTTG GTGCTCTTTA TCTACAGAAT CCAAGACCTT TCAAGAAAGG TCTTGGATTC

103' TTTTCTTCAG GACTAGGTA CATAAAGCCA CCTTTTATG ATTTGTTGAA ATTTCTCACT
          *****
121" TTTTCTTCAG GACTAGGTA CATAAAGCCA CCTTTTATG ATTTGTTGAA ATTTCTCACT

163' CCATCCCTTT TGCTAGTGAT CATGGGTCCT CAGAGGTCAG ACTTGGTGTC CTTGGATAAA
          *****
181" CCATCCCTTT TGCTAGTGAT CATGGGTCCT CAGAGGTCAG ACTTGGTGTC CTTGGATAAA

223' GAGCATGAAG CAACAGTGGC TGAACCAGAG TTGGAACCCA GATGCTCTTT CCACTAAGCA
          *****
241" GAGCATGAAG CAACAGTGGC TGAACCAGAG TTGGAACCCA GATGCTCTTT CCACTAAGCA
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283' TACAAC TTTC CATTAGATAA CACCTCCCTC CCACCCCAAC CAAGCAGCTC CAGTGCACCA
*****
301" TACAAC TTTC CATTAGATAA CACCTCCCTC CCACCCCAAC CAAGCAGCTC CAGTGCACCA

343' CTTTCTGGAG CATAAACATA CCTTAACTTT ACAACTTGAG TGGCCTTGAA TACTGTTCTT
*****
361" CTTTCTGGAG CATAAACATA CCTTAACTTT ACAACTTGAG TGGCCTTGAA TACTGTTCTT

403' ATCTGGAATG TGCTGTTCTC TTTCATCTTC CTCTATTGAA GCCCTCCTAT TCCTCAATGC
*****
421" ATCTGGAATG TGCTGTTCTC TTTCATCTTC CTCTATTGAA GCCCTCCTAT TCCTCAATGC

463' CTTGCTCCAA CTGCCTTTGG AAGATTCTGC TCTTATGCCT CCACTGGAAT TAATGTCTTA
*****
481" CTTGCTCCAA CTGCCTTTGG AAGATTCTGC TCTTATGCCT CCACTGGAAT AAATGTCTTA

523' GTACCACTTG TCTATTCTGC TATATAGTCA GTCCTTACAT TGCTTTCTTC TTCTGATAGA
*****
541" GTACCACTTG TCTATTCTGC TATATAGTCA GTCCTTACAT TGCTTTCTTC TTCTGATAGA

583' CCAAAC TCTT TAAGGAC-AA GTACCTAGTC TTATCTATTT CTAGATCCCC CACATTACTC
*****
601" CCAAAC TCTT TAAGGACAAA GTACCTAGTC TTATCTATTT CTAGATCCCC CACATTAA

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1st Nucleotide Sequence

File Name : Reference Seq. gnu
Sequence Size : 5505

2nd Nucleotide Sequence

File Name : RDB7322R. fasta (Complementary)
Sequence Size : 684

Unit Size to Compare = 1
Pick up Location = 1



[99.122% / 683 bp] INT/OPT. Score : < 2278/ 2656 >

661' GTTTGTGGAA CTGATTCTA TGTGAAGCAC ATGTGCCCT TCACTCTGTT AACATGCATT

* *****

1"

TTA AACATGCATT

721' AG-AAAATA AATCTTTTGA AAA-GTTGTA GTATGCCCC TAAGAGCAGT AACAGTTCCT

** ***** ***** ** ***** ***** ***** *****

14" AGAAAAATA AATCTTTTGA AAAGTTGTA GTATGCCCC TAAGAGCAGT AACAGTTCCT

779' AGAACTCTC TAAATGCTT AG-AAAAAGA TTTATTTTAA ATTACCT-CC CCAATAAAAT

***** ***** ** ***** ***** ***** ** *****

74" AGAACTCTC TAAATGCTT AGAAAAAGA TTTATTTTAA ATTACCTCC CCAATAAAAT

837' GATTGGCTGG CTTATCTTCA CCATCATGAT AGCATCTGTA ATTAAGTAA AAAAAATAAT

***** ***** ***** ***** ***** *****

134" GATTGGCTGG CTTATCTTCA CCATCATGAT AGCATCTGTA ATTAAGTAA AAAAAATAAT

897' TATGCCATTA AAAGAAATC ATCCATGATC TTGTTCTAAC ACCTGCCACT CTAGTACTAT

***** ***** ***** ***** ***** *****

194" TATGCCATTA AAAGAAATC ATCCATGATC TTGTTCTAAC ACCTGCCACT CTAGTACTAT

957' ATCTGTCACA TGGTACTATG ATAAAGTTAT CTAGAAATAA AAAAGCATAC AATTGATAAT

***** ***** ***** ***** ***** * *****

254" ATCTGTCACA TGGTACTATG ATAAAGTTAT CTAGAAATAA AAAAGCATAC AATTGATAAT

1017' TCACCAAATT GTGGAGCTTC AGTATTTTAA ATGTATATTA AAATTAATTT ATTTAAAGA

***** ***** ***** ***** ***** *****

314" TCACCAAATT GTGGAGCTTC AGTATTTTAA ATGTATATTA AAATTAATTT ATTTAAAGA

1077' TCAAAGAAAA CTTTCGTCAT ACTCCGTATT TGATAAGGAA CAAATAGGAA GTGTGATGAC

***** ***** ***** ***** ***** *****

374" TCAAAGAAAA CTTTCGTCAT ACTCCGTATT TGATAAGGAA CAAATAGGAA GTGTGATGAC

1137' TCAGGTTTGC CCTGAGGGGA TGGCCATCA GTTGCAAATC GTGGAATTTCT CTCTGACATA

***** ***** ***** ***** ***** *****

434" TCAGGTTTGC CCTGAGGGGA TGGCCATCA GTTGCAAATC GTGGAATTTCT CTCTGACATA



1197' ATGAAAAGAT GAGGGTGCAT AAGTTCTCTA GTAGGGTGAT GATATAAAAA GCCACCGGAG

 494" ATGAAAAGAT GAGGGTGCAT AAGTTCTCTA GTAGGGTGAT GATATAAAAA GCCACCGGAG

 1257' CACTCCATAA GGCACAAACT TTCAGAGACA GCAGAGCACA CAAGCTTCAT CAAGATCTGG

 554" CACTCCATAA GGCACAAACT TTCAGAGACA GCAGAGCACA CAAGCTTCAT CAAGATCTGG

 1317' CCTCGGCGGC CAAGCTTGGC AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA

 614" CCTCGGCGGC CAAGCTTGGC AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA

 1377' AAACATTAAG AAGGGCCCAG CGCCATTCTA CCCACTCGAA GACGGGACCG CCGGCGAGCA
 ***** *
 674" AAACATTAAG A