



Posi.: pGL3 Control Vector
(SV40 promoter)

Nega.: Empty Vector

PENK: pGL4-phPENK (RDB#7293)

TG: pGL4-phTG (RDB#7304)

AQP3: pGL4-phAQP3 (RDB#7311)

HPGD: pGL4-phHPGD (RDB#7457)

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.01.25

1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5484

2nd Nucleotide Sequence

File Name : RDB7311F.fasta
Sequence Size : 718

Unit Size to Compare = 1
Pick up Location = 1

[96.350% / 685 bp] INT/OPT.Score : < 405/ 2444 >

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1' GGCCTAACT GGCCGGTACC
                                     * * * *****
1" GTGAGAATTT GGCAAGTCCG GGGACAATAC TNATNCTGCG ATCCAATCGT GTGCCGTACC

20' TGAGCTCGCT AGCCTCGAGG ATGGTGAATC CCCATCTCCA CTAAAAAAC AAANAATTAG
***** ***** ***** ***** ***** ***. *****
61" -GAGCTCGCT AGCCTCGAGG ATGGTGAATC CCCATCTCCA CTAAAAAAC AAAATATTAG

80' CTGGGCATGG TGGTGTGCAC CTGTAATCCC AGCTAATCGG GAGGNCTGAA GCAGGAGAAT
***** ***** ***** ***** ***** ***** *****
120" CTGGGCATGG TGGTGTGCAC CTGTAATCCC AGCTAATCGG GAGG-CTGAA GCAGGAGAAT

140' CACTTGAACC TGGGAGGTGG AGGTTGCAGG GAGCCNGAGA TCACGCCATT GCACTCCACC
***** ***** ***** ***** ***** ***** *****
179" CACTTGAACC TGGGAGGTGG AGGTTGCAGG GAGCC-GAGA TCACGCCATT GCACTCCACC

200' TAGGCGACAG AGAGAGACTC CGTCTANAAA AAAAAAAGA GACAGACTCT TCCTTGCTG
***** ***** ***** ** ***** ***** *****
238" TAGGCGACAG AGAGAGACTC CGTCTA-AAA AAAAAAAGA GACAGACTCT TCCTTGCTG
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260' GGGGTAAGTC AGATGGGNAG AGGAGAGGGT TAAAAACAGC TGGGACTCAG CCTGCTGGCA
***** ** ***** ***** ***** *****
297" GGGGTAAGTC AGATGGG-AG AGGAGAGGGT TAAAAACAGC TGGGACTCAG CCTGCTGGCA

320' AACATGTGNG CATGTGGCAT GTCGGGGCAA CTGCAGCTCA GCCTCTGGAG CCATGTGAGN
***** * ***** ***** ***** ***** *****
356" AACATGTG-G CATGTGGCAT GTCGGGGCAA CTGCAGCTCA GCCTCTGGAG CCATGTGAG-

380' CAATGCACGC AGGTACACGT GTGACAAGCT AGGTCACCTA GCCATGTTCA NACAGGCATG
***** ***** ***** ***** ***** *****
414" CAATGCACGC AGGTACACGT GTGACAAGCT AGGTCACCTA GCCATGTTCA -ACAGGCATG

440' TGCACAGCCA CGAGGAATGC CCAGCCGTAC AATTAGGCAC ANCAGGACAT CCGCCATGTG
***** ***** ***** ***** * ***** *****
473" TGCACAGCCA CGAGGAATGC CCAGCCGTAC AATTAGGCAC A-CAGGACAT CCGCCATGTG

500' TAGACACAGC TGTGGACATA GCTGGCCAGG ACNATGCGAC ACACGACGTG CTCATAGCAC
***** ***** ***** ** ***** ***** *****
532" TAGACACAGC TGTGGACATA GCTGGCCAGG AC-ATGCGAC ACACGACGTG CTCATAGCAC

560' AGGGAGAAGG GCCCATGAAG TCTNGGTTGG AACTCAGCAC GTGTGTCTGT GTGCCACCT
***** ***** ** ***** ***** ***** *****
591" AGGGAGAAGG GCCCATGAAG TCT-GGTTGG AACTCAGCAC GTGTGTCTGT GTGCCACCT

620' GAGTCTGGAC TGCTNGCCCC TCTGACACTA GCTGTCCCCT TGAAGGTCG GTGCCTTATC
***** **** ***** ***** ***** **** ***** ****
650" GAGTCTGGAC TGCT-GCCCC TCTGACACTA GCTGTCCC- TGAAGGTCG GTGCC-TATC

680' TGTCNTGAC AGAAGAGACA GTGTTGCTTC TCACTTGGG CTCGCAGCCT CCTCCTNCCT
*** .**** **

707" TGT-CTGAC GAAA

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1st Nucleotide Sequence

File Name : Reference Seq.gnu
Sequence Size : 5484



2nd Nucleotide Sequence

File Name : RDB7311R.fasta (Complementary)

Sequence Size : 673

Unit Size to Compare = 1

Pick up Location = 1

[79.809% / 629 bp] INT/OPT.Score : < 420/ 1412 >

661' GAAGGGTCGG TGCCTTATCT GTCNTGACA GAAGAGACAG TGTTGCTTCT CACTTGGGGC

** * * .**

1" CCTCACACAC TCCAGCCGN CCACTCCACA AAAACANGCT CTCACNNGG

721' TGCAGCCTC CTCCTNCCTG CCTGAACTG AGGATCTGTT GGGTCCAGTC ATCCTGGAGA

***** ** *. *. * **** *. * * **** ***** **** **

51" TGCAG---- CT-CTCTCNG CCTCCAACNG A-GATC--GG GGGTCCAGTC ATCC---GGA

781' GATGCGNGCC AGTTTCTTTC TGACAGGTCT CCTCCTGCCC GCAAGGAAGT GGGGTGANTC

* *** ** * * * * . ***** * * . **** ***** **** * * *

100" AAAGCG-GCC AG-GTC-TTC NACAGGGTCT CCT-CNGCCC GCAAGGAAG- GGGGGGA-TC

841' ACAGGGCGCA GGTGGTCTCT ATGACAGCTG CATCCTCTCC AGCCATGGNC CCTGAACCT

***** ** ***** * . ***** * ***** ***** * . * * *****

154" ACAGGGCGCA GG-GGTCTC- AANACAGC-G CATCCTCTCC AGCCA--GGC CC-GAACCC-

901' GCCTATAATC CCACCATTGG CTCTCAGATC TGCCTAAGCN CTCTCAGCCC CCTTGACGTC

***** ** * ***** * * ***** ***** ***** * * . *****

207" GCCTA-AATC CCACCA-TGG CTCTCAGATC -GCCTAAGC- CTCTCAGCCC CC-NGACGTC

961' CCCTCCCTTA AGCGCCCTCC GAAGGCCACC NCGTCCCTCA AA-GCTCCTC AACTCCATG

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

262" CCCTCC-TA AGCGCCCTCC GAAGGCCACC -CGTCCCTCA AAGGCTCCTC AACTCCATG

1020' CCCGCAGCTC CCTCCACCCG GCNGTCCGCA CCAGCCTCCC AGCCGAGGTG GGGCGGGGGC

***** ***** * . ***** ***** ***** *****

320" CCCGCAGCTC CCTCCACCCG GGGTCCGCA CCAGCCTCCC AGCCGAGGTG GGGCGGGGGC



1080' -GAGGGGGC- GCGCANCTCC TCGGCGCTCC GGGACTGCAG GCGGGGGCTG CAGGGCGGGC
 ***** ***** * ***** ***** ***** *****
 380" GGAGGGGGCG GCGCACTCCT TCGGCGCTCC GGGACTGCAG GCGGGGGCTG CAGGGCGGGC

 1138' GGGGCCNCGT GTC-TCCAGC GTCCTATAA AGGGAGCCAC CAGCGCTGGA GGCCGCTGNC
 ***** ** *** ***** ***** ***** ***** *****
 440" GGGGCCCGGT GTCTTCCAGC GTCCTATAA AGGGAGCCAC CAGCGCTGGA GGCCGCTGCT

 1197' TCGCTGCGCC ACCGCCTCCC GCCACCCCTG CCGGCCGAC AGCGCCGCG CCTGCCCGC
 ***** **** ***** **** ***** *** ***** *** *** *****
 500" CGGCTGCGCC ACCG-CTCCC GCCA-CCCTG -CCG-CCGAC ----GCGCGC GCTG-CCCGC

 1257' CATGGGTCGA CAGAAGGAGC T-GGTGTCAT CAAGATCTGG CCTCGGCGGC CAAGCTTGGC
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 551" CA-GGGTAGG ACGAAGAGGA TGGGTNTTAC GTATAGGNTC CGGGNCCGT TACGGTT-TC

 1316' AATCCGGTAC TGTTGGTAAA GCCACCATGG AAGATGCCAA AAACATTAAG AAGGGCCCAG
 * ** ***** *
 609" TTTGATGTTT TGTTGTTTTT GGTTTTCTAG CATTTTTTTT TTTTTTTTTT TTTTCGTTTT

 1376' CGCCATTCTA CCCACTCGAA GACGGGACCG CCGGCGAGCA GCTGCACAAA GCCATGAAGC

 669" TTTTC