

RIKEN clone ID: IRAK022A12

Vector : pCMV-SPORT6

Gene	PPKCSH		
Accession No.	BC015154.1	1625 bp	1..1625
	<i>CDS</i>	- bp	<1..603

● Plasmid DNA purification

Date : 100601 Culture : LB (100 ug/ml Ampicillin) 10 ml → 37°C O/N

Date : 100602 Purification : QIAGEN Miniprep kit → dH₂O 100 ul

● Digestion by restriction enzyme / Concentration calibration

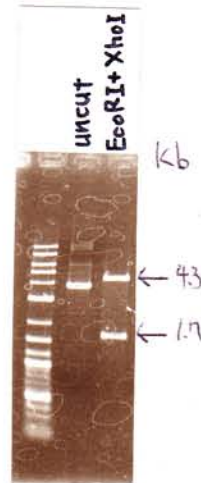
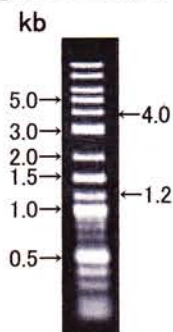
Date : 100602

DNA concentration (O.D.): 51.0 ng/ul

DNA	2 ul
Enzyme (EcoRI+XhoI)	0.5+0.5 ul
Buffer H	1 ul
dH ₂ O	6 ul
Total	10 ul

Electrophoresis: 1% agarose gel, 1 × TAE Buffer

Marker: 2-Log DNA Ladder (NEB#N3200L)



<Expected digestion pattern from BC015154.1.1>

4339, 1668

● Adjust plasmid DNA solution to 25 ng/ul ~preparation for shipping~

Date : 100705 Shipped : 25 ng/ul, 40 ul

Final concentration: 25 ng/ul

DNA (51.0 ng/ul)	78 ul
10 × TE	15.9 ul
dH ₂ O	65.2 ul
Total	159.1 ul

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.06.10

1st Nucleotide Sequence
File Name : BC015154.1.gnu
Sequence Size : 1625

2nd Nucleotide Sequence

File Name : IRAK022A12_Reverse2_007_10060913VH.fasta
Sequence Size : 760

Unit Size to Compare = 6
Pick up Location No. = 1

[707 / 724 bp] INT/OPT. Score : < 2328 / 2733 >

1' CTGAGAGAGG GGAGSAGAGS
1" GTCGCCGAAT TCCTGGGAGTA TGGTGGACCC ACGCGTCCGG CTGAGAGAGA GGAGSAGAGS
22' GAGGANTCCG AGGTGGACGG GGAGGAGGCC AAGCGGAGCA GCCCTGCTGA GGAAAGCAAA
61" GAGGATTCGG AGGTGGACGG GGAGGAGGCC AAGCGGAGCA GCCCTGCTGA GGAAAGCAAA
82' ATGCGCCCTT ACGACAGACA GACGCAAGCC TTCATCGATG CTGGCCAGGA GGCCCGCAAC
121" ATGCGCCCTT ACGACAGACA GACGCAAGCC TTCATCGATG CTGGCCAGGA GGCCCGCAAC
142' AAGTTGAGGG AGGCCGAGCG GTGCTGAGG GACATGAGAG AGTCCATCAG GAACTGAGG
181" AAGTTGAGGG AGGCCGAGCG GTGCTGAGG GACATGAGAG AGTCCATCAG GAACTGAGG
202' CAAGAGATT CTTTGACTT TGGCCCAAC GGGGAGTTTG CTTAACCCTA CAGCCATGG
241" CAAGAGATT CTTTGACTT TGGCCCAAC GGGGAGTTTG CTTAACCCTA CAGCCATGG
262' TNGSAGCTCA CACCAACGA ATAGGTCTAC CGCTCTGACC CCTTCAAGCT TGTCTCGAG
301" TNGSAGCTCA CACCAACGA ATAGGTCTAC CGCTCTGACC CCTTCAAGCT TGTCTCGAG
322' AAACCCAAAC TGGGGAGCTG TCCCAACAGC CTTGGACACT GGGGCTCAGG GATTGAGCCC
361" AAACCCAAAC TGGGGAGCTG TCCCAACAGC CTTGGACACT GGGGCTCAGG GATTGAGCCC
382' GACCAAGACA AGTTCAATGC CATGAGATAT GAGCAAGACA CGGGCTACTG GCAGGGCCCC
421" GACCAAGACA AGTTCAATGC CATGAGATAT GAGCAAGACA CGGGCTACTG GCAGGGCCCC
442' AACCTCTCA CCACCTGGG CTTCTCTGC GGGAAAGAGA CCAATGATAC CAGCAACACA
481" AACCTCTCA CCACCTGGG CTTCTCTGC GGGAAAGAGA CCAATGATAC CAGCAACACA
502' GAGCCCAATC GTCGCGAGTA CCTCATGAGC CTGATGAGGC CAGCCCGCTG CCCCGAGACA
541" GAGCCCAATC GTCGCGAGTA CCTCATGAGC CTGATGAGGC CAGCCCGCTG CCCCGAGACA
562' CCGCCTGAAG CACCCACCG- AAGATGACA TACGAGCTC TAG-CTGGAT GGGCGCAGA-
601" CCGCCTGAAG CACCCACCGA AAGATGACA TACGAGCTC TAGCTGGAT GGGCGCAGAG
619' GGTGAGCGGG GAGTGGAGT CTCGTGAGC TGGCCAGCA A-GGGGAGG GGGGGCCCT
661" GGTGAGCGGG GAGTGGAGT CTCGTGAGC TGGCCAGCA A-GGGGAGG GGGGGCCCT
678' GAGGAAAGAG GACCCAGAG GGCACCTAT CAACTGAT CCCCAATGTC CCTGCTTTT
721" GAGGAAAGAG GACCCAGAG GCCCT-TAT C-ACTGATG CCC

[GENETYX : Nucleotide Sequence Homology Data]

Date : 2010.06.10

1st Nucleotide Sequence
File Name : BC015154.1.gnu
Sequence Size : 1625

2nd Nucleotide Sequence

File Name : IRAK022A12_M13_E03_100602150M.fasta (Complementary)
Sequence Size : 631

Unit Size to Compare = 6
Pick up Location No. = 1

[518 / 536 bp] INT/OPT. Score : < 1636 / 1930 >

1081' TACTGCACATC TCAGGCTGG GCTTACAGAT GAGACTCA AAAAAAATA ATAAATATA
1" TCCAGCCT-- GGNACAGAGG GA-ACCTGC- AAAAGANN- AT-ATAT-A
1141' TAAGAAAA TAGACAGAT CTCAGGCTG CTCACCTCT GGCCTGAAAT GATCTCCCA
44" TAAG-AAA TA-ACAAGT CTCAGGCTG CTC-ACT-CT GGCCTGAAAT GATCTCCCA
1201' CCTTAGCTC CCGAG-GGC GGGACTTACA GCGAAACATC ACCAATGCA GCTATCCCA
100" CCTAGGCTC CCGAGTGGG CCGSACTTACA GCGAAACATC ACCAATGCA GCTATCCCA
1260' GCTTCTTAT CTGGTCTTC TCTTCCCCA GAACCTAAG AAGGCATSA GCCAGCCCT
160" GCTTCTTAT CTGGTCTTC TCTTCCCCA GAACCTAAG AAGGCATSA GCCAGCCCT
1320' GATGTCGCT CACCCGACC CTCTGGGCT GGCCTGAGCT CTGTTGCTC CTCTGTTGC
220" GATGTCGCT CACCCGACC CTCTGGGCT GGCCTGAGCT CTGTTGCTC CTCTGTTGC
1380' GCGAGACTT TGTGGGGCT TCGTGCCTG CTCTGGGCT CAGGGGGGG TGTCTCAGT
280" GCGAGACTT TGTGGGGCT TCGTGCCTG CTCTGGGCT CAGGGGGGG TGTCTCAGT
1440' TCCGAGGCC CAACAGCCTT CAAGAATGG TAAAGAGCT TGCCTTCCCT GGGCCTCCCA
340" TCCGAGGCC CAACAGCCTT CAAGAATGG TAAAGAGCT TGCCTTCCCT GGGCCTCCCA
1500' CTTTGTGAC TCGCCCAAC ACCCCAGCC CTGTGCTGC CACCCCTCTT AGTGGAGAT
400" CTTTGTGAC TCGCCCAAC ACCCCAGCC CTGTGCTGC CACCCCTCTT AGTGGAGAT
1560' AGTGAATGAC TTGACTTGT ACCTCAATAC AATTAATGT ATCCCCACC CAAAAAATA
460" AGTGAATGAC TTGACTTGT ACCTCAATAC AATTAATGT ATCCCCACC CAAAAAATA
1620' AAAAAA
520" AAAAAAGGC GGCCTCTTA GATATCCTT CAGGGGGGCC AAGCTTACGC GTACCCAGCT