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Product datasheet for SC323429

PHKG2 (NM_000294) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	PHKG2 (NM_000294) Human Untagged Clone
Tag:	Tag Free
Symbol:	PHKG2
Synonyms:	GSD9C
Mammalian Cell Selection:	None
Vector:	pCMV6-XL5
E. coli Selection:	Ampicillin (100 ug/mL)

Fully Sequenced ORF:

>OriGene ORF within SC323429 sequence for NM_000294 edited (data generated by NextGen Sequencing)

ATGACGCTGGACGTGGGGCCGGAGGATGAGCTGCCCGACTGGGCCGCCGCCAAAGAGTTT
TACCAGAAGTACGACCCTAAGGACGTCATCGGCAGAGGAGTGAGCTCTGTGGTCCGCCGT
TGTGTTCATCGAGCTACTGGCCACGAGTTTGCGGTGAAGATTATGGAAGTGACAGCTGAG
CGGCTGAGTCCTGAGCAGCTGGAGGAGGTGCGGGAAGCCACACGGCGAGAGACACACATC
CTTCGCCAGGTCGCCGGCCACCCCCACATCATCACCCTCATCGATTCCTACGAGTCTTCT
AGCTTCATGTTCCTGGTGTTTGACCTGATGCGGAAGGGAGAGCTGTTTGACTATCTCACA
GAGAAGGTGGCCCTCTCTGAAAAGGAAACCAGGTCCATCATGCGGTCTCTGCTGGAAGCA
GTGAGCTTTCTCCATGCCAACAACATTGTGCATCGAGATCTGAAGCCCGAGAATATTCTC
CTAGATGACAATATGCAGATCCGACTTTCAGATTTCGGGTTCTCCTGCCACTTGGAACCT
GGCGAGAAGCTTCGAGAGTTGTGTGGGACCCCAGGGTATCTAGCGCCAGAGATCCTTAAA
TGCTCCATGGATGAAACCCACCCAGGCTATGGCAAGGAGGTCGACCTCTGGGCCTGTGGG
GTGATCTTGTTCACACTCCTGGCTGGCTCGCCACCCTTCTGGCACCGGCGGCAGATCCTG
ATGTTACGCATGATCATGGAGGGCCAGTACCAGTTCAGTTCCCCCGAGTGGGATGACCGT
TCCAGCACTGTCAAAGACCTGATCTCCAGGCTGCTGCAGGTGGATCCTGAGGCACGCCTG
ACAGCTGAGCAGGCCCTACAGCACCCCTTCTTTGAGCGTTGTGAAGGCAGCCAACCCTGG
AACCTCACCCCCCGCCAGCGGTTCCGGGTGGCAGTGTGGACAGTGCTGGCTGCTGGACGA
GTGGCCCTAAGCACCCATCGTGTACGGCCACTGACCAAGAATGCACTGTTGAGGGACCCT
TATGCGCTGCGGTCAGTGCGGCACCTCATCGACAACTGTGCCTTCCGGCTCTACGGGCAC
TGGGTAAAGAAAGGGGAGCAGCAGAACCGGGCGGCTCTCTTTCAGCACCGGCCCCCTGGG
CCTTTTCCCATCATGGGCCCTGAAGAGGAGGGAGACTCTGCTGCTATAACTGAGGATGAG
GCCGTGCTTGTGCTGGGCTAG

Clone variation with respect to NM_000294.2

View online »

5' Read Nucleotide Sequence:

>OriGene 5' read for mutant NM_000294 unedited
ACCGCCCGTTTGAGCAAATGGGCGGTAGGCGCTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAG
TGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGCGAATTCGGCACGAGGGCGCAGCTCG
CGTCGACCCTGGCTCCTCTGCCTGCCCCCTCAGGCCCCCGCCTCCTTCAGGATGACGCTGGACGTGGGGC
CGGAGGATGAGCTGCCCGACTGGGCCGCCGCCAAAGAGTTTTACCAGAAGTACGACCCTAAGGACGTCAT
CGGCAGAGGAGTGAGCTCTGTGGTCCCGCCGTTGTGTTCATCGAGCTACTGGGCCACGAGTTTTGCGGGT
GATGATTATGGGAAGTGACAGCTGAGCGGGCTGAGTTCCTGGAGCAGCTGGGAGGAAGGGGCCGGGAGCC
CACACGGCAAGAGAACACACATCCCTTCGCAAGGTCGGCCGGCCACCCCCCACATAATCCCCCTCATCAA
TTCTAAGAAGTCTTTCTGGCTCCAGGTTCCGGGGGTTGGACTTGTGGGCGGAAGGAGAACCTGTTGGACT
ACCTAACGAAAAAAGTGGCCCCCTCTCGAAAAAGGAAAAAAGTCCCCCATGCGCGTCCCTCTTTTGAGAG
CGTTGAGCTTCTTCTATGCAAACCCACTTTTGTCCTGAAGATCTAGAGCCGGAAAATTCTCTCTGATGAC
ACAATGCGATACGCATTTTACATTCGGGTTCTGCGCCTGGAACCCGCGAGAGACTCTAAGTGTGTGTGGC
CCAAGGATCATCGCCAGATACTCAAAGTCCTGTGAGACACCGCGCTGCGAGAGGTCACACCTGGCCGTGG
GGATCTGTACACTCGTGTCGCGCACCTTTTGCCGCGGATCGAGTGCGACTCAGGACTCAGCTAGTCCAGT
GTAGAGCATCACCTGAACGATTCACGGTGGAG

Kinase Domain Sequence:

>SC323429 kinase domain raw sequence. By performing BLASTX analysis with this sequence against NCBI refernce protein database, you can confirm the presence of the kinase-deficient mutation
CSMTKMGCAATGGGCGKAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCA
GAATTTTGTAATACGACTCACTATAGGGCGGCCGCGAATTCGGCACGAGGGCGCAGCTCGCGTCGACCCT
GGCTCCTCTGCCTGCCCCCTCAGGCCCCCGCCTCCTTCAGGATGACGCTGGACGTGGGGCCGGAGGATGA
GCTGCCCGACTGGGCCGCCGCCAAAGAGTTTTACCAGAAGTACGA

Restriction Sites: Please inquire

ACCN: NM_000294

Insert Size: 1640 bp

OTI Disclaimer: Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).

OTI Annotation: This kinase-deficient mutant clone was generated by created by site-directed mutagenesis from the corresponding wild-type clone. See details in "Application of active and kinase-deficient kinome collection for identification of kinases regulating hedgehog signaling." Cell. 2008 May p536-548.

Components: The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).

Reconstitution Method:
1. Centrifuge at 5,000xg for 5min.
2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.
3. Close the tube and incubate for 10 minutes at room temperature.
4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.
5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.

RefSeq: NM_000294.1, NP_000285.1

RefSeq Size:	1571 bp
RefSeq ORF:	1221 bp
Locus ID:	5261
UniProt ID:	P15735
Cytogenetics:	16p11.2
Domains:	pkinase, TyrKc, S_TKc
Protein Families:	Druggable Genome, Protein Kinase
Protein Pathways:	Calcium signaling pathway, Insulin signaling pathway
Gene Summary:	Phosphorylase kinase is a polymer of 16 subunits, four each of alpha, beta, gamma and delta. The alpha subunit includes the skeletal muscle and hepatic isoforms, encoded by two different genes. The beta subunit is the same in both the muscle and hepatic isoforms, and encoded by one gene. The gamma subunit also includes the skeletal muscle and hepatic isoforms, and the hepatic isoform is encoded by this gene. The delta subunit is a calmodulin and can be encoded by three different genes. The gamma subunits contain the active site of the enzyme, whereas the alpha and beta subunits have regulatory functions controlled by phosphorylation. The delta subunit mediates the dependence of the enzyme on calcium concentration. Mutations in this gene cause glycogen storage disease type 9C, also known as autosomal liver glycogenosis. Alternatively spliced transcript variants encoding different isoforms have been identified in this gene.[provided by RefSeq, Feb 2010] Transcript Variant: This variant (1) encodes the longer isoform (1). Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.