

Product datasheet for **SC109374**

KRAS (NM_004985) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	KRAS (NM_004985) Human Untagged Clone
Tag:	Tag Free
Symbol:	KRAS
Synonyms:	C-K-RAS; c-Ki-ras2; CFC2; K-Ras; K-RAS2A; K-RAS2B; K-RAS4A; K-RAS4B; KI-RAS; KRAS1; KRAS2; NS; NS3; RALD; RASK2
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL6</u>
E. coli Selection:	Ampicillin (100 ug/mL)



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Fully Sequenced ORF:

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>OriGene sequence for NM_004985 edited
GAATTCGGCACGAGGCGGCGGAGGCAGCAGCGGCGGCGGAGTGGCGGCGGCGAAGGTGG
CGGCGGCTCGGCCAGTACTCCCGGCCCCCGCCATTTCCGACTGGGAGCGAGCGCGGCGCA
GGCACTGAAGGCGGCGGCGGGCCAGAGGCTCAGCGGCTCCCAGGTGCGGGAGAGAGGCC
TGCTGAAAATGACTGAATATAAACTTGTGGTAGTTGGAGCTGGTGGCGTAGGCAAGAGTG
CCTTGACGATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGG
ATTCCTACAGGAAGCAAGTAGTAATTGATGGAGAAACCTGTCTCTTGATATTCTCGACA
CAGCAGGTCAAGAGGAGTACAGTCAATGAGGGACCAGTACATGAGGACTGGGGAGGGCT
TTCTTTGTGATTTGCCATAAATAACTAAATCATTTGAAGATATTCACCATTATAGAG
AACAAATTAAGAGTTAAGGACTCTGAAGATGTACCTATGGTCTAGTAGGAAAATAAT
GTGATTTGCCCTTAGAACAGTAGACACAAAACAGGCTCAGGACTTAGCAAGAAGTTATG
GAATTCCTTTTATTGAAACATCAGCAAAGACAAGACAGGGTGTGATGATGCCTTCTATA
CATTAGTTCGAGAAATTCGAAAACATAAAGAAAAGATGAGCAAAGATGGTAAAAAGAAGA
AAAAGAAGTCAAAGACAAAGTGTGAATTATGTAATACAATTTGACTTTTTTCTTAAG
GCATACTAGTACAAGTGGTAATTTTGTACATTACCTAAATTATTAGCATTGTTTTAG
CATTACCTAATTTTTTCTGCTCCATGCAGACTGTTAGCTTTTACCTTAAATGCTTATT
TTAAAATGACAGTGGAAGTTTTTTTTCTCGAAGTGCCAGTATCCCAGAGTTTTGGTT
TTTGAAGTAGCAATGCCTGTGAAAAAGAACTGAATACCTAAGATTTCTGTCTTGGGGTT
TTTGGTGCATGCAGTTGATTACTTCTTATTTTCTTACCAATTGTGAATGTTGGTGTGAA
ACAAATTAATGAAGCTTTTGAATCATCCCTATTCTGTGTTTTATCTAGTCACATAAATGG
ATTAATTAATAATTTAGTTGAGACCTTCTAATGGTTTTTACTGAAACATTGAGGGAAC
ACAAATTTATGGCTTCTGATGATGATCTTCTAGGCATCATGCCTATAGTTTGCAT
CCCTGACGAATGTAAGXXXXXXXXXXXXXXXXXXXXXXXXXAATGGTTTCTTGATAATTG
TGTAAGTAAATGTTTTTAGAACCCAGCAGTTACCTTAAAGCTGAATTTATATTTAGTAACT
TCTGTGTTAATACTGGATAGCATGAATTCTGCATTGAGAACCTGAATAGCTGTCATAAAA
TGAAACTTTCTTTCTAAAGAAAGATACTCACATGAGTTCTTGAAGAATAGTCATAACTAG
ATTAAGATCTGTGTTTTAGTTAATAGTTTGAAGTGCCTGTTGGGATAATGATAGGTAA
TTTAGATGAATTTAGGGGAAAAAAGTTATCTGCAGAAATGTTGAGGGCCCATCTCCCC
CCACACCCACAGAGCTAACTGGGTTACAGTGTTTTATCCGAAAGTTTCCAATCCACT
GTCTTGTTTTCATGTTGAAAAACTTTTGCATTTTCTTTGAGTGCCAATTTCTTAC
TAGTACTATTTCTAATGTAACATGTTTACCTGGAAATGATTTTAACTATTTTTGTATAG
TGTAAGTGAACATGCACATTTTGTACATTGTGCTTTCTTTTGTGGACATATGCAGTG
TGATCCAGTTGTTTTCCATCATTGGTTGCGCTGACCTAGGAATGTTGGTCATATCAAAC
ATTAATAATGACCACTCTTTAATTGAAATTACTTTAAATGTTTATAGGAGTATGTGC
TGTGAAGTGATCTAAAATTTGTAATATTTTGTGCATGAACTGACTACTCCTAATTATTG
TAATGTAATAAAAATAGTTACAGTGACAAAAAAAAAAAAAAAAAACTCGAC
    
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5' Read Nucleotide Sequence:

>OriGene 5' read for NM_004985 unedited
 TATTACACCCGCCGTTGCCGCAAAGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAA
 GCAGAGCTCATTTAGGTGACACTATAGAATACAAGCTACTTGTTCTTTTTGCAGCGGCCG
 CGAATTCGGCACGAGGCGGGCGGAGGCAGCAGCGGCGGGCGGCAGTGGCGGGCGGAAGGTG
 GCGGGCGTCTGGCCAGTACTCCCGGCCCGCCATTTCCGACTGGGAGCGAGCGGGCGC
 AGGCACTGAAGGCGGGCGGGGCCAGAGGCTCAGCGGCTCCAGGTGCGGGAGAGAGGC
 CTGCTGAAAATGACTGAATATAAACTTGTGGTAGTTGGAGCTGGTGGCGTAGGCAAGGT
 GCCTTGACGATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAG
 GATTCCTACAGGAAGCAAGTAGTAATTGATGGAGAAACCTGTCTCTTGGATATTCTCGAC
 ACAGCAGGTCAAGAGGAGTACAGTGCAATGAGGGACCAGTACATGAGGACTGGGGAGGGC
 TTTCTTTGTGATTTGCCATAAATAACTAAATCATTGGAAGATATTCACCATTATAGA
 GAACAAATTAAGAGTTAAGGACTCTGAAGATGTACCTATGGTCTAGTAGGAAATAAA
 TGTGATTTGCCTTCTAGAACAGTAGACACANAACAGGCTCAGGACTTAGCAAGAAGTTAT
 GGAATTCCTTNTATTGAAACATCAGCAAAGACAAGACAGGGTGTGATGATGCCTTCTAT
 ACATTAGNTCGAGAAATNCGAAACATANAGANAGATGAGCANAGATGGGTAAGAAG
 AAAAGAAGTCNAAGACAAGTGTGTAANTATGTAATACCATTNGTACTTTTNTCTTAAG
 CATACTAGTACAAGGGTAATTTTTGTACATTACACTAAATT

3' Read Nucleotide Sequence:

>OriGene 3' read for NM_004985 unedited
 NGGGAAATCTATGNACCGCGCCGATTCTANGTCGAGTTTTTTTTTTTTTTTTTTTGTAC
 TGTAACTATTTTTATTACATTACAATAATTAGGAGTAGTACAGTTCATGACAAAAATTTA
 CAAATTTTAGATCACTTCACAGCACATACTCCTATAAACATTTAAAAGTTAATTTCAATT
 AAAAGAGTGGTCATTTTTAAATGTTTGATATGACCAACATTCCTAGGTCAGCGCAACAAA
 TGAATGAAAACAACCTGGATCACACTGCATATGTCCACAAAAGAAAGCACAATGTACAAA
 ATGTGCATGTTTCAGTTTACACTATACAAAAATAGTTAAAATACATTCAGGTAACATG
 TTACATTAAGAAATAGTACTAGTAAGAAATGGCACTCAAAGGAAAAATGCAAAAGTATT
 TTCAACATGAAAACACAAGACAGTGAATTGAAAACCTTCGGATAAAAACACTGTAACCCA
 GTTAGCTCTGTGGGGGTGTGGGGGAAGAGATGGGCCCTCAACATTTCTGCAGATAACTT
 TTTTCCCTAAAATTCATCTAAATTACCTATCATTATCCCAAACAGGCCTTCAAACATTT
 AAATAAAAACACAGATCTTAATCTAGTTATGACTATTCTTCAAGAACTCATGTGAGTATC
 TTTCTTTAGAAAAGAAAGTTTCATTTTATGACAGCTATTCACGTTCTCAATGCAGAATTCA
 TGCTATCCAGTATTAACACAGAAAGTACTAAATATAAATTCAGCTTTAAGGTAACGTCTG
 GGTNTCTAAAAACATTTCTACACAATTATCAAGAAACATTACTTTTTGACAATGGGAATC
 TTAATAGTTTTGCTGTCTAAAAAAAATCCCTAAAAAGTTATTACTGGTTGAAGAAAAAT
 GTTAGA

Restriction Sites:

NotI-NotI

ACCN:

NM_004985

Insert Size:

2067 bp

OTI Disclaimer: Due to the inherent nature of this plasmid, standard methods to replicate additional amounts of DNA in *E. coli* are highly likely to result in mutations and/or rearrangements. Therefore, OriGene does not guarantee the capability to replicate this plasmid DNA. Additional amounts of DNA can be purchased from OriGene with batch-specific, full-sequence verification at a reduced cost. Please contact our customer care team at custsupport@origene.com or by calling 301.340.3188 option 3 for pricing and delivery.

The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. [More info](#)

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_004985.3](#), [NP_004976.2](#)

RefSeq Size: 5312 bp

RefSeq ORF: 567 bp

Locus ID: 3845

UniProt ID: [P01116](#)

Cytogenetics: 12p12.1

Domains: ras, RAS, RHO, RAB

Protein Families: Druggable Genome

Protein Pathways: Acute myeloid leukemia, Axon guidance, B cell receptor signaling pathway, Bladder cancer, Chemokine signaling pathway, Chronic myeloid leukemia, Colorectal cancer, Dorso-ventral axis formation, Endometrial cancer, ErbB signaling pathway, Fc epsilon RI signaling pathway, Gap junction, Glioma, GnRH signaling pathway, Insulin signaling pathway, Long-term depression, Long-term potentiation, MAPK signaling pathway, Melanogenesis, Melanoma, Natural killer cell mediated cytotoxicity, Neurotrophin signaling pathway, Non-small cell lung cancer, Pancreatic cancer, Pathways in cancer, Progesterone-mediated oocyte maturation, Prostate cancer, Regulation of actin cytoskeleton, Renal cell carcinoma, T cell receptor signaling pathway, Thyroid cancer, Tight junction, VEGF signaling pathway

Gene Summary:

This gene, a Kirsten ras oncogene homolog from the mammalian ras gene family, encodes a protein that is a member of the small GTPase superfamily. A single amino acid substitution is responsible for an activating mutation. The transforming protein that results is implicated in various malignancies, including lung adenocarcinoma, mucinous adenoma, ductal carcinoma of the pancreas and colorectal carcinoma. Alternative splicing leads to variants encoding two isoforms that differ in the C-terminal region. [provided by RefSeq, Jul 2008]

Transcript Variant: This variant (b) is composed of five exons and lacks exon 4a which the longer transcript variant (a) includes. This predominant variant (b) has a cds that terminates in exon 4b and encodes isoform b. 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.