

## **Product datasheet for SC126782**

## KRAS (NM 033360) Human Untagged Clone

**Product data:** 

**Product Type: Expression Plasmids** 

**Product Name:** KRAS (NM\_033360) Human Untagged Clone

Tag: Tag Free **KRAS** Symbol:

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: pCMV6-XL4

E. coli Selection: Ampicillin (100 ug/mL)

**Fully Sequenced ORF:** >OriGene ORF sequence for NM\_033360 edited

ATGACTGAATATAAACTTGTGGTAGTTGGAGCTGGTGGCGTAGGCAAGAGTGCCTTGACG ATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGATTCCTAC AGGAAGCAAGTAGTAATTGATGGAGAAACCTGTCTCTTGGATATTCTCGACACAGCAGGT GTATTTGCCATAAATAATACTAAATCATTTGAAGATATTCACCATTATAGAGAACAAATT CCTTCTAGAACAGTAGACACAAAACAGGCTCAGGACTTAGCAAGAAGTTATGGAATTCCT TTTATTGAAACATCAGCAAAGACAAGACAGAGAGTGGAGGATGCTTTTTATACATTGGTG AGAGAGATCCGACAATACAGATTGAAAAAAATCAGCAAAGAAGAAAAAGACTCCTGGCTGT

GTGAAAATTAAAAAATGCATTATAATGTAA

5' Read Nucleotide Sequence:

>OriGene 5' read for NM\_033360 unedited

CGGCCGCAATTCGGCACCAGGCAGCAGCGGCGGCGGCGGCGGCGAAGGTGGCG CACTGAAGGCGGCGGGGGCCAGAGGCTCAGCGGCTCCCAGGTGCGGAGAGAGGCCTG CTGAAAATGACTGAATATTTCTTGTGGTAGTTGGAGCTGGTGGCGTAGGCAAGAGTGCCT TGACGATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATAGAGGATT CCTACAGGAAGCAAGTAGTAATTGATGGAGAAACCTGTCTCTTGGATATTCTCGACACAG CAGGTCAAGAGGAGTACAGTGCAATGAGGGACCAGTACATGAGGACTGGGGAGGGCTTTC TTTGTGTATTTGCCATAAATAATACTAAATCATTTGAAGATATTCACCATTATAGAGAAC ATTTGCCTTCTAGAACAGTAGACACAAAACAGGCTCAGGACTTAGCAAGAAGTTATGGAA TTCCTTTTATTGAAACATCAGCAAAGACAAGAACAGGGTGTTGATGATGCCTTCTATACA

TTAGTTCGAGAAATTCGAAACATTAAGAAAGATGAGCANAGATGGTNAAA



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3' Read Nucleotide Sequence:

OTI Disclaimer:

>OriGene 3' read for NM\_033360 unedited ATATAATCAAGTTTATTCCTTTAAAACAATGAAGTGATTTACATAAAGTAGCTTGATCGA AGAGTTTCAGTGGAATCGTAGCAAAACAATTATAGAGCTGGCACAGAGACCAAACCCCTT CTTTGCAAAACTAAAATACGCATCGTGTTATCTCTGGGTCGTATACCAAAGGCCTTAGTA AGATATTACAGACCACACTAGCACTACCTAAGGACCGGGATTATGTCTCTTGTTTGGGGA GTCAGGAGTTCGAGACCAGCCTGGCCAACAGGGTGAAACCCCGTCTCTCCTAAAAATACA AAAATTATTTGAGTGTAGTGGCACACGCCTGTAATCCCAGCTACTCAGGAGGCCGAGGCA CGAGAATCGCTTGAACCTGCGAGATGGAGGTTGCATGGAGCTGAGATGGCGCCACTGCAT TTAAGAATTTTCCCTTTGATGGAACATCCCCGGTAACCAATCAACGGAAGGTTTAACTGG TTCCCGATATCAGCCCGACTTTTGATTCCCTAAGAGACCTTTTACCCGTACCTCTGTTAA TCTCCCCTCCACCGCCACGGGCCCGCCCCTTCCTCCCATGTGGGCACCCCCCTCGTCCCC TGGTATGTTCATATTGTACCGTGTCGCTCGCCGCTTGCGCCTATCCCTCAGCCACGCGCT TCGCCCATGTCGCGCCGGTCCGCACGCCCCACGCCCGAGCCCCCTACCA

Restriction Sites: Notl-Notl
ACCN: NM\_033360
Insert Size: 3900 bp

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 <a href="mailto:customercare">customercare</a> team at <a href="mailto:customercare

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. <u>More info</u>

**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: <u>NM 033360.2</u>, <u>NP 203524.1</u>

RefSeq Size: 5436 bp



## KRAS (NM\_033360) Human Untagged Clone - SC126782

RefSeq ORF: 570 bp Locus ID: 3845

UniProt ID: P01116
Cytogenetics: 12p12.1

**Domains:** ras, RAN, 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 (a) is composed of six exons, including exon 4a, which the shorter transcript variant (b) lacks. This rare variant (a) has a cds that terminates in exon 4a and encodes a unique C-terminus, compared to isoform a. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent

with the reference genome assembly. The genomic coordinates used for the transcript record

were based on alignments.