

## Product datasheet for **SC323501**

### **RIOK2 (NM\_018343) Human Untagged Clone**

#### **Product data:**

Product Type:	Expression Plasmids
Product Name:	RIOK2 (NM_018343) Human Untagged Clone
Tag:	Tag Free
Symbol:	RIOK2
Synonyms:	RIO2
Mammalian Cell Selection:	None
Vector:	<u><a href="#">pCMV6-XL4</a></u>
E. coli Selection:	Ampicillin (100 ug/mL)



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**Fully Sequenced ORF:** >OriGene ORF within SC323501 sequence for NM\_018343 edited (data generated by NextGen Sequencing)

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ATGGGGAAAGTGAATGTGGCCAAGTTGCGTTACATGAGCCGAGATGACTTCAGGGTCTTG
ACCGCGGTTGAAATGGGCATGAAGAACCATGAAATTGTTCCCGGCAGTTTGATTGCTTCT
ATAGCCAGCCTTAAACATGGTGGCTGTAATAAAGTTTTAAGAGAATTAGTGAAACATAAA
CTCATAGCTTGGGAGCGTACAAAACGTCCAGGGCTATCGTTGACAAATGCAGGATAT
GATTACTAGCTTTGAAAACACTTCTTCTAGGCAAGTAGTTGAGTCTGTTGGAAACCAG
ATGGGTGTTGGCAAAGAATCAGATATTTACATTGTTGCAATGAAGAAGGACAACAATTT
GCATTAAGCTTTCACAGACTAGGAAGAACCTCGTTTCGAAATTTGAAAAACAAACGCGAT
TATCATAAACATAGGCACAATGTGTCTTGGCTTTATTTATCTCGTCTCTGCCATGAAG
GAATTTGCCTATATGAAGGCATTGTATGAGAGGAAATTTCCAGTTCCAAAGCCAATTGAT
TACAATCGTCATGCAGTGGTCATGGAACCTATAAATGGTATCCACTATGTCAGATACAC
CATGTTGAAGATCCTGCATCAGTATATGATGAAGCTATGGAACCTAATTGTCAAACCTGCA
AATCATGGGCTGATTCATGGAGCKTTTAAATGAATTTAATCTCATTTTGGATGAAAGTGAC
CATATCACCATGATTGATTTTCCACAGATGGTTTCAACTTCTCATCCCAATGCTGAGTGG
TATTTTGACAGAGATGTTAAATGCATTAAGATTTCTTTATGAAACGTTTCAGCTACGAA
AGTGAGCTTTTTCCAACTTTTAAGGATATCAGGAGAGAAGACACTCTTGATGTGGAGGTT
TCTGCCAGTGGCTACACAAAGGAAATGCAGGCAGATGATGAACCTGCTTACCTTAGGT
CCAGATGATAAAAATATTGAAACAAAAGAGGGATCTGAATTTCTCATTTTCAGATGGAGAA
GTGGCAGAAAAAGCAGAGGTTTACAGGTCAGAAAATGAAAGTGAACGGAACCTGTCTAGAA
GAATCAGAGGGCTGCTATTGCAGATCATCTGGAGACCCTGAACAAATAAAGGAAGACAGT
TTATCAGAAGAGAGTGTGATGCACGGAGTTTGAATGACTGAATTCATCAAGCTTTA
GAAGAAATAAAAAGGCGAGGTTGTTGAAAACAACCTGTAACCTGAATTTTCTGAGGAGAAA
AACAGAACTGAAAATTACAACAGGCAAGATGGTCAGAGAGTTCAAGGAGGAGTCCCTGCT
GGCTCTGACGAGTATGAAGATGAATGCCCTCATCTAATTGCCCTTGTGCTATTAATAGA
GAATTCAGGCCTTTCAGAGATGAAGAAAATGTGGGAGCTATGAATCAGTATAGAACAAGA
ACTCTGAGTATCACTTCTTCAGGCAGTGTGTAAGCTGTTCAACAATTCCTCCAGAACTG
GTGAAACAGAAGGTGAAACGTCAGTTGACAAAACAGCAAAAATCAGCTGTCAGACGTCGA
TTGCAGAAAGGAGAAGCAATATATTTACCAAGCAACGTAGGGAAAACATGCAAAAATATC
AAATCAAGTTTGAAGCAGCTAGCTTTTGGGAGAATAA
    
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Clone variation with respect to NM\_018343.2  
 447 a=>t;453 a=>t;683 a=>c;684 t=>k;1045 g=>a;1641 c=>t

**5' Read Nucleotide Sequence:** >OriGene 5' read for mutant NM\_018343 unedited

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CCCCGCCGTTTCAGCAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGA
ACCGTCAGAATTTTGAATACGACTCACTATAGGGCGGCCGCAATTCGGCACGAGGGTCGTCGGAGAGG
CATCTGGGTTTCGACTGGGGCCGCATGGGAAAAGTGAATGTGGCCAAGTTGCGTTACATGAGCCGAGAT
GACTTCAGGGTCTTGACCGCGTTGAAATGGGCATGAAGAACCATGAAATTGTTCCCGGCAGTTTGATTG
CTTCTATAGCCAGCCTTAAACATGGTGGCTGTAATAAAGTTTTAAGAGAATTAGTGAAAACATAAACTCA
TAGCTTGGGGAGCGTACCCAAAACGTCCAGGGCTATCGTTGACAAATGCAGGATATGATTACCTAGCT
TTGAAAACCTTTTCTTCTAGGCAAGTAGTTGAGTCCGGTGGAAACCCAGAGGGTGGTTGGCAAAGAATC
AGATATTAATGGTGCAAAGGAGAAGGGACAACATTTCTTAAACCTCACACATAGAAAAACCTGTTCC
AATTTGAAAACACAACGCATATATAAACCTAGGCCATGTGGCTGGCTAATTATCTCTCATGGCCGAGAGA
TTCCTATAAGCCTGTGAGAGAGAATCCGTTCAACGAAGTATCACACACCACC
    
```

**Kinase Domain Sequence:** >SC323501 kinase domain raw sequence. By performing [BLASTX](#) analysis with this sequence against NCBI reference protein database, you can confirm the presence of the kinase-deficient mutation

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GWCCCATGTTGAGWCCTGCATCAGTATATGATGAAGCTATGGAACCTAATTGTCAAACCTGCAAAATCATGG
GCTGATTCATGGAGCGTTTAAATGAATTTAATCTCATTTTGGATGAAAGTGACCATATCACCATGATTGAT
TTTCCACAGATGGTTTCAACTTCTCATCCCAATGCTGAGTGGTATTTTGACAGAGATGTTAAATGCATTA
AAGATTTCTTTATGAAACGTTTCAGCTACGAAAGTGAAGCTTTTTC
    
```

<b>Restriction Sites:</b>	Please inquire
<b>ACCN:</b>	NM_018343
<b>Insert Size:</b>	2110 bp
<b>OTI Disclaimer:</b>	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).
<b>OTI Annotation:</b>	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." <a href="#">Cell. 2008 May p536-548.</a>
<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"><li>1. Centrifuge at 5,000xg for 5min.</li><li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li><li>3. Close the tube and incubate for 10 minutes at room temperature.</li><li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li><li>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.</li></ol>
<b>RefSeq:</b>	<a href="#">NM_018343.1</a> , <a href="#">NP_060813.1</a>
<b>RefSeq Size:</b>	1832 bp
<b>RefSeq ORF:</b>	1659 bp
<b>Locus ID:</b>	55781
<b>UniProt ID:</b>	<a href="#">Q9BVS4</a>
<b>Cytogenetics:</b>	5q15
<b>Domains:</b>	RIO
<b>Protein Families:</b>	Druggable Genome, Protein Kinase

**Gene Summary:**

Serine/threonine-protein kinase involved in the final steps of cytoplasmic maturation of the 40S ribosomal subunit. Involved in export of the 40S pre-ribosome particles (pre-40S) from the nucleus to the cytoplasm. Its kinase activity is required for the release of NOB1, PNO1 and LTV1 from the late pre-40S and the processing of 18S-E pre-rRNA to the mature 18S rRNA (PubMed:19564402). Regulates the timing of the metaphase-anaphase transition during mitotic progression, and its phosphorylation, most likely by PLK1, regulates this function (PubMed:21880710).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (1) represents the longer transcript and 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.