

Product datasheet for SC119567

Retinoic Acid Receptor beta (RARβ) (NM_000965) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Retinoic Acid Receptor beta (RARβ) (NM_000965) Human Untagged Clone
Tag:	Tag Free
Symbol:	Retinoic Acid Receptor beta
Synonyms:	HAP; MCOPS12; NR1B2; RARbeta1; RRB2
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL5</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>OriGene ORF within SC119567 sequence for NM_000965 edited (data generated by NextGen Sequencing)

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ATGTTTGACTGTATGGATGTTCTGTCTGAGTCTGGGCAAATCCTGGATTTCTACACT
GCGAGTCCGTCCTCTGCATGCTCCAGGAGAAAGCTCTCAAAGCATGCTTCAGTGGATTG
ACCCAAACCGAATGGCAGCATCGGCACACTGCTCAATCAATTGAAACACAGACACCAGC
TCTGAGGAACTCGTCCCAAGCCCCCATCTCCACTTCTCCCCCTCGAGTGTACAAAACC
TGCTTCGTCTGCCAGGACAAATCATCAGGGTACCACTATGGGGTCAGCGCCTGTGAGGGA
TGTAAGGGCTTTTTCCGCAGAAGTATTCAGAAGAATATGATTTACTTGTCCAGGAT
AAGAACTGTGTTATTAATAAAGTACCAGGAATCGATGCCAATACTGTGACTCCAGAAG
TGCTTTGAAGTGGGAATGTCAAAGAATCTGTCAGGAATGACAGGAACAAGAAAAAGAAG
GAGACTTCGAAGCAAGAATGCACAGAGAGCTATGAAATGACAGCTGAGTTGGACGATCTC
ACAGAGAAGATCCGAAAAGCTCACCAGGAACTTTCCCTTCACTCTGCCAGCTGGGTAAA
TACACCACGAATTCAGTGTGACCATCGAGTCCGACTGGACCTGGGCTCTGGGACAAA
TTCAGTGAAGTGGCCACCAAGTGCATTATTAAGATCGTGGAGTTTGCTAAACGTCTGCCT
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ATCCTGATTCTTAGAATTTGCACCAGGTATACCCAGAACAAAGACACCATGACTTTCTCA
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AGTGCTAAAGGTGCAGAGCGTGAATTACCTTGAAAATGGAAAATCCTGGATCAATGCCA
CCTCTCATTCAAGAAATGCTGGAGAATTCTGAAGGACATGAACCTTGACCCCAAGTTCA
AGTGGGAACACAGCAGAGCACAGTCTAGCATCTACCCAGCTCAGTGGAAAACAGTGGG
GTCAGTCAGTCACCACTCGTGAATAA

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Clone variation with respect to NM_000965.3



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5' Read Nucleotide Sequence:

>OriGene 5' read for NM_000965 unedited
 GCATTTTGTATACGACTCACTATAGGGCGGCCGCAATTCGCACGAGGGTCTGTCATAA
 TTCATGGATTCGGGNGCTGGGAAAAAGACCAACAGCCTACGTGCCAAAAAGGGCAGAG
 TTTGATGGAGTTGGTGGACTTTTCTATGCCATTTGCCTCCACACCTAGAGGATAAGCAC
 TTTTGCAGACATTCAGTGAAGGGAGATCATGTTTGACTGTATGGATGTTCTGTCAGTGA
 GTCCTGGGCAAATCCTGGATTTCTACTGCGAGTCCGTCTTCTGCATGCTCCAGGAGA
 AAGCTCTCAAAGCATGTTTCAGTGGATTGACCCAAACCGAATGGCAGCATCGGCACACTG
 CCAATCAATTGAAACACAGAGCACAGCTCTGAGGAACCTGCCAAGCCCCCATCTC
 CACTTCTCCCCCTCGAGTGACAAACCCTGCTTCGTCTGCCAGGACAAATCATCAGGGT
 ACCACTATGGGGTCAGCGCCTGTGAGGGATGTAAGGGCTTTTTCCGCAGAAGTATTCAGA
 AGAATATGATTTACACTTGTCCAGAGATAAGAACTGTGTTATTAATAAAGTCACCAGGA
 ATCGATGCCAATACTGTCGACTCCAGAAGTCTTTGAAGTGGGAATGCCAAAGAATCTG
 TCAGGAATGACAGGGAACAGAAAAAGAGAGACTTCGAAGCAAGAATGCACAGAGAGCT
 ATGAAATGACAGCTGAGTTGGACGATCTCACAGAGAAGATCCGAAAGCTCNACCAGAAAC
 TTTCCCTCACTCTGCCAGCTGGGTAATAACACCACGAATTCAGTGTGACCATCGAGTT
 CGACTGGACCTGGGCCTCTGGGACAAATTCATTGAACTGGCCACCAGTGCATTATTAAGA
 TCGGNGAGATTGCTAAACGCTTGCTGGTTCAGTGGCTTGACATCGCAAACN

3' Read Nucleotide Sequence:

>OriGene 3' read for NM_000965 unedited
 GGGGCTTTTGTGTGTTTTATGCTTTGCCGGNANACTCCTGGGAAAAGGTAACAGTATAT
 GAACATAGAAAGCATTGTTAAACAAACAATCTCAATGTACAAACAGAGCCAGTAAAAGTA
 CATCACAGACTTGCTAATATATCAAAAAAAAAAATCCACTAGTGTAAATGAGAACT
 AAGAACTGACACTTGTATCTGTAAACCACTCTACCACAGCTTTCACTCTGCTTCATAGT
 GATTGAACAAGGTCAAAGGAGGCAGATTCTATGCCTGTTCTTTGGGAGTTGTTAATATT
 AATTAGCCCTTGGCATCAAGAAGGCTGGAAAAAAAAATCCCAATATCAGGCATGAATCA
 GGAAGGACTAGAGTTACATGGTCCAGGTGGTAGACCAGCCTGTAATTATCCCATGAA
 ATTTCCCTAATGGCTTGTGAACAAGTAAACAAAAAATTAACACTGAAAAGTGTCTGCTC
 TTGGAGGCTATCATTACTGTAAAAAATTTTTTTTTAACTGTGTAGTTATGTCATTAAC
 AAGTAATAAACCACTTTTAATTTAAAGTACATTAACAATTGAACAAATGACATTTGATT
 AACTGAACTGGCAGTTACTACTGATACAGAATTCTCTTCTGCTAGTGCAGGGAATTTGTAT
 ACTTTTACTGGCAACATGAAATAAAAGATGCAGTTTGAGAGCATTAGAAAGAGCAAAGA
 CAAGCCTCCCTACTAACCAAAAGTAGAATATCTCTAGCCTTATCTTGTACTGTACATA
 ATTCCTGTCCATAGACCTGTTTCCCTACCTTGAGTCTTGACTATTCCCCGAAACCCACAC
 AGTTATTTTCTTGAACCTAGGTAACCTGACCAGCAACCTATTTCTTAACCCTCGCGGCC
 TGGCTCATTTTGTATTTTGCAAAAAAACAGGAAAC

Restriction Sites:

NotI-NotI

ACCN:

NM_000965

Insert Size:

2900 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).

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_000965.2](#), [NP_000956.2](#)

RefSeq Size: 3119 bp

RefSeq ORF: 1347 bp

Locus ID: 5915

UniProt ID: [P10826](#)

Cytogenetics: 3p24.2

Domains: HOLI, zf-C4

Protein Families: Druggable Genome, Nuclear Hormone Receptor, Transcription Factors

Protein Pathways: Non-small cell lung cancer, Pathways in cancer, Small cell lung cancer

Gene Summary: This gene encodes retinoic acid receptor beta, a member of the thyroid-steroid hormone receptor superfamily of nuclear transcriptional regulators. This receptor localizes to the cytoplasm and to subnuclear compartments. It binds retinoic acid, the biologically active form of vitamin A which mediates cellular signalling in embryonic morphogenesis, cell growth and differentiation. It is thought that this protein limits growth of many cell types by regulating gene expression. The gene was first identified in a hepatocellular carcinoma where it flanks a hepatitis B virus integration site. Alternate promoter usage and differential splicing result in multiple transcript variants. [provided by RefSeq, Mar 2014]

Transcript Variant: This variant (1, also known as beta-2) is a predominant transcript. This variant can initiate translation from an upstream AUG site and also from a downstream, in-frame AUG site (PMID: 12118004). The isoform (1) represented in this RefSeq is derived from the upstream AUG start codon. 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.