

## Product datasheet for **SC323520**

### Activin A Receptor Type IB (ACVR1B) (NM\_004302) Human Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	Activin A Receptor Type IB (ACVR1B) (NM_004302) Human Untagged Clone
Tag:	Tag Free
Symbol:	Activin A Receptor Type IB
Synonyms:	ACTRIB; ACVRLK4; ALK4; SKR2
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 SC323520 sequence for NM\_004302 edited (data generated by NextGen Sequencing)

```

ATGGCGGAGTCGGCCGGAGCCTCCTCCTTCTTCCCCCTTGTGTGCTCCTGCTCGCCGGC
AGCGGCGGGTCCGGGCCCCGGGGGTCCAGGCTGTGTGTGCGTGCACCAGCTGCCTC
CAGGCCAACTACACGTGTGAGACAGATGGGCTGCATGGTTTCCATTTTCAATCTGGAT
GGGATGGAGCACCATGTGCGCACCTGCATCCCCAAAGTGGAGCTGGTCCCTGCCGGGAAG
CCCTTCTACTGCCTGAGCTCGGAGGACCTGCGCAACACCCACTGCTGCTACACTGACTAC
TGCAACAGGATCGACTTGAGGGTGCCAGTGGTCACTCAAGGAGCCTGAGCACCCGTCC
ATGTGGGCGCCGGTGGAGCTGGTAGGCATCATCGCCGGCCGGTGTTCCTCCTGTTCCCTC
ATCATCATCATTGTTTTCTTGTGATTAACTATCATCAGCGTGTCTATCACAACCGCCAG
AGACTGGACATGGAAGATCCCTCATGTGAGATGTGTCTCCTCAAAGACAAGACGCTCCAG
GATCTTGTCTACGATCTCACCCTCAGGGTCTGGCTCAGGGTTACCCCTCTTTGTCCAG
CGCACAGTGGCCGAACCATCGTTTTACAAGAGATTATTGGCAAGGGTCGGTTTGGGGAA
GTATGGCGGGGCCGCTGGAGGGTGGTGTGTGGCTGTGATGATATTCTTCTCTCGTGAA
GAACGGTCTTGGTTCAGGGAAGCAGAGATATACCAGACGGTCATGCTGCGCCATGAAAC
ATCCTTGGATTTATTGCTGCTGACAATAAAGATAATGGCACCTGGACACAGCTGTGGCTT
GTTTCTGACTATCATGAGCACGGGTCCCTGTTTATTATCTGAACCGGTACACAGTGACA
ATTGAGGGGATGATTAAGCTGGCCTTGTCTGCTGTAGTGGGCTGGCACACCTGCACATG
GAGATCGTGGGCACCCAAGGGAAGCCTGGAATTGCTCATCGAGACTTAAAGTCAAAGAAC
ATTCTGGTGAAGAAAAATGGCATGTGTGCCATAGCAGACCTGGGCTGGCTGTCCGTCAT
GATGCAGTCACTGACACCATTGACATTGCCCGAATCAGAGGGTGGGACCAAACGATAC
ATGGCCCTGAAGTACTTGATGAAACCATTAATATGAAACACTTTGACTCCTTTAAATGT
GCTGATATTTATGCCCTCGGGCTTGTATATTGGGAGATTGCTCGAAGATGCAATTCGGA
GGAGTCCATGAAGAATATCAGCTGCCATATTACGACTTAGTGCCCTCTGACCCCTCCATT
GAGGAAATGCGAAAGTTGTATGTGATCAGAAGCTGCGTCCCAACATCCCCAACTGGTGG
CAGAGTTATGAGGCACTGCGGGTGTGGGAAGATGATGCGAGAGTGTGGTATGCCAAC
GGCGCAGCCCGCTGACGGCCCTGCGCATCAAGAAGACCCTCTCCAGCTCAGCGTGCAG
GAAGACGTGAAGATCTAA
    
```

Clone variation with respect to NM\_004302.4  
701 a=>t;702 a=>g

**5' Read Nucleotide Sequence:**

>OriGene 5' read for mutant NM\_004302 unedited

```

CCGCCGTCGAGCAATGGGCGGTAGGCGCTGTACGGTTGGGAGGTTCTATATAAGCAGAGCTCGTTTAGTG
AACCGTCAGAATCTTGAATACGACTCACTATAGGGCGGCCGGAATTCGGCACGAGGCTGGGCTGCGGC
GGCGGCGGCGGGTGGTACTATGGCGGAGTCGGCCGGAGCCTCCTCCTTCTTCCCCCTTGTGTCCCTC
CTGCTCGCCGGCAGCGGGGTCGGGCCCCGGGGGTCCAGGCTCTGCTGTGTGCGTGCACCAGCTGCC
TCCAGGCCAACTACACGTGTGAGACAGATGGGCTGCATGGTTTCCATTTTCAATCTGGATGGGGATGG
GAGGCACCATGTGCGCACCTGCATCCCCAAAGTGGAGCTGGTCCCTGCCGGGAAAGCCCTTCTACTGCC
GAGCTCGGAGAACCTGCGCAACAACCCACTGCTGCTACTGACTACTGCAACAGGATCGACTTGGAGG
TTGCTAGTGGTCACCCCGAGGAAACCCTGAGC
    
```

**Kinase Domain Sequence:**

>SC323520 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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CCTTAGAGATWTGGCAGGGTCGGTTTGGGGAAGTATGGCGGGGCCGCTGGAGGGTGGTGTGTGGCTGT
GATGATATTCTTCTCTGTAAGAACGGTCTTGGTTCAGGGAAGCAGAGATATACCAGACGGTCATGCTG
CGCCATGAAAACATCCTTGGATTTATTGCTGCTGACAATAAAGATAATGGCACCTGGACACAGCTGTGGC
TTGTTTCTGACTATCATGAGCACGGTCCCTGTTTATTATCTGA
    
```

**Restriction Sites:**

Please inquire

**ACCN:**

NM\_004302

<b>Insert Size:</b>	3300 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_004302.3</a> , <a href="#">NP_004293.1</a>
<b>RefSeq Size:</b>	4540 bp
<b>RefSeq ORF:</b>	1518 bp
<b>Locus ID:</b>	91
<b>UniProt ID:</b>	<a href="#">P36896</a>
<b>Cytogenetics:</b>	12q13.13
<b>Domains:</b>	Activin_recp, pkinase, TyrKc, S_TKc, GS
<b>Protein Families:</b>	Druggable Genome, Protein Kinase, Transmembrane
<b>Protein Pathways:</b>	Adherens junction, Chronic myeloid leukemia, Colorectal cancer, Cytokine-cytokine receptor interaction, Endocytosis, MAPK signaling pathway, Pancreatic cancer, Pathways in cancer, TGF-beta signaling pathway

**Gene Summary:**

This gene encodes an activin A type IB receptor. Activins are dimeric growth and differentiation factors which belong to the transforming growth factor-beta (TGF-beta) superfamily of structurally related signaling proteins. Activins signal through a heteromeric complex of receptor serine kinases which include at least two type I and two type II receptors. This protein is a type I receptor which is essential for signaling. Mutations in this gene are associated with pituitary tumors. Alternate splicing results in multiple transcript variants. [provided by RefSeq, Jun 2010]

Transcript Variant: This variant (1) encodes isoform (a). 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.