

Product datasheet for RC206829L4V

OriGene Technologies, Inc.

9620 Medical Center Drive, Ste 200 Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com CN: techsupport@origene.cn

TBX3 (NM_016569) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type: Lentiviral Particles

Product Name: TBX3 (NM 016569) Human Tagged ORF Clone Lentiviral Particle

Symbol: TBX3

Synonyms: TBX3-ISO; UMS; XHL

Mammalian Cell

Selection:

Puromycin

Vector: pLenti-C-mGFP-P2A-Puro (PS100093)

Tag: mGFP

ACCN: NM_016569 **ORF Size:** 2229 bp

ORF Nucleotide

- - -

Sequence:

The ORF insert of this clone is exactly the same as(RC206829).

OTI Disclaimer: 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

OTI Annotation: This clone was engineered to express the complete ORF with an expression tag. Expression

varies depending on the nature of the gene.

RefSeg: NM 016569.3

 RefSeq Size:
 4814 bp

 RefSeq ORF:
 2232 bp

 Locus ID:
 6926

 UniProt ID:
 015119

Cytogenetics: 12q24.21

Domains: T-box

Protein Families: Druggable Genome, Transcription Factors





ORIGENE

MW: 79.4 kDa

Gene Summary:

This gene is a member of a phylogenetically conserved family of genes that share a common DNA-binding domain, the T-box. T-box genes encode transcription factors involved in the regulation of developmental processes. This protein is a transcriptional repressor and is thought to play a role in the anterior/posterior axis of the tetrapod forelimb. Mutations in this gene cause ulnar-mammary syndrome, affecting limb, apocrine gland, tooth, hair, and genital development. Alternative splicing of this gene results in three transcript variants encoding different isoforms; however, the full length nature of one variant has not been determined. [provided by RefSeq, Jul 2008]