

Product datasheet for RC211955L3V

OriGene Technologies, Inc.

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Manic Fringe (MFNG) (NM_002405) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type: Lentiviral Particles

Product Name: Manic Fringe (MFNG) (NM_002405) Human Tagged ORF Clone Lentiviral Particle

Symbol: Manic Fringe
Mammalian Cell Puromycin

Selection:

Vector:

pLenti-C-Myc-DDK-P2A-Puro (PS100092)

Tag: Myc-DDK

ACCN: NM_002405

ORF Size: 963 bp

ORF Nucleotide

The ORF insert of this clone is exactly the same as(RC211955).

OTI Disclaimer:

Sequence:

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.

RefSeq: <u>NM 002405.2</u>

 RefSeq Size:
 2040 bp

 RefSeq ORF:
 966 bp

 Locus ID:
 4242

 UniProt ID:
 000587

Cytogenetics: 22q13.1

Domains: Fringe

Protein Families: Druggable Genome

Protein Pathways: Notch signaling pathway





MW: 36 kDa

Gene Summary:

This gene is a member of the glycosyltransferase 31 gene family. Members of this gene family, which also includes the LFNG (GeneID: 3955) and RFNG (GeneID: 5986) genes, encode evolutionarily conserved glycosyltransferases that act in the Notch signaling pathway to define boundaries during embryonic development. While their genomic structure is distinct from other glycosyltransferases, these proteins have a fucose-specific beta-1,3-N-acetylglucosaminyltransferase activity that leads to elongation of O-linked fucose residues on Notch, which alters Notch signaling. The protein encoded by this gene may control Notch signaling in claudin-low breast cancer. [provided by RefSeq, May 2018]