

Product datasheet for SC313303

OriGene Technologies, Inc.

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FGFR1 Oncogene Partner (FGFR1OP) (NM 007045) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: FGFR1 Oncogene Partner (FGFR1OP) (NM_007045) Human Untagged Clone

Tag: Tag Free

FGFR1 Oncogene Partner Symbol:

FGFR1OP; FOP Synonyms:

Mammalian Cell

Neomycin

Selection:

Vector: pCMV6-Entry (PS100001) E. coli Selection: Kanamycin (25 ug/mL)

Fully Sequenced ORF: >SC313303 representing NM_007045.

Blue=Insert sequence Red=Cloning site Green=Tag(s)

GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC

ATGGCGGCGACGGCCGCAGTGGTGGCCGAGGAGGACACGGAGCTGCGGGACCTGCTGGTGCAGACG CTGGAGAACAGCGGGGTCCTGAACCGCATCAAGGCTGAACTCCGAGCAGCTGTTTTTTAGCACTAGAG GAGCAAGAAAAAGTAGAGAACAAAACTCCTTTAGTTAATGAGAGCCTGAAAAAGTTTTTAAATACCAAA GACGGTCGTTTAGTGGCTAGTCTTGTTGCAGAATTTCTTCAGTTTTTTAACCTTGACTTTACTTTGGCT GTTTTTCAACCTGAAACTAGCACACTGCAAGGTCTCGAAGGTCGAGAGAATTTAGCCCGAGATTTAGGT ATAATTGAAGCAGAAGGTACTGTGGGTGGACCCTTATTATTAGAAGTGATCAGGCGCTGTCAACAGAAA GAGGGAAAAACAAGTGCACAGACAACACCAAGTAAGATACCAAGGTATAAAGGACAAGGTAAGAAGAAG ACAAGCGGGCAGAAGGCTGGTGACAAGAAGGCCAATGATGAGGCCAATCAGAGTGATACAAGTGTCTCC TTGTCAGAACCCAAGAGCAAAAGCAGCCTTCACTTACTGTCCCATGAAACAAAAATTGGATCTTTTCTA AGCAACAGAACTTTAGATGGCAAAGACAAAGCTGGCCTTTGTCCAGATGAAGATGATATGGAAGGAGAT GCAGGAAGTCTGGCCTCGCTCTCGGATGCACCCCCCTTAAAAAGTGGACTCAGCTCCCTGGCGGGAGCC CCTTCTTTAAAAGACTCTGAGAGTAAAAGGGGAAATACAGTTTTGAAAGATCTGAAATTGATCAGTGAT AAAATTGGATCACTTGGATTAGGAACTGGAGAAGATGATGATGTTGATGATTTTAATAGTACCAGC GACATCAATACCAGTGATAAGCTTGATGACCTCACACAGATCTGACTGTATCCCAGCTCAGTGATGTT

GCGGATTATCTGGAAGATGTTGCATAG

ACGCGTACGCGCCCCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT

TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

Restriction Sites: Sgfl-Mlul





ACCN: NM 007045

Insert Size: 1200 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).

OTI Annotation: This TrueClone is provided through our Custom Cloning Process that includes sub-cloning

> into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

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.

NM 007045.3 RefSeq:

RefSeq Size: 3736 bp RefSeq ORF: 1200 bp Locus ID: 11116 **UniProt ID:** 095684 Cytogenetics:

Protein Families: Druggable Genome

6q27

MW: 43.1 kDa

Gene Summary: This gene encodes a largely hydrophilic centrosomal protein that is required for anchoring

microtubules to subcellular structures. A t(6;8)(q27;p11) chromosomal translocation, fusing this gene and the fibroblast growth factor receptor 1 (FGFR1) gene, has been found in cases of myeloproliferative disorder. The resulting chimeric protein contains the N-terminal leucinerich region of this encoded protein fused to the catalytic domain of FGFR1. Alterations in this gene may also be associated with Crohn's disease, Graves' disease, and vitiligo. Alternatively spliced transcript variants that encode different proteins have been identified. [provided by

RefSeq, Jul 2013]

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