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Product datasheet for SC313017

NSFL1C (NM_018839) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	NSFL1C (NM_018839) Human Untagged Clone
Tag:	Tag Free
Symbol:	NSFL1C
Synonyms:	dJ776F14.1; P47; UBX1; UBXD10; UBXN2C
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC313017 representing NM_018839. Blue=Insert sequence Red=Cloning site Green=Tag(s) GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGGCGGCGGAGCGACAGGAGGCGCTGAGGGAGTTCGTGGCGGTGACGGGCGCCGAGGAGGACCGGGCC CGCTTCTTTCTCGAGTCGGCCGGCTGGGACTTGCAGATCGCGCTAGCGAGCTTTTATGAGGACGGAGGG GATGAAGACATTGTGACCATTTCGCAGGCAACCCCCAGTTCAGTGTCCAGAGGCACAGCCCCCAGTGAT AATAGAGTGACATCCTTCAGAGACCTCATTCATGACCAAGATGAAGATGAGGAGGAAGAGGAAGGCCAG AGGTTTTATGCTGGGGGCTCAGAGAGAAGTGGACAGCAGATTGTTGGCCCTCCCAGGAAGAAAAGTCCC AACGAGCTGGTGGATGATCTCTTTAAAGGTGCCAAAGAGCATGGAGCTGTAGCTGTGGAGCGAGTGACC AAGAGCCCTGGAGAGACCAGTAAACCGAGAGTTCATGTAGTATTGAAACTCTGGAAGAGTGGATTCAGC CTGGATAATGGAGAACTCAGAAGCTACCAAGACCCATCCAATGCCCAGTTTCTGGAGTCTATCCGCAGA GGGGAGGTGCCAGCAGAGCTTCGGAGGCTAGCTCACGGTGGACAGGTGAACTTGGATATGGAGGACCAT CGGGACGAGGACTTTGTGAAGCCCAAAGGAGCCTTCAAAGCCTTCACTGGCGAGGGTCAGAAACTGGGC AGCACTGCCCCCCAGGTGTTGAGTACCAGCTCTCCAGCCCAACAGGCAGAAAATGAAGCCAAAGCCAGC TCTTCCATCTTAATCGACGAATCAGAGCCTACCACAAACATCCAAATTCGGCTTGCAGACGGCGGGAGG CTGGTGCAGAAATTTAACCACAGCCACAGGATCAGCGACATCCGACTCTTCATCGTGGATGCCCGGCCA GCCATGGCTGCCACCAGCTTTATCCTCATGACTACTTTCCCGAACAAAGAGCTGGCTGATGAGAGCCAG ACCCTGAAGGAAGCCAACCTGCTCAATGCTGTCATCGTGCAGCGGTTAACATAA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
Restriction Sites:	SgfI-MluI
ACCN:	NM_018839
Insert Size:	1020 bp

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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.
RefSeq:	NM_018839.4
RefSeq Size:	3475 bp
RefSeq ORF:	1020 bp
Locus ID:	55968
UniProt ID:	Q9UNZ2
Cytogenetics:	20p13
Domains:	UBX, FAF
MW:	37.3 kDa
Gene Summary:	N-ethylmaleimide-sensitive factor (NSF) and valosin-containing protein (p97) are two ATPases known to be involved in transport vesicle/target membrane fusion and fusions between membrane compartments. A trimer of the protein encoded by this gene binds a hexamer of cytosolic p97 and is required for p97-mediated regrowth of Golgi cisternae from mitotic Golgi fragments. Alternative splicing results in multiple transcript variants. A related pseudogene has been identified on chromosome 8. [provided by RefSeq, May 2011] Transcript Variant: This variant (2) lacks an alternate in-frame exon in the central coding region, compared to variant 1, resulting in an isoform (b) that is shorter than 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.