

Product datasheet for SC110747

NLRP3 (NM_004895) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	NLRP3 (NM_004895) Human Untagged Clone
Tag:	Tag Free
Symbol:	NLRP3
Synonyms:	AGTAVPRL; All; AVP; C1orf7; CIAS1; CLR1.1; DFNA34; FCAS; FCAS1; FCU; KEFH; MWS; NALP3; PYPAF1
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL4</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>OriGene ORF within SC110747 sequence for NM_004895 edited (data generated by NextGen Sequencing)

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ATGAAGATGGCAAGCACCCTGCAAGCTGGCCAGGTACCTGGAGGACCTGGAGGATGTG
GACTTGAAGAAATTTAAGATGCACTTAGAGGACTATCCTCCCCAGAAGGGCTGCATCCCC
CTCCCCAGGGGTCAGACAGAGAAGGCAGACCATGTGGATCTAGCCACGCTAATGATCGAC
TTCAATGGGGAGGAGAAGGCGTGGGCCATGGCCGTGTGGATCTTCGCTGCGATCAACAGG
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GTTTTCGAATCCCCTGTGATATGCCAGGAAGACAGCATTGAAGAGGAGTGGATGGGTTTA
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CAGAACCTGGGGTGTCTGAAATGTATTTCAATTATGAGACAAAAAGTGCCTTAGAAACA
CTTCAAGAAGAAAAGCCTGAGCTGACCGTCGTCTTTGAGCCTTCTTGGTAG
    
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Clone variation with respect to NM_004895.4
786 g=>a

5' Read Nucleotide Sequence:

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>OriGene 5' read for NM_004895 unedited
CGCGAATTCGGCACCAGGGGAAACCTTTCTTCCATGGCTCAGGACACACTCCTGGATCGA
GCCAACAGGAGAAGTTCTGTGTGGACCGAAGCCTAAGGACCCTGAAAACAGCTGCAGAT
GAAGATGGCAAGCACCCGCTGCAAGCTGGCCAGGTACCTGGAGGACCTGGAGGATGTGGA
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CCCGAGGGGTGAGACAGAGAAGGCAGACCATGTGGATCTAGCCACGCTAATGATCGACTT
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TGTGAGCCTCAACAACGCTACACACGACTGCGTCTCATCAAGGAGCACCCGGAGCCAGCAG
GAGAAGGGACAGAGCTTCTGGCCATCGGCNAGAACAAGAAGTGTGAGAACCCCGTGAGT
CCCATTAGATGGAGTTGCTGTTTGACCCCGATG
    
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Restriction Sites:

NotI-NotI

ACCN:

NM_004895

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).
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:	<ol style="list-style-type: none"> 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:	<u>NM_004895.3</u> , <u>NP_004886.3</u>
RefSeq Size:	4484 bp
RefSeq ORF:	3111 bp
Locus ID:	114548
UniProt ID:	<u>Q96P20</u>
Cytogenetics:	1q44
Domains:	LRR, LRR_RI, PAAD_DAPIN
Protein Families:	Druggable Genome
Protein Pathways:	NOD-like receptor signaling pathway

Gene Summary:

This gene encodes a pyrin-like protein containing a pyrin domain, a nucleotide-binding site (NBS) domain, and a leucine-rich repeat (LRR) motif. This protein interacts with the apoptosis-associated speck-like protein PYCARD/ASC, which contains a caspase recruitment domain, and is a member of the NLRP3 inflammasome complex. This complex functions as an upstream activator of NF-kappaB signaling, and it plays a role in the regulation of inflammation, the immune response, and apoptosis. The SARS-CoV 3a protein, a transmembrane pore-forming viroporin, has been shown to activate the NLRP3 inflammasome via the formation of ion channels in macrophages. Mutations in this gene are associated with familial cold autoinflammatory syndrome (FCAS), Muckle-Wells syndrome (MWS), chronic infantile neurological cutaneous and articular (CINCA) syndrome, neonatal-onset multisystem inflammatory disease (NOMID), keratoendotheliitis fugax hereditaria, and deafness, autosomal dominant 34, with or without inflammation. Multiple alternatively spliced transcript variants encoding distinct isoforms have been identified for this gene. Alternative 5' UTR structures are suggested by available data; however, insufficient evidence is available to determine if all of the represented 5' UTR splice patterns are biologically valid. [provided by RefSeq, Aug 2020]

Transcript Variant: This variant (1) represents the longest transcript and encodes the longest isoform (a). Both variants 1 and 3 encode the same isoform. **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. **CCDS Note:** This CCDS representation uses the 5'-most in-frame start codon, which is conserved in primates, rat, kangaroo rat, dolphin, cow, cat, elephant, tenrec and armadillo. An alternative downstream start codon, which is more widely conserved and has a stronger Kozak signal, also exists. It is possible that leaky scanning by ribosomes would allow the downstream start codon to be used, at least some of the time. The use of the downstream start codon would result in a protein that is 2 aa shorter at the N-terminus. There is no experimental evidence showing which start codon is preferentially used in vivo.