

## Product datasheet for **TR305382**

### NLRP3 Human shRNA Plasmid Kit (Locus ID 114548)

#### Product data:

Product Type:	shRNA Plasmids
Product Name:	NLRP3 Human shRNA Plasmid Kit (Locus ID 114548)
Locus ID:	114548
Synonyms:	AGTAVPRL; All; AVP; C1orf7; CIAS1; CLR1.1; DFNA34; FCAS; FCAS1; FCU; KEFH; MWS; NALP3; PYPAF1
Vector:	pRS (TR20003)
E. coli Selection:	Ampicillin
Mammalian Cell Selection:	Puromycin
Format:	Retroviral plasmids
Components:	NLRP3 - Human, 4 unique 29mer shRNA constructs in retroviral untagged vector(Gene ID = 114548). 5µg purified plasmid DNA per construct 29-mer scrambled shRNA cassette in pRS Vector, TR30012, included for free.
RefSeq:	<a href="#">NM_001079821</a> , <a href="#">NM_001127461</a> , <a href="#">NM_001127462</a> , <a href="#">NM_001243133</a> , <a href="#">NM_004895</a> , <a href="#">NM_183395</a> , <a href="#">NM_001079821.1</a> , <a href="#">NM_001079821.2</a> , <a href="#">NM_004895.1</a> , <a href="#">NM_004895.2</a> , <a href="#">NM_004895.3</a> , <a href="#">NM_004895.4</a> , <a href="#">NM_183395.1</a> , <a href="#">NM_183395.2</a> , <a href="#">NM_001127461.1</a> , <a href="#">NM_001127461.2</a> , <a href="#">NM_001127462.1</a> , <a href="#">NM_001127462.2</a> , <a href="#">NM_001243133.1</a> , <a href="#">BC117211</a> , <a href="#">BC143359</a> , <a href="#">BC143362</a> , <a href="#">BC143363</a> , <a href="#">NM_004895.5</a>
UniProt ID:	<a href="#">Q96P20</a>



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<b>Summary:</b>	<p>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 hereditarian, 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]</p>
<b>shRNA Design:</b>	<p>These shRNA constructs were designed against multiple splice variants at this gene locus. To be certain that your variant of interest is targeted, please contact <a href="mailto:techsupport@origene.com">techsupport@origene.com</a>. If you need a special design or shRNA sequence, please utilize our <a href="#">custom shRNA service</a>.</p>
<b>Performance Guaranteed:</b>	<p>OriGene guarantees that the sequences in the shRNA expression cassettes are verified to correspond to the target gene with 100% identity. One of the four constructs at minimum are guaranteed to produce 70% or more gene expression knock-down provided a minimum transfection efficiency of 80% is achieved. Western Blot data is recommended over qPCR to evaluate the silencing effect of the shRNA constructs 72 hrs post transfection. To properly assess knockdown, the gene expression level from the included scramble control vector must be used in comparison with the target-specific shRNA transfected samples.</p> <p>For non-conforming shRNA, requests for replacement product must be made within ninety (90) days from the date of delivery of the shRNA kit. To arrange for a free replacement with newly designed constructs, please contact Technical Services at <a href="mailto:techsupport@origene.com">techsupport@origene.com</a>. Please provide your data indicating the transfection efficiency and measurement of gene expression knockdown compared to the scrambled shRNA control (Western Blot data preferred).</p>