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# Product datasheet for TR315663

### HSPC142 (BABAM1) Human shRNA Plasmid Kit (Locus ID 29086)

## **Product data:**

| Product Type:                | shRNA Plasmids   |
|------------------------------|--|
| Product Name:                | HSPC142 (BABAM1) Human shRNA Plasmid Kit (Locus ID 29086)  |
| Locus ID:                    | 29086  |
| Synonyms:                    | C19orf62; HSPC142; MERIT40; NBA1   |
| Vector:                      | pRS (TR20003)  |
| E. coli Selection:           | Ampicillin   |
| Mammalian Cell<br>Selection: | Puromycin  |
| Format:                      | Retroviral plasmids  |
| Components:                  | <ul> <li>BABAM1 - Human, 4 unique 29mer shRNA constructs in retroviral untagged vector(Gene ID = 29086). 5μg purified plasmid DNA per construct</li> <li>29-mer scrambled shRNA cassette in pRS Vector, TR30012, included for free.</li> </ul>   |
| RefSeq:                      | <u>NM 001033549</u> , <u>NM 001288756</u> , <u>NM 001288757</u> , <u>NM 014173</u> , <u>NM 014173.1</u> , <u>NM 014173.2</u> ,<br><u>NM 014173.3</u> , <u>NM 001033549.1</u> , <u>NM 001033549.2</u> , <u>NM 001288757.1</u> , <u>NM 001288756.1</u> ,<br><u>BC006244</u> , <u>BC091491</u> , <u>BC000788</u> , <u>NM 014173.4</u> |
| UniProt ID:                  | <u>Q9NWV8</u>  |



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#### CRIGENE HSPC142 (BABAM1) Human shRNA Plasmid Kit (Locus ID 29086) – TR315663

| Summary:      | Component of the BRCA1-A complex, a complex that specifically recognizes 'Lys-63'-linked<br>ubiquitinated histones H2A and H2AX at DNA lesions sites, leading to target the BRCA1-<br>BARD1 heterodimer to sites of DNA damage at double-strand breaks (DSBs). The BRCA1-A<br>complex also possesses deubiquitinase activity that specifically removes 'Lys-63'-linked<br>ubiquitin on histones H2A and H2AX. In the BRCA1-A complex, it is required for the complex<br>integrity and its localization at DSBs. Component of the BRISC complex, a multiprotein<br>complex that specifically cleaves 'Lys-63'-linked ubiquitin in various substrates<br>(PubMed:24075985, PubMed:26195665). In these 2 complexes, it is probably required to<br>maintain the stability of BABAM2 and help the 'Lys-63'-linked deubiquitinase activity<br>mediated by BRCC3/BRCC36 component. The BRISC complex is required for normal mitotic<br>spindle assembly and microtubule attachment to kinetochores via its role in deubiquitinating<br>NUMA1 (PubMed:26195665). Plays a role in interferon signaling via its role in the<br>deubiquitination of the interferon receptor IFNAR1; deubiquitination increases IFNAR1<br>activity by enhancing its stability and cell surface expression (PubMed:24075985). Down-<br>regulates the response to bacterial lipopolysaccharide (LPS) via its role in IFNAR1<br>deubiquitination (PubMed:24075985).[UniProtKB/Swiss-Prot Function] |
|---------------|---|
| shRNA Design: | 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 <u>techsupport@origene.com</u> .<br>If you need a special design or shRNA sequence, please utilize our <u>custom shRNA service</u> .  |
| Performance   | OriGene guarantees that the sequences in the shPNA expression cassettes are verified to   |

PerformanceOriGene guarantees that the sequences in the shRNA expression cassettes are verified toGuaranteed:correspond to the target gene with 100% identity. One of the four constructs at minimum are<br/>guaranteed to produce 70% or more gene expression knock-down provided a minimum<br/>transfection efficiency of 80% is achieved. Western Blot data is recommended over qPCR to<br/>evaluate the silencing effect of the shRNA constructs 72 hrs post transfection. To properly<br/>assess knockdown, the gene expression level from the included scramble control vector must<br/>be used in comparison with the target-specific shRNA transfected samples.

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 techsupport@origene.com. Please provide your data indicating the transfection efficiency and measurement of gene expression knockdown compared to the scrambled shRNA control (Western Blot data preferred).

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