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# Datasheet for ABIN3095050 RNF8 Protein (AA 1-485) (Strep Tag)

1 Image



### Overview

| Quantity:                     | 1 mg  |
|-------------------------------|---|
| Target:                       | RNF8  |
| Protein Characteristics:      | AA 1-485                                      |
| Origin:                       | Human   |
| Source:                       | Tobacco (Nicotiana tabacum)                   |
| Protein Type:                 | Recombinant                                   |
| Purification tag / Conjugate: | This RNF8 protein is labelled with Strep Tag. |
| Application:                  | ELISA, Western Blotting (WB), SDS-PAGE (SDS)  |

## Product Details

|           | have a special request, please contact us.  |
|-----------|---|
|           | system, a different complexity of the protein could make another tag necessary. In case you |
|           | Sequence without tag. The proposed Strep-Tag is based on experience s with the expression   |
|           | SFCSYCINEW MKRKIECPIC RKDIKSKTYS LVLDNCINKM VNNLSSEVKE RRIVLIRERK AKRLF                     |
|           | FEAIIQAKNK ELEQTKEEKE KMQAQKEEVL SHMNDVLENE LQCIICSEYF IEAVTLNCAH                           |
|           | AEQAQQQARV EQLEKTFQEE EQHLQGLEIA QGEKDLKQQL AQALQEHWAL MEELNRSKKD                           |
|           | ASQRSLQMFK VTMSRILRLK IQMQEKHEAV MNVKKQTQKG NSKKVVQMEQ ELQDLQSQLC                           |
|           | CESGQPVKSQ GKGEVASTPS DNLDPKLTAL EPSKTTGAPI YPGFPKVTEV HHEQKASNSS                           |
|           | EYEVTEEDWE TIYPCLSPKN DQMIEKNKEL RTKRKFSLDE LAGPGAEGPS NLKSKINKVS                           |
|           | RNHCVLKQNP EGQWTIMDNK SLNGVWLNRA RLEPLRVYSI HQGDYIQLGV PLENKENAEY                           |
| Sequence: | MGEPGFFVTG DRAGGRSWCL RRVGMSAGWL LLEDGCEVTV GRGFGVTYQL VSKICPLMIS                           |

Characteristics:

Key Benefits:

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- · Made in Germany from design to production by highly experienced protein experts.
- Protein expressed with ALICE® and purified by multi-step, protein-specific process to ensure correct folding and modification.
- These proteins are normally active (enzymatically functional) as our customers have reported (not tested by us and not guaranteed).
- State-of-the-art algorithm used for plasmid design (Gene synthesis).

This protein is a **made-to-order protein** and will be made for the first time for your order. Our experts in the lab will ensure that you receive a correctly folded protein.

The big advantage of ordering our **made-to-order proteins** in comparison to ordering custom made proteins from other companies is that there is no financial obligation in case the protein cannot be expressed or purified.

#### Expression System:

- ALICE®, our Almost Living Cell-Free Expression System is based on a lysate obtained from Nicotiana tabacum c.v.. This contains all the protein expression machinery needed to produce even the most difficult-to-express proteins, including those that require post-translational modifications.
- During lysate production, the cell wall and other cellular components that are not required for
  protein production are removed, leaving only the protein production machinery and the
  mitochondria to drive the reaction. During our lysate completion steps, the additional
  components needed for protein production (amino acids, cofactors, etc.) are added to
  produce something that functions like a cell, but without the constraints of a living system all that's needed is the DNA that codes for the desired protein!

#### Concentration:

- The concentration of our recombinant proteins is measured using the absorbance at 280nm.
- The protein's absorbance will be measured in several dilutions and is measured against its specific reference buffer.
- We use the Expasy's ProtParam tool to determine the absorption coefficient of each protein.

#### Purification:

Two step purification of proteins expressed in Almost Living Cell-Free Expression System (ALICE®):

- 1. In a first purification step, the protein is purified from the cleared cell lysate using StrepTag capture material. Eluate fractions are analyzed by SDS-PAGE.
- Protein containing fractions of the best purification are subjected to second purification step through size exclusion chromatography. Eluate fractions are analyzed by SDS-PAGE and Western blot.

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| Product Details  |  |
|------------------|--|
| Purity:          | >80 % as determined by SDS PAGE, Size Exclusion Chromatography and Western Blot. |
| Endotoxin Level: | Low Endotoxin less than 1 EU/mg (< 0.1 ng/mg)                                    |
| Grade:           | Crystallography grade  |

# Target Details

| Target:           | RNF8   |
|-------------------|--|
| Alternative Name: | RNF8 (RNF8 Products)   |
| Background:       | E3 ubiquitin-protein ligase RNF8 (hRNF8) (EC 2.3.2.27) (RING finger protein 8) (RING-type E3       |
|                   | ubiquitin transferase RNF8),FUNCTION: E3 ubiquitin-protein ligase that plays a key role in DNA     |
|                   | damage signaling via 2 distinct roles: by mediating the 'Lys-63'-linked ubiquitination of histone  |
|                   | H2A and H2AX and promoting the recruitment of DNA repair proteins at double-strand breaks          |
|                   | (DSBs) sites, and by catalyzing 'Lys-48'-linked ubiquitination to remove target proteins from      |
|                   | DNA damage sites. Following DNA DSBs, it is recruited to the sites of damage by ATM-               |
|                   | phosphorylated MDC1 and catalyzes the 'Lys-63'-linked ubiquitination of histones H2A and           |
|                   | H2AX, thereby promoting the formation of TP53BP1 and BRCA1 ionizing radiation-induced foc          |
|                   | (IRIF). Also controls the recruitment of UIMC1-BRCC3 (RAP80-BRCC36) and PAXIP1/PTIP to             |
|                   | DNA damage sites. Also recruited at DNA interstrand cross-links (ICLs) sites and catalyzes 'Lys    |
|                   | 63'-linked ubiquitination of histones H2A and H2AX, leading to recruitment of FAAP20/C1orf86       |
|                   | and Fanconi anemia (FA) complex, followed by interstrand cross-link repair. H2A ubiquitinatior     |
|                   | also mediates the ATM-dependent transcriptional silencing at regions flanking DSBs in cis, a       |
|                   | mechanism to avoid collision between transcription and repair intermediates. Promotes the          |
|                   | formation of 'Lys-63'-linked polyubiquitin chains via interactions with the specific ubiquitin-    |
|                   | conjugating UBE2N/UBC13 and ubiquitinates non-histone substrates such as PCNA.                     |
|                   | Substrates that are polyubiquitinated at 'Lys-63' are usually not targeted for degradation. Also   |
|                   | catalyzes the formation of 'Lys-48'-linked polyubiquitin chains via interaction with the ubiquitin |
|                   | conjugating UBE2L6/UBCH8, leading to degradation of substrate proteins such as CHEK2,              |
|                   | JMJD2A/KDM4A and KU80/XRCC5: it is still unclear how the preference toward 'Lys-48'- versu         |
|                   | 'Lys-63'-linked ubiquitination is regulated but it could be due to RNF8 ability to interact with   |
|                   | specific E2 specific ligases. For instance, interaction with phosphorylated HERC2 promotes the     |
|                   | association between RNF8 and UBE2N/UBC13 and favors the specific formation of 'Lys-63'-            |
|                   | linked ubiquitin chains. Promotes non-homologous end joining (NHEJ) by promoting the 'Lys-         |
|                   | 48'-linked ubiquitination and degradation the of KU80/XRCC5. Following DNA damage,                 |
|                   | mediates the ubiquitination and degradation of JMJD2A/KDM4A in collaboration with RNF168           |
|                   | leading to unmask H4K20me2 mark and promote the recruitment of TP53BP1 at DNA damage               |

sites (PubMed:11322894, PubMed:14981089, PubMed:17724460, PubMed:18001824, PubMed:18001825, PubMed:18006705, PubMed:18077395, PubMed:18337245, PubMed:18948756, PubMed:19015238, PubMed:19124460, PubMed:19202061, PubMed:19203578, PubMed:19203579, PubMed:20550933, PubMed:21558560, PubMed:21857671, PubMed:21911360, PubMed:22266820, PubMed:22373579, PubMed:22531782, PubMed:22705371, PubMed:22865450, PubMed:22980979). Following DNA damage, mediates the ubiquitination and degradation of POLD4/p12, a subunit of DNA polymerase delta. In the absence of POLD4, DNA polymerase delta complex exhibits higher proofreading activity (PubMed:23233665). In addition to its function in damage signaling, also plays a role in higher-order chromatin structure by mediating extensive chromatin decondensation. Involved in the activation of ATM by promoting histone H2B ubiquitination, which indirectly triggers histone H4 'Lys-16' acetylation (H4K16ac), establishing a chromatin environment that promotes efficient activation of ATM kinase. Required in the testis, where it plays a role in the replacement of histones during spermatogenesis. At uncapped telomeres, promotes the joining of deprotected chromosome ends by inducing H2A ubiquitination and TP53BP1 recruitment, suggesting that it may enhance cancer development by aggravating telomere-induced genome instability in case of telomeric crisis. Promotes the assembly of RAD51 at DNA DSBs in the absence of BRCA1 and TP53BP1 Also involved in class switch recombination in immune system, via its role in regulation of DSBs repair. May be required for proper exit from mitosis after spindle checkpoint activation and may regulate cytokinesis. May play a role in the regulation of RXRA-mediated transcriptional activity. Not involved in RXRA ubiquitination by UBE2E2 (PubMed:11322894, PubMed:14981089, PubMed:17724460, PubMed:18001824, PubMed:18001825, PubMed:18006705, PubMed:18077395, PubMed:18337245, PubMed:18948756, PubMed:19015238, PubMed:19124460, PubMed:19202061, PubMed:19203578, PubMed:19203579, PubMed:20550933, PubMed:21558560, PubMed:21857671, PubMed:21911360, PubMed:22266820, PubMed:22373579, PubMed:22531782, PubMed:22705371, PubMed:22865450, PubMed:22980979). {EC0:0000269|PubMed:11322894, EC0:0000269|PubMed:14981089, ECO:0000269|PubMed:17724460, ECO:0000269|PubMed:18001824, ECO:0000269|PubMed:18001825, ECO:0000269|PubMed:18006705, ECO:0000269|PubMed:18077395, ECO:0000269|PubMed:18337245, ECO:0000269|PubMed:18948756, ECO:0000269|PubMed:19015238, ECO:0000269|PubMed:19124460, ECO:0000269|PubMed:19202061, ECO:0000269|PubMed:19203578, ECO:0000269|PubMed:19203579, ECO:0000269|PubMed:20550933, ECO:0000269|PubMed:21558560, ECO:0000269|PubMed:21857671, ECO:0000269|PubMed:21911360,

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# Target Details

| EC0:0000269 PubMed:22266820, EC0:0000269 PubMed:22373579,   |
|---|
| EC0:0000269 PubMed:22531782, EC0:0000269 PubMed:22705371,   |
| ECO:0000269 PubMed:22865450, ECO:0000269 PubMed:22980979,   |
| ECO:0000269 PubMed:23233665}.   |
| 55.5 kDa  |
| 076064  |
| Production of Molecular Mediator of Immune Response   |
|   |
| In addition to the applications listed above we expect the protein to work for functional studies |
| as well. As the protein has not been tested for functional studies yet we cannot offer a          |
| guarantee though.   |
| ALiCE®, our Almost Living Cell-Free Expression System is based on a lysate obtained from          |
| Nicotiana tabacum c.v This contains all the protein expression machinery needed to produce        |
| even the most difficult-to-express proteins, including those that require post-translational      |
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| something that functions like a cell, but without the constraints of a living system - all that's |
| needed is the DNA that codes for the desired protein!   |
| For Research Use only   |
|   |
| Liquid  |
| The buffer composition is at the discretion of the manufacturer. If you have a special request,   |
| please contact us.  |
| Avoid repeated freeze-thaw cycles.  |
| -80 °C  |
|   |
|   |

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Handling
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Expiry Date:

Unlimited (if stored properly)

### Images



**Image 1.** "Crystallography Grade" protein due to multi-step, protein-specific purification process

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