Datasheet for ABIN5709277

# CETN2 Protein (AA 1-172, full length) (His-SUMO Tag)

1 Image

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## Overview

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|---|---|
| Quantity: | 100 µg |
| Target: | CETN2 |
| Protein Characteristics: | AA 1-172, full length |
| Origin: | Human |
| Source: | Escherichia coli (E. coli) |
| Protein Type: | Recombinant |
| Purification tag / Conjugate: | This CETN2 protein is labelled with His-SUMO Tag. |
| Application: | SDS-PAGE (SDS) |

## Product Details

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| Sequence: | MASNFKKANM ASSSQRKRMS PKPELTEEQK QEIREAFDLF DADGTGTIDV KELKVAMRAL GFEPKKEEIK KMISEIDKEG TGKMNFGDFL TVMTQKMSEK DTKEEILKAF KLFDDDETGK ISFKNLKRVA KELGENLTDE ELQEMIDEAD RDGDGEVSEQ EFLRIMKKTS LY |
| Purification: | SDS-PAGE |
| Purity: | > 90 % |

## Target Details

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| Target: | CETN2 |
| Alternative Name: | CETN2 (CETN2 Products) |
| Background: | Plays a fundamental role in microtubule organizing center structure and function. Required for centriole duplication and correct spindle formation. Has a role in regulating cytokinesis and |

## Target Details

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| | genome stability via cooperation with CALM1 and CCP110.Involved in global genome nucleotide excision repair (GG-NER) by acting as component of the XPC complex. Cooperatively with RAD23B appears to stabilize XPC. In vitro, stimulates DNA binding of the XPC:RAD23B dimer.The XPC complex is proposed to represent the first factor bound at the sites of DNA damage and together with other core recognition factors, XPA, RPA and the TFIIH complex, is part of the pre-incision (or initial recognition) complex. The XPC complex recognizes a wide spectrum of damaged DNA characterized by distortions of the DNA helix such as single-stranded loops, mismatched bubbles or single-stranded overhangs. The orientation of XPC complex binding appears to be crucial for inducing a productive NER. XPC complex is proposed to recognize and to interact with unpaired bases on the undamaged DNA strand which is followed by recruitment of the TFIIH complex and subsequent scanning for lesions in the opposite strand in a 5'-to-3' direction by the NER machinery. Cyclobutane pyrimidine dimers (CPDs) which are formed upon UV-induced DNA damage esacpe detection by the XPC complex due to a low degree of structural perurbation. Instead they are detected by the UV-DDB complex which in turn recruits and cooperates with the XPC complex in the respective DNA repair.Component of the TREX-2 complex (transcription and export complex 2), composed of at least ENY2, GANP, PCID2, DSS1, and either centrin CETN2 or CETN3 . The TREX-2 complex functions in docking export-competent ribonucleoprotein particles (mRNPs) to the nuclear entrance of the nuclear pore complex (nuclear basket). TREX-2 participates in mRNA export and accurate chromatin positioning in the nucleus by tethering genes to the nuclear periphery . |
| Molecular Weight: | 35.7 kDa |
| UniProt: | P41208 |
| Pathways: | DNA Damage Repair, M Phase |

## Application Details

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| Application Notes: | Optimal working dilution should be determined by the investigator. |
| Restrictions: | For Research Use only |

## Handling

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| Format: | Liquid |
| Concentration: | 0.1-2 mg/mL |
| Buffer: | 20 mM Tris-HCl based buffer, pH 8.0 |

## Handling

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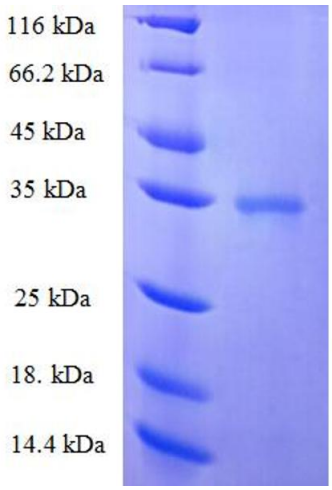
| Storage: | -80 °C,4 °C,-20 °C |
| Storage Comment: | Store at -20°C, for extended storage, conserve at -20°C or -80°C. Repeated freezing and thawing is not recommended. Store working aliquots at 4°C for up to one week. |

## Images




**SDS-PAGE**

**Image 1.**