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Lieferung & Zahlungsart

siehe unsere Liefer- und Versandbedingungen

Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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Datasheet

ATXN2 (Human) Recombinant Protein (Q01)

Catalog Number: H00006311-Q01

Regulation Status: For research use only (RUO)

Product Description: Human ATXN2 partial ORF (NP_002964, 1214 a.a. - 1313 a.a.) recombinant protein with GST-tag at N-terminal.

Sequence:
PQNSFPAAQQTVFTIHPSHVQPAYTNPPHMAHVPQAH VQSGMVPSHPTAHAPMMLMTTQPPGGPQAALAQSAL QPIPVSTTAHFPYMTHPSVQAHHQQQL

Host: Wheat Germ (in vitro)

Theoretical MW (kDa): 36.74

Applications: AP, Array, ELISA, WB-Re
(See our web site product page for detailed applications information)

Protocols: See our web site at http://www.abnova.com/support/protocols.asp or product page for detailed protocols

Preparation Method: *in vitro* wheat germ expression system

Purification: Glutathione Sepharose 4 Fast Flow

Storage Buffer: 50 mM Tris-HCl, 10 mM reduced Glutathione, pH=8.0 in the elution buffer.

Storage Instruction: Store at -80°C. Aliquot to avoid repeated freezing and thawing.

Entrez GeneID: 6311

Gene Symbol: ATXN2

Gene Alias: ATX2, FLJ46772, SCA2, TNRC13

Gene Summary: The autosomal dominant cerebellar ataxias (ADCA) are a heterogeneous group of neurodegenerative disorders characterized by progressive degeneration of the cerebellum, brain stem and spinal cord. Clinically, ADCA has been divided into three groups: ADCA types I-III. Defects in this gene are the cause of spinocerebellar ataxia type 2 (SCA2). SCA2 belongs to the autosomal dominant cerebellar ataxias type I (ADCA I) which are characterized by cerebellar ataxia in combination with additional clinical features like optic atrophy, ophthalmoplegia, bulbar and extrapyramidal signs, peripheral neuropathy and dementia. SCA2 is caused by expansion of a CAG repeat in the coding region of this gene. Longer expansions result in earlier onset of the disease. Alternatively spliced transcript variants encoding different isoforms have been identified but their full length sequence has not been determined. [provided by RefSeq]