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Lieferung & Zahlungsart

siehe unsere Liefer- und Versandbedingungen

Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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Datasheet

GTF2H2 (Human) Recombinant Protein (P01)

Catalog Number: H00002966-P01

Regulation Status: For research use only (RUO)

Product Description: Human GTF2H2 full-length ORF (AAH05345, 1 a.a. - 165 a.a.) recombinant protein with GST-tag at N-terminal.

Sequence:
MDEEPERTKRWEGGYERTWEILKEDESGSLKATIEDIL FKAKRKRVFEHHGQVRLGMMRHLYVVVDGSRTMED QDLKPNRLTCTLKLLEYFVEEYFDQNPISQIGIIVTKSKR AEKLTELSGNPRKHITSLKKAVDMTCHGEPSLYNSLSI AMQTLKLVLYIMYN

Host: Wheat Germ (in vitro)

Theoretical MW (kDa): 43.89

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: 2966

Gene Symbol: GTF2H2

Gene Alias: BTF2, BTF2P44, MGC102806, T-BTF2P44, TFIIH

Gene Summary: This gene is part of a 500 kb inverted duplication on chromosome 5q13. This duplicated region contains at least four genes and repetitive elements which make it prone to rearrangements and deletions. The repetitiveness and complexity of the sequence have also caused difficulty in determining the organization of this genomic region. This gene is within the telomeric copy of the duplication. Deletion of this gene sometimes accompanies deletion of the neighboring SMN1 gene in spinal muscular atrophy (SMA) patients but it is unclear if deletion of this gene contributes to the SMA phenotype. This gene encodes the 44 kDa subunit of RNA polymerase II transcription initiation factor IIH which is involved in basal transcription and nucleotide excision repair. Transcript variants for this gene have been described, but their full length nature has not been determined. A second copy of this gene within the centromeric copy of the duplication has been described in the literature. It is reported to be different by either two or four base pairs; however, no sequence data is currently available for the centromeric copy of the gene. [provided by RefSeq]