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YB91973Mu01

A Disintegrin And Metalloproteinase With Thrombospondin 1 (ADAMTS1)

Organism: *Mus musculus* (Mouse)

Instruction manual

FOR IN VITRO USE AND RESEARCH USE ONLY

NOT FOR USE IN DIAGNOSTIC OR THERAPEUTIC PROCEDURES

4th Edition (Revised in August, 2012)

[DESCRIPTION]

Protein Names: A Disintegrin And Metalloproteinase With Thrombospondin 1

Synonyms: ADAMTS1

Species: Mouse

Size: 100 μ g

Source: *Escherichia coli*-derived

Subcellular Location: Secreted, extracellular space, extracellular matrix.

[PROPERTIES]

Residues: His560~Pro911 (Accession # P97857), with N-terminal His-Tag.

Grade & Purity: >95%, 40 kDa as determined by SDS-PAGE reducing conditions.

Formulation: Supplied as liquid form in Phosphate buffered saline(PBS), pH 7.4.

Endotoxin Level: <1.0 EU per 1 μ g (determined by the LAL method).

Applications: SDS-PAGE; WB; ELISA; IP.

(May be suitable for use in other assays to be determined by the end user.)

Predicted Molecular Mass: 40.2 kDa

Predicted isoelectric point: 8.8

[PREPARATION]

Reconstitute in sterile PBS, pH7.2~pH7.4.



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[STORAGE AND STABILITY]

Storage: Avoid repeated freeze/thaw cycles.

Store at 2-8°C for one month.

Aliquot and store at -80°C for 12 months.

Stability Test: The thermal stability is described by the loss rate of the target protein. The loss rate was determined by accelerated thermal degradation test, that is, incubate the protein at 37°C for 48h, and no obvious degradation and precipitation were observed. (Referring from China Biological Products Standard, which was calculated by the Arrhenius equation.) The loss of this protein is less than 5% within the expiration date under appropriate storage condition.

[SEQUENCES]

The target protein is fused with N-terminal His-tag, its sequence is listed below.

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MGHHHHHSGSEF-H      GSWGPWGPWG      DCSRTC GG V      QYTMRECDNP      VPKNGGKYCE      GKRVR YRSCN      IEDCPDNNGK
TFREEQCEAH NEFSKASFGN EPTVEWTPKY AGVSPKDRCK LTCEAKGIGY FFVLQPKVVD GTPCSPDSTS VCVQGQC VKA
GCDRIIDSKK      KFDKCGVC GG      NGSTCKKMSG      IVTSTRPGYH      DIVTIPAGAT      NIEVKHRNQR      GSRNNGSFLA
IRAADGTIILNGNFTLSTLE      QDLTYKGTVL      RYSGSSAALE      RIRSF SPLKE      PLTIQVLMVG      HALRPKIKFT      YFMKKKTESF
NAIPTFSEWV IEEWGECSKT CGSGWQRRVV QCRDINGHPA SECAKEVKPA STRPCADLPC P
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