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YB91251Hu01

Tumor Necrosis Factor Ligand Superfamily, Member 7 (TNFSF7)

Organism: Homo sapiens (Human)

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: Tumor Necrosis Factor Ligand Superfamily, Member 7

Synonyms: TNFSF7, CD70, CD27L, CD27LG

Species: Human

Size: 100 μ g

Source: *Escherichia coli*-derived

Subcellular Location: Membrane; Single-pass type II membrane protein.

[PROPERTIES]

Residues: Gln47~Val191 (Accession # P32970), with two N-terminal Tags, His-tag and GST-tag.

Grade & Purity: >95%, 43 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: 43.1 kDa

Predicted isoelectric point: 6.8

[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 two N-terminal Tags, His-tag and GST-tag, its sequence is listed below.

MRNKKFELGLEFPNLPYYIDGDVKTQSMAIIRYIADKHNLGGCPKERAIEISMLEGAVLDIRYGVSR IAYSKDFETLKVDFLSKLPEML

KMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAI PQIDKYLKSSKYIAWPLQGWQATFGGGDHPP

KSDGSTSGSGHHHHHSAGLVPRGSTAIGMKETA AAKFERQHMDSPDLGTLEVLFGGPLGSPEF-QLPL

ESLGWDVAEL

QLNHTGPQQD

PRLYWQGGPA

LGRSFLHGPE

LDKGQLRIHR

DGIYMVHIQV

TLAICSSTTA

SRHHPTTLAV

GICSPASRSI

SLLRLSFHQG CTIASQRLTP LARGDTLCTN LTGTLLPSRN TDETFFGVQW V