

RPA548Hu02 100µg
Intercellular Adhesion Molecule 1 (ICAM1)
Organism Species: Homo sapiens (Human)
Instruction manual

FOR IN VITRO USE AND RESEARCH USE ONLY NOT FOR USE IN CLINICAL DIAGNOSTIC PROCEDURES

9th Edition (Revised in Jul, 2013)

## [PROPERTIES]

Residues: Asn26~Glu480 (Accession # P05362),

with N-terminal GST-tag.

Host: E. coli

Subcellular Location: Membrane; Single-pass

type I membrane protein.

**Purity: >95%** 

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

Formulation: Supplied as lyophilized form in PBS,

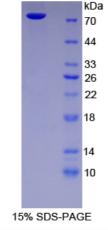
pH7.4, containing 5% sucrose, 0.01% sarcosyl.

Predicted isoelectric point: 5.8

Predicted Molecular Mass: 75.8kDa

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

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



## [ <u>USAGE</u> ]

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



## [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 GST-tag, its sequence is listed below. MSPILGYWKI KGLVQPTRLL LEYLEEKYEE HLYERDEGDK WRNKKFELGL EFPNLPYYID GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL DIRYGVSRIA YSKDFETLKV DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK KRIEAIPQID KYLKSSKYIA WPLQGWQATF GGGDHPPKSD GGPLGS- NAQTS VSPSKVILPR GGSVLVTCST SCDQPKLLGI ETPLPKKELL LPGNNRKVYE LSNVQEDSQP MCYSNCPDGQ STAKTFLTVY WTPERVELAP LPSWQPVGKN LTLRCQVEGG APRANLTVVL LRGEKELKRE PAVGEPAEVT TTVLVRRDHH GANFSCRTEL DLRPQGLELF ENTSAPYQLQ TFVLPATPPQ LVSPRVLEVD TQGTVVCSLD GLFPVSEAQV HLALGDQRLN PTVTYGNDSF SAKASVSVTA EDEGTQRLTC AVILGNQSQE TLQTVTIYSF PAPNVILTKP EVSEGTEVTV KCEAHPRAKV TLNGVPAQPL GPRAQLLLKA TPEDNGRSFS CSATLEVAGQ LIHKNQTREL RVLYGPRLDE RDCPGNWTWP ENSQQTPMCQ AWGNPLPELK CLKDGTFPLP IGESVTVTRD LEGTYLCRAR STQGEVTRKV TVNVLSPRYE