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YBA142Hu01 100 μ g

Intercellular Adhesion Molecule 5 (ICAM5)

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: Arg409~Pro674 (Accession # Q9UMF0), with two N-terminal Tags, His-tag and GST-tag.

Host: *E. coli*

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

Purity: >95%

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

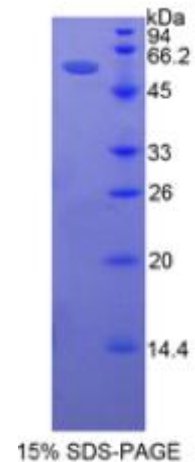
Formulation: Supplied as lyophilized form in PBS, pH7.4, containing 5% sucrose, 0.01% sarcosyl.

Predicted isoelectric point: 5.7

Predicted Molecular Mass: 60.0kDa

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

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



[USAGE]



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

MSPILGYWKI KGLVQPTRLL LEYLEEKYEE HLYERDEGDK WRNKKFELGL EFPNLPYYID
GDVKLTQ SMA IIRYIADKHN MLGGCPKERA EISMLEGAVL DIRYGVSR IA YSKDFETLKV
DFLSKLP EML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK
KRIEAI PQID KYLKSSKYIA WPLQG WQATF GGGDHPPKSD GSTSGSGHHH HHSAGLVPR
GSTA IGMKET AAA KFERQH M DSPDLGTLEV LFQ GPLG SEF- RL DDSDC PRSWT
W P E G P E Q T L R C E A R G N P E P S V H C A R S D G G A V L A L G L L G P V T R A L S G T Y R C
KAANDQGEAV KDVTLTVEYA PALDSVGCPE RITWLEGTEA SLSCVAHGVP PPDVICVRSG
ELGAVIEGLLRVAREHAGTY RCEATNPRGS AAKNVAITVE YGPRFEEPSC PSNWTWVEGS
G R L F S C E V D G K P Q P S V K C V G S G G A T E G V L L P L A P P D P S P R A P R I P R V L A P
GIYVCNATNRHGSAKTVVV SAESPPEMDE STCP