RPA178Hu02 100μg
Alpha-2-Heremans Schmid Glycoprotein (aHSG)
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: Ala19~Leu300 (Accession # P02765),

with two N-terminal Tags, His-tag and GST-tag.

Host: *E. coli*

Subcellular Location: Secreted.

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.

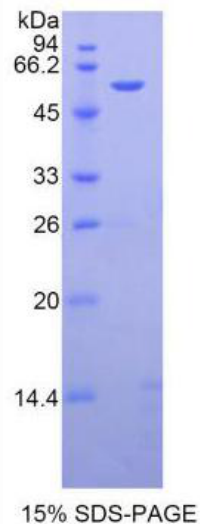**Predicted isoelectric point:** 5.2

Predicted Molecular Mass: 62.2kDa

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

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

kDa
94
66.2
45
33
26
20
14.4

15% SDS-PAGE

[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
GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL DIRYGVSRIA YSKDFETLKV
DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK
KRIEAIPQID KYLKSSKYIA WPLQGWQATF GGGDHPPKSD GSTSGSGHHH HHHSAGLVPR
GSTAIGMKET AAAKFERQHM DSPDLGTLEV LFQGPLGSEF- AP HGPGLIYRQP
NCDDPETEEA ALVAIDYINQ NLPWGYKHTL NQIDEVKVWP QQPSGELFEI EIDTLETTCH
VLDPTPVARC SVRQLKEHAV EGDCDFQLLK LDGKFSVVYA KCDSSPDSAE DVRKVCQDCP
LLAPLNDTRV VHAAKAALAA FNAQNNGSNF QLEEISRAQL VPLPPSTYVE FTVSGTDCVA
KEATEAAKCN LLAEKQYGFC KATLSEKLGG AEVAVTCTVF QTQPVTSQPQ PEGANEAVPT
PVVDPDAPPS PPLGAPGLPP AGSPPDSHVL