

RPC888Bo01 100µg

Chromogranin B (CHGB)

Organism Species: *Bos taurus*; Bovine (Cattle)

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: Leu309~Glu484 (Accession # P23389),
with two N-terminal Tags, His-tag and GST-tag.

Host: *E. coli*

Subcellular Location: Cytoplasmic vesicle,
secretory vesicle membrane; Peripheral
membrane protein; Luminal side.

Purity: >95%

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

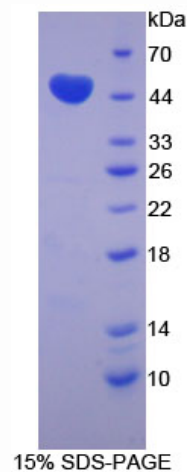
Formulation: Supplied as lyophilized form in PBS,
pH7.4, containing 5% sucrose, 0.01% sarcosyl.

Predicted isoelectric point: 5.9

Predicted Molecular Mass: 51.8kDa

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 KGLVQPTRL L LEYLEEKYEE HLYERDEGDK WRNKKFELGL EFPNLPYYID
GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL DIRYGVSR IA YSKDFETLKV
DFLSKLP EML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFP KLVCFK
KRIEAI PQID KYLKSSKYIA WPLQG WQATF GGGDHPPKSD GSTSGSGHHH HHSAGLVPR
GSTAIGMKET AA AKFERQHM DSPDLGTLEV LFQG PLGSEF-LE EGA EYGEEVR
RHSA AQAPGD LQGARFGGRG RGEHQALRRP SEESLEQENK RHGLSPDLNM
AQQYSE ESEE ERGPAPGPSY RARGG EAAAY STLGQTDEKR FLGETHHRVQ
ESQRDKARRR L PGELRNYLD YGEEKGEEAA RGKWQPQ GDP RDADENREEA
RLRGKYAPH HITE