

RPH108Hu01 100µg

Sulfatase 1 (SUL)

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: Pro609~Gly871 (Accession # Q8IWU6),
with two N-terminal Tags, His-tag and GST-tag.

Host: *E. coli*

Subcellular Location: Endoplasmic reticulum.

Golgi apparatus, Golgi stack. Cell surface.

Purity: >95%

Endotoxin Level: <1.0EU per 1µg

(determined by the LAL method).

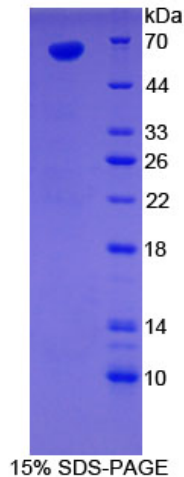
Formulation: Supplied as lyophilized form in PBS,
pH7.4, containing 5% sucrose, 0.01% sarcosyl.

Predicted isoelectric point: 8.3

Predicted Molecular Mass: 63.1kDa

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 KGLVQPTRLLEYLEEKYEE HLYERDEGDK WRNKKFELGL EFPNLPYYID
GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL DIRYGVSRIA YSKDFETLKV
DFLSKLPEML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK
KRIEAIPQID KYLKSSKYIA WPLQGWQATF GGGDHPKSD GSTSGSGHHH HHSAGLVPR
GSTAIGMKET AAKFERQHM DSPDLGTLLEV LFQGPLGSEF- PT TVRVTHKCFI
LPNDSIHCER ELYQSARAWK DHKAYIDKEI EALQDKIKNL REVRGHLKRR KPEECSCSKQ
SYYNKEKGVK KQEKLKSHLH PFKEAAQEVDSKLQLFKENN RRRKKERKEK
RRQRKGEECS LPGLTCFTHD NNHWQTAPFW NLGSFCACTS SNNNTYWCLR
TVNETHNLF CEFATGFLEY FDMNTDPYQL TNTVHTVERG ILNQLHVQLM ELRSCQGYKQ
CNPRPKNL DVGNKDGGSYDL HRGQLWDGWE G