

RPB773Rb01 100µg
Recombinant Transglutaminase 1, Keratinocyte (TGM1)
Organism Species: Oryctolagus cuniculus (Rabbit)
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: Met433~His692 (Accession # P22758),
with two N-terminal Tags, His-tag and GST-tag.

Host: *E. coli*

Subcellular Location: Membrane; Peripheral
membrane protein.

Purity: >95%

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

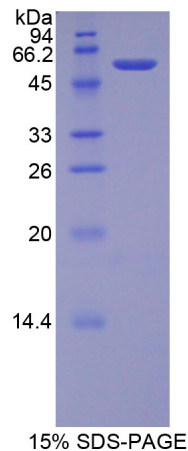
Formulation: Supplied as lyophilized form in PBS,
pH7.4, containing 5% sucrose, 0.01% sarcosyl.

Predicted isoelectric point: 5.8

Predicted Molecular Mass: 61.2kDa

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
GDVKLTQSMA IIRYIADKHN MLGGCPKERA EISMLEGAVL DIRYGVSRIA YSKDFETLKV
DFLSKLP EML KMFEDRLCHK TYLNGDHVTH PDFMLYDALD VVLYMDPMCL DAFPKLVCFK
KRIEAIQID KYLKSSKYIA WPLQGQWQATF GGGDHPPKSD GSTSGSGHHH HHSAGLVPR
GSTAIGMKET AAKFERQHM DSPDLGTLEV LFQGPLGSEF-MDIYFDEN MKPLEHLNRD
SVWNFHVWND CWMKRPDLP S GFDGWQVVDA TPQETSSGIF CCGPCSVESV
KNGLYVMKYD TPFIFAEVNS DKVYWQRQDD GSKFIVYVEE KAIGTLIVTK AVRSHMREDI
THIYKHPEGS DAERKAVETA AAHGSKPNVY DSRDSAEDVA MQVEAQDAVM QQDLTVSVVL
TNRSSSRRTV KLHLYLSVTF YTGVTGSIFK ESKKEVVLAA GSSDSVMPV AYKEYRPHLV
DQGAMLLNVS GH