

RPB480Ra01 50 μ g
Recombinant Mannose Binding Lectin (MBL)
Organism Species: Rattus norvegicus (Rat)
Instruction manual

FOR IN VITRO USE AND RESEARCH USE ONLY
NOT FOR USE IN CLINICAL DIAGNOSTIC PROCEDURES

12th Edition (Revised in Aug, 2016)

[**PROPERTIES**]

Source: Prokaryotic expression.

Host: *E. coli*

Residues: Glu19~Asp244

Tags: N-terminal His-Tag

Tissue Specificity: Liver.

Subcellular Location: Secreted.

Purity: >95%

Traits: Freeze-dried powder

Buffer formulation: PBS, pH7.4, containing 1mM DTT, 5% trehalose, 0.01% sarcosyl and Proclin300.

Original Concentration: 200ug/mL

Applications: SDS-PAGE; WB; ELISA; IP; CoIP; Purification; Amine Reactive Labeling.

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

Predicted isoelectric point: 6.0

Predicted Molecular Mass: 25.3kDa

Accurate Molecular Mass: 30kDa as determined by SDS-PAGE reducing conditions.

Phenomenon explanation:

The possible reasons that the actual band size differs from the predicted are as follows:

1. Splice variants: Alternative splicing may create different sized proteins from the same gene.
2. Relative charge: The composition of amino acids may affects the charge of the protein.
3. Post-translational modification: Phosphorylation, glycosylation, methylation etc.
4. Post-translation cleavage: Many proteins are synthesized as pro-proteins, and then cleaved to give the active form.
5. Polymerization of the target protein: Dimerization, multimerization etc.

[**USAGE**]

Reconstitute in PBS (pH7.4) to a concentration of 0.1-1.0 mg/mL. Do not vortex.

[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. 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. The loss rate is less than 5% within the expiration date under appropriate storage condition.

[SEQUENCE]

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ET LTEGAQSSCP VIACSSPGLN GFPKGDGHDG
AKGEGEPGQ GLRGLQGGPG KVGPA GPPGN PGSKGATGPK GDRGESVEFD
TTNIDLEIAA LRSELRAMRK WLLSMSENV GK KYFMSSVR RMPLNRAKAL
CSELQGT VAT PRNAEENRAI QNVAKDVAFL GITDQRTENV FEDLTGNRVR
YTNWNEGEPN NVGSGENCVV LLTNGKWNDV PCSDSFLVVC EFS D
    
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[IDENTIFICATION]

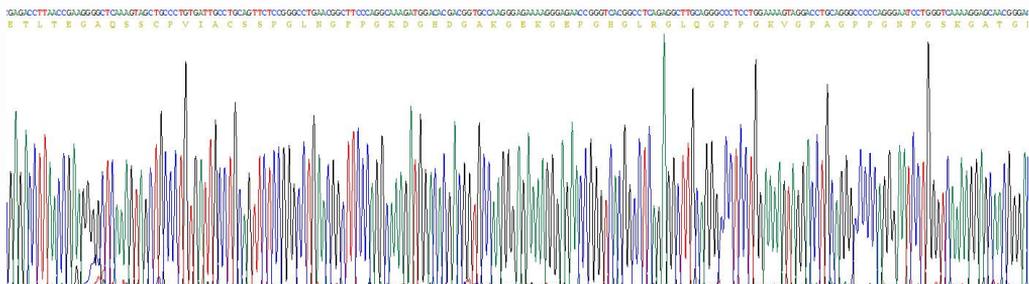


Figure 1. Gene Sequencing (Extract)

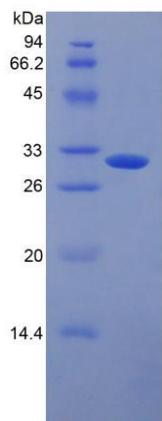


Figure 2. SDS-PAGE