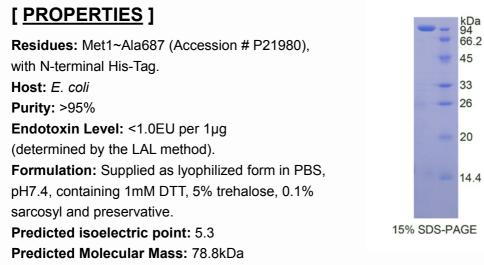
RPB830Hu01 10μg Recombinant Transglutaminase 2, Tissue (TGM2) Organism Species: Homo sapiens (Human) *Instruction manual*

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



Accurate Molecular Mass: 100kDa as determined by SDS-PAGE reducing conditions. **Applications:** SDS-PAGE; WB; ELISA; IP.

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

Note: 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.

[<u>USAGE</u>]

Reconstitute in sterile PBS, pH7.2-pH7.4.

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[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.

[<u>SEQUENCES</u>]

The target protein is fused with N-terminal His-Tag, its sequence is listed below. MGHHHHHHSGSEF-MAEELVLERC DLELETNGRD HHTADLCREK LVVRRGQPFW LTLHFEGRNY EASVDSLTFS VVTGPAPSQE AGTKARFPLR DAVEEGDWTA TVVDQQDCTL SLQLTTPANA PIGLYRLSLE ASTGYQGSSF VLGHFILLFN AWCPADAVYL DSEEERQEYV LTQQGFIYQG SAKFIKNIPWNFGQFEDGIL DICLILLDVN PKFLKNAGRD CSRRSSPVYV GRVVSGMVNC NDDQGVLLGR WDNNYGDGVS PMSWIGSVDI LRRWKNHGCQ RVKYGQCWVF AAVACTVLRC LGIPTRVVTN YNSAHDQNSN LLIEYFRNEF GEIQGDKSEM IWNFHCWVES WMTRPDLQPG YEGWQALDPT PQEKSEGTYC CGPVPVRAIK EGDLSTKYDA PFVFAEVNAD VVDWIQQDDG SVHKSINRSL IVGLKISTKS VGRDEREDIT HTYKYPEGSS EEREAFTRAN HLNKLAEKEE TGMAMRIRVG QSMNMGSDFD VFAHITNNTA EEYVCRLLLC ARTVSYNGIL GPECGTKYLL NLNLEPFSEK SVPLCILYEK YRDCLTESNL IKVRALLVEP VINSYLLAER DLYLENPEIK IRILGEPKQK RKLVAEVSLQ NPLPVALEGC TFTVEGAGLT EEQKTVEIPD PVEAGEEVKV RMDLLPLHMG LHKLVVNFES DKLKAVKGFR NVIIGPA

[REFERENCES]

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