RPB451Hu01 50µg

Recombinant Early Growth Response Protein 2 (EGR2)

Organism Species: Homo sapiens (Human)

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*

Residuess: Gly147~Cys403

Tags: N-terminal His Tag

Tissue Specificity: Nucleus

Purity: > 97%

Traits: Freeze-dried powder

Buffer formulation: 20mM Tris, 150mM NaCl, pH8.0, containing 1mM EDTA, 1mM DTT, 0.01% SKL, 5% Trehalose and Proclin300.

Original Concentration: 200μg/mL

Applications: Positive Control; Immunogen; SDS-PAGE; WB.

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

Predicted isoelectric point: 9.1

Predicted Molecular Mass: 31.3kDa

Accurate Molecular Mass: 36kDa 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 20mM Tris, 150mM NaCl (pH8.0) to a concentration of 0.1-1.0 mg/mL. Do not vortex.

[STORAGE AND STABILITY]

Storage: Avoid repeated freeze/thaw cycles.

Store at 2-8ºC for one month.

Aliquot and store at -80ºC 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]

GPLG
VCTMSQTQPD LDHLYSPPPP PPPYSGCAGD LYQDPSAFLS AATTSTSSSL
AYPPPPSYPS PKPATDPGLF PMIPDYPGFF PSQCQRDLHG TAGPDRKPFP
CPLDTLRVPP PLTPLSTIRN FTLGGPSAGV TGPGASGGSE GPRLPGSSSA
AAAAAAAAAY NPHHLPLRPI LRPRKYPNRP SKTPVHERPY PCPAEGCDRR
FSRSDELTRH IRIHTGHKPF QCRICMRNFS RSDHLTTHIR THTGEKPFAC
DYC

[IDENTIFICATION]

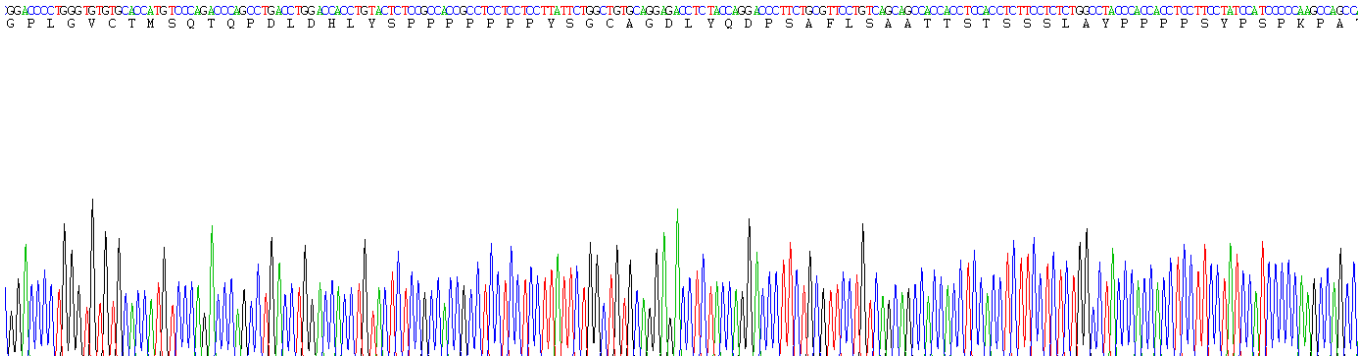

Figure. Gene Sequencing (Extract)

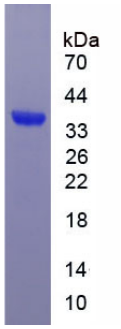

Figure. SDS-PAGE