

#### RPE293Hu01 100µg

### Recombinant Rac-GTPase Activating Protein 1 (RACGAP1)

**Organism Species: Homo sapiens (Human)** 

Instruction manual

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

10th Edition (Revised in Jan, 2014)

# [PROPERTIES]

Residues: Met106~Trp539

Tags: Two N-terminal Tags, His-tag and GST-tag

Accession: Q9H0H5

Host: E. coli

**Subcellular Location:** Nucleus, Cytoplasm, cytoskeleton, spindle, Cytoplasmic vesicle, secretory vesicle, acrosome, Cleavage furrow, Midbody, Cell membrane, Peripheral membrane protein, Cytoplasmic side.

**Purity: >90%** 

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

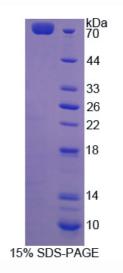
**Formulation:** Supplied as lyophilized form in PBS, pH7.4, containing 5% trehalose, 0.01% sarcosyl.

Predicted isoelectric point: 8.9

Predicted Molecular Mass: 78.1kDa

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 sequence of the target protein is listed below.

MLMCD TSGSIQLSEE QKSALAFLNR GQPSSSNAGN KRLSTIDESG SILSDISFDK TDESLDWDSS LVKTFKLKKR EKRRSTSRQF VDGPPGPVKK TRSIGSAVDQ GNESIVAKTT VTVPNDGGPI EAVSTIETVP YWTRSRRKTG TLQPWNSDST LNSRQLEPRT ETDSVGTPQS NGGMRLHDFV SKTVIKPESC VPCGKRIKFG KLSLKCRDCR VVSHPECRDR CPLPCIPTLI GTPVKIGEGM LADFVSQTSP MIPSIVVHCV NEIEQRGLTE TGLYRISGCD RTVKELKEKF LRVKTVPLLS KVDDIHAICS LLKDFLRNLK EPLLTFRLNR AFMEAAEITD EDNSIAAMYQ AVGELPQANR DTLAFLMIHL QRVAQSPHTK MDVANLAKVF GPTIVAHAVP NPDPVTMLQD IKROPKVVFR I I SI PI FYW