

RPD331Ra01 100µg

Recombinant Calcium/Calmodulin Dependent Protein Kinase II Alpha (CAMK2a)

Organism Species: Rattus norvegicus (Rat)

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: Met1~His478

Tags: Two N-terminal Tags, His-tag and T7-tag

Accession: P11275

Host: *E. coli*

Subcellular Location: Cell junction, synapse,
presynaptic cell membrane.

Purity: >90%

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

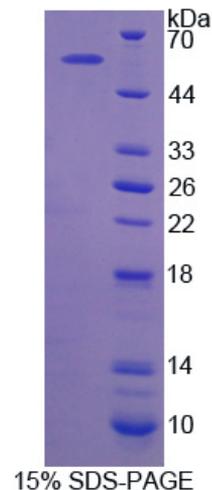
Formulation: Supplied as lyophilized form in PBS,
pH7.4, containing 5% trehalose, 0.01% sarcosyl.

Predicted isoelectric point: 6.6

Predicted Molecular Mass: 57.8kDa

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.

MATITCTRFT EYQLFEELG KGAFSVVRRK VKVLAGEQYA AKIINTKKLS ARDHQKLERE
ARICRLLKHP NIVRLHDSIS EEGHHYLIFD LVTGGELFED IVAREYYSEA DASHCIQIQL
EAVLHCHQMG VVHRDLKPEN LLLASKLKGA AVKLADFGLA IEVEGEQQAW FGFAGTPGYL
SPEVLRKDPY GKPVDLWACG VILYILLVGY PPFWDEDQHR LYQQIKAGAY DFPSPEWDTV
TPEAKDLINK MLTINPSKRI TAAEALKHPW ISHRSTVASC MHRQETVDCL KKFNARRKLLK
GAILTTMLAT RNFSGGKSGG NKKNDGVKES SESTNTTIED EDTKVRKQEI IKVTEQLIEA
ISNGDFESYT KMCDPGMTAF EPEALGNLVE GLDFHRFYFE NLWSRNSKPV HTTILNPHIH
LMGDESACIA YIRITQYLDA GGIPRTAQSE ETRVWHRRDG KWQIVHFHRS GAPSVLPH