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YBE806Hu01 100μg

Recombinant Glutamate Receptor,

Ionotropic, N-Methyl-D-Aspartate 2A (GRIN2A)

Organism Species: Homo sapiens (Human)

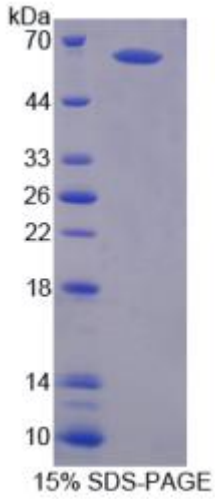
Instruction manual

FOR IN VITRO USE AND RESEARCH USE ONLY

NOT FOR USE IN CLINICAL DIAGNOSTIC PROCEDURES

10th Edition (Revised in Jan, 2014)

[PROPERTIES]



Residues: Pro31~Ala555

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

Accession: Q12879

Host: *E. coli*

Subcellular Location: Cell membrane; Multi-pass membrane protein. Cell junction.

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: 5.3

Predicted Molecular Mass: 62.5kDa

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^{O}C for one month.

Aliquot and store at -80^{O}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^{O}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.

PPALNIAVML GHSHDVTERE LRTLWGPEQA AGLPLDVNVV ALLMNRTDPK SLITHVCDLM SGARIHGLVF GDDTDQEAVA QMLDFISSHT FVPILGIHGG ASMIMADKDP TSTFFQFGAS IQQQATVMLK IMQDYDWHVF SLVTTIFPGY REFISFVKTT VDNSFVGWDM QNVITLDTSF EDAKTQVQLK KIHSSVILLY CSKDEAVLIL SEARSLGLTG YDFFWIVPSL VSGNTELIPK EFPSGLISVS YDDWDYSLEA RVRDGIGILT TAASSMLEKF SYIPEAKASC YGQMERPEVP MHTLHPFMVNVTWDGKDLSFTEEGYQVHPRLVVIVLNKDREWEKVGKWEN HTLSLRHAVW PRYKSFSDCE PDDNHLSIVT LEEAPFVIVE DIDPLTETCV RNTVPCRKFV KINNSTNEGM NVKKCCKGFC IDILKKLSRT VKFTYDLYLV TNGKHGKKVN NVWNGMIGEV VYQRAVMAVG SLTINEERSE VVDFSVPFVE TGISVMVSRS NGTVSPSAFL EPFSA

[REFERENCES]

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3. Endele S., *et al.* (2010) Nat. Genet. 42:1021-1026.

4. Lesca G., *et al.* (2013) Nat. Genet. 45:1061-1066.