EPB214Hu51 100ug

Eukaryotic Aspartate Aminotransferase (AST)

Organism Species: Homo sapiens (Human)

Instruction manual

FOR IN VITRO USE AND RESEARCH USE ONLY

NOT FOR USE IN CLINICAL DIAGNOSTIC PROCEDURES

11th Edition (Revised in May, 2016)

[PROPERTIES]

Source: Eukaryotic expression.

Host: Yeast

Residues: Ala2~Gln413

Tags: N-terminal His Tag

Homology: Mouse 90%, Rat 90%

Tissue Specificity: Kidney, stomach, liver, intestine.

Subcellular Location: Cytoplasm.

Purity: >95%

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

Traits: Freeze-dried powder

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

Original Concentration: 200ug/mL

Predicted isoelectric point: 6.6

Predicted Molecular Mass: 47.5kDa

Accurate Molecular Mass: 48kDa as determined by SDS-PAGE reducing conditions.

Applications: SDS-PAGE; WB; ELISA; IP; CoIP; EMSA; Reporter Assays; Purification; Amine Reactive Labeling.

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

[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 2-8°C for one month.

Aliquot and store at -80°C for 12 months.

Stability Test: The thermal stability is described by the loss rate. 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]

APPSVFAEV PQAQPVLVFK LTADFREDPD PRKVNLGVGA YRTDDCHPWV
LPVVKKVEQK IANDNSLNHE YLPILGLAEF RSCASRLALG DDSPALKEKR
VGGVQSLGGT GALRIGADFL ARWYNGTNNK NTPVYVSSPT WENHNAVFSA
AGFKDIRSYR YWDAEKRGLD LQGFLNDLEN APEFSIVVLH ACAHNPTGID
PTPEQWKQIA SVMKHRFLFP FFDSAYQGFA SGNLERDAWA IRYFVSEGFE
FFCAQSFSKN FGLYNERVGN LTVVGKEPES ILQVLSQMEK IVRITWSNPP
AQGARIVAST LSNPELFEEW TGNVKTMADR ILTMRSELRA RLEALKTPGT
WNHITDQIGM FSFTGLNPKQ VEYLVNEKHI YLLPSGRINV SGLTTKNLDY
VATSIHEAVT KIQ

[IDENTIFICATION]

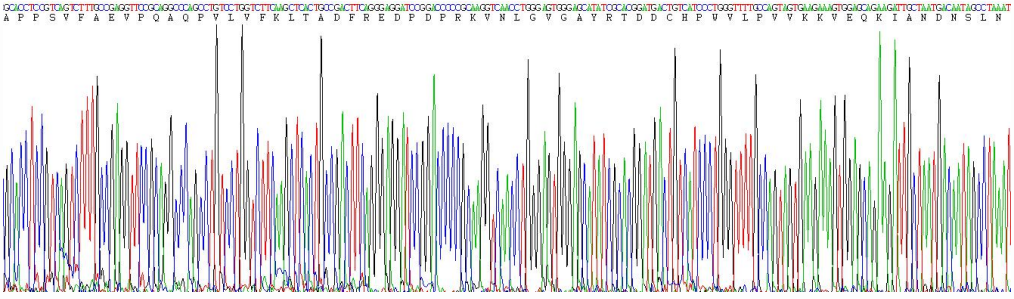

Figure 1. Gene Sequencing (extract)

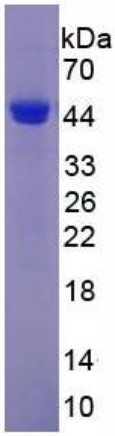

Figure 2. SDS-PAGE