

YBE837Hu01 100µg

Recombinant Aldehyde Dehydrogenase 7 Family, Member A1 (ALDH7A1) **Organism Species: Homo sapiens (Human)**

Instruction manual

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

9th Edition (Revised in Jul, 2013)

[PROPERTIES]

Residues: Met1~Gln539 (Accession # P49419).

with N-terminal His-Tag.

Host: E. coli

Subcellular Location: Mitochondrion.

Cytoplasm,

cytosol.

Purity: >95%

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: 8.2

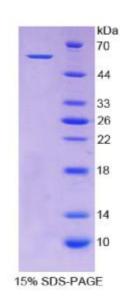
Predicted Molecular Mass: 59.7kDa

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 target protein is fused with N-terminal His-Tag, its sequence is listed below. MG H H H H H H S G S - MW R L P R A L C V HA A K T S K L S G PW S R PA A F M S TL L I N Q P Q YA WLKELGLREE NEGVYNGSWG GRGEVITTYC PANNEPIARV RQASVADYEE TVKKAREAWK IWADIPAPKR GEIVRQIGDA LREKIQVLGS LVSLEMGKIL VEGVGEVQEY VDICDYAVGL SRMIGGPILP SERSGHALIE QWNPVGLVGI ITAFNFPVAV YGWNNAIAMI CGNVCLWKGA PTTSLISVAV TKIIAKVLED NKLPGAICSL TCGGADIGTA MAKDERVNLL SFTGSTQVGK QVGLMVQERF GRSLLELGGN NAIIAFEDAD LSLVVPSALF AAVGTAGQRC TTARRLFIHE SIHDEVVNRL KKAYAQIRVG NPWDPNVLYG PLHTKQAVSM FLGAVEEAKK EGGTVVYGGK VMDRPGNYVE PTIVTGLGHD ASIAHTETFA PILYVFKFKN EEEVFAWNNE VKQGLSSSIF TKDLGRIFRW LGPKGSDCGI VNVNIPTSGA EIGGAFGGEK HTGGGRESGS DAWKQYMRRS TCTINYSKDL PLAQGIKFQ