

P90776Hu01 100µg
Pyruvate Dehydrogenase Alpha (PDHa)
Organism: Homo sapiens (Human)
Instruction manual

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

6th Edition (Revised in March, 2013)

[PROPERTIES]

Residues: Phe30~Ser390 (Accession # P08559),
with N-terminal His-Tag.

Host: *E. coli*

Subcellular Location: Mitochondrion matrix.

Purity: >95%

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

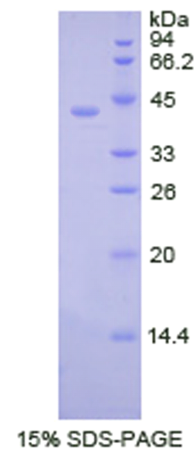
Formulation: Supplied as lyophilized form in PBS,
pH7.4, containing 5% sucrose, 0.01% sarcosyl.

Predicted isoelectric point: 6.5

Predicted Molecular Mass: 41.7kDa




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.

Unique product Superb quality Client favorite Nicest service  ISO9001:2008;  ISO13485:2003; 

11271 Richmond Avenue, H104, Houston, TX 77082, USA | Toll free: 001-888-960-7402 | Fax: 001-832-538-0088 | Email: mail@uscnk.us | Http://www.uscnk.us
Export Processing Zone, Wuhan 430056, P.R.China | Toll free: 0086-800-880-0687 | Fax: 0086-27-8425-9551 | Email: mail@uscnk.com | Http://www.uscnk.com

[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.
MGHHHHHSGSEF- F ANDATFEIKK CDLHRLEEGP PVTTVLTR ED GLKYYRMMQT
VRRMELKADQ LYKQKIIRGF CHLCDGQEAC CVGLEAGINP TDHLITAYRA HGFTFTRGLS
VREILAELTG RKGCGAKGKG GSMHMYAKNF YGGNGIVGAQ VPLGAGIALA CKYNGKDEV C
LTLYGDGAAN QGQIFEAYNM AALWKLPCIF ICENNRYGMG TSVVERAAAST DYYKRGDFIP
GLRVDGMDIL CVREATRFAA AYCRSGKGPI LMELQTYRYH GHSMSPGV S YRTREEIQEV
RSKSDPIMLL KDRMVNSNLA SVEELKEIDV EVRKEIEDAA QFATADPEPP LEELGYHIYS
SDPPFEVRGA NQWIKFKSVS