RPD541Hu01 100µg
Recombinant Cytochrome P450 26B1 (CYP26B1)
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~Val512 (Accession # Q9NR63), with two N-terminal Tags, His-tag and T7-tag.

Host: *E. coli*

Subcellular Location: Endoplasmic reticulum membrane; Peripheral membrane protein. Microsome membrane.

Purity: >95%

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

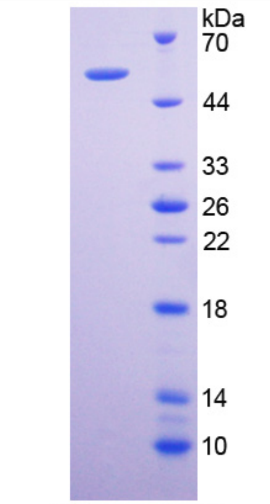
Formulation: Supplied as lyophilized form in PBS, pH7.4, containing 5% trehalose, 0.01% sarcosyl.

Predicted isoelectric point: 8.8

Predicted Molecular Mass: 61.3kDa

Applications: SDS-PAGE; WB; ELISA; IP.

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



15% SDS-PAGE

[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°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 two N-terminal Tags, His-tag and T7-tag, its sequence is listed below.

MGSSHHHHHH SSGLVPRGSH MASMTGGQQM GRGSEF- MLFEGLDLVS ALATLAACLV
SVTLLLAVSQ QLWQLRWAAT RDKSCKLPIP KGSMGFPLIG ETGHWLLQGS GFQSSRREKY
GNVFKTHLLG RPLIRVTGAE NVRKILMGEH HLVSTEWPRS TRMLLGPNTV SNSIGDIHRN
KRKVFSKIFS HEALESYLPK IQLVIQDTLR AWSSHPEAIN VYQEAQKLTF RMAIRVLLGF
SIPEEDLGHL FEVYQQFVDN VFSLPVDLPF SGYRRGIQAR QILQKGLEKA IREKLQCTQG
KDYLDALDLL IESSKEHGKE MTMQELKDGT LELIFAAYAT TASASTSLIM QLLKHPTVLE
KLRDELRAHG ILHSGGCPCE GTLRLDTLSG LRYLDCVIKE VMRLFTPISG GYRTVLQTFE
LDGFQIPKGW SVMYSIRDTH DTAPVFKDVN VFDPDRFSQA RSEDKDGRFH
YLPFGGGVRT CLGKHLAKLF LKVLAVELAS TSRFELATRT FPRITLVPVL HPVDGLSVKF
FGLDSNQNEI LPETEAMLSA TV