

P93066Hu02 100μg

Apelin (APLN)

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: Ser24~Phe77 (Accession # Q9ULZ1),
with two N-terminal Tags, His-tag and MBP-tag.

Host: *E. coli*

Subcellular Location: Secreted.

Purity: >95%

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

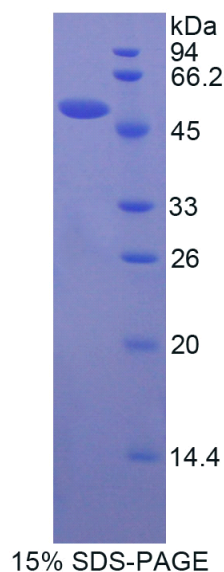
Formulation: Supplied as lyophilized form in PBS,
pH7.4, containing 5% sucrose, 0.01% sarcosyl.

Predicted isoelectric point: 6.3

Predicted Molecular Mass: 52.7kDa

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**;  **CE**

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

MKIEEGKLVI WINGDKGYNG LAEVGKKFEK DTGIKVTVEH PDKLEEKFPQ VAATGDGPDI
IFWAHDRFGG YAQSGLLAEI TPDKAFQDKL YPFTWDAVRY NGKLIAYPIA VEALSLIYNK
DLLPNPPKTW EEIPALDKEL KAKGKSALMF NLQEPYFTWP LIAADGGYAF KYENGKYDIK
DVGVDNAGAK AGLTFLVDLI KNKHMNADTD YSIAEAAFNK GETAMTINGP WAWSNIDTSK
VNYGVTVLPT FKGQPSKPFV GVLSAGINAA SPNKELAKEF LENYLLTDEG LEAVNKDKPL
GAVALKSYEE ELAKDPRIAA TMENAQKGEI MPNIPQMSAF WYAVRTAVIN AASGRQTVDE
ALKDAQTGST SGSGHHHHHH SAGLVPRGST AIGMKETAAA KFERQHMDSP DLGTLEVLVQ
GPLGSEF- SLMPLPD GNGLEDGNVR HLVQPRGSRN GPGPWQGGRR KFRRQRPRLS
HKGPMPIF