

9F, No. 108, Jhouzih St.,Taipei, Taiwan Tel: + 886-2-8751-1888 Fax: + 886-2-6602-1218 E-mail: sales@abnova.com

Datasheet

XPNPEP1 polyclonal antibody

Catalog Number: PAB14395

Regulation Status: For research use only (RUO)

Product Description: Goat polyclonal antibody raised

against synthetic peptide of XPNPEP1.

Immunogen: A synthetic peptide corresponding to

human XPNPEP1.

Sequence: C-LIRETQPISKQH

Host: Goat

Theoretical MW (kDa): 69.9

Reactivity: Human

Applications: ELISA, WB-Ti

(See our web site product page for detailed applications

information)

Protocols: See our web site at

http://www.abnova.com/support/protocols.asp or product

page for detailed protocols

Specificity: Approx 80 KDa band observed in human heart, skeletal muscle and pancreas lysates (calculated

MW of 69.9 KDa according to NP_065116.2).

Form: Liquid

Purification: Antigen affinity purification

Concentration: 0.5 mg/mL

Recommend Usage: ELISA (1:32000)

Western Blot (0.3-1 ug/mL)

The optimal working dilution should be determined by

the end user.

Storage Buffer: In Tris saline, pH 7.3 (0.5% BSA,

0.02% sodium azide)

Storage Instruction: Store at -20°C.

Aliquot to avoid repeated freezing and thawing.

Entrez GenelD: 7511

Gene Symbol: XPNPEP1

Gene Alias: SAMP, XPNPEP, XPNPEPL, XPNPEPL1

Gene Summary: X-prolyl aminopeptidase (EC 3.4.11.9) proline-specific metalloaminopeptidase specifically catalyzes the removal of any unsubstituted N-terminal amino acid that is adjacent to a penultimate proline residue. Because of its specificity toward proline, it has been suggested that X-prolyl aminopeptidase is important in the maturation and degradation of peptide hormones, neuropeptides, and tachykinins, as well as in the digestion of otherwise resistant dietary protein thereby complementing the pancreatic peptidases. Deficiency of X-prolyl aminopeptidase results excretion of large amounts imino-oligopeptides in urine (Blau et al., 1988 [PubMed 3141711]).[supplied by OMIM]

References:

1. Exploring proteomes and analyzing protein processing by mass spectrometric identification of sorted N-terminal peptides. Gevaert K, Goethals M, Martens L, Van Damme J, Staes A, Thomas GR, Vandekerckhove J. Nat Biotechnol. 2003 May;21(5):566-9. Epub 2003 Mar 31.