

HAV-VP1-P2A (residues 722-830)

Hepatitis A Virus Coat Protein VP1- Core Protein P2A

recombinant, *E. coli*

Cat. No.	Amount
PR-1113	100 μ g

For *in vitro* use only
Quality guaranteed for 12 months
Store at -20°C

Avoid freeze / thaw cycles

Form

Liquid. Supplied in 10 mM CBB pH 9.6, 0.1% SDS and 50% glycerol.

Application

Recombinant HAV-VP1-P2A Antigen may be used in ELISA and Western blots, excellent for detection of HAV with minimal specificity problems.

Specificity

Immunoreactive with sera of HAV-infected individuals.

Molecular Weight

51.2 kDa

Purity

>90% by SDS-PAGE

Description

The protein contains the HAV Coat protein VP1 and core protein P2A immunodominant regions, amino acids 722-830.

HAV core proteins are purified by proprietary chromatographic techniques.

Background

Forty-two antigenic domains were identified across the hepatitis A virus (HAV) polyprotein by using a set of 237 overlapping 20-mer synthetic peptides spanning the entire HAV polyprotein and a panel of serum samples from acutely HAV-infected patients. The term "antigenic domain" is used in this study to define a protein region spanned with consecutive overlapping immunoreactive peptides.

Nineteen antigenic domains were found within the structural proteins, and 22 were found within the nonstructural proteins, with 1 domain spanning the junction of VP1 and P2A proteins. Five of these domains were considered immunodominant, as judged by both the breadth and the strength of their immunoreactivity. One domain is located within the VP2 protein at position 57-90 aa. A second domain, located at position 767-842 aa, contains the C-terminal part of the VP1 protein and the entire P2A protein. A third domain, located at position 1403-1456 aa, comprises the C-terminal part of the P2C protein and the N-terminal half of the P3A protein. The fourth domain, located at position 1500-1519 aa, includes almost the entire P3B, and the last domain, located at position 1719-1764 aa, contains the C-terminal region of the P3C protein and the N-terminal region of the P3D protein. It is interesting to note that four of the five most immunoreactive domains are derived from small HAV proteins and/or encompass protein cleavage sites separating different HAV proteins.

Selected References:

Haro *et al.* (2003) Liposome entrapment and immunogenic studies of a synthetic lipophilic multiple antigenic peptide bearing VP1 and VP3 domains of the hepatitis A virus: a robust method for vaccine design. *FEBS. Lett.* **540**:133.

Costa-Mattioli *et al.* (2002) Molecular evolution of hepatitis A virus: a new classification based on the complete VP1 protein. *J. Virol.* **76**:9516.

Emerson *et al.* (2002) Identification of VP1/2A and 2C as virulence genes of hepatitis A virus and demonstration of genetic instability of 2C. *J. Virol.* **76**:8551.



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Kang *et al.* (2002) A proposed vestigial translation initiation motif in VP1 of hepatitis A virus. *Virus Res.* **87**:11.

Martin *et al.* (1999) Maturation of the hepatitis A virus capsid protein VP1 is not dependent on processing by the 3Cpro proteinase. *J. Virol.* **73**:6220.

Graff *et al.* (1999) Hepatitis A virus capsid protein VP1 has a heterogeneous C terminus. *J. Virol.* **73**:6015.