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Rabbit Anti-Simian Rotavirus VP4 antibody

SL17494R

Product Name:	Simian Rotavirus VP4
Chinese Name:	辛诺柏病毒糖VP4/外层衣壳蛋白VP4/猴轮状病毒VP4抗体
Alias:	Hemagglutinin; VP4_ROTSS; Outer Capsid protein VP4 (Hemagglutinin); Outer capsid protein VP4; RVA s4gp1; RVAs4gp1; VP4; Outer capsid protein VP4; Outer capsid protein VP5*; Simian Rotavirus VP5*.
Organism Species:	Rabbit
Clonality:	Polyclonal
React Species:	Simian Rotavirus
Applications:	ELISA=1:500-1000IHC-P=1:400-800IHC-F=1:400-800ICC=1:100-500IF=1:100-500（Paraffin sections need antigen repair） not yet tested in other applications. optimal dilutions/concentrations should be determined by the end user.
Molecular weight:	58/85kDa
Form:	Lyophilized or Liquid
Concentration:	1mg/ml
immunogen:	KLH conjugated synthetic peptide derived from Simian Rotavirus VP4:201-300/776
Lsotype:	IgG
Purification:	affinity purified by Protein A
Storage Buffer:	0.01M TBS(pH7.4) with 1% BSA, 0.03% Proclin300 and 50% Glycerol.
Storage:	Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. The lyophilized antibody is stable at room temperature for at least one month and for greater than a year when kept at -20°C. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.
PubMed:	PubMed
Product Detail:	Simian Rotavirus VP4 (Outer Capsid protein VP4) (Hemagglutinin) functions as a spike-forming protein that mediates virion attachment to the host epithelial cell receptors and plays a major role in cell penetration, determination of host range restriction and virulence. Rotavirus entry into the host cell probably involves multiple sequential contacts between the outer capsid proteins VP4 and VP7, and the cell receptors. According to the considered strain, VP4 seems to essentially target sialic acid

	and/or the integrin heterodimer ITGA2/ITGB1. VP4 is a homotrimer and adopts a dimeric appearance above the capsid surface, while forming a trimeric base anchored inside the capsid layer. The priming trypsin cleavage triggers its rearrangement into rigid spikes with approximate two-fold symmetry of their protruding parts. After an unknown second triggering event, cleaved VP4 may undergo another rearrangement, in which two VP5* subunits fold back on themselves and join a third subunit to form a tightly associated trimer, shaped like a folded umbrella. VP4 interacts with host ITGA2 (via ITAG2 I-domain); this interaction occurs when ITGA2 is part of the integrin heterodimer ITGA2/ITGB1. VP4 interacts with host integrin heterodimer TGA4/ITGB1 and ITGA4/ITGB7. Proteolytic cleavage by trypsin results in activation of VP4 functions and greatly increases infectivity. The penetration into the host cell is dependent on trypsin treatment of VP4. It produces two peptides, VP5* and VP8* that remain associated with the virion. **Function:** Spike-forming protein that mediates virion attachment to the host epithelial cell receptors and plays a major role in cell penetration, determination of host range restriction and virulence. Rotavirus entry into the host cell probably involves multiple sequential contacts between the outer capsid proteins VP4 and VP7, and the cell receptors. According to the considered strain, VP4 seems to essentially target sialic acid and/or the integrin heterodimer ITGA2/ITGB1 (By similarity). Outer capsid protein VP5*: forms the spike 'foot' and 'body'. Acts as a membrane permeabilization protein that mediates release of viral particles from endosomal compartments into the cytoplasm. In integrin-dependent strains, VP5* targets the integrin heterodimer ITGA2/ITGB1 for cell attachment (By similarity). VP8* forms the head of the spikes. It is the viral hemagglutinin and an important target of neutralizing antibodies. In sialic acid-dependent strains, VP8* binds to host cell sialic acid, most probably a ganglioside, providing the initial contact. **Subunit:** VP4 is a homotrimer (Potential). VP4 adopts a dimeric appearance above the capsid surface, while forming a trimeric base anchored inside the capsid layer. Only hints of the third molecule are observed above the capsid surface. It probably performs a series of molecular rearrangements during viral entry. Prior to trypsin cleavage, it is flexible. The priming trypsin cleavage triggers its rearrangement into rigid spikes with approximate two-fold symmetry of their protruding parts. After an unknown second triggering event, cleaved VP4 may undergo another rearrangement, in which two VP5* subunits fold back on themselves and join a third subunit to form a tightly associated trimer, shaped like a folded umbrella. VP5* is a homotrimer (Potential). The trimer is coiled-coil stabilized by its C-terminus, however, its N-terminus, known as antigen domain or 'body', seems to be flexible allowing it to self-associate either as a dimer or a trimer. The two- to three-fold reorganization and fold-back of VP5* may be linked to membrane penetration, by exposing its hydrophobic region. Interacts with host ITGA2 (via ITAG2 I-domain); this interaction occurs when ITGA2 is part of the integrin heterodimer ITGA2/ITGB1. Interacts with host integrin heterodimer ITGA4/ITGB1 and ITGA4/ITGB7.

Subcellular Location:
Outer capsid protein VP4: Virion. Host rough endoplasmic reticulum (Potential). Note=Immature double-layered particles assembled in the cytoplasm bud across the membrane of the endoplasmic reticulum, acquiring during this process a transient lipid membrane that is modified with the ER resident viral glycoproteins NSP4 and VP7; these enveloped particles also contain VP4. As the particles move towards the interior of the ER cisternae, the transient lipid membrane and the non-structural protein NSP4 are lost, while the virus surface proteins VP4 and VP7 rearrange to form the outermost virus protein layer, yielding mature infectious triple-layered particles.
Outer capsid protein VP8*: Virion. Note=Outer capsid protein.
Outer capsid protein VP5*: Virion. Note=Outer capsid protein.

Post-translational modifications:
Proteolytic cleavage by trypsin results in activation of VP4 functions and greatly increases infectivity. The penetration into the host cell is dependent on trypsin treatment of VP4. It produces two peptides, VP5* and VP8* that remain associated with the virion.

Similarity:
Belongs to the rotavirus VP4 family.

SWISS:
P12473

Gene ID:
7011406

Database links:
Entrez Gene: 7011406 ROTSS

SwissProt: P12473 ROTSS

Important Note:
This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.