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## SARS-CoV-2 S protein (126-264 aa) Polyclonal antibody Catalog Number: 28869-1-AP 1 Publications

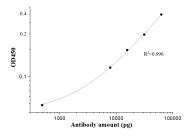


Basic Information	Catalog Number: 28869-1-AP	GenBank Accession Number: NC_045512	Purification Method: Antigen affinity purification
	Size: 150ul, Concentration: 500 ug/ml by Nanodrop; Source: Rabbit Isotype: IgG	GeneID (NCBI):	<u> </u>
		Full Name:	
		SARS-CoV-2 Spike Protein	
		Calculated MW: 141 kDa	
	Immunogen Catalog Number: AG30679		
Applications	Tested Applications: ELISA		
	Cited Applications: WB, IP		
	Species Specificity: Virus		
De elsevers d'Inferme etien	Coronaviruses (CoVs) infect human and animals and cause varieties of diseases, including respiratory, enteric, renal, and neurological diseases. CoV uses its spike protein to recognize ACE2 as its receptors and mediate membrane fusion and virus entry into host cells(PMID: 32221306). Each monomer of trimeric S protein is about 180 kDa, and contains two subunits, S1 and S2,S1 recognizes and binds to host receptors, and subsequent conformational changes in S2 facilitate fusion between the viral envelope and the host cell membrane(PMID: 19198616). Although the amino acid sequences of the S-glycoprotein were found to be different between the various HCoV, the structures showed high similarity, but the best 3D structural overlap shared by SARS-CoV and SARS-CoV-2, consistent with the shared ACE2 predicted receptor (PMID: 32522207). The spike protein of CoVs can be a target for vaccine and therapeutic development (PMID: 19198616). 28869-1-AP is specific for spike protein of SARS-COV-2, that antigen region is 126-264aa.		
Background Information	renal, and neurological diseases. Co membrane fusion and virus entry int kDa, and contains two subunits, S1 au changes in S2 facilitate fusion betwee the amino acid sequences of the S-gl showed high similarity, but the best shared ACE2 predicted receptor (PMI therapeutic development (PMID: 191	V uses its spike protein to recognize o host cells(PMID: 32221306). Each nd S2,S1 recognizes and binds to ho een the viral envelope and the host ycoprotein were found to be differe 3D structural overlap shared by SAI D: 32522207). The spike protein of	e ACE2 as its receptors and mediate monomer of trimeric S protein is about 180 ost receptors, and subsequent conformational cell membrane(PMID: 19198616). Although ent between the various HCoV, the structures RS-CoV and SARS-CoV-2, consistent with the CoVs can be a target for vaccine and
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Notable Publications	renal, and neurological diseases. Co membrane fusion and virus entry int kDa, and contains two subunits, S1 and changes in S2 facilitate fusion betwee the amino acid sequences of the S-gl showed high similarity, but the best shared ACE2 predicted receptor (PMI therapeutic development (PMID: 191 region is 126-264aa.	V uses its spike protein to recognize o host cells(PMID: 32221306). Each nd S2,S1 recognizes and binds to ho een the viral envelope and the host ycoprotein were found to be differe 3D structural overlap shared by SAI D: 32522207). The spike protein of	e ACE2 as its receptors and mediate monomer of trimeric S protein is about 180 ost receptors, and subsequent conformational cell membrane(PMID: 19198616). Although ent between the various HCoV, the structures RS-CoV and SARS-CoV-2, consistent with the CoVs can be a target for vaccine and
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For technical support and original validation data for this product please contact: T: 1 (888) 4PTGLAB (1-888-478-4522) (toll free E: proteintech@ptglab.com in USA), or 1(312) 455-8498 (outside USA) W: ptglab.com

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## Selected Validation Data



SARS-CoV-2 Spike Antibody (28869-1-AP) tested by ELISA.SARS-CoV-2 Spike protein was coated onto microtiter plates at 0.15 µg/well and then incubated with a dilution series of SARS-CoV-2 Spike Antibody (28869-1-AP). Bound antibodies were detected with HRP conjugated anti-Rabbit IgG followed by incubation with HRP Substrate and then measuring the resulting absorbance at 450 nm.