



SARS-CoV Matrix Antibody

Cat. No.: 3527

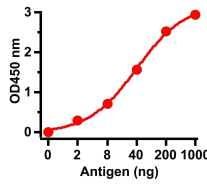


Figure 1 ELISA Test

Antibodies: SARS-CoV Matrix Antibody, 3527 (1 µg/mL). A direct ELISA was performed using immunogen as coating antigen and the anti-SARS-CoV Matrix antibody as the capture antibody. Secondary: Goat anti-rabbit IgG

Ψ Specifications

HOST SPECIES:	Rabbit
SPECIES REACTIVITY:	Virus
HOMOLOGY:	Predicted reactivity based on immunogen sequence: SARS-CoV-2 Matrix protein: (identity 77%, homology 93%)
IMMUNOGEN:	Anti-SARS-CoV Matrix antibody (3527) was raised against a peptide corresponding to 13 amino acids near the amino-terminus of SARS-CoV Matrix protein. The immunogen is located within the first 50 amino acids of SARS-CoV Matrix.
TESTED APPLICATIONS:	ELISA
APPLICATIONS:	SARS-CoV Matrix antibody can be used for the detection of SARS-CoV Matrix protein in ELISA. It will detect 5 ng of free peptide at 1 µg/mL.

Ψ Properties

PURIFICATION:	SARS-CoV Matrix Antibody is affinity chromatography purified via peptide column.
CLONALITY:	Polyclonal
ISOTYPE:	IgG

CONJUGATE:	Unconjugated
PHYSICAL STATE:	Liquid
BUFFER:	SARS-CoV Matrix Antibody is supplied in PBS containing 0.02% sodium azide.
CONCENTRATION:	1 mg/mL
STORAGE CONDITIONS:	SARS-CoV Matrix antibody can be stored at 4 °C for three months and -20 °C, stable for up to one year. As with all antibodies care should be taken to avoid repeated freeze thaw cycles. Antibodies should not be exposed to prolonged high temperatures.

Ψ Additional Info

OFFICIAL SYMBOL:	M
ALTERNATE NAMES:	SARS-CoV Matrix Antibody: Membrane protein, E1 glycoprotein, M protein
ACCESSION NO.:	P59596
PROTEIN GI NO.:	30173398
GENE ID:	1489672
USER NOTE:	Optimal dilutions for each application to be determined by the researcher.

Ψ Background and References

BACKGROUND:	Coronavirus disease 2019 (COVID-19), formerly known as 2019-nCoV acute respiratory disease, is an infectious disease caused by SARS-CoV-2, a virus closely related to the SARS virus (1). The disease is the cause of the 2019–20 coronavirus outbreak (2). The structure of 2019-nCoV consists of the following: a spike protein (S), hemagglutinin-esterase dimer (HE), a membrane glycoprotein (M), an envelope protein (E) a nucleocapsid protein (N) and RNA. The membrane (M) protein or matrix protein is the most abundant structural protein and defines the shape of the viral envelope (3). It is an integral membrane protein involved in the budding of the viral particles and interacts with S (Spike) protein. It involves in organization of the nucleoprotein inside, which includes many copies of the N (nucleocapsid) protein bound to the genomic RNA. The M protein holds dominant cellular immunogenicity and has been determined as a protective antigen in humoral responses, which suggests it would serve as a potential target in vaccine design (4).
REFERENCES:	1) Gorbalenya. bioRxiv: 2020.
	2) Hui et al. Int J Infect Dis. 2020;91:264-266.
	3) Neuman, et al. J Struct Biol. 2011;174(1):11-22.
	4) Liu et al. J Infect Dis. 2010;202(8):1171-80.

Ψ CITATIONS

CITATIONS:	1)Jaume, et al. Anti-severe acute respiratory syndrome coronavirus spike antibodies trigger infection of human immune cells via a pH- and cysteine protease-independent FcγR pathway. J Virol. 2011 Oct;85(20):10582-97. doi: 10.1128/JVI.00671-11. Epub 2011 Jul 20.PMID: 21775467
	2)Quijano-Rubio, et al. De novo design of modular and tunable allosteric biosensors. bioRxiv. 2020 Jul 20;2020.07.18.206946. doi: 10.1101/2020.07.18.206946.PMID: 32743576

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