

DESCRIPTION

Species Reactivity	SARS-CoV-2
Specificity	Detects SARS-CoV-2 membrane (M) protein in direct ELISAs.
Source	Monoclonal Mouse IgG _{2B} Clone # 1041508
Purification	Protein A or G purified from hybridoma culture supernatant
Immunogen	<i>E. coli</i> -derived SARS-CoV-2 membrane (M) protein with a C-terminal His tag Arg101-Gln222 Accession # YP_0097243693
Conjugate	Alexa Fluor 350 Excitation Wavelength: 346 nm Emission Wavelength: 442 nm
Formulation	Supplied 0.2mg/ml in 1X PBS with RDF1 and 0.09% Sodium Azide *Contains <0.1% Sodium Azide, which is not hazardous at this concentration according to GHS classifications. Refer to the Safety Data Sheet (SDS) for additional information and handling instructions.

APPLICATIONS

Please Note: Optimal dilutions should be determined by each laboratory for each application. [General Protocols](#) are available in the Technical Information section on our website.

Immunocytochemistry	Optimal dilution of this antibody should be experimentally determined.
Immunohistochemistry	Optimal dilution of this antibody should be experimentally determined.

PREPARATION AND STORAGE

Shipping	The product is shipped with polar packs. Upon receipt, store it immediately at the temperature recommended below.
Stability & Storage	Protect from light. Do not freeze. 12 months from date of receipt, 2 to 8 °C as supplied

BACKGROUND

SARS-CoV-2, which causes the global pandemic coronavirus disease 2019 (Covid-19), belongs to a family of viruses known as coronaviruses that are commonly comprised of four structural proteins: Spike protein(S), Envelope protein (E), Membrane protein (M), and Nucleocapsid protein (N) (1). M protein is the most abundant structural protein in the coronavirus membrane, and it is predicted to span the membrane three times, with a short N-terminal domain outside the viral envelope and a long C-terminal domain inside the virion (2). SARS-CoV-2 M protein is a 222 amino acid (aa) glycoprotein that is composed of an 18 aa N-terminal domain on the viral surface, 3 transmembrane domains, and a 122 aa C-terminal domain inside the viral envelope. SARS-CoV-2 M protein shares 89.14%, 98.6%, 98.2%, and 38.36% aa similarity with SARS-CoV-1, bat SARS-CoV, pangolin SARS-CoV, and MERS-CoV M proteins, respectively (3). The M protein of coronavirus plays an important role in assembly of viral particles by interacting with other structural proteins, especially with the E protein (4, 5). In SARS-CoV-2, M protein, combined with E protein, regulates intracellular trafficking of the S Protein and its unique furin-mediated processing (6).

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