# RB571, RB572, RB573, RB574, RB575, RB576, RB577 and RB578 antibodies recognize a fragment of the membrane M protein from SARS-CoV-2 by ELISA

Philippe Hammel<sup>1</sup>, Frederic Zenhausern<sup>2,3,4</sup>

<sup>1</sup> Geneva Antibody Facility, Faculty of Medicine, University of Geneva, 1 rue Michel Servet, CH-1211, Geneva, Switzerland; <sup>2</sup> Center for Applied NanoBioscience and Medicine, The University of Arizona, Phoenix, AZ 85004, USA; <sup>3</sup> Whitespace Enterprise Corporation, 1305 Auto Drive, Tempe, AZ 85284, USA; <sup>4</sup> School of Pharmaceutical Sciences, University of Geneva, 1 rue Michel Servet, CH-1211, Geneva, Switzerland

## Abstract

The recombinant antibodies RB571, RB572, RB573, RB574, RB575, RB576, RB577 and RB578 detect by ELISA a synthetic peptide from the SARS-CoV-2 M protein.

## Introduction

The SARS-CoV membrane (M) protein is the most abundant structural protein, driving virus assembly and budding into the lumen of the endoplasmic reticulum-Golgi intermediary compartment (ERGIC) via interactions with the E, S and N proteins (Siu *et al.*, 2008). Here we describe the ability of eight recombinant antibodies (RB571, RB572, RB573, RB574, RB575, RB576, RB577 and RB578) to detect by ELISA a C-terminal fragment of the cytosolic domain of the SARS-CoV-2 M protein (UniProt P0DTC5).

#### **Materials & Methods**

Antibodies: ABCD RB571, ABCD RB572, ABCD RB573, ABCD RB574, ABCD RB575, ABCD RB576, ABCD RB577 and ABCD RB578 antibodies (ABCD nomenclature, https://web.expasy.org/ abcd/) were produced by the Geneva Antibody Facility (http://www.unige.ch/medecine/antibodies/) as miniantibodies with the antigen-binding VHH portion fused to a mouse IgG2A Fc. HEK293 suspension cells (growing in FreeStyle<sup>™</sup> 293 Expression Medium, Gibco #12338) were transiently transfected with the vector coding for the VHH-Fc of each antibody. Supernatants (50-100 mg/L) were collected after 5 days.

Antigen: The antibodies were raised against an Nbiotinylated synthetic peptide, corresponding to the last 33 cytosolic C-terminal residues (DSGFAAYSRYRIGNYKLNTDHSS SSDNIALLVQ). This peptide was also used as antigen for ELISA detection. As a negative control, an N-biotinylated peptide corresponding to the last 31 C-terminal residues (NIVNVSLVKPSFYVYSRVKNLNSSRVPDLLV) of the SARS-CoV-2 E protein (UniProt P0DTC4) was used.

**Protocol:** The whole procedure was carried out at room temperature. Biotinylated peptides at saturating concentration (10 pmol/well) were immobilized on streptavidin-coated ELISA plates (Pierce #15124) for 30 min. Each well was rinsed three times with 100  $\mu$ l of washing buffer (PBS + 0.5% (w/v) BSA + 0.05% (w/v) Tween20), then incubated for 1 hour with 50  $\mu$ l of RB antibody-containing supernatant diluted in washing buffer (Fig. 1). After rinsing 3 times (100  $\mu$ l washing buffer), wells were incubated with horseradish peroxidase-coupled

Geneva University Library Open Access Publications https://oap.unige.ch/journals/abrep | ISSN 2624-8557 goat anti-mouse IgG (Bio-Rad #170-6516, dilution 1:1000, 50  $\mu$ l per well) for 30 min. After 3 rinses, Tetramethylbenzidine (TMB) substrate (Sigma #T5569) was added (50  $\mu$ l per well). The reaction was stopped by the addition of 25  $\mu$ l of 2 M H<sub>2</sub>SO<sub>4</sub>. The absorbance (OD) was measured at 450 nm, and the absorbance at 570 nm was subtracted.

### Results

Antibodies RB571, RB572, RB574, RB576, RB577 and, to a lesser extent, RB573, RB575 and RB578 bound in a concentration-dependent manner to the SARS-CoV-2 M peptide against which they were raised, but not against an unrelated peptide (Fig. 1). Note that the peptidic antigen used here is a short cytosolic domain of the M protein; it does not fold into a complex structure, nor contains glycosylation sites (Fung and Liu, 2018). Accordingly, it is reasonable to expect that the RB antibodies will also recognize the full-length protein. Further experiments will be necessary to determine if this is the case, and in which experimental procedures the antibodies can be used.



**Fig. 1.** Specific binding of RB antibodies to the target M peptide (ratio signal:background >2), but not to the control peptide (shown only for RB574; all other background curves are superimposed), as detected by ELISA.

#### References

Fung TS, Liu DX. Post-translational modifications of coronavirus proteins: roles and function. Future Virol. 2018; 13:405-430. PMID:32201497

Siu YL, Teoh KT, Lo J, et al. The M, E, and N structural proteins of the severe acute respiratory syndrome coronavirus are required for efficient assembly, trafficking, and release of viruslike particles. J Virol. 2008; 82:11318-30. PMID:18753196

#### Acknowledgments

This work was co-sponsored by NASA TRISH contract #NNX16AO69A/CAT0001.



This work is licensed under a Creative Commons Attribution 4.0 International License.