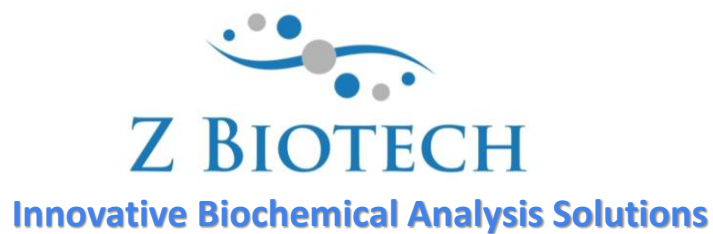


# SAR-CoV-2 RBD Peptide Array User Manual



**Website:** <http://www.zbiotech.com/home.html>

**Tel:** (720) 285-3587

**Email:** [info@zbiotech.com](mailto:info@zbiotech.com)

For Research Use Only

Copyright 2021, Z Biotech, LLC. All Rights Reserved.

## Introduction

Z Biotech's SARS-CoV-2 Receptor-Binding Domain (RBD) Peptide Array has been developed to help researchers identify, profile, and compare specific IgG, IgA, and IgM antibody responses to the RBD or detect and validate protein interactions with various RBD sequences. The RBD Peptide Arrays include RBD WT sequences and mutations of the Alpha, Beta, Gamma, Delta, Omicron, and other variants. The RBD Peptide Arrays are available in high-content and customizable, multi-well formats suitable for high-throughput assays.

This manual is provided as a comprehensive guide to help the researcher acquire clear results from the assay. Please read through carefully before starting your experiment.

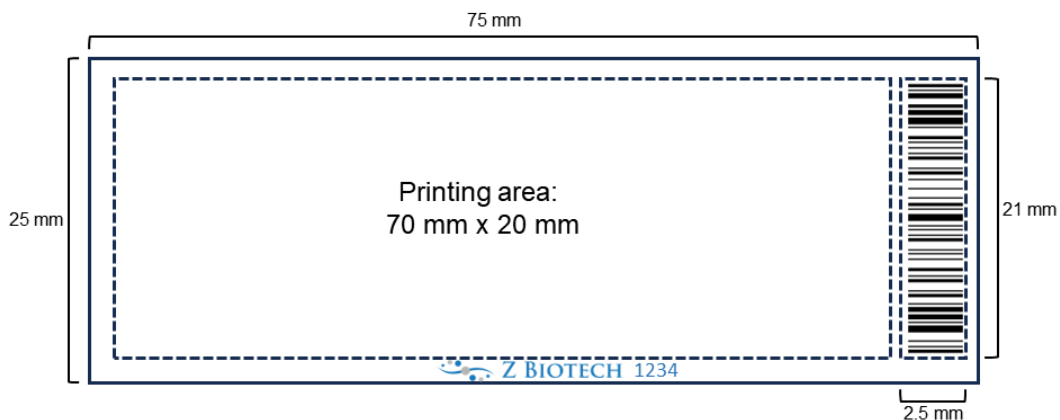
## Handling and Storage

Store the bag of slides and any buffers in a 4°C refrigerator. Purchased slides and buffers should be used within 6 months.

Allow the bag of slides to equilibrate to room temperature at least 20 minutes before opening. After opening, re-seal any unused slides in the moisture barrier bag with a desiccant inside and restore at 4°C. Handle the slides in a clean, dust free environment. Wear gloves and hold the slides on the edges. When adding sample do not touch the pipette tip to the array surface. When removing sample, gently touch the pipette tip at the corner of the well of the cassette and tilt the slide so that the sample pools to that corner. Avoid contact with the surface of the slides.

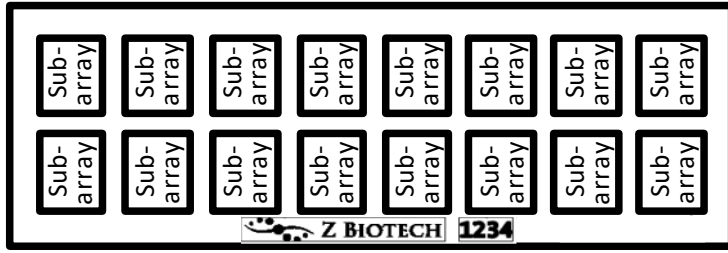
## Array Map/Schematic

SARS-CoV-2 RBD Peptide Array slides have 8 or 16 subarrays depending on the customer's request. Arrays are printed on the side with the "Z Biotech" label and 4-digit number ID facing upward. The "Z Biotech" label is located on the bottom center from a landscape view. The number ID is consistent with the barcode ID on the bottom from a portrait view. Dimensions and array maps are shown below.



Array Map:

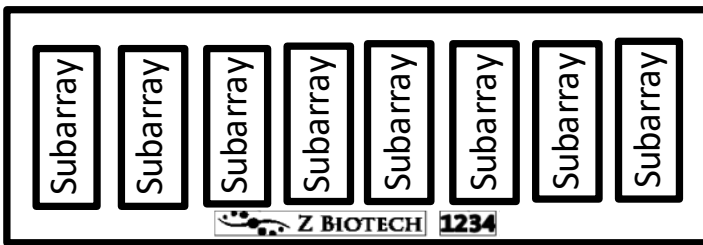
16-subarray Slide



Below is an example layout of a 16-subarray assay, if the customer were to choose 35 RBD peptides for inclusion on the array. A similar layout with more replicates would be made for the 8-subarray layout.

RP1	RP1	RP1	RP1	RP2	RP2	RP2	RP2	RP3	RP3	RP3	RP3
RP4	RP4	RP4	RP4	RP5	RP5	RP5	RP5	RP6	RP6	RP6	RP6
RP7	RP7	RP7	RP7	RP8	RP8	RP8	RP8	RP9	RP9	RP9	RP9
RP10	RP10	RP10	RP10	RP11	RP11	RP11	RP11	RP12	RP12	RP12	RP12
RP13	RP13	RP13	RP13	RP14	RP14	RP14	RP14	RP15	RP15	RP15	RP15
RP16	RP16	RP16	RP16	RP17	RP17	RP17	RP17	RP18	RP18	RP18	RP18
RP19	RP19	RP19	RP19	RP20	RP20	RP20	RP20	RP21	RP21	RP21	RP21
RP22	RP22	RP22	RP22	RP23	RP23	RP23	RP23	RP24	RP24	RP24	RP24
RP25	RP25	RP25	RP25	RP26	RP26	RP26	RP26	RP27	RP27	RP27	RP27
RP28	RP28	RP28	RP28	RP29	RP29	RP29	RP29	RP30	RP30	RP30	RP30
RP31	RP31	RP31	RP31	RP32	RP32	RP32	RP32	RP33	RP33	RP33	RP33
RP34	RP34	RP34	RP34	RP35	RP35	RP35	RP35	NC	NC	NC	NC
PC2	PC2	PC2	PC2	PC3	PC3	PC3	PC3	PC4	PC4	PC4	PC4
Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	M	M	M	M

8-subarray Slide



## SAR-CoV-2 RBD Peptide Identification List:

NO.	SEQUENCE	TYPE	START	END
1	RVQPTESIVRFPNIT	WT	319	333
2	FPNITNLCPFGEVFN	WT	329	343
2-A	FPNITNLCPFDEVFN	Mutant		
3	GEVFNATRFASVYAW	WT	339	353
3-A	GEVFKATRFASVYAW	Mutant		
3-B	GEVFNATIFASVYAW	Mutant		
3-C	GEVFNATKFASVYAW	Mutant		
3-D	GEVFNATTFASVYAW	Mutant		
4	SVYAWNRRKRISNCVA	WT	349	363
4-A	SVYAWKRRKRISNCVA	Mutant		
5	SNCVADYSVLYNSAS	WT	359	373
5-A	SNCVADYSVLYNLAP	Mutant		
6	YNSASFSTFKCYGVS	WT	369	383
6-A	YNLAPFFTFKCYGVS	Mutant		
7	CYGVSPTKLNDLCFT	WT	379	393
7-A	CYGLSPTKLNDLCFT	Mutant		
7-B	CYGVSLTKLNDLCFT	Mutant		
8	DLCFTNVYADSFVIR	WT	389	403
9	SFVIRGDEVQRQIAPG	WT	399	413
9-A	SFVIRGDEVQRQMAPG	Mutant		
10	QIAPGQTGKIADYNY	WT	409	423
10-A	QIAPGQTGNIADYNY	Mutant		
10-B	QIAPGQTGTIADYNY	Mutant		
10-C	QIAPGQTGMIADYNY	Mutant		
10-D	QIAPGQTGRIADYNY	Mutant		
11	ADYNYKLPDDFTGCV	WT	419	433
12	FTGCVIAWNSNNLDS	WT	429	443
12-A	FTGCVVAWNSNNLDS	Mutant		
12-B	FTGCVIAWNSKNLDS	Mutant		
12-C	FTGCVIAWNSKNLDS	Mutant		
13	NNLDSKVGGNLYNYLY	WT	439	453
13-A	NKLDSKVSIGNYNYLY	Mutant		
13-B	NNLDSKVDGNYNYLY	Mutant		
13-C	NNLDSKVVGNYNYLY	Mutant		
13-D	NNLDSKVAIGNYNYLY	Mutant		
13-E	NNLDSKVGGNFNYLY	Mutant		
13-F	NNLDSKVGGNCFNYLY	Mutant		
13-G	NNLDSKVGGNSNYLY	Mutant		
13-H	NNLDSKVGGNRYNYLY	Mutant		
13-I	NNLDSKVGGNQYNYLY	Mutant		
14	YNYLYRFRKSNLKP	WT	449	463
14-A	YNYRYRFRKSNLKP	Mutant		
14-B	YNYPYRFRKSNLKP	Mutant		

<b>14-C</b>	YNY <b>Q</b> YRLFRKSNLKP	Mutant		
<b>14-D</b>	YNYLYR <b>F</b> FRKSNLKP	Mutant		
<b>14-E</b>	YNYL <b>F</b> RRLFRKSNLKP	Mutant		
<b>14-F</b>	YNYL <b>S</b> RRLFRKSNLKP	Mutant		
<b>15</b>	SNLKPFERDISTEIY	WT	459	473
<b>16</b>	STEIYQ <b>A</b> <b>S</b> <b>T</b> PCNGV	WT	469	483
<b>16-A</b>	STEIYQ <b>V</b> GSTPCNGV	Mutant		
<b>16-B</b>	STEIYQ <b>G</b> GSTPCNGV	Mutant		
<b>16-C</b>	STEIYQAG <b>N</b> TPCNGV	Mutant		
<b>16-D</b>	STEIYQAG <b>T</b> TPCNGV	Mutant		
<b>16-E</b>	STEIYQAG <b>I</b> TPCNGV	Mutant		
<b>16-F</b>	STEIYQAG <b>R</b> TPCNGV	Mutant		
<b>16-G</b>	STEIYQAG <b>S</b> KPCNGV	Mutant		
<b>16-H</b>	STEIYQAG <b>S</b> RPCNGV	Mutant		
<b>16-I</b>	STEIYQAG <b>S</b> IPCNGV	Mutant		
<b>17</b>	PCNGV <b>E</b> GFNCY <b>F</b> PLQ	WT	479	493
<b>17-A</b>	PCNGV <b>K</b> GFNCYFPLQ	Mutant		
<b>17-B</b>	PCNGV <b>Q</b> GFNCYFPLQ	Mutant		
<b>17-C</b>	PCNGV <b>A</b> GFNCYFPLQ	Mutant		
<b>17-D</b>	PCNGV <b>E</b> GFNCY <b>S</b> PLQ	Mutant		
<b>17-E</b>	PCNGV <b>E</b> GFNCY <b>Y</b> PLQ	Mutant		
<b>18</b>	<b>Y</b> FPL <b>Q</b> S <b>Y</b> GFQPT <b>N</b> GV	WT	489	503
<b>18-A</b>	<b>Y</b> SPLQSYGFQPTNGV	Mutant		
<b>18-B</b>	<b>Y</b> FPL <b>R</b> S <b>S</b> <b>F</b> RPT <b>Y</b> GV	Mutant		
<b>18-C</b>	<b>Y</b> FPLQ <b>A</b> YGFQPTNGV	Mutant		
<b>18-D</b>	<b>Y</b> FPLQ <b>P</b> YGFQPTNGV	Mutant		
<b>18-E</b>	<b>Y</b> FPLQ <b>T</b> YGFQPTNGV	Mutant		
<b>18-F</b>	<b>Y</b> FPLQSYGFQPT <b>Y</b> GV	Mutant		
<b>18-G</b>	<b>Y</b> FPLQSYGFQPT <b>R</b> GV	Mutant		
<b>18-H</b>	<b>Y</b> FPLQSYGFQPT <b>D</b> GV	Mutant		
<b>18-I</b>	<b>Y</b> FPLQSYGFQPT <b>H</b> GV	Mutant		
<b>19</b>	PTNGVGYQP <b>Y</b> RVVVL	WT	499	513
<b>19-1</b>	PT <b>Y</b> GVGYQP <b>Y</b> RVVVL	Mutant		
<b>19-2</b>	PT <b>Y</b> GVG <b>H</b> Q <b>Y</b> RVVVL	Mutant		
<b>20</b>	RVVVLSFELL <b>H</b> APAT	WT	509	523
<b>20-A</b>	RVVVLSFELL <b>H</b> T <b>P</b> AT	Mutant		
<b>20-B</b>	RVVVLSFELL <b>H</b> S <b>P</b> AT	Mutant		
<b>20-C</b>	RVVVLSFELL <b>H</b> <b>P</b> AT	Mutant		
<b>21</b>	HAPATVCGPK <b>K</b> STNL	WT	519	533
<b>22</b>	KSTNLVKN <b>K</b> CVNF	WT	529	541

## Controls

NC: Negative control, Print Buffer

PC2: Positive control 2, Human IgG (0.1 mg/mL)

PC3: Positive control 3, Mouse IgG (0.1 mg/mL)

PC4: Positive control 4, Rabbit IgG (0.1 mg/mL)

Marker: Anti-human IgG, Cy3 (0.01 mg/mL) and anti-Human IgG, Alexa647 (0.01 mg/mL)

## **Materials Required**

- Arrayed glass slides
- 16 or 8-subarray cassettes
- Glycan Array Blocking Buffer (GABB, Item #10106), add 1% BSA (10 mg/ml) if needed
- Glycan Array Assay Buffer (GAAB, Item #10107), add 1% BSA (10 mg/ml) if needed
- Laser fluorescence scanner (able to scan at the wavelength of your fluorophore)
- Coplin jar
- Adhesive slide cover film

## **Preparation of Assay Samples**

Prepare samples or antibodies of interest in a centrifuge tube by diluting with the Glycan Array Assay Buffer. We recommend a range of 50  $\mu\text{g/ml}$  to 0.1  $\mu\text{g/ml}$  concentration, although some experimentation may be required to establish the concentration that will provide the highest binding signals with the lowest background fluorescence. This is often accomplished by applying a different dilution of samples to different wells of the array. For the fluorescently labelled streptavidin, we recommend a concentration of 1  $\mu\text{g/mL}$ . Calculate the volume of sample needed depending on how many slides and subarrays are to be assayed. **We recommend using 100  $\mu\text{L}$  volume of sample per well for 16 subarray cassettes and 200  $\mu\text{L}$  for 8 subarray cassettes to ensure full and even coverage of the printed area throughout incubation for every step of the assay.** If necessary, the assay can be done successfully with a minimal volume of 60  $\mu\text{L}$  per well for 16 subarray cassettes and 80  $\mu\text{L}$  for 8 subarray cassettes. We caution that using a minimal volume in the wells has an increased risk of the array drying out during the assay and may also cause unequal distribution of the sample across the arrayed surface which may result in signal variation. Please ensure each sample is homogeneous and thoroughly mixed.

## **Assay Protocol**

### Part 1 – Blocking

*Handle the slide in a clean, dry environment. Use gloves and avoid touching the slide surface.*

1. Let the arrayed slides equilibrate to room temperature (20-30 minutes) before opening the moisture barrier bag.
2. Add GABB to each subarray well.
3. Cover the wells with adhesive film to prevent evaporation and incubate slide on shaker at 80 rpm for 30 min. Longer incubation time is acceptable, but not necessary.

*Make sure the orbital shaker is completely flat. If the slide is sloped in any direction during incubation, it can cause variation in binding and detection.*

## Part 2 – Binding Assay

1. Unless the sample of interest is bacteria or cells, centrifuge samples briefly to avoid adding irrelevant particles to the array.
2. Remove blocking buffer from each well by gently touching a pipette tip to the corner of the well, tipping the slide so that the sample pools to that corner, and pipetting off buffer. Avoid touching the array surface. Have the replacement buffer ready before removing the old buffer to ensure the array does not dry out.
3. Wash the wells three times by adding GAAB to each well and shaking the array at 80 rpm for 5 min. Remove the buffer and repeat.
4. Immediately apply the sample of interest to each well. Avoid leaving air bubbles.
5. Seal the wells with adhesive film to prevent evaporation. If the sample is fluorescently labelled, cover with aluminum foil to keep it in the dark. Incubate on a shaker for 1 hour at 80 rpm. If the samples can easily aggregate, shake at higher speed to prevent protein aggregation. Longer incubation time may increase binding signal, especially for weakly binding samples.

*Avoid allowing the slides to dry out at any point during the assay, especially during long incubation times. Make sure the adhesive film is sealed around each well.*

If your samples are fluorescently labelled, go directly to Part 6 – Final Wash and Dry.

## Part 3 – Wash

1. Remove buffer or sample from each well by gently touching a pipette tip to the corner of the well, tipping the slide so that the sample pools to that corner, and pipetting off buffer. Avoid touching the array surface.
2. Immediately add GAAB to each well. Incubate on the shaker for 5 minutes at 80 rpm. Completely remove the buffer by pipette and repeat this step twice more. Avoid allowing the slide to dry out by having your next wash or sample ready before you remove the buffer.

If your sample is biotinylated, go directly to Part 5 – Fluorescent Staining.

## Part 4 – Binding of Biotinylated Antibody (Sandwich Assay Format)

1. Unless the secondary biotinylated antibody sample is bacteria or cells, centrifuge samples briefly to avoid adding irrelevant particles to the array.
2. After completely removing the third GAAB wash, immediately add the secondary biotinylated antibody to each well. Seal the wells with adhesive film and incubate on the shaker for 1 hour at 80 rpm. Shaking at a faster speed can prevent protein aggregation. Longer incubation time is acceptable, but not necessary.
3. After incubation repeat Part 3 – Wash.

## Part 5 – Fluorescent Staining

1. Centrifuge fluorescent labeled streptavidin samples briefly to avoid adding irrelevant particles to the array.
2. After completely removing the third GAAB wash, immediately add the fluorescently labelled streptavidin sample. Seal the wells with adhesive film and shield the wells from light with aluminum foil. Incubate on the shaker at 80 rpm for 1 hour. Longer incubation time is acceptable, but not necessary.

## Part 6 – Final Wash and Dry

1. Remove sample from each well by gently touching a pipette tip to the corner of the well, tipping the slide so that the liquid pools to that corner, and pipetting off. Avoid touching the array surface.
2. Briefly rinse each well with GAAB.
3. Completely remove the buffer by pipette. Avoid touching the array surface. Repeat steps 2 and 3.
4. Disassemble the cassette from the slide. For the provided cassette this can be done by holding the slide with one hand at the top and bottom edges and sliding out the cassette clips one by one with the other hand. If your provided cassette has metal clips they can be removed by rotating the clip outwards from the bottom of the slide. When the clips have been removed place the slide on the table and hold a small outer edge of the slide to the table as you gently peel the cassette off.
5. Immediately immerse the slide in a Coplin jar or beaker full of GAAB. Do not touch the surface of the array or allow the array surface to touch the sides of the beaker or jar.
6. Place the jar or beaker on a shaker at 80 rpm for 10 minutes.
7. Decant the buffer from the jar or beaker while holding the slide in place (only touch the edge of the slide) and then add sterile de-ionized water to immerse the slide.
8. Place the jar or beaker on the shaker at 80 rpm for 2 minutes.
9. Decant the water from the jar or beaker. Repeat once more with fresh de-ionized water.
10. Allow the slide to dry completely in a clean, dust free environment before scanning.

## **Analysis**

Scan the slide in a laser fluorescence scanner at the wavelength of emission for the fluorophore used. Adjust the laser power and PMT to obtain the highest possible signals without any being saturated (saturated positive control signal is okay). Analyze data with microarray analysis software. If there is specific binding the signal intensity should be higher than the background signal (area where there are no printed spots). Fluorescent signal due to specific binding to your sample of interest should be both dose-dependent with your sample dilution (unless the sample concentration range is too high and glycan binding is saturated) and should have positive binding signal after signal from control assays has been subtracted. Our standard method of comparing signal intensities is to quantify the median signal intensity data and subtract the background intensity. Subtracting signal from negative control spots as well as the same spots on a negative control assay (assay with only detection antibodies and fluorophore) will give more accurate specific binding data.

Interpretation of Control Signals:

Negative Control (Print Buffer): The negative control should produce a signal close to the intensity of the background. Since there is no binding involved with the negative control, any other signals around the negative control's intensity are also not true binding.

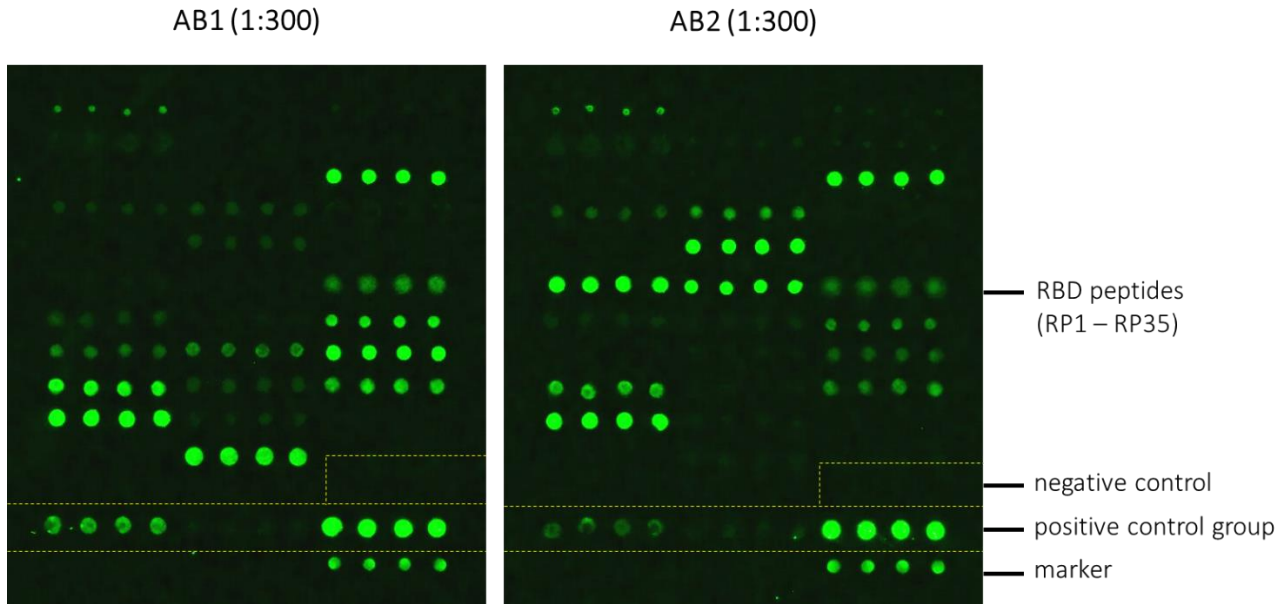
Marker: The array marker should show fluorescence signal regardless of the assay. It is there primarily to aid with orientation of the array map during analysis.

IgG (PC2, PC3, PC4): IgG is an antibody found in blood that is a primary component of humoral immunity. If the glycan-binding or secondary antibody sample is an anti-IgG from human, rabbit, or mouse it should bind to the respective IgG control.

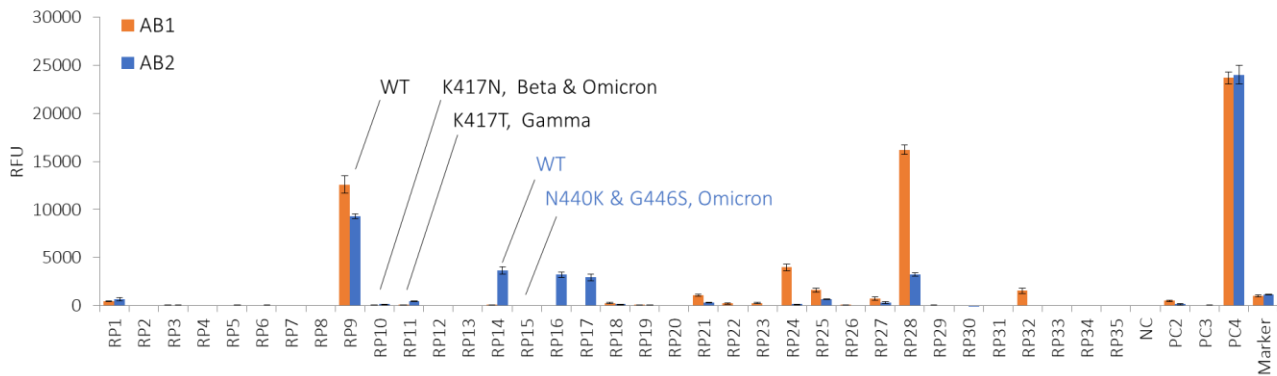


### Typical Binding Assay Result from the SARS-CoV-2 RBD Peptide Array

Example: SARS-CoV-2 RBD Peptide Array in 16-subarray format. Subarrays were assayed with two different antibodies (AB1 and AB2) (1:300 dilution), followed by a secondary antibody (anti-rabbit IgG, Cy3). Array was scanned with a microarray scanner at 532nm wavelength. All positive controls and the marker show binding as expected. Negative control (NC) shows no binding.



Comparison of RBD peptide bindings, AB1 and AB2 (1:300)



## Troubleshooting

Condition	Possible Causes	Potential Solutions
High Background	<ul style="list-style-type: none"> <li>• Sample concentration is too high</li> <li>• Concentration of fluorescent samples is too high</li> <li>• Arrays are not thoroughly washed</li> <li>• Slide drying out during assay</li> <li>• Excessive particles in the samples due to sample aggregation, dust, etc.</li> </ul>	<ul style="list-style-type: none"> <li>• Use a lower concentration range of samples. Consider a wider range if you are unsure where the detection limit is</li> <li>• Apply longer times for washing steps and use a higher shaking rate</li> <li>• Make sure wash buffer and sample is completely removed before the next step</li> <li>• Make sure adhesive film fully seals the wells to avoid evaporation</li> <li>• Centrifuge the samples prior to assay to avoid adding irrelevant particles</li> <li>• If you think that the sample is aggregating during incubation, try shaking at a higher speed</li> </ul>
Signal Variation	<ul style="list-style-type: none"> <li>• Slide drying out during assay</li> <li>• Binding samples are not equally distributed in the wells</li> <li>• Sample aggregation during incubation</li> <li>• Bubbles during incubation</li> </ul>	<ul style="list-style-type: none"> <li>• Make sure wells are sealed to prevent evaporation during incubation</li> <li>• Apply a larger volume of sample to each well to ensure equal distribution</li> <li>• Use a higher shaking rate during incubation</li> <li>• Make sure samples are homogeneous, mixed thoroughly, and do not leave bubbles on the array surface</li> </ul>
Unexpected Binding	<ul style="list-style-type: none"> <li>• Cross-contamination between wells or other sources</li> <li>• Sample contamination</li> </ul>	<ul style="list-style-type: none"> <li>• Make sure to use sterilized pipette tips and tubes used for sample application and preparation</li> <li>• Ensure cassette is pressed firmly to the slide so that there are no gaps to allow leaking between wells</li> <li>• Be careful not to cross contaminate samples when applying to the wells, even during wash steps</li> </ul>