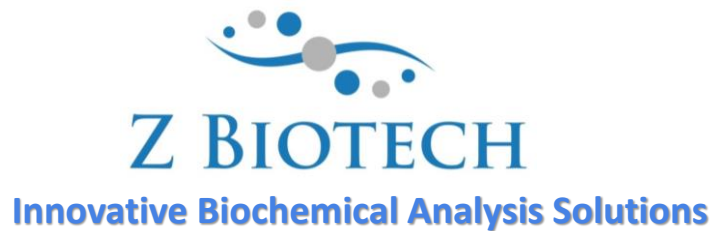


# MUC1 Glycopeptide Array User Manual



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## Introduction

Mucin 1 (MUC1) is a transmembrane glycoprotein, and it is one of several mucin proteins that make up mucus. The extracellular domain of MUC1 consists of a variable number of 20-amino-acid tandem repeats, and these repeats are highly O-glycosylated.  $\alpha$ -N-acetylgalactosamine (GalNAc, Tn) is attached to the hydroxyl group of threonine (Thr) and serine (Ser) of the tandem repeats and further extended with galactose (Gal), N-acetylglucosamine (GlcNAc), or GalNAc to form eight different core structures. These structures can be further modified by sialylation, sulfation, acetylation, fucosylation, and polylactosamine extension.

MUC1 is expressed on the surface of normal epithelial cells. However, changes in glycosylation patterns occur in various pathological conditions. For example, aberrant glycosylation of MUC1 has prevented cancer cells from forming core-2-based glycans. Therefore, cancer-associated MUC1 is hypoglycosylated with short carbohydrate structures such as Tn (GalNAc-Ser or -Thr) and STn (Neu5Ac-6-GalNAc-Thr). This unique feature makes MUC1 an ideal cancer-specific antigen for therapeutics development.

ZBiotech has developed a robust chemoenzymatic synthesis and microarray platform that enables the production and screening of a large MUC1 glycopeptide library. The first version of our MUC1 glycopeptide array includes 62 MUC1 glycopeptides and 1 unglycosylated peptide. Each glycopeptide is 23-mer in length and modified with carbohydrate structures such as Tn (GalNAc-Ser or -Thr) or STn (Neu5Ac-6-GalNAc-Ser or -Thr). This array platform allows researchers to identify, profile and compare specific antibody responses; as well as detect and validate protein interactions with various glycoforms of MUC1 peptides. This microarray platform is highly sensitive and has low background by using our proprietary surface coating and glycan immobilization technology.

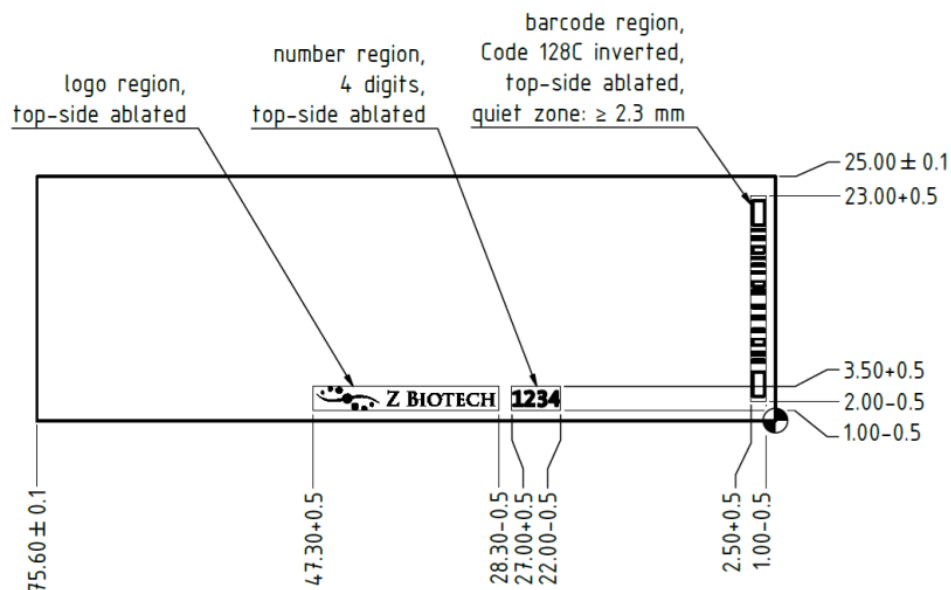
## Handling and Storage

Store the bag of slides and any buffers in a 4°C refrigerator if they are to be assayed within 24 hours upon receipt. For long term storage keep the bag of slides at -20°C. Avoid freezing and thawing multiple times. 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 refreeze.

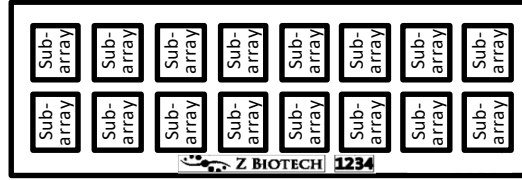
## Array Map/Schematic

MUC1 Glycopeptide Array slides have either 8 or 16 subarrays. 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 slides)

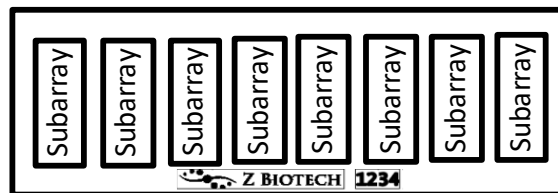
16-subarray Slide



1	1	1	1	2	2	2	2	3	3	3	3	4	4	4	4
5	5	5	5	6	6	6	6	7	7	7	7	8	8	8	8
9	9	9	9	10	10	10	10	11	11	11	11	12	12	12	12
13	13	13	13	14	14	14	14	15	15	15	15	16	16	16	16
17	17	17	17	18	18	18	18	19	19	19	19	20	20	20	20
21	21	21	21	22	22	22	22	23	23	23	23	24	24	24	24
25	25	25	25	26	26	26	26	27	27	27	27	28	28	28	28
29	29	29	29	30	30	30	30	31	31	31	31	32	32	32	32
33	33	33	33	34	34	34	34	35	35	35	35	36	36	36	36
37	37	37	37	38	38	38	38	39	39	39	39	40	40	40	40
41	41	41	41	42	42	42	42	43	43	43	43	44	44	44	44
45	45	45	45	46	46	46	46	47	47	47	47	48	48	48	48
49	49	49	49	50	50	50	50	51	51	51	51	52	52	52	52
53	53	53	53	54	54	54	54	55	55	55	55	56	56	56	56
57	57	57	57	58	58	58	58	59	59	59	59	60	60	60	60
61	61	61	61	62	62	62	62	63	63	63	63	NC	NC	NC	NC
PC1	PC1	PC1	PC1	PC2	PC2	PC2	PC2	PC3	PC3	PC3	PC3	PC4	PC4	PC4	PC4
Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	M	M	M	M

### Array Map (8-subarray slides):

8-subarray Slide



1	1	1	1	1	1	2	2	2	2	2	2	3	3	3	3	3	3	4	4	4	4	4	4	5	5	5	5	5	5	6	6	6	6	6	6
7	7	7	7	7	7	8	8	8	8	8	8	9	9	9	9	9	9	10	10	10	10	10	10	11	11	11	11	11	11	12	12	12	12	12	12
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19	19	19	19	19	19	20	20	20	20	20	20	21	21	21	21	21	21	22	22	22	22	22	22	23	23	23	23	23	23	24	24	24	24	24	24
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37	37	37	37	37	37	38	38	38	38	38	38	39	39	39	39	39	39	40	40	40	40	40	40	41	41	41	41	41	41	42	42	42	42	42	42
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49	49	49	49	49	49	50	50	50	50	50	50	51	51	51	51	51	51	52	52	52	52	52	52	53	53	53	53	53	53	54	54	54	54	54	54
55	55	55	55	55	55	56	56	56	56	56	56	57	57	57	57	57	57	58	58	58	58	58	58	59	59	59	59	59	59	60	60	60	60	60	60
61	61	61	61	61	61	62	62	62	62	62	62	63	63	63	63	63	63	NC	NC	NC	NC	NC	NC	PC1	PC1	PC1	PC1	PC1	PC1	PC1	PC1	PC1	PC1	PC1	PC1
PC3	PC3	PC3	PC3	PC3	PC3	PC4	PC4	PC4	PC4	PC4	PC4	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	Blank	M	M	M	M	M	M

## MUC1 Glycopeptide Identification List

#	Sequence
1	PPAHGVT(GalNAc)SAPDTRPAPGSTAPPA
2	PPAHGVTS(GalNAc)APDTRPAPGSTAPPA
3	PPAHGVTSAPDT(GalNAc)RPAPGSTAPPA
4	PPAHGVTSAPDTRPAPGS(GalNAc)TAPPA
5	PPAHGVTSAPDTRPAPGST(GalNAc)APPA
6	PPAHGVT(GalNAc)S(GalNAc)APDTRPAPGSTAPPA
7	PPAHGVT(GalNAc)SAPDT(GalNAc)RPAPGSTAPPA
8	PPAHGVT(GalNAc)SAPDTRPAPGS(GalNAc)TAPPA
9	PPAHGVT(GalNAc)SAPDTRPAPGST(GalNAc)APPA
10	PPAHGVTS(GalNAc)APDT(GalNAc)RPAPGSTAPPA
11	PPAHGVTS(GalNAc)APDTRPAPGS(GalNAc)TAPPA
12	PPAHGVTS(GalNAc)APDTRPAPGST(GalNAc)APPA
13	PPAHGVTSAPDT(GalNAc)RPAPGS(GalNAc)TAPPA
14	PPAHGVTSAPDT(GalNAc)RPAPGST(GalNAc)APPA
15	PPAHGVTSAPDTRPAPGS(GalNAc)T(GalNAc)APPA
16	PPAHGVT(GalNAc)S(GalNAc)APDT(GalNAc)RPAPGSTAPPA
17	PPAHGVT(GalNAc)S(GalNAc)APDTRPAPGS(GalNAc)TAPPA
18	PPAHGVT(GalNAc)S(GalNAc)APDTRPAPGST(GalNAc)APPA
19	PPAHGVT(GalNAc)SAPDT(GalNAc)RPAPGS(GalNAc)TAPPA
20	PPAHGVT(GalNAc)SAPDT(GalNAc)RPAPGST(GalNAc)APPA
21	PPAHGVT(GalNAc)SAPDTRPAPGS(GalNAc)T(GalNAc)APPA
22	PPAHGVTS(GalNAc)APDT(GalNAc)RPAPGS(GalNAc)TAPPA
23	PPAHGVTS(GalNAc)APDT(GalNAc)RPAPGST(GalNAc)APPA
24	PPAHGVTS(GalNAc)APDTRPAPGS(GalNAc)T(GalNAc)APPA
25	PPAHGVTSAPDT(GalNAc)RPAPGS(GalNAc)T(GalNAc)APPA
26	PPAHGVT(GalNAc)S(GalNAc)APDT(GalNAc)RPAPGS(GalNAc)TAPPA
27	PPAHGVT(GalNAc)S(GalNAc)APDT(GalNAc)RPAPGST(GalNAc)APPA
28	PPAHGVT(GalNAc)S(GalNAc)APDTRPAPGS(GalNAc)T(GalNAc)APPA
29	PPAHGVT(GalNAc)SAPDT(GalNAc)RPAPGS(GalNAc)T(GalNAc)APPA
30	PPAHGVTS(GalNAc)APDT(GalNAc)RPAPGS(GalNAc)T(GalNAc)APPA
31	PPAHGVT(GalNAc)S(GalNAc)APDT(GalNAc)RPAPGS(GalNAc)T(GalNAc)APPA
32	PPAHGVT(Neu5Ac-6-GalNAc)SAPDTRPAPGSTAPPA
33	PPAHGVTS(Neu5Ac-6-GalNAc)APDTRPAPGSTAPPA
34	PPAHGVTSAPDT(Neu5Ac-6-GalNAc)RPAPGSTAPPA
35	PPAHGVTSAPDTRPAPGS(Neu5Ac-6-GalNAc)TAPPA
36	PPAHGVTSAPDTRPAPGST(Neu5Ac-6-GalNAc)APPA
37	PPAHGVT(Neu5Ac-6-GalNAc)S(Neu5Ac-6-GalNAc)APDTRPAPGSTAPPA
38	PPAHGVT(Neu5Ac-6-GalNAc)SAPDT(Neu5Ac-6-GalNAc)RPAPGSTAPPA
39	PPAHGVT(Neu5Ac-6-GalNAc)SAPDTRPAPGS(Neu5Ac-6-GalNAc)TAPPA
40	PPAHGVT(Neu5Ac-6-GalNAc)SAPDTRPAPGST(Neu5Ac-6-GalNAc)APPA
41	PPAHGVTS(Neu5Ac-6-GalNAc)APDT(Neu5Ac-6-GalNAc)RPAPGSTAPPA
42	PPAHGVTS(Neu5Ac-6-GalNAc)APDTRPAPGS(Neu5Ac-6-GalNAc)TAPPA
43	PPAHGVTS(Neu5Ac-6-GalNAc)APDTRPAPGST(Neu5Ac-6-GalNAc)APPA
44	PPAHGVTSAPDT(Neu5Ac-6-GalNAc)RPAPGS(Neu5Ac-6-GalNAc)TAPPA
45	PPAHGVTSAPDT(Neu5Ac-6-GalNAc)RPAPGST(Neu5Ac-6-GalNAc)APPA
46	PPAHGVTSAPDTRPAPGS(Neu5Ac-6-GalNAc)T(Neu5Ac-6-GalNAc)APPA
47	PPAHGVT(Neu5Ac-6-GalNAc)S(Neu5Ac-6-GalNAc)APDT(Neu5Ac-6-GalNAc)RPAPGSTAPPA
48	PPAHGVT(Neu5Ac-6-GalNAc)S(Neu5Ac-6-GalNAc)APDTRPAPGS(Neu5Ac-6-GalNAc)TAPPA
49	PPAHGVT(Neu5Ac-6-GalNAc)S(Neu5Ac-6-GalNAc)APDTRPAPGST(Neu5Ac-6-GalNAc)APPA
50	PPAHGVT(Neu5Ac-6-GalNAc)SAPDT(Neu5Ac-6-GalNAc)RPAPGS(Neu5Ac-6-GalNAc)TAPPA
51	PPAHGVT(Neu5Ac-6-GalNAc)SAPDT(Neu5Ac-6-GalNAc)RPAPGST(Neu5Ac-6-GalNAc)APPA
52	PPAHGVT(Neu5Ac-6-GalNAc)SAPDTRPAPGS(Neu5Ac-6-GalNAc)T(Neu5Ac-6-GalNAc)APPA
53	PPAHGVTS(Neu5Ac-6-GalNAc)APDT(Neu5Ac-6-GalNAc)RPAPGS(Neu5Ac-6-GalNAc)TAPPA
54	PPAHGVTS(Neu5Ac-6-GalNAc)APDT(Neu5Ac-6-GalNAc)RPAPGST(Neu5Ac-6-GalNAc)APPA
55	PPAHGVTS(Neu5Ac-6-GalNAc)APDTRPAPGS(Neu5Ac-6-GalNAc)T(Neu5Ac-6-GalNAc)APPA
56	PPAHGVTSAPDT(Neu5Ac-6-GalNAc)RPAPGS(Neu5Ac-6-GalNAc)T(Neu5Ac-6-GalNAc)APPA
57	PPAHGVT(Neu5Ac-6-GalNAc)S(Neu5Ac-6-GalNAc)APDT(Neu5Ac-6-GalNAc)RPAPGS(Neu5Ac-6-GalNAc)TAPPA
58	PPAHGVT(Neu5Ac-6-GalNAc)S(Neu5Ac-6-GalNAc)APDT(Neu5Ac-6-GalNAc)RPAPGST(Neu5Ac-6-GalNAc)APPA
59	PPAHGVT(Neu5Ac-6-GalNAc)S(Neu5Ac-6-GalNAc)APDTRPAPGS(Neu5Ac-6-GalNAc)T(Neu5Ac-6-GalNAc)APPA
60	PPAHGVT(Neu5Ac-6-GalNAc)SAPDT(Neu5Ac-6-GalNAc)RPAPGS(Neu5Ac-6-GalNAc)T(Neu5Ac-6-GalNAc)APPA
61	PPAHGVTS(Neu5Ac-6-GalNAc)APDT(Neu5Ac-6-GalNAc)RPAPGS(Neu5Ac-6-GalNAc)T(Neu5Ac-6-GalNAc)APPA
62	PPAHGVT(Neu5Ac-6-GalNAc)S(Neu5Ac-6-GalNAc)APDT(Neu5Ac-6-GalNAc)RPAPGS(Neu5Ac-6-GalNAc)T(Neu5Ac-6-GalNAc)APPA
63	PPAHGVTSAPDTRPAPGSTAPPA

## Controls

NC: Negative control, Print Buffer

PC1: Positive control 1, Biotinylated PEG (0.01 mg/mL)

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 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 glycan-binding protein samples or secondary antibodies of interest in a centrifuge tube by diluting with the Glycan Array Assay Buffer. We recommend a range of 50 µg/ml to 0.1 µg/ml concentration for protein samples, 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 µg/mL. Calculate the volume of sample needed depending on how many slides and subarrays are to be assayed. **We recommend using 100 µL volume of sample per well for 16 subarray cassettes and 200 µL 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 µL per well for 16 subarray cassettes and 80 µL 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 blocking buffer 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 glycan binding protein 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 glycan binding protein 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 the 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 glycan-binding protein 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 glycan-binding 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 Controls (Print Buffer):** The negative controls should produce little to no signal. Since there is no binding involved with the negative control, any other signals around the negative control's intensity are also not binding.

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

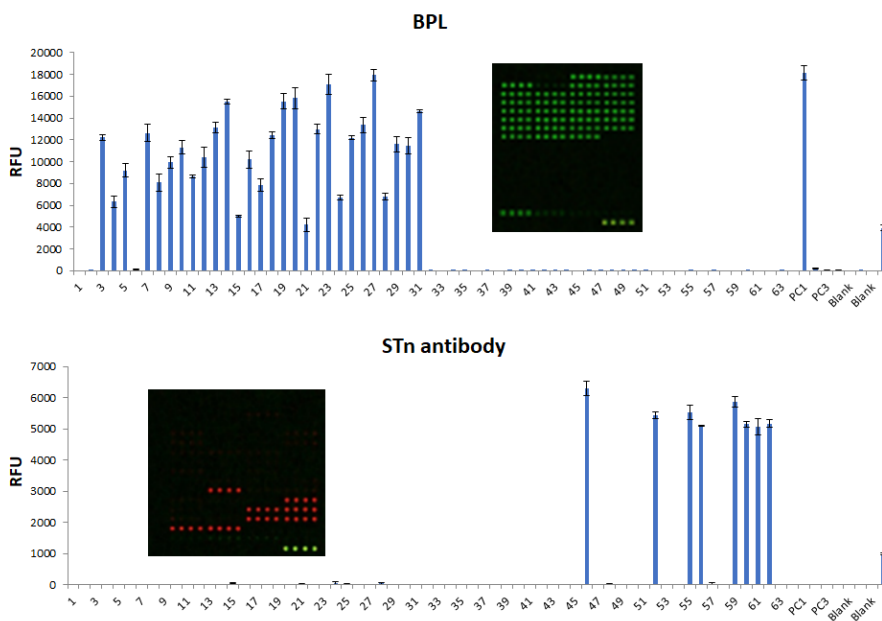
**Biotinylated PEG (PC1):** This positive control will bind directly to the fluorescent labelled streptavidin. If your glycan-binding protein sample is already fluorescently labelled, or in any case where the addition of fluorescent labelled streptavidin to the array was not preformed (Part 5 – Fluorescent staining) this positive control will not be reactive.

**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 MUC1 Glycopeptide Array

Example 1 is of one well on a MUC1 Glycopeptide Array slide (16-subarray) was assayed with glycan-binding protein biotinylated *Bauhinia purpurea* agglutinin (BPL) lectin (10 µg/mL),

followed by Streptavidin-Cy3. Example 2 is of one well on a MUC1 Glycopeptide Array slide (16-subarray) was assayed with STn antibody AF647, CC49 (1 µg/ml). The array was scanned with InnoScan 710 microarray scanner.



## Troubleshooting

Condition	Possible Causes	Potential Solutions
High Background	<ul style="list-style-type: none"> <li>• Concentration of glycan-binding protein samples 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 protein 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>• Glycan-binding protein 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>