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LEGENDplex™

Multi-Analyte Flow Assay Kit

SARS-CoV-2 Serological IgM Mix and Match Subpanel

Please read the entire manual before running the assay.

BioLegend.com

It is highly recommended that this manual be read in its entirety before using this product. Do not use this kit beyond the expiration date.

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Chapter 1: KIT DESCRIPTION

Introduction

Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) is a single stranded RNA virus that belongs to the *Coronaviridae* family. SARS-CoV-2 caused COVID-19 pandemic declared in 2020. Among other symptoms, the viral infection may lead to respiratory diseases and pulmonary failure which can be fatal. SARS-CoV-2 is structurally composed of 4 main proteins (spike glycoprotein, envelope, membrane and nucleocapsid proteins) and several accessory proteins. The coronavirus spike (S) glycoprotein contains a receptor binding domain (RBD) and is a viral fusion protein on the outer envelope of the virion that plays a critical role in viral infection by mediating fusion of the viral and cellular membranes. IgG, IgA and IgM are three types of immunoglobulins that are targeted in COVID-19 serological testing. IgA and IgM are produced during early stages of viral infection. The IgA response declines quickly during infection, while the IgM response dissipates at a slower rate. The IgG response develops gradually and its levels are sustained after infection. Studying the expression profiles of immunoglobulins against viral proteins after infection is critical for understanding the humoral immune response to Coronavirus.
The LEGENDplex™ SARS-CoV-2 Serological IgM Panel is a bead-based multiplex assay, utilizing fluorescence–encoded beads suitable for analyzing by various flow cytometers. This panel allows simultaneous measurement IgM antibodies against SARS-CoV-2 Spike S1 and RBD proteins. The panel has been validated for human serum and plasma samples. For flexible customization, please visit www.biolegend.com/legendplex.

This assay is for research use only.

Principle of the Assay

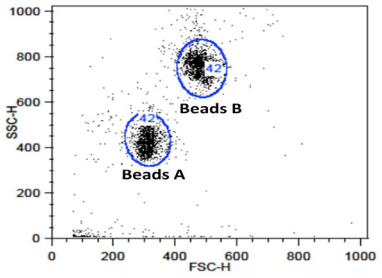
BioLegend's LEGENDplex™ assays are bead-based immunoassays that use the same basic principle as sandwich immunoassays. Beads are differentiated by size and internal fluorescence intensities. The surface of each bead set is first conjugated with specific proteins, and then used as capture beads for that particular analyte. When a selected panel of capture beads is mixed and incubated with samples containing target analytes, each analyte binds to its specific capture beads. After washing, biotinylated detection antibody binds to the bound target in samples and standard forming a capture bead-analyte-detection antibody complex. Streptavidin-phycoerythrin (SA-PE) is subsequently added, providing fluorescent signal intensities in proportion to the amount of the bound analytes. Since the beads are differentiated by size and internal fluorescence intensity, analyte-specific populations can be segregated and PE fluorescent signal quantified. The concentration of a particular analyte is determined using a standard curve generated in the same assay.

Beads Usage

The LEGENDplex™ beads-based assay usually includes two sets of beads. Each set has a unique size that can be identified based on their forward scatter (FSC) and side scatter (SSC) profiles (Beads A and Beads B, Figure 1). Each bead set can be further resolved based on their internal fluorescence intensities. The internal dye can be detected using either the FL3, FL4, or APC channels, depending on the type of flow cytometer used. The smaller A Beads consists of 6 bead populations (A4, A5, A6, A7, A8, A10) and the larger B Beads consists of 7 bead populations (B2, B3, B4, B5, B6, B7, B9) (Figure 2-3).

The SARS-CoV-2 Serological IgM Panel uses only 2 of the 13 bead populations (B2 and B5) distinguished by size and internal fluorescent dye.

Figure 1. Beads Differentiated by Size



Beads A = smaller beads

Beads B = larger beads

Figure 2. Beads A Classification by FL4

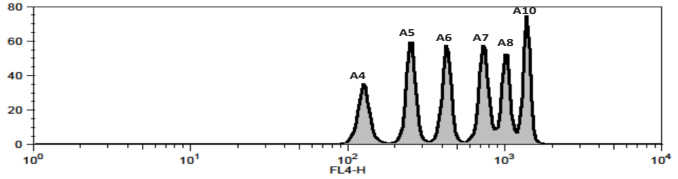
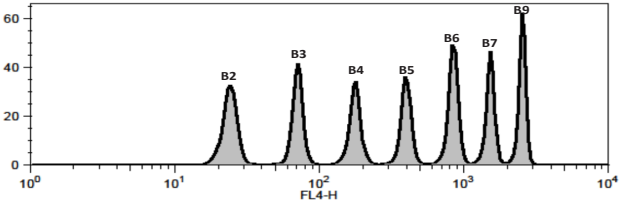


Figure 3. Beads B Classification by FL4



For Beads usage in the full panel, please refer to Table 1 below.

Table 1. Bead ID* and Panel Target Selection

Target	Bead ID	SARS-CoV-2 Serological IgM Panel Cat. # 741211 or 741212	Mix & Match	Top Standard Concentrations
Anti-Spike S1 IgM	**B2**	√		The top standard concentrations of each target may vary and may be subject to change from lot to lot. Please refer to the lot-specific Certificate of Analysis (CoA) for this information.
Anti-S1 RBD IgM	**B5**	√		

*Bead ID is used to associate a bead population to a particular analyte when using the LEGENDplex™ data analysis software program. For further information regarding the use of the program please visit **biolegend.com/en-us/legendplex**

Storage Information

Recommended storage for all original kit components is between 2°C and 8°C. DO NOT FREEZE Pre-mixed Beads, Detection Antibodies or SA-PE.

- Once the standards have been sufficiently reconstituted, immediately transfer contents into polypropylene vials. DO NOT STORE RECONSTITUTED STANDARDS IN GLASS VIALS.
- Upon reconstitution, leftover top standard should be stored at ≤-70°C for use within one month. Avoid multiple (>2) freeze-thaw cycles. Discard any leftover diluted standards.

Materials Supplied

The LEGENDplex™ kit contains reagents for 100 tests, listed in the table below. When assayed in duplicate, this is enough for an 8-point standard curve and 40 samples.

For the Mix and Match Subpanels, individual beads are provided at 13X concentration. The Buffer Set contains Setup Beads, all Buffers, Plate Sealers, Matrix, and SA-PE.

Kit Components	Quantity	Volume	Cat #
Capture Beads* (see tables below for more information)	**Varies**	**Varies**	**Varies**
SARS-CoV-2 Serological Panel IgM Det. Ab	1 bottle	3.5 mL	741209
SARS-CoV-2 Serological IgM Panel Standard	1 vial	Lyophilized	741210
LEGENDplex™ Buffer Set D	1	--	740375
Filter Plate* or V-bottom Plate**	1 plate	--	740377* or 740379**

* For kit with filter plate. ** For kit with V-bottom plate. Only one plate is provided for each kit.

Capture beads for Mix and Match Subpanels

Bead Name	Quantity	Volume	Cat #
SARS-CoV-2 Spike S1 Protein Capture Bead B2, 13X	1 vial	270 µL	741211
SARS-CoV-2 S1 RBD Capture Bead B5, 13X	1 vial	270 µL	741212

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LEGENDplex™ Buffer Set D (Cat#: 740375)

Components	Quantity	Volume	Part #
Setup Beads 1: FITC Beads	1 vial	1 mL	77840
Setup Beads 2: PE Beads	1 vial	1 mL	77842
Setup Beads 3: Raw Beads	1 vial	2 mL	77844
LEGENDplex™ SA-PE	1 bottle	3.5 mL	77743
LEGENDplex™ Assay Buffer	2 bottles	25 mL	77562
LEGENDplex™ Wash Buffer, 20X	1 bottle	25 mL	77564
Plate Sealers	4 sheets	--	78101

No plate is included in Buffer Set D. Plate needs to be ordered separately. Please order the correct type of plate based on the preferred assay protocol (Cat# 740377 or 740378 for Filter Plate and Cat# 740379 for V-bottom Plate)

Materials to be Provided by the End-User

- A flow cytometer equipped with two lasers (e.g., a 488 nm blue laser or 532 nm green laser and a 633-635 nm red laser) capable of distinguishing 575 nm and 660 nm or a flow cytometer equipped with one laser (e.g., 488 nm blue laser) capable of distinguishing 575 nm and 670 nm.

Partial list of compatible flow cytometers:

Flow Cytometer	Reporter Channel	Channel Emission	Classification Channel	Channel Emission	Compensation needed?
BD FACSCalibur™	FL2	575 nm	FL4	660 nm	No*
BD Accuri™ C6	FL2	585 nm	FL4	675 nm	No*
BD FACSCanto™, BD FACSCanto™ II	PE	575 nm	APC	660 nm	No*
BD™ LSR, LSR II BD LSRFortessa™	PE	575 nm	APC	660 nm	No*
Gallios™	PE	575 nm	APC	660 nm	No*
CytoFLEX	PE	585 nm	APC	660 nm	No*
NovoCyte	PE	572 nm	APC	660 nm	No*
Attune™ NxT	PE	574 nm	APC	670 nm	No*

***Compensation is not required for the specified flow cytometers when set up properly.**

For setting up various flow cytometers, please visit: **www.biolegend.com/**

legendplex and click on the **Instrument Setup** tab.

- Multichannel pipettes capable of dispensing 5 µL to 200 µL
- Reagent reservoirs for multichannel pipette
- Polypropylene microfuge tubes (1.5 mL)
- Laboratory vortex mixer
- Sonicator bath (e.g., Branson Ultrasonic Cleaner model #B200, or equivalent)
- Aluminum foil
- Absorbent pads or paper towels
- Plate shaker (e.g., Lab-Line Instruments model #4625, or equivalent)
- Tabletop centrifuges (e.g., Eppendorf centrifuge 5415 C, or equivalent)
- 1.1 mL Mini FACS tubes

If the assay is performed in a filter plate:

- A vacuum filtration unit (Millipore MultiScreen ® HTS Vacuum Manifold, cat # MSVMHTS00 or equivalent). Instructions on how to use the vacuum manifold can be found at the supplier's website.
- A vacuum source (mini vacuum pump or line vacuum, e.g., Millipore Vacuum Pump, catalog # WP6111560, or equivalent)
- If needed, additional Filter plates can be ordered from BioLegend (Cat# 740377 or 740378).

If the assay is performed in a V-bottom plate:

- Centrifuge with a swinging bucket adaptor for microtiter plates (e.g., Beckman Coulter Allegra™ 6R Centrifuge with MICROPLUS CARRIER adaptor for GH3.8 and JS4.3 Rotors) .
- If needed, additional V-bottom plates can be ordered from BioLegend (Cat# 740379).

Precautions

- All blood components and biological materials should be handled as potentially hazardous. Follow universal precautions as established by the Center for Disease Control and Prevention and by the Occupational Safety and Health Administration when handling and disposing of infectious agents.
- Sodium azide has been added to some reagents as a preservative. Although the concentrations are low, sodium azide may react with lead and copper plumbing to form highly explosive metal azides. On disposal, flush

with a large volume of water to prevent azide build-up.

- Do not mix or substitute reagents from different kits or lots. Reagents from different manufacturers should not be used with this kit.
- Do not use this kit beyond its expiration date.
- SA-PE and beads are light-sensitive. Minimize light exposure.

Chapter 2: ASSAY PREPARATION

Sample Collection and Handling

Preparation of Serum Samples:

- Allow the blood to clot for at least 30 minutes and centrifuge for 20 minutes at 1,000 x *g*.
- Remove serum and assay immediately or aliquot and store samples at ≤-20°C. Avoid multiple (>2) freeze/thaw cycles.
- When using frozen samples, it is recommended that samples be thawed completely, mixed and centrifuged to remove particulates prior to use.

Preparation of Plasma Samples:

- Plasma collection should be collected using an anti-coagulant (e.g., EDTA, Heparin, Citrate). Centrifuge for 20 minutes at 1,000 x *g* within 30 minutes of blood collection.
- Remove plasma and assay immediately, or aliquot and store samples at ≤-20°C. Avoid multiple (>2) freeze/thaw cycles.
- When using frozen samples, it is recommended that samples be thawed completely, mixed well and centrifuged to remove particulates.

Reagent Preparation

Preparation of Protein-Immobilized Beads

1. The individual beads (13X) need to be combined with one another and diluted with Assay Buffer to create a 1X working solution of beads prior to use.
2. Sonicate each bead vial for 1 minute in a sonicator bath and then vortex for 30 seconds to completely resuspend the beads.
3. Calculate and prepare a 1X beads working solution based on the desired number of reactions and plex-size of your assay (i.e. the number of individual bead vials) following the steps described below.

    A. Total volume (µL) = **30** x (number of reactions)

    B. Volume needed from each 13X beads vial (µL) = **2.3** x (number of

reactions)

C. Assay Buffer needed (µL) = A – B x (number of individual beads vials to be mixed)

Note: calculations for total volume include a 20% excess to account for any loss during pipetting.

Example: to prepare 50 reactions for a 5-plex assay

A. Total volume (µL) = **30** x 50 = 1500 µL

B. Volume per beads vial needed (µL) = **2.3** x 50 = 115 µL

C. Assay Buffer needed (µL) = A – B x (number of individual beads vials) =1500 – (115 x 5) = 925 µL

Combine 115 µL of each beads vial (5 vials) with 925 µL of assay buffer to get the desired final volume of 1500 µL of 1X working solution of beads.

Preparation of Wash Buffer

- Bring the 20X Wash Buffer to room temperature and mix to bring all salts into solution.
- Dilute 25 mL of 20X Wash Buffer with 475 mL deionized water. Store unused portions between 2°C and 8°C for up to one month.

Standard Preparation

1. Prior to use, reconstitute the lyophilized SARS-CoV-2 Serological IgM Panel Standard with 250 µL Assay Buffer.
2. Mix and allow the vial to sit at room temperature for 10 minutes, and then transfer the standard to an appropriately labeled polypropylene microcentrifuge tube. This will be used as the top standard C7.

   Note: The top standard concentrations may be subject to change from lot to lot (please visit **biolegend.com/en-us/legendplex** to download a lot-specific certificate of analysis).

3. Label 6 polypropylene microcentrifuge tubes as C6, C5, C4, C3, C2 and C1, respectively.
4. Add 75 µL of Assay Buffer to each of the six tubes. Prepare 1:4 dilution of the top standard by transferring 25 µL of the top standard C7 to the C6 tube and mix well. This will be the C6 standard.
5. In the same manner, perform serial 1:4 dilutions to obtain C5, C4, C3, C2 and C1 standards (**see the table below using the top standard at 500,000 pg/mL as an example**). Assay Buffer will be used as the 0 pg/mL standard

(C0).

Tube/Standard ID	Serial Dilution	Assay Buffer to add (µL)	Standard to add	Final Conc. (pg/mL)
C7	--	--	--	500,000
C6	1:4	75	25 µL of C7	125,000
C5	1:16	75	25 µL of C6	31250
C4	1:64	75	25 µL of C5	7812.5
C3	1:256	75	25 µL of C4	1953.1
C2	1:1024	75	25 µL of C3	488.2
C1	1:4096	75	25 µL of C2	122.1
C0	--	75	--	0

Sample Dilution

- A 200-fold dilution for serum and plasma samples is recommended before being tested (e.g. dilute 2 uL of sample with 18 uL ofLEGENDplexTM Assay Buffer and further serially dilute 5 uL of that mixture into 95 uL of LEGENDplexTM Assay Buffer). The user may modify this dilution factor.

- **Adding serum or plasma samples without dilution will result in low assay accuracy and possibly, clogging of the filter plate.**

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Chapter 3: ASSAY PROCEDURE

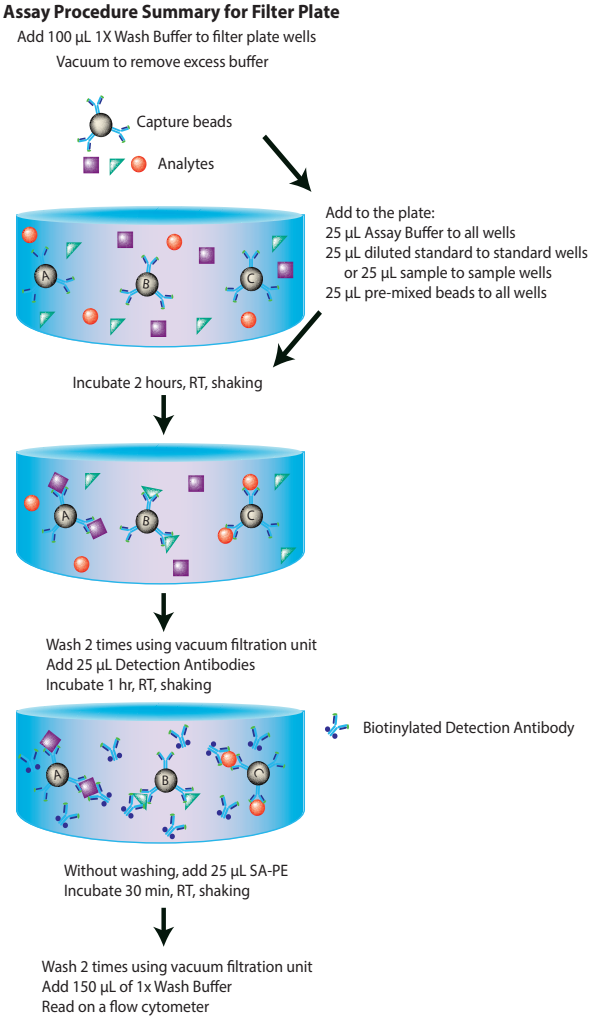
The LEGENDplex™ assay can be performed in a filter plate, or in a V-bottom plate.

- The Filter plate assay procedure is recommended due to its good sample to sample consistency, assay robustness and ease of handling. The filter plate assay procedure requires a vacuum filtration unit for washing (see **Materials to be Provided by the End-User, page 7)**. If you have performed bead-based multiplex assays before, your lab may already have the vacuum filtration unit set up.
- If the Filter plate assay procedure is not possible or if you prefer, the assay can be performed in a V-bottom plate.

Performing the Assay Using a Filter Plate

- Allow all reagents to warm to room temperature (20-25°C) before use.
- Set the filter plate on an inverted plate cover at all times during assay setup and incubation steps, so that the bottom of the plate does not touch any surface. Touching a surface may cause leakage.
- Keep the plate upright during the entire assay procedure, including the washing steps, to avoid losing beads.
- The plate should be placed in the dark or wrapped with aluminum foil for all incubation steps.
- **Standards and samples should be run in duplicate and arranged on the plate in a vertical configuration convenient for data acquisition and analysis (as shown in attached PLATE MAP, page 29). Be sure to load standards in the first two columns. If an automation device is used for reading, the orientation and reading sequence should be carefully planned.**

1. Pre-wet the plate by adding 100 µL of LEGENDplex™ 1X Wash Buffer to each well and let it sit for 1 minute at room temperature. To remove the excess volume, place the plate on the vacuum manifold and apply vacuum. Do not exceed 10” Hg of vacuum. Vacuum until wells are drained (5-10 seconds). Blot excess Wash Buffer from the bottom of the plate by pressing the plate on a stack of clean paper towels. Place the plate on top of the inverted plate cover.


Assay Procedure Summary for Filter Plate
Add 100 µL 1X Wash Buffer to filter plate wells
Vacuum to remove excess buffer
Capture beads
Analytes
Add to the plate:
25 µL Assay Buffer to all wells
25 µL diluted standard to standard wells
or 25 µL sample to sample wells
25 µL pre-mixed beads to all wells
A
B
C
Incubate 2 hours, RT, shaking
Wash 2 times using vacuum filtration unit
Add 25 µL Detection Antibodies
Incubate 1 hr, RT, shaking
Biotinylated Detection Antibody
Without washing, add 25 µL SA-PE
Incubate 30 min, RT, shaking
Wash 2 times using vacuum filtration unit
Add 150 µL of 1x Wash Buffer
Read on a flow cytometer

2. Load the plate as shown in the table below (in the order from left to right)
For measuring serum or plasma samples:

	Assay Buffer	Standard	Sample*
Standard Wells	25 µL	25 µL	--
Sample Wells	25 µL	--	25 µL

*See **Sample Dilution on page 12**

3. Vortex mixed beads bottle for 30 seconds. Add 25 µL of mixed beads to each well. The volume should be 75 µL in each well after beads addition. (Note: During addition of the beads, shake mixed beads bottle intermittently to avoid bead settling).

4. Seal the plate with a plate sealer. **To avoid plate leaking, do not apply positive pressure to the sealer when sealing the plate**. Wrap the entire plate, including the inverted plate cover, with aluminum foil. Place the plate on a plate shaker, secure it with a rubber band and shake at approximate 500 rpm for 2 hours at room temperature.

5. **Do not invert the plate**! Place the plate on the vacuum manifold and apply vacuum as before in Step 1. Add 200 µL of 1X Wash Buffer to each well. Remove Wash Buffer by vacuum filtration. Blot excess Wash Buffer from the bottom of the plate with an absorbent pad or paper towels. Repeat this washing step once more.

6. Add 25 µL of Detection Antibodies to each well.

7. Seal the plate with a fresh plate sealer. Wrap the entire plate, including the inverted plate cover, with aluminum foil. Place the plate on a plate shaker and shake at approximately 500 rpm for 1 hour at room temperature.

8. **Do not vacuum!** Add 25 µL of SA-PE to each well directly.

9. Seal the plate with a fresh plate sealer. Wrap the entire plate, including the inverted plate cover, with aluminum foil. Place the plate on a plate shaker and shake at approximate 500 rpm for 30 minutes at room temperature.

10. Repeat step 5 above.

11. Add 150 µL of 1X Wash Buffer to each well. Resuspend the beads on a plate shaker for 1 minute.

12. Read samples on a flow cytometer, preferably within the same day of the assay (Note: Prolonged sample storage can lead to reduced signal).

If the flow cytometer is equipped with an autosampler, read the plate directly using the autosampler. **Please be sure to program the autosampler**

to resuspend beads in the well immediately before taking samples. The probe height may need to be adjusted when using an autosampler.

If an autosampler is not available, the samples can be transferred from the filter plate to micro FACS (or FACS) tubes and read manually.

Performing the Assay Using a V-bottom Plate

- Allow all reagents to warm to room temperature (20-25°C) before use.
- Keep the plate upright during the entire assay procedure, except during the washing steps, to avoid losing beads.
- The plate should be placed in the dark or wrapped with aluminum foil for all incubation steps.
- Standards and samples should be run in duplicate and arranged on the plate in a vertical configuration convenient for data acquisition and analysis (as shown in attached PLATE MAP, page 29). Be sure to load standards in the first two columns. If an automation device is used for reading, the orientation and reading sequence should be carefully planned.

1. Load the plate as shown in the table below (in the order from left to right)
For measuring serum or plasma samples:

	Assay Buffer	Standard	Sample*
Standard Wells	25 µL	25 µL	--
Sample Wells	25 µL	--	25 µL

*See **Sample Dilution on page 12**

2. Vortex mixed beads for 30 seconds. Add 25 µL of mixed beads to each well. The total volume should be 75 µL in each well after beads addition. (Note: During beads addition, shake mixed beads bottle intermittently to avoid bead settling).

3. Seal the plate with a plate sealer. Cover the entire plate with aluminum foil to protect the plate from light. Shake at 800 rpm on a plate shaker for 2 hours at room temperature **(Depending on the shaker, the speed may need to be adjusted. The optimal speed is one that is high enough to keep beads in suspension during incubation, but not too high that it may cause sample to spill from the wells)**.

4. Centrifuge the plate at 1050 rpm (~250 g) for 5 minutes, using a swinging bucket rotor (G.H 3.8) with microplate adaptor (Please refer to **Materials to be Provided by the End-User, page 7).** Do not use excessive centrifugation speed as it may make it harder to resuspend beads in later steps. **Make sure the timer of the centrifuge works properly and standby to make sure the centrifuge reaches preset speed.**

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5. Immediately after centrifugation, dump the supernatant into a biohazard waste container by quickly inverting and flicking the plate **in one continuous and forceful motion**. The beads pellet may or may not be visible after dumping the supernatant. Loss of beads should not be a concern as the beads will stay in the tip of the well nicely. Blot the plate on a stack of clean paper towel and drain the remaining liquid from the well as much as possible. Be careful not to disturb the bead pellet.

   Alternatively, removal of the supernatant may be completed using a multichannel pipette set at 75 µL. Try to remove as much liquid as possible without removing any beads. Be sure to change pipette tips between each row or column.

6. Wash the plate by dispensing 200 µL of 1X Wash Buffer into each well and incubate for one minute. Repeat step 4 and 5 above. A second wash is optional, but may help reduce background.

7. Add 25 µL of Detection Antibodies to each well.

8. Seal the plate with a new plate sealer. Cover the entire plate with aluminum foil to protect the plate from light. Shake at 800 rpm on a plate shaker for 1 hour at room temperature.

9. **Do not wash the plate!** Add 25 µL of SA-PE to each well directly.

10. Seal the plate with a new plate sealer. Wrap the entire plate with aluminum foil and shake the plate on a plate shaker at approximate 800 rpm for 30 minutes at room temperature.

11. Repeat step 4, and 5.

12. (This washing step is optional but helps to reduce the background.) Wash the plate by dispensing 200 µL of 1X Wash Buffer into each well and incubate for one minute. Repeat step 4 and 5 above.

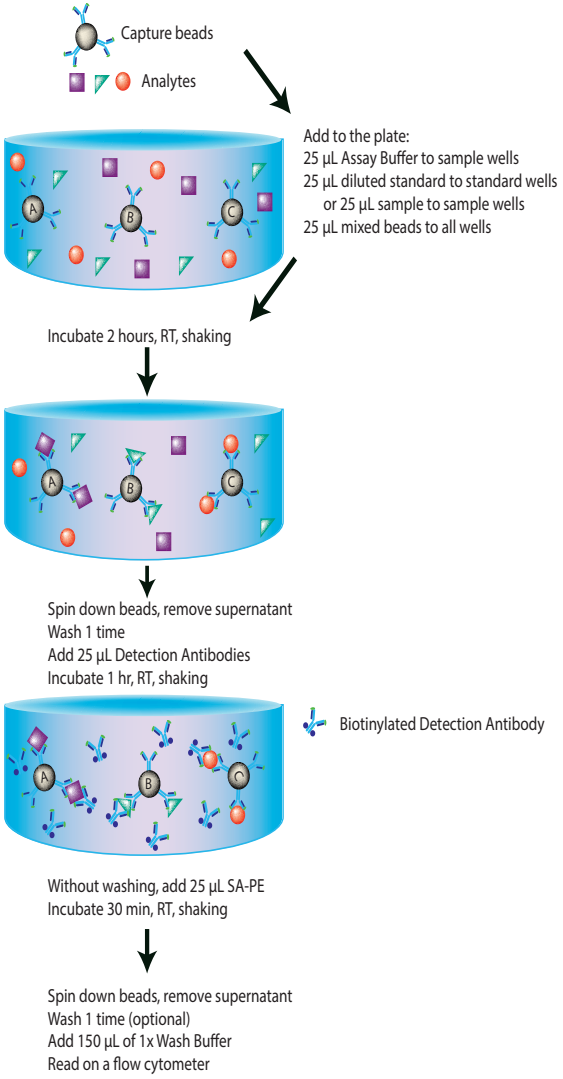
13. Add 150 µL of 1X Wash Buffer to each well. Resuspend the beads by pipetting.

14. Read samples on a flow cytometer, preferably within the same day of the assay (Note: Prolonged sample storage can lead to reduced signal).

    If the flow cytometer is equipped with an autosampler, the samples can be read directly. **Please be sure to program the autosampler to resuspend beads in the well immediately before taking samples. The probe height may need to be adjusted when using an autosampler**.

    If an autosampler is not available, the samples can be transferred from the plate to micro FACS (or FACS) tubes and read manually.

Assay Procedure Summary for V-bottom Plate



Chapter 4: FLOW CYTOMETER SETUP

In order to generate reliable data, the flow cytometer must be set up properly before data acquisition.

The setup instructions have been removed from this manual and uploaded onto our website to save paper.

To access the setup instructions, please visit: **www.biolegend.com/legendplex** and click on the **Instrument Setup** tab.

Chapter 5: DATA ACQUISITION AND ANALYSIS

Data Acquisition

1. Before reading samples, make sure that the flow cytometer is set up properly.

2. Create a new template or open an existing template (for details on how to create a cytometer-specific template, please refer to the Flow Cytometer Setup Guide).

3. Vortex each sample for 5 seconds before analysis.

4. Set the flow rate to low. Set the number of beads to be acquired to about 300 per analyte (e.g., acquire 2,100 beads for a 7-plex assay or 3,000 beads for a 13-plex assay). Do not set to acquire total events as samples may contain large amounts of debris. Instead, create a large gate to include both Beads A and Beads B (gate A+B) and set to acquire the number of events in gate A + B. This will exlude majority of the debris.

   Note: Do not acquire too few or too many beads. Too few beads acquired may result in high CVs and too many beads acquired may result in slow data analysis later.

5. Read samples.

   When reading samples, set the flow cytometer to setup mode first and wait until bead population is stabilized before recording or switching to acquisition mode.

   To simplify data analysis using the LEGENDplex™ Data Analysis Software, read samples in the same order as shown on the PLATE MAP attached at the end of the manual. For an in-plate assay, read column by column (A1, B1, C1...A2, B2, C2...).

When naming data files, try to use simple names with a consecutive numbering for easy data analysis (e.g. for standards, C0.001, C0.002, C1.003, C1.004, C2.005, C2.006, C3.007, C3.008, ... C7.015, C7.016; for samples, S1.017, S1.018, S2.019, S2.020, S3.021, S3.022…)

Store all FCS files in the same folder for each assay. If running multiple assays, create a separate folder for each assay.

6. Proceed to data analysis using LEGENDplex™ Data Analysis Software when data acquisition is completed.

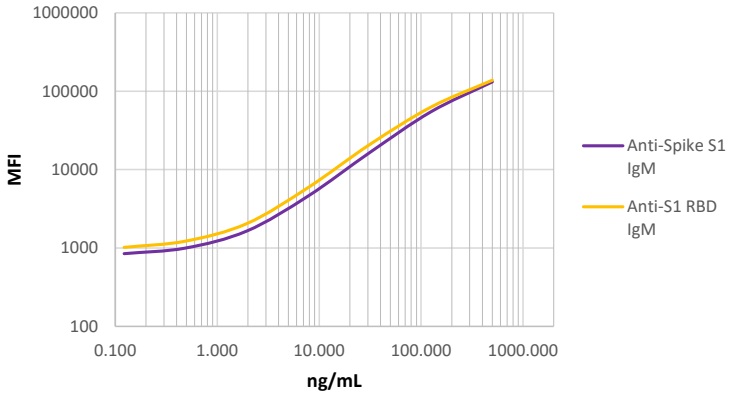
Data Analysis

- The assay FCS files should be analyzed using BioLegend's LEGENDplex™ data analysis software. The program is offered free of charge with the purchase of any LEGENDplex™ assay. For further information regarding acccess to, and use of the program please visit **biolegend.com/en-us/legendplex**.
- Concentrations reported below C2 of the standard curve should be considered inconclusive.

Chapter 6: ASSAY CHARACTERIZATION

Representative Standard Curve

This standard curve was generated using the LEGENDplex™ SARS-CoV-2 Serological IgM Panel for demonstration purposes only. A standard curve must be run with each assay.



Assay Sensitivity

The assay sensitivity or limit of detection (LOD) is the theoretical limit of detection calculated using the LEGENDplex™ Data Analysis Software by applying a 5-parameter curve fitting algorithm. The formula for assay sensitivity presented below is (Mean LOD + 2STDEV).

Analyte	Sensitivity (ng/mL) (N = 26)
Anti-Spike S1 IgM	0.312
Anti-S1 RBD IgM	0.243

Cross-Reactivity

The following anti- human Sars-CoV-2 antibodies were tested at 5000 ng/mL using the LEGENDplex™ SARS-CoV-2 Serological IgM Panel. No or negligible cross-reactivity was observed for either Anti-Spike S1 IgM and Anti-S1 RBD IgM analytes.

Anti-S1 RBD IgG
Anti-Nucleocapsid Protein IgG
Anti-S1 RBD IgA
Anti-S1 IgA
Anti-Nucleocapsid Protein IgM

Accuracy (Spike Recovery)

Serum and plasma samples were pre-diluted with Assay Buffer then spiked with target recombinant antibodies at three different levels within the assay range. The spiked samples were then assayed, and the measured concentrations were compared with the expected values.

Analyte	% of Recovery in Serum (N=8)	% of Recovery in Plasma (N=24)
Anti-Spike S1 IgM	102%	103%
Anti-S1 RBD IgM	104%	109%

Linearity of Dilution

Serum and plasma samples were pre-diluted with Assay Buffer, spiked with target recombinant antibody, then serially diluted 2, 4, 8 fold in Assay Buffer and assayed.

The measured concentrations of serially diluted samples were then compared with the concentration of the lowest dilution based on serial dilution factor used.

Analyte	% Linearity	
	Serum (N=8)	Plasma (N=24)
Anti-Spike S1 IgM	108%	108%
Anti-S1 RBD IgM	108%	104%

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Intra-Assay Precision

Two samples with different concentrations of each target antibody were analyzed in one assay with 16 replicates per sample. The intra-assay precision is shown below.

Analyte	Sample	Mean (ng/mL)	STDEV	%CV
Anti-Spike S1 IgM	Sample 1	30.01	4.00	13%
	Sample 2	7.01	0.39	6%
Anti-S1 RBD IgM	Sample 1	30.84	3.61	12%
	Sample 2	7.27	0.43	6%

Inter-Assay Precision

Two samples with different concentrations of each target antibody were analyzed in ten independent assays with four replicates per sample. The inter-assay precision is shown below.

Analyte	Sample	Mean (ng/mL)	STDEV	%CV
Anti-Spike S1 IgM	Sample 1	31.69	4.90	15%
	Sample 2	7.45	1.75	23%
Anti-S1 RBD IgM	Sample 1	32.81	4.16	13%
	Sample 2	7.91	2.13	27%

Biological Samples

The values in this section are provided for reference only. The assays provided in this kit are intended for research use only.

Human serum samples from 32 donors were tested for the endogenous levels of the target antibodies. Samples were collected before vaccination, 2 weeks after the 1st dose of vaccination and 2 weeks after the 2nd dose of vaccination and assayed with the LEGENDplex™ SARS-CoV-2 Serological IgM Panel. Pre-existing SARS-CoV-2 reactive antibodies have been reported at low levels in healthy donor cohorts[1], inconclusive data may reflect this phenomenon and can be verified with clinical information. The samples were diluted 200-fold in Assay Buffer. For samples where the MFI was below the MFI of standard C2 (0.488 ng/mL) and the concentrations that were below the limit of detection (LOD) concentration were excluded from the calculation of % detectable. Users may modify this cutoff. The concentrations after multiplying by the dilution factor are shown below (in ng/mL).

Analyte	Vaccination	Range (ng/mL)	% Detectable	Median (ng/mL)
Anti-Spike S1 IgM	Before Vax	0 - 406.8	6%	18.7
	1st Dose	30.6 - 4349.2	75%	145.2
	2nd Dose	30.5 - 3261.6	88%	216.3
Anti-S1 RBD IgM	Before Vax	0 - 331.9	16%*	26.7
	1st Dose	12.3 - 1080.4	66%	91.2
	2nd Dose	11.7 - 1091.2	75%	191.0

[1]K.W. Ng *et al., Science* 10.1126/science.abe1107 (2020)

*The increase of detactable samples for Anti-S1 RBD IgM in before vaccinated samples maybe due to the lower limit of detection value of the Anti-Spike S1 RBD IgM compared to the Anti-Spike S1 IgM assay.

TROUBLESHOOTING

Problem	Possible Cause	Solution
Bead population shifting upward or downward during acquisition	The strong PE signal from high concentration samples or standards may spill over to classification Channel (e.g., FL3/FL4/APC) and mess up the bead separation.	Optimize instrument settings using Kit Setup Beads, and make appropriate compensation between channels.
Filter plate will not vacuum or some wells clogged	Vacuum pressure is insufficient or vacuum manifold does not seal properly.	Increase vacuum pressure such that 0.2 mL buffer can be suctioned in 3-5 seconds. Clean the vacuum manifold and make sure no debris on the manifold. Press down the plate on the manifold to make a good seal.
	Samples have insoluble particles or sample is too viscous (e.g., serum and plasma samples)	Centrifuge samples just prior to assay setup and use supernatant. If high lipid content is present, remove lipid layer after centrifugation. Sample may need dilution if too viscous. If some wells are still clogged during washing, try the following: 1). Add buffer to all the wells, pipette up and down the clogged wells and vacuum again. 2). Use a piece of clean wipe, wipe the under side of the clogged wells and vacuum again. 3). Take a thin needle (e.g., insulin needle), while holding the plate upward, poke the little hole under each of the clogged wells and vacuum again. Do not poke too hard or too deep as it may damage the filter and cause leaking.
	Filter plate was used without pre-wet.	Pre-wet plate with wash buffer before running the assay.

Insufficient bead count or slow reading	Beads inappropriately prepared	Sonicate bead vials and vortex just prior to addition. Agitate mixed beads intermittently in reservoir while pipetting this into the plate.
	Samples cause beads aggregation due to particulate matter or viscosity.	Centrifuge samples just prior to assay setup and use supernatant. If high lipid content is present, remove lipid layer after centrifugation. Sample may need dilution if too viscous.
	Beads were lost during washing for in-tube assay	Make sure beads are spun down by visually check the pellet (beads are in light blue or blue color). Be very careful when removing supernatant during washing.
	Probe might be partially clogged.	Sample probe may need to be cleaned, or if needed, probe should be removed and sonicated.
Plate leaked	Vacuum pressure set too high	Adjust vacuum pressure such that 0.2 mL buffer can be suctioned in 3-5 seconds. Do not exceed 10” Hg of vacuum.
	Plate set directly on table or absorbent towels during incubations or reagent additions	Set plate on plate holder or raised edge so bottom of filter is not touching any surface.
	Liquid present on the under side of the plate after vacuum	After washing, press down plate firmly on a stack of clean paper towels to dry the underside of the plate.
	Pipette touching and damaged plate filter during additions.	Pipette to the side of wells.
High Background	Background wells were contaminated	Avoid cross-well contamination by changing tips between pipetting when performing the assay using a multichannel pipette.
	Insufficient washes	The background may be due to non-specific binding of SA-PE. Increase number of washes.
Debris (FSC/SSC) during sample acquisition	Debris or platelet may exist in sample solution.	Centrifuge samples before analyzing samples. Remove platelet as much as possible.

Variation between duplicate samples	Beads aggregation	Sonicate and vortex the Beads prior to use.
	Multichannel pipette may not be calibrated or inconsistent pipetting	Calibrate Pipette. Ensure good pipetting practice. Prime pipette before use may help.
	Plate washing was not uniform	Make sure all reagents are vacuumed out completely in all wash steps.
	Samples may contain particulate matters.	Centrifuge samples just prior to assay setup and use supernatant. If high lipid content is present, remove lipid layer after centrifugation. Sample may need dilution if too viscous.
Low or poor standard curve signal	The standard was incorrectly reconstituted, stored or diluted	Follow the protocol to reconstitute, store and dilute standard. Double check your calculation.
	Wrong or short incubation time	Ensure the time of all incubations was appropriate.
Signals too high, standard curves saturated	PMT value for FL2/PE set too high	Make sure the PMT setting for the reporter channel is appropriate
	Plate incubation time was too long	Use shorter incubation time.
Sample readings are out of range	Samples contain no or below detectable levels of analyte	Make sure the experiment to generate the samples worked. Use proper positive controls.
	Samples concentrations higher than highest standard point.	Dilute samples and analyze again.
	Standard curve was saturated at higher end of curve.	Make sure the PMT setting for the reporter channel is appropriate. Use shorter incubation time if incubation time was too long
Missed beads populations during reading, or distribution is unequal	Sample may cause some beads to aggregate.	Centrifuge samples just prior to assay setup and use supernatant. If high lipid content is present, remove lipid layer after centrifugation. Sample may need dilution if too viscous.
	Beads populations are not mixed properly	Make sure all bead populations are mixed. and in similar numbers.

Notes

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PLATE MAP (for in-plate assay)

	1	2	3	4	5	6	7	8	9	10	11	12
A	**C0**	**C4**	Sample1	Sample5	Sample 9	Sample 13	Sample 17	Sample 21	Sample 25	Sample 29	Sample 33	Sample 37
B	**C0**	**C4**	Sample1	Sample5	Sample 9	Sample 13	Sample 17	Sample 21	Sample 25	Sample 29	Sample 33	Sample 37
C	**C1**	**C5**	Sample2	Sample6	Sample 10	Sample 14	Sample 18	Sample 22	Sample 26	Sample 30	Sample 34	Sample 38
D	**C1**	**C5**	Sample2	Sample6	Sample 10	Sample 14	Sample 18	Sample 22	Sample 26	Sample 30	Sample 34	Sample 38
E	**C2**	**C6**	Sample3	Sample7	Sample 11	Sample 15	Sample 19	Sample 23	Sample 27	Sample 31	Sample 35	Sample 39
F	**C2**	**C6**	Sample3	Sample7	Sample 11	Sample 15	Sample 19	Sample 23	Sample 27	Sample 31	Sample 35	Sample 39
G	**C3**	**C7**	Sample4	Sample8	Sample 12	Sample 16	Sample 20	Sample 24	Sample 28	Sample 32	Sample 36	Sample 40
H	**C3**	**C7**	Sample4	Sample8	Sample 12	Sample 16	Sample 20	Sample 24	Sample 28	Sample 32	Sample 36	Sample 40

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