

# BioLegend®

## LEGENDplex™

**Human Kidney Function Panel 1  
Mix and Match Subpanel  
(For Urine Sample)**

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

Kidneys are vital organs that perform a variety of important functions: filtration of the waste products from blood and maintenance of the body's water, electrolyte and acid-base status. Therefore, kidney damage can be life threatening. Kidney injuries can be divided into two classes, namely acute and chronic injuries, which are both associated with other diseases such as diabetes and congestive heart failure. Drugs can also induce kidney injuries.

The detection and monitoring of kidney injury at an early stage is important, not only for disease management, but also for drug safety in clinical trials. In the past, measurement of kidney function was based on serum creatinine, blood urea nitrogen (BUN), and electrolyte enzymes. These parameters are poor and often give false positive or negative results. Novel biomarkers have promised to detect kidney damage earlier than those traditional markers. The LEGENDplex™ Human Kidney Function Panel can be used to profile kidney functional changes using multiple biomarkers. This panel can be a valuable research tool to a wide variety of scientific disciplines, from toxicity screening of drug candidates to basic and translational biomedical research.

The LEGENDplex™ Human Kidney Function Panel 1 is a multiplex bead-based assay panel, using fluorescence-encoded beads suitable for use on various flow cytometers. This panel allows simultaneous quantification of 9 human proteins, including IGFBP7, B2M ( $\beta$ 2-microglobulin), Cystatin C, Clusterin (ApoJ), EGF, Albumin, OPN (Osteopontin), TFF3 (Trefoil factor 3), and Uromodulin. This assay panel provides high detection sensitivities and broad dynamic ranges. The panel has been validated for urine samples. **For serum/plasma samples, due to the different dilution factors of the analytes, please use other panels that are specifically designed and validated for that sample type.**

The Human Kidney Function Panel 1 is designed to allow flexible customization within the panel. Please visit [www.biolegend.com/legendplex](http://www.biolegend.com/legendplex) for more information on how to mix and match within the panel.

### Principle of the Assay

BioLegend's LEGENDplex™ assays are bead-based immunoassays using the same basic principle as sandwich immunoassays.

Beads are differentiated by size and internal fluorescence intensities. Each bead set is conjugated with a specific antibody on its surface and serves as the capture beads for that particular analyte. When a selected panel of capture beads is mixed and incubated with a sample containing target analytes specific to the capture antibodies, each analyte will bind to its specific capture beads. After washing, a biotinylated detection antibody cocktail is added, and each detection antibody in the cocktail will bind to its specific analyte bound on the capture

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beads, thus forming capture bead-analyte-detection antibody sandwiches. Streptavidin-phycoerythrin (SA-PE) is subsequently added, which will bind to the biotinylated detection antibodies, providing fluorescent signal intensities in proportion to the amount of bound analytes.

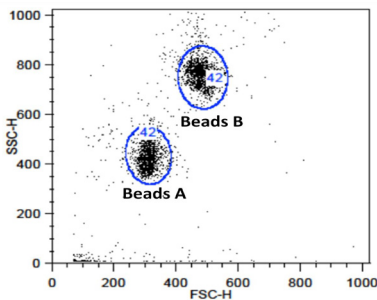
Since the beads are differentiated by size and internal fluorescence intensity on a flow cytometer, analyte-specific populations can be segregated and PE fluorescent signal quantified. The concentration of a particular analyte is determined using a standard curve generated in the same assay.

### Beads Usage

The LEGENDplex bead-based assay system uses 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 FL3, FL4, or APC channel, depending on the type of flow cytometer used. The smaller Beads (A) consist of 6 (shown in Figure 2) bead populations and 5 of them (A4, A5, A6, A7 and A8) are used for the Human Kidney Function Panel 1. The larger Beads (B) consist of 7 (shown in Figure 3) bead populations and 4 of them (B3, B4, B7 and B9) are used for this panel.

Using a total of 9 bead populations distinguished by size and internal fluorescent dye, the Human Kidney Function Panel 1 allows simultaneous detection of 9 proteins in a single sample. Each analyte is associated with a particular bead set as indicated (Figures 2-3 and Table 1).

**Figure 1. Beads Differentiated by Size**

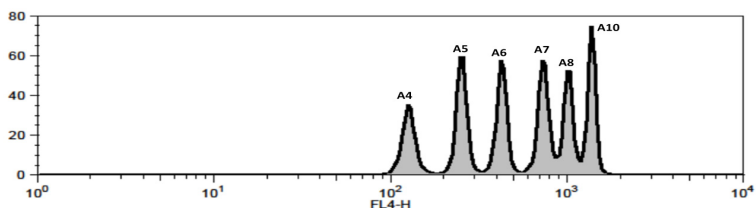


Beads A = smaller beads

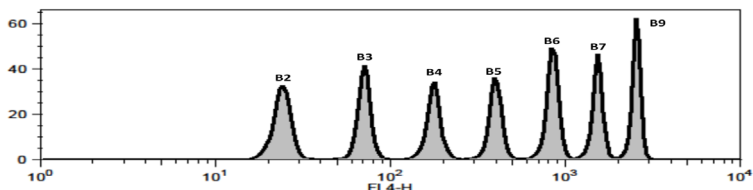
Beads B = larger beads

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**Figure 2. Beads A Classification by FL4**



**Figure 3. Beads B Classification by FL4**



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

**Table 1. Panel Targets and Bead ID\***

Target	Bead ID	Mix & Match	Top Standard Concentrations
IGFBP7	A4		The top standard concentration of each target may vary and may subject to change from lot to lot. Please refer to the lot-specific Certificate of Analysis for this information.
$\beta$ 2-microglobulin	A5		
Cystatin C	A6		
Clusterin	A7		
EGF	A8		
Albumin	B3		
OPN	B4		
TFF3	B7		
Uromodulin	B9		

\*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](http://biolegend.com/en-us/legendplex)

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## 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 reconstituted, immediately transfer contents into polypropylene vials. DO NOT STORE RECONSTITUTED STANDARDS IN GLASS VIALS.
- Upon reconstitution, leftover standard should be stored at  $\leq -70^{\circ}\text{C}$  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 #
<b>Capture Beads* (see tables below for more information)</b>	<b>varies</b>	<b>varies</b>	<b>varies</b>
LEGENDplex™ Human Kidney Function Panel 1 Detection Antibodies	1 bottle	3.3 mL	740579
LEGENDplex™ Kidney Function Panel 1 Standard	1 vial	lyophilized	740580
LEGENDplex™ Buffer Set G	1		740539
Filter Plate* or V-bottom Plate**	1 Plate		740377* or 740379**

\* For assay with filter plate. \*\* For assay with V-bottom plate.



## Human Kidney Function Panel 1 Mix and Match SubPanel

### Capture beads for Mix and Match Subpanels\*

Bead Name	Quantity	Volume	Cat#
LEGENDplex™ Human IGFBP7 Capture Bead A4, 13X	1 vial	270 µL	740472
LEGENDplex™ Human β2-microglobulin Capture Bead A5, 13X	1 vial	270 µL	740567
LEGENDplex™ Human Cystatin C Capture Bead A6, 13X	1 vial	270 µL	740568
LEGENDplex™ Human Apo J (Clusterin) Capture Bead A7, 13X	1 vial	270 µL	740569
LEGENDplex™ Human EGF Capture Bead A8, 13X	1 vial	270 µL	740570
LEGENDplex™ Human Albumin Capture Bead B3, 13X	1 vial	270 µL	740571
LEGENDplex™ Human Osteopontin Capture Bead B4, 13X	1 vial	270 µL	740572
LEGENDplex™ Human TFF3 Capture Bead B7, 13X	1 vial	270 µL	740573
LEGENDplex™ Human Uromodulin Capture Bead B9, 13X	1 vial	270 µL	740574

\* Please refer to Beads ID and Panel-Specific Target Selection table (Table 1), to see which capture beads are included in each panel.

### LEGENDplex™ Buffer Set G (Cat#: 740539)

Setup Beads: PE Beads	1 vial	1 mL	77842
Setup Beads: Raw Beads	1 vial	1.8 mL	77844
LEGENDplex™ SA-PE	1 bottle	3.3 mL	77743
LEGENDplex™ Assay Buffer	1 bottle	25 mL	77562
LEGENDplex™ Wash Buffer, 20X	1 bottle	25 mL	77564
Lyophilized Standard Resconstitution Buffer	1 vial	1 mL	75241
Plate Sealers	4 sheets		78101

No plate is included in Buffer Set G. Plate need 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)

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## **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:**

<b>Flow Cytometer</b>	<b>Reporter Channel</b>	<b>Channel Emission</b>	<b>Classification Channel</b>	<b>Channel Emission</b>	<b>Compensation needed?</b>
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/instrumentplex](http://www.biolegend.com/instrumentplex) 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 5415C, or equivalent)

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### **If the assay is performed in a filter plate:**

- A vacuum filtration unit (Millipore MultiScreen<sup>®</sup> 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 plate 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 plate 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 Urine Samples:

- Urine: Collect first-morning, mid-stream urine samples in a sterile container. To remove heavy sediment, centrifuge for 10 minutes at 1,000 x g. Remove supernatant and assay immediately or store at  $-70^{\circ}\text{C}$ . Avoid repeated freeze-thaw cycles.

***NOTE: Because there are very high levels of Albumin in saliva, care must be taken to avoid contamination of reagents and samples from end-user's saliva. Consider utilizing a face mask or shield.***

### Reagent Preparation

#### Preparation of Antibody-Immobilized Beads

Sonicate Pre-mixed Beads bottle for 1 minute in a sonicator bath and then vortex for 30 seconds prior to use. If no sonicator bath is available, increase the vortexing time to 1 minute to completely resuspend the 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  $2^{\circ}\text{C}$  and  $8^{\circ}\text{C}$  for up to one month.

### Standard Preparation

1. Prior to use, reconstitute the lyophilized Human Kidney Function Panel 1 Standard Cocktail with 250  $\mu\text{L}$  Lyophilized Standard Reconstitution Buffer

**Important: the standard must be reconstituted in the Lyophilized Standard Reconstitution Buffer in order to obtain optimal standard curves.**

2. Mix and allow the vial to sit at room temperature for 10 minutes, and then transfer the standard to an appropriately labeled polypropylene microfuge tube. This will be used as the top standard C7.
3. Label 6 polypropylene microfuge tubes as C6, C5, C4, C3, C2 and C1, respectively.

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**Note: The top standard concentrations of analytes in this panel were set at various concentrations, but may be subject to change from lot to lot (please visit [biolegend.com/en-us/legendplex](http://biolegend.com/en-us/legendplex) to download a lot-specific certificate of analysis ).**

4. Add 75  $\mu\text{L}$  of Assay Buffer to each of the six tubes. Prepare 1:4 dilution of the top standard by transferring 25  $\mu\text{L}$  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 1000 ng/mL as an example). Assay Buffer will be used as the 0 ng/mL standard (C0).

Tube/Standard ID	Serial Dilution	Assay Buffer to add ( $\mu\text{L}$ )	Standard to add	Final Conc. (ng/mL)
C7	--	--	--	1000
C6	1:4	75	25 $\mu\text{L}$ of C7	250
C5	1:16	75	25 $\mu\text{L}$ of C6	62.5
C4	1:64	75	25 $\mu\text{L}$ of C5	15.6
C3	1:256	75	25 $\mu\text{L}$ of C4	3.91
C2	1:1024	75	25 $\mu\text{L}$ of C3	0.98
C1	1:4096	75	25 $\mu\text{L}$ of C2	0.24
C0	--	75	--	0

### Sample Dilution

- Urine samples should be diluted at 100-fold with Assay Buffer as described in the table below. If further sample dilution is needed, the dilution should be done with Assay Buffer.

Sample	Dilution (1:100)
Urine	2 $\mu\text{L}$ of samples + 198 $\mu\text{L}$ of Assay Buffer

## Chapter 3: ASSAY PROCEDURE

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

- The in-filter plate assay procedure requires a vacuum filtration unit for washing (see **Materials to be Provided by the End-User, page 8**). If you have performed bead-based multiplex assays before, your lab may already have the vacuum filtration unit set up.
- If the in-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 with an absorbent pad or paper towels. Place the plate on top of the inverted plate cover.
  2. Load all the wells including standards and samples wells with 25 µL of Assay Buffer.
  3. Load 25 µL of either prepared standards to corresponding standard wells or diluted samples to sample wells.
  4. 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.

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(Note: During addition of the beads, shake mixed beads bottle intermittently to avoid bead settling).

5. 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 and shake at approximate 500 rpm for 2 hours at room temperature.
6. **Do not invert the plate!** Place the plate on the vacuum manifold and apply vacuum as before in Step 1. Add 200  $\mu\text{L}$  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.
7. Add 25  $\mu\text{L}$  of Detection Antibodies to each well.
8. 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.
9. **Do not vacuum!** Add 25  $\mu\text{L}$  of SA-PE to each well directly.
10. 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.
11. Repeat step 6 above.
12. Add 150  $\mu\text{L}$  of 1X Wash Buffer to each well. Resuspend the beads on a plate shaker for 1 minute.
13. Read samples on a flow cytometer, preferably within the same day of the assay (Note: Prolonged sample storage can lead to reduced signal).

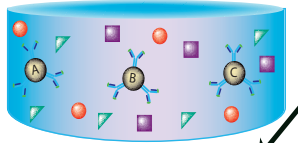
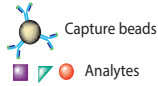
If the flow cytometer is equipped with an autosampler, read the plate directly using the autosampler. **Please be sure to program the autosampler to resuspend beads in the well immediately before taking samples. The probe height may need to be adjusted when using an autosampler.**

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

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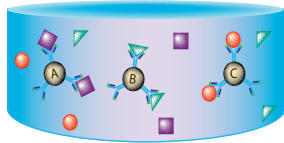
## Assay Procedure Summary for Filter Plate

Add 100  $\mu\text{L}$  1X Wash Buffer to filter plate wells  
Vacuum to remove excess buffer

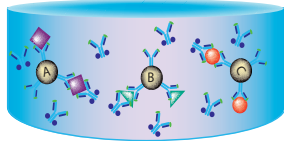



Add to the plate:  
25  $\mu\text{L}$  Assay Buffer to all wells  
25  $\mu\text{L}$  diluted standard to standard wells  
or 25  $\mu\text{L}$  sample to sample wells  
25  $\mu\text{L}$  pre-mixed beads to all wells

Incubate 2 hours, RT, shaking



Wash 2 times using vacuum filtration unit  
Add 25  $\mu\text{L}$  Detection Antibodies  
Incubate 1 hr, RT, shaking



 Biotinylated Detection Antibody

Without washing, add 25  $\mu\text{L}$  SA-PE  
Incubate 30 min, RT, shaking

Wash 2 times using vacuum filtration unit  
Add 150  $\mu\text{L}$  of 1x Wash Buffer  
Read on a flow cytometer



### 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, 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 of plate. If an automation device is used for reading, the orientation and reading sequence should be carefully planned.
1. Load all the wells including standards and samples wells with 25  $\mu$ L of Assay Buffer.
  2. Load 25  $\mu$ L of either prepared standards to corresponding standard wells or diluted samples to sample wells.
  3. Vortex mixed beads for 30 seconds. Add 25  $\mu$ L of mixed beads to each well. The total volume should be 75  $\mu$ L in each well after beads addition. (Note: During beads addition, shake mixed beads bottle intermittently to avoid bead settling).
  4. 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 so it causes spill from the wells**).
  5. Centrifuge the plate at 1050 rpm (~250 g) for 5 minutes, using a swinging bucket rotor (Ex: G.H 3.8) with microplate adaptor (Please refer to **Materials to be Provided by the End-User, page 8**). 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.**
  6. Immediately after centrifugation, dump the supernatant into a sink by quickly inverting and flicking the plate **in one continuous and forcefull motion**. Do not worry about losing beads even if the pellet is not visible. 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  $\mu$ L. Try to remove as much liquid as possible

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without removing any beads. Be sure to change pipette tips between each row or column.

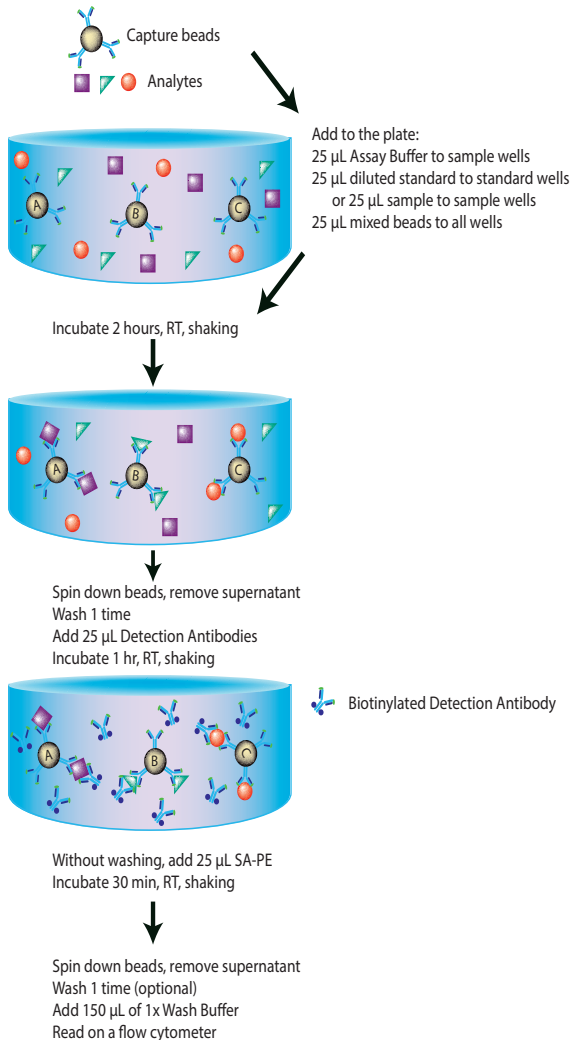
7. Wash the plate by dispensing 200  $\mu\text{L}$  of washing buffer into each well and incubate for one minute. Repeat step 5 and 6 above. A second wash is optional, but may help reduce background.
8. Add 25  $\mu\text{L}$  Detection Antibodies to each well.
9. Seal the plate with a new plate sealer. 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.
- 10. Do not wash the plate!** Add 25  $\mu\text{L}$  of SA-PE to each well directly.
11. 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.
12. Repeat step 5 and 6 above.
13. Wash the plate by dispensing 200  $\mu\text{L}$  of washing buffer into each well and incubate for one minute. Repeat step 5 and 6 above. This final wash is optional, it may help reduce background.
14. Add 150  $\mu\text{L}$  of 1X Wash Buffer to each well. Resuspend the beads by pipetting.
15. 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.

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## Assay Procedure Summary for V-bottom Plate



## Chapter 4: FLOW CYTOMETER SETUP

In order to generate accurate 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](http://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 2,700 beads for a 9-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 exclude majority of 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...).

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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.

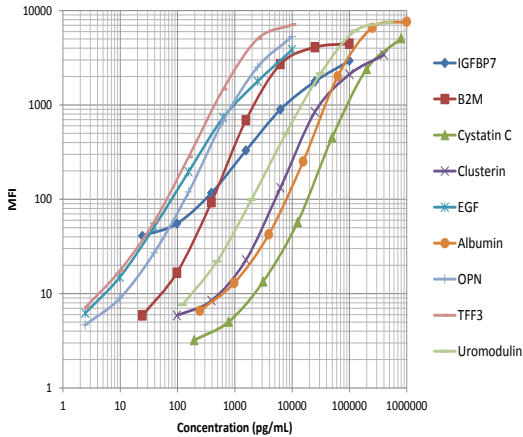
### **Data Analysis**

- 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 access to, and use of the program please visit [biolegend.com/en-us/legendplex](https://www.biolegend.com/en-us/legendplex).

## Chapter 6: ASSAY CHARACTERIZATION

### Representative Standard Curve

This standard curve was generated using the LEGENDplex™ Human Kidney Function Panel 1 for demonstration purposes only. A standard curve must be run with each assay.



### Assay Sensitivity

The assay sensitivity is the theoretical limit of detection calculated using the LEGENDplex™ Data Analysis Software by applying a 5-parameter curve fitting algorithm. Assay Sensitivity presented here is  $\leq \text{Mean LOD} + 2 \times \text{STDEV LOD}$ .

Analyte	LOD in Assay Buffer (pg/mL)
Human IGFBP7	34.0
Human B2M	18.6
Human Cystatin C	181.7
Human Clusterin	131.2
Human EGF	1.6
Human Albumin	366.5
Human OPN	3.5
Human TFF3	2.4
Human Uromodulin	61.0

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### Cross-Reactivity

The following human purified or recombinant proteins were tested individually using the LEGENDplex™ Human Kidney Function Panel 1. There was negligible cross-reactivity found for all of the proteins tested.

OPN detection reagents are specific to the full length form of this protein.

Albumin	B2M	Clusterin	Cystatin C	EGF	FABP1	FABP3
IGFBP7	IL-4	IL-6	IL-18	IL-21	IL-22	IL-12
IP-10	KIM-1	MCP-1	M-SCF	MMP-1	NGAL	OPN
Renin	RBP4	STNF RI	TFF3	TIMP-1	TIMP-2	TRANCE
Uro-modulin	VEGF 121					

### Linearity of Dilution

For testing linearity of dilution, urine samples (n=10) were first diluted 100-fold with Assay Buffer, then serially diluted 1:2, 1:4, 1:8 with Assay Buffer and assayed. The measured concentrations of serially diluted samples were then compared with the concentration of 100-fold diluted urine samples based on serial dilution factor used.

Analyte	Urine
Human IGFBP7	110%
Human B2M	105%
Human Cystatin C	103%
Human Clusterin	90%
Human EGF	108%
Human Albumin	81%
Human OPN	104%
Human TFF3	105%
Human Uromodulin	103%

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## Spike Recovery

For spike recovery, urine samples (n=8) were first diluted 100-fold with Assay Buffer, then target proteins were spiked at three different levels into samples. The spiked samples were assayed, and the measured concentrations were compared with expected values.

Analyte	Urine
Human IGFBP7	113%
Human B2M	109%
Human Cystatin C	107%
Human Clusterin	98%
Human EGF	104%
Human Albumin	102%
Human OPN	100%
Human TFF3	98%
Human Uromodulin	101%

## Intra-Assay Precision

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

Analyte	Sample	Mean (ng/mL)	STDEV	%CV
Human IGFBP7	Sample 1	0.48	0.05	10%
	Sample 2	1.71	0.21	12%
Human B2M	Sample 1	0.54	0.04	7%
	Sample 2	1.94	0.18	9%
Human Cystatin C	Sample 1	4.08	0.22	5%
	Sample 2	13.7	1.04	8%
Human Clusterin	Sample 1	2.17	0.29	13%
	Sample 2	7.22	0.53	7%
Human EGF	Sample 1	0.06	0.005	8%
	Sample 2	0.20	0.02	9%



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Human Albumin	Sample 1	6.03	0.6	10%
	Sample 2	18.1	1.54	9%
Human OPN	Sample 1	0.05	0.005	9%
	Sample 2	0.18	0.02	9%
Human TFF3	Sample 1	0.05	0.004	8%
	Sample 2	0.18	0.01	8%
Human Uromodulin	Sample 1	3.25	0.24	7%
	Sample 2	10.1	0.77	8%

### Inter-Assay Precision

Two samples with different concentrations of each target protein were analyzed in three independent assays with 4 replicates per sample. The resulting inter-assay precision is shown below.

Analyte	Sample	Mean (ng/mL)	STDEV	%CV
Human IGFBP7	Sample 1	0.34	0.11	31%
	Sample 2	1.52	0.18	12%
Human B2M	Sample 1	0.48	0.04	8%
	Sample 2	1.72	0.15	9%
Human Cystatin C	Sample 1	3.14	0.28	9%
	Sample 2	12.1	1.16	10%
Human Clusterin	Sample 1	1.38	0.26	19%
	Sample 2	5.42	0.94	17%
Human EGF	Sample 1	0.05	0.004	8%
	Sample 2	0.18	0.02	10%
Human Albumin	Sample 1	4.72	0.77	16%
	Sample 2	0.18	0.02	10%
Human OPN	Sample 1	0.04	0.01	12%
	Sample 2	0.16	0.01	8%
Human TFF3	Sample 1	0.05	0.01	12%
	Sample 2	0.16	0.01	8%
Human Uromodulin	Sample 1	2.86	0.26	8%
	Sample 2	9.09	0.77	9%

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**Biological Samples**

**Urine**

Normal human urine samples from 16 different donors were tested for endogenous levels of proteins. The range and mean concentrations (ng/mL) measured are shown below.

Analyte	Urine (n=16)	
Human IGFBP7	Range	17.9-179.5
	Mean	74.7
Human B2M	Range	19.2-298.1
	Mean	106.7
Human Cystatin C	Range	14.0-123.4
	Mean	40.6
Human Clusterin	Range	18.4-103.9
	Mean	44.9
Human EGF	Range	7.7-111.7
	Mean	36.4
Human Albumin	Range	734-9,935
	Mean	3651
Human OPN	Range	6.9-176.1
	Mean	49.5
Human TFF3	Range	5.1-77.5
	Mean	38.6
Human Uromodulin	Range	1,221-19,508
	Mean	6,533

## 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)	<p>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.</p> <p>If some wells are still clogged during washing, try the following:</p> <ol style="list-style-type: none"> <li>1). Add buffer to all the wells, pipette up and down the clogged wells and vacuum again.</li> <li>2). Use a piece of clean wipe, wipe the under side of the clogged wells and vacuum again.</li> <li>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.</li> </ol>
	Filter plate was used without pre-wet.	Pre-wet plate with wash buffer before running the assay.

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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.

## Human Kidney Function Panel 1 Mix and Match SubPanel

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.

# Human Kidney Function Panel 1 Mix and Match SubPanel

**PLATE MAP (for in-plate assay)**

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



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