BioLegend®

Enabling Legendary Discovery™

LEGENDplex™

Multi-Analyte Flow Assay Kit

Human Diabesity Panel
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

Diabesity is a term describing type 2 diabetes occurring in relation to obesity. The pathologies of these two diseases are linked by processes which revolve around insulin resistance and hyperinsulinemia. The prevalence of diabesity has increased tremendously over the past few decades due to the modern obesity epidemic. The health impact of diabesity includes long-term diabetic complications and increased risk for stroke, heart attack, and end-stage kidney disease. Specific diabetes related metabolic targets and adipokines participate in a complex feedback cycle that controls hunger and energy metabolism, and can be used to analyze the metabolic profiles of diabesity patients. Accurate quantification of these important biomarkers is essential to better understanding this global disease.

The Human Diabesity Panel is a multiplex bead-based assay panel, which contains fluorescence–encoded beads suitable for use on various flow cytometers. This panel allows for the simultaneous quantification of 11 human proteins involved in diabesity, including PAI-1, GLP-1 (Total), Insulin, C-Peptide, TNF-α, Glucagon, Leptin, Cortisol, IL-1β, IL-6 and GLP-1 (Active). This assay panel provides broader dynamic ranges than traditional ELISA methods and has been validated for use with tissue culture supernatant, serum, and plasma samples.

This assay is for research use only.

The LEGENDplex™ Human Diabesity Panel is configured as shown below depending on sample types and required dilutions:

Catalog No.	Plex Size	Targets	Recommended Sample Type	Recommended Dilution Factor
740909 740910	11-plex	PAI-1, GLP-1 (Total), Insulin, C-Peptide, TNF-α, Glucagon, Leptin, Cortisol*, IL-1β, IL-6 and GLP-1 (Active)	**Tissue Culture**	**Varies**
740911 740912	7-plex	GLP-1 (Total), C-Peptide, TNF-α, Glucagon, IL-1β, IL-6 and GLP-1 (Active)	**Serum, Plasma**	**1:2**
740913 740914	4-plex	PAI-1, Insulin, Leptin, Cortisol*	**Serum, Plasma**	**1:8**

* This panel includes a competitive assay for human cortisol. A cortisol tracer is provided in this kit which will need to be diluted 100-fold before using it in the assay. This cortisol tracer will be added to all wells before adding the beads. The competition between the cortisol tracer and the standard cortisol will form

an inverted standard curve compared to the other targets (see Representative Standard Curve on page 23). Due to the nature of the assay, the standard curve will have the highest signal at the lowest standard cortisol concentration and the signal will decrease as the standard cortisol concentration increases. Note: The cortisol tracer is for the cortisol assay ONLY and does not affect any other target.

The LEGENDplex™ Human Diabesity Panel is designed to allow flexible customization within the panel. Please visit 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, 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 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.

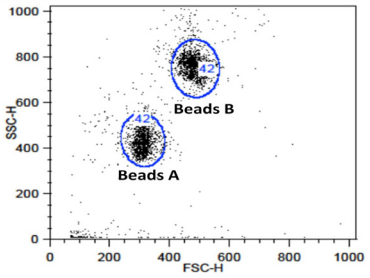
Since the beads are differentiated by size and internal fluorescence intensity on a flow cytometer, analyte-specific populations can be segregated and PE fluorescent signal quantified. The concentration of a particular analyte is determined using a standard curve generated in the same assay.

Beads Usage

The Human Diabesity Panel uses two sets of beads. Each set has a unique size that can be identified based on its forward scatter (FSC) and side scatter (SSC) profiles (Beads A and Beads B, Figure 1). The individual beads in each 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 consists of 6 bead populations (A4, A5, A7, A8, A10) and the larger Beads B consists of 7 bead populations (B3, B4, B5, B6, B7, B9) (Figure 2-3). Five populations of A beads and six populations of B beads are used in this panel.

Using a total of 11 bead populations, distinguished by size and internal fluorescent dye, the Human Diabesity Panel allows simultaneous detection of 11 proteins in a single sample. Each analyte is associated with a particular bead ID as indicated (Figures 2-3 and Table 1).

Figure 1. Beads Differentiated by Size



Beads A = smaller beads

Beads B = larger beads

Figure 2. Beads A Classification by FL4

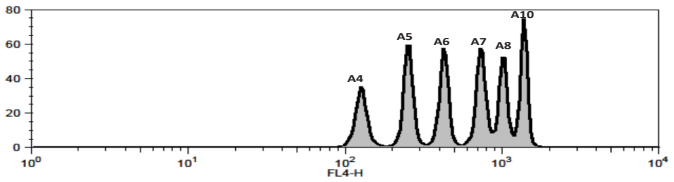
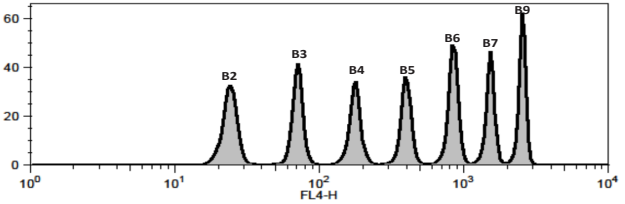


Figure 3. Beads B Classification by FL4



LEGENDplex™ Human Diabesity Panel Mix and Match Subpanel

For Beads usage in the full panel as well as sample specific subpanels, please refer to Table 1 below.

Table 1. Panel Targets and Bead ID*

Target	Bead ID	Diabesity Panel (11-plex) Cat. # 740909 or 740910	Diabesity Panel (7-plex) Cat. # 740911 or 740912	Diabesity Panel (4-plex) Cat. # 740913 or 740914	Top Standard Concentrations
PAI-1	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.
GLP-1 (Total)	A5	√	√		
Insulin	A7	√		√	
C-Peptide	A8	√	√		
TNF-α	A10	√	√		
Glucagon	B3	√	√		
Leptin	B4	√		√	
Cortisol**	B5	√		√	
IL-1β	B6	√	√		
IL-6	B7	√	√		
GLP-1 (Active)	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.**

**For the Cortisol assay, customer needs to order the LEGENDplex™ Human Cortisol Tracer, 100X separately (Cat#740917).

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.

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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**
Human Diabesity Panel Detection Antibodies	1 bottle	3.3 mL	740916
Human Diabesity Panel Standard	1 vial	Lyophilized	740915
Human Cortisol Tracer, 100X*	1 vial	50 µL	740917
LEGENDplex™ Buffer Set A	1		740368
Filter Plate** or V-bottom Plate***	1 plate		76187** or 76883***

* For kits containing cortisol assay ONLY

** 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****

Kit Components	Quantity	Volume	Cat. #
LEGENDplex™ Human PAI-1 Capture Bead A4, 13X	1 vial	270 µL	740918
LEGENDplex™ Human GLP-1 (Total) Capture Bead A5, 13X	1 vial	270 µL	740919
LEGENDplex™ Human Insulin Capture Bead A7, 13X	1 vial	270 µL	740920
LEGENDplex™ Human C-Peptide Capture Bead A8, 13X	1 vial	270 µL	740921
LEGENDplex™ Human TNF-α Capture Bead A10, 13X	1 vial	270 µL	740922
LEGENDplex™ Human Glucagon Capture Bead B3, 13X	1 vial	270 µL	740923
LEGENDplex™ Human Leptin Capture Bead B4, 13X	1 vial	270 µL	741262
LEGENDplex™ Human Cortisol Capture Bead B5, 13X	1 vial	270 µL	740925
LEGENDplex™ Human IL-1β Capture Bead B6, 13X	1 vial	270 µL	740669
LEGENDplex™ Human IL-6 Capture Bead B7, 13X	1 vial	270 µL	740927
LEGENDplex™ Human GLP-1 (Active) Capture Bead B9, 13X	1 vial	270 µL	740928

******** Please refer to **Panel Targets and Bead ID (Table 1, page 6),** to see which capture beads are included in each panel.

LEGENDplex™ Buffer Set A (Cat#: 740368)

Components	Quantity	Volume	Part #
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™ Matrix B	1 vial	Lyophi-lized	77549
LEGENDplex™ Assay Buffer	1 bottle	25 mL	77562
LEGENDplex™ Wash Buffer, 20X	1 bottle	25 mL	77564
Plate Sealers	4 sheets		78101

No plate is included in Buffer Set A. 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	Reporter 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)
- Micro FACS tubes, 1.1 mL (if the flow cytometer does not contain an autosampler)
- 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)

If the assay is performed in a filter plate (recommended):

- 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 (optional):

- 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.
- Matrix B for LEGENDplex™ kits contains components of human origin and should be handled as potentially hazardous. The raw material has been screened for infectious diseases and is negative for HIV, HBV and HCV using FDA-approved test methods.
- 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

Note: Due to the nature of certain targets in this panel, it is recommended to add protease inhibitors (especially DPPIV inhibitor) to the samples immediately after blood collection to reduce target degradation. Samples were treated with a solution of DPPIV inhibitor (Millipore-Sigma Cat#K4264) and Bovine Aprotinin (Millipore-Sigma Cat#616370) at 1 µmol/mL and 300 KIU/mL respectively in 1X PBS. The ratio for adding this protease inhibitor solution to blood is 1:50 meaning for each mL of blood collected, 20 µL of the inhibitor solution should be added. It is also recommended to assay freshly collected samples.

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). 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.

Preparation of Tissue Culture Supernatant:

- Centrifuge the sample to remove debris and assay immediately. If not possible, aliquot and store samples at ≤-20°C. Avoid multiple (>2) freeze/thaw cycles.

Reagent Preparation

Preparation of Antibody-Immobilized Beads

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.

1. Sonicate each bead vial for 1 minute in a sonicator bath and then vortex for 30 seconds to completely resuspend the beads.
2. 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.

Preparation of Matrix B (for Serum or Plasma Samples Only)

- Add 5.0 mL LEGENDplex™ Assay Buffer to the bottle containing lyophilized Matrix B. Allow at least 15 minutes for complete reconstitution. Vortex to mix well. Leftover reconstituted Matrix B should be stored at ≤-70°C for up to one month.

Preparation of 1X Cortisol Tracer (For Panels with Cortisol Assay Only)

- Prior to use, vortex Human Cortisol Tracer, 100X briefly and use a tabletop centrifuge to release any liquid trapped on the vial cap.
- Dilute Human Cortisol Tracer, 100X into 1X using LEGENDplex™ Assay Buffer. For example, if 4 mL of Cortisol Tracer is needed, then add 40 µL of Human Cortisol Tracer, 100X to 3960 µL of LEGENDplex™ Assay Buffer.

Standard Preparation

1. Prior to use, reconstitute the lyophilized Human Diabesity Standard with 250 µL LEGENDplex™ 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 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 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 10,000 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	--	--	--	10,000
C6	1:4	75	25 µL of C7	2,500
C5	1:16	75	25 µL of C6	625
C4	1:64	75	25 µL of C5	156.25
C3	1:256	75	25 µL of C4	39.01
C2	1:1024	75	25 µL of C3	9.77
C1	1:4096	75	25 µL of C2	2.44
C0	--	75	--	0

Sample Dilution

For cell culture supernatant, serum and plasma samples, follow panel specific dilution recommendations below:

- **For Human Diabesity Panel (11-plex):**

  Tissue culture samples are the recommended sample type. For tissue culture supernatant samples, the levels of analyte can vary greatly from sample to sample. To test tissue culture supernatant samples, a preliminary experiment may be required to determine the appropriate dilution factor. If further dilution is desired, dilution should be done with corresponding fresh cell culture medium or Assay Buffer as a diluent to ensure accurate measurement.

- **For Human Diabesity Panel (7-plex):**

  Serum or plasma samples must be diluted 2-fold with Assay Buffer as described in the table below.

Sample	Dilution (1:2)	Final Dilution Fold
Serum, Plasma	50 µL + 50 µL (Assay Buffer)	2

  If further dilution is desired, dilution should be done with Matrix B to ensure accurate measurement.

- **For Human Diabesity Panel (4-plex):**

  Serum or plasma samples must be diluted 8-fold with Assay Buffer as described in the table below.

Sample	Dilution (1:8)	Final Dilution Fold
Serum, Plasma	25 µL + 175 µL (Assay Buffer)	8

  If further dilution is desired, dilution should be done with Matrix B to ensure accurate measurement.

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. This procedure requires a vacuum filtration unit for washing (see **Materials to be Provided by the End-User, page 9)**. 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 37). 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.
2. **For measuring tissue culture supernatant samples in 11-plex**, load the plate as shown in the table below (in the order from left to right):

	Cell Culture Medium or Assay Buffer	Standard	Sample*
Standard Wells	25 µL	25 µL	---
Sample wells	25 µL	---	25 µL

For measuring serum or plasma samples in 7-plex and 4-plex, load the plate as shown in the table below (in the order from left to right):

	Matrix B	Assay Buffer	Standard	Sample*
Standard Wells	25 µL	---	25 µL	---
Sample wells	---	25 µL	---	25 µL

*See **Sample Dilution on page 14**

3. **For the 11-plex and 4-plex panels ONLY.** Vortex 100-fold diluted Human Diabesity Cortisol Tracer briefly. Add 25 µL of Human Diabesity Cortisol Tracer to each well.

4. Vortex mixed beads bottle for 30 seconds. Add 25 µL of mixed beads to each well. The volume should be 100 µL (for panels with cortisol assay) or 75 µL (for panels without cortisol assay) in each well after beads addition. (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 with a rubber band 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 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.

7. Add 25 µL 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 µL 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.

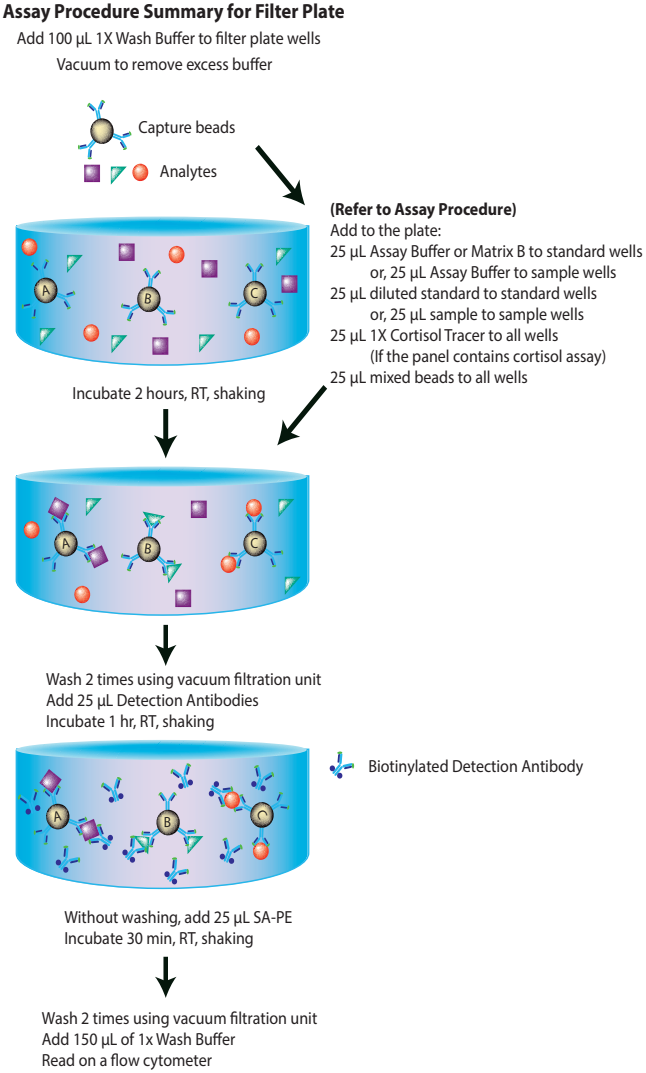
11. Repeat step 6 above.

12. Add 150 µL 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.



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 37). 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. **For measuring tissue culture supernatant samples in 11-plex,** load the plate as shown in the table below (in the order from left to right):

	Cell Culture Medium or Assay Buffer	Standard	Sample*
Standard Wells	25 µL	25 µL	---
Sample wells	25 µL	---	25 µL

For measuring serum or plasma samples in 7-plex, and 4-plex, load the plate as shown in the table below (in the order from left to right):

	Matrix B	Assay Buffer	Standard	Sample*
Standard Wells	25 µL	---	25 µL	---
Sample wells	---	25 µL	---	25 µL

*See **Sample Dilution on page 14**

2. **For the 11-plex and 4-plex panels ONLY.** Vortex 100-fold diluted Human Diabesity Cortisol Tracer briefly. Add 25 µL of Human Diabesity Cortisol Tracer to each well.

3. Vortex mixed beads for 30 seconds. Add 25 µL of mixed beads to each well. The total volume should be 100 µL (for panels with cortisol assay) or 75 µL (for panels without cortisol assay) 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 that it may cause**

sample to spill from the wells).

5. 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 9).** 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 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 100 µL (for panels with cortisol assay) or 75 µL (for panels without cortisol assay). Try to remove as much liquid as possible without removing any beads. Be sure to change pipette tips between each row or column.

7. Wash the plate by dispensing 200 µL of 1X Wash 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 µL of 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 µL 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.

13. (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.

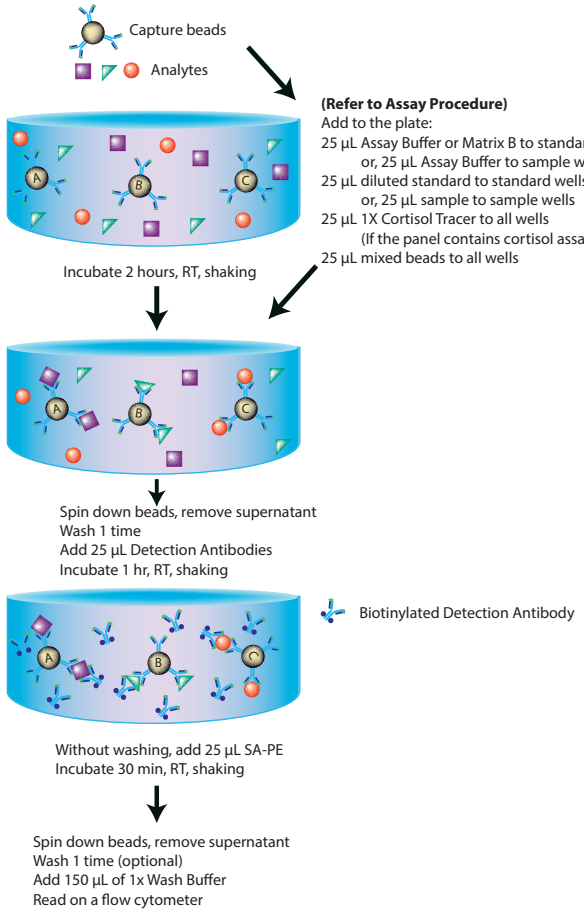
14. Add 150 µL of 1X Wash Buffer to each well. Resuspend the beads by pipetting.

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.

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 900 beads for a 3-plex assay or 3,000 beads for a 10-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 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.

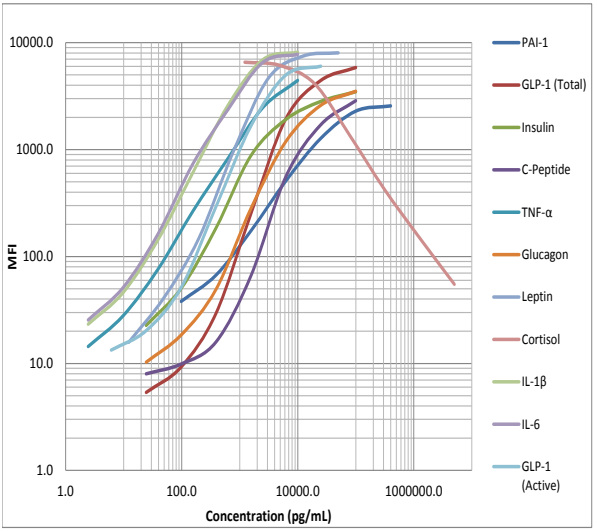
Data Analysis

- 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 access to, and use of the program please visit **biolegend.com/en-us/legendplex.**

Chapter 6: ASSAY CHARACTERIZATION

Representative Standard Curve

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



Assay Sensitivity

The assay sensitivity or minimum detectable concentration (MDC) is the theoretical limit of detection calculated using the LEGENDplex™ Data Analysis Software by applying a 5-parameter curve fitting algorithm.

Analyte	Sensitivity in Cell Culture Media (pg/mL) (N = 12)		Sensitivity in Serum (pg/mL) (N = 12)	
	Mean	STDEV	Mean	STDEV
PAI-1	63.3	20.0	43.4	13.0
GLP-1 (Total)	13.0	5.8	11.9	4.8
Insulin	17.0	6.7	16.2	5.4
C-Peptide	15.6	6.5	21.2	6.0
TNF-α	1.0	0.5	0.8	0.5
Glucagon	13.8	6.3	11.4	5.5

Leptin	6.0	2.1	6.5	1.8
Cortisol	1026.6	430.8	947.8	360.8
IL-1β	1.1	0.6	0.84	0.6
IL-6	1.2	0.7	0.8	0.6
GLP-1 (Active)	4.7	1.9	3.9	2.2

Cross-Reactivity

Human target proteins or peptides were tested individually at the indicated concentrations below using the LEGENDplex™ Human Diabesity Panel, with negligible cross-reactivity observed for non-intended targets.

Analyte	Conc. (ng/mL)	Analyte	Conc. (ng/mL)
PAI-1	4,000	Leptin	500
GLP-1 (Total)	1,000	Cortisol	50,000
Insulin	1,000	IL-1β	100
C-Peptide	1,000	IL-6	100
TNF-α	100	GLP-1 (Active)	250
Glucagon	1,000		

The following human proteins or peptides were tested at 50 ng/mL or higher. None or negligible cross-reactivity was found.

Visfatin	IGFBP-6	NGAL	RBP4	PDGF-AA	sCD40L
Ghrelin	IGFBP-2	Adiponectin	ALPL	PDGF-BB	sCD25
PPY	IGFBP-4	Adipsin	ACP5	TGF-α	SDF-1
PYY	IGFBP-3	OPN	RANKL	VEGF	sST2
Amylin	IGFALS	OPG	BMP-2	Apo A I	sRAGE
Proinsulin	Fibrinogen	MPO	DKK-1	Apo B100	CX3XL1
NPY	Antithrombin	SAA	Angio-2	Apo C	sCD130
Oxyntomodulin	Plasminogen	CRP	EPO	Apo D	IL-33
OCN	Prothrombin	VCAM-1	FGF-basic	Apo E	IL-11
IGFBP-7	Factor XIII	MMP-9	GM-CSF	sTREM-1	IL-15

Accuracy (Spike Recovery)

For spike recovery in cell culture medium, RPMI or DMEM with 10% FBS were spiked with target proteins at three different levels within the assay range. For spike recovery in serum and EDTA plasma, samples were first diluted 2-fold or 8-fold* with Assay Buffer and spiked with target proteins 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 Spike Recovery		
	Tissue Culture Supernatant (N= 2)	Serum (N = 8)	EDTA Plasma (N = 8)
PAI-1	103%	62%*	58%*
GLP-1 (Total)	91%	71%	85%
Insulin	104%	69%*	59%*
C-Peptide	99%	44%	107%
TNF-α	103%	74%	66%
Glucagon	97%	101%	112%
Leptin	97%	68%*	94%*
Cortisol	107%	142%*	160%*
IL-1β	101%	104%	126%
IL-6	99%	82%	96%
GLP-1 (Active)	94%	71%	73%

Linearity of Dilution

Tissue culture samples were spiked with target proteins with known concentrations in the assay range, then serially diluted 2, 4, and 8-fold with Assay Buffer and assayed.

Serum and EDTA plasma samples were initially diluted two-fold, or eight-fold* in Assay Buffer and then spiked with target proteins with known concentrations in the assay range. The spiked samples were then serially diluted 2, 4, and 8-fold with Matrix B and assayed. *Refer to the table on the next page.

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		
	Tissue Culture Supernatant (N= 2)	Serum (N = 4)	Plasma (N = 4)
PAI-1	98%	130%*	106%*
GLP-1 (Total)	90%	116%	113%
Insulin	93%	83%*	91%*
C-Peptide	92%	137%	135%
TNF-α	98%	140%	146%
Glucagon	86%	93%	89%
Leptin	68%	95%*	99%*
Cortisol	107%	105%*	115%*
IL-1β	97%	93%	99%
IL-6	81%	131%	136%
GLP-1 (Active)	96%	112%	118%

Intra-Assay Precision

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

Analyte	Sample	Mean (pg/mL)	STDEV	%CV
PAI-1	Sample 1	14,44.8	401.1	10%
	Sample 2	6,022.5	387.7	6%
GLP-1 (Total)	Sample 1	401.1	27.0	7%
	Sample 2	2,016.3	59.4	3%
Insulin	Sample 1	355.4	34.4	10%
	Sample 2	2,079.7	124.1	6%
C-Peptide	Sample 1	441.2	40.2	9%
	Sample 2	2,194.0	89.5	4%
TNF-α	Sample 1	47.0	4.3	9%
	Sample 2	189.2	14.9	8%
Glucagon	Sample 1	470.0	33.8	7%
	Sample 2	2,466.4	102.3	4%

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Leptin	Sample 1	180.81	10.3	6%
	Sample 2	755.8	28.4	4%
Cortisol	Sample 1	22,387.6	2,614.5	12%
	Sample 2	104,818.9	3,662.5	3%
IL-1β	Sample 1	51.1	2.6	5%
	Sample 2	177.5	7.9	4%
IL-6	Sample 1	44.1	3.0	7%
	Sample 2	169.7	11.0	6%
GLP-1 (Active)	Sample 1	112.9	10.3	9%
	Sample 2	511.6	17.2	3%

Inter-Assay Precision

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

Analyte	Sample	Mean (pg/mL)	STDEV	%CV
PAI-1	Sample 1	997.5	124.9	13%
	Sample 2	5,472.2	432.9	8%
GLP-1 (Total)	Sample 1	354.2	51.8	15%
	Sample 2	1,837.2	146.9	8%
Insulin	Sample 1	252.7	54.9	22%
	Sample 2	1,623.4	184.0	11%
C-Peptide	Sample 1	330.4	25.5	8%
	Sample 2	1,851.4	140.6	8%
TNF-α	Sample 1	34.2	5.8	17%
	Sample 2	157.7	6.9	4%
Glucagon	Sample 1	443.1	87.1	20%
	Sample 2	2,365.2	368.0	16%
Leptin	Sample 1	153.0	34.8	23%
	Sample 2	677.6	49.6	7%
Cortisol	Sample 1	16,819.8	3,758.6	22%
	Sample 2	94,405.2	10,028.6	11%

IL-1β	Sample 1	37.5	5.1	14%
	Sample 2	148.1	6.1	4%
IL-6	Sample 1	33.6	5.8	17%
	Sample 2	144.3	7.4	5%
GLP-1 (Active)	Sample 1	98.2	4.5	5%
	Sample 2	512.5	66.1	13%

Biological Samples

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

The Human Diabesity Panel was validated using human serum and EDTA plasma samples. End user can assay with other plasma types (Citrate, Heparin) but EDTA is the recommended plasma sample type. (For more information on sample collection and treatment, see page 11).

Fasting and Post-feeding serum and EDTA plasma samples were collected from donors (n=20). Donors fasted 12 hours prior to donating the fasting blood samples. Blood was collected again 60 minutes after the donors were fed. Protease inhibitor solution was added to the blood samples immediately after collection.

Serum and EDTA Plasma (Samples are paired)

Normal human serum samples (N = 17) were tested for levels of the target proteins. The concentrations (pg/mL) measured are shown below.

Analyte	Fasting		Post-feeding	
	Range	Median	Range	Median
PAI-1	60,048.7-287,989.0	90,690.2	58,536.7-170,307.4	25,886.6
GLP-1 (Total)	37.7-866.6	104.8	29.8-918.8	92.1
Insulin	198.4-1,295.9	771.7	959.0-6,562.2	2,906.0
C-Peptide	454.8-6,736.6	1,556.3	1,442.8-14,088.0	4,222.9
TNF-α	1.3-46.4	2.4	1.2-51.4	1.8
Glucagon	21.5-517.8	48.8	18.6-551.8	37.1
Leptin	1,021.6-72,686.8	12,672.7	420.6-5,5097.8	9,626.2
Cortisol	36,713.2-914,545.6	425,380.1	137,223.5-866,319.1	242,251.8

IL-1β	4.1-56.4	9.0	1.9-55.3	3.1
IL-6	0.6-18.8	2.3	0.6-17.7	1.4
GLP-1 (Active)	3.1-125.5	15.8	11.8-137.0	23.0

ND = Non-detectable

Normal human EDTA plasma samples (N=17) were tested for levels of the target proteins. The concentrations (pg/mL) measured are shown below.

Analyte	Fasting		Post-feeding	
	Range	Median	Range	Median
PAI-1	6,295.7-34,429.0	16,320.2	6,573.7-35,202.6	15,829.2
GLP-1 (Total)	107.2-1,079.0	215.7	86.4-954.5	204.1
Insulin	190.9-6,341.4	478.2	1,082.3-8,428.7	2,490.9
C-Peptide	610.2-5,085.0	1,533.1	1,505.7-13,881.7	4,773.8
TNF-α	1.3-141.9	2.7	1.2-98.8	3.4
Glucagon	29.1-1,011.0	73.7	21.5-751.1	61.9
Leptin	546.8-62,549.0	17,390.3	890.2-58,561.9	11,314.2
Cortisol	87,668.8-842,905.7	333,042.0	110,244.0-670,975.6	191,356.3
IL-1β	0.8-80.8	2.5	1.6-75.2	2.9
IL-6	0.9-25.9	1.9	0.6-26.6	2.1
GLP-1 (Active)	3.1-164.4	25.1	6.9-165.9	75.1

Diabetic Serum and EDTA Plasma (Samples are paired)

Diabetic patient serum samples (N = 3) were collected and tested for levels of the target proteins. The concentrations (pg/mL) measured are shown below.

Analyte	Fasting		Post-feeding	
	Range	Median	Range	Median
PAI-1	59,286.3-100,866.5	72,237.5	52,963.8-84,284.8	63,231.0
GLP-1 (Total)	104.8-827.1	466.0	86.4-494.6	290.5

Insulin	318.0-1,553.8	935.9	2,590.9-4,537.8	2,724.7
C-Peptide	904.6-2,523.6	1,704.5	2,374.2-4,676.7	2.902.9
TNF-α	1.4-17.3	1.7	1.4-10.9	1.5
Glucagon	29.1-591.7	310.4	ND-277.1	250.1
Leptin	9,535.8-41,061.1	35,298.2	3,922.5-36,569.6	31,995.0
Cortisol	226,180.6-328,461.9	314,881.2	180,147.5-517,312.6	342,283.0
IL-1β	ND-46.8	46.8	ND-17.5	17.5
IL-6	0.6-29.0	1.3	1.5-9.1	5.3
GLP-1 (Active)	ND-185.4	180.4	7.9-91.6	49.7

ND = Non-detectable

Diabetic patient EDTA plasma samples (N = 3) were collected and tested for levels of the target proteins. The concentrations (pg/mL) measured are shown below.

Analyte	Fasting		Post-feeding	
	Range	Median	Range	Median
PAI-1	10,423.4-34,049.8	17,173.8	13,589.8-26,267.5	17,890.2
GLP-1 (Total)	112.1-628.8	179.3	112.1-543.8	241.4
Insulin	325.5-1,212.3	768.9	1,382.5-1,802.6	1,662.6
C-Peptide	1,238.3-2,089.8	1,900.0	2,283.9-5,553.4	2,580.4
TNF-α	1.5-10.4	2.5	1.4-9.6	3.2
Glucagon	62.7-378.3	94.9	30.7-322.5	176.2
Leptin	6,355.4-36,569.6	33,020.2	4,387.4-49,362.6	34,118.3
Cortisol	226,180.6-346,944.3	230,163.4	78,281.8-456,763.9	328,461.9
IL-1β	ND-28.5	28.5	2.0-21.3	11.7
IL-6	2.1-15.0	3.9	1.4-10.8	6.1
GLP-1 (Active)	23.0-115.7	69.3	37.9-89.0	63.5

ND = Non-detectable

Cell Culture Supernatant

Human PBMC cells (1 x 10^6 cells/mL) were cultured under 10 µg/mL of PHA. Unstimulated PBMC cells were used as a control. Supernatants were collected 24 hours after stimulation, and assayed. The concentrations (pg/mL) are shown below.

Analyte	Control	PHA Stimulation
PAI-1	830.2	1,118.7
GLP-1 (Total)	ND	ND
Insulin	ND	21.7
C-Peptide	36.2	92.4
TNF-α	4.1	541.5
Glucagon	ND	ND
Leptin	ND	3.5
Cortisol	ND	ND
IL-1β	224.5	758.4
IL-6	5,464.2*	12,940.0
GLP-1 (Active)	ND	8.9

ND = Non-detectable

*Donor might have had inflammatory conditions.

Cultured media of normal human pre-adipocytes and mature adipocytes as well as diabetic adipocytes were purchased from a commercial source and tested for levels of the target proteins. The concentrations (pg/mL) are shown below.

Analyte	Pre-adipocytes	Mature Adipocytes	Diabetic Adipocytes
PAI-1	16,143.4	1,563.2	3,383.8
GLP-1 (Total)	ND	ND	ND
Insulin	ND	7,646.1	9,155.5
C-Peptide	ND	ND	ND
TNF-α	ND	ND	ND
Glucagon	ND	ND	ND
Leptin	ND	106.4	648.4
Cortisol	5,154.1	489,974.9	526,382.9
IL-1β	ND	ND	ND
IL-6	ND	ND	ND
GLP-1 (Active)	ND	ND	ND

ND = Non-detectable

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 underside 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 underside 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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