ab197422 - Human Bone Metabolism Antibody Array (41 Targets) - Quantitative

Instructions for Use

For the Quantitative measurementof 41 Human Bone Metabolism cytokines in serum, plasma, cell culture media, other body fluid, cell and tissue lysates.

This product is for research use only and is not intended for diagnostic use.

Version 6a Last Updated 04 June 2026

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1. BACKGROUND

Abcam's Human Bone Metabolism Antibody Array (41 Targets)-Quantitative ab197422 can be used for quantitative measurement of 41 Human Bone Metabolism cytokines. Suitable for serum, plasma, cell culture media, other body fluid, cell and tissue lysates.

Targets: Activin A, aFGF (FGF-1), Amphiregulin, bFGF, BMP-4, BMP-9, E-Selectin, ICAM-1 (CD54), IGF-1, IL-1 alpha (IL-1 F1), IL-1 beta (IL-1 F2), IL-6, IL-8 (CXCL8), IL-11, IL-17A, MCP-1 (CCL2), M-CSF, MIP-1 alpha (CCL3), MMP-2, MMP-9, MMP-13, Osteoactivin (GPNMB), P-Cadherin, RANK (TNFRSF11A), SDF-1 alpha (CXCL12 alpha), Sonic Hedgehog N-Terminal (Shh-N), TGF beta 1, TGF beta 2, TNF alpha, VCAM-1 (CD106), VE-Cadherin (CDH5), BMP-2, BMP-6, BMP-7, DKK-1, MMP-3, Osteoprotegerin (TNFRSF11B), Osteopontin (SPP1), PDGF-BB, TGF beta 3, TRANCE (TNFSF11).

The analytes measured by this kit are split across 2 different arrays on different slides, both of which are provided in the kit.

Quantitative antibody arrays can be used to quantitate up to 40 cytokines with as little as 50 µL of sample. Arrays are available for 400 Human and 200 mouse proteins.

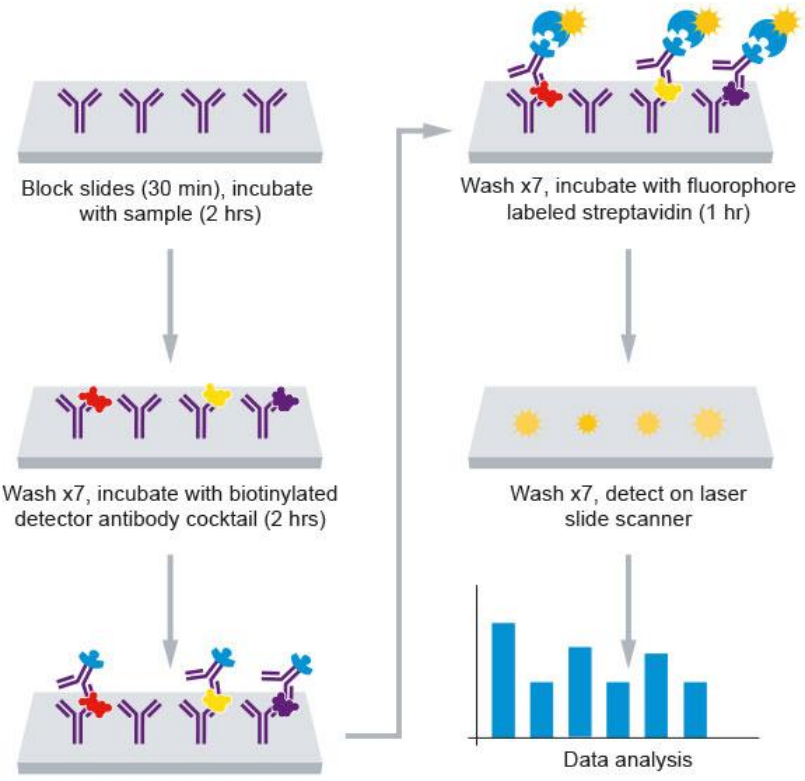
Each glass slide is spotted with 16 identical antibody arrays and is provided with a 16 well gasket to allow separate samples to be applied to each array. Each antibody is spotted in quadruplicate on each array. For reproducible quantitation, eight of the arrays are used with a cocktail of protein standards to produce a standard curve. The same 8 standard curve arrays can be used across multiple slides, allowing measurement of 22 experimental samples with 2 slides, 36 with 3 slides etc.

For high through-put, 4 slides can be nested into a tray matching a standard microplate (not supplied), allowing automated processing with a liquid handling workstation.

Array processing can be completed within one working day (see workflow diagram below) and arrays can be analyzed with a wide number of laser glass slide array / gene microarray scanners (see scanner requirements available under the Protocols section here). If you don't have a suitable scanner then we recommend our membrane

antibody arrays, which can be analyzed with any WB chemiluminescent reader. See below for a schematic protocol, the fluorophore is a dye with equivalent to excitation/ emission to Cy3.

2. ASSAY SUMMARY



3. PRECAUTIONS

Please read these instructions carefully prior to beginning the assay.

All kit components have been formulated and quality control tested to function successfully as a kit. Modifications to the kit components or procedures may result in loss of performance.

4. STORAGE AND STABILITY

Store kit at -20ºC immediately upon receipt.

Once thawed, for short-term storage, store the glass slide, cytokine standard mix, detection antibody cocktail and fluorophore labeled streptavidin at ≤ -20°C and the sample diluent, wash buffers, slide washed/dryer and adhesive device sealer at 2-8°C.

Refer to list of materials supplied for storage conditions of individual components. Observe the storage conditions for individual prepared components in the Reagent Preparation section.

5. MATERIALS SUPPLIED

Item	Quantity			Storage Condition (Before Preparation)
	8 Tests	22 Tests	50 Tests	
Slide incubation chamber and frame	2 Units	4 Units	8 Units	-20ºC
Cy3 equivalent dye-conjugated Streptavidin	2 X 5 µL	4 X 5 µL	8 X 5 µL	-20ºC
Sample Diluent	2 X 15 mL	2 X 15 mL	4 X 15 mL	-20ºC
20X Wash Buffer I	4 X 30 mL	6 X 30 mL	12 X 30 mL	-20ºC
20X Wash Buffer II	2 X 30 mL	2 X 30 mL	4 X 30 mL	-20ºC
Slide Washer/Dryer (30 mL Centrifuge Tube)	2 Units	2 Units	4 Units	-20ºC
Human Bone Metabolism Array (31 T) Biotinylated Antibody Cocktail	1 X 25 µL	2 X 25 µL	4 X 25 µL	-20ºC
Human Bone Metabolism Array (31 T) Glass Slide	1 Slide	2 Slides	4 Slides	-20ºC
Human Bone Metabolism Array (31 T) Lyophilized Cytokine Standard Mix	1 Vial (lyophilized)	2 Vials (lyophilized)	4 Vials (lyophilized)	-20ºC
Human Bone Metabolism Array (10 T) Biotinylated Antibody Cocktail	1 X 25 µL	2 X 25 µL	4 X 25 µL	-20ºC
Human Bone Metabolism Array (10 T) Glass Slide	1 Slide	2 Slides	4 Slides	-20ºC
Human Bone Metabolism Array (10 T) Lyophilized Cytokine Standard Mix	1 Vial (lyophilized)	2 Vials (lyophilized)	4 Vials (lyophilized)	-20ºC
Adhesive film	2 Units	4 Units	8 Units	-20ºC

6. MATERIALS REQUIRED, NOT SUPPLIED

These materials are not included in the kit, but will be required to successfully utilize this assay:

- Pipettors, pipet tips and other common lab consumables.
- Distilled Water.
- Orbital shaker or oscillating rocker.
- Laser scanner for fluorescence detection.
- Aluminum foil.
- 1.5 mL Polypropylene microcentrifuge tubes.

7. LIMITATIONS

- Assay kit intended for research use only. Not for use in diagnostic procedures
- Do not mix or substitute reagents or materials from other kit lots or vendors. Kits are QC tested as a set of components and performance cannot be guaranteed if utilized separately or substituted.

8. TECHNICAL HINTS

Multiple slide array kits

- Some of our quantitative antibody array kits are provided with different arrays on different slides within the kit to make up the total array. If this kit has multiple array maps in Section 12 of this protocol, then it is one of those kits. In these cases, there are different sets of reagents provided for the different arrays. The glass array slide, lyophilized protein standards and detection antibody cocktails are specific for each different array and cannot be mixed between arrays - ensure that you use the correct components together for each array. The other reagents can be used with any of the arrays.The protocol instructions below are for each individual array within the set.

Handling glass array slides

- Do not touch the surface of the slides, as the microarray slides are very sensitive. Hold the slides by the edges only.
- Handle all buffers and slides with latex free gloves.
- Handle glass array slidein clean environment.
- Because there is no barcode on the slide, transcribe the slide serial number from the slide bag to the back of the slide with a permanent marker before discarding the slide bag. Once the slide is disassembled, you might not have enough info to distinguish one slide from the other.

Incubation

- Completely cover array area with sample or buffer during incubation.
- Avoid foaming during incubation steps.
- Perform all incubation and wash steps under gentle rotation.
- Cover the incubation chamber with adhesive film during incubation, particularly when incubation is more than 2 hours or <70 µL of sample or reagent is used.
- Several incubation steps such as step 13.1 (blocking), step 13.2 (sample incubation), step 13.6 (detection antibody incubation), or step 13.9 (Fluorophore-labeled streptavidin incubation) may be done overnight at 2-8°C.
- Please make sure to cover the incubation chamber tightly to prevent evaporation.

Completely air dry the glass array slide

- Take out the glass array slidefrom the box, and let it equilibrate to room temperature inside the sealed plastic bag for 30 minutes.
- Remove slide from the plastic bag; peel off the cover film, and let it air dry at room temperature for another 1.5 hours.
- Note: Incomplete drying of slides before use may cause the formation of “comet tails”.

Using the slide scanner and data extraction software with the quantitative antibody array slides

- Using the following guidelines, along with scanner settings that reduce the background as much as possible, you should get very good results (inter-assay and intra-assay CV <15%).
- Most gene microarray laser scanners are compatible with GAL file formats, which define a grid matching the array map. You may request a GAL file from Abcam at no charge.
- Scan using Cy3-compatible (green; 532 nm) laser only.

- Define the area for signal capture for all spots as a circle with 110-120 micron diameter, ignoring any “comet tails”. In some cases, you may need to manually align circles in the super-imposed grid to match the antibody spots on the array.
- Use MEDIAN signal values, not the total or the mean. This minimizes the influence of “comet tails” and outlier data.
- Use local background correction (also using Median value).
- The laser power, photomultiplier tube (PMT) or other signal gain settings of the scanner may be used to increase spot signal intensities and/or to reduce background signals. Optimal settings will generate:
    - Strong positive control signals, where POS1>POS2>POS3
    - Low and even background signals
    - A wide range of signal intensities for antibody spots
- Adjusting the brightness and contrast settings on your data extraction software can improve the quality of the scanned image. Changing these settings only affects the image as seen on your computer monitor and has no net effect on the data that can be extracted from the image.
- For any given analyte, you should only compare fluorescence data generated using the same laser power, PMT and/or signal gain settings for all sub-arrays for which you wish to compare the results. However, you may scan all slides at multiple settings to obtain optimal signal responses for each analyte. For example, you may use data obtained with a higher PMT value for weaker signals and data obtained with a lower PMT for stronger signals.
- We recommend that if you are using the same standard curve across multiple slides, that you reserve 2 arrays from each additional slide and use them with 2 dilutions of protein standards, e.g. dilutions 3 and 6. These can be used to confirm that there is no significant difference in linearity of response between different slides.

9. REAGENT PREPARATION

Keep all reagents at RT during preparation. Reagents should only be used in their 1X working concentration.

9.1. **1X Wash Buffer I**

Dilute 20X Wash Buffer I 20-fold with distilled or deionized water to prepare the 1X Wash Buffer I.

9.2. **1X Wash Buffer II**

Dilute 20X Wash Buffer II 20-fold with distilled or deionized water to prepare the 1X Wash Buffer II.

9.3. **1X Human Bone Metabolism Array (31 T) Biotinylated Antibody Cocktail**

Reconstitute the detection antibody by adding 1.4 mL of Sample Diluent to the tube. Spin briefly.

9.4. **1X Human Bone Metabolism Array (10 T) Biotinylated Antibody Cocktail**

Reconstitute the detection antibody by adding 1.4 mL of Sample Diluent to the tube. Spin briefly.

9.5. **Cy3 equivalent dye-conjugated Streptavidin**

After briefly spinning down, add 1.4 mL of Sample Diluent to Cy3 equivalent dye-conjugated streptavidin tube. Mix gently.

9.6. **Sample Diluent**

Sample Diluent is provided Ready to Use.

10. STANDARD PREPARATION

- **Prepare serially diluted standards immediately prior to use.**
- **Always prepare a fresh set of standards for every use.**
- **There is only one vial of standard provided in the two-slide kit, which is enough to make two standard curves.**
- **Reconstitute the lyophilized standard within one hour of usage.**
- **If you need to use the standard over two different days, store only the Std1 dilution at -80°C.**

*Note: Since the starting concentration of each cytokine is different, theserial concentrations from **Standard #1** to **Standard #7** for each cytokine are varied which can be found in the section Array Map and Analyte Standard Concentrations. The same standard curve can be used across multiple slides if you are running all slides at the same time. In this case, we recommend to include a Std3 and Control in the slides without standard curve for slide normalization. If you are testing the slides separately, you should run a full standard curve on each slide.*

10.1 Reconstitute the Standard Mix (lyophilized) by adding 500 µL Sample Diluent to the tube. For best recovery, always quick-spin vial prior to opening. Dissolve the powder thoroughly by a gentle mix. Label the tube as **Standard #1**.

10.2 Label 7 further tubes as Tube #2 to Tube #8.

10.3 Add 200 µL Sample Diluent into tube # 2-7.

10.4 Pipette 100 µL**Standard #1** into tube #2 and mix gently.

10.5 Perform 5 more serial dilutions by adding 100 µL**Standard #2** to tube #3 and so on.

10.6 Add 100 µL Sample Diluent to tube #8 (**Control**). Do not add standard cytokines or samples to tube #8 (**Control**), which will be used as Negative control. For best results, include a set of standards on each slide.

Standard Dilution Preparation Table

Standard #	Sample to Dilute	Volume to Dilute (µL)	Volume of Diluent (µL)
1	See section 10.1		
2	Standard #1	100	200
3	Standard #2	100	200
4	Standard #3	100	200
5	Standard #4	100	200
6	Standard #5	100	200
7	Standard #6	100	200
8 (Control)	-	-	100



11. SAMPLE PREPARATION

- Use serum-free conditioned media if possible.
- If serum-containing conditioned media is required, it is highly recommended that complete medium be used as a control since many types of sera contains cytokines.
- We recommend the following parameters for other samples: 50 to 100 µL of original or diluted serum, plasma, cell culture media, or other body fluid, or 50-500 µg/mL of protein for cell and tissue lysates.
- If you experience high background or the readings exceed the detection range, further dilution of your sample is recommended.

12. ARRAY MAP & ANALYTE STANDARD CONCENTRATIONS

POS – Positive Control

NEG – Negative Control

BLANK – No Antibody

Human Bone Metabolism Antibody Array - Quantitative (31 Targets) (ab197423) Array Map

POS1	POS2	Activin A
aFGF	AR	bFGF
BMP-4	BMP-9	E-Selectin
ICAM-1	IGF-1	IL-1α
IL-1β	IL-6	IL-8
IL-11	IL-17	MCP-1
M-CSF	MIP-1α	MMP-2
MMP-9	MMP-13	Osteoactivin
P-Cadherin	RANK	SDF-1α
Shh N	TGFβ1	TGFβ2
TNFα	VCAM-1	VE-Cadherin

Human Bone Metabolism Antibody Array - Quantitative (10 Targets) (ab197424) Array Map

POS1	POS2
BMP-2	BMP-6
BMP-7	DKK-1
MMP-3	OPG
OPN	PDGF-BB
TGFβ3	TRANCE

Note: After reconstitution of the lyophilized cytokine standard mix, the 8-point cytokine concentration used for generating the standard curve of a given antigen is listed below. The detection sensitivity of each protein in one experiment is user dependent.

Human Bone Metabolism Array (31 T) Serial Standard Concentration (pg/ml)

(pg/ml)	Cntrl	Std7	Std6	Std5	Std4	Std3	Std2	Std1
Activin A	0	137	412	1,235	3,704	11,111	33,333	100,000
aFGF	0	274	823	2,469	7,407	22,222	66,667	200,000
AR	0	5	16	49	148	444	1,333	4,000
bFGF	0	14	41	123	370	1,111	3,333	10,000
BMP-4	0	27	82	247	741	2,222	6,667	20,000
BMP-9	0	27	82	247	741	2,222	6,667	20,000
E-Selectin	0	27	82	247	741	2,222	6,667	20,000
ICAM-1	0	55	165	494	1,481	4,444	13,333	40,000
IGF-1	0	137	412	1,235	3,704	11,111	33,333	100,000
IL-1α	0	3	8	25	74	222	667	2,000
IL-1β	0	1	3	10	30	89	267	800
IL-6	0	3	8	25	74	222	667	2,000
IL-8	0	1	2	5	15	44	133	400
IL-11	0	27	82	247	741	2,222	6,667	20,000
IL-17	0	14	41	123	370	1,111	3,333	10,000
MCP-1	0	3	8	25	74	222	667	2,000
M-CSF	0	5	16	49	148	444	1,333	4,000
MIP-1α	0	14	41	123	370	1,111	3,333	10,000
MMP-2	0	137	412	1,235	3,704	11,111	33,333	100,000
MMP-9	0	14	41	123	370	1,111	3,333	10,000
MMP-13	0	11	33	99	296	889	2,667	8,000
Osteoactivin	0	14	41	123	370	1,111	3,333	10,000
P-Cadherin	0	137	412	1,235	3,704	11,111	33,333	100,000
RANK	0	137	412	1,235	3,704	11,111	33,333	100,000
SDF-1α	0	14	41	123	370	1,111	3,333	10,000
Shh N	0	55	165	494	1,481	4,444	13,333	40,000
TGFβ1	0	55	165	494	1,481	4,444	13,333	40,000
TGFβ2	0	110	329	988	2,963	8,889	26,667	80,000
TNFα	0	3	8	25	74	222	667	2,000
VCAM-1	0	549	1,646	4,938	14,815	44,444	133,333	400,000
VE-Cadherin	0	274	823	2,469	7,407	22,222	66,667	200,000

Human Bone Metabolism Array (10 T) Serial Standard Concentration (pg/ml)

(pg/ml)	Cntrl	Std7	Std6	Std5	Std4	Std3	Std2	Std1
BMP-2	0	14	41	123	370	1,111	3,333	10,000
BMP-6	0	27	82	247	741	2,222	6,667	20,000
BMP-7	0	274	823	2,469	7,407	22,222	66,667	200,000
DKK-1	0	137	412	1,235	3,704	11,111	33,333	100,000
MMP-3	0	137	412	1,235	3,704	11,111	33,333	100,000
OPG	0	27	82	247	741	2,222	6,667	20,000
OPN	0	55	165	494	1,481	4,444	13,333	40,000
PDGF-BB	0	3	8	25	74	222	667	2,000
TGFβ3	0	27	82	247	741	2,222	6,667	20,000
TRANCE	0	274	823	2,469	7,407	22,222	66,667	200,000

13. ASSAY PROCEDURE

- **Please prepare all reagents immediately prior to use.**

13.1 Add 100 µL Sample Diluent into each well and incubate at room temperature for 30 minutes to block slides.

13.2 Decant buffer from each well. Add 100 µL standard cytokines or samples to each well. Incubate arrays at room temperature for 1-2 hours. (Longer incubation time is preferable for higher signals)

Note: We recommend using 50 to 100 µL of original or diluted serum, plasma, conditioned media, or other body fluid, or 50-500 µg/mL of protein for cell and tissue lysates.

13.3 Cover the incubation chamber with adhesive film during incubation if less than 70 µL of sample or reagent is used.

Note: This step may be done overnight at 2-8°C for best results.

13.4 Wash: Decant the samples from each well, and wash 5 times (5 minutes each) with 150 µL of 1X Wash Buffer I at room temperature with gentle shaking. Completely remove wash buffer in each wash step. Dilute 20X Wash Buffer I with H_2O.

13.5 (Optional for Cell and Tissue Lysates): Put the glass array slidewith frame into a box with 1X Wash Buffer I (cover the whole glass slide and frame with Wash Buffer I), and wash at room temperature with gentle shaking for 20 minutes.

13.6 Decant the 1X Wash Buffer I from each well, wash 2 times (5 minutes each) with 150 µL of 1X Wash Buffer II at room temperature with gentle shaking. Completely remove wash buffer in each wash step. Dilute 20X Wash Buffer II with H_2O.

Note: Incomplete removal of the wash buffer in each wash step may cause "dark spots". (i.e. Background signal is higher than that of the spot.)

13.7 Reconstitute the detection antibody as shown in the Reagent Preperation section.

13.8 Add 80 µL of the detection antibody cocktail to each well. Incubate at room temperature for 1-2 hour. (Longer incubation time is preferable for higher signals and backgrounds). Note: incubation may be done at 2-8°C for overnight.

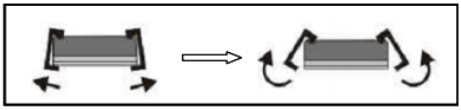
13.9 Decant the samples from each well, and wash 5 times with 150 µL of 1X Wash Buffer I and then 2 times with 150 µL of 1X Wash Buffer II at room temperature with gentle shaking. Completely remove wash buffer in each wash step.

13.10 Reconstitute the Cy3 equivalent dye-conjugated streptavidin as shown in the Reagent Preperation section.

13.11 Add 80 µL of Cy3 equivalent dye-conjugated streptavidin to each well. Cover the device with aluminum foil to avoid exposure to light orincubate in dark room. Incubate at room temperature for 1 hour.

13.12 Decant the samples from each well, and wash 5 times with 150 µL of 1X Wash Buffer I at room temperature with gentle shaking. Completelyremove wash buffer in each wash step.

13.13 Disassemble the device by pushing clips outward from the slide side. Carefully remove the slide from the gasket. (Be careful not to touch the surface of the array side.)



13.14 Place the slide in the slide Washer/Dryer (a 4-slide holder/centrifuge tube), add enough 1X Wash Buffer I (about 30 mL) to cover the whole slide, and then gently shake at room temperature for 15 minutes. Decant Wash Buffer I. Wash with 1X Wash Buffer II (about 30 mL)with gentle, and gently shake at room temperature for 5 minutes.

13.15 Remove water droplets completely by one of the following ways:

a). Put the glass array slideinto the Slide Washer/Dryer, and dry the glass array slideby centrifuge at 1,000 rpm for 3 minutes without cap.

b) Dry the glass array slidewith a compressed N_2 stream.

c) Gently apply suction with a pipette to remove water droplets.

Donot touch the array, only the sides.

13.16 Imaging: The signals can be visualized through use of a laser scanner equipped with a Cy3 wavelength such as Axon GenePix. Make sure that the signal from the well containing the highest standard concentration (**Standard #1**) receives the highest possible reading, yet remains unsaturated.

Note: In case the signal intensity for different analytes varies greatly in the same array, we recommend using multiple scans, with a higher PMT for low signal analytes, and a low PMT for high signal analytes.

13.17 Data extraction can be done with most of the microarray analysissoftware (GenePix, ScanArray Express, ArrayVision, or MicroVigene).

14. CALCULATIONS

14.1 Data extraction can be done with most commercially available microarray analysis software (GenePix, ScanArray Express or MicroVigene). Standard curves and extrapolated values will need to be calculated separately. You may use a standard curve performed on one slide to calculate values on other slides, so long as all of those slides were processed in parallel in the same batch.

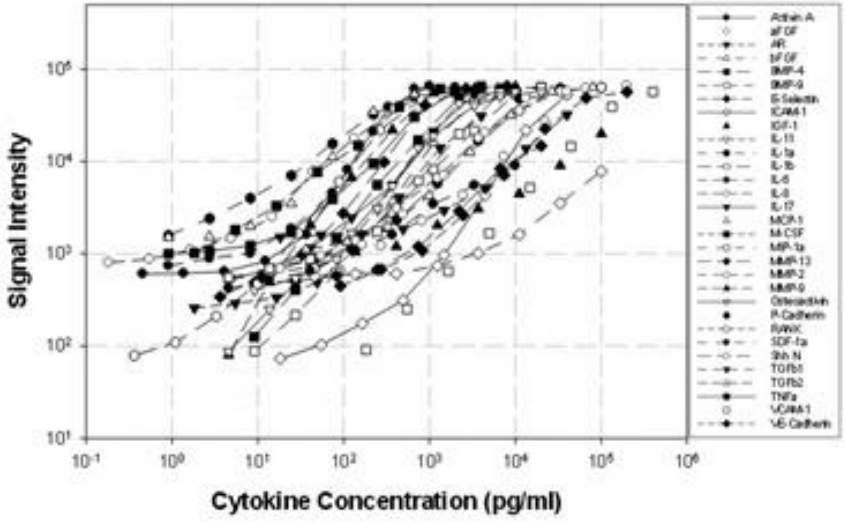
14.2 There are 2 positive control spots in each array - POS1 and POS2. We recommend that researchers select one of the arrays used for the standard curve to be the reference array, calculate the ratio of POS1/POS2 in that array and then use that ratio to calculate an adjusted average of POS1 and POS2 in each array (i.e. by multiplying POS2 by the ratio from the reference array and taking the average of the result of that multiplication and POS1). Researchers should then normalise the values in each array back to the reference array using the ratio of the adjusted average and the POS1 value for the reference array. The reason for using the ratio to calculate an adjusted average is that the POS1 signal is several times that of POS2, so using a conventional average would skew the impact of POS1 over POS2.

15. TYPICAL DATA

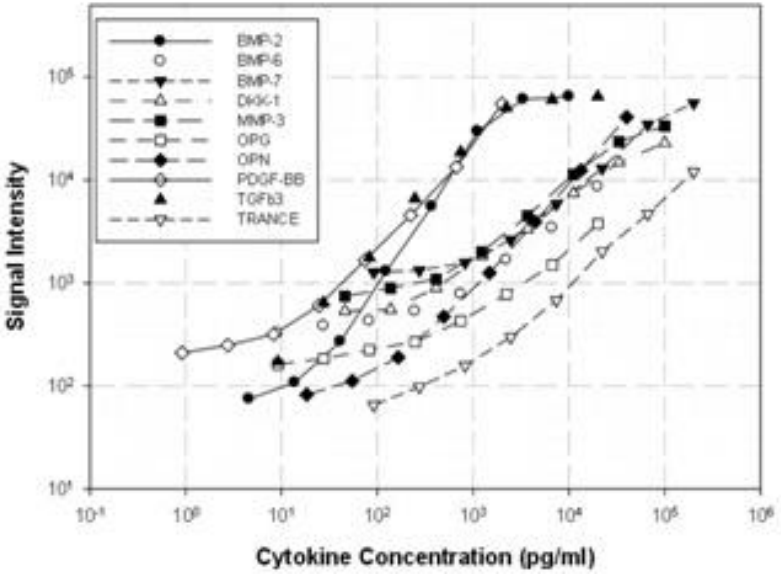
Typical results obtained with Abcam Antibody Arrays:

Standard curves

Human Bone Metabolism Array-Quantitative (31 T) (ab197423)
Standard Curves



Human Bone Metabolism Array-Quantitative (10 T) (ab197424)
Standard Curves



System recovery

The antibody pairs used in the kits have been tested to recognize their specific antigen. The spiking recovery rate of the cytokines by the kits in serum and cell culture media can be found in their individual manuals.

- Human Bone Metabolism Array (31 T) - Quantitative (ab197423)
- Human Bone Metabolism Array (10 T) - Quantitative (ab197424)

16. TROUBLESHOOTING

Problem	Cause	Recommendation
Weak Signal	Inadequate detection	Increase laser power and PMT parameters
	Inadequate reagent volumes or improper dilution	Check pipettes and ensure correct preparation
	Short incubation time	Ensure sufficient incubation time and change sample incubation step to overnight
	Too low protein concentration insample	Don't make too low dilution or concentratesample
	Improper storage of kit	Store kit as suggested temperature. Don't freeze/thaw the slide.
Uneven signal	Bubble formed during incubation	Avoid bubble formation during incubation
	Arrays are not completed covered byreagent	Completely cover arrays with solution
	Reagent evaporation	Cover the incubation chamber with adhesive film during incubation
Poor standard curve	Cross-contamination from neighboring wells	Avoid overflowing wash buffer
	Comet tail formation	Air dry the slide for at least 1 hour before usage
	Inadequate standard reconstitution or Improper dilution	Reconstitute the lyophilized standard well at room temperature before making serial dilutions. Check pipettes and ensure proper serial dilutions.

	Inadequate detection	Increase laser power that the highest standard concentration for each cytokine receives the highest possible reading yet remains unsaturated.
	Use freeze-thawed cytokine standards	Always use new cytokine standard vial for new sets of experiment. Discard any leftover.
Highbackground	Overexposure	Lower the laser power
	Dark spots	Completely remove wash buffer in each wash step.
	Insufficient wash	Increase wash time and use more wash buffer
	Dust	Work in clean environment
	Slide is allowed to dry out.	Don’t dry out slides during experiment.

17. NOTES

Technical Support

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For all technical or commercial enquiries please go to:
https://www.abcam.com/en-us/contact-us
https://www.abcam.cn/contact-us (China)
https://www.abcam.co.jp/contact-us (Japan)