

Version 2 Last updated 29 October 2021

# ab277722 Human Met SimpleStep ELISA<sup>®</sup> Kit (c-Met)

For the quantitative measurement of Met in human serum, plasma, cell culture supernatant, cell and tissue extract.

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

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## 1. Overview

Met *in vitro* SimpleStep ELISA® (Enzyme-Linked Immunosorbent Assay) kit is designed for the quantitative measurement of Met protein in human serum, plasma, cell culture supernatant, cell and tissue extract.

The SimpleStep ELISA® employs an affinity tag labeled capture antibody and a reporter conjugated detector antibody which immunocapture the sample analyte in solution. This entire complex (capture antibody/analyte/detector antibody) is in turn immobilized via immunoaffinity of an anti-tag antibody coating the well. To perform the assay, samples or standards are added to the wells, followed by the antibody mix. After incubation, the wells are washed to remove unbound material. TMB Development Solution is added and during incubation is catalyzed by HRP, generating blue coloration. This reaction is then stopped by addition of Stop Solution completing any color change from blue to yellow. Signal is generated proportionally to the amount of bound analyte and the intensity is measured at 450 nm. Optionally, instead of the endpoint reading, development of TMB can be recorded kinetically at 600 nm.

Met, also known as Hepatocyte Growth Factor Receptor (HGFR) or Proto-Oncogene c-Met (c-Met) is a receptor tyrosine kinase that transduces signals from the extracellular matrix into the cytoplasm by binding to hepatocyte growth factor ligand. Met regulates many physiological processes including proliferation, scattering, morphogenesis and survival. Ligand binding at the cell surface induces autophosphorylation of Met on its intracellular domain that provides docking sites for downstream signaling molecules. The recruitment of these downstream effectors by Met leads to the activation of several signaling cascades including the RAS-ERK, PI3 kinase-AKT, or PLC gamma-PKC. During embryonic development, Met signaling plays a role in gastrulation, development and migration of muscles and neuronal precursors, angiogenesis and kidney formation. In adults, Met participates in wound healing as well as organ regeneration and tissue remodeling. Met promotes also differentiation and proliferation of hematopoietic cells. Human and mouse Met are 90% identical on their amino acids sequences.

## 2. Protocol Summary

Prepare all reagents, samples, and standards as instructed



Add 50  $\mu$ L standard or sample to appropriate wells



Add 50  $\mu$ L Antibody Cocktail to all wells



Incubate at room temperature for 1 hour



Aspirate and wash each well three times with 350  $\mu$ L 1X Wash Buffer  
PT



Add 100  $\mu$ L TMB Development Solution to each well and incubate  
for 10 minutes.



Add 100  $\mu$ L Stop Solution and read OD at 450 nm

### 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.
- We understand that, occasionally, experimental protocols might need to be modified to meet unique experimental circumstances. However, we cannot guarantee the performance of the product outside the conditions detailed in this protocol booklet.
- Reagents should be treated as possible mutagens and should be handled with care and disposed of properly. Please review the Safety Datasheet (SDS) provided with the product for information on the specific components.
- Observe good laboratory practices. Gloves, lab coat, and protective eyewear should always be worn. Never pipet by mouth. Do not eat, drink or smoke in the laboratory areas.
- All biological materials should be treated as potentially hazardous and handled as such. They should be disposed of in accordance with established safety procedures.

### 4. Storage and Stability

**Store kit at +4°C immediately upon receipt. Kit has a storage time of 1 year from receipt, providing components have not been reconstituted.**

Refer to list of materials supplied for storage conditions of individual components.

## 5. 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.

## 6. Materials Supplied

Item	Quantity	Storage Condition
Human Met Capture Antibody 10X	600 µL	+4°C
Human Met Detector Antibody 10X	600 µL	+4°C
Human Met Lyophilized Recombinant Protein	2 Vials	+4°C
Antibody Diluent 4BI	6 mL	+4°C
Cell Extraction Buffer PTR 5X	10 mL	+4°C
Sample Diluent NS	50 mL	+4°C
Wash Buffer PT 10X	20 mL	+4°C
TMB Development Solution	12 mL	+4°C
Stop Solution	12 mL	+4°C
SimpleStep Pre-Coated 96-Well Microplate	96 Wells	+4°C
Plate Seal	1	+4°C

## 7. Materials Required, Not Supplied

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

- Microplate reader capable of measuring absorbance at 450 or 600 nm.
- Method for determining protein concentration (BCA assay recommended).
- Deionized water.
- Multi- and single-channel pipettes.
- Tubes for standard dilution.
- Plate shaker for all incubation steps.
- Optional: Phenylmethylsulfonyl Fluoride (PMSF) (or other protease inhibitors).

## 8. Technical Hints

- Samples generating values higher than the highest standard should be further diluted in the appropriate sample dilution buffers.
- Avoid foaming or bubbles when mixing or reconstituting components.
- Avoid cross contamination of samples or reagents by changing tips between sample, standard and reagent additions.
- Ensure plates are properly sealed or covered during incubation steps.
- Complete removal of all solutions and buffers during wash steps is necessary to minimize background.
- As a guide, typical ranges of sample concentration for commonly used sample types are shown below in Sample Preparation (section 11).
- All samples should be mixed thoroughly and gently.
- Avoid multiple freeze/thaw of samples.
- Incubate ELISA plates on a plate shaker during all incubation steps.
- When generating positive control samples, it is advisable to change pipette tips after each step.

- To avoid high background always add samples or standards to the well before the addition of the antibody cocktail.
- This kit is sold based on number of tests. A 'test' simply refers to a single assay well. The number of wells that contain sample, control or standard will vary by product. Review the protocol completely to confirm this kit meets your requirements. Please contact our Technical Support staff with any questions.



## 9. Reagent Preparation

- Equilibrate all reagents to room temperature (18-25°C) prior to use. The kit contains enough reagents for 96 wells. The sample volumes below are sufficient for 48 wells (6 x 8-well strips); adjust volumes as needed for the number of strips in your experiment.
- Prepare only as much reagent as is needed on the day of the experiment. Capture and Detector Antibodies have only been tested for stability in the provided 10X formulations.

### 9.1 1X Cell Extraction Buffer PTR (For cell and tissue extracts only):

Prepare 1X Cell Extraction Buffer PTR by diluting Cell Extraction Buffer PTR 5X to 1X with deionized water. To make 10 mL 1X Cell Extraction Buffer PTR combine 8 mL deionized water and 2 mL Cell Extraction Buffer PTR 5X. Mix thoroughly and gently. If required protease inhibitors can be added.

### 9.2 1X Wash Buffer PT:

Prepare 1X Wash Buffer PT by diluting Wash Buffer PT 10X with deionized water. To make 50 mL 1X Wash Buffer PT combine 5 mL Wash Buffer PT 10X with 45 mL deionized water. Mix thoroughly and gently.

### 9.3 Antibody Cocktail:

Prepare Antibody Cocktail by diluting the capture and detector antibodies in Antibody Diluent 4BI. To make 3 mL of the Antibody Cocktail combine 300  $\mu$ L 10X Capture Antibody and 300  $\mu$ L 10X Detector Antibody with 2.4 mL Antibody Diluent 4BI. Mix thoroughly and gently.

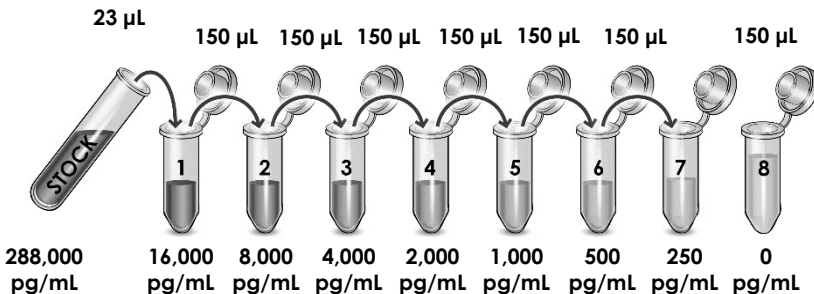
## 10. Standard Preparation

- Always prepare a fresh set of standards for every use.
- Discard working standard dilutions after use as they do not store well.
- The following section describes the preparation of a standard curve for duplicate measurements (recommended).

**IMPORTANT:** If the protein standard vial has a volume identified on the label, reconstitute the Met by adding that volume of Diluent indicated on the label. Alternatively, if the vial has a mass identified, reconstitute the Met standard by adding 500  $\mu\text{L}$  Diluent. Hold at room temperature for 10 minutes and mix gently. This is the 288,000  $\text{pg/mL}$  **Stock Standard** Solution.

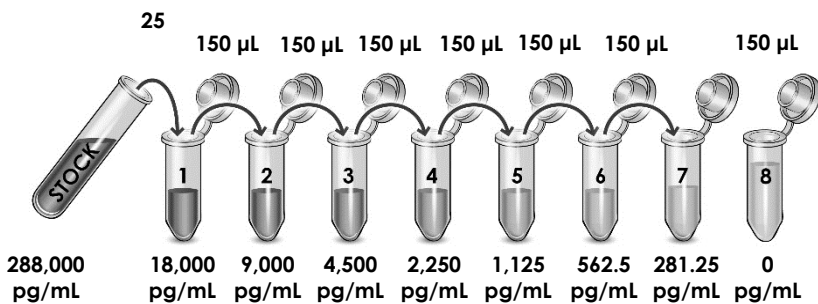
10.1 For **serum, plasma and cell culture supernatant samples** follow these instructions:

- 10.1.1 Reconstitute the Met standard sample by adding Sample Diluent NS.
- 10.1.2 Label eight tubes, Standards 1– 8.
- 10.1.3 Add 391  $\mu\text{L}$  of Sample Diluent NS into tube number 1 and 150  $\mu\text{L}$  of Sample Diluent NS into numbers 2-8.
- 10.1.4 Use the Stock Standard to prepare the following dilution series. Standard #8 contains no protein and is the Blank control:



**10.2** For **cell and tissue extract samples** follow these instructions:

- 10.2.1 Reconstitute the Met standard sample by adding 1X Cell Extraction Buffer PTR.
- 10.2.2 Label eight tubes, Standards 1– 8.
- 10.2.3 Add 375  $\mu$ L of 1X Cell Extraction Buffer PTR into tube number 1 and 150  $\mu$ L of 1X Cell Extraction Buffer PTR into numbers 2-8.
- 10.2.4 Use the Stock Standard to prepare the following dilution series. Standard #8 contains no protein and is the Blank control:



## 11. Sample Preparation

Typical Sample Dynamic Range	
Sample Type	Range
Serum	0.3 - 10%
Plasma - Citrate	0.3 - 10%
Plasma - EDTA	0.3 - 10%
Plasma - Heparin	0.3 - 10%
Cell Culture Media*	≤25%
A431 Cell Extract	8 - 250 µg/mL

\*Based on spiked sample

### 11.1 Plasma:

Collect plasma using citrate, EDTA or heparin. Centrifuge samples at 2,000 x g for 10 minutes. Dilute samples at least 1:10 into Sample Diluent NS and assay. Store un-diluted plasma samples at -20°C or below for up to 3 months. Avoid repeated freeze-thaw cycles.

### 11.2 Serum:

Samples should be collected into a serum separator tube. After clot formation, centrifuge samples at 2,000 x g for 10 minutes and collect serum. Dilute samples at least 1:10 into Sample Diluent NS and assay. Store un-diluted serum at -20°C or below. Avoid repeated freeze-thaw cycles.

### 11.3 Cell Culture Supernatants:

This kit reacts with bovine c-Met present in bovine serum. To avoid the background signal caused by the bovine c-Met, it is recommended to culture cells in media without serum supplements. Centrifuge cell culture media at 2,000 x g for 10 minutes to remove debris. Collect supernatants. Dilute samples at least 1:4 into Sample Diluent NS and assay. Store un-diluted samples at -20°C or below. Avoid repeated freeze-thaw cycles.

### 11.4 Preparation of extracts from cell pellets:

11.4.1 Collect non-adherent cells by centrifugation or scrape to collect adherent cells from the culture flask. Typical

centrifugation conditions for cells are 500 x g for 5 minutes at 4°C.

- 11.4.2 Rinse cells twice with PBS.
- 11.4.3 Solubilize pellet at  $2 \times 10^7$  cell/mL in chilled 1X Cell Extraction Buffer PTR.
- 11.4.4 Incubate on ice for 20 minutes.
- 11.4.5 Centrifuge at 18,000 x g for 20 minutes at 4°C.
- 11.4.6 Transfer the supernatants into clean tubes and discard the pellets.
- 11.4.7 Assay samples immediately or aliquot and store at -80°C. The sample protein concentration in the extract may be quantified using a protein assay.
- 11.4.8 Dilute samples to desired concentration in 1X Cell Extraction Buffer PTR.

### **11.5 Preparation of extracts from adherent cells by direct lysis (alternative protocol):**

- 11.5.1 Remove growth media and rinse adherent cells 2 times in PBS.
- 11.5.2 Solubilize the cells by addition of chilled 1X Cell Extraction Buffer PTR directly to the plate (use 750  $\mu$ L - 1.5 mL 1X Cell Extraction Buffer PTR per confluent 15 cm diameter plate).
- 11.5.3 Scrape the cells into a microfuge tube and incubate the lysate on ice for 15 minutes.
- 11.5.4 Centrifuge at 18,000 x g for 20 minutes at 4°C.
- 11.5.5 Transfer the supernatants into clean tubes and discard the pellets.
- 11.5.6 Assay samples immediately or aliquot and store at -80°C. The sample protein concentration in the extract may be quantified using a protein assay.
- 11.5.7 Dilute samples to desired concentration in 1X Cell Extraction Buffer PTR.

### **11.6 Preparation of extracts from tissue homogenates:**

- 11.6.1 Tissue lysates are typically prepared by homogenization of tissue that is first minced and thoroughly rinsed in PBS to remove blood (dounce homogenizer recommended).
- 11.6.2 Homogenize 100 to 200 mg of wet tissue in 500  $\mu$ L – 1 mL of chilled 1X Cell Extraction Buffer PTR. For lower amounts of tissue adjust volumes accordingly.
- 11.6.3 Incubate on ice for 20 minutes.
- 11.6.4 Centrifuge at 18,000 x g for 20 minutes at 4°C.

- 11.6.5 Transfer the supernatants into clean tubes and discard the pellets.
- 11.6.6 Assay samples immediately or aliquot and store at  $-80^{\circ}\text{C}$ . The sample protein concentration in the extract may be quantified using a protein assay.
- 11.6.7 Dilute samples to desired concentration in 1X Cell Extraction Buffer PTR.

## 12. Plate Preparation

- The 96 well plate strips included with this kit are supplied ready to use. It is not necessary to rinse the plate prior to adding reagents.
- Unused plate strips should be immediately returned to the foil pouch containing the desiccant pack, resealed and stored at 4°C.
- For each assay performed, a minimum of two wells must be used as the zero control.
- For statistical reasons, we recommend each sample should be assayed with a minimum of two replicates (duplicates).
- Differences in well absorbance or “edge effects” have not been observed with this assay.

## 13. Assay Procedure

- Equilibrate all materials and prepared reagents to room temperature prior to use.
  - We recommend that you assay all standards, controls and samples in duplicate.
- 13.1** Prepare all reagents, working standards, and samples as directed in the previous sections.
  - 13.2** Remove excess microplate strips from the plate frame, return them to the foil pouch containing the desiccant pack, reseal and return to 4°C storage.
  - 13.3** Add 50 µL of all sample or standard to appropriate wells.
  - 13.4** Add 50 µL of the Antibody Cocktail to each well.
  - 13.5** Seal the plate and incubate for 1 hour at room temperature on a plate shaker set to 400 rpm.
  - 13.6** Wash each well with 3 x 350 µL 1X Wash Buffer PT. Wash by aspirating or decanting from wells then dispensing 350 µL 1X Wash Buffer PT into each well. Wash Buffer PT should remain in wells for at least 10 seconds. Complete removal of liquid at each step is essential for good performance. After the last wash invert the plate and tap gently against clean paper towels to remove excess liquid.
  - 13.7** Add 100 µL of TMB Development Solution to each well and incubate for 10 minutes in the dark on a plate shaker set to 400 rpm.

*Given variability in laboratory environmental conditions, optimal incubation time may vary between 5 and 20 minutes.*

*Note: The addition of Stop Solution will change the color from blue to yellow and enhance the signal intensity about 3X. To avoid signal saturation, proceed to the next step before the high concentration of the standard reaches a blue color of O.D.600 equal to 1.0.*
  - 13.8** Add 100 µL of Stop Solution to each well. Shake plate on a plate shaker for 1 minute to mix. Record the OD at 450 nm. This is an endpoint reading.
  - 13.9** Alternative to 13.7 – 13.8: Instead of the endpoint reading at 450 nm, record the development of TMB Substrate kinetically. Immediately after addition of TMB Development Solution begin recording the blue color development with elapsed



time in the microplate reader prepared with the following settings:

<b>Mode</b>	<b>Kinetic</b>
Wavelength:	600 nm
Time:	up to 20 min
Interval:	20 sec - 1 min
Shaking:	Shake between readings

Δ **Note:** that an endpoint reading can also be recorded at the completion of the kinetic read by adding 100 µL Stop Solution to each well and recording the OD at 450 nm.

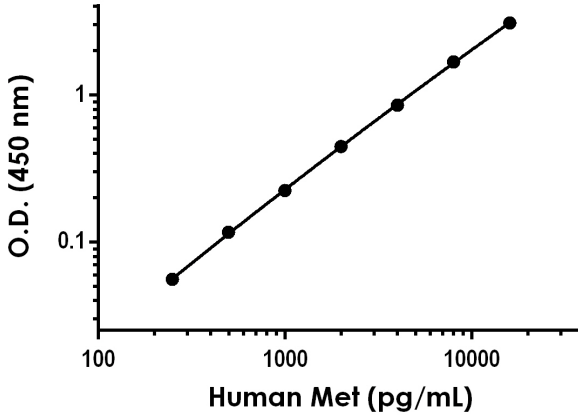
**13.10** Analyze the data as described below.

## 14. Calculations

- 14.1 Calculate the average absorbance value for the blank control (zero) standards. Subtract the average blank control standard absorbance value from all other absorbance values.
- 14.2 **Create a standard curve** by plotting the average blank control subtracted absorbance value for each standard concentration (y-axis) against the target protein concentration (x-axis) of the standard. Use graphing software to draw the best smooth curve through these points to construct the standard curve.
  - Δ **Note:** Most microplate reader software or graphing software will plot these values and fit a curve to the data. A four parameter curve fit (4PL) is often the best choice; however, other algorithms (e.g. linear, semi-log, log/log, 4 parameter logistic) can also be tested to determine if it provides a better curve fit to the standard values.
- 14.3 Determine the concentration of the target protein in the sample by interpolating the blank control subtracted **absorbance values against the standard curve**. Multiply the resulting value by the appropriate sample dilution factor, if used, to obtain the concentration of target protein in the sample.
- 14.4 Samples generating absorbance values greater than that of the highest standard should be further diluted and reanalyzed. Similarly, samples which measure at an absorbance values less than that of the lowest standard should be retested in a less dilute form.

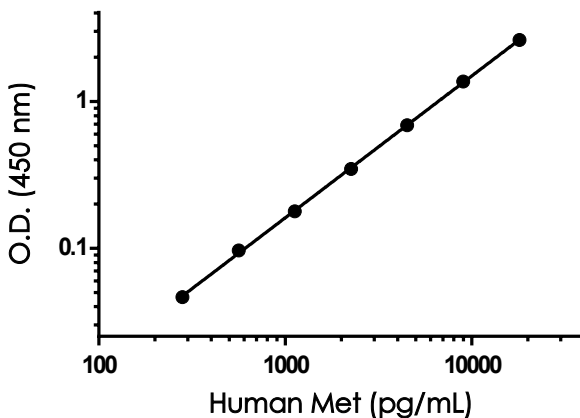
## 15. Typical Data

Typical standard curve – data provided for demonstration purposes only. A new standard curve must be generated for each assay performed.



Standard Curve Measurements			
Concentration (pg/mL)	O.D 450 nm		Mean O.D
	1	2	
0.00	0.060	0.059	0.060
250	0.114	0.117	0.116
500	0.178	0.174	0.176
1,000	0.281	0.287	0.284
2,000	0.510	0.504	0.507
4,000	0.930	0.901	0.915
8,000	1.785	1.696	1.740
16,000	3.196	3.104	3.150

**Figure 1.** Example of human Met standard curve in Sample Diluent NS. The Met standard curve was prepared as described in Section 10. Raw data values are shown in the table. Background-subtracted data values (mean +/- SD) are graphed.



Standard Curve Measurements			
Concentration (pg/mL)	O.D 450 nm		Mean O.D
	1	2	
0.00	0.054	0.053	0.053
281.25	0.102	0.099	0.100
562.5	0.149	0.150	0.150
1,125	0.232	0.232	0.232
2,250	0.396	0.407	0.401
4,500	0.724	0.757	0.741
9,000	1.416	1.425	1.420
18,000	2.673	2.681	2.677

**Figure 2.** Example of human Met standard curve in 1X Cell Extraction Buffer PTR. The Met standard curve was prepared as described in Section 10. Raw data values are shown in the table. Background-subtracted data values (mean +/- SD) are graphed.

## 16. Typical Sample Values

### SENSITIVITY –

The MDD was determined by calculating the mean of zero standard replicates and adding 2 standard deviations then extrapolating the corresponding concentration.

Sample Diluent Buffer	n=	Minimal Detectable Dose
Sample Diluent NS	16	81.6 pg/mL
1X Cell Extraction Buffer PTR	15	67.4 pg/mL

### RECOVERY –

Three concentrations of Met recombinant protein were spiked in duplicate to the indicated biological matrix to evaluate signal recovery in the working range of the assay.

Sample Type	Average % Recovery	Range (%)
3% Serum	90	78-111
5% Plasma - Citrate	94	84 - 113
3% Plasma - EDTA	103	99 - 108
5% Plasma - Heparin	104	91 - 113
25% Cell Culture Media*	104	99 - 110
100 µg/mL A431 Cell Extract	89	77 - 106

\*Media is RPMI 1640 containing 0% fetal bovine serum.

## Linearity of Dilution

Linearity of dilution is determined based on interpolated values from the standard curve. Linearity of dilution defines a sample concentration interval in which interpolated target concentrations are directly proportional to sample dilution.

Native Met was measured in the following biological samples in a 2-fold dilution series. Sample dilutions are made in Sample Diluent NS.

Dilution Factor	Interpolated value	10% Human Serum	10% Human Plasma (Citrate)	10% Human Plasma (EDTA)	10% Human Plasma (Heparin)
Undiluted	pg/mL	11,984	8,558	9,102	9,295
	<b>% Expected value</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>
2	pg/mL	5,542	4,291	4,544	4,351
	<b>% Expected value</b>	<b>92</b>	<b>100</b>	<b>100</b>	<b>94</b>
4	pg/mL	2,734	2,269	2,382	2,253
	<b>% Expected value</b>	<b>91</b>	<b>106</b>	<b>105</b>	<b>97</b>
8	pg/mL	1,366	1,150	1,247	1,083
	<b>% Expected value</b>	<b>91</b>	<b>108</b>	<b>110</b>	<b>93</b>
16	pg/mL	672.9	619.2	585.3	552.8
	<b>% Expected value</b>	<b>90</b>	<b>116</b>	<b>103</b>	<b>95</b>

Recombinant Met was spiked into the following biological samples and diluted in a 2-fold dilution series in Sample Diluent NS.

Dilution Factor	Interpolated value	25% Cell Culture Media*
Undiluted	pg/mL	14,681
	<b>% Expected value</b>	<b>100</b>
2	pg/mL	7,008
	<b>% Expected value</b>	<b>95</b>
4	pg/mL	3,430
	<b>% Expected value</b>	<b>93</b>
8	pg/mL	1,785
	<b>% Expected value</b>	<b>97</b>
16	pg/mL	877.3
	<b>% Expected value</b>	<b>96</b>

\*Media is RPMI 1640 containing 0% fetal bovine serum.

Native Met was measured in the following biological samples in a 2-fold dilution series. Sample dilutions are made in 1X Cell Extraction Buffer PTR.

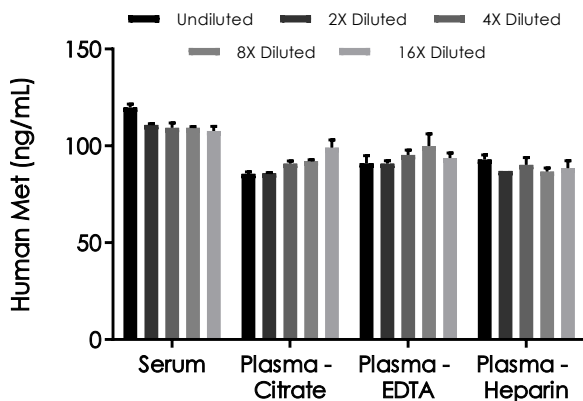
Dilution Factor	Interpolated value	250 µg/mL A431 Extract
Undiluted	pg/mL	12,275
	<b>% Expected value</b>	<b>100</b>
2	pg/mL	6,328
	<b>% Expected value</b>	<b>103</b>
4	pg/mL	3,225
	<b>% Expected value</b>	<b>105</b>
8	pg/mL	1,616
	<b>% Expected value</b>	<b>105</b>
16	pg/mL	838.6
	<b>% Expected value</b>	<b>109</b>

### PRECISION –

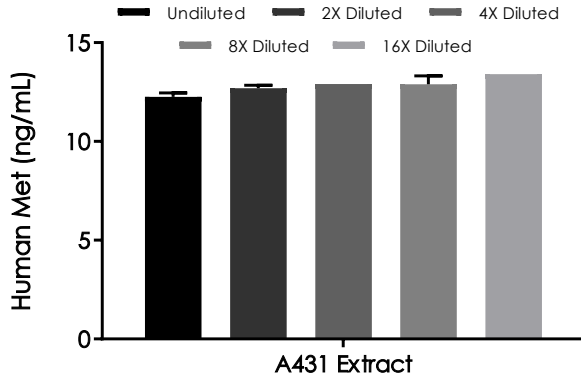
Mean coefficient of variations of interpolated values of Met from two concentrations of human serum within the working range of the assay.

	Intra- Assay	Inter- Assay
n =	8	3
CV(%)	3.3	4.4

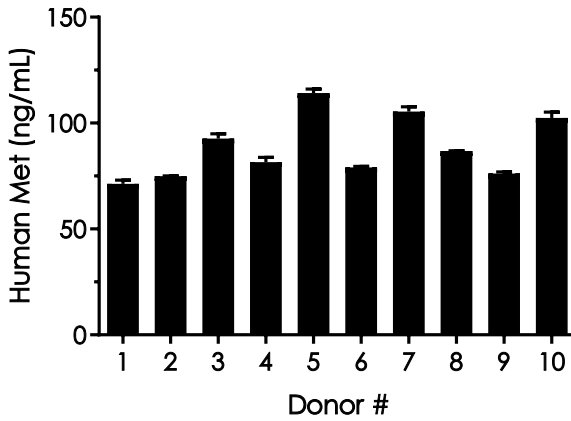




**Figure 3.** Interpolated concentrations of native Met in human serum and plasma samples. The concentrations of Met were measured in duplicates, interpolated from the Met standard curves and corrected for sample dilution. Undiluted samples are as follows: serum 10%, plasma (citrate) 10%, plasma (EDTA) 10% and plasma (heparin) 10%. The interpolated dilution factor corrected values are plotted (mean +/- SD, n=2). The mean Met concentration was determined to be 111.4 ng/mL in neat serum, 90.7 ng/mL in neat plasma (citrate), 94.1 ng/mL in neat plasma (EDTA) and 89.0 ng/mL in neat plasma (heparin).



**Figure 4.** Interpolated concentrations of native Met in human A431 cell based on a 250 µg/mL extract load. The concentrations of Met were measured in duplicate and interpolated from the Met standard curve and corrected for sample dilution. The interpolated dilution factor corrected values are plotted (mean +/- SD, n=2). The mean Met concentration was determined to be 12.8 ng/mL in A431 extract.



**Figure 5.** Serum from ten individual healthy human female donors was measured in duplicate. Interpolated dilution factor corrected values are plotted (mean +/- SD, n=2). The mean Met concentration was determined to be 88.5 ng/mL with a range of 71.3 – 114.2 ng/mL.

## 17. Assay Specificity

This kit recognizes both native and recombinant human Met protein in serum, plasma (citrate, EDTA and heparin), and cell culture supernatant, cell and tissue extract samples only.

Urine, milk, saliva and cerebrospinal fluid samples have not been tested with this kit.

### **CROSS REACTIVITY**

Recombinant human HGF was prepared at 16 ng/mL and assayed for cross reactivity. No cross-reactivity was observed.

### **INTERFERENCE**

Recombinant human HGF was prepared at 50 ng/mL and 2 ng/mL and tested for interference. 50 ng/mL human HGF increased interpolated value of 2 ng/mL human Met 2.04-fold (104%). 2 ng/mL human HGF with increased interpolated value of 2 ng/mL human Met 1.14-fold (14%).

## 18. Species Reactivity

This kit recognizes human Met protein.

Other species reactivity was determined by measuring 2% serum samples of various species, interpolating the protein concentrations from the human standard curve, and expressing the interpolated concentrations as a percentage of the protein concentration in human serum assayed at the same dilution.

<b>Species</b>	<b>% Reactivity</b>
Mouse	580
Rat	957
Cow	288
Rhesus Macaque Monkey	334

Recombinant mouse Met was prepared at 4.0 - 0.5 ng/mL range and assayed for reactivity. 392% reactivity was observed.

Please contact our Technical Support team for more information.

## 19. Troubleshooting

Problem	Reason	Solution
<b>Poor standard curve</b>	Inaccurate Pipetting	Check pipettes
	Improper standard dilution	Prior to opening, briefly spin the stock standard tube and dissolve the powder thoroughly by gentle mixing
<b>Low Signal</b>	Incubation times too brief	Ensure sufficient incubation times; increase to 2 or 3 hour standard/sample incubation
	Inadequate reagent volumes or improper dilution	Check pipettes and ensure correct preparation
	Incubation times with TMB too brief	Ensure sufficient incubation time until blue color develops prior addition of Stop solution
<b>Large CV</b>	Plate is insufficiently washed	Review manual for proper wash technique. If using a plate washer, check all ports for obstructions.
	Contaminated wash buffer	Prepare fresh wash buffer
<b>Low sensitivity</b>	Improper storage of the ELISA kit	Store your reconstituted standards at -80°C, all other assay components 4°C. Keep TMB Development Solution protected from light.
<b>Precipitate in Diluent</b>	Precipitation and/or coagulation of components within the Diluent.	Precipitate can be removed by gently warming the Diluent to 37°C.

# 20. Notes

## Technical Support

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