

## ab260064 – Human C-Peptide SimpleStep ELISA® Kit

For the quantitative measurement of C-Peptide in human serum, plasma (heparin), cell culture supernatant, and urine.

For research use only - not intended for diagnostic use.

For overview, typical data and additional information please visit: [www.abcam.com/ab260064](http://www.abcam.com/ab260064)

This kit is available in a 384-well plate format. This plate utilizes smaller volumes of standards and samples per well. Directions for using this format can be found on pg 9.

**Storage and Stability:** Store kit at 2-8°C immediately upon receipt. Refer to list of materials supplied for storage conditions of individual components. Observe the storage conditions for individual prepared components in the Standard Preparation and Reagent preparation sections.

### Materials Supplied

Item	Quantity	Storage Condition
Human C-Peptide Capture Antibody 10X	600 µL	+4°C
Human C-Peptide Detector Antibody 10X	600 µL	+4°C
Human C-Peptide Lyophilized Recombinant Protein	2 Vials	+4°C
Antibody Diluent 4BI	6 mL	+4°C
Sample Diluent NS	12 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

### Materials Required, Not Supplied

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

Microplate reader capable of measuring absorbance at 450 or 600 nm.

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).

### 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.

**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.

**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 µL 10X Capture Antibody and 300 µL 10X Detector Antibody with 2.4 mL Antibody Diluent 4BI. Mix thoroughly and gently.

### 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).

1. Reconstitute the C-Peptide standard sample by adding the volume of Sample Diluent NS indicated on the protein vial label. Hold at room temperature for 10 minutes. Mix thoroughly and gently. This is the 4,000 pg/mL **Stock Standard** Solution.
2. Label eight tubes, Standards 1–8.
3. Add 380 µL of Sample Diluent NS into tube number 1 and 150 µL of Sample Diluent NS into numbers 2-8.
4. Use the **Stock Standard** to prepare the following dilution series. Standard #8 contains no protein and is the Blank control:

Standard #	Dilution Sample	Volume to Dilute (µL)	Volume of Diluent (µL)	Starting Conc. (pg/mL)	Final Conc. (pg/mL)
1	<b>Stock Standard</b>	20	380	4,000	200
2	Standard#1	150	150	200	100
3	Standard#2	150	150	100	50
4	Standard#3	150	150	50	25
5	Standard#4	150	150	25	12.5
6	Standard#5	150	150	12.5	6.25
7	Standard#6	150	150	6.25	3.13
8	Blank Control	0	150	0	0

## Sample Preparation

Typical Sample Dynamic Range	
Sample Type	Range
Serum	0.4 – 12.5%
Plasma – Heparin	1.6 – 12.5%
Urine	1:3,200 – 1:200
Cell Culture Media*	≤50%

\*Based on spiked sample

**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 1:8 into Sample Diluent NS and assay. Store un-diluted serum at -20°C or below. Avoid repeated freeze-thaw cycles.

**Plasma** Collect plasma using heparin. Centrifuge samples at 2,000 x g for 10 minutes. Dilute samples at least 1:8 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. Note: This kit is incompatible with plasma (citrate, EDTA) samples.

**Cell Culture Supernatants** Centrifuge cell culture media at 2,000 x g for 10 minutes to remove debris. Collect supernatants. Dilute samples at least 1:2 into Sample Diluent NS and assay. Store un-diluted samples at -20°C or below. Avoid repeated freeze-thaw cycles.

**Urine** Centrifuge urine at 2,000 x g for 10 minutes to remove debris. samples at least 1:200 into Sample Diluent NS and assay. Store un-diluted urine samples at -20°C or below. Avoid repeated freeze-thaw cycles.

## 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.

## 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.

1. Prepare all reagents, working standards, and samples as directed in the previous sections.
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.
3. Add 50 µL of all sample or standard to appropriate wells.
4. Add 50 µL of the Antibody Cocktail to each well.
5. Seal the plate and incubate for 1 hour at room temperature on a plate shaker set to 400 rpm.
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.
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.
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.
9. Alternative to 7 – 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:

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

**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.

Download our ELISA guide for technical hints, results, calculation, and troubleshooting tips:

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## Additional information

### ASSAY SPECIFICITY

This kit is designed for the quantification of human C-Peptide.

The standard protein in this kit is full length human C-Peptide.

Milk, CSF, cell and tissue extract samples have not been tested with this kit.

This kit is incompatible with plasma (citrate) and plasma (EDTA) samples.

### CROSS REACTIVITY

Recombinant human mature insulin and human proinsulin were prepared at 200 pg/mL and 50 ng/mL and assayed for cross reactivity. No cross-reactivity was observed.

### INTERFERENCE

Recombinant human mature insulin and human proinsulin were prepared at 200 pg/mL and 50 ng/mL and tested for interference. No interference with was observed.

### SPECIES REACTIVITY

Other species reactivity was determined by measuring 3% 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.

Reactivity < 3% was determined for the following species: Mouse, Rat, Cow.

Other species reactivity not determined.

### CALIBRATION

This immunoassay is calibrated against a highly purified human C-Peptide. The NIBSC/WHO unclassified purified human C-Peptide preparation 13/146 was evaluated in this kit.

The dose response curve of the unclassified standard C-Peptide parallels the SimpleStep standard curve. To convert sample values obtained with the SimpleStep Human C-Peptide kit to approximate NIBSC mg/mL, use the equation below.

NIBSC (13/146) approximate value (mg/mL) = 1.077 x SimpleStep Human C-Peptide value (mg/mL).

### CALCULATION

- Calculate the average absorbance value for the blank control (zero) standards. Subtract the average blank control standard absorbance value from all other absorbance values.
- 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.

△ 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.

- 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.
- 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.

### 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	0.061	0.059	0.060
3.13	0.090	0.086	0.088
6.25	0.141	0.137	0.139
12.5	0.226	0.221	0.223
25	0.400	0.421	0.410
50	0.806	0.799	0.802
100	1.535	1.600	1.567
200	3.051	3.034	3.043

Table 1. Example of human C-Peptide standard curve in Sample Diluent NS. The C-Peptide standard curve was prepared as described in the Standard Preparation section. The table shows raw data values.

### TYPICAL SAMPLE VALUES

#### Sensitivity:

The calculated minimal detectable dose (MDD) is 1.45 pg/mL. The MDD was determined by calculating the mean of zero standard replicates (n=25) and adding 2 standard deviations then extrapolating the corresponding concentration.

#### Recovery

Three concentrations of C-Peptide 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 (%)
2% Serum	100 - 110	105
2% Plasma – Heparin	85 - 102	92
1: 3,200 Urine	101 - 107	103
50% Cell Culture Media*	88 - 92	90

\*Media is RPMI 1640 containing 10% 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 C-Peptide 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	12.5% Human Serum	12.5% Human Plasma (Heparin)	1:200 Human Urine
Undiluted	pg/mL	146	71	162
	<b>% Expected value</b>	100	100	100
2	pg/mL	78	38	77
	<b>% Expected value</b>	106	107	95
4	pg/mL	41	21	39
	<b>% Expected value</b>	112	119	96
8	pg/mL	21	10	20
	<b>% Expected value</b>	115	116	96
16	pg/mL	11	NL	10
	<b>% Expected value</b>	118	NL	98

NL – Non-Linear

Recombinant C-Peptide was spiked into the following biological samples in a 2-fold dilution series. Sample dilutions are made in Sample Diluent NS.

Dilution Factor	Interpolated value	50% Cell Culture Media
Undiluted	pg/mL	81
	<b>% Expected value</b>	100
2	pg/mL	46
	<b>% Expected value</b>	113
4	pg/mL	22
	<b>% Expected value</b>	106
8	pg/mL	11
	<b>% Expected value</b>	112
16	pg/mL	6
	<b>% Expected value</b>	109

## Precision

Mean coefficient of variations of interpolated values of C-Peptide from two concentrations of serum within the working range of the assay.

	Intra-assay	Inter-assay
<b>N=</b>	8	3
<b>CV (%)</b>	2.6	3.7

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## DIRECTIONS FOR 384-WELL PLATE FORMAT:

### Materials Supplied for 384-well Format

Item	Quantity	Storage Condition
Human C-Peptide Capture Antibody 10X	600 $\mu$ L	+4°C
Human C-Peptide Detector Antibody 10X	600 $\mu$ L	+4°C
Human C-Peptide Lyophilized Recombinant Protein	2 Vials	+4°C
Antibody Diluent 4BI	6 mL	+4°C
Sample Diluent NS	50 mL	+4°C
Wash Buffer PT 10X	20 mL	+4°C
TMB Development Solution	2 x 12 mL	+4°C
Stop Solution	2 x 12 mL	+4°C
SimpleStep Pre-Coated 384-Well Microplate	384 wells	+4°C
Plate Seal	1	+4°C

### Materials Required, Not Supplied

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

Microplate reader capable of measuring absorbance at 450 or 600 nm in a 384-well plate.

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).

Optional: Automated liquid handler.

### Reagent Preparation

Equilibrate all reagents to room temperature (18-25°C) prior to use. The kit contains enough reagents for one full plate. The sample volumes below are sufficient for running all 384 wells; adjust volumes as needed for the number of samples and dilution scheme for 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.

**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.

**Antibody Cocktail:** Prepare Antibody Cocktail by diluting the capture and detector antibodies in Antibody Diluent 4BI. To make 6 mL of the Antibody Cocktail combine 600  $\mu$ L 10X Capture Antibody and 600  $\mu$ L 10X Detector Antibody with 4.8 mL Antibody Diluent 4BI. Mix thoroughly and gently.

## 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).

1. Reconstitute the C-Peptide standard sample by adding the volume of Sample Diluent NS indicated on the protein vial label. Hold at room temperature for 10 minutes. Mix thoroughly and gently. This is the 4,000 pg/mL **Stock Standard** Solution.
2. Label eight tubes, Standards 1– 8.
3. Add 380  $\mu$ L of Sample Diluent NS into tube number 1 and 75  $\mu$ L of Sample Diluent NS into numbers 2-8.
4. Use the **Stock Standard** to prepare the following dilution series. Standard #8 contains no protein and is the Blank control:

Standard #	Dilution Sample	Volume to Dilute ( $\mu$ L)	Volume of Diluent ( $\mu$ L)	Starting Conc. (pg/mL)	Final Conc. (pg/mL)
1	<b>Stock Standard</b>	20	380	4,000	200
2	Standard#1	75	75	200	100
3	Standard#2	75	75	100	50
4	Standard#3	75	75	50	25
5	Standard#4	75	75	25	12.5
6	Standard#5	75	75	12.5	6.25
7	Standard#6	75	75	6.25	3.13
8	Blank Control	0	75	0	0

### Plate Preparation

The 384-well plate included with this kit are supplied ready to use. It is not necessary to rinse the plate prior to adding reagents.

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.

## Assay Procedure for 384-well Plate Format

Equilibrate all materials and prepared reagents to room temperature prior to use.  
We recommend that you assay all standards, controls and samples in duplicate.

1. Prepare all reagents, working standards, and samples as directed in the previous sections.
2. Add 12.5  $\mu\text{L}$  of all sample or standard to appropriate wells.
3. Add 12.5  $\mu\text{L}$  of the Antibody Cocktail to each well.
4. Seal the plate and incubate for 1 hour at room temperature on a plate shaker set to 700 rpm.
5. Wash each well with 3 x 100  $\mu\text{L}$  1X Wash Buffer PT. Wash by aspirating or decanting from wells then dispensing 100  $\mu\text{L}$  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.
6. Add 25  $\mu\text{L}$  of TMB Development Solution to each well and incubate for 10 minutes in the dark on a plate shaker set to 700 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.<sub>600</sub> equal to 1.0.

7. Add 25  $\mu\text{L}$  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. Proper mixing of the Stop Solution is required for proper measurement.
8. Alternative to 6 – 7: 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:

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

**Note** that an endpoint reading can also be recorded at the completion of the kinetic read by adding 25  $\mu\text{L}$  Stop Solution to each well and recording the OD at 450 nm.

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