

ab326894 – Human CKM SimpleStep ELISA® Kit – Chemiluminescent

For the quantitative measurement of CKM in human serum, plasma (heparin), plasma (EDTA), plasma (citrate), urine, cell extract, and tissue extract.
For research use only - not intended for diagnostic use.
Patent pending.

For overview, typical data and additional information please visit: www.abcam.com/ab326894

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.

Limitations: All data, except typical standard curve and sensitivity were collected using the colorimetric version of this kit (ab264617).

Materials Supplied

Item	Quantity 1 x 96 tests	Storage Condition
Human CKM Capture Antibody 10X	600 µL	+4°C
Human CKM Detector Antibody 10X	600 µL	+4°C
Human CKM Lyophilized Recombinant Protein	2 Vials	+4°C
Antibody Diluent 5BI	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
ChemiHRP Reagent A	3 mL	+4°C
ChemiHRP Reagent B	3 mL	+4°C
SimpleStep Pre-Coated Black 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:

Luminometer with the following settings: 0.5-1 second/well read time; summation mode (all wavelengths).

Method for determining protein concentration (BCA assay recommended).

Deionized water.

Multi- and single-channel pipettes.

Tubes for standard dilution.

Orbital microplate shaker for all incubation steps: capable of 750 rpm shaking speed.

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.

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.

Antibody Cocktail: Prepare Antibody Cocktail by diluting the capture and detector antibodies in Antibody Diluent 5BI. 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 5BI. Mix thoroughly and gently.

Lumi HRP Development Solution: Just prior to use, prepare Lumi HRP Development Solution by mixing equal volume of the ChemiHRP Reagent A and the ChemiHRP Reagent B. To make 3 mL of the Lumi HRP Development Solution combine 1.5 mL of ChemiHRP Reagent A and 1.5 mL of ChemiHRP Reagent B. Mix thoroughly and gently by inversion or slow pipetting (Avoid shaking or vortexing). Protect the prepared solution from light until use.

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 **CKM** protein standard by adding the volume indicated on the protein vial label. For **serum** and plasma **samples measurements**, use Sample Diluent NS. For **cell** and tissue **samples measurements**, use Sample Diluent 1X Cell Extraction Buffer PTR. Hold at room temperature for 10 minutes and mix thoroughly and gently. This is the 32,000 pg/mL **Stock Standard #1** Solution.
1. Label nine tubes, Standards 1–9.
2. Use the same Sample Diluent as used to resuspend the Stock Standard #1 to prepare the standard curve. Add 0 µL of Sample Diluent into tube number 1 and 150 µL of Sample Diluent into numbers 2-9.
3. Use the **Stock Standard #1** to prepare the following dilution series. Standard #9 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	Stock Standard #1	150	0	32,000	32,000
2	Stock Standard #1	75	150	32,000	10,666
3	Standard#2	75	150	10,666	3,555
4	Standard#3	75	150	3,555	1,185
5	Standard#4	75	150	1,185	395
6	Standard#5	75	150	395	131.7
7	Standard#6	75	150	131.7	43.9
8	Standard#7	75	150	43.9	14.6
9	Blank Control	0	150	0	0

Sample Preparation

Typical Sample Dynamic Range	
Sample Type	Range
Serum	1:128 - 1:16
Plasma - Citrate	1:128 - 1:8
Plasma - EDTA	1:64 - 1:8
Plasma - Heparin	1:128 - 1:8
Urine*	< 25%
Skeletal Muscle Tissue extract	31.25 ng/mL - 500 ng/mL

*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 1:16 into Sample Diluent NS and assay. Store un-diluted serum at -20°C or below. Avoid repeated freeze-thaw cycles.

Plasma Collect plasma using citrate, EDTA or 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.

Urine Centrifuge urine at 2,000 x g for 10 minutes to remove debris. Dilute samples at least 1:4 into Sample Diluent NS and assay. Store un-diluted urine samples at -20°C or below. Avoid repeated freeze-thaw cycles.

Preparation of extracts from cell pellets 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. Rinse cells twice with PBS. Solubilize pellet at 2x10⁷ cell/mL in chilled

1X Cell Extraction Buffer PTR. Incubate on ice for 20 minutes. Centrifuge at 18,000 x g for 20 minutes at 4°C. Transfer the supernatants into clean tubes and discard the pellets. Assay samples immediately or aliquot and store at -80°C. The sample protein concentration in the extract may be quantified using a protein assay. Dilute samples to desired concentration in 1X Cell Extraction Buffer PTR.

Preparation of extracts from tissue homogenates Tissue lysates are typically prepared by homogenization of tissue that is first minced and thoroughly rinsed in PBS to remove blood (dounce homogenizer recommended). Homogenize 100 to 200 mg of wet tissue in 500 μL – 1 mL of chilled 1X Cell Extraction Buffer PTR. For lower amounts of tissue adjust volumes accordingly. Incubate on ice for 20 minutes. Centrifuge at 18,000 x g for 20 minutes at 4°C. Transfer the supernatants into clean tubes and discard the pellets. Assay samples immediately or aliquot and store at -80°C. The sample protein concentration in the extract may be quantified using a protein assay. Dilute samples to desired concentration in 1X Cell Extraction Buffer PTR.

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 30 minutes at room temperature on a plate shaker set to 750 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 30 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 50 μL of prepared Lumi HRP Development Solution to each well and incubate for 1 minute in the dark on a plate shaker set to 750 rpm. Further optimization of incubation time vs signal strength can be performed if needed. Avoid introducing bubbles into the wells.
8. Measure the produced light of each well using a microplate luminometer with the following settings: 1 second/well read time in summation mode (all wavelengths). Relative light unit (RLU) readings may vary between luminometer models. It is recommended to configure

- instrument settings according to the manufacturer's specifications. Note: Relative light unit (RLU) values may change over the course of the 15-minute reading window.
9. Analyze the data as described below.

Mode:	Luminescence
Instrument settings:	Endpoint
Detection Mode:	All wavelengths
Read Time:	0.5-1 sec
Read:	Top

Note For microplate readers with Pre-Read Optimization option, the Read Height as well as Microplate Optimization is recommended before the first read.

Download our ELISA guide for technical hints, results, calculation, and troubleshooting tips:
<https://www.abcam.com/en-us/technical-resources/guides/elisa-guide>

Technical Support
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Additional information

ASSAY SPECIFICITY

This kit is designed for the quantification of human CKM.

Native signal was detected in serum, plasma (citrate), plasma (EDTA), plasma (heparin), cell extract, and tissue extract sample types.

Spiked protein experiments were used to validate urine sample types.

Cell culture supernatant, saliva, CSF and milk samples have not been tested with this kit.

CROSS REACTIVITY

50 ng/mL of recombinant human CKMB and 50 ng/mL of recombinant human CKBB were tested for cross reactivity. No cross reactivity was observed.

INTERFERENCE

50 ng/mL of recombinant human CKMB and 50 ng/mL of recombinant human CKBB were tested for interference. No interference was observed.

SPECIES REACTIVITY

This kit recognizes human and monkey CKM protein.

Other species reactivity was determined by measuring 1:16 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.

Interpolated values were below the detectable range of the assay for the following species: Mouse, Rat, Cow

Other species reactivity not determined.

CALCULATION

- Preconfigured protocols are available when using SoftMax Pro software from Molecular Devices.
- Calculate the average chemiluminescence value for the blank control (zero) standards. Subtract the average blank control standard chemiluminescence value from all other chemiluminescence values.
- Create a standard curve by plotting the average blank control subtracted chemiluminescence 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 chemiluminescence 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 chemiluminescence 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 chemiluminescence values greater than that of the highest standard should be further diluted and reanalyzed. Similarly, samples which measure at chemiluminescence 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)	RLU		Mean RLU
	1	2	
0	112	112	112
14.63	683	552	618
43.90	3,334	2,708	3,021
131.69	11,505	10,270	10,888
395.06	42,680	41,673	42,177
1,185.1	120,564	115,790	118,177
3,555.5	351,444	338,231	344,838
10,666.6	998,713	993,064	995,889
32,000	2,553,324	2,600,196	2,576,760

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

Standard Curve Measurements			
Concentration (pg/mL)	RLU		Mean RLU
	1	2	
0	98	98	98
14.63	445	447	446
43.90	2,153	2,065	2,109
131.69	9,608	9,052	9,330
395.06	31,443	31,800	31,622
1,185.1	98,588	90,837	94,713
3,555.5	310,542	295,902	303,222
10,666.6	881,105	859,249	870,177
32,000	2,511,172	2,477,829	2,494,501

Table 2. Example of human CKM standard curve in Sample Diluent 1X Cell Extraction Buffer PTR. The CKM standard curve was prepared as described in the Standard Preparation section. The table shows raw data values.

TYPICAL SAMPLE VALUES

Sensitivity:

The minimal detectable dose (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	13	2.67 pg/mL
1X Cell Extraction Buffer PTR	12	2.35 pg/mL

Recovery

Three concentrations of CKM 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 (%)
3.125% Serum	112	100 - 120
3.125% Plasma - Citrate	108	102 - 114
3.125% Plasma - EDTA	104	103 - 106
3.125% Plasma - Heparin	103	97 - 113
25% Urine	84	82 - 86
125 ng/mL Skeletal Muscle Tissue extract	105	103 - 106

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 CKM 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	6.25% Human Serum	12.5% Human Plasma (Citrate)	12.5% Human Plasma (EDTA)	12.5% Human Plasma (Heparin)
Undiluted	pg/mL	2,232.1	1,765.0	949.9	3,187.8
	% Expected value	100	100	100	100
2	pg/mL	1,097.3	924.2	480.9	1,480.4
	% Expected value	98	105	101	93
4	pg/mL	560.5	440.4	244.3	723.9
	% Expected value	100	100	103	91
8	pg/mL	287.2	241.2	102.1	387.3
	% Expected value	103	109	86	97
16	pg/mL	NL	93.4	NL	158.5
	% Expected value		85		80

NL – Non-Linear

Recombinant CKM was spiked into the following biological samples and then diluted in a 2-fold dilution series. Sample dilutions are made in Sample Diluent NS.

Dilution Factor	Interpolated value	25% Human Urine
Undiluted	pg/mL	977.6
	% Expected value	100
2	pg/mL	537.9
	% Expected value	110
4	pg/mL	280.6
	% Expected value	115
8	pg/mL	144.6
	% Expected value	118
16	pg/mL	70.5
	% Expected value	115

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

Dilution Factor	Interpolated value	500 ng/mL Human Skeletal Muscle Tissue Extract
Undiluted	pg/mL	2,116.9
	% Expected value	100
2	pg/mL	1,072.5
	% Expected value	101
4	pg/mL	544.7
	% Expected value	103
8	pg/mL	278.2
	% Expected value	105
16	pg/mL	132.3
	% Expected value	100

Precision

Mean coefficient of variations of interpolated values of CKM from a single concentration of human serum within the working range of the assay.

	Intra-assay	Inter-assay
n=	8	3
CV (%)	3.6	2.3

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

<https://www.abcam.com/en-us/technical-resources/guides/elisa-guide>

Technical Support

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