

Version 1 Last updated 7 September 2018

# ab221832 Human Cytochrome C SimpleStep ELISA<sup>®</sup> Kit

For the quantitative measurement of Cytochrome C in human cell and tissue extracts and subcellular fractions.

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

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## 1. Overview

Cytochrome C *in vitro* SimpleStep ELISA<sup>®</sup> (Enzyme-Linked Immunosorbent Assay) kit is designed for the quantitative measurement of Cytochrome C protein in human cell and tissue extracts and subcellular fractions.

The SimpleStep ELISA<sup>®</sup> 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.

Cytochrome C is 11 kDa mitochondrial intermembrane space electron carrier protein. The oxidized form of the cytochrome C heme group can accept an electron from the heme group of the cytochrome c1 subunit of cytochrome reductase. Cytochrome C then transfers this electron to the cytochrome oxidase complex, the final protein carrier in the mitochondrial electron-transport chain. Cytochrome C also plays a role in apoptosis. Suppression of the anti-apoptotic members or activation of the pro-apoptotic members of the Bcl-2 family leads to altered mitochondrial outer membrane permeability resulting in release of cytochrome C into the cytosol. Binding of cytochrome C to Apaf-1 triggers the activation of caspase-9, which then accelerates apoptosis by activating other caspases.

## 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 6 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 Cytochrome C Capture Antibody 10X	600 µL	+4°C
Human Cytochrome C Detector Antibody 10X	600 µL	+4°C
Human Cytochrome C Lyophilized Recombinant Protein	2 Vials	+4°C
Antibody Diluent CPI	6 mL	+4°C
Wash Buffer PT 10X	20 mL	+4°C
Cell Extraction Buffer PTR 5X	10 mL	+4°C
Cell Extraction Enhancer Solution 50X	1 mL	+4°C
Denaturant	500 µL	+4°C
TMB Development Solution	12 mL	+4°C
Stop Solution	12 mL	+4°C
Sample Diluent NS	12 mL	+4°C
Anti-tag coated microplate (12 x 8 well strips)	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.

- The provided Antibody Diluents and Sample Diluents contain protease inhibitor aprotinin. Additional protease inhibitors can be added if required.
- The provided Cell Extraction Buffer 5X contains phosphatase inhibitors and protease inhibitor aprotinin. Additional protease inhibitors can be added if required.
- The provided Cell Extraction Enhancer Solution 50X may precipitate when stored at + 4°C. To dissolve, warm briefly at + 37°C and mix gently. The Cell Extraction Enhancer Solution 50X can be stored at room temperature to avoid precipitation.
- **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:

Prepare 1X Cell Extraction Buffer PTR by diluting Cell Extraction Buffer PTR 5X and 50X Cell Extraction Enhancer Solution 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 Cell Extraction Buffer PTR + Enhancer

Prepare 1X Cell Extraction Buffer PTR + Enhancer by diluting 5X Cell Extraction Buffer PTR and 50X Cell Extraction Enhancer Solution to 1X with deionized water. To make 10 mL 1X Cell Extraction Buffer PTR + Enhancer combine 7.8 mL deionized water, 2 mL 5X Cell Extraction Buffer PTR and 200  $\mu$ L 50X Cell Extraction Enhancer Solution. Mix thoroughly and gently. If required protease inhibitors can be added.

### 9.3 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.

### 9.4 Antibody Cocktail:

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

## 10. Standard Preparation

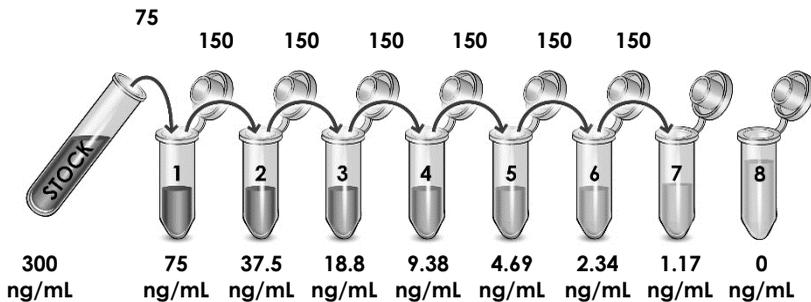
- Always prepare a fresh set of standards for every use.
- Discard working standard dilutions after use as they do not store well.
- The following section describes the preparation of a standard curve for duplicate measurements (recommended).

**10.1** Reconstitute the human Cytochrome C lyophilized standard protein by adding 500  $\mu\text{L}$  1X Cell Extraction Buffer PTR + Enhancer. Mix thoroughly and gently. Hold at room temperature for 10 minutes and mix gently. This is the 300 ng/mL **Stock Standard** Solution.

**10.2** Label eight tubes, Standards 1– 8.

**10.3** Add 225  $\mu\text{L}$  1X Cell Extraction Buffer PTR +Enhancer into tube number 1 and 150  $\mu\text{L}$  of 1X Cell Extraction Buffer PTR + Enhancer into numbers 2-8.

**10.4** 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
Human Heart Tissue Extract	0.31 – 20 µg/mL
Human Colon Tissue Extract	1.56 – 50 µg/mL
Human Skeletal Muscle Tissue Extract	0.78 – 25 µg/mL
HepG2 Cell Extract	1.56 – 50 µg/mL
PC-3 Cell Extract	0.78 – 50 µg/mL
THP-1 Cell Extract	3.13 – 50 µg/mL

### 11.1 Preparation of extracts from cell pellets:

- 11.1.1 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.
- 11.1.2 Rinse cells twice with PBS.
- 11.1.3 Solubilize pellet at  $2 \times 10^7$  cell/mL in chilled 1X Cell Extraction Buffer PTR + Enhancer.
- 11.1.4 Incubate on ice for 20 minutes.
- 11.1.5 Centrifuge at 18,000 x g for 20 minutes at 4°C.
- 11.1.6 Transfer the supernatants into clean tubes and discard the pellets.
- 11.1.7 At this point extract samples can be aliquoted and stored at -80°C. The sample protein concentration in the extract may be quantified using a protein assay.
- 11.1.8 To 8 volume parts of extract add 1 volume part of Denaturant. Mix thoroughly and gently.
- 11.1.9 Incubate samples at room temperature for 10 minutes.
- 11.1.10 Dilute samples 40-fold in 1X Cell Extraction Buffer PTR. Mix thoroughly and gently.
- 11.1.11 Dilute samples further to desired concentration in 1X Cell Extraction Buffer PTR + Enhancer.

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

- 11.2.1 Remove growth media and rinse adherent cells 2 times in PBS.
- 11.2.2 Solubilize the cells by addition of chilled 1X Cell Extraction Buffer PTR + Enhancer directly to the plate (use 750  $\mu$ L - 1.5 mL 1X Cell Extraction Buffer PTR + Enhancer per confluent 15 cm diameter plate).
- 11.2.3 Scrape the cells into a microfuge tube and incubate the lysate on ice for 15 minutes.
- 11.2.4 Centrifuge at 18,000 x g for 20 minutes at 4°C.
- 11.2.5 Transfer the supernatants into clean tubes and discard the pellets.
- 11.2.6 At this point extract samples can be aliquoted and stored at -80°C. The sample protein concentration in the extract may be quantified using a protein assay.
- 11.2.7 To 8 volume parts of extract add 1 volume part of Denaturant. Mix thoroughly and gently.
- 11.2.8 Incubate samples at room temperature for 10 minutes.
- 11.2.9 Dilute samples 40-fold in 1X Cell Extraction Buffer PTR. Mix thoroughly and gently.
- 11.2.10 Dilute samples further to desired concentration in 1X Cell Extraction Buffer PTR + Enhancer.

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

- 11.3.1 Tissue lysates are typically prepared by homogenization of tissue that is first minced and thoroughly rinsed in PBS to remove blood (dounce homogenizer recommended).
- 11.3.2 Homogenize 100 to 200 mg of wet tissue in 500  $\mu$ L – 1 mL of chilled 1X Cell Extraction Buffer PTR + Enhancer. For lower amounts of tissue adjust volumes accordingly.
- 11.3.3 Incubate on ice for 20 minutes.
- 11.3.4 Centrifuge at 18,000 x g for 20 minutes at 4°C.
- 11.3.5 Transfer the supernatants into clean tubes and discard the pellets.
- 11.3.6 At this point extract samples can be aliquoted and stored at -80°C. The sample protein concentration in the extract may be quantified using a protein assay.
- 11.3.7 To 8 volume parts of extract add 1 volume part of Denaturant. Mix thoroughly and gently.
- 11.3.8 Incubate samples at room temperature for 10 minutes.

11.3.9 Dilute samples 40-fold in 1X Cell Extraction Buffer PTR. Mix thoroughly and gently.

11.3.10 Dilute samples further to desired concentration in 1X Cell Extraction Buffer PTR + Enhancer.

#### **11.4 Subcellular fractions**

11.4.1 To 8 volume parts of a fraction add 1 volume part of Denaturant. Mix thoroughly and gently.

11.4.2 Incubate samples at room temperature for 10 minutes.

11.4.3 Dilute samples 40-fold in 1X Cell Extraction Buffer PTR. Mix thoroughly and gently.

11.4.4 If needed, dilute samples further to desired concentration in 1X Cell Extraction Buffer PTR + Enhancer.

## **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.
- Prepare all reagents, working standards, and samples as directed in the previous sections.

**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. Complete removal of liquid at each step is essential for good performance. After the last wash invert the plate and blot it against clean paper towels to remove excess liquid.

**13.7** Add 100 µL of TMB Development Solution to each well and incubate for 6 minutes in the dark on a plate shaker set to 400 rpm.

**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 15 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  $\mu$ L Stop Solution to each well and recording the OD at 450 nm.

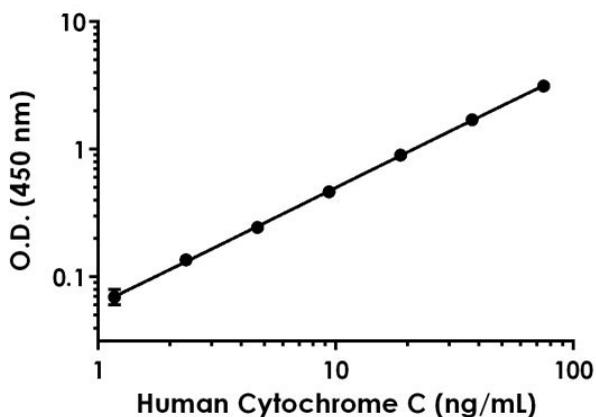
**13.10** Analyze the data as described below.

## 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 (ng/mL)	O.D 450 nm		Mean O.D
	1	2	
0	0.070	0.067	0.069
1.17	0.146	0.131	0.138
2.34	0.207	0.203	0.205
4.69	0.327	0.299	0.313
9.38	0.557	0.514	0.535
18.8	0.993	0.949	0.971
37.5	1.781	1.765	1.773
75	3.215	3.208	3.212

**Figure 1.** Example of human Cytochrome C standard curve in 1X Cell Extraction Buffer PTR + Enhancer. The Cytochrome C 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 calculated minimal detectable dose (MDD) is 1.1 ng/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 recombinant human Cytochrome C 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 (%)
5 µg/mL Human Heart Tissue Extract	104	101 - 106
25 µg/mL HepG2 Cell Extract	107	105 - 110

## 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 Cytochrome C was measured in the following biological samples in a 2-fold dilution series. Sample dilutions are made in 1X Cell Extraction Buffer PTR + Enhancer.

Dilution Factor	Interpolated value	20 µg/mL Human Heart Tissue Extract	50 µg/mL Human Colon Tissue Extract	25 µg/mL Human Skeletal Muscle Tissue Extract
Undiluted	ng/mL	33.73	37.27	45.71
	<b>% Expected value</b>	100	100	100
2	ng/mL	17.13	15.80	20.92
	<b>% Expected value</b>	102	85	92
4	ng/mL	8.739	7.914	9.779
	<b>% Expected value</b>	104	85	86
8	ng/mL	4.572	3.940	5.184
	<b>% Expected value</b>	108	85	91
16	ng/mL	2.345	1.979	2.967
	<b>% Expected value</b>	111	85	104

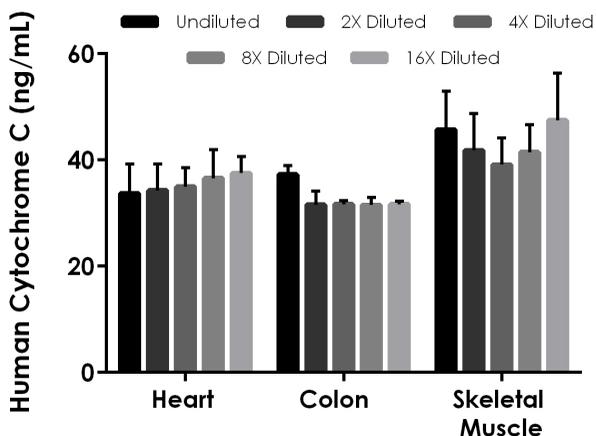
Native Cytochrome C was measured in the following biological samples in a 2-fold dilution series. Sample dilutions are made in 1X Cell Extraction Buffer PTR + Enhancer.

Dilution Factor	Interpolated value	50 µg/mL HepG2 Cell Extract	50 µg/mL PC-3 Cell Extract	50 µg/mL THP-1 Cell Extract
Undiluted	ng/mL	46.64	83.47	18.79
	<b>% Expected value</b>	100	100	100
2	ng/mL	22.69	41.61	9.502
	<b>% Expected value</b>	97	100	101
4	ng/mL	11.65	20.51	5.035
	<b>% Expected value</b>	100	98	107
8	ng/mL	5.755	9.963	2.477
	<b>% Expected value</b>	99	95	105
16	ng/mL	2.719	4.859	1.081
	<b>% Expected value</b>	93	93	92

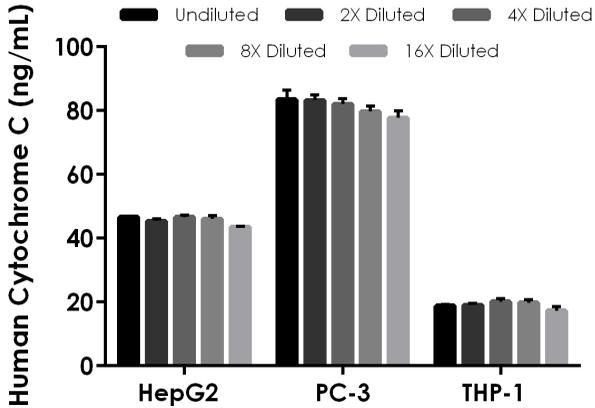
#### PRECISION –

Mean coefficient of variations of interpolated values from three concentrations of human heart tissue extract within the working range of the assay.

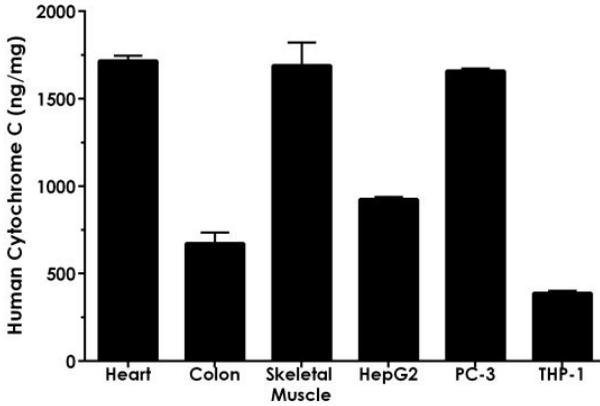
	Intra-Assay	Inter-Assay
n =	3	5
CV(%)	2.8	6.3



**Figure 2.** Interpolated concentrations of native Cytochrome C in human heart tissue extract based on a 20 µg/mL extract load, colon tissue extract based on a 50 µg/mL extract load, and skeletal muscle tissue extract based on a 25 µg/mL extract load. The concentrations of Cytochrome C were measured in duplicate and interpolated from the Cytochrome C standard curve and corrected for sample dilution. The interpolated dilution factor corrected values are plotted (mean +/- SD, n=2). The mean Cytochrome C concentration was determined to be 35.41 ng/mL in heart tissue extract, 32.74 ng/mL in colon tissue extract, and 43.12 ng/mL in skeletal muscle tissue extract.



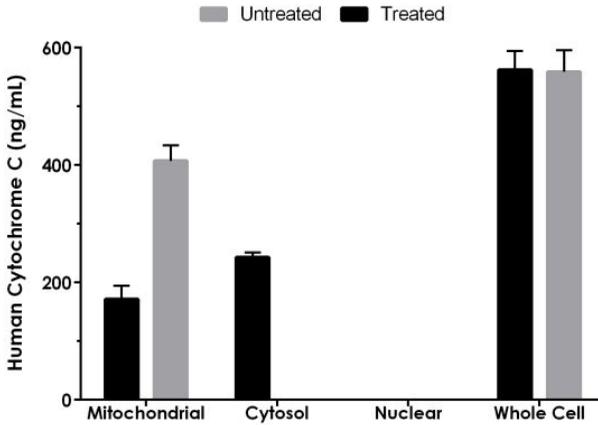
**Figure 3.** Interpolated concentrations of native Cytochrome C in HepG2 cell extract, PC-3 cell extract, and THP-1 cell extract samples based on a 50 µg/mL extract load. The concentrations of Cytochrome C were measured in duplicate and interpolated from the Cytochrome C standard curve and corrected for sample dilution. The interpolated dilution factor corrected values are plotted (mean +/- SD, n=2). The mean Cytochrome C concentration was determined to be 45.64 ng/mL in HepG2 cell extract, 81.23 ng/mL in PC-3 cell extract, and 19.01 ng/mL in THP-1 cell extract.



**Figure 4.** Interpolated concentrations of native Cytochrome C in human extract samples. The concentrations of Cytochrome C were measured in three different dilutions in duplicate and interpolated from the Cytochrome C standard curve and corrected for sample dilution. The interpolated dilution factor corrected values are plotted in ng of Cytochrome C per mg of extract (mean +/- SD, n=3). Cytochrome C concentration was determined to be 1716 ng/mg heart tissue extract, 670.1 ng/mg in colon tissue extract, 1689 ng/mg in skeletal muscle tissue extract, 924.2 ng/mg in HepG2 cell extract, 1658 ng/mg in PC-3 cell extract, and 386.2 ng/mg in THP-1 cell extract samples.

## 17. Assay Specificity

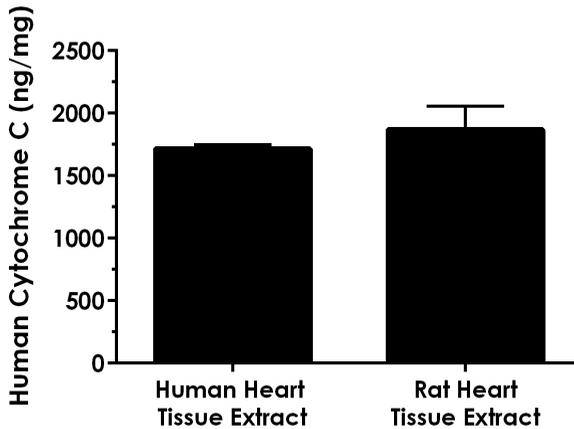
This kit recognizes both native and recombinant human Cytochrome C protein in cell and tissue extract, and subcellular fraction samples only.



**Figure 5.** Comparison Cytochrome C distribution in subcellular fractions derived from  $3.7 \times 10^3$  HeLa cells and whole cells cultured in the presence (treated) or absence (untreated) of  $1 \mu\text{M}$  staurosporine for 4 hours. Cells were collected directly after treatment and subcellular fractions were prepared using a cell fractionation kit (ab109719). Fractions were processed as described in section 11.10. and assayed. The concentrations of Cytochrome C were measured in three different dilutions of the fraction samples in duplicates and interpolated from the Cytochrome C standard curve. The interpolated values are plotted (mean  $\pm$  SD,  $n=3$ ). The mean Cytochrome C concentration was determined be 171.4 ng/mL in the treated cytosol fraction, 242.8 in the treated mitochondrial fraction, 562.0 in the treated whole cell sample, 407.2 ng/mL in the untreated mitochondrial fraction, and 558.9 ng/mL in the untreated whole cell sample. Cytochrome C was not detectable in the untreated cytosol fraction and in both nuclear fractions.

## 18. Species Reactivity

This kit recognizes human Cytochrome C protein.



Other species reactivity was determined by measuring a 20  $\mu\text{g/mL}$  extract load of human and rat heart tissue extract samples, interpolating the protein concentrations from the human standard curve, and expressing the interpolated concentrations as a percentage of the protein concentration in the human heart tissue extract. Cross-reactivity was determined to be 100% in rat heart extract. Due to 100% amino acids sequence identity of rat and mouse Cytochrome C, the same cross-reactivity can be assumed for mouse Cytochrome C.

Please contact our Technical Support team for more information.

## 19. Troubleshooting

Problem	Reason	Solution
<b>Difficulty pipetting lysate; viscous lysate.</b>	Genomic DNA solubilized	Prepare 1X Cell Extraction Buffer PTR (without enhancer). Add enhancer to lysate after extraction.
<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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