



# **ab207616 – Mouse APE (Apex1) SimpleStep ELISA<sup>®</sup> Kit**

## Instructions for Use

For the quantitative measurement of mouse APE (Apex1) protein in mouse cell culture supernatants and cell and tissue extracts.

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

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## 1. BACKGROUND

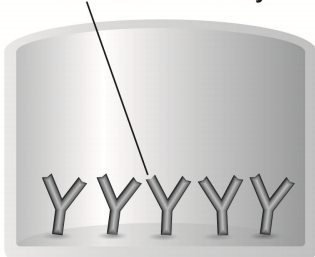
Mouse APE (Apex1) *in vitro* SimpleStep ELISA® (Enzyme-Linked Immunosorbent Assay) kit is designed for the quantitative measurement of mouse APE protein in mouse cell culture supernatants and cell and tissue extracts.

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 substrate 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.

Mouse APE is a multifunctional protein that binds DNA and RNA and plays a central role in the cellular response to oxidative stress. The two major activities of APE are DNA repair and redox regulation of transcription factors. APE functions as an apurinic/apyrimidinic (AP) endodeoxyribonuclease in the DNA base excision repair (BER) pathway of DNA lesions induced by oxidative and alkylating agents. The C-terminal region of APE is responsible for base excision repair activities. Notably, this repair activity is suppressed by phosphorylation. The N-terminal region of APE may regulate the DNA binding capabilities of a variety of transcription factors through redox stimulation. Mouse APE has 98% and 94% identity to rat and human APE, respectively.

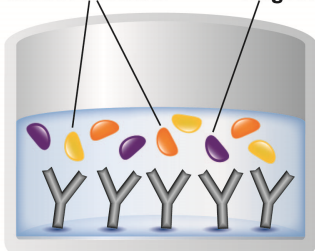
## 2. ASSAY SUMMARY

Immobilization Antibody



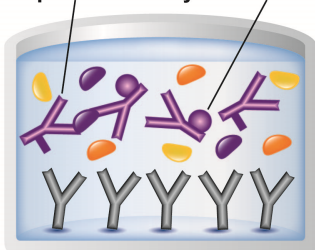
Remove appropriate number of antibody coated well strips. Equilibrate all reagents to room temperature. Prepare all reagents, samples, and standards as instructed.

Matrix Proteins Target Analyte



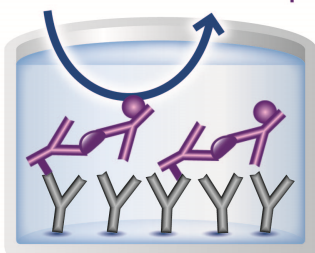
Add standard or sample to appropriate wells.

Capture Antibody Detector Antibody



Add Antibody Cocktail to all wells. Incubate at room temperature.

Substrate Color Development



Aspirate and wash each well. Add TMB Substrate to each well and incubate. Add Stop Solution at a defined endpoint. Alternatively, record color development kinetically after TMB substrate addition.

## 3. PRECAUTIONS

**Please read these instructions carefully prior to beginning the assay.**

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

## 4. STORAGE AND STABILITY

**Store kit at 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 Reagent and Standard Preparation sections.

## 5. MATERIALS SUPPLIED

Item	Amount	Storage Condition (Before Preparation)
10X Mouse APE Capture Antibody	600 µL	+2-8°C
10X Mouse APE Detector Antibody	600 µL	+2-8°C
Mouse APE Lyophilized Recombinant Protein	2 Vials	+2-8°C
Antibody Diluent 4BI	6 mL	+2-8°C
10X Wash Buffer PT	20 mL	+2-8°C
5X Cell Extraction Buffer PTR	10 mL	+2-8°C
50X Cell Extraction Enhancer Solution	1 mL	+2-8°C
TMB Substrate	12 mL	+2-8°C
Stop Solution	12 mL	+2-8°C
Sample Diluent NS	50 mL	+2-8°C
Pre-Coated 96 Well Microplate (12 x 8 well strips)	96 Wells	+2-8°C
Plate Seal	1	+2-8°C

### 6. 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.
- 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).

### 7. LIMITATIONS

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

### 8. TECHNICAL HINTS

- 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 50X Cell Extraction Enhancer Solution may precipitate when stored at + 4°C. To dissolve, warm briefly at + 37°C and mix gently. The 50X Cell Extraction Enhancer Solution 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 (For cell and tissue extracts only)

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

*NOTE: Do NOT add 50X enhancer to the 1X Cell Extraction Buffer PTR*

### 9.2 1X Wash Buffer PT

Prepare 1X Wash Buffer PT by diluting 10X Wash Buffer PT with deionized water. To make 50 mL 1X Wash Buffer PT combine 5 mL 10X Wash Buffer PT 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

Prepare serially diluted standards immediately prior to use. Always prepare a fresh set of positive controls for every use.

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 APE standard by adding that volume of Diluent indicated on the label. Alternatively, if the vial has a mass identified, reconstitute the APE standard by adding 0.5 mL Diluent. Hold at room temperature for 10 minutes and mix gently. This is the 60,000 pg/mL **Stock Standard** Solution.

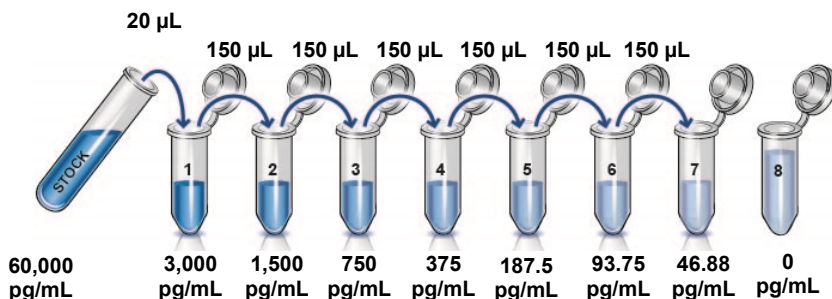
10.1 For **cell culture supernatant samples** follow these instructions:

10.1.1 Reconstitute the APE standard by adding Sample Diluent NS.

10.1.2 Label eight tubes, Standards 1–8.

10.1.3 Add 380  $\mu$ L of Sample Diluent NS into tube number 1 and 150  $\mu$ 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:



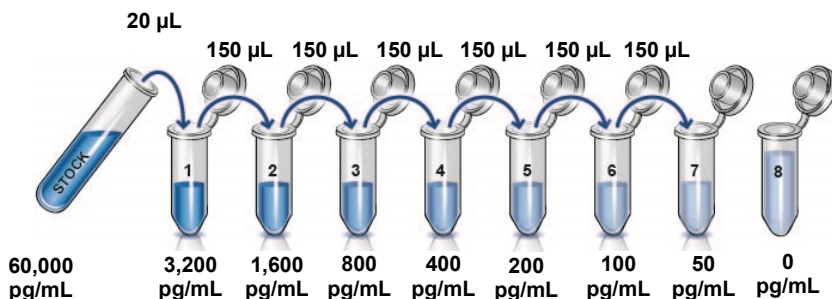
10.2 For **cell and tissue extract samples** follow these instructions:

10.2.1 Reconstitute the APE standard by adding 1X Cell Extraction Buffer PTR by pipette.

10.2.2 Label eight tubes, Standards 1–8.

10.2.3 Add 355  $\mu\text{L}$  of 1X Cell Extraction Buffer PTR into tube number 1 and 150  $\mu\text{L}$  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
RPMI Base Media	1:160 – 1:10
Mouse C2C12 Cell Extract	18.75 – 150 µg/mL
Mouse NIH 3T3 Cell Extract	0.78 – 3.13 µg/mL
Rat PC12 Cell Extract	3.13 – 12.5 µg/mL
Human PC3 Cell Extract	6.25 – 100 µg/mL

### 11.1 Cell Culture Supernatants

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

### 11.2 Preparation of extracts from cell pellets

- 11.2.1 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.
- 11.2.2 Rinse cells twice with PBS.
- 11.2.3 Solubilize pellet at  $2 \times 10^7$  cell/mL in chilled 1X Cell Extraction Buffer PTR.
- 11.2.4 Incubate on ice for 20 minutes.
- 11.2.5 Centrifuge at 18,000 x g for 20 minutes at 4°C.
- 11.2.6 Transfer the supernatants into clean tubes and discard the pellets.

- 11.2.7 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.
- 11.2.8 Dilute samples to desired concentration in 1X Cell Extraction Buffer PTR.
- 11.3 **Preparation of extracts from adherent cells by direct lysis (alternative protocol)**
  - 11.3.1 Remove growth media and rinse adherent cells 2 times in PBS.
  - 11.3.2 Solubilize the cells by addition of chilled 1X Cell Extraction Buffer PTR directly to the plate (use  $750\ \mu\text{L}$  -  $1.5\ \text{mL}$  1X Cell Extraction Buffer PTR per confluent  $15\ \text{cm}$  diameter plate).
  - 11.3.3 Scrape the cells into a microfuge tube and incubate the lysate on ice for 15 minutes.
  - 11.3.4 Centrifuge at  $18,000 \times g$  for 20 minutes at  $4^{\circ}\text{C}$ .
  - 11.3.5 Transfer the supernatants into clean tubes and discard the pellets.
  - 11.3.6 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.
  - 11.3.7 Dilute samples to desired concentration in 1X Cell Extraction Buffer PTR.
- 11.4 **Preparation of extracts from tissue homogenates**
  - 11.4.1 Tissue lysates are typically prepared by homogenization of tissue that is first minced and thoroughly rinsed in PBS to remove blood (dounce homogenizer recommended).
  - 11.4.2 Homogenize 100 to 200 mg of wet tissue in  $500\ \mu\text{L}$  -  $1\ \text{mL}$  of chilled 1X Cell Extraction Buffer PTR. For lower amounts of tissue adjust volumes accordingly.
  - 11.4.3 Incubate on ice for 20 minutes.

- 11.4.4 Centrifuge at 18,000 x g for 20 minutes at 4°C.
- 11.4.5 Transfer the supernatants into clean tubes and discard the pellets.
- 11.4.6 Assay samples immediately or aliquot and store at -80°C. The sample protein concentration in the extract may be quantified using a protein assay.
- 11.4.7 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.**
- **It is recommended to 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. 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 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.

*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:*

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

13.9 Analyze the data as described below.



## 14. CALCULATIONS

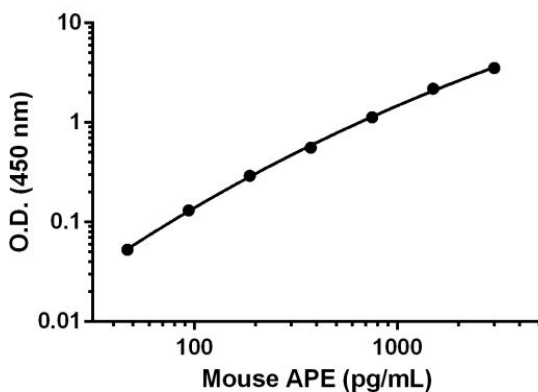
- 14.1 Calculate the average absorbance value for the blank control (zero) standards. Subtract the average blank control standard absorbance value from all other absorbance values.
- 14.2 Create a standard curve by plotting the average blank control subtracted absorbance value for each standard concentration (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.

*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.

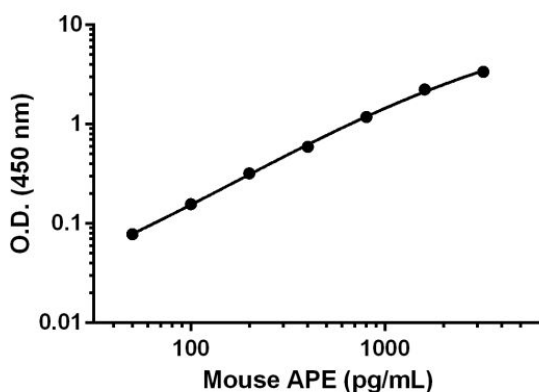
## 15. TYPICAL DATA

**TYPICAL STANDARD CURVE** – Data provided for **demonstration purposes only**. A new standard curve must be generated for each assay performed.



Standard Curve Measurements			
Conc. (pg/mL)	O.D. 450 nm		Mean O.D.
	1	2	
0	0.093	0.112	0.102
46.88	0.154	0.157	0.155
93.75	0.237	0.232	0.234
187.5	0.399	0.390	0.395
375	0.657	0.668	0.663
750	1.241	1.233	1.237
1,500	2.268	2.315	2.291
3,000	3.600	3.667	3.637

**Figure 1.** Example of mouse APE standard curve in Sample Diluent NS. The APE standard curve was prepared as described in Section 10. Raw data values are shown in the table. Background-subtracted data values (mean  $\pm$  SD) are graphed.



Standard Curve Measurements			
Conc. (pg/mL)	O.D. 450 nm		Mean O.D.
	1	2	
0	0.067	0.062	0.065
50	0.144	0.142	0.143
100	0.224	0.219	0.221
200	0.382	0.389	0.386
400	0.670	0.645	0.657
800	1.252	1.248	1.250
1,600	2.298	2.314	2.306
3,200	3.462	3.431	3.447

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

## 16. TYPICAL SAMPLE VALUES

### SENSITIVITY –

The calculated minimal detectable dose (MDD) is determined by calculating the mean of zero standard replicates and adding 2 standard deviations then extrapolating the corresponding concentration. The MDD is dependent on the Sample Diluent buffer used:

Sample Diluent Buffer	n=	Minimal Detectable Dose
Sample Diluent NS	24	28.8 pg/mL
1X Cell Extraction Buffer PTR	24	4.6 pg/mL

### RECOVERY –

Three concentrations of mouse APE 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 (%)
RPMI Base Media (10%)	100%	98 – 104%

### 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 APE was measured in mouse C2C12 and NIH 3T3 cell extracts, rat PC12 cell extract, and human PC3 cell extract in a 2-fold dilution series. Sample dilutions were made in 1X Cell Extraction Buffer PTR.

Recombinant mouse APE was spiked into 10% RPMI Base Media and diluted in a 2-fold dilution series in Sample Diluent NS.

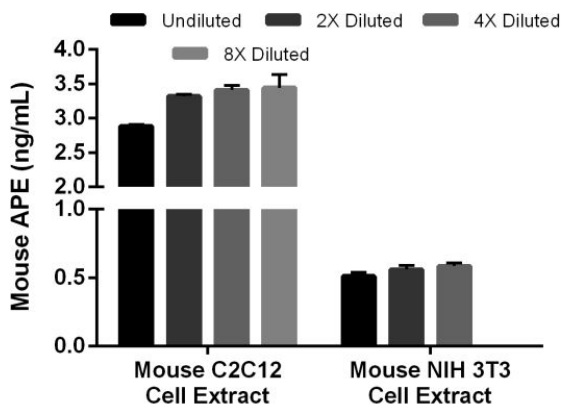
Dilution Factor	Interpolated value	150 µg/mL Mouse C2C12 Cell Extract	3.13 µg/mL Mouse NIH 3T3 Cell Extract	12.5 µg/mL Rat PC12 Cell Extract	100 µg/mL Human PC3 Cell Extract	10% RPMI Base Media
Undiluted	pg/mL	2,882.50	509.55	1,942.59	2,603.78	1,662.31
	% Expected value	100	100	100	100	100
2	pg/mL	1659.62	278.27	1059.48	1362.83	757.22
	% Expected value	115	109	109	105	91
4	pg/mL	852.46	145.82	549.60	713.91	402.21
	% Expected value	118	114	113	110	97
8	pg/mL	430.37	NL	NL	366.69	208.60
	% Expected value	119	NL	NL	113	100
16	pg/mL	NL	NL	NL	191.82	101.5
	% Expected value	NL	NL	NL	118	98

NL – Non-Linear

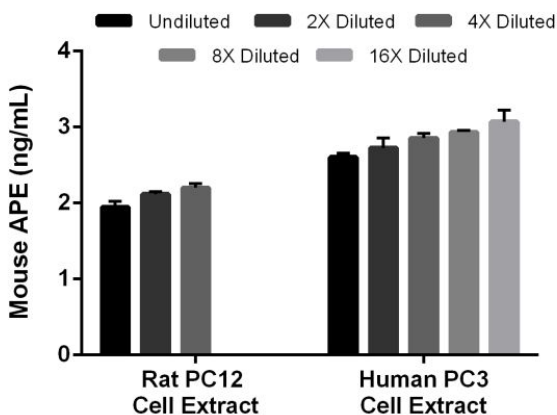
## PRECISION –

Mean coefficient of variations of interpolated values of APE in 3 concentrations of mouse C2C12 cell extract within the working range of the assay.

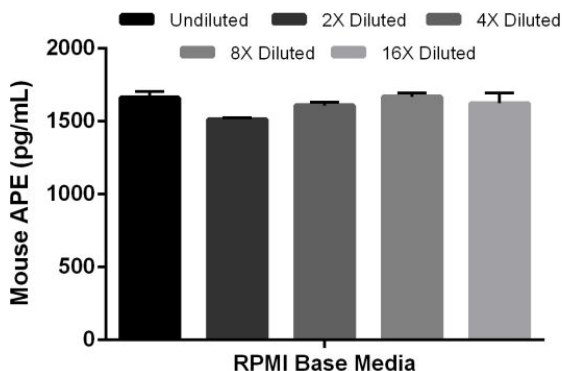
	Intra-Assay	Inter-Assay
n=	8	3
CV (%)	3.1	8.8



**Figure 3.** Interpolated concentrations of native APE in mouse C2C12 cell extract and NIH 3T3 cell extract based on 150  $\mu\text{g/mL}$  and 3.13  $\mu\text{g/mL}$  extract loads, respectively. The concentrations of APE were measured in duplicate and interpolated from the APE standard curve and corrected for sample dilution. The interpolated dilution factor corrected values are plotted (mean  $\pm$  SD,  $n=2$ ). The mean APE concentration was determined to be 3.26 ng/mL in C2C12 cell extract and 0.55 ng/mL in NIH 3T3 cell extract.



**Figure 4.** Interpolated concentrations of native APE in rat PC12 cell extract and mouse PC3 cell extract based on 12.5  $\mu\text{g/mL}$  and 100  $\mu\text{g/mL}$  extract loads, respectively. The concentrations of APE were measured in duplicate and interpolated from the APE standard curve and corrected for sample dilution. The interpolated dilution factor corrected values are plotted (mean  $\pm$  SD,  $n=2$ ). The mean APE concentration was determined to be 2.09 ng/mL in rat PC12 cell extract and 2.84 ng/mL in mouse PC3 cell extract.



**Figure 5.** Interpolated concentrations of spiked APE in RPMI Base Media. The concentrations of APE were measured in duplicates, interpolated from the APE standard curve and corrected for sample dilution. Undiluted samples are as follows: RPMI Base Media 10%. The interpolated dilution factor corrected values are plotted (mean  $\pm$  SD,  $n=2$ ). The mean APE concentration was determined to be 1,616 pg/mL in RPMI Base Media 10%.



### **17. ASSAY SPECIFICITY**

This kit recognizes both native and recombinant mouse APE protein in cell culture supernatant, cell and tissue extract samples only.

Serum and plasma samples are not suitable for this assay.

#### **CROSS REACTIVITY**

Recombinant human APE protein was prepared at 3,200 pg/mL in 1X Cell Extraction Buffer PTR and assayed in a 2-fold dilution series for cross-reactivity. On average, human APE protein is 52% cross-reactive to Mouse APE with a standard deviation of 6%. For example, 3,200 pg/mL of Human APE protein interpolates as 1,664 pg/mL of Mouse APE protein.

Please contact our Technical Support team for more information

## 18. TROUBLESHOOTING

Problem	Cause	Solution
Difficulty pipetting lysate; viscous lysate.	Genomic DNA solubilized	Prepare 1X Cell Extraction Buffer PTR (without enhancer). Add enhancer to lysate after extraction.
Poor standard curve	Inaccurate Pipetting	Check pipettes
	Improper standard dilution	Prior to opening, briefly spin the stock standard tube and dissolve the powder thoroughly by gentle mixing
Low Signal	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
Large CV	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
Low sensitivity	Improper storage of the ELISA kit	Store your reconstituted standards at -80°C, all other assay components 4°C. Keep TMB substrate solution protected from light.
Precipitate in Diluent	Precipitation and/or coagulation of components within the Diluent.	Precipitate can be removed by gently warming the Diluent to 37°C.

### 19. NOTES

## Technical Support

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