

Protocol for AGRP(83-132)-Amide ENZYME IMMUNOASSAY KIT

(Cat. No. EK-003-53)
(range: 0-100 ng/ml)



PHOENIX PHARMACEUTICALS, INC.

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CAUTION:

Investigational device. Limited by law to investigational use.
For research use only. Not for use in diagnostic procedures.

KIT CONTENTS

1. EIA assay buffer concentrate (20x, 50ml)..... **Catalog no. EK-BUF**
2. Pre-coated EIA plate (96 wells, 1 plate)
3. Acetate plate sealer (APS) (3 pieces)
4. Primary AGRP (83-132)-amide antibody (1 vial)
5. Standard AGRP (83-132)-amide peptide (1 vial)
6. Biotinylated AGRP (83-132) (1 vial)
7. Positive control (2 vials)
8. Streptavidin-horseradish peroxidase (SA-HRP) concentrate (30 μ l)
9. Substrate solution (12ml)
10. 2N HCl (Stop solution) (15ml)

ADDITIONAL MATERIALS, NOT INCLUDED

1. Microtiter plate reader (450nm) (required)
2. Micropipette with disposable pipette tips (required)
3. Absorbent material for blotting (required)
4. Vortex (required)
5. Curve-fitting software capable of 4 parameter logistics (recommended)
6. Orbital plate shaker (300-400rpm) (recommended)
7. Microtiter plate washer (recommended)
8. Multi-channel pipette (50-100 μ l) (recommended)
9. Solution reservoir (recommended)
10. Centrifuge (optional)
11. EDTA Lavender Vacutainer blood collection tubes (optional)..... **Catalog no. VT-6450**
12. Aprotinin (30 TIU) (optional) **Catalog no. RK-APRO**
13. C18 SEP-COLUMN (optional)..... **Catalog no. RK-SEPCOL-1**
14. Buffer A (optional) **Catalog no. RK-BA-1**
15. Buffer B (optional) **Catalog no. RK-BB-1**

STORAGE

1. Store the kit at 4°C upon receipt. Do not freeze.
2. It is highly recommended that all solutions be used as soon as possible after reconstitution.
3. Any unused strips/columns may be removed from the pre-coated immunoplate. Please place strips back in the original zip-lock foil pouch with a desiccant, reseal, and store at 4°C. Do not allow moisture to accumulate on the wells.
4. If necessary, store the 1x assay buffer at 4°C.
5. If necessary, store any reconstituted solutions of standard peptide, biotinylated peptide, antibody and SA-HRP at 4°C.

REFERENCES

1. Porstmann, T. and Kiessig, S.T., Enzyme Immunoassay Techniques, An Overview, *Journal of Immunological Methods*, 150: 5-21 (1992).
2. Avrameas, S., Amplification Systems in Immunoenzymatic Techniques, *Journal of Immunological Methods*, 150: 23-32 (1992).

Phoenix Pharmaceuticals, Inc. guarantees that its products conform to the information contained in this publication. The purchaser must determine the suitability of the product for their particular needs and establish optimum sample concentrations.

INTRODUCTION

This kit is designed to measure the concentration of a specific peptide and its related peptides based on the principle of a “competitive” enzyme immunoassay.

GENERAL DESIGN OF THIS KIT

The immunoplate in this kit is pre-coated with a secondary antibody, whose nonspecific binding sites are blocked. The secondary antibody can bind to the Fc fragment of the primary antibody. This primary antibody’s Fab fragment will then be competitively bound by both the biotinylated peptide and the targeted peptide in either the standard peptide solution or the unknown sample. The biotinylated peptide interacts with streptavidin-horseradish peroxidase (SA-HRP) which catalyzes the substrate solution. The intensity of the resulting yellow color is directly proportional to the amount of biotinylated peptide-SA-HRP complex, but inversely proportional to the amount of the targeted peptide (in either the standard peptide solution or the unknown sample). This is due to competition between the biotinylated peptide and the target peptide for binding with the primary antibody. A standard curve can be established by plotting the measured O.D. as a function of the various known standard peptide concentrations. Unknown peptide concentration in samples can then be determined via extrapolation based on this standard curve.

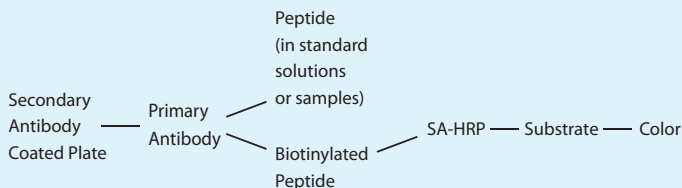


Figure 1. Diagram of the molecular interactions used in this kit

SUMMARY OF ASSAY PROTOCOL

Add 50 μ l/well of standard, sample, or positive control, along with 25 μ l/well of primary antibody and biotinylated peptide to each well

▼
Incubate at room temperature (20-23°C) for 2 hours

▼
Wash immunoplate 4 times with 350 μ l/well of 1x assay buffer

▼
Add 100 μ l/well of SA-HRP solution

▼
Incubate at room temperature (20-23°C) for 1 hour

▼
Wash immunoplate 4 times with 350 μ l/well of 1x assay buffer

▼
Add 100 μ l/well of TMB substrate solution

▼
Incubate at room temperature (20-23°C) for 1 hour

▼
Terminate reaction with 100 μ l/well of 2N HCl

▼
Read absorbance O.D. at **450nm** and calculate results

Note: Read this protocol in its entirety before starting the assay. Each kit contains reagents sufficient for 96 wells and is capable of assaying 40 duplicate samples.

ASSAY PROTOCOL

Note: The kit and all its components should be equilibrated to room temperature (20-23°C) before opening any vials and starting the assay. Before opening any Eppendorf tubes for reconstitution, briefly centrifuge at ~3,000rpm for 5 seconds to ensure that all the lyophilized material is at the bottom of the tube.

1. Dilute the 20x EIA assay buffer concentrate with 950ml of distilled water. Mix thoroughly before use. This will be the 1x assay buffer solution used to dilute or reconstitute all other samples and reagents during the assay.

Note: If crystals appear in the 20x assay buffer, the bottle can be placed in a warm water bath for approximately 30 minutes or until no crystals are visible.

2. Reconstitute the standard AGRP (83-132)-amide in 1ml of the 1x assay buffer and vortex thoroughly. Allow the solution to sit at least 10 minutes at room temperature (20-23°C) to completely dissolve in solution. This will be the standard stock solution.

Note: Vortex immediately before use.

3. Reconstitute the primary AGRP (83-132)-amide antibody in 5ml of 1x assay buffer and vortex thoroughly. Allow the solution to sit for at least 5 minutes at room temperature to completely dissolve.
4. Reconstitute the biotinylated AGRP (83-132)-amide in 5ml of 1x assay buffer and vortex thoroughly. Allow the solution to sit for at least 5 minutes at room temperature to completely dissolve.
5. Reconstitute the positive control in 200 μ l of 1x assay buffer and vortex thoroughly. Allow the solution to sit for at least 5 minutes at room temperature to completely dissolve.

Prepare peptide standard solutions as follows:

Standard ID / Number	1x Assay Buffer Volume	Standard Peptide Volume	Concentration
Stock	1000 μ l	(powder)	1000ng/ml
#1	900 μ l	100 μ l of stock	100ng/ml
#2	900 μ l	100 μ l of #1	10ng/ml
#3	900 μ l	100 μ l of #2	1ng/ml
#4	900 μ l	100 μ l of #3	0.1ng/ml
#5	900 μ l	100 μ l of #4	0.01ng/ml

Figure 2. Table of the standard dilutions

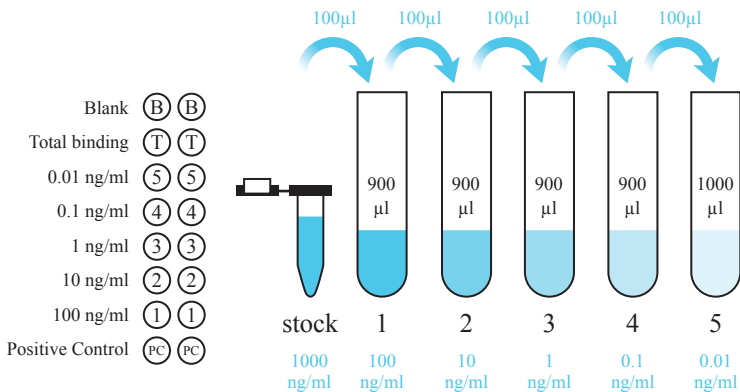


Figure 3. Immunoplate loading map

Figure 4. Visual guide of the standard dilutions

6. Prepare the standard dilutions from the rehydrated standard peptide as shown in Figure 2 and Figure 4 on the previous page. Vortex the tube thoroughly after each serial dilution.
7. Leave wells A1 and A2 on the immunoplate empty as blanks.
8. Add 50 μ l of 1x assay buffer into wells B1 and B2. These will represent total binding (of the biotinylated peptide).
9. Add 50 μ l of the least concentrated peptide standard solution (#5) to wells C1 and C2. Next, add peptide standard #4 into wells D1 and D2, and so forth, continuing in the opposite order of the standard dilution.
Note: Standard peptides should always be assayed in duplicate.
10. Add 50 μ l of rehydrated positive control into wells H-1 and H-2.
Note: Positive controls should always be assayed in duplicate.
11. Add 50 μ l of any unknown/prepared samples into their designated wells, again in duplicate.
Note: Each laboratory must determine the appropriate dilution factors and preparation for their samples to ensure that peptide levels are detectable and within the linear range of the standard curve.
12. Add 25 μ l of rehydrated primary AGRP (83-132)-amide antibody into each well **except** the blank wells (A1 and A2).
Note: A multi-channel pipette is **NOT** recommended to load the primary antibody.
13. Add 25 μ l of rehydrated biotinylated AGRP (83-132)-amide into each well **except** the blank wells (A1 and A2).
Note: A multi-channel pipette is **NOT** recommended to load the biotinylated peptide.
14. Seal the immunoplate with an acetate plate sealer (APS). Incubate the immunoplate for 2 hours at room temperature (20-23°C).
Note: Orbital shaking at 300-400 rpm is recommended for the duration of the incubation.
15. Centrifuge the SA-HRP vial (3,000-5,000 rpm for 5 seconds) to mix. Pipette 12 μ l of SA-HRP into 12ml of 1x assay buffer and vortex the solution thoroughly.

16. Remove the APS from the immunoplate and discard the contents of the wells. Wash each well with 350µl of 1x assay buffer, discard the buffer, invert the immunoplate, and blot the plate dry. Repeat 4 times.

17. Add 100µl of SA-HRP solution into each well.

18. Reseal the immunoplate with an APS. Incubate for 1 hour at room temperature (20-23°C).

Note: Orbital shaking at 300-400 rpm is recommended for the duration of the incubation.

19. Remove the APS from the immunoplate and discard the contents of the wells. Wash each well with 350µl of 1x assay buffer, discard the buffer, invert the immunoplate, and blot the plate dry. Repeat 4 times.

20. Add 100µl of the TMB substrate solution into each well.

Note: TMB is light-sensitive. After the addition of the TMB substrate solution, it is strongly recommended to cover the immunoplate to protect it from light.

21. Reseal the immunoplate with an APS. Incubate for 1 hour at room temperature (20-23°C).

Note: Orbital shaking at 300-400 rpm is recommended for the duration of the incubation.

22. Remove the APS from the immunoplate. Do **NOT** wash or the immunoplate or discard the contents of the wells.

23. Add 100µl of 2N HCl into each well to stop the reaction. The color in the wells should change from blue to yellow. Gently tap the plate to ensure thorough mixing.

Note: Proceed to the next step within 20 minutes.

24. Load the immunoplate onto a microtiter plate reader and measure absorbance O.D. at 450nm.

ADDITIONAL RECOMMENDATIONS

- Reagents of different lot numbers should never be mixed.
- Plasma, serum, culture media, tissue homogenate, CSF, urine, or any biological fluid can be assayed as long as the level of peptide in the sample is high enough for the sensitivity of the specific kit.
- High levels of interfering proteins may cause variations within sample results. Therefore, it is imperative to select the appropriate sample preparation procedure to obtain optimal results. Please consult the literature for specific methodology.
- When handling the plate, avoid touching the bottom. Any fingerprints or blots may affect the O.D. readings.
- Manual washing may cause high duplicate coefficient variations. To reduce this factor, liquid from the plate should be removed by inverting and blotting the plate on an absorbent material.
- Each time a new tip is used, make sure the tip is secure and free of air bubbles. For better intra-assay variation, aspirate and expel a reagent or sample back into its container a few times to wet the pipette walls prior to loading the pipette.
- Avoid submerging the whole pipette tip into reagents and samples. Droplets can accumulate at the end of the tip, causing an excess of solution to be loaded into the well and affecting assay results.
- Performing this procedure outside of the recommended room temperature (20-23°C) may affect assay results.
- Any modifications to the existing protocol (i.e. standard dilutions, pipetting technique, washing technique, incubation time or temperature, storage conditions, and kit expiration) may affect the sensitivity, specificity and results of the assay.

CALCULATION OF RESULTS

1. Label the X-axis (log scale) with the concentration of standards #5 through #1 (0.01 to 100 ng/ml).
2. Label the Y-axis (linear scale) as absorbance (O.D.) at 450nm.
3. Average all duplicate readings (standards, positive control, samples) and subtract the average blank O.D. reading.
4. Plot the O.D. for each standard peptide concentration directly above its X-axis coordinate.
5. Draw the best fit curve through these data points. It should show a direct relationship between peptide concentration and absorbance. As the standard peptide concentration increases, the yellow color decreases, thereby reducing absorbance (O.D.).

Note: We strongly recommend using curve-fitting software capable of 4 parameter logistics or log-logit functionality.

6. To determine the peptide concentration in any unknown samples, first locate its absorbance (O.D.) on the Y-axis. Draw a horizontal line across the graph from that absorbance to the intersection with the standard curve. The X-axis coordinate at this intersection point will correspond to the peptide concentration (ng/ml) in the assayed sample.

Note: Multiply the measured peptide concentration by any dilution factor(s) used while preparing the original sample.

7. Refer to the QC Data Sheet for acceptable values of the positive controls.

SUGGESTED METHOD FOR PEPTIDE EXTRACTION

Note: We strongly recommend performing a peptide extraction for all samples. This will help eliminate interfering molecules found in biological fluids, and allow for sample dilution or concentration.

General Blood Withdrawal and Plasma Collection:

1. Collect blood samples into Lavendar Vacutainer tubes (Catalog no. VT-6450), which contain EDTA and can hold up to 7ml of blood.
2. Gently rock the Lavendar Vacutainer tubes several times immediately after collection of blood to avoid coagulation.
3. Transfer the blood to centrifuge tubes containing aprotinin (Catalog no. RK-APRO), and gently rock several more times to inhibit the activity of proteases.

Note: We recommend 0.6 TIU, or 100 μ l, of Aprotinin per 1ml of blood collected. If the Lavendar Vacutainer tubes are centrifuge-safe, the Aprotinin may be added directly to them.

4. Centrifuge the blood at 1,600 x g for 15 minutes at 4°C and collect the plasma.

Note: Plasma can be kept at -70°C and will remain stable for up to one month.

5. For peptide extraction from sample, acidify the plasma with an equal amount of Buffer A (Catalog no. RK-BA-1). Mix and centrifuge at 6,000 to 17,000 x g for 20 minutes at 4°C. This will be loaded onto the C-18 SEP-COLUMN.

Note: We recommend using at least 1ml of plasma for peptide extraction. It may be possible to perform the extraction using smaller volumes as long as volumes of reconstituting and eluting buffer are adjusted accordingly.

General Tissue Preparation:

1. Boil tissue in 75% HoAc (Acetic Acid) for 20 minutes at 100°C.
2. Homogenize tissue in lysis buffer, usually with a low pH.
3. Centrifuge the tissue homogenate at 12,000rpm for 20 to 30 minutes at 4°C.
4. For peptide extraction from sample, take 1ml of supernatant and combine with 1ml of Buffer A (Catalog no. RK-BA-1) to acidify sample. Centrifuge at 6,000 to 17,000 x g for 20 minutes and collect the supernatant. This will be loaded onto the C-18 SEP-COLUMN. Performing the centrifugation on ice helps to inhibit peptidases.

Note: If a separate protein assay is required, designate and remove an aliquot before addition of Buffer A. This buffer contains materials which may interfere with protein analysis.

Extraction of Peptides from Sample:

1. Equilibrate a SEP-COLUMN containing 200mg of C18 (Catalog no. RK-SEPCOL-1). Wash with 1ml of Buffer B (Catalog no. RK-BB-1) once, followed by 3ml of Buffer A three (3) times.
2. Load the acidified sample (plasma, serum, tissue, etc.) solution onto the pre-equilibrated C-18 SEP-COLUMN.
3. Slowly wash the column with 3ml of Buffer A twice and discard the wash.
4. Elute the peptide slowly with 3ml of Buffer B once and collect the eluant into a polystyrene tube.

Note: Ensure there is a constant flow for all solutions during the extraction procedure. For optimal sample processing and recovery, do not allow air bubbles to enter the C-18 matrix.

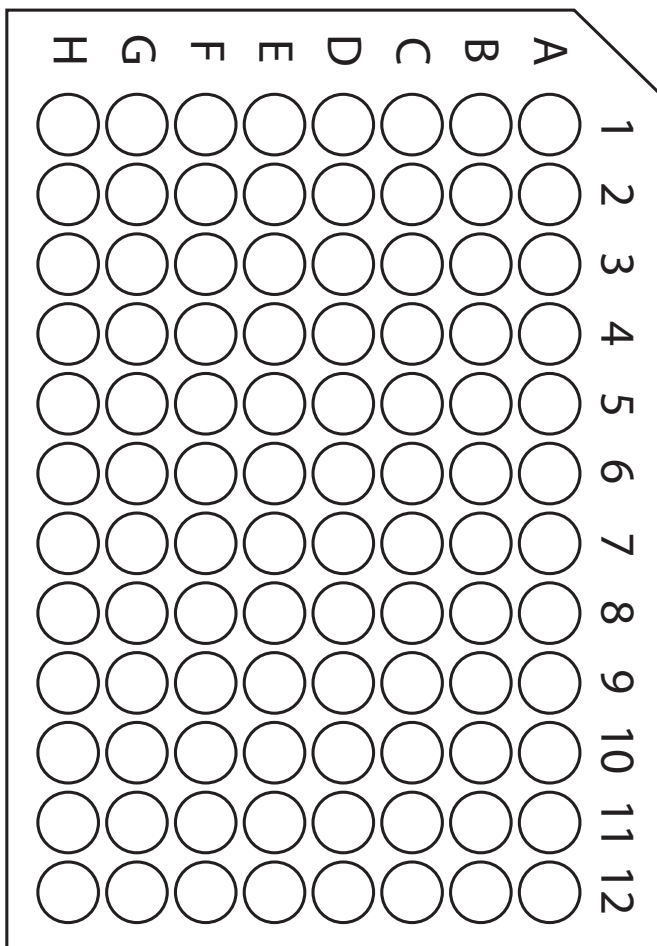
5. Evaporate eluant to dryness in a centrifugal concentrator or by a suitable substitute method.

Note: A combination of a centrifugal concentrator (i.e. Speedvac) and a lyophilizer (freeze-dryer) produces the best results. First, use a centrifugal concentrator to dry the sample for approximately 15 minutes, removing the organic layer. Snap-freeze the remaining sample and freeze-dry overnight using a lyophilizer. If a centrifugal concentrator is not accessible, freeze-drying overnight using a lyophilizer will be sufficient.

6. Keep the dried extract at -20°C and perform the assay as soon as possible. Use the 1x assay buffer to reconstitute the dried extract to the desired concentration. If the peptide value does not fall within the range of detection, dilute or concentrate the sample accordingly.

Note: For example, if 1ml of plasma was extracted, dried, and then reconstituted in 250 μl of 1x assay buffer, then the original sample would have now have undergone a 4x concentration.

ASSAY DIAGRAM



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