

## Introduction

**Bradford Protein Assay Kit** is a quick and ready-to-use colorimetric assay for total protein quantitation. When coomassie dye binds protein in an acidic medium, an immediate shift in absorption maximum occurs from 465 nm to 595 nm with a concomitant color change from brown to blue. Performing the assay is simple: combine a small amount of protein sample with the assay reagent, mix well, incubate briefly and measure the absorbance at 595 nm. Protein concentrations are estimated by reference to absorbances obtained for a series of standard protein dilutions, which are assayed alongside the unknown samples. Because the color response with coomassie is non-linear with increasing protein concentration, a standard curve must be completed with each assay.

## Package Information

Components	C0120
Bradford assay reagent	500 ml
BSA standard	10 ml, 2 mg/ml

## Storage

Store at 2-8°C and protect from light.

## Preparation of BSA Standard

Use Table 1 as a guide to prepare a set of protein standards.

**Table 1.** Preparation of Diluted BSA Standards

Dilution Scheme for Standard Test Tube and Microplate Protocol (Working range: 100-1500 µg/mL)

Vial	Volume of Diluent	Volume and Source of BSA	Final BSA Concentration
A	0	300 µL of Stock	2000 µg/mL
B	125 µL	375 µL of Stock	1500 µg/mL
C	325 µL	325 µL of Stock	1000 µg/mL
D	175 µL	175 µL of vial B dilution	750 µg/mL
E	325 µL	325 µL of vial C dilution	500 µg/mL
F	325 µL	325 µL of vial E dilution	250 µg/mL
G	325 µL	325 µL of vial F dilution	125 µg/mL
H	400 µL	100 µL of vial G dilution	25 µg/mL
I	400 µL	0	0 µg/mL (Blank)

Dilution Scheme for Micro Test Tube and Microplate Protocol (Working range: 1-25 µg/mL)

Vial	Volume of Diluent	Volume and Source of BSA	Final BSA Concentration
A	2370 µL	30 µL of Stock	25 µg/mL
B	4950 µL	50 µL of Stock	20 µg/mL
C	3970 µL	30 µL of Stock	15 µg/mL
D	2500 µL	2500 µL of vial B dilution	10 µg/mL
E	2000 µL	2000 µL of vial D dilution	5 µg/mL
F	1500 µL	1500 µL of vial E dilution	2.5 µg/mL
G	5000 µL	0	0 µg/mL (Blank)

## Test Tube Protocol

### A. Standard Test Tube Protocol (Working range: 100-1500 µg/mL)

- Pipette 30 µL of each standard or unknown sample into appropriately labeled test tubes.
- Add 1.5 mL of Bradford reagent to each tube and mix well.
- Incubate samples for 5 min at room temperature.
- With the spectrophotometer set to 595 nm, zero the instrument on a cuvette filled only with water. Subsequently, measure the absorbance of all the samples.
- Substrate the average 595 nm measurement for the Blank replicates from the 595 nm measurements of all other individual standard and unknown sample replicates.
- Prepare a standard curve by plotting the average blank-corrected 595 nm measurements for each BSA standard vs. its concentration in µg/mL. Use the standard curve to determine the protein concentration of each unknown sample.

### B. Micro Test Tube Protocol (Working range: 1-25 µg/mL)

- Pipette 1 mL of each standard or unknown sample into appropriately labeled test tubes.
- Add 1 mL of Bradford reagent to each tube and mix well.
- Incubate samples for 5 min at room temperature.
- With the spectrophotometer set to 595 nm, zero the instrument on a cuvette filled only with water. Subsequently, measure the absorbance of all the samples.
- Substrate the average 595 nm measurement for the Blank replicates from the 595 nm measurements of all other individual standard and unknown sample replicates.
- Prepare a standard curve by plotting the average blank-corrected 595 nm measurements for each BSA standard vs. its concentration in µg/mL. Use the standard curve to determine the protein concentration of each unknown sample.

## Microplate Protocol

### A. Standard Microplate Protocol (Working range: 100-1500 µg/mL)

- Pipette 5 µL of each standard or unknown sample into appropriate microplate wells.
- Add 200 µL of Bradford reagent to each well and mix with plate shaker for 30 seconds.
- Incubate plate for 5 min at room temperature.

4. Measure the absorbance at or near 595 nm with a plate reader.
5. Subtract the average 595 nm measurement for the Blank replicates from the 595 nm measurements of all other individual standard and unknown sample replicates.
6. Prepare a standard curve by plotting the average blank-corrected 595 nm measurements for each BSA standard vs, its concentration in  $\mu\text{g/mL}$ . Use the standard curve to determine the protein concentration of each unknown sample.

**Note:** If using curve-fitting algorithms associated with a microplate reader, a four-parameter (quadratic) or best-fit curve will provide more accurate results than a purely linear fit. If plotting results by hand, a point-to-point curve is preferable to a linear fit to the standard points.

**B. Micro Microplate Protocol (Working range: 1-25  $\mu\text{g/mL}$ )**

1. Pipette 100  $\mu\text{L}$  of each standard or unknown sample into appropriately labeled test tubes.
2. Add 100  $\mu\text{L}$  of Bradford reagent to each well and mix with plate shaker for 30 seconds.
3. Incubate plate for 5 min at room temperature.
4. Measure the absorbance at or near 595 nm with a plate reader.
5. Subtract the average 595 nm measurement for the Blank replicates from the 595 nm measurements of all other individual standard and unknown sample replicates.
6. Prepare a standard curve by plotting the average blank-corrected 595 nm measurements for each BSA standard vs, its concentration in  $\mu\text{g/mL}$ . Use the standard curve to determine the protein concentration of each unknown sample.

**Note:** If using curve-fitting algorithms associated with a microplate reader, a four-parameter (quadratic) or best-fit curve will provide more accurate results than a purely linear fit. If plotting results by hand, a point-to-point curve is preferable to a linear fit to the standard points.