

Jul 01, 2022

## Bradford protein assay – Protein concentration measurement (single 595 nm read)

Daniel C Moreira<sup>1</sup><sup>1</sup>Universidade de Brasília

1 Works for me

Share

[dx.doi.org/10.17504/protocols.io.14egnx3ml5d/v1](https://dx.doi.org/10.17504/protocols.io.14egnx3ml5d/v1)

Daniel Moreira  
Universidade de Brasília

### ABSTRACT

This protocol describes how to measure the concentration of total protein in a sample performing the Bradford's assay using microtiter plates. Procedures are slightly modifications based on the method described in M.M. Bradford, A rapid and sensitive method for the quantitation of microgram quantities of protein utilizing the principle of protein-dye binding, Anal. Biochem. 72 (1976) 248–254.

### DOI

[dx.doi.org/10.17504/protocols.io.14egnx3ml5d/v1](https://dx.doi.org/10.17504/protocols.io.14egnx3ml5d/v1)

### PROTOCOL CITATION

Daniel C Moreira 2022. Bradford protein assay – Protein concentration measurement (single 595 nm read). **protocols.io**  
<https://dx.doi.org/10.17504/protocols.io.14egnx3ml5d/v1>

### KEYWORDS

Protein, Protein determination, Colorimetric assay, Bradford, Microtiter plate, Microplate

### LICENSE

————— This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

### CREATED

Jul 22, 2019

### LAST MODIFIED

Jul 01, 2022

### PROTOCOL INTEGER ID

26075

## MATERIALS

**users Catalog #1001150**

RAD Catalog #5000006

Aldrich Catalog #A0281

Corning® 96 well NBS™ Microplate Sigma

Aldrich Catalog #CLS3651

 UV-transparent cuvettes **BIO-**

RAD Catalog #1702511

 **Coomassie Brilliant Blue G Sigma**

Aldrich Catalog #B0770

Ethanol Fisher

Scientific Catalog #10538071

Phosphoric acid solution **Sigma**


Aldrich Catalog #W290017

Microplate Reader

Molecular Devices 8002482 [↗](#)

Multi-mode microplate readers (Absorbance, Fluorescence (top/bottom read), and Luminescence (top/bottom read)). Ranges: Abs, 200–1000 nm; FL, 250–850 nm; Lumi, 250–850 nm. Light source: Xenon flashlamp. Detector: Silicon photodiode, Photomultiplier tube. Readtypes: Endpoint, Kinetic, Spectrum scan, and Well scan.

### Bradford's protein reagent preparation

- 1 Prepare a solution containing 0.01% (w/v) Coomassie Brilliant Blue G-250 (e.g., B0770, Sigma-Aldrich), 4.7% (v/v) ethanol, and 8.5% (v/v) phosphoric acid as described in the next steps.
- 2 Weight 100 mg of Coomassie Brilliant Blue G-250 (e.g., B0770, Sigma-Aldrich) and dilute it in 50 mL of ethanol using a magnetic stirrer at room temperature.
- 3 

**In a fume hood, slowly add 100 mL of 85% (w/v) phosphoric acid (e.g., W290017, Sigma-Aldrich) to the previous solution and homogenize.**

- 4 **Dilute the resulting solution to a final volume of 1,000 mL with distilled water<sup>1</sup>.** Filter through a Whatman No. 1 paper (or equivalent). Store at room temperature protected from light.

<sup>1</sup> Alternatively, you can use commercially available ready-to-use reagents (e.g., 5000006, Bio-Rad).

#### Protein standard solutions preparation

- 5 **Prepare a 4 mg/mL bovine serum albumin (BSA, e.g., A0281, Sigma-Aldrich) stock solution in PBS<sup>2</sup>.**

*Example:* Dilute 6 mg in a final volume of 1.5 mL.

<sup>2</sup> If compatible<sup>3</sup>, use the same solvent/buffer in which the sample to be analyzed was prepared to make the BSA standard solutions.

<sup>3</sup> Check buffer components incompatibility with the Bradford reagent. There are several available online. For example: [http://www.bio-rad.com/webroot/web/pdf/lsr/literature/Bulletin\\_6852.pdf](http://www.bio-rad.com/webroot/web/pdf/lsr/literature/Bulletin_6852.pdf) and <https://www.sigmaaldrich.com/content/dam/sigma-aldrich/docs/Sigma/Bulletin/b6916bul.pdf>.

#### 6

**Check the BSA concentration in the stock solution.** Read it at 280 nm in an UV-transparent cuvette and use the equation below to calculate the actual BSA concentration.

$$BSA (mg/mL) = \left( \frac{Abs_{280} \times 10}{6.6} \right) \times dilution$$

*Example:* If you diluted 50 µL of the BSA stock solution in a final volume of 1,000 µL and it resulted in a absorbance of 0.130, you have:

$$BSA (mg/mL) = \left( \frac{0.130 \times 10}{6.6} \right) \times 20$$

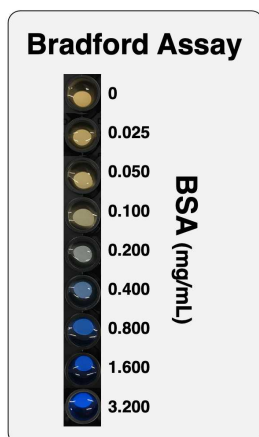
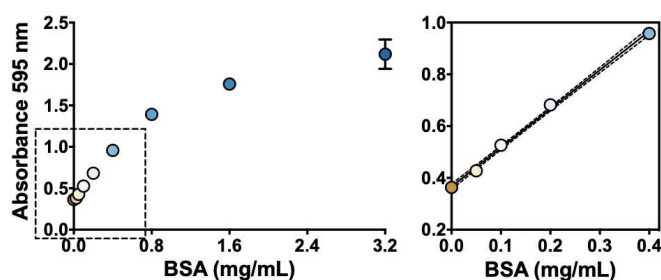
$$BSA (mg/mL) = 3.94$$

- 7 **Prepare several BSA solutions at concentrations from 0.05 to 0.40 mg/mL<sup>4</sup> using PBS (or the relevant buffer/solvent) in Eppendorf tubes.**

*Example:* If your stock solution is 3.94 mg/mL, first prepare a 0.4 mg/mL (50.8 µL to a final volume of 500 µL) and then dilute it serially to 0.20, 0.10, and 0.05 mg/mL (e.g., 100 µL of the previous solution + 100 µL of PBS).

<sup>4</sup> Under the conditions described in this protocol, the change in absorbance at 595 nm is linear within the 0.05–0.40 mg/mL BSA range (see figure below).

**Note:** There is another reading procedure that extends the linear range of the assay, which is to read at two wavelengths, 450 nm and 590 nm, and plot A<sub>590</sub>/A<sub>450</sub> versus BSA concentration (see the protocol "Bradford protein assay – Protein concentration measurement (A<sub>590A</sub>/A<sub>450</sub> ratio)")




## Sample preparation

- 8 Dilute samples in appropriate buffer (e.g., PBS; see section/step 5) to achieve an expected concentration<sup>5</sup> that lies within the concentration range of the standard curve (0.05–0.04 mg/mL; see section/step 7).

*Example:* Considering that rat liver contains ~100 mg protein/g wet weight, if you have a rat liver extract/homogenate that was prepared diluting the tissue sample 1:20 (resulting in ~5 mg protein/mL), you need to further dilute by a factor of least 15 (total dilution 1:300, resulting in ~0.333 mg/mL) before proceeding with the assay.

<sup>5</sup> If an estimate of protein concentration for your tissue/cell sample is not available, test several concentrations.

## Assay

- 9 

Add 260  $\mu$ L of water to at least three wells of a 96-well microtiter plate.

These will be the microplate reader blanks (also known as 'auto zero' or 'reference wells').

- 10 Add 10  $\mu$ L of each BSA standard solution to at least three wells of a 96-well microtiter plate.

Remember to prepare a zero/blank standard, which is the buffer used to prepare the standards but with no BSA.

- 11 Add 10  $\mu$ L of each sample to at least three wells of a 96-well microtiter plate.

Ideally, you should use several dilutions of the sample and check whether there is a linear response between signal (absorbance at 595 nm) and amount of sample. One convenient assay of doing it is to pipet several volumes (e.g., 1, 2, 5, 10  $\mu$ L) and add it up to 10  $\mu$ L with the appropriate buffer. This also maximizes the chance of getting at least one dilution of the sample within the dynamic range of the standard curve for unknown samples.

Example:

- Dilution 1 – 1 µL sample + 9 µL buffer;
- Dilution 2 – 2 µL sample + 8 µL buffer;
- Dilution 3 – 5 µL sample + 5 µL buffer;
- Dilution 4 – 10 µL sample.

## 12 Add 250 µL of Bradford's protein reagent to each well containing BSA standards or samples.

If available, use a positive displacement pipette device (e.g., Multipette M4, Eppendorf) to avoid bubbles.

Do not add Bradford's protein reagent to wells containing 260 µL water. These are used just as blanks for the microplate reader.

## 13 Incubate the 96-well microtiter plate at room temperature for 5 min.

## 14 Read the microplate at 595 nm.

Read before 1 h of incubation. At high protein concentrations, precipitation begins after 10–15 minutes.

Alternatively, also acquire absorbances at 450 nm and 590 nm (see step 7).

### Calculation

## 15

Calculate the average absorbance for each BSA standard and samples using the absorbance values at 595 nm of the triplicates.

BSA mg/mL	Absorbance at 595 nm			
	Read 1	Read 2	Read 3	Average
0.00	0.362	0.363	0.365	0.363
0.05	0.418	0.428	0.436	0.427
0.10	0.521	0.529	0.529	0.526
0.20	0.681	0.680	0.685	0.682
0.40	0.961	0.960	0.952	0.958

BSA standard solutions.

Sample	Absorbance at 595 nm			
	Read 1	Read 2	Read 3	Average
Rat liver homogenate (1:500)	0.532	0.540	0.537	0.536

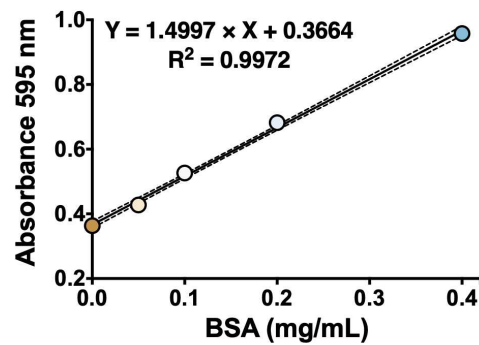
Sample example: 5 µL of rat liver homogenate (1:500, w/v) + 5 µL PBS.

## 16 Build a standard curve.

Plot the average absorbance value at 595 nm on the Y- axis *versus* BSA concentration in mg/mL on the X-axis.

Calculate a linear regression ( $Y = a \times X + b$ ; e.g., 'add a linear trendline' in Microsoft Excel).

Example:



## 17 Calculate protein concentration in samples using the equation generated in the previous step.

Interpolate unknown protein concentration from the standard curve and multiply by all dilutions.

$$\text{Protein (mg/mL)} = \left( \frac{(\text{AVG } A_{595} - b)}{a} \right) \times \text{Dilution1} \times \text{Dilution2}$$

Example:

For this example (see step 15), the dilution factors are 500 (a rat liver homogenate was prepared at 1:500, w/v) and 2 (5 µL were added to the microplate and added up to 10 µL with buffer).

$$\text{Protein (mg/mL)} = \left( \frac{(0.536 - 0.3664)}{1.4997} \right) \times 500 \times 2$$

$$\text{Protein (mg/mL)} = 113.09$$

For tissues, the final result is often expressed as mg protein per gram of wet weight (mg/gww) assuming 1 g/mL. Thus, this rat liver sample used as example would have 113.09 mg/gww.