

DEC 12, 2022

WORKS FOR ME

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## Chloroform-methanol protein precipitation from microalgae and Pierce BCA assay

COMMENTS 0

DOI

[dx.doi.org/10.17504/protocols.io.yxmvm2e25g3p/v1](https://dx.doi.org/10.17504/protocols.io.yxmvm2e25g3p/v1)Ying-Yu Hu<sup>1</sup>, Christopher Lord<sup>1</sup>, Zoe V Finkel<sup>1</sup><sup>1</sup>Dalhousie UniversityMarine Microbial Macroecology Lab  
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### ABSTRACT

Chlorophyll, phospholipids, sucrose, glycerol and some detergent in crude protein extracted from microalgae can interfere the Pierce BCA protein assay. In order to remove these interference, bead miller extracted protein is precipitated by chloroform-methanol prior to BCA assay. The resulting precipitation is dissolved into Sarcosine-Tris solution. Low limit of detection is about 5 ug/mL.

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### PROTOCOL CITATION

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### KEYWORDS

Protein , Microalgae, Chloroform-methanol precipitation, Pierce BCA assay

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73284

SAFETY WARNINGS

Use fume-hood when handling methanol and chloroform.

All waste containing methanol and chloroform shall be collected in waste container for halogenated organic solvents.

## Reagent preparation

- 1 Tris buffer [M] 5 mM (pH 8.0)  
Add  500 µL [M] 1 M  8.0 Tris into 100 mL MilliQ water  
 Tris(hydroxymethyl)aminomethane hydrochloride 1M pH 8.0 RNase free **Fisher Scientific Catalog #AAJ60080AK**
- 2 20% Sarcosine  
Dilute 2 part 30% N-lauroylsarcosine sodium salt with 1 part [M] 5 mM (pH 8.0) Tris buffer  
 N-lauroylsarcosine sodium salt solution (30%) **Sigma Aldrich Catalog #61747**

1h 12m

## Protein precipitation

- 3 Thaw protein extract
- 4 Turn on refrigerate centrifuge

### Equipment

**CENTRIFUGE 5430 R**

NAME

Eppendorf

BRAND


MP2231000510

SKU

- 5 Turn on incubator/shaker, preheat to  37 °C


Equipment	
<b>SHAKING INCUBATOR</b>	NAME
71L	TYPE
Corning® LSE™	BRAND
6753	SKU

6 Prepare ice-bath


7 Well mix the extract and then transfer  100 µL of extract to 2 mL microtube (Abdos tubes give better precipitation results), in replicate.

Equipment	
<b>Micro Centrifuge Tubes</b>	NAME
Abdos	BRAND
P10203	SKU

#### Note


8 In the fume hood, add  400 µL methanol


 Methanol **Sigma Aldrich Catalog #34860**


9 Gently vortex for  00:00:30 by using a tube insert 30s

Equipment	
VWR ANALOG VORTEX MIXER	NAME
VWR	BRAND
10153-838	SKU
With tube insert	SPECIFICATIONS

10 In the fume hood, add  100  $\mu$ L chloroform  
 Chloroform (HPLC grade) **Sigma Aldrich Catalog #439142-4L**


11 Gently vortex for  00:00:30 by using a tube insert 30s

12 In the fume hood, add  300  $\mu$ L MilliQ


13 Gently vortex for  00:00:30 by using a tube insert 30s

14 Incubate  On ice for  00:30:00 30m

15  20000 rcf, 4°C, 00:10:00 10m

16 In the fume hood, remove upper phase by leaving about  250  $\mu$ L liquid

Note

17 In the fume hood, add  300  $\mu$ L methanol

18 Gently mix the liquid until bottom layer disappear and the solution is homogenous.



Note

19  20000 rcf, 4°C, 00:10:00

10m



20 In the fume hood, remove all solvent.

Note

21 If pellet tends to be aspired with solvent, add another  300  $\mu$ L methanol, gently vortex, and  
 20000 rcf, 4°C, 00:10:00

10m





22 In the fume hood, remove most solvent by using 1000  $\mu$ L pipet tip, and then remove the rest by using 100  $\mu$ L pipet tip. Do not remove pellet with solvent.

23 Dry pellet in vacuum desiccator for at least  00:30:00 at  Room temperature

30m


Note

## BCA assay

24 Add  5  $\mu\text{L}$  20% sarcosine and  95  $\mu\text{L}$   5 mM (pH 8.0) Tris buffer to dry protein pellet, incubate at  37 °C for 15 to 30 min.

25 Use tube insert, vortex all tubes for 15 to 30 min until pellet is completely re-dissolved.

26 BSA standard solutions

 Thermo Scientific™ Pierce™ Bovine Serum Albumin Standard 2 mg/mL (50 mL) Thermo Scientific Catalog #Thermo Scientific™ 0023210


Standard	20% sarcosine (uL)	5 mM Tris (uL)	2 mg/mL BSA (uL)	Final Conc. (mg/mL)
SD1	5	95	0	0
SD2	25	470	5	0.02
SD3	25	463	12	0.048
SD4	25	450	25	0.1
SD5	25	425	50	0.2
SD6	25	375	100	0.4
SD7	25	275	200	0.8
SD8	25	225	250	1

27 Vortex and then use reverse pipetting: transfer  100  $\mu\text{L}$  standard solutions into the corresponding tubes, except for SD1 (it has already been 100  $\mu\text{L}$ ).



28 Use the following formula to determine the total volume of working reagent (WR) required. Consider leaving several mL of extra volume:

$$(\# \text{ standards} + \# \text{ samples}) \times \left( \text{img alt="pipette icon" data-bbox="350 845 390 865"} 800 \mu\text{L} \right) = \text{total volume WR required}$$

29 Prepare WR by mixing 50 parts of BCA reagent A with 1 part of BCA Reagent B in a 50 mL falcon tube

- 30 Use one tip and reverse pipetting: Add  800  $\mu$ L WR into each tube, make sure that the tip doesn't have contact with the solution, so that samples are not cross-contaminated.

Note

- 31 Vortex each tube, shake and incubate at  37 °C for  00:30:00

30m

- 32 Remove samples from the incubator.

- 33 Load samples into microplate in duplicate:

Note

### Equipment

#### 96-Well Microplates

Polystyrene, Clear,

Greiner Bio-One

82050-760

NAME

TYPE

BRAND

SKU

- 34 Shake for 5 s at 600 rpm in a continuous and high force mode  
Read endpoint 562 nm with a measurement time 100 ms

### Equipment

#### Varioskan LUX Multimode Microplate Reader

Thermo Fisher

VL0L00D0

NAME

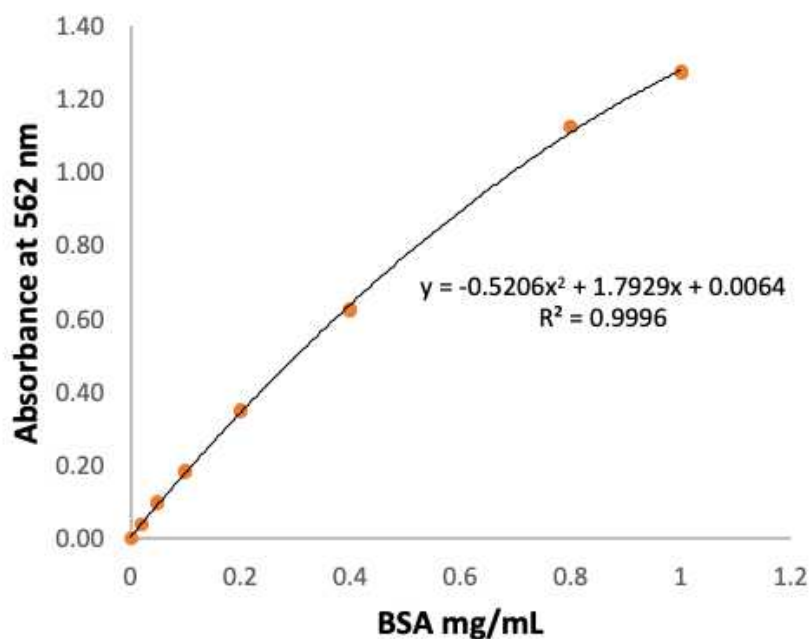
BRAND

SKU

## Calculation

- 35 Subtract the average 562 nm absorbance measurement of the blank standard replicates from the 562 nm measurements of all other individual **standard**.
- 36 Subtract the average 562 nm absorbance measurement of the blank sample (filter) replicates from the 562 nm measurements of all other individual **sample**.
- 37 Prepare a standard curve by plotting the average Blank-corrected 562 nm measurement for each BSA standard versus its concentration in mg/ml. The standard curve is quadratic.





- 38 For the calculation convenience, plot BSA concentration (Conc) versus Corrected absorbance (Abs) to obtain a standard curve as following:

$$\text{Conc\_mg/mL} = a \times \text{Abs}^2 + b \times \text{Abs} + c$$

Use the corrected measured absorbance of samples (Abs) to calculate the total protein concentration (Conc\_mg/mL) from each sample.

- 39 Protein\_mg/filter = Conc\_mg/mL X PEB\_mL

Where PEB is the volume of protein extraction buffer used to extract protein from microalgae sample.