FEB 13, 2019

OPEN ACCESS

DOI:
[dx.doi.org/10.17504/protocols.io.vg3e3yn](https://doi.org/10.17504/protocols.io.vg3e3yn)

External link:
<https://doi.org/10.1371/journal.pone.0210123>

Protocol Citation: Paloma Varela 2019. Size Exclusion Chromatography coupled to Multi Angle Light Scattering (SECMALS). **protocols.io**
<https://dx.doi.org/10.17504/protocols.io.vg3e3yn>

MANUSCRIPT CITATION:
 Varela PF, Velours C, Aumont-Niçaise M, Pineau B, Legrand P, Poquet I (2019) Biophysical and structural characterization of a zinc-responsive repressor of the MarR superfamily. PLoS ONE 14(2): e0210123. doi: [10.1371/journal.pone.0210123](https://doi.org/10.1371/journal.pone.0210123)

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

Protocol status: Working

Size Exclusion Chromatography coupled to Multi Angle Light Scattering (SECMALS)

PLOS One

Paloma
Varela¹

¹Institute for Integrative Biology of the Cell, CEA, CNRS, Université Paris-Saclay, Gif-sur-Yvette, France

Paloma Varela

MATERIALS

To determine the oligomeric state of ZitR_{MG}, 50 ml of fully purified protein sample at approximately 1-4 mg.ml⁻¹ were loaded on a KW-803 column (Shodex) equilibrated at 0.5 ml.min⁻¹ flow rate (Shimadzu HPLC system) and supplemented with either 1 mM ZnSO₄ or 1 mM EDTA (Fig. S1). Detection was performed using a MiniDAWN TREOS multi angle light scattering detector and an Optilab T-REX differential refractometer (Wyatt Technology) (biophysics platform, LEBS/IMAGIF). Molar mass and hydrodynamic radius were calculated with the Astra 6.1.1.17 software using a differential index of refraction (dn/dc) value of 0.183 ml.g⁻¹.

Created: Nov 09, 2018

Last Modified: Feb 13, 2019

PROTOCOL integer ID:
17659