Video Article

Online Size-exclusion and Ion-exchange Chromatography on a SAXS Beamline

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Abstract

Biological small angle X-ray scattering (BioSAXS) is a powerful technique in molecular and structural biology used to determine solution structure, particle size and shape, and surface-to-volume ratio of macromolecules. The technique is applicable to a very wide variety of solution conditions spanning a broad range of concentrations, pH values, ionic strengths, temperatures, additives, etc., but the sample is required to be monodisperse. This caveat led to the implementation of liquid chromatography systems on SAXS beamlines. Here, we describe the upstream integration of size-exclusion (SEC) and ion-exchange chromatography (IEC) on a beamline, different methods for optimal background subtraction, and data reduction. As an example, we describe how we use SEC- and IEC-SAXS on a fragment of the essential vaccinia virus protein D5, consisting of a D5N helicase domain. We determine its overall shape and molecular weight, showing the hexameric structure of the protein.

Video Link

The video component of this article can be found at https://www.jove.com/video/54861/

Introduction

BioSAXS is a powerful tool to determine the shape of nano-sized objects. The scattering of X-rays by a solution containing macromolecules, sized in the nm range, is recorded at very low angles. This angular range contains information about global parameters: the radius of gyration; the largest intraparticle distance; the particle shape; and the degree of folding, denaturation, or disorder. The technique does not require crystals, and the macromolecule stays in solution and thus can be kept in conditions mimicking certain important parameters of the cell, such as ionic strength, pH, etc. The knowledge of these factors might help to determine, for example, the physiologically relevant oligomeric state of a protein of interest or to validate a proposed model of a complex. The characterization of protein-protein interactions in different buffer conditions, the creation of models of missing domains, the refinement of homology models, and the determination of discrete folded and unfolded states can be performed quickly and easily.

As with any technique, BioSAXS has intrinsic weaknesses: aggregated or denatured samples, mixtures of particles, heterogeneous samples, radiation damage, and buffer mismatches may result in un-interpretable data. For many analysis methods, it is implicitly assumed that the sample is monodispersive, a requirement that is often difficult to obtain in practice. In many cases, the degradation of the sample is subtle and cannot be detected in the data on its own, and any attempt to interpret the data gives inaccurate or even misleading results. To overcome these obstacles, the combination of size-exclusion chromatography (SEC) and SAXS was implemented on many beamlines to ensure data quality and to make this technique more accessible for increasingly difficult samples. Recently, we added a new method to the repertoire by developing online ion-exchange chromatography (IEC)-coupled SAXS. Both techniques are opening SAXS to a wide range of biological particles formerly impossible to analyze. The choice of which method to use depends on the biophysical properties of the particles of interest.

SEC separates macromolecules by their size, whereby at least a 10% difference in apparent molecular mass is needed for the separation. Physical limitations of the column and physiological properties of the samples, like hydrophobic surfaces, flexibility, and lack of stability, also complicate data collection, analysis, and interpretation.

Ion-exchange chromatography, which separates molecules based on their charge and, hence, their binding affinity to the IEC column, can be used instead of or in addition to SEC. The total charge can be readily manipulated by changing the pH, or varying the salt concentration of the buffer, providing a relatively simple method for the controlled elution of the molecules from the IEC column. By using the charge, the separation of similar types and sizes of molecules, which would otherwise be difficult to separate, can be performed routinely with IEC. Additionally, IEC has the advantage of being able to deal with diluted samples, allowing one to avoid the concentration steps, which carry the potential risk of radiation damage, and buffer mismatches may result in un-interpretable data. For many analysis methods, it is implicitly assumed that the sample is monodispersive, a requirement that is often difficult to obtain in practice. In many cases, the degradation of the sample is subtle and cannot be detected in the data on its own, and any attempt to interpret the data gives inaccurate or even misleading results. To overcome these obstacles, the combination of size-exclusion chromatography (SEC) and SAXS was implemented on many beamlines to ensure data quality and to make this technique more accessible for increasingly difficult samples. Recently, we added a new method to the repertoire by developing online ion-exchange chromatography (IEC)-coupled SAXS. Both techniques are opening SAXS to a wide range of biological particles formerly impossible to analyze. The choice of which method to use depends on the biophysical properties of the particles of interest.

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DEN Selon le protocole de préparation en ligne et de génération d'échantillon de la protéine D5 supprimée, il est nécessaire de minimiser les pertes. Pour cette raison, la dernière étape de purification est en ligne directement avant l'acquisition de données SAXS, afin d'augmenter la probabilité de collecter un bon échantillon.

1. Description de la préparation en ligne et de la génération d'échantillon d'une protéine D5 supprimée

**NOTE:** Le construct D5323-785 (Figure 1A) a été cloné, exprimé et purifié selon la description précédente.

1. **Clone the construct into the pProEx HTb vector**

1.1.1. Perform a polymerase chain reaction (PCR) on D5R using the 5'-GCACATGGAATATTATATATGCACTTTTACGGAGATGAAATATCCTCTATGA-3' and 5'-ATGCAGGGAGATTGAATGAAATATCCTCTATGA-3' primers and a PCR reaction mix with polymerase, following the manufacturer's advice.

1.2. Purify the PCR fragments via spin columns, following the manufacturer's advice.

1.3. Digest the PCR fragments and the plasmid with the Ncol and HindIII restriction enzymes, following the manufacturer's recommendations for buffer composition and incubation time.

1.4. Run the fragments on a 1% agarose gel in 0.5x TAE buffer (20 mM Tris, 10 mM acetic acid, and 0.5 mM EDTA) and stain the gel with DNA dye.

1.5. Expose the gel to UV light. Caution: Wear personal safety equipment! Cut out the bands of the digested PCR fragments and the digested plasmid and purify the DNA using a gel purification spin column kit, following the manufacturer's recommendations.

1.6. Ligate the purified PCR fragments into the plasmid using a fast ligation kit, following the manufacturer's recommendations.

1.7. Transform via heat shock the product from the ligation reaction into competent bacteria optimized for plasmid amplification.

1.8. Add half of the ligation product to a vial of bacteria.

1.9. Incubate the reaction tube on ice for 20 min.

1.10. Incubate the tube at 42 °C for 30 s.

1.11. Place the tube on ice for 2 min.

1.12. Add 1 mL of Luria Bertani (LB) Broth (Miller) without antibiotics and let the cells recover at 37 °C for 1 h.

1.13. Spin down the cells at 16,100 x g for 3 s in a tabletop microtube centrifuge and remove most of the medium.

1.14. Spread the cells onto LB agar plates with ampicillin (50 µg/mL final) and let the colonies grow at 37 °C overnight.

1.15. Put a colony into 3 mL of LB with ampicillin (50 µg/mL final) and grow the culture at 37 °C, shaking at 160 rpm overnight.

1.16. Follow the instruction of the miniprep kit to extract the plasmid.

1.17. Send a sample of the plasmid for sequencing and analyze the sequence for the absence of mutations and for the correct insertion.

1.18. Transform the pProEx HTb D5323-785 construct into bacteria optimized for protein expression (use 1 µL and follow the steps in step 1.1). Spread the bacteria onto an LB agar plate with ampicillin (50 µg/mL final).

1.19. To create a starting culture, put one colony in 300 mL of LB with ampicillin (50 µg/mL final) and grow the bacteria at 37 °C, shaking at 160 rpm overnight.

2. Inoculate 12 x 1 L of LB in the presence of ampicillin (50 µg/mL final), each with 20 mL of the pProEx HTb D5323-785 bacteria starter culture at 37 °C until an OD$_{600}$ = 0.3 is reached. Reduce the temperature to 18 °C and induce expression at an OD$_{600}$ = 0.5 with 1 mM IPTG. Incubate the cultures, shaking them at 160 rpm and 18 °C overnight.

3. Harvest the bacteria by centrifugation at 50,000 x g and at 4 °C for 30 min. Resuspend the bacterial pellets in approximately 150 mL of lysis buffer (50 mM Tris-HCl [pH 7], 150 mM NaCl, 5 mM MgCl$_2$, 10 mM β-mercaptoethanol, and 10% glycerol) with 1x protease inhibitor and 25 units (U)/10 mL DNase. Lyse the bacteria via sonication on ice (1-inch probe, 50% power, 0.5-s pulse, 0.5-s pause, 3x 5 min).

4. Load the supernatant onto a nickel affinity column (Ni-column, 1.5-mL bed volume), and wash it with 10 column volumes (CV) of binding buffer (50 mM Tris-HCl [pH 7], 150 mM NaCl, 10 mM β-mercaptoethanol, and 10% glycerol), 10 CV of washing buffer (50 mM Tris-HCl [pH 7], 1 M NaCl, 10 mM β-mercaptoethanol, and 10% glycerol), and 10 CV of imidazole wash (50 mM Tris-HCl [pH 7], 150 mM NaCl, 10 mM β-mercaptoethanol, 10% glycerol, and 30 mM imidazole). Elute the D5323-785 (20 mM Tris-HCl [pH 7], 150 mM NaCl, 10 mM β-mercaptoethanol, 10% glycerol, and 200 mM imidazole).
5. Inspect the different purification steps via sodium dodecyl sulfate (SDS)-polyacrylamide gel electrophoresis (PAGE).
   1. Load 2-20 μL of each purification step flow-through mixed with 1x loading dye (2x; 4% SDS, 20% glycerol, 120 mM Tris-HCl [pH 6.8], and 0.02% weight/volume bromophenol blue) on a 10% SDS gel and run them at 200 V in 1x Laemmli running buffer (25 mM Tris, 0.192 M glycine, and 0.1% SDS).
   2. Stain the gel with a ready-to-use Coomassie blue solution.

6. Exchange the buffer of the eluted protein with binding buffer using a desalting column according to the manufacturer's manual.
7. Cleave the His-tag by adding Tobacco Etch Virus nuclear-inclusion-a endopeptidase (TEV, 1 mg/100 mg of protein) to the protein solution. Incubate at room temperature overnight.
8. Check the digestion by performing SDS-PAGE (see step 1.5).
9. Equilibrate the Ni-column in binding buffer. Let the protein solution pass through and wash the beads with 2 CV of imidazole washing buffer while collecting the flow-through.
10. Concentrate the protein using a centrifugal concentrator to a final volume of 0.5 mL.
11. Inject the concentrated protein onto a size-exclusion column equilibrated with gel filtration buffer (20 mM Tris-HCl [pH 7], 150 mM NaCl, 10% glycerol, and 1 mM dithiothreitol [DTT]).
12. Collect the flow-through in 0.5-mL fractions.
13. Check the presence and purity of the protein in the peak samples by performing SDS-PAGE (see step 1.5).
14. Combine the fractions of the eluted peak of DS323.785. Dilute the sample to 25 mM NaCl and 5% glycerol while keeping the Tris and DTT concentrations constant. (for 5 mL of protein solution in 20 mM Tris-HCl [pH 7], 150 mM NaCl, 10% glycerol, and 1 mM DTT, first add 5 mL of 20 mM Tris-HCl [pH 7] and 1 mM DTT, and then add 20 mL of 20 mM Tris-HCl [pH 7], 5% glycerol, and 1 mM DTT).
15. Load the sample onto an ion-exchange column. Use buffer A (20 mM Tris [pH 7], 25 mM NaCl, 5% glycerol, and 1 mM DTT) and buffer B (20 mM Tris [pH 7], 1 M NaCl, 5% glycerol, and 1 mM DTT) to form a salt gradient from 25 mM to 1 M.
16. Collect the eluted protein in 1.5-mL fractions.
17. Check the presence and purity of the protein in the peak samples by performing SDS-PAGE (see step 1.5 and Figure 1B).
18. Reconcentrate the protein solution in a centrifugal concentrator to a final volume of 0.5 mL.
19. Run the concentrated protein on a size-exclusion column in gel filtration buffer (20 mM Tris-HCl [pH 7], 150 mM NaCl, 5% glycerol, and 1 mM DTT; see step 1.11).

2. Data Collection

NOTE: Request beam time as early as possible. For ESRF, guidelines on available access types and on how to submit an application can be found at:
http://www.esrf.eu/UsersAndScience/UserGuide/Applying. After the acceptance of the proposal and an invitation for the experiment, all participants have to complete a safety training. After validation of the training, fill in the "A-form" (via the ESRF user portal) to declare the researchers visiting the beamline for the experiment, along with the required safety information on the samples. Contact the local contact person to discuss the experiment.

1. SEC-SAXS data collection

NOTE: For online purification, use the high-performance liquid chromatography (HPLC) system installed at BM29. The system consists of an in-line degasser, a binary pump, a valve for buffer selection and gradients, an autosampler, a UV-VIS array photospectrometer, and a conductometer. It is directly attached to the flow-through capillary of the SAXS exposure unit.13
   1. Put 1 mL of the gel filtration buffer aside. Connect the buffer bottle to the SEC system (the default is Port A).
   2. Choose the flow rate depending on the column in use. Note: For the size-exclusion column used here, the flow rate is 0.1 mL/min.
   3. Flush the pumps and the upstream tubes via the "auto-purge" function.
   4. Wait until the system is filled with the buffer and connect the column. Equilibrate the column by passing at least 1.5 CV.
   5. Interlock the hatch and measure the buffer set aside in step 2.1.1, using the sample changer to control for variation of the signal due to radiation damage. Only continue if there is no radiation damage to the buffer.
   6. Switch the beamline control system to HPLC mode. Make a test run of buffer, collecting 200 frames with 1 s per frame. Write down the number of counts given by the detector in the summed intensity plot.
   NOTE: The signal should match the previously measured buffer, and the summed intensity over time should remain constant. If the signal does not match or is not constant, a longer equilibration of the system is required.
   7. Spin down the sample at 13,000 x g in a tabletop microtube centrifuge for at least 10 min.
   8. Fill the sample into an HPLC-compatible glass vial (provided) and put it into the auto-injector. Note the well position.
   9. Interlock the experimental hatch using standard procedure, as explained in the User Safety Training.
   10. Log into and create a folder for data storage through the beamline control software.
   11. Program the HPLC system using the "quick batch" feature. Set the storage location for the UV data to the folder created in step 2.1.10. Make sure to activate the automatic ASCII conversion of the UV data, storing the ASCII file in the same folder.
   1. Choose the injection volume and well position. Add the measurement to queue by pressing the "Start" button. The software will ask to save the batch. Prepare for saving, but do not press the "Save" button, as this automatically starts the measurement.
   12. Set up data collection parameters in the beamline control software. Choose the number of frames so that the total data collection time is in slight excess of the acquisition time defined in step 2.1.2.
   13. Open the safety shutter and start SAXS data collection using the beamline control software. Verify that the data are correctly acquired. Compare the newly collected data to the data collected in step 2.1.6 and check that the number of counts in the summed intensity remains constant for at least 100 frames and matches the value from step 2.1.6.
   1. Start the SEC run by pressing the "Save" button, as prepared in step 2.1.11, and note the frame number displayed in the camserver software when the injection is completed and UV data acquisition starts.
3. SEC-SAXS Data Reduction & Analysis

1. Open the data in data acquisition in ISPyB by pressing the “Go” button. Determine in the overview which frames of the SAXS data collection correspond to the elution peak. Verify that the radius of gyration is stable throughout the peak.

2. Confirm that the automated buffer correction was performed correctly. Load frames from the central part of the peak into a program that performs manipulations with experimental SAXS data files and average them. Then, load the automatically generated buffer file and check whether the high q regions of the averaged frames and the buffer frames match.

3. Compare the frames acquired throughout the peak quantitatively using the CORMAP test.
   1. Load the automatically created subtractions (*.sub.dat files) of frames covering the region of interest.
   2. Scale them to each other by pressing the “Scale” button.
   3. Compare them using the “Data Comparison” feature. There should be no systematic changes between the frames throughout the peak.

4. Open all *_sub.dat frames of interest, merge them using the "Merge" button, and save the merged file in .dat format.

5. Determine the radius of gyration with the "Radius of Gyration" tool in the program, noting the first data point in the Guinier range for later cropping of the data at low resolution.

6. Determine the pair-distance distribution function with the "Distance Distribution" tool in the program and save the resulting .out file as gnom.out.

4. Ab Initio Modeling

1. On a Unix machine, run a 40 x ab initio model reconstruction program without symmetry restrictions. Create a new folder and copy the gnom.out file to it. Run the program as follows:
   for (( i = 1; i <= 40; i++ )); do dammif gnom.out -m s -p dammifp1_$i; done

2. Analogously, run an ab initio model reconstruction program with symmetry restrictions for six-fold symmetry in a second folder:
   for (( i = 1; i <= 40; i++ )); do dammif gnom.out -m s -p dammifp6_$i; done
3. Align all ab initio model reconstruction program output files (*-1.pdb). In the two folders from steps 4.1 and 4.2, run damaver -a *-1.pdb.
4. Open the union of all models (damaver.pdb) as well as the model filtered to the correct volume (damfilt.pdb) in a suitable molecular visualization software and compare them.
5. Open the damsel.log file in a text editor. The model listed as the "reference" at the bottom of the file is the most representative model.

5. IEC-SAXS Data Reduction, Analysis, and Modeling

1. In the program that performs the manipulation with experimental SAXS data files, load about 50 SAXS frames from each mixing step of the buffer run, press the "AVERAGE" button, and save the results.
2. Based on the auto-processing results available via ISPyB, identify which frames of the experiment correspond to the elution of the protein and verify that the (preliminary) radius of gyration is stable throughout the peak.
3. Load the frames into the experimental SAXS data files manipulation program and average them, as done for the buffer frames (see step 5.1). Then, load the buffer files generated in step 5.1 and compare the high q regions (above 4.2 nm$^{-1}$) to find a buffer that matches the average from the peak.
   NOTE: There should be no systematic offset between the average from the peak and the buffer. If the sample curve seems to fall between two buffer curves, interpolate their curves by calculating the average.
4. Subtract the buffer identified as the best match from the average scattering curve of the peak fraction and save the resulting subtracted file. In addition, create subtracted curves using the average buffer curves from the preceding and following mixing steps to estimate the error margin of the subtraction.
5. Repeat steps 5.3 and 5.4 individually for the left and right halves of the peak and compare the results to those from step 5.4 to check for stability of the signal throughout the peak.
6. Follow steps 3.5 and 3.6 for all three subtracted curves from step 5.4.
7. Compare the results for all three subtracted curves.
   Note: Only results that remain robust within the error margin of subtraction can be trusted.
8. Perform modeling as in steps 4.1 and 4.2 for the best subtraction identified in step 5.3.
9. Follow step 4.3 to 4.5 to align the models and to identify the most representative one.

6. Comparison of the Results

1. Run a program to superimpose 3D structures on the representative models of the SEC (step 4.5) and IEC-SAXS data (step 5.9) with P6 symmetry: supcomb model_sec.pdb model_iec.pdb
2. Import the model_sec.pdb and the model_iec-r.pdb into a molecular visualization software.
3. Open the .fir files of the modelSec.pdb and the modeliec-r.pdb in a spreadsheet and create a 2D graph of experimental and calculated scattering curves.

Representative Results

The results of the model-free invariant analysis are listed in Table 1. The analysis of the D5$_{323-785}$ SEC-SAXS data showed a molecular mass estimate (from a Porod analysis) of 345 kDa versus 338 kDa, observed using IEC-SAXS. Both are in agreement with the expected mass of 6 times 53.5 kDa (321 kDa) for a hexamer. The ab initio modeling of both data sets was undertaken with no imposed symmetry (SEC-SAXS: $\chi^2 = 0.88$, IEC-SAXS: $\chi^2 = 3.1$) and using C6 symmetry (SEC-SAXS: $\chi^2 = 1.0$, IEC-SAXS: $\chi^2 = 4$). As the overall fits to the scattering data for both reconstructions are comparable in both cases (Figure 1D and E), C6 symmetry can be assumed. Thus, the model corresponds to a hexagonal cone-like structure with a central channel, which appears partially obstructed (SEC: Figure 1F; IEC: Figure 1G, overlay Figure 1H). An examination of individual models before averaging shows that this obstruction is likely to be an artifact of the averaging process.
Figure 1: SAXS data analysis and comparison of D5<sub>323-785</sub> (figure adapted from References 12 and 18). A) Schematic domain structure of D5 protein and D5<sub>323-785</sub>. B) Offline ion-exchange chromatogram with the indication of the three peaks. Orange curve: Absorbance at 280 nm (au), blue curve: percentage of buffer B. Percentages of buffer B at the peaks are indicated. C) Online ion-exchange chromatogram. Color key as in B. Additionally, the measured intensity is indicated in green. The experimental scattering curve and calculated curve of the model obtained by SEC-SAXS D) and IEC E) data analysis of D5<sub>323-785</sub>. F) Bead model of D5<sub>323-785</sub> based on SEC data and G) IEC data. H) Overlay of the SEC and IEC models. The panels in F) to H) were created using a molecular visualization software<sup>24</sup>. Please click here to view a larger version of this figure.
Data-collection parameters

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Instrument:</td>
<td>ESRF BM29</td>
</tr>
<tr>
<td>Wavelength (Å)</td>
<td>0.99</td>
</tr>
<tr>
<td>q-range (Å(^{-1}))</td>
<td>0.0032 – 0.49</td>
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<tr>
<td>Sample-to-detector distance</td>
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<tr>
<td>Exposure time (sec)</td>
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<tr>
<td>Concentration range</td>
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<tr>
<td>Temperature (K)</td>
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<tr>
<td>Detector</td>
<td>Pilatus 1M (Dectris)</td>
</tr>
<tr>
<td>Flux (photons/s)</td>
<td>(1 \times 10^{12})</td>
</tr>
<tr>
<td>Beam size (µm(^2))</td>
<td>700 × 700</td>
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</tbody>
</table>

Structural parameters for D5\(323-785\), SEC

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(I_0) (cm(^{-1})) [from Guinier]</td>
<td>0.0237</td>
</tr>
<tr>
<td>(R_g) (Å) [from Guinier]</td>
<td>48</td>
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<tr>
<td>(q_{\text{max}}R_g - q_{\text{min}}R_g) used for Guinier</td>
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<tr>
<td>(D_{\text{max}}) (Å) [from (p(r))]</td>
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</tr>
<tr>
<td>q-range used for (p(r)) (Å(^{-1}))</td>
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</tr>
<tr>
<td>Porod volume (V_p) (Å(^3)) [from Scatter]</td>
<td>((570 \pm 5) \times 10^{3})</td>
</tr>
<tr>
<td>Molecular mass (M_r) (kDa) [from (V_p)]</td>
<td>345</td>
</tr>
<tr>
<td>Calculated monomeric (M_r) from sequence (kDa)</td>
<td>321</td>
</tr>
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</table>

Structural parameters for D5\(323-785\), IEC

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>(I_0) (cm(^{-1})) [from Guinier]</td>
<td>0.386</td>
</tr>
<tr>
<td>(R_g) (Å) [from Guinier]</td>
<td>46.5 ± 0.1</td>
</tr>
<tr>
<td>(q_{\text{max}}R_g - q_{\text{min}}R_g) used for Guinier</td>
<td>0.44 - 1.29</td>
</tr>
<tr>
<td>(D_{\text{max}}) (Å) [from (p(r))]</td>
<td>120</td>
</tr>
<tr>
<td>q-range used for (p(r)) (Å(^{-1}))</td>
<td>0.03 - 0.18</td>
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<tr>
<td>Porod volume (V_p) (Å(^3)) [from Scatter]</td>
<td>((577 \pm 5) \times 10^{3})</td>
</tr>
<tr>
<td>Molecular mass (M_r) (kDa) [from (V_p)]</td>
<td>339</td>
</tr>
<tr>
<td>Calculated hexameric (M_r) from sequence (kDa)</td>
<td>321</td>
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</tbody>
</table>

Table 1: SAXS data parameters. The table summarizes the parameters of SAXS data acquisition and analysis.

Discussion

For many macromolecules, a final purification step using chromatography is required prior to SAXS data collection to obtain a good quality data set. However, not all samples remain stable; they may be prone to aggregation or re-equilibration to a mixture of oligomerization states. Therefore, a final online purification step on the beamline is required to minimize the time between purification and data collection in order to obtain the best-quality SAXS data. Depending on the biophysical properties of the protein of interest, SEC-SAXS or IEC-SAXS might be chosen to obtain optimal sample quality. Here, on a protein construct derived from the helicase/primase D5, both techniques are explained and discussed.

Acquisition of SEC-SAXS data is becoming more and more standardized and is available on many BioSAXS beamlines. Data analysis, especially background subtraction, is relatively straightforward and easy. However, a stable buffer signal and the sufficient separation of the macromolecular species remains essential. Therefore, it is critical to reserve enough time to equilibrate the column thoroughly. Failure of this method can be due to persistent contaminants of similar size to the protein of interest, low concentrations, and radiation-sensitive buffers.

In practice, initially, SEC-SAXS is likely to be used as the method of choice for most macromolecular samples. Still, many purification protocols require a prior IEC step due to the presence of contaminants or aggregation. Given that each concentration and chromatography step is associated with losses of sample (estimated at 30-50%) and time, direct IEC-SAXS is advantageous. For samples that cannot be purified by SEC, be it due to the presence of similarly sized "contaminants" or because they severely aggregate at the necessary concentrations, IEC-SAXS would always be the better-suited approach. Also, the higher flow rates supported by many IEC columns can help to reduce the transit time.
between purification and measurement. In the example presented here, IEC was used with a step elution, which allows for the separation of the close peaks of D5_{323-785} from contaminants by carefully choosing the salt concentration steps. In principle, the number of steps is unlimited, but practically, at least 1 step per peak is required, and not too many should be chosen. For the background subtraction method described above, it is crucial to measure a relatively high number of different buffer compositions in order to find the matching one.

A shared downside of both techniques is the lack of precise protein concentration information. Due to this, precise mass determination based on forward scattering is not possible. For globular proteins such as D5_{323-785}, the Porod volume provides an alternative, albeit less precise, mass estimate, but for highly flexible or disordered proteins, this approach would not be valid.

A variation of the step-wise gradient IEC-SAXS method presented here is the use of a linear gradient instead. While it is possible to work with as many steps as desired to isolate sub-peaks using a step-wise elution, in the linear gradient approach, it is required to optimize the gradient conditions carefully in order to separate the peaks entirely before starting the SAXS experiment. Background subtraction in this approach could be done frame-wise and could be verified by the comparison of the individual frames, but it requires more advanced data handling, and a dedicated software does not exist yet.

The choice of a suitable column is critical for both techniques, as it determines the separation of the macromolecular species. Size-exclusion columns differ in loading capacity, the size range of separable macromolecules, and resolution, while ion-exchange columns vary in the kind and the density of their immobilized charges.

While the protocol presented here is specific to the ESRF beamline BM29, adaptation to any other SAXS beamline is, in principle, straightforward. The main requirements are a sufficiently high X-ray flux and a suitable detector (ideally single-photon-counting), to acquire reasonable signal-to-noise data in the range of seconds or less, and an online liquid chromatography system capable of creating gradients. The exact implementation would, of course, depend on the local beamline environment.

The results obtained on D5_{323-785} using the two methods differ slightly. The radius of gyration is slightly smaller for the IEC data than for the SEC data, and the local minima of the scattering curve are shifted to slightly larger scattering vectors. This means that the D5_{323-785} measured with IEC-SAXS is slightly more compact than the D5_{323-785} measured with SEC-SAXS. This might be due to differences in the sample preparation, in the time between purification and measurement (IEC is faster), or, less likely, to a contaminant in the SEC-purified sample. The bead models obtained completely independently with both methods are comparable (Figure 1H). D5_{323-785} shows the expected hollow, hexameric structure 56.

In conclusion, online ion-exchange and online size-exclusion chromatography are important biochemical purification methods that can be coupled directly to SAXS. The background subtraction of IEC-SAXS data is slightly more difficult and ambiguous than for SEC-SAXS, but it is nevertheless possible. Depending on the biophysical properties of the protein of interest, both SEC and IEC-SAXS allow for the optimization of species separation with inherent advantages. Providing that the validation steps (as described) are correctly observed, the resulting data can be analyzed with confidence, and models can be determined using the standard tools available within the community. Together, both techniques allow online separation for a broad range of biological macromolecules, yielding data not accessible via standard static measurements.

### Disclosures

The authors have nothing to disclose.

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### References


