Generating a Calibration Curve with UHPLC Size Exclusion Column

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Overview

Size Exclusion Chromatography (SEC) is a technique for the separation of large molecules such as proteins and polymers based on their size in solution. To determine the hydrodynamic radius (R_h) of an unknown, a calibration curve can be generated with polymer standards. The relative retention times are plotted against the log MW for each respective standard, and a polynomial regression analysis is performed. Here we demonstrate the use of protein standards, with wellcharacterized hydrodynamic radii and molar masses, to generate calibration curves.

Figure 1 highlights the separation of common protein standards using a gel filtration standard for analytical and large-scale size exclusion analysis. **Table 1** shows a summary of relative elution times for these standards analyzed by SEC. Relative retention times plotted are then plotted against the log R_h for each respective standard, and a polynomial regression analysis is performed.

Figure 2 shows the calibration curve using a third order polynomial regression generated from standards and log R_h . Based upon the elution volume or retention time for NIST mAb (**Figure 3**), the measured R_h is 50.2 Å. This is within 97.2 % of the reported value of 5.2 Å for NIST mAb.

LC Conditions

Column:	Biozen™ 1.8 μm dSEC-2, 200 Å		
Part No.:	<u>00H-4787-E0</u>		
Dimensions:	300 x 4.6 mm		
Mobile Phase:	200 mM Potassium Phosphate, 250 mN		
	Potassium Chloride, pH 6.2		
Flow Rate:	0.35 mL/min		
Injection Volume:	10 μL		
Temperature:	25 °C		
Detection:	UV @ 280 nm		
Sample:	Protein Standards		

In summary, using a calibration curve generated by well-characterized standards can be used to determine the hydrodynamic radius of an unknown. Further, it may potentially be used for a stability indicating or biosimilarity method, as changes in post-translational modification such as deamidation and glycosylation can be detected with a well-developed analytical SEC method.

Table 1. Retention Times for Protein Standards

Analyte	Retention Time (min)	Relative Elution Volume (mL)	Theoretical R _h (Å)
Bovine Thyroglobulin	5.489	3.85	86
IgA	6.122	4.3	76
lgG	6.99	4.91	51
Ovalbumin	8.447	5.93	28
Myoglobin, horse heart	9.389	6.59	18.4
NIST mAb	7.078	4.97	52

Figure 1. SEC Chromatograms for Protein Standards

Chromatographic overlays of protein standards, y-axis normalized. Black- Thyroglobulin, Teal- Gamma Globulin (IgA/IgG), Red- Ovalbumin, Green- Myoglobin



Figure 2. Calibration Curve, Hydrodynamic Radius (R_h)

Calibration curve generating using relative elution volume of protein standards, plotted against log R_h . A third order polynomial regression was used to calculate R_h of various analytical samples.



Figure 3. Representative SEC Chromatogram for NIST mAb

Retention time for NIST mAb is 7.078 min. Extrapolated hydrodynamic radius is 50.2 Å



Have questions or want more details on implementing this method? We would love to help! Visit www.phenomenex.com/Chat to get in touch with one of our Technical Specialists



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