

Absolute molecular weight



Molecular size



Zetasizer µV



Light scattering
FOR PROTEINS



Integrated Dual Capability

- SEC-LS
- DLS

Introducing the Zetasizer μV with integrated dual light scattering capability

A highly sensitive batch DLS instrument and a powerful SEC-LS detector, in a single package.

Add the power of advanced light scattering technology to your size exclusion chromatography system (SEC-LS), or use in cuvette mode for large aggregate detection. Uses dynamic light scattering (DLS) to measure molecule size, and static light scattering to determine molecular weight.

Use as an SEC-LS detector to measure absolute size and molecular weight

Connect the Zetasizer μV to your SEC system using standard chromatography tubing

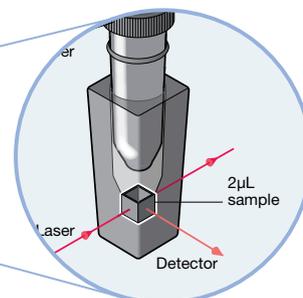
- Measure protein size and molecular weight
- No column calibration
- Determine protein oligomeric state
- Measure the polydispersity of each peak
- Low volume 8μL flow cell
- Compatible with any SEC system



Takes only seconds to change from Flow mode to Cuvette mode

Simply remove the flow cell and insert a cuvette

- No calibration required
- Minimum of 2μL of sample
- Absolute size measurement
- Sensitive detection of the presence of aggregates
- Screen buffers for crystallisation conditions
- Determine protein melting point or aggregation temperature
- Measure molecular weight and second virial coefficient

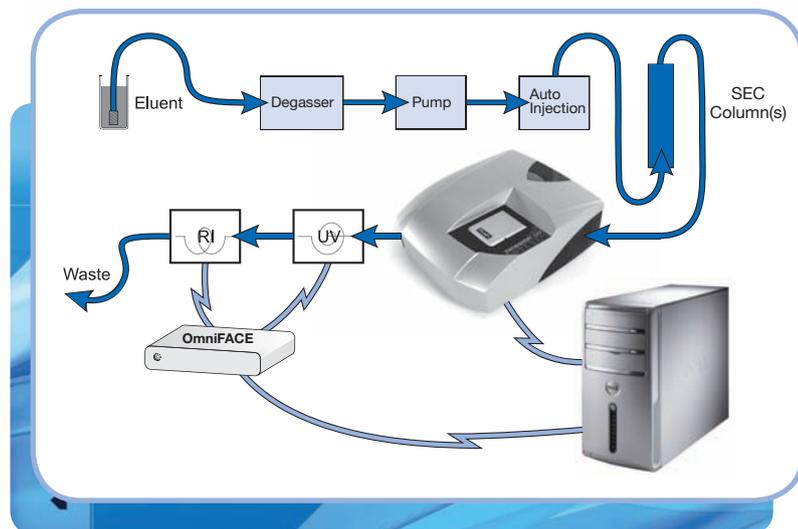


The Zetasizer μV as an SEC-LS detector

Buy as complete size exclusion chromatography system, or add to your existing SEC modules.

The Zetasizer μV uses static light scattering (SLS) to measure absolute molecular weight in conjunction with a concentration detector and dynamic light scattering (DLS) to measure size. DLS is an absolute technique, and hence the size measured is independent of the elution volume of the material. Measurements of molecular weight by SLS are also independent of the sample elution volume.

As the molecular weight and size of the protein monomer are measured, an eluted peak can unambiguously be characterised as the monomer oligomer, or higher order aggregate. Unlike conventional SEC, any material/column interactions will not interfere with this identification.



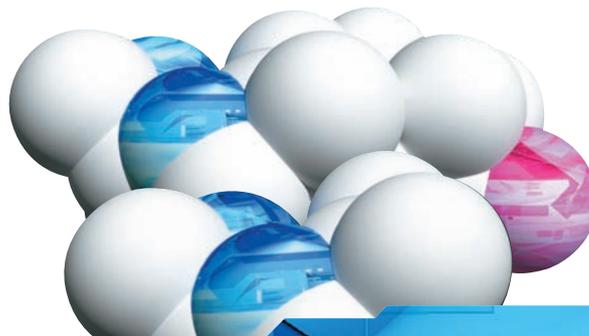
- No column calibration required
- Simple to install, just add in series with any other detectors such as UV or RI
- Autosampler connectivity
- Identify eluted material by size and absolute molecular weight
- Laser stability and optical setup means excellent baseline stability and signal-to-noise allowing maximum sensitivity
- 8μL flow cell minimises band broadening
- View the correlation function at every time point to assess data quality

The Zetasizer μ V for **cuvette mode measurements**

Optimised for simplicity and accuracy

Designed for protein applications, the Zetasizer μ V combines the highest sensitivity, a minimum 2 μ L volume requirement with high precision rapid temperature control to provide fast, accurate and absolute results.

- Automated signal attenuator – enables the measurement of any sample concentration
- High power stable laser – improves the speed of measurement and accuracy
- Condensation control, humidity sensor enables dry air input when required
- Uses the world's favourite DLS software to provide extensive functionality while maintaining ease of use



Benefits for protein measurements

The exceptional ease of operation of the system ensures that the power of the system is available to every operator

- Investigate the stability of the protein in your buffer
- Highly sensitive to the early onset of aggregation
- Determine potential stability by measuring the melting point or aggregation temperature
- The sensitivity and minimum 2 μ L sample volume means only 40ng of a 65kDa protein is required
- Use the second virial coefficient to study solubility and suitability for crystallization
- Measure the molecular weight using the Debye plot method



SEC-LS applications

Oligomeric state

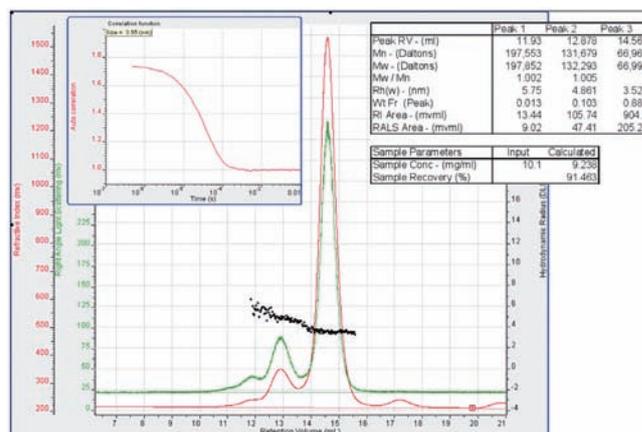
The activity of many proteins depends on their oligomeric state. Separation of a mixed population of protein oligomers allows the measurement of both the size and molecular weight of each and the subsequent determination of their oligomeric state.

Quantitation

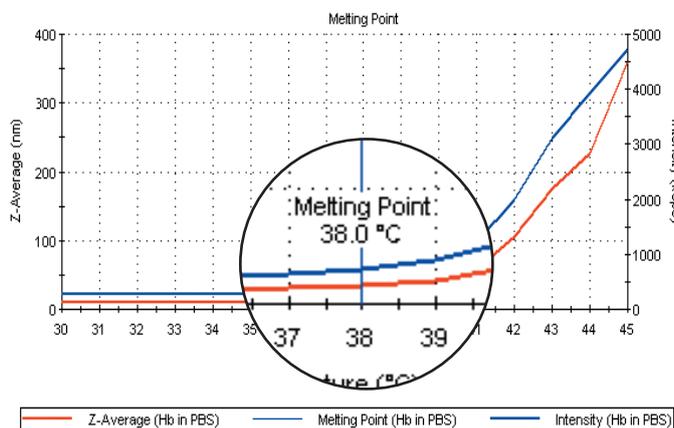
It is of great interest to many researchers to determine the fraction of the total population that is aggregated or has formed oligomers. Separation of the populations allows them to be fully characterised. Molecular weight, concentration and proportion can be measured for each peak.

Conjugation

Many proteins are conjugated with other molecules such as sugars, detergents or poly-ethylene glycol (PEG). The ability to add two concentration detectors means that conjugate analyses can be performed to determine the molecular weight and composition of the complex.



Cuvette (batch) applications



Aggregate detection

Light scattering is an ideal technique to determine the early onset of aggregation of a stressed protein, from the appearance of the first oligomers to aggregates up to a micron in size.

Buffer screening

As the measurement is completely non-invasive it can be performed in the native buffer to optimise storage conditions over a wide concentration range.

Protein stability

Stability can also be predicted from the temperature required to denature the protein. In the simplest case, the higher the melting point, the longer the shelf life of the protein.

Software designed for chromatography specialists - OmniSEC GPC/SEC

OmniSEC is a powerful yet easy to use GPC/SEC software suite providing data acquisition, analysis and reporting, and instrument control when used with Malvern Viscotek GPC systems.

This software can be used to control the Zetasizer μV alongside your SEC control software, when integrating with third-party instrumentation such as ÄKTA systems.

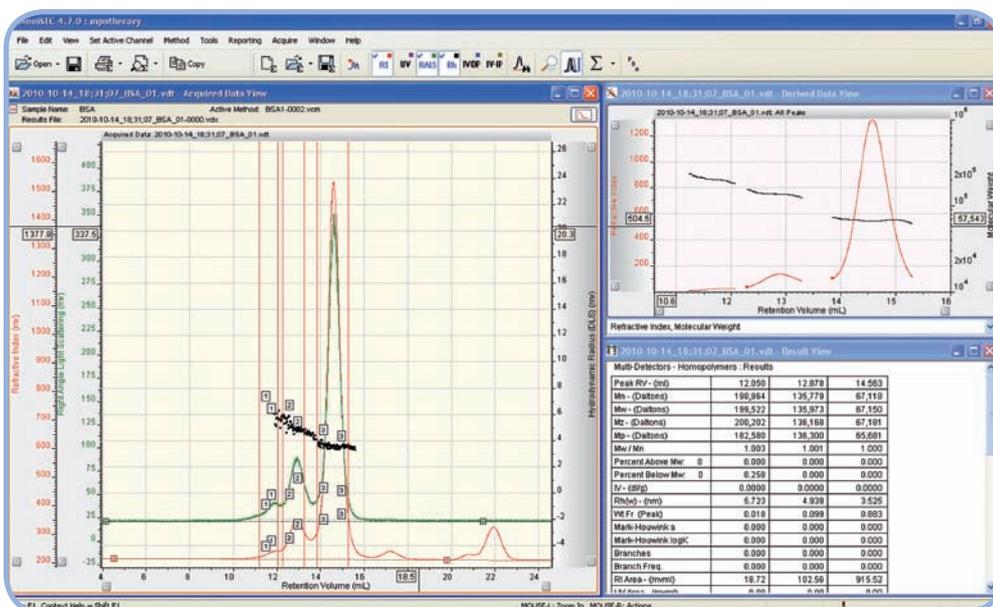
With a complete Malvern SEC-LS system simply load your samples and the software controls all the sequencing, enabling truly automatic unattended operation.

Support is provided for:

- Multiple detectors
- Absolute molecular weight
- Absolute molecular size
- Protein analysis
- Molecular conformation/branching
- Conjugate analysis
- Conventional calibration

OmniSEC contains many convenient and productive features:

- Two clicks from raw data to results
- Built-in, intuitive report designer
- Manual or fully automatic baseline setting
- Automatic determination of dn/dc , UV extinction coefficient and A_2
- Proven asymmetric band broadening corrections
- Integrated help system to guide users
- Full export capability of raw data, results and intermediate calculations
- Enables compliance with 21 CFR part 11



Batch DLS software designed for protein scientists

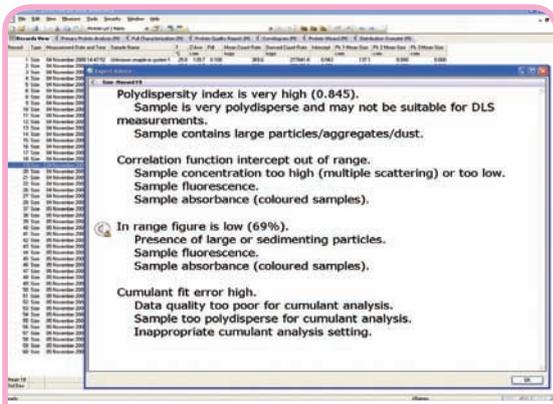
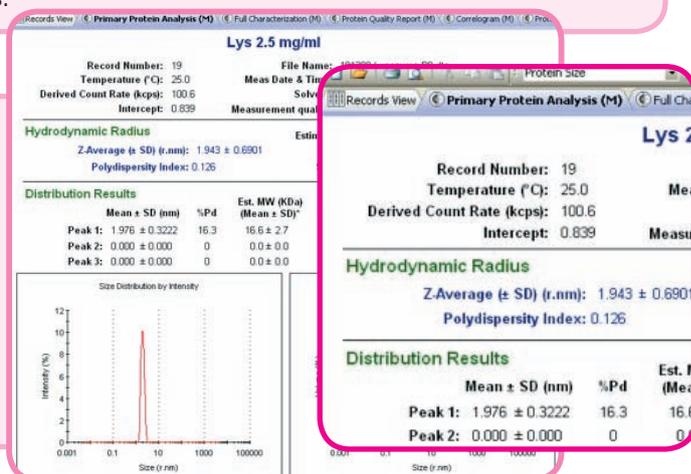
It's no coincidence that our user-friendly, flexible and intuitive software is also the world's most popular.

SOPs

Standard operating procedures (SOPs) simplify the way measurements are performed. Any measurement procedure can be customized to the specific needs of a test or sample. Each SOP can be saved so that experiments can be repeated with identical protocols.

Protein Workspace

The default setup of the software is customized for the analysis of proteins and biomolecules. Everything about this interface, from the parameters reported, the views of the results, the units used and the measurement procedures are geared to support the requirements of the protein specialist.



Expert Advice System

Producing the data is now easy, but how good is it? The Zetasizer µV incorporates an expert advice system that utilises the expertise of Malvern scientists to examine data quality and assist with method improvement.

Protein utilities

This set of tools is designed to help the user with experimental design and interpretation of the data. Assistance is available for recommended sample concentrations and 'what if' scenarios are available to provide shape estimates such as the Perrin factor, prolate and oblate axial ratios, as well as an estimate of molecular weight from the size measured.

Protein wizard

This wizard is an expert report in the software that can assess your sample from a number of points of view. It can give an idea of the total proportion of aggregates in a sample, the ratios of possible oligomeric structures, and can also suggest whether a sample might be suitable for crystallization trials.

Integrated dual capability - protein size and MW in batch *and* flow

Specifications

Zetasizer μ V

System specifications

General	Temperature control range	2°C - 90°C +/- 0.1°C*
	Measurement angle	90°
	Condensation control	Purge facility using dry air
	Standard laser	60mW, 830nm
	Correlator	Min. sample time 480ns, max. 3600s. 264 channels
Options	21 CFR part 11 software	Enables an operating mode that assists with ER/ES compliance
System	Compliance	CE, Product: laser class 1, EN 60825-1:2001 and CDRH
	Dimensions, weight, power	System 350mm x 410mm x 170mm (W,D,H), 14kg, 100W
	Minimum PC specification	Pentium P4 PC 2.8GHz Dual core processor, 2GB RAM, 160GB hard disk drive, 1024 x 768 screen resolution, CD-ROM drive, USB port, Windows XP Pro (SP3), Windows Vista or Windows 7. <i>Note: Only the 32-bit Windows 7 operating system is supported.</i>

Specifications for operation in cuvette mode

	Parameters measured	Hydrodynamic size, molecular weight of Molecular solutions, e.g. proteins
Size	Size range (radius)	0.15nm - 1 micron**
	Minimum sample volume	2 μ L
	Sensitivity	0.1mg/mL of 15kDa protein
Molecular weight	Molecular weight range (estimated from hydrodynamic diameter)	342Da to >10 ⁶ Da†
	Molecular weight range (calculated using Debye plot)	980Da to >10 ⁶ Da†
	Minimum sample volume	2 μ L
Software		
	Results output	Molecular size, molecular weight, A2, size distribution

Specifications for operation in chromatography detector mode

	Parameters measured	Molecular weight, Molecular size
	Flow cell volume	8 μ L
Molecular weight	Molecular weight range	<500Da to >10 ⁶ Da†
Software		
	Results output	Mn, Mw, Mz, Mp, Mw/Mn, Rh, Weight Fraction, Concentration, dn/dc, dA/dc. A2 ††

OmniFACE interface specification

	Acquisition	2 channels RI, UV
	Dimensions, weight, power	260mm x 260mm x 60mm (WxDxH) + power adapter, max. 65W

Notes * Temperature accuracy, 0.1°C at 25°C, 0.2°C at 2°C and 0.5°C at 90°C **Peak mode range (radius), 0.3nm - 0.5 microns, sample dependent
† Sample dependent ††When used in conjunction with a concentration detector

Malvern Instruments Limited

Groveswood Road • Malvern
Worcestershire • UK • WR14 1XZ
Telephone: +44 (0)1684 892456
Facsimile: +44 (0)1684 892789

Malvern Instruments Worldwide

Sales and service centres in over 50 countries.
For details visit www.malvern.com/contact



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