

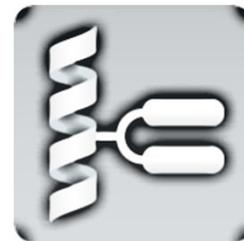
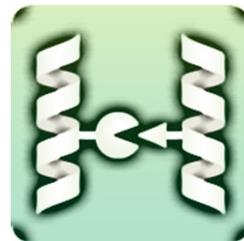


Beyond Aggregates:

Light Scattering Tools for Biophysical Characterization and Quantitation

Sophia Kenrick

Wyatt Technology Corporation





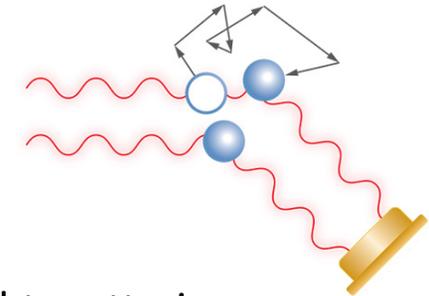
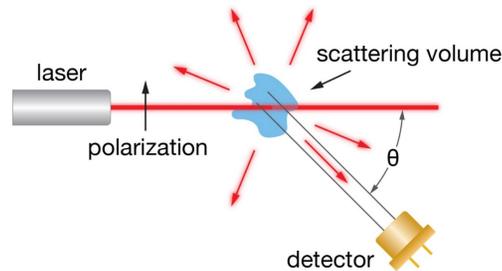
About Wyatt Technology Corporation

- ✓ Founded in 1982 by Dr. Philip J. Wyatt to commercialize multi-angle light scattering (MALS)
- ✓ Award-winning, robust, low maintenance, easy to use instruments that have been validated by thousands of peer-reviewed publications
- ✓ Leading provider of light scattering instruments for solution-based characterization of macromolecules and nanoparticles:
molar mass, size, charge, & interactions
- ✓ Pioneer of SEC-MALS and FFF-MALS, now standard analytical tools in protein, biopharma, biopolymer, synthetic polymer labs and more
- ✓ Pioneer of plate-based dynamic light scattering (DLS), an essential technology for high-throughput protein and nanoparticle formulation





Light scattering provides critical attributes

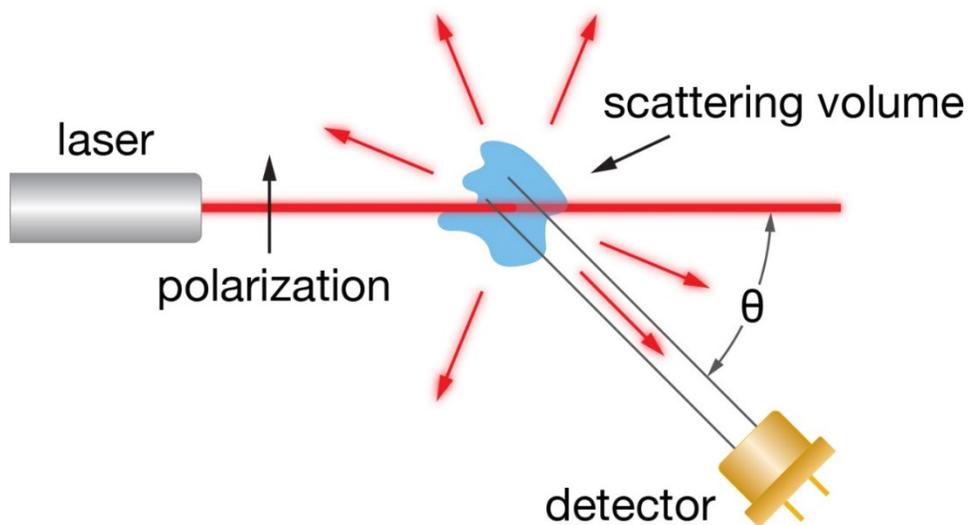


Static light scattering

Dynamic light scattering

Identity	<ul style="list-style-type: none"> ✓ Molar mass ✓ Size (RMS radius) ✓ Conjugation/loading Extinction coefficient ✓ Concentration 	<ul style="list-style-type: none"> ✓ Hydrodynamic size Conformation
Quality	<ul style="list-style-type: none"> ✓ Aggregate amount and size Fragment amount and size Heterogeneity 	<ul style="list-style-type: none"> ✓ Aggregate size Viscosity
Stability	<ul style="list-style-type: none"> Reversible associations ✓ Second virial coefficient 	<ul style="list-style-type: none"> ✓ Diffusion interaction parameter ✓ Transition temperatures

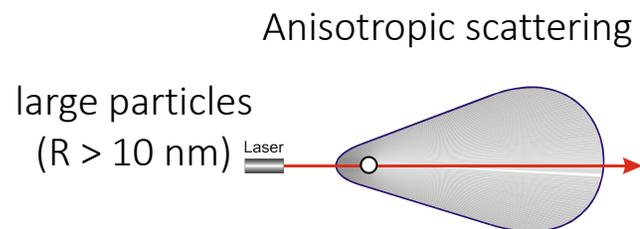
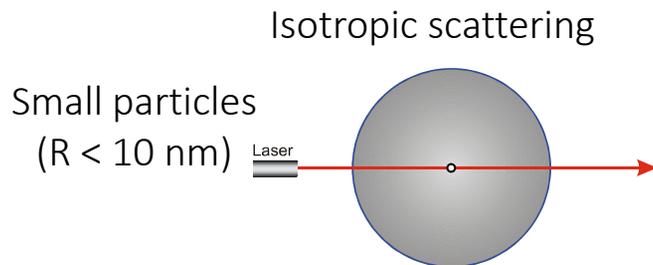
Multi-Angle Light Scattering



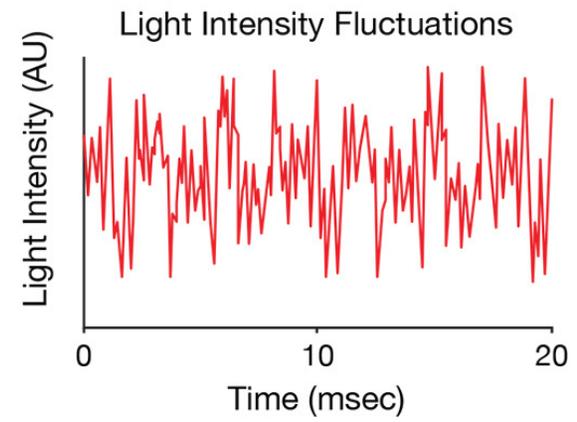
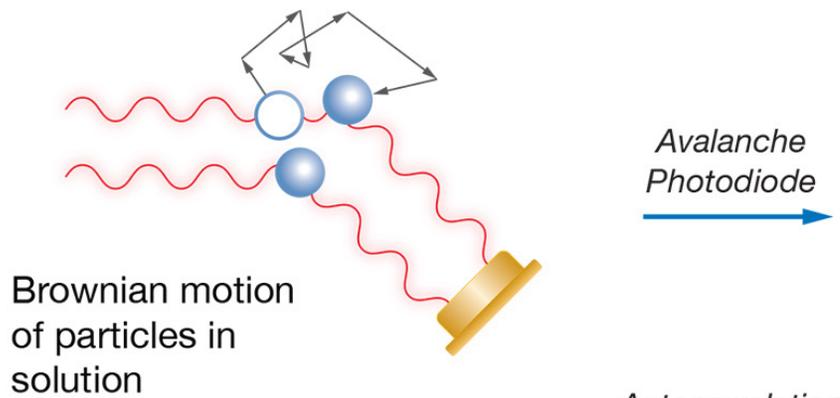
The amount of light scattered at 0° is directly proportional to the molar mass and mass concentration

$$I_{scattered} \propto M \cdot c \cdot \left(\frac{dn}{dc} \right)^2$$

The variation of scattered light with scattering angle is proportional to the average size of the scattering molecules.

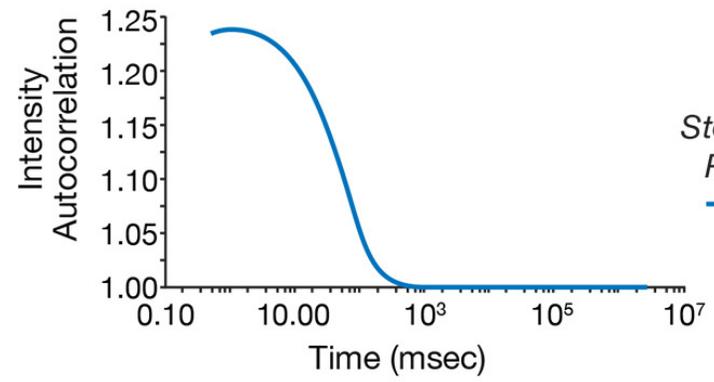


Dynamic light scattering (DLS)

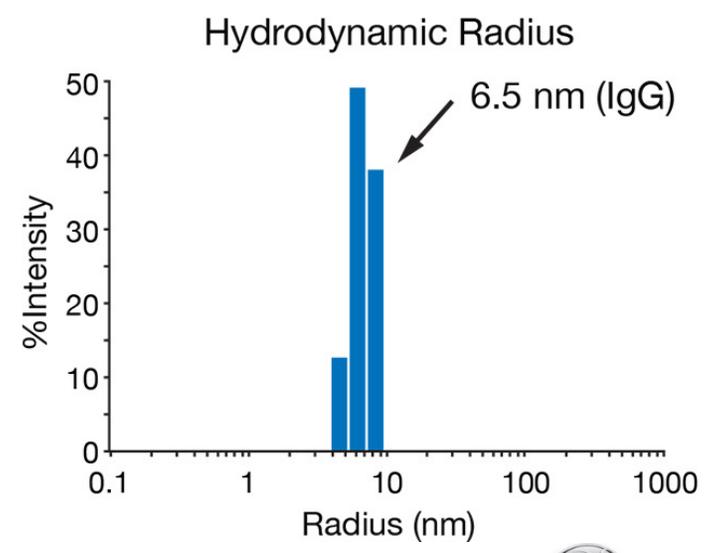


Autocorrelation Analysis

Decay rate \propto Diffusion coefficient



Stokes-Einstein Relationship



Typical MALS hardware setup and applications



SEC-MALS of biomolecules

- Proteins, polysaccharides, nucleic acids, conjugates
- Measure monomer and aggregate molar mass, molar mass distribution and polydispersity (M_w/M_n)
- Characterize branching and degree of conjugation



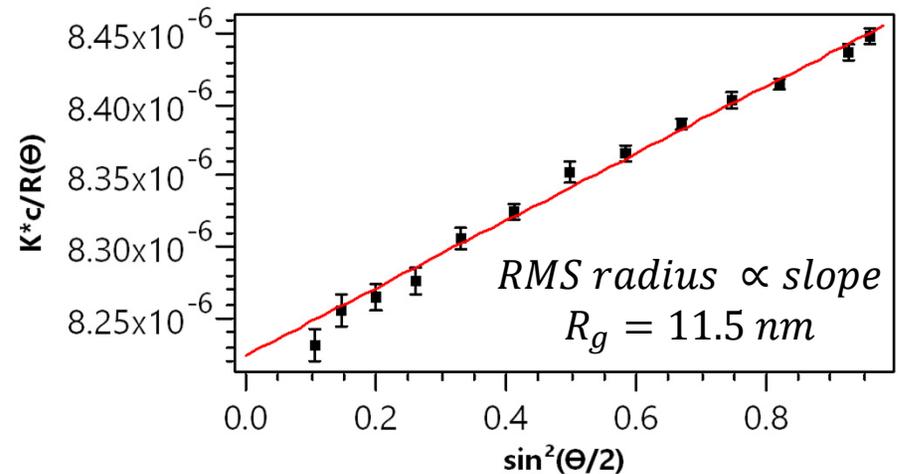
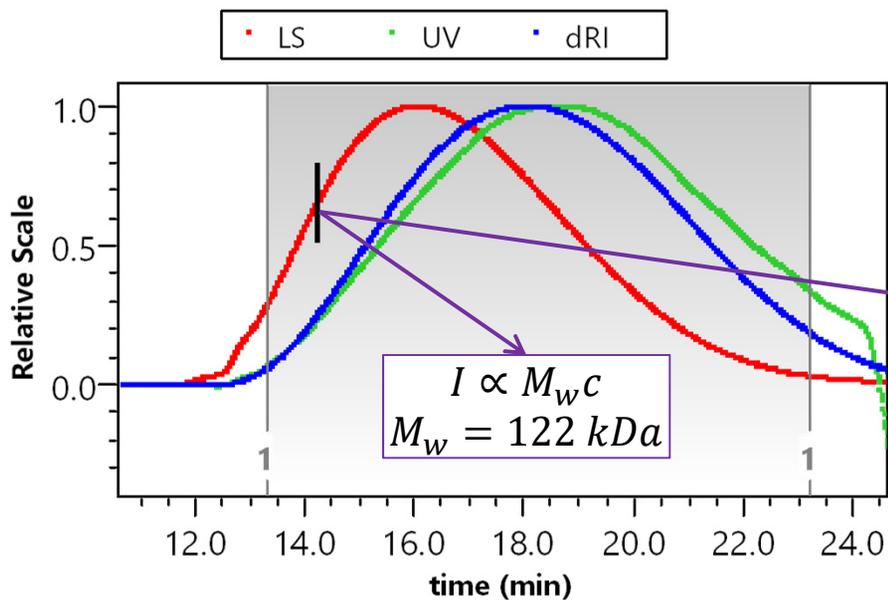
Eclipse AF4-MALS of BioNPs

- Viral vectors, EVs/exosomes, lipid or other NPs
- Isolate, identify, and quantify nanoparticle size, molar mass, and concentration
- Characterize shape/structure and payload/cargo content



Example: Online Molar Mass and RMS Radius

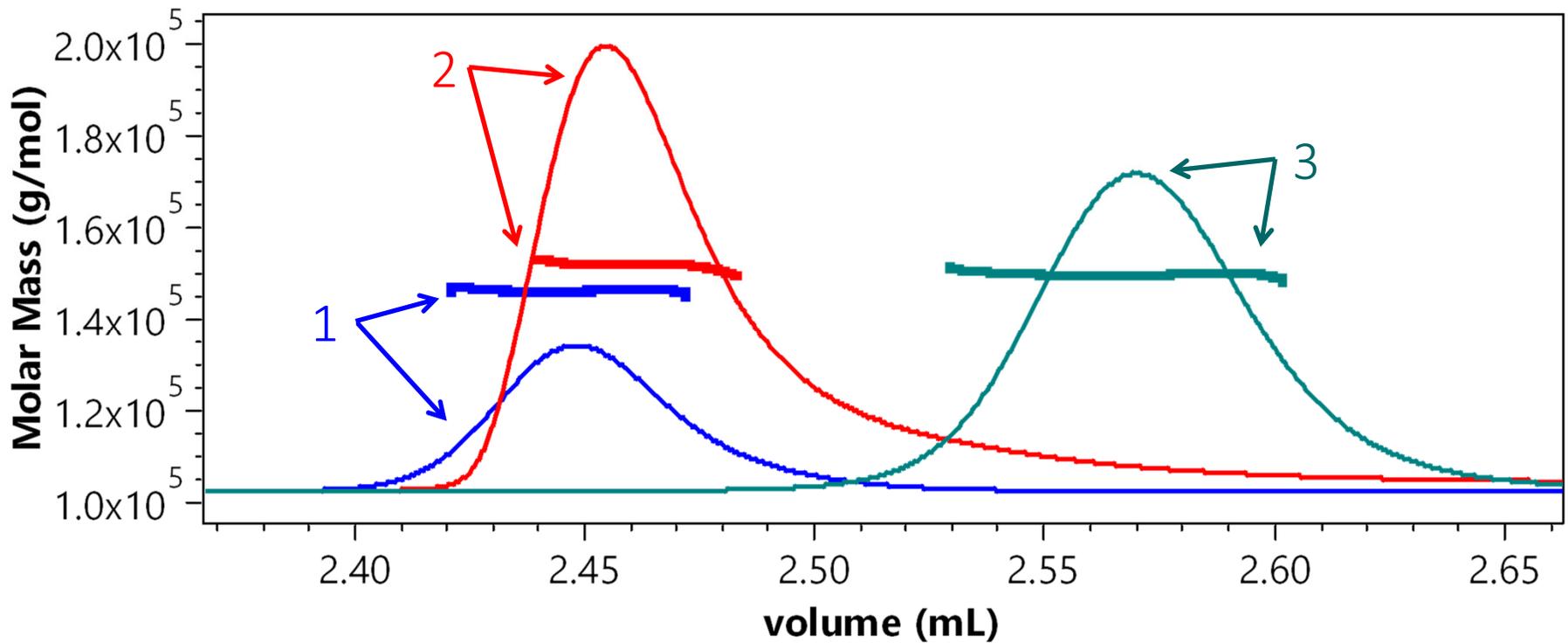
Light scattering and refractive index data are measured for each eluting slice to yield *absolute* molecular weight, R_g , and (with DLS) R_h .





Example: Online Molar Mass and RMS Radius

Light scattering and refractive index data are measured for each eluting slice to yield *absolute* molecular weight, R_g , and (with DLS) R_h .

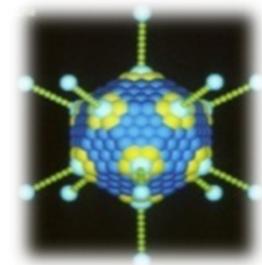
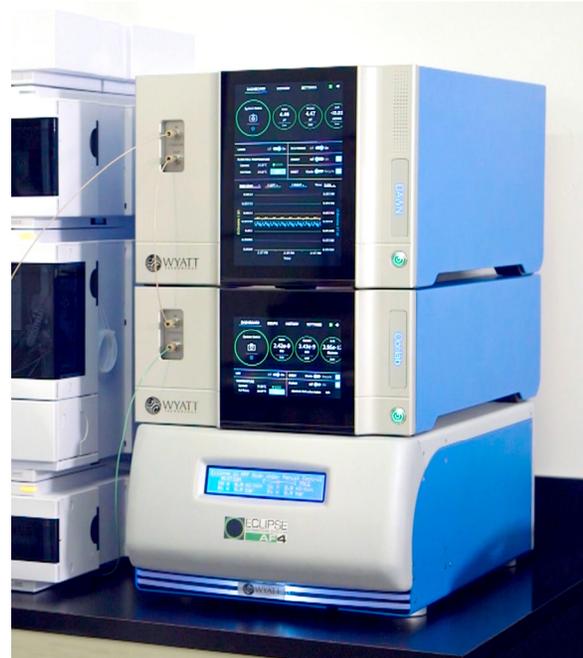


Case Study 1: Adenovirus

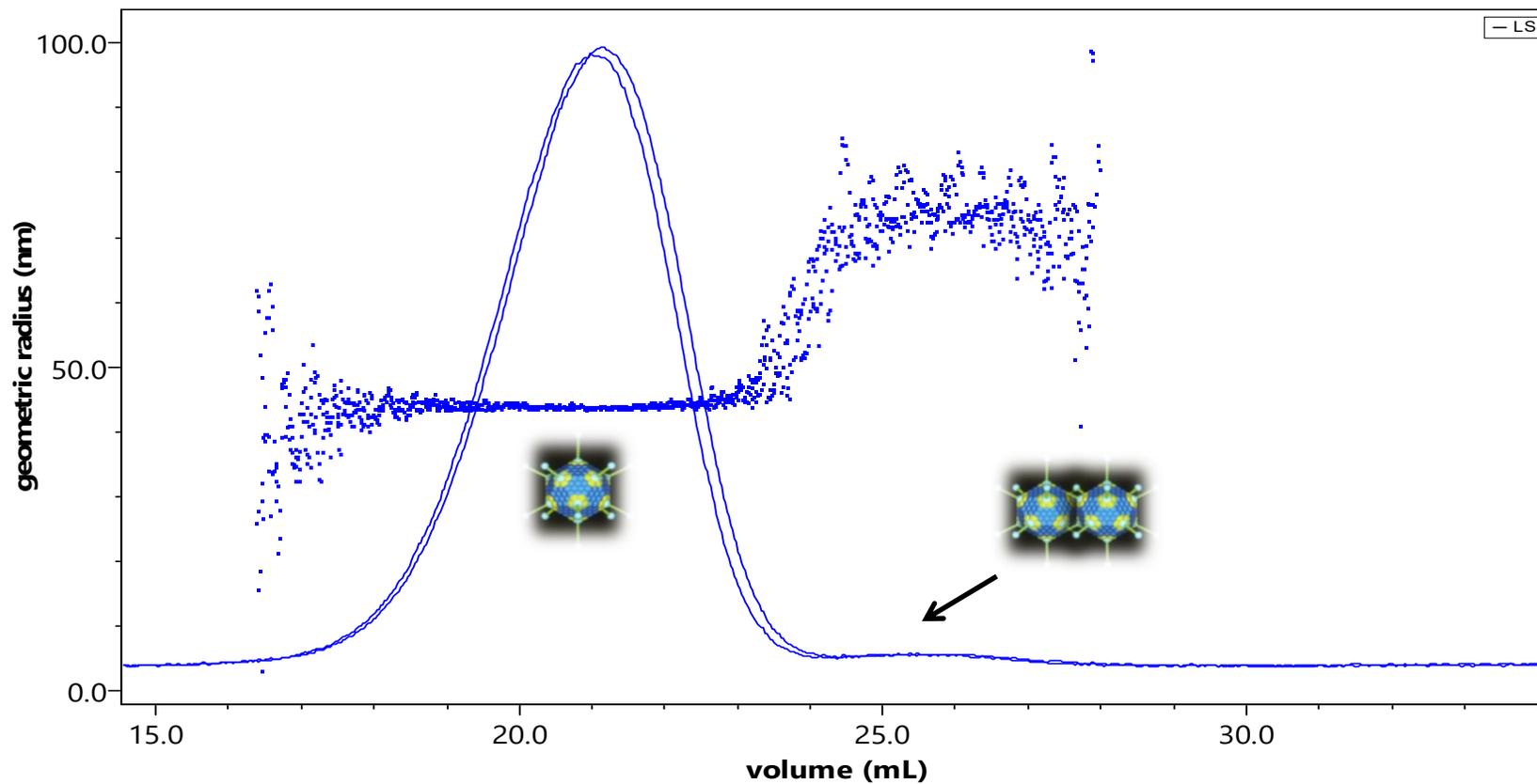
Measure size of monomer and aggregates

Quantify number of aggregates

Relate aggregation to stress conditions



Adenovirus



- Small amount of aggregates will not be detected by batch DLS.
- R_g and R_h can be measured by MALS and online DLS, respectively.



Quantitation: size, particle counts, aggregate%

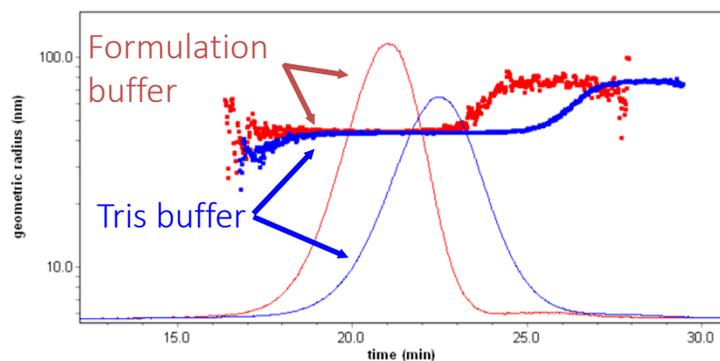
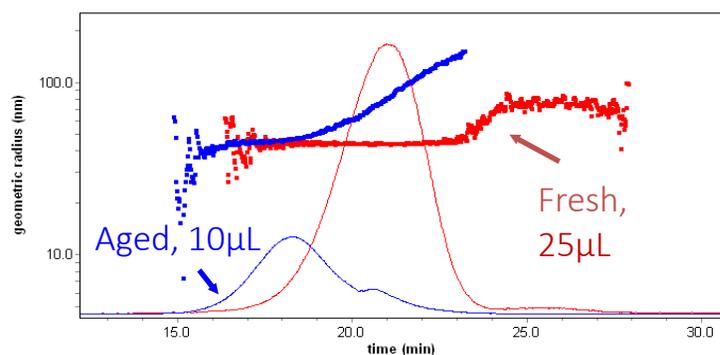
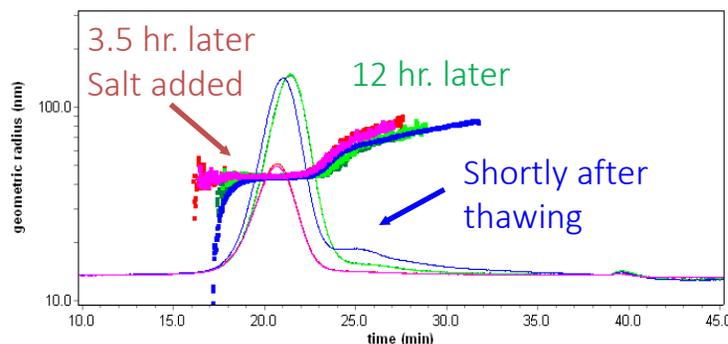
	Monomer		Aggregate				
	Radius (nm)	Number of particles	Radius (nm)	Number of particles	% by number (MALS)	% by mass (MALS)	% by UV peak area
Run 1	43.7	1.8×10^{10}	77	1.4×10^7	0.08%	2.76%	0.83%
Run 2	44	1.7×10^{10}	82	1.0×10^7	0.06%	2.09%	1.06%
Average	43.9	1.75×10^{10}	80	1.2×10^7	0.07%	2.4%	0.9%

Good reproducibility was obtained for both sizing and particle counting, despite very low amount of aggregate.

MALS provides more accurate quantitation of aggregate than traditional UV method.

- UV peak area may overestimate the percentage of large aggregates
- Scattering contribution in UV data is significant for particle radius >50 nm

How do stressors change the vector?



Freeze-thaw

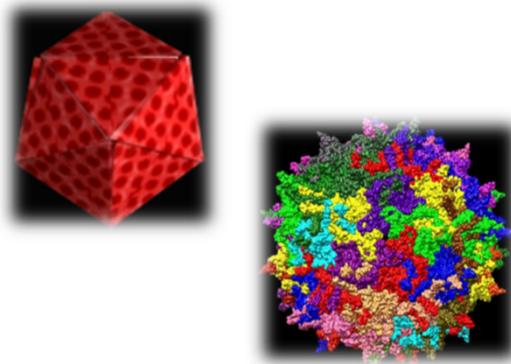
- Isolate and quantify virus size with Eclipse AF4-MALS
- Sensitive and robust aggregation assessment

Fresh vs. aged

- Elution time and peak shape are not representative of size distribution
- Eclipse fractionation with DAWN MALS detector quantifies absolute size

Buffer effects

- Measure differences in size distribution between buffers
- Quantify number of particles: 1.7×10^{10} for each case

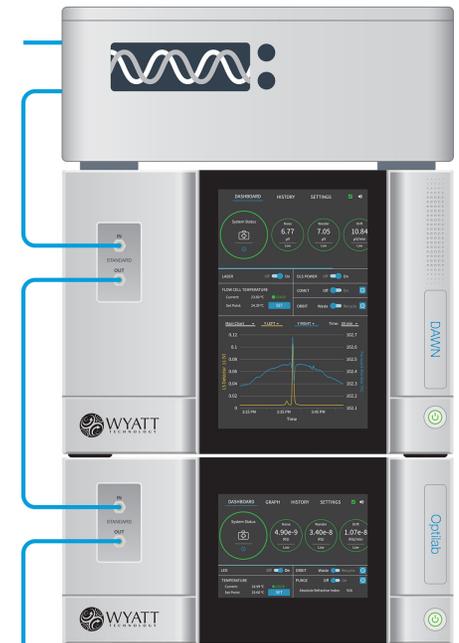


Case Study 2: Adeno-associated virus (AAV)

Comparison of separation techniques

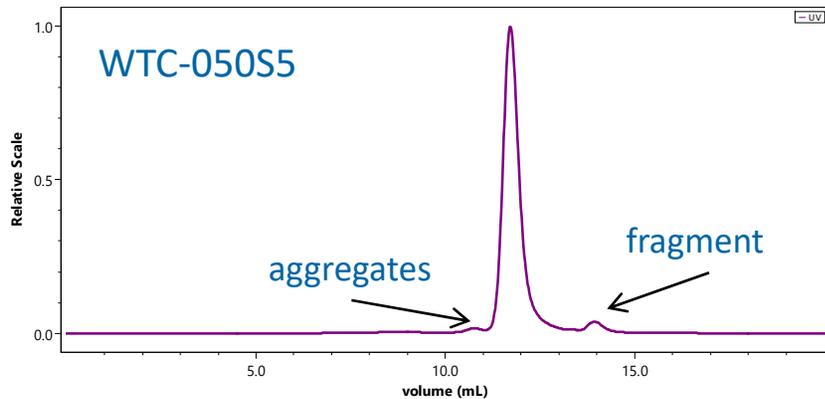
Quantify genetic payload

Determine structure



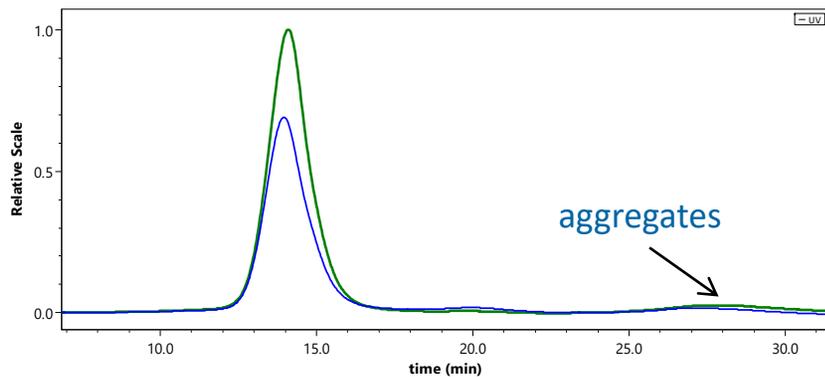


AAV by SEC-MALS and Eclipse AF4-MALS



SEC-MALS

- SEC may be able to resolve monomer and oligomer
- SEC is not be the right tool to quantify large aggregates



Eclipse AF4-MALS

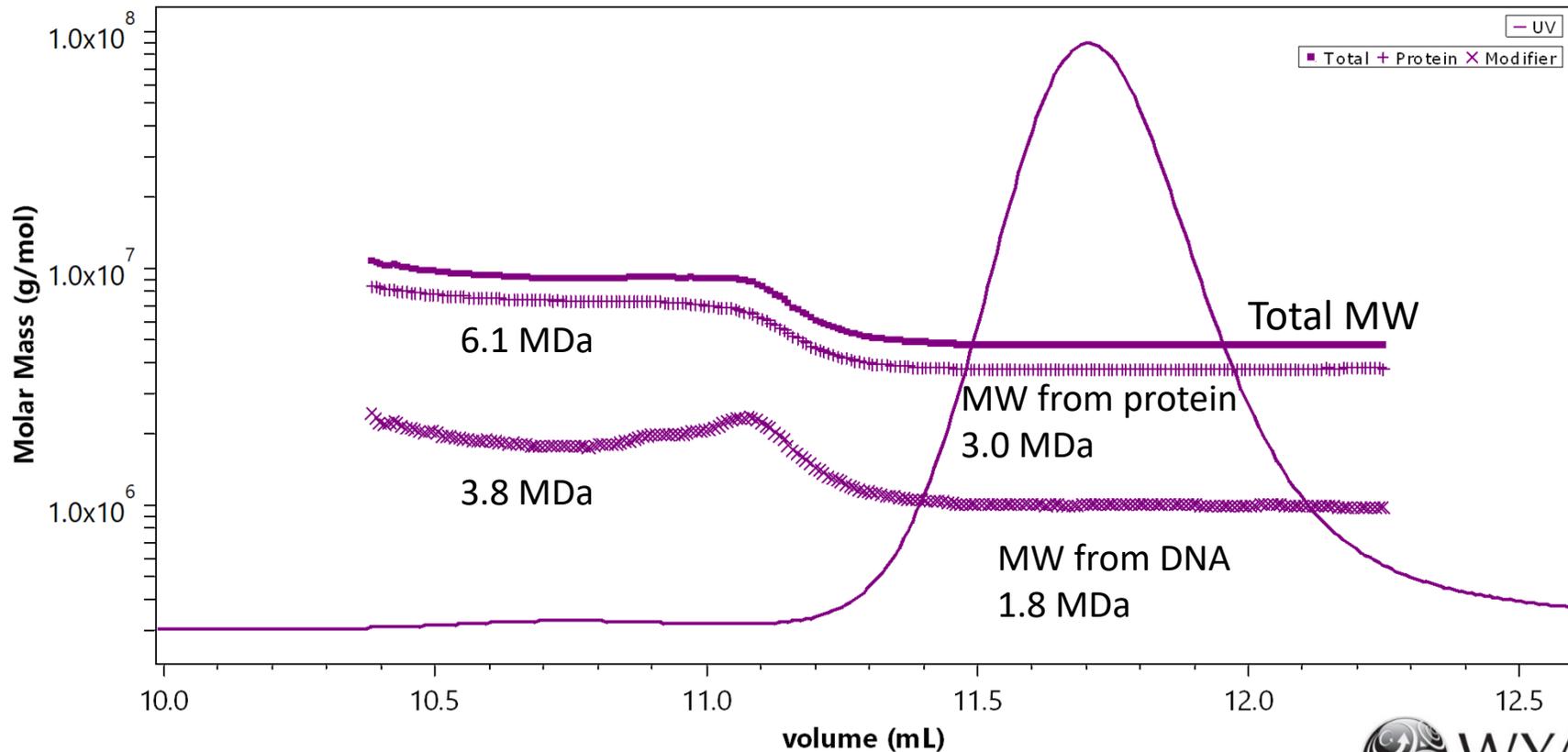
- AF4 provides better separation of confirmation of aggregate %
- HMW aggregates visible by AF4-MALS may be removed by SEC column



AAV genetic payload by SEC with multi-detection

Quantify genetic payload

- SEC/FFF cannot resolve empty and filled AAVs, but the apparent MW data from MALS and dRI may correlate to the percentage of full AAV

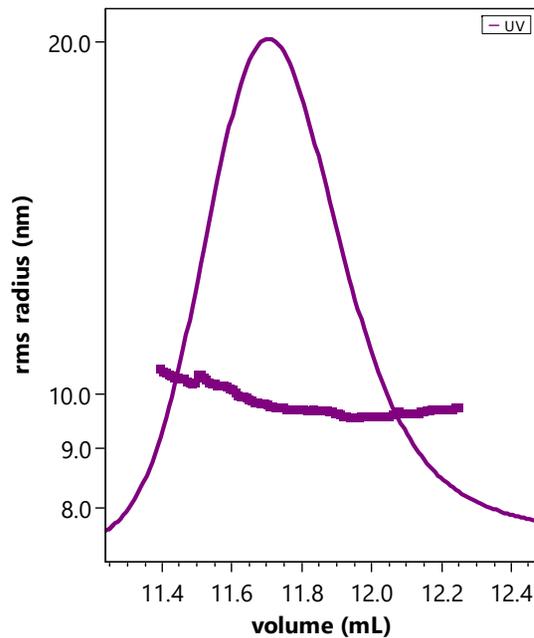




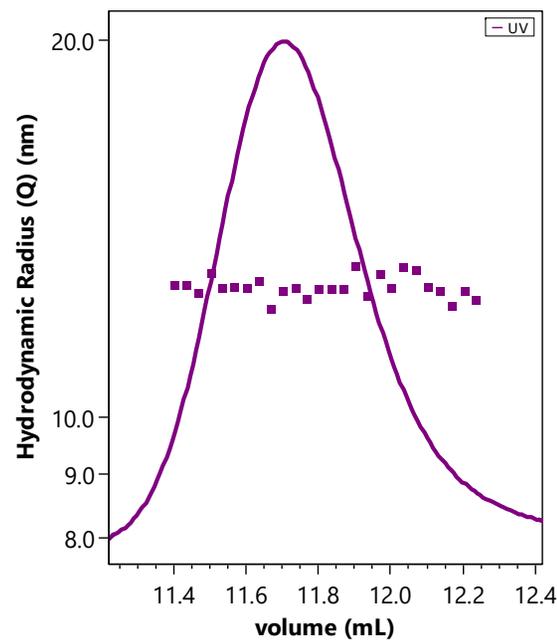
AAV structure by SEC with multi-detection

Confirm payload and measure shape

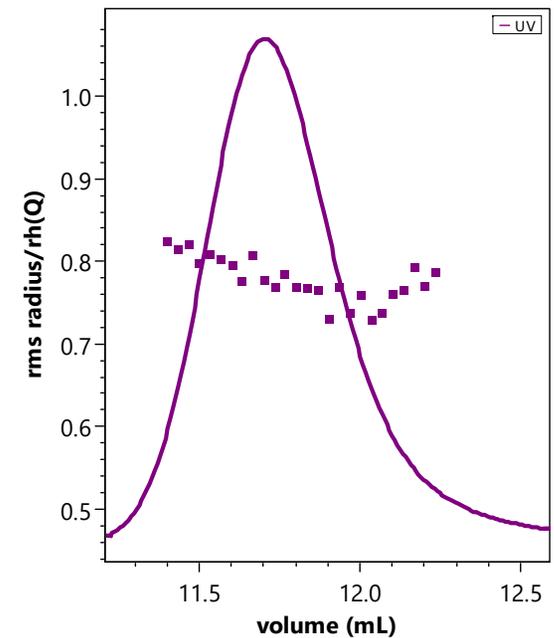
R_g from MALS

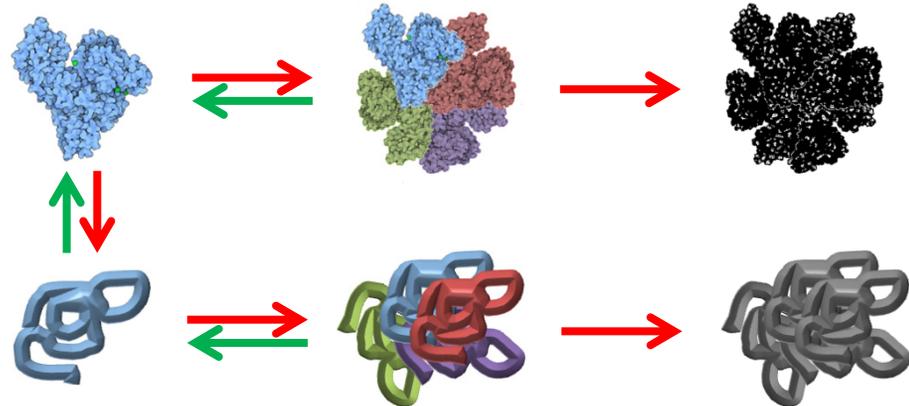
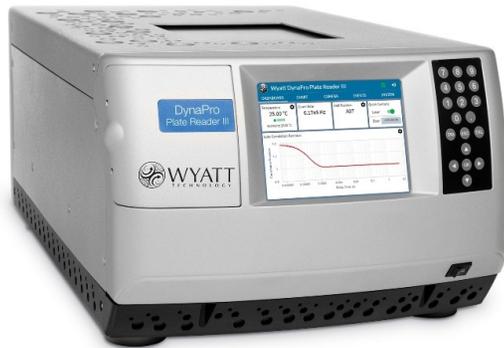


R_h from DLS



$R_g/R_h \sim 0.8$
filled sphere





Case Study 3: Formulation stability

High-throughput aggregate screening

Colloidal stability: k_D and A_2

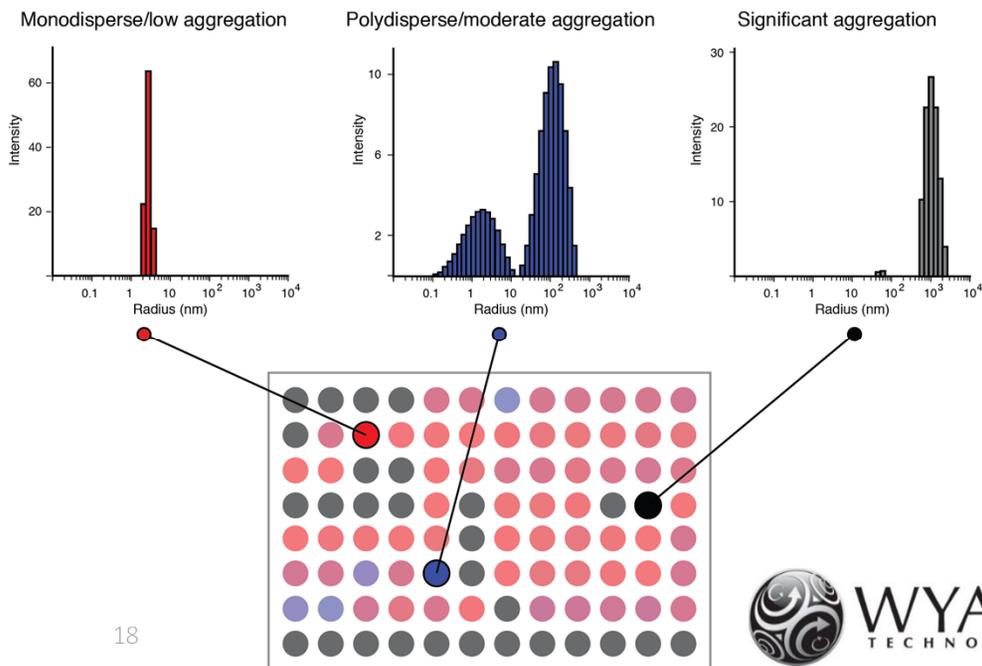
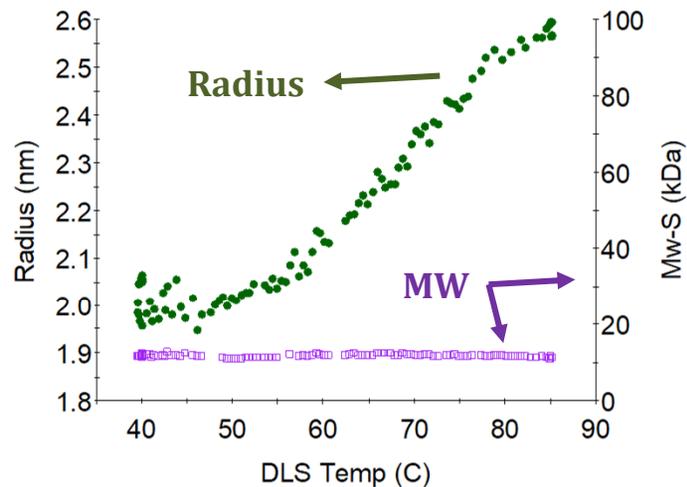
Conformational stability: T_m and T_{agg}



Benefits of batch DLS

Screening and characterization tool for formulation development

- High-throughput, low volume quality control for aggregates
- Perform studies as a function of time and temperature
- Screen small-molecule drugs: promiscuous inhibitors and binders
- Measure formulation viscosity





Measure interactions among molecules

Dynamic light scattering:

Diffusion Interaction Parameter, k_D

$$D_t = D_0(1 + k_D c)$$

$k_D < 0$ attraction

$k_D > 0$ repulsion

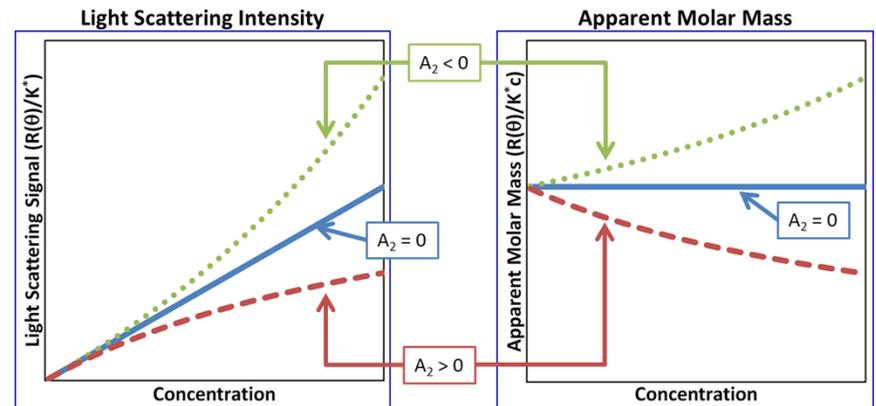
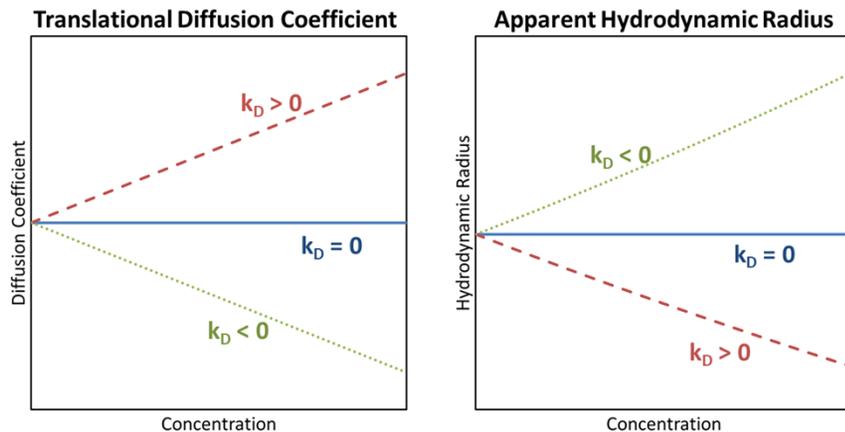
Static light scattering:

Second virial coefficient, A_2

$$R/K^* = Mc[1 - 2A_2Mc]$$

$A_2 < 0$ attraction

$A_2 > 0$ repulsion





Why measure concentration dependence?

k_D correlates with solution properties

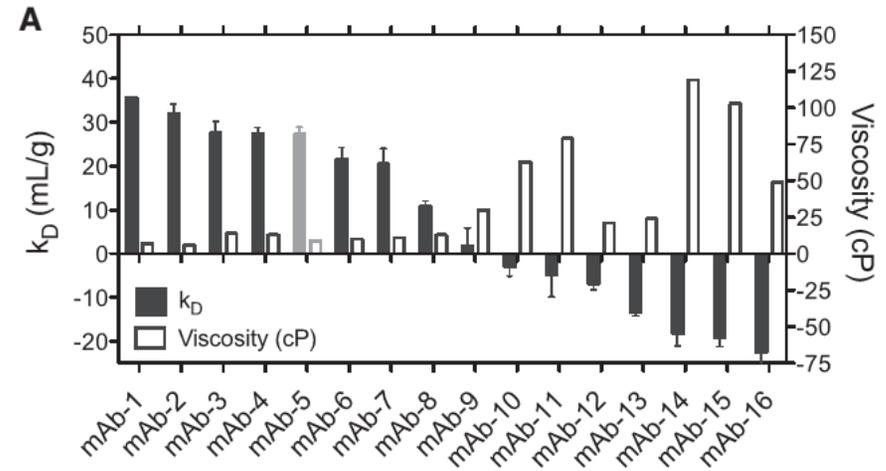
- $k_D > 0$ correlates to low viscosity
- $k_D \lesssim 0$ correlates to high viscosity
- $k_D \lesssim 0$ correlates with particles formation (e.g., after agitation)

Sample formulation space and determining key stability attributes.

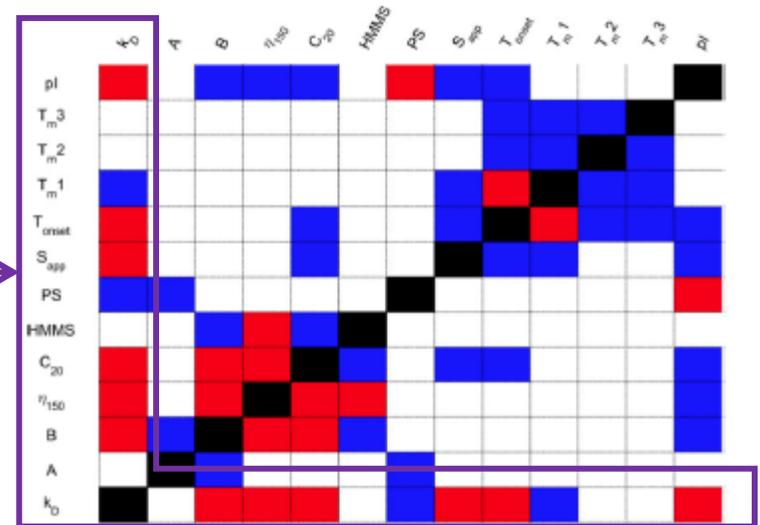
- Interactions as a function of pH, excipient, salts, etc.
- Observe correlations between k_D , A_2 , and T_{agg}

Positive correlation between k_D and many other stability-indicating parameters!

Tomar D.S., et al. (2018) *Pharm. Res.* 35:193.



Connolly, B.D. et al. *Biophys. J.* (2012) 103(1):69-78.

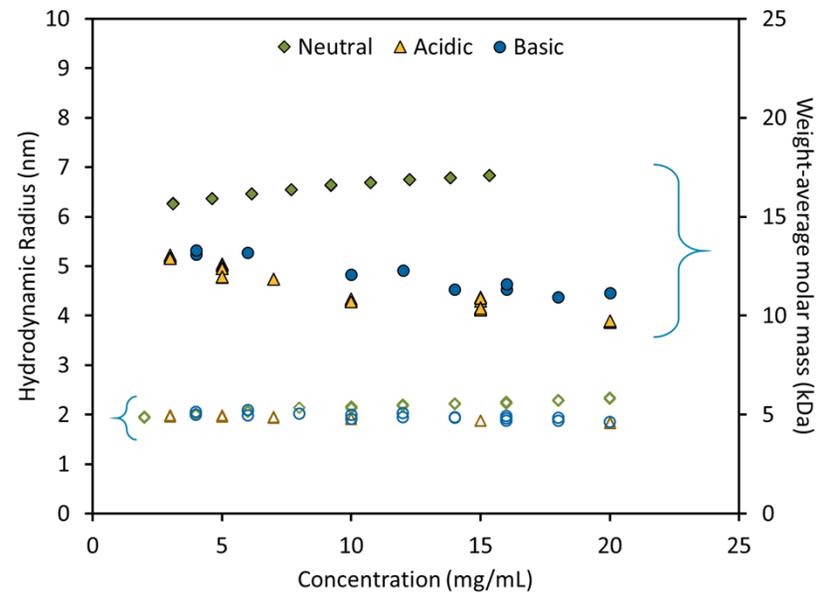




Quantify colloidal stability, k_D and A_2

Formulation pH influences intermolecular interactions.

- Neutral pH causes undesirable attractive interactions
- Acidic and basic pH exhibit net repulsive interactions



DLS

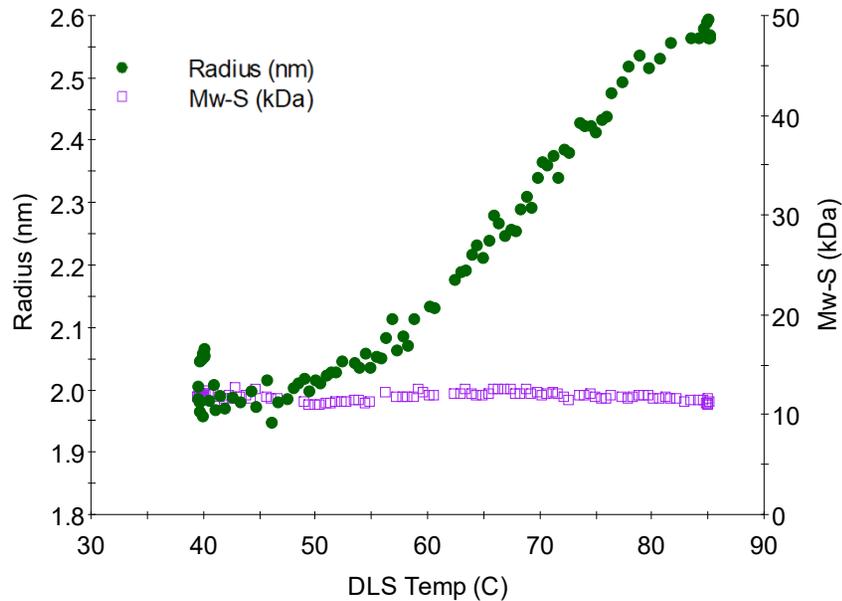
SLS

	R_h (nm)	k_D (mL/g)	M_w (kDa)	A_2 (mol · mL/g ²)
Neutral	1.9	-8.5	15.0	-4.8×10^{-4}
Acidic	2.0	+4.6	13.5	$+7.3 \times 10^{-4}$
Basic	2.1	+3.7	14.7	$+5.0 \times 10^{-4}$



Conformational stability from temperature

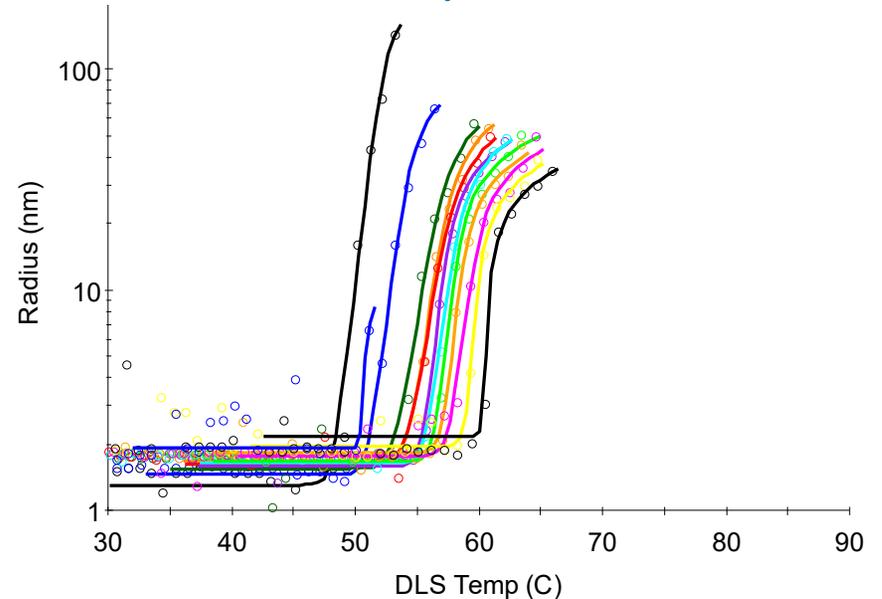
Acidic pH



Acidic pH provides conformational stability.

- Midpoint unfolding temperature $T_m = 69\text{ }^\circ\text{C}$
- Confirm unfolding (not aggregation) via constant measured M_w

Basic pH



Basic pH shows aggregation at elevated temperature

- Onset of aggregation/unfolding happens at lower T compared to acidic pH
- T_{agg} varies with concentration, ranging from 48 °C to 60 °C



Conclusion

Light scattering is not just for protein molecules and aggregates!

- Assess wide range of biotherapeutics, protein conjugates, and higher order structures.
- Extend characterization and quantitation to viruses, gene therapy and drug delivery vectors.

Static and dynamic light scattering provide a wide range of solutions for formulation stability.

- Measure nonspecific interactions and propensity to aggregate with DLS (k_D) or SLS (A_2).
- Characterize conformational stability (T_m , T_{agg} , time to aggregation, etc.)

Combine with complementary information for complete characterization.



For More Information

Sample application notes, webinars, & more at www.wyatt.com/Library.

Search over 14,000 peer-reviewed publications that feature Wyatt instruments at www.wyatt.com/Bibliography.

For information about a particular topic:

- Light Scattering Solutions: www.wyatt.com/Solutions
- SEC-MALS: www.wyatt.com/SEC-MALS
- DLS: www.wyatt.com/DLS
- CG-MALS: www.wyatt.com/CG-MALS

