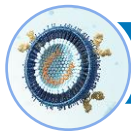


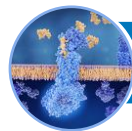
# Determination of Critical Quality Attributes for ADC, NanoDDS and Gene Delivery tools from Research to Production

**Dr. Abhigyan Sengupta and  
Dr. David Golonka**

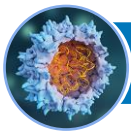
# Applications in Focus



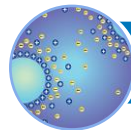
Vaccines



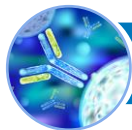
Protein



Gene Therapy



Nanoparticle



Biotherapeutics



Polymer

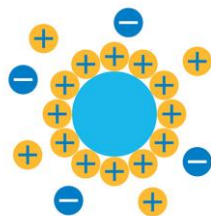
## Biophysical Properties of Interest



Molar Mass



Size



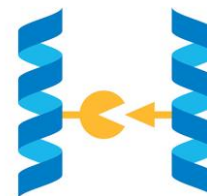
Charge



Interaction

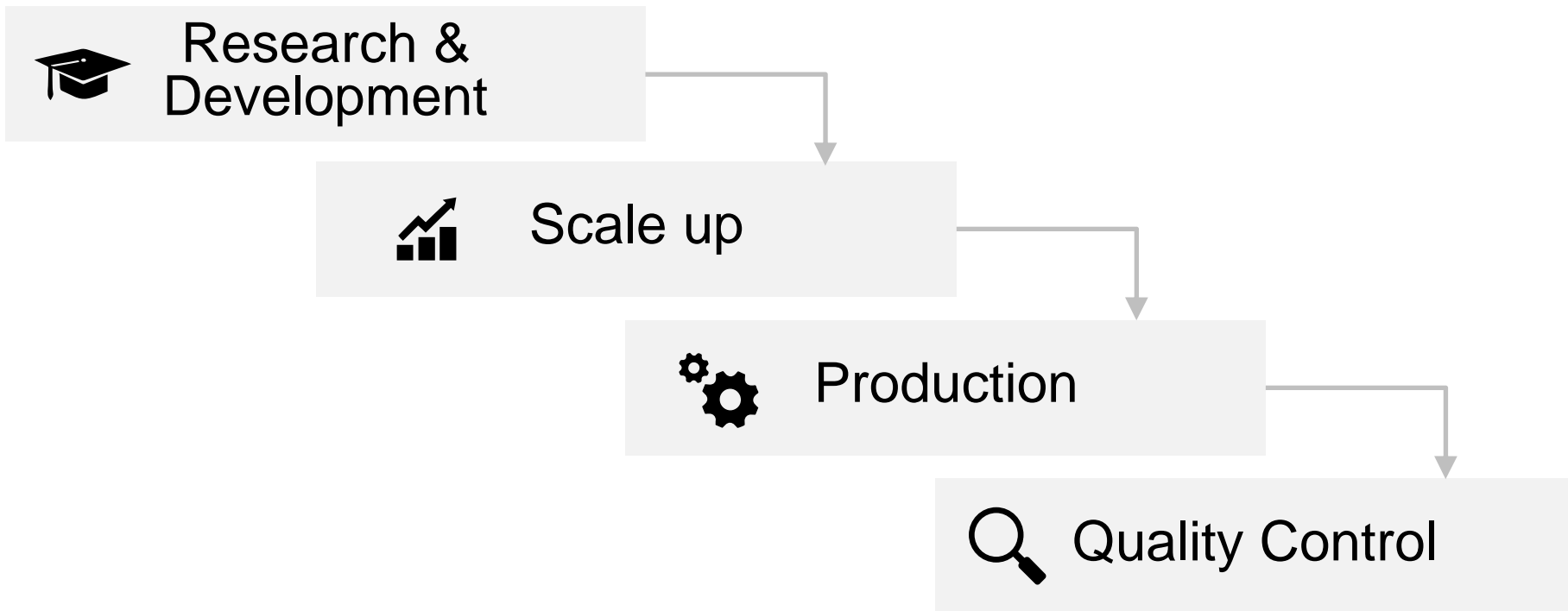


Conformation



Conjugation

# Steps of Drug Development - Research to Production





## Batch systems

DLS



HTP-DLS



## Chromatography

SEC-MALS

IEX-MALS



AF4-MALS



## Process

RT-MALS



Dynamic Light  
Scattering (DLS)

Multi-Angle Light Scattering (MALS)



## Batch systems

DLS



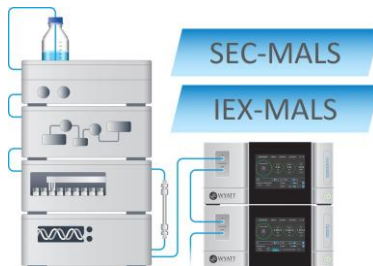
HTP-DLS



## Chromatography

SEC-MALS

IEX-MALS



AF4-MALS



## Process

RT-MALS



Dynamic Light  
Scattering (DLS)

Multi-Angle Light Scattering (MALS)

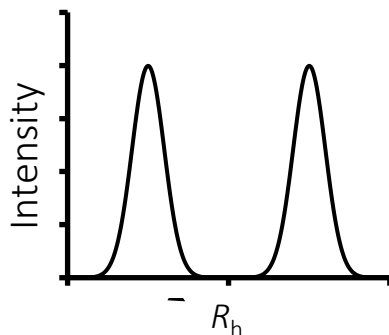
# Dynamic Light Scattering



## Theory

### Measurement of hydrodynamic size

Determination of the diffusion coefficient from which the hydrodynamic radius is derived.



## What can you measure?

- Size, size distribution and polydispersity
- Aggregate detection
- Protein quality
- Molar mass and particle concentration

### NanoStar II

#### ZetaStar

- Disposable or quartz cuvettes
- Walk-up experiments
- Low sample volume
- Aggregate detection
- Protein quality

### Plate Reader III



- Wellplates (96, 384, 1536)
- Formulation Screening
- Colloidal stability ( $A_2/B_{22}$ ,  $k_D$ )
- Thermal stability ( $T_{onset}$ ,  $T_m$ ,  $T_{agg}$ )
- Viscosity
- Compatible with robotic systems

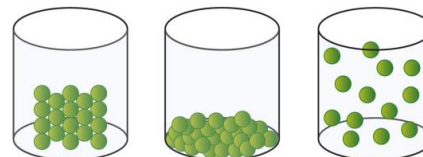
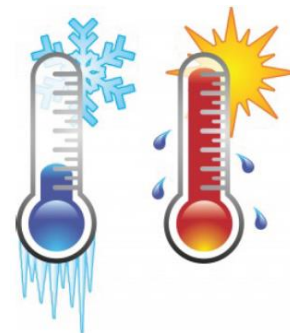
# DLS Application Example

## Formulation Screening



# DLS Application Examples – Formulation Screening

- Background: Antibody drug candidates can be screened by accelerated stability studies
- Experiment: Compare two antibody candidates in multiple formulations
  - Formulation Buffer
  - pH 4, 20 mM Na Citrate
  - pH 5, 20 mM Na Acetate
  - pH 6, 0 mM NaCl, 20 mM Histidine
  - pH 6, 150 mM NaCl, 20 mM Histidine
  - pH 7, 20 mM phosphate - potassium
- Challenges:
  - Limited sample amount
  - Time restrictions

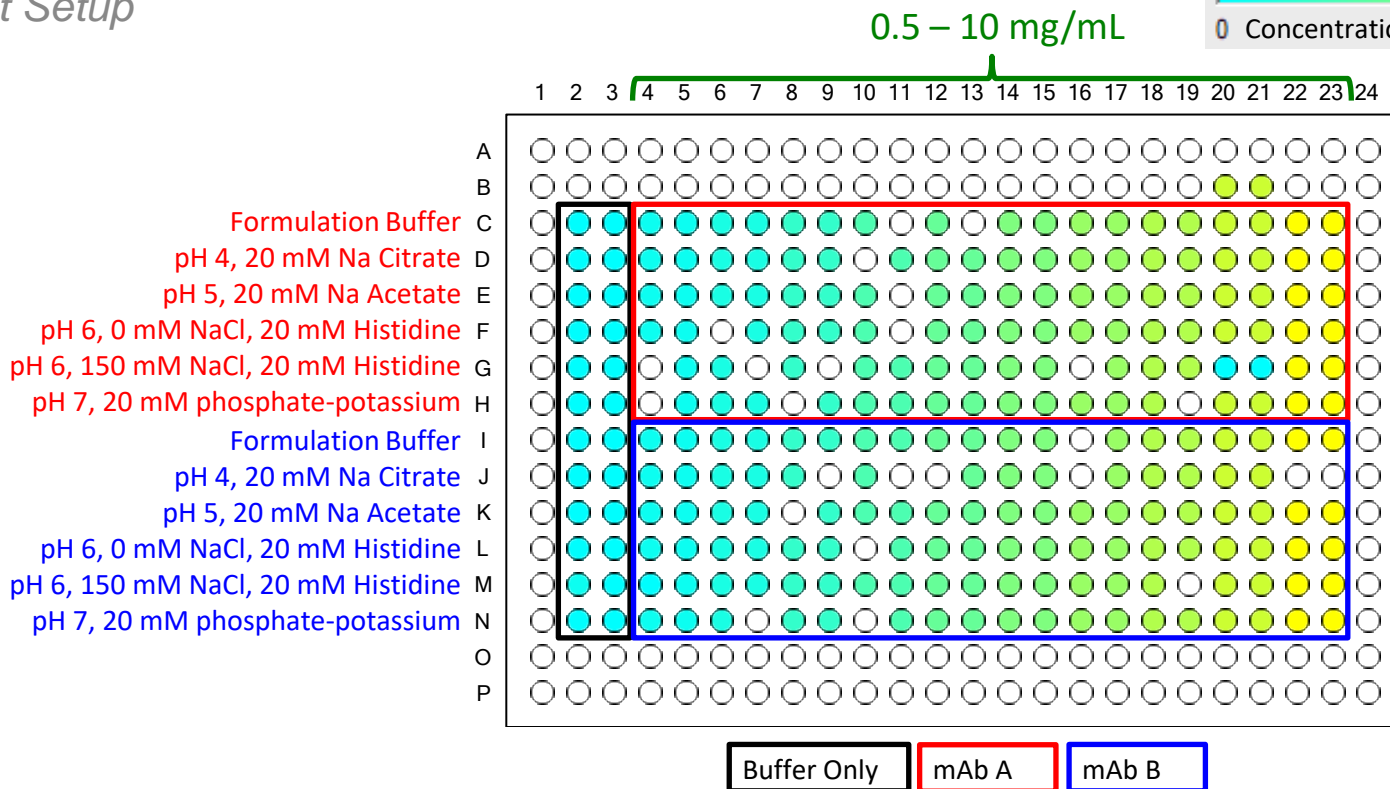






# DLS Application Examples – Formulation Screening

## Experiment Setup



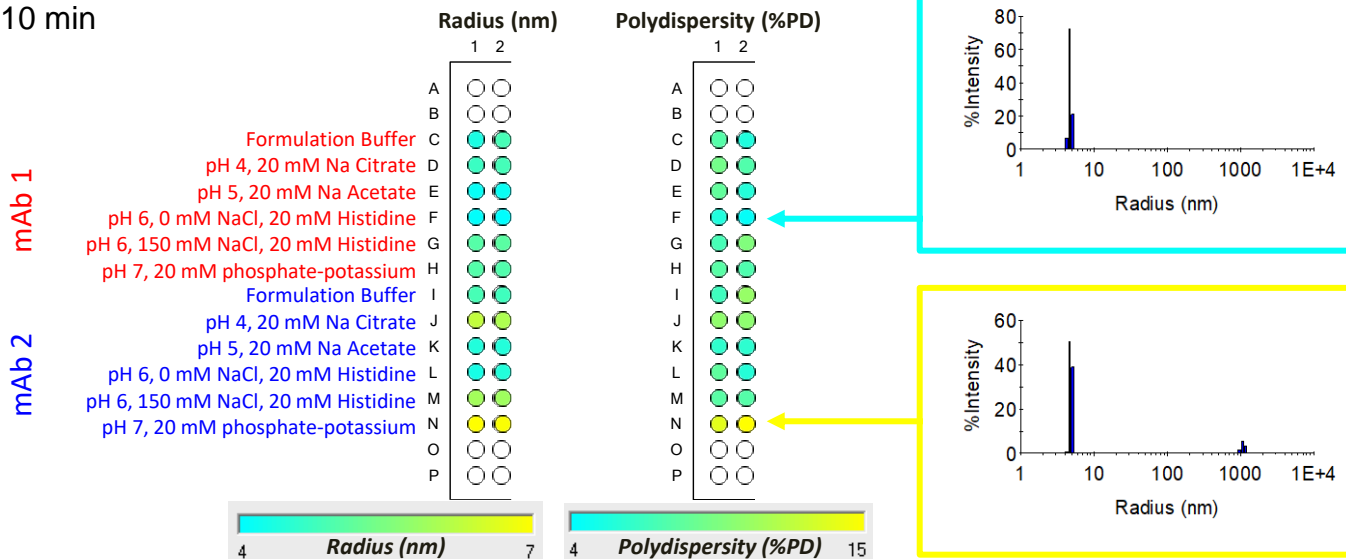


# DLS Application Examples – Formulation Screening

## Purity and Aggregation

Total Samples: 24

Total Time: 10 min



Quickly screen average size and polydispersity with spectral viewer

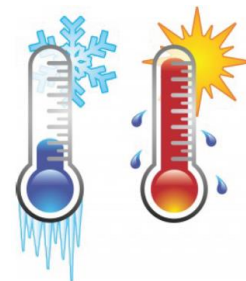
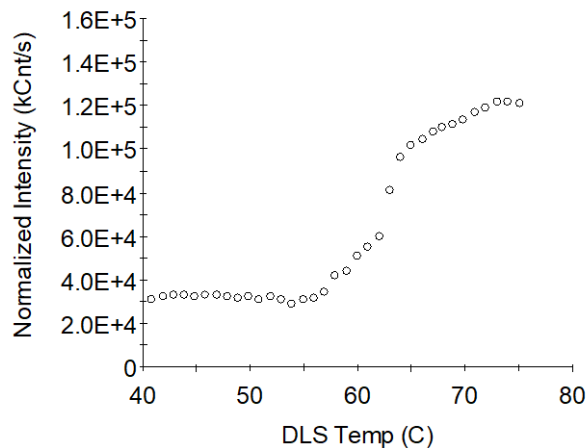
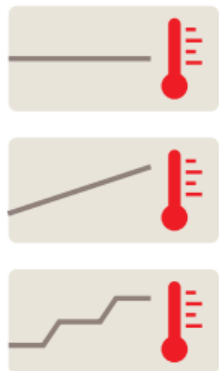
DLS sensitive to low concentration of large aggregates



# DLS Application Examples – Formulation Screening

## Thermal Stability Study

### TN7001 Measuring Temperature Transitions Using the DynaPro Plate Reader



#### 1. Select temperature profiles

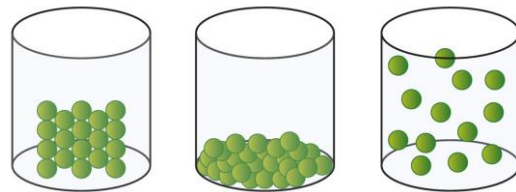
Combine multiple profiles  
for complex protocols.



# DLS Application Examples – Formulation Screening

*Colloidal Stability,  $k_D$  and  $A_2$*

- Diffusion Interaction Parameter,  $k_D$ 
  - measured by DLS
  - Measure of protein-protein interactions + some smaller contributions
  - Usually well correlated to  $A_2$
- Second Virial Coefficient  $A_2$ 
  - Measured by SLS
  - Direct measure of protein-protein interactions


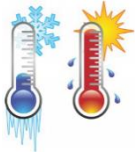



Relate to long-term stability

Traditionally challenging to measure



# DLS Application Examples – Formulation Screening

| Case Study: Conclusion |                                    | Sample Purity<br> | Thermal Stability<br> |                                     | Colloidal Stability<br> | Sum |
|------------------------|------------------------------------|---|--|-------------------------------------|--|-----|
|                        |                                    | Rh, %PD, Histogram  | Temp Ramp  | Temp Cycle                          | kD & A2  |     |
| mAb 1                  | pH 4, 20 mM Na Citrate             | <input type="checkbox"/>  | <input checked="" type="checkbox"/>  | <input checked="" type="checkbox"/> | <input type="checkbox"/>   | -2  |
|                        | pH 5, 20 mM Na Acetate             | <input checked="" type="checkbox"/>   | <input checked="" type="checkbox"/>  | <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/>  | 0   |
|                        | pH 6, 0 mM NaCl, 20 mM Histidine   | <input checked="" type="checkbox"/>   | <input type="checkbox"/>   | <input type="checkbox"/>            | <input checked="" type="checkbox"/>  | 2   |
|                        | pH 6, 150 mM NaCl, 20 mM Histidine | <input type="checkbox"/>  | <input type="checkbox"/>   | <input type="checkbox"/>            | <input type="checkbox"/>   | 0   |
|                        | pH 7, 20 mM phosphate - potassium  | <input type="checkbox"/>  | <input type="checkbox"/>   | <input type="checkbox"/>            | <input type="checkbox"/>   | 0   |
| mAb 2                  | pH 4, 20 mM Na Citrate             | <input type="checkbox"/>  | <input type="checkbox"/>   | <input type="checkbox"/>            | <input type="checkbox"/>   | 0   |
|                        | pH 5, 20 mM Na Acetate             | <input checked="" type="checkbox"/>   | <input type="checkbox"/>   | <input type="checkbox"/>            | <input checked="" type="checkbox"/>  | 2   |
|                        | pH 6, 0 mM NaCl, 20 mM Histidine   | <input checked="" type="checkbox"/>   | <input type="checkbox"/>   | <input type="checkbox"/>            | <input checked="" type="checkbox"/>  | 2   |
|                        | pH 6, 150 mM NaCl, 20 mM Histidine | <input type="checkbox"/>  | <input type="checkbox"/>   | <input checked="" type="checkbox"/> | <input type="checkbox"/>   | -1  |
|                        | pH 7, 20 mM phosphate - potassium  | <input checked="" type="checkbox"/>   | <input type="checkbox"/>   | <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/>  | -3  |

# ELS Application Example

## mRNA-LNP development and production



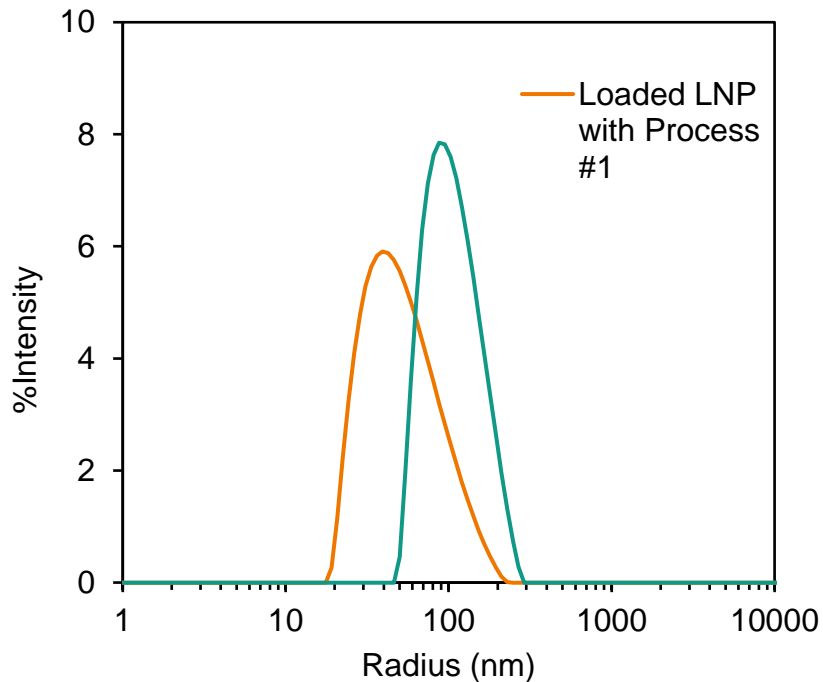
# RNA-LNP development and production

- Helper lipid (DSPC, DOPE ...)
- Ionizable lipid (MC3, SM102 ...)
- Cholesterol
- Lipid-anchored PEG (DMP-PEG)
- mRNA





# Assessing LNP preparation processes



## Rapid screening of product and process development

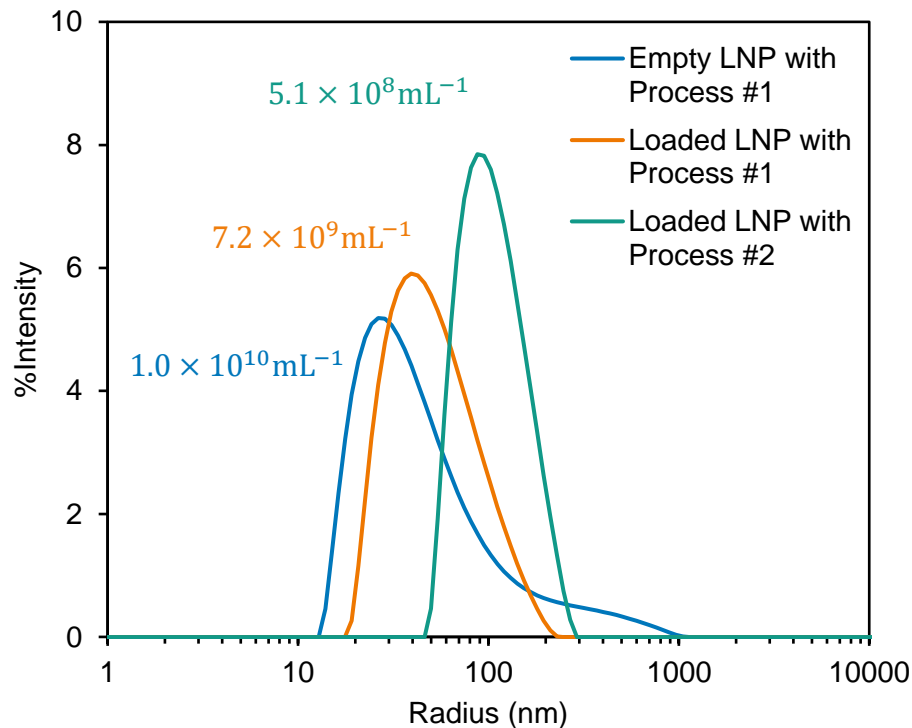
Assess various mixing process or devices

- Process #1: With Microfluidics-mixing
- Process #2: Without Microfluidics-mixing





# Characterizing size and particle concentration of LNPs

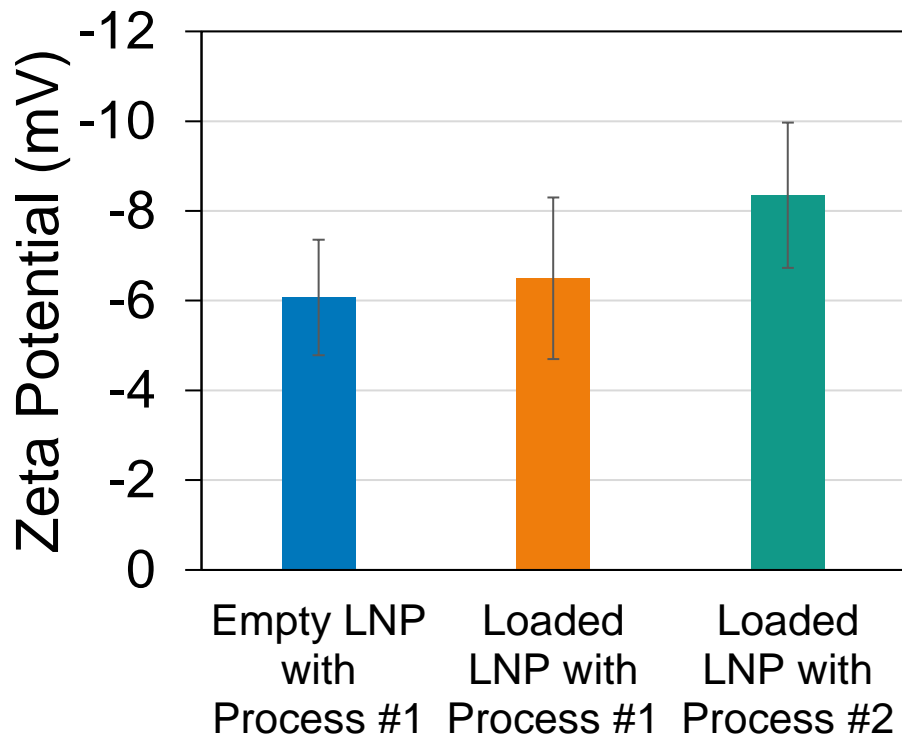


## Determine size, polydispersity and size distribution of empty and loaded LNPs

- Empty LNP exhibit noticeable broad distribution
- Loaded LNP median is clearly larger (~ 45 nm)
- Particle concentration is quickly determined  
~1 $\times 10^{10}$  particles/mL



# Characterizing charge / zeta potential of LNPs



ELS determines charge / zeta potential of LNPs, which is intrinsically related to the ability to enter specific organs and cells and deliver its payload effectively and where needed.

- All samples are negatively charged under test conditions
- Process conditions seem to have no or little influence on LNP surface charge
- Measurements can be performed under physiological conditions

ZetaStar provides rapid answers for scientists to make faster and more informed decisions to improve LNP size consistency

## Summary – DLS and ELS

- Fast and reliable measurements
- Identification of aggregates
- Automated measurements of large sample sets
- Powerful technique for proteins from research to production
  - Characterization of protein candidates and formulation screening in research
  - Assessing sample quality during scale up and production at-line
  - Quality control for protein products
- Zeta potential and structural insight for charged particles like LNPs



## Batch systems

DLS



HTP-DLS



## Chromatography

SEC-MALS

IEX-MALS



AF4-MALS



## Process

RT-MALS



Dynamic Light Scattering (DLS)

Multi-Angle Light Scattering (MALS)

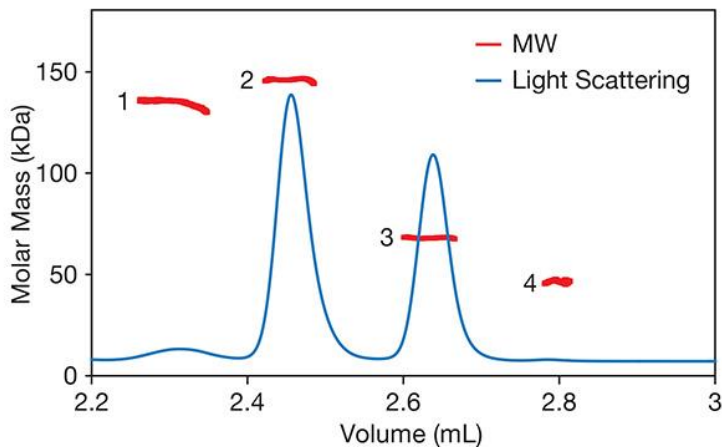
SEC-MALS

IEX-MALS

# Multi-Angle Light Scattering

## Theory

### Absolute Molar Mass Distribution



## What can you measure?

### miniDAWN & DAWN

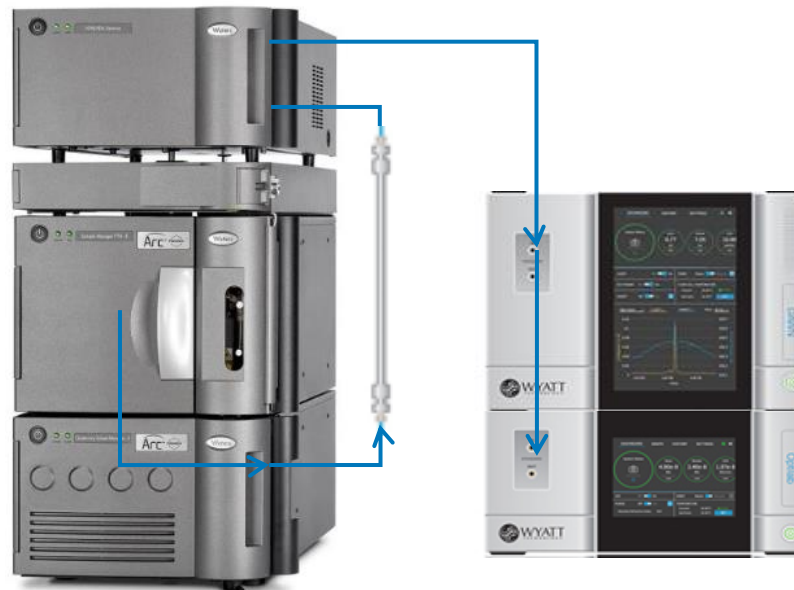
- Molar masses from 200 Da up to 10 MDa or 1 GDa
- No protein standards needed (no assumptions)
- Identification & quality
- Purification & aggregates
- Oligomerization state & complexes
- Conjugate analysis (glycol-proteins, PEGylated proteins, antibody drug conjugates, AAV)
- 21 CFR part 11

### microDAWN

- for UHPLC and  $\mu$ SEC

# SEC-MALS - Hardware

- ✓ Quantitative multi-wavelength UV
- ✓ Steady pressure during injection
- ✓ Pulseless pump



SEC-MALS interfaces to standard U/HPLC-SEC instrumentation

# SEC-MALS Application Example

## Protein Conjugate Analysis



# MALS Application Examples – Protein Conjugate Analysis

Waters™



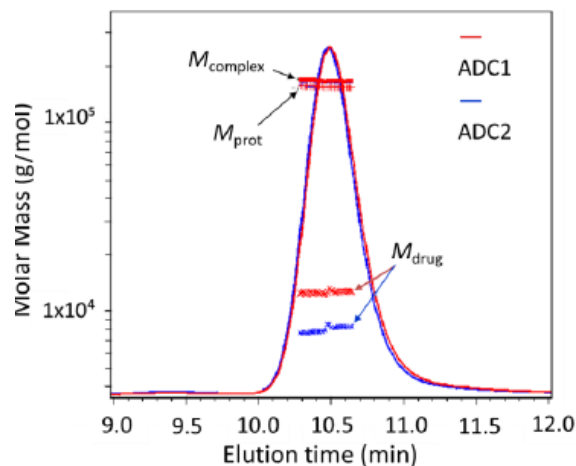
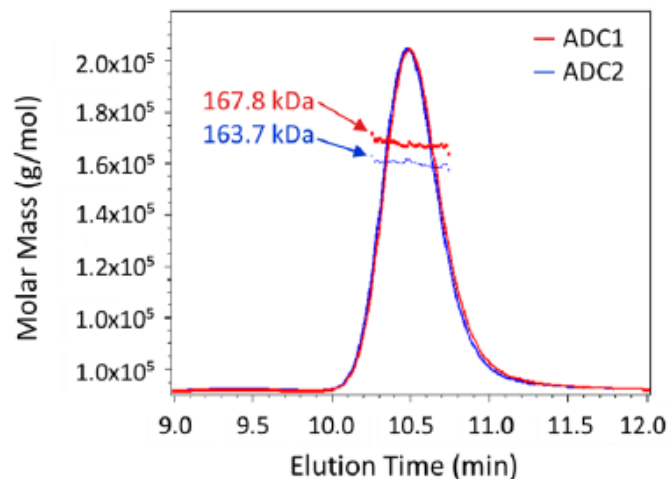
- Protein conjugate analysis uses MALS + UV + RI and measures:
  - Amount component A                      -                      Amount component B
  - Molar mass component A                -                      Molar mass component B
  - Molar mass of the complex
  
- Protein conjugate analysis is used for:
  - Glycosylated proteins
  - PEGylated proteins
  - Membrane protein
  - Protein-protein-complex
  - Antibody-Drug-Ratios





# Antibody-Drug-Ratio by Protein Conjugate

- Requirements
  - UV extinction coefficients and  $dn/dc$  values for antibody and drug need to be known
  - Antibody and drug must differ either in the UV extinction coefficient or in the  $dn/dc$  value
  - The modifier mass should be at least 5 % of the total molar mass
- Molar mass of a single drug molecule is 1.25 kDa



|      | $M_w$ (kDa) |          |      | DAR  |
|------|-------------|----------|------|------|
|      | Complex     | Antibody | Drug |      |
| ADC1 | 167.8       | 155.2    | 12.6 | 10.1 |
| ADC2 | 163.7       | 155.6    | 8.1  | 6.5  |

# SEC-MALS Application Example

## Characterizing AAV

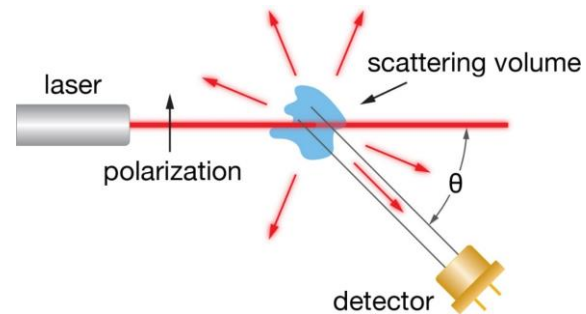


# Multi-angle light scattering (MALS) solution for AAV

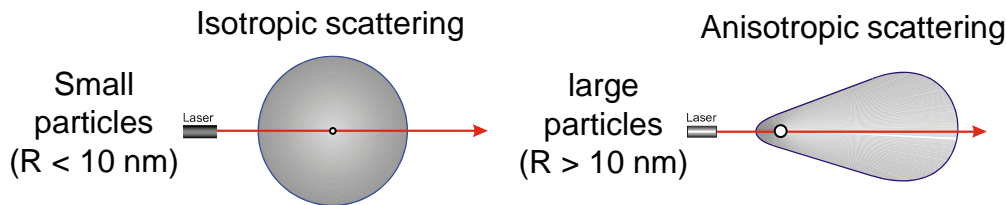
## SEC-MALS

*For AAV production and QC  
(4 CQAs in a single assay)*

- ✓ Identity (molar mass)
- ✓ Particle concentration
- ✓ Capsid content
- ✓ Purity (aggregation)



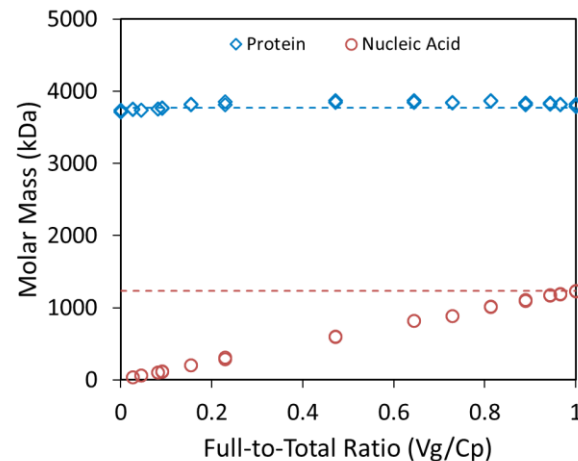
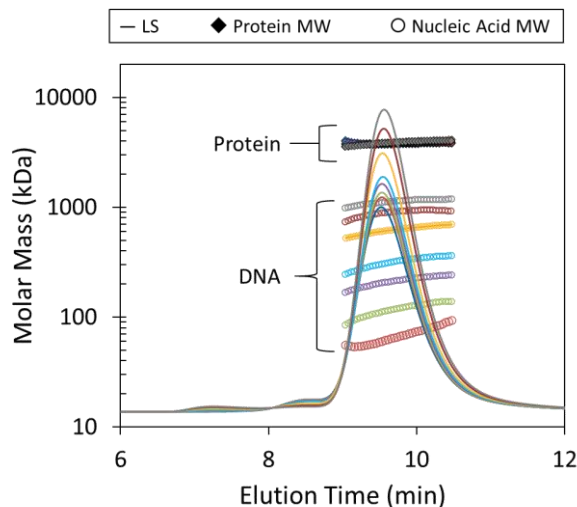
$$I_{\text{scattered}} \propto M \cdot c \cdot \left( \frac{dn}{dc} \right)^2$$





## CQA #1: Identity (Molar Mass)

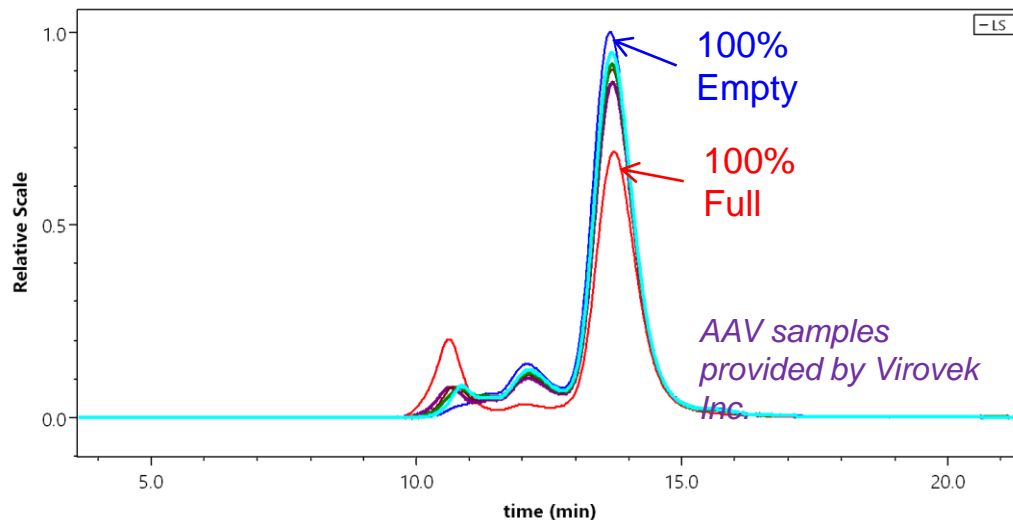
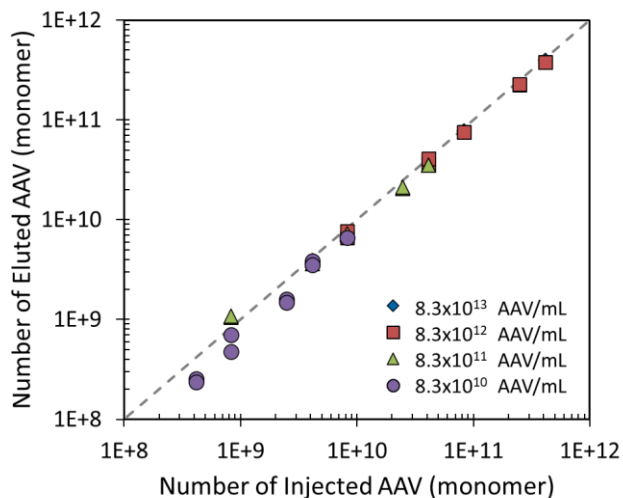
- MALS directly measures molar mass of each AAV sample to identify
  - Oligomeric state (monomer, dimer, higher order oligomer)
  - Capsid content (empty, full, or mixture)
  - Presence of self-complementary DNA or other nonideal DNA loading





## CQA #2: Particle concentration

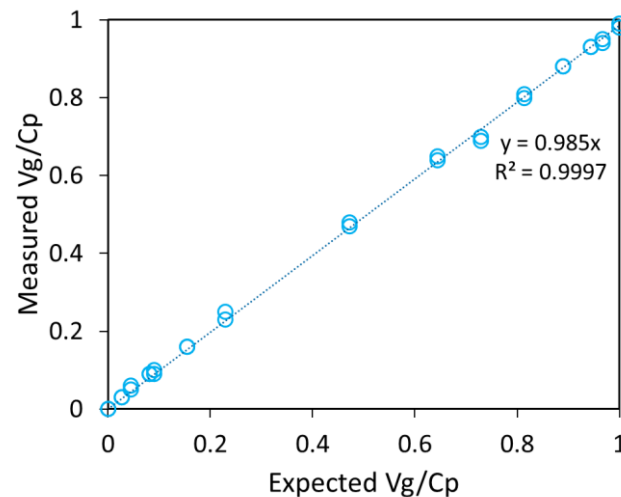
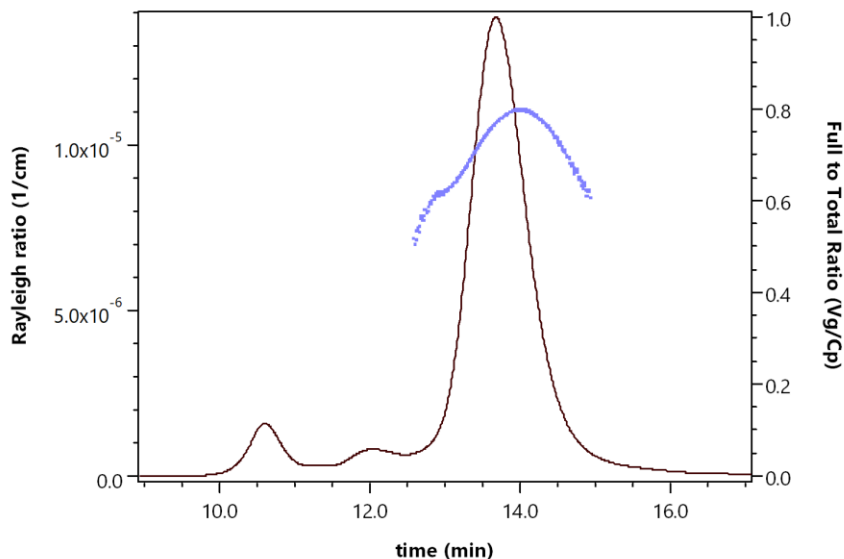
- SEC-MALS combined with UV and RI provides total, full, and empty AAV concentration.
  - Well-tested method that has been applied to serotypes 1, 2, 5, 6, 8, 9, 10
  - Complementary to AUC, ddPCR, ELISA, and other methods
  - Only assumption is 100% mass recovery





## CQA #3: Capsid content (Vg/Cp or full/total)

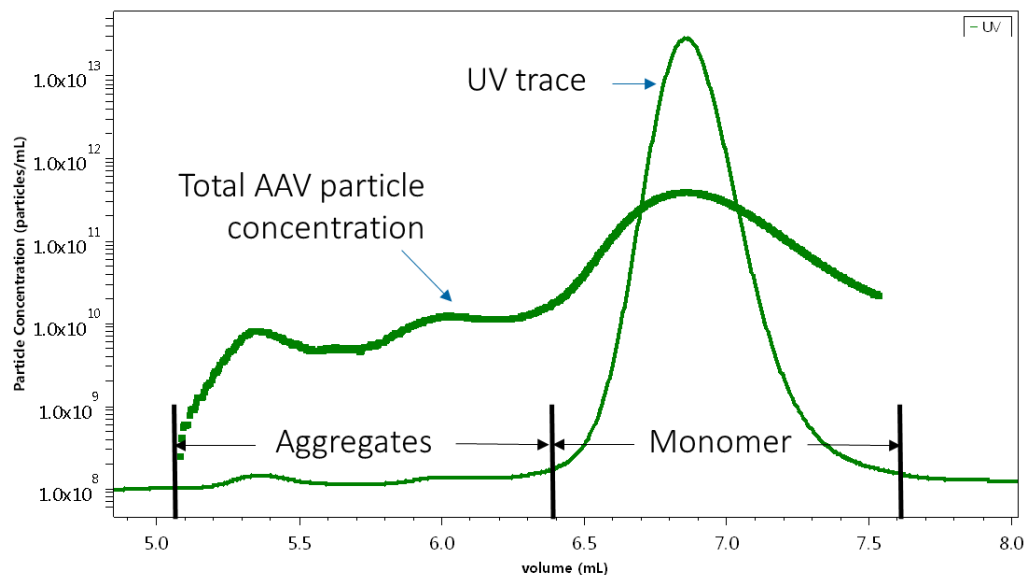
- Simultaneous with CQA 1, SEC-UV-MALS-RI provides capsid content (CQA 2).
  - Excellent correlation with AUC data to provide orthogonal, complementary information
  - Measured capsid content is linear and extends across a wide dynamic range





## CQA #4: Purity (quantify aggregation)

- Particle concentrations are calculated for each data slice to quantify percent monomer and aggregates.
- SEC column may remove large aggregates and FFF is a better alternative. Please read Wyatt AN2004.



|            | Concentration<br>[particles/mL] | Content<br>[%] |
|------------|---------------------------------|----------------|
| Monomer    | $4.22 \times 10^{13}$           | 94.6           |
| Aggregates | $0.24 \times 10^{13}$           | 5.4            |
| Total      | $4.46 \times 10^{13}$           | 100            |

## Summary – SEC-MALS

- Measurements are absolute
  - No protein standards needed (no assumptions)
- 200 Da up to 1 GDa
- Automated measurements of large sample sets
- Powerful technique for proteins and AAV from research to production
  - Identify proteins, oligomeric states and purity of samples
  - Analyze modified proteins, protein-DNA-conjugates or protein-protein-complex
  - In-depth quality control for protein and AAV products





## Batch systems

DLS



HTP-DLS



## Chromatography

SEC-MALS

IEX-MALS



AF4-MALS



## Process

RT-MALS



Dynamic Light  
Scattering (DLS)

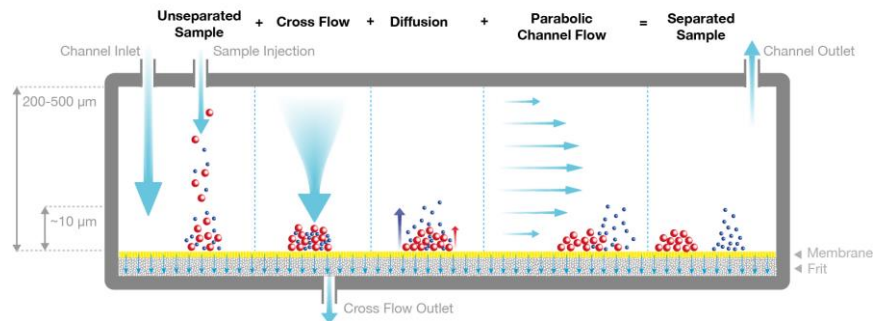
Multi-Angle Light Scattering (MALS)

# Field-Flow Fractionation



## Theory

### Orthogonal Separation Technique



- Laminar channel flow transports the sample
- Cross flow through membrane retains sample
- Separation based on cross flow / channel flow ratio
- Separation depends upon diffusion speed, hydrodynamic radius

## What can you measure?

### Eclipse FFF System

- Orthogonal technique to SEC
- Separation of sticky proteins, larger complexes, viruses, particles
- 21 CFR part 11

# Eclipse FFF-MALS System

## DAWN MALS detector

Measures molar mass and radius  $R_g$   
 $R_h$  with integrated DLS detector

## Optilab dRI detector

Measures concentration

## Eclipse FFF control module

Regulates the flows for the separation  
Monitors all pressures and flows

## HPLC

Pump  
Autosampler  
UV detector  
Fraction collector

## FFF Channel

Separation in a flow field  
No stationary phase



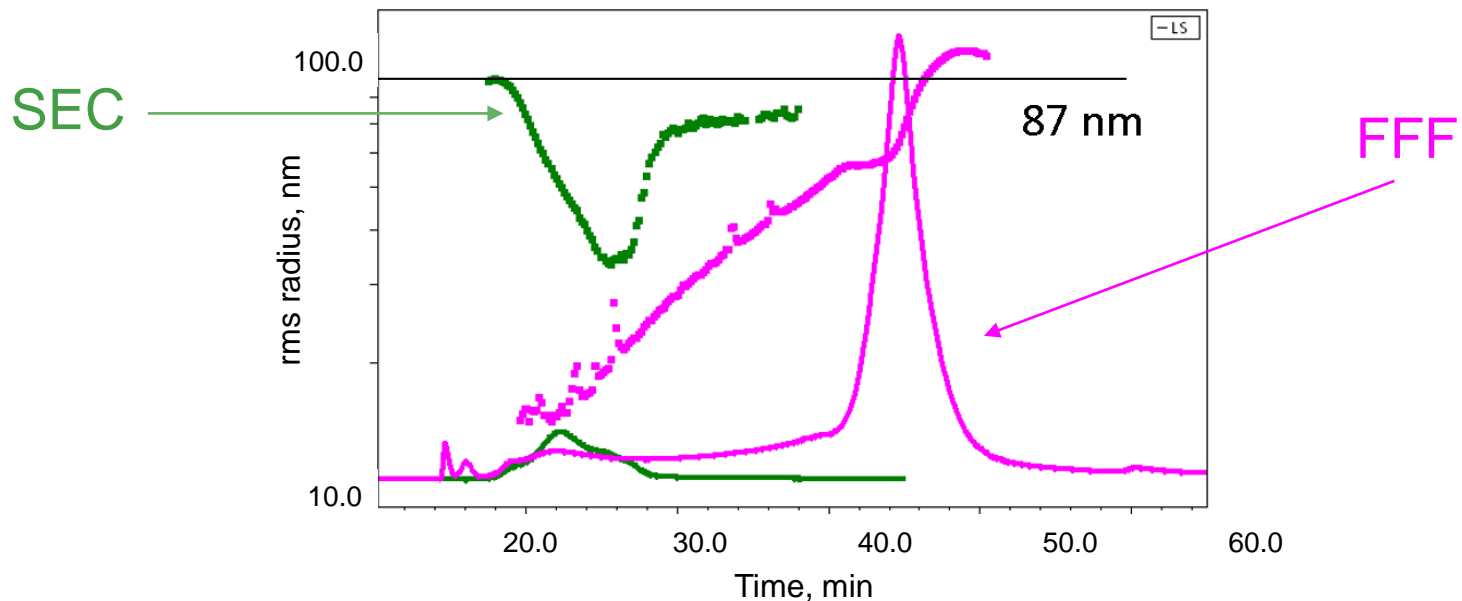
|     | Challenges   |
|-----|--|
|     | SEC-MALS   |
| AAV | Good method for multiple CQAs<br>May remove large aggregates             |
| AD  | High risk of low recovery and<br>insufficient resolution, not a good fit |
| LV  |  |

|     | Challenges  |  |
|-----|---|--|
|     | SEC-MALS  | DLS  |
| AAV | Good method for multiple CQAs<br>May remove large aggregates          | Good screening method<br>Low resolution and low quantitation for in-depth characterization |
| AD  | High risk of low recovery and insufficient resolution, not a good fit |  |
| LV  |   |  |

|     | Challenges  |  | Solutions  |
|-----|---|--|--|
|     | SEC-MALS  | DLS  | FFF-MALS   |
| AAV | Good method for multiple CQAs<br>May remove large aggregates          | Good screening method<br><br>Low resolution and low quantitation for in-depth characterization | Orthogonal method for AAV aggregate quantification   |
| AD  | High risk of low recovery and insufficient resolution, not a good fit |  | Preferred method for high resolution separation, proper quantification of size/concentration/aggregation, and in-depth characterization (empty vs. full) |
| LV  |   |  |  |

## Should we choose SEC or FFF

- SEC: poor mass recovery, compromised separation resolution, filters off larger components
- FFF: good mass recovery, high resolution, no sample degradation



# FFF-MALS Application Example

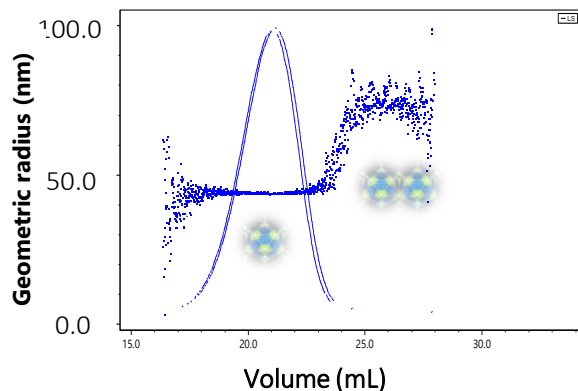
## Characterizing Viral Vectors





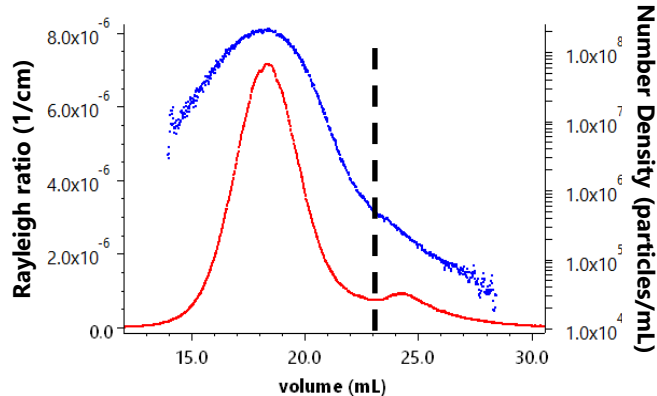
# Adenovirus characterized by FFF-MALS

Detect aggregation with high sensitivity and resolution



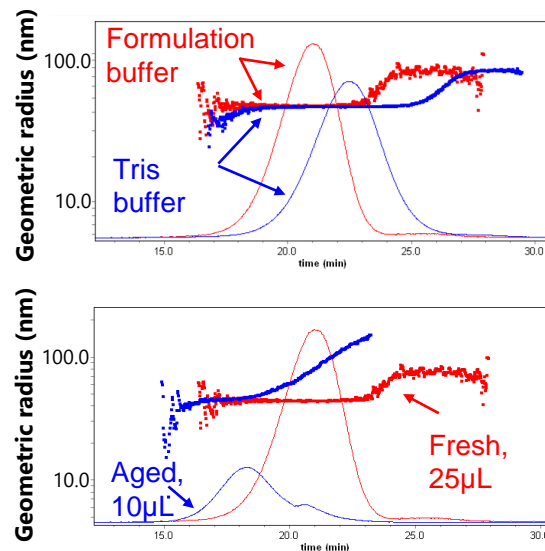
The minute amount of dimer cannot be detected by DLS.

Quantify physical titer and estimate empty to full ratio

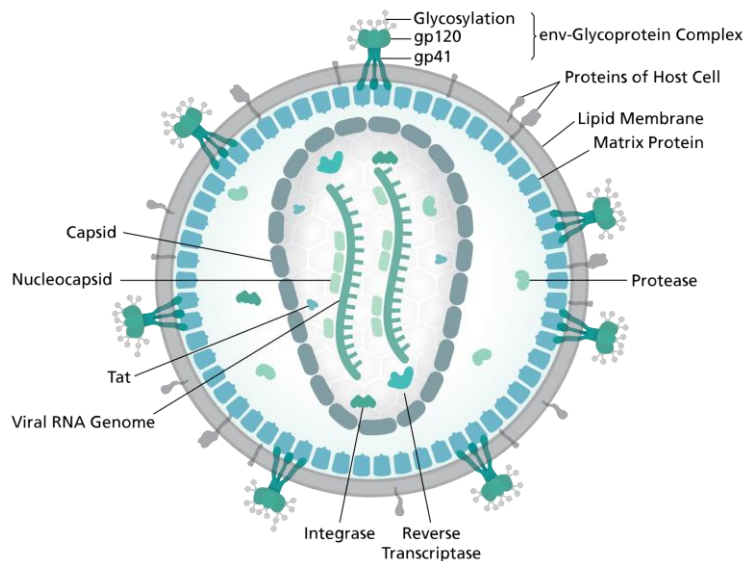


|                              |                      |
|------------------------------|----------------------|
| Monomer, mL <sup>-1</sup>    | $6.5 \times 10^{10}$ |
| Aggregates, mL <sup>-1</sup> | $8.8 \times 10^7$    |

Study formulation and stability



# Lentivirus (LV)

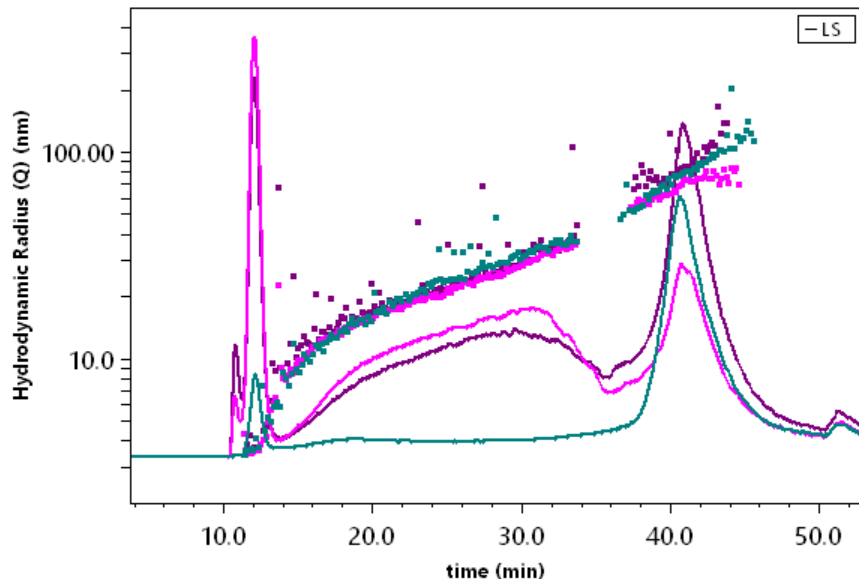
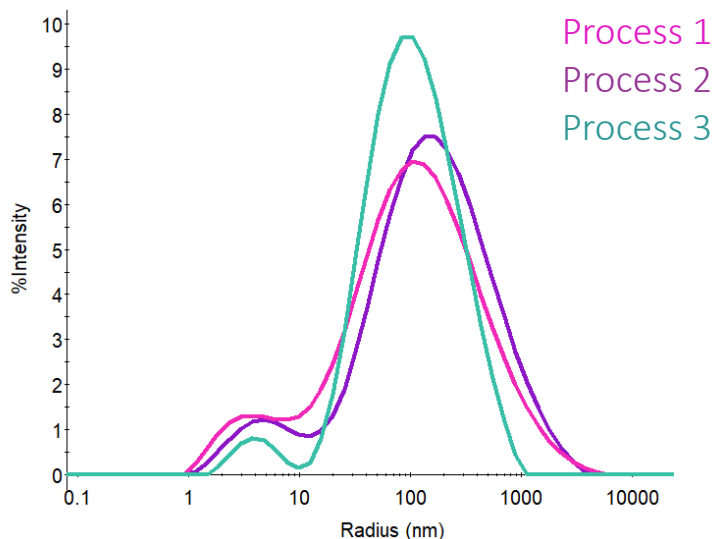


- A subtype of gamma retrovirus
- Used in both gene and cell therapies
- Genetic payload is low compared to the total capsid mass
- More complex than AAV and AD due to its large size and size heterogeneity
- Lack of characterization tools
- Low recovery and no separation by SEC



## LV: understand the manufacturing parameters

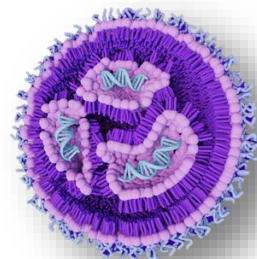
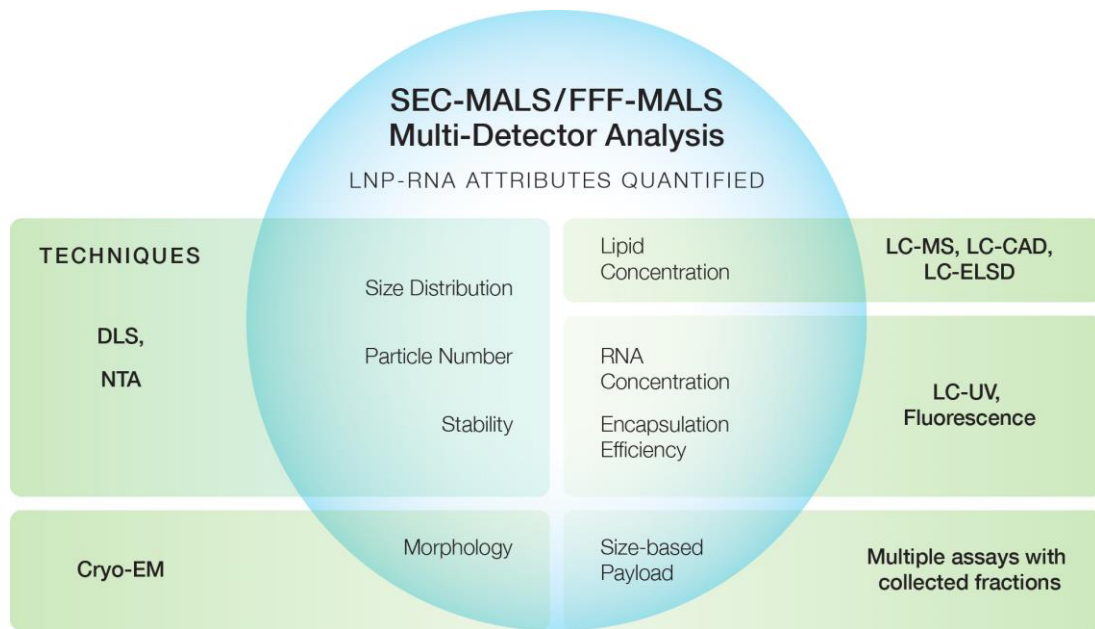
- LVs from 3 slightly different process conditions. DLS to screen the samples first.
- FFF-MALS provides good resolution for LV and impurities, thus enables better understanding and control of manufacturing parameters and conditions.



# FFF-MALS Application Example

## Characterizing LNP

- SEC-MALS and FFF-MALS provide comprehensive LNP characterization and multi-attribute quantitation.



# MALS-DLS-UV-dRI following SEC or FFF

*SEC or FFF provides size-based separation*

- Online detectors – MALS, DLS, UV, and dRI – provide data for biophysical analysis to quantify attributes



DAWN® (MALS-QELS)

- ✓ Molar mass
- ✓ Radius ( $R_g$ ,  $R_h$ ), shape
- ✓ Particle concentration



UV (260 nm)

- ✓ Concentration
- ✓ Composition



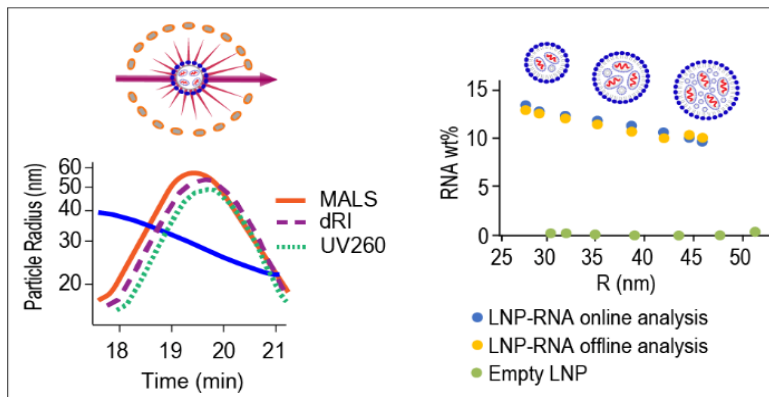
Optilab® (dRI)

- ✓ Concentration
- ✓ Composition



# LNP-siRNA by SEC/FFF-MALS-UV-dRI

## Size-based RNA payload



X. Jia, et al, "Enabling online determination of the size-dependent RNA content of lipid nanoparticle-based RNA formulations", submitted.

## Offline analysis:

**Total mass:** use dRI signal from SEC

**RNA mass:**

- 1) Fractions collected;
- 2) LNP disrupted by 2% Triton X-100 and diluted;
- 3) Analyzed by UHP-RPC-UV(260 nm) for RNA quantitation.

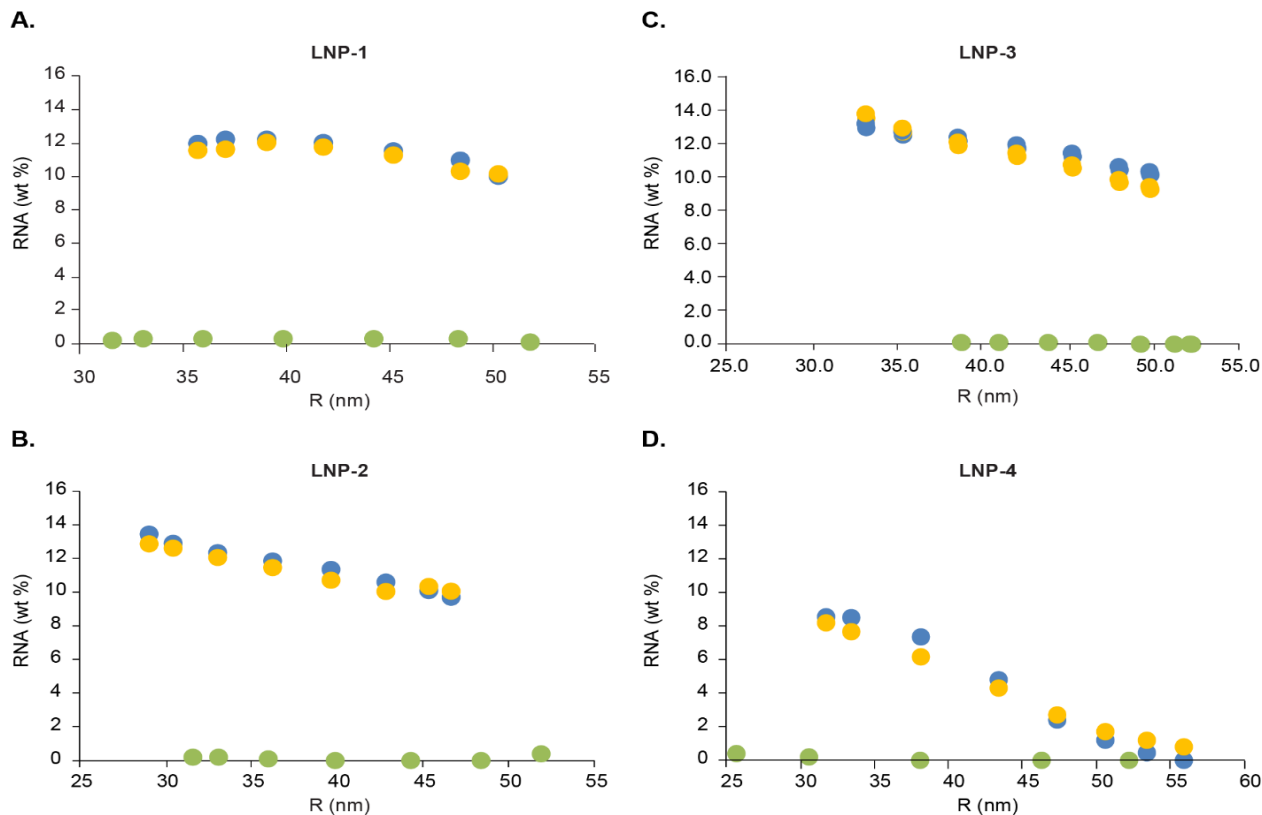
**New**

## Online analysis (Wyatt LNP method):

Use data from **online multiple-detector** and **Wyatt LNP Analysis** to calculate lipid and RNA concentration of each eluting slice



# LNP-siRNA by SEC/FFF-MALS-UV-dRI



LNP-RNA, offline

LNP-RNA, online

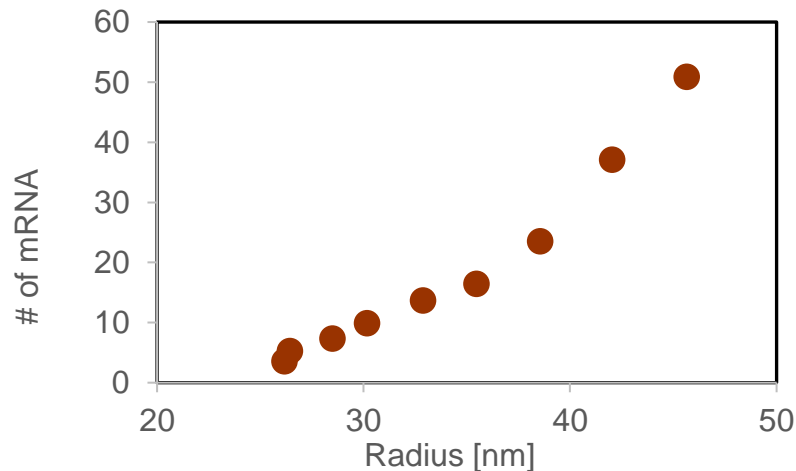
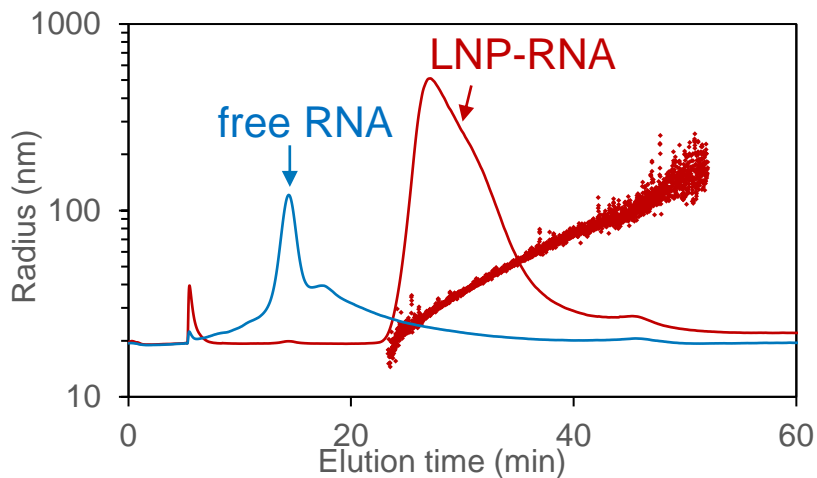
Empty LNP, online





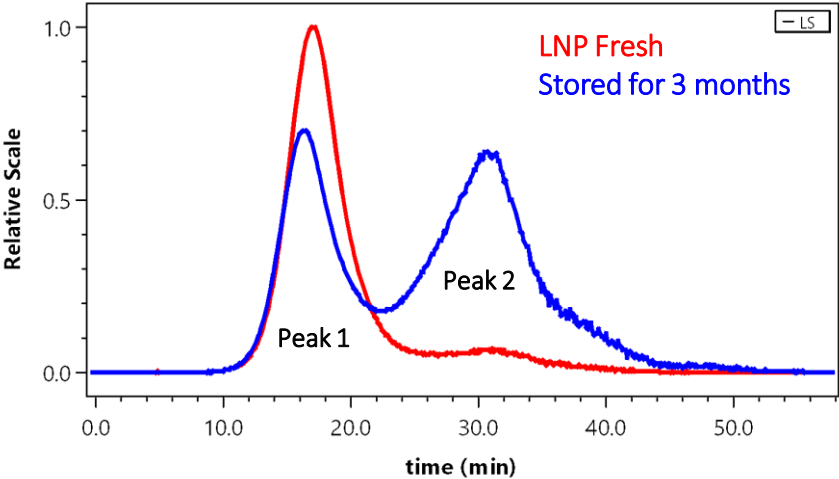
# Lipid nanoparticle (LNP) encapsulated nucleic acids

- LNP is emerging as a platform to formulate various gene drug substance.
- Use FFF-MALS-UV-dRI to quantify MW and size distribution, RNA encapsulation efficiency, payload distribution, and structural information.

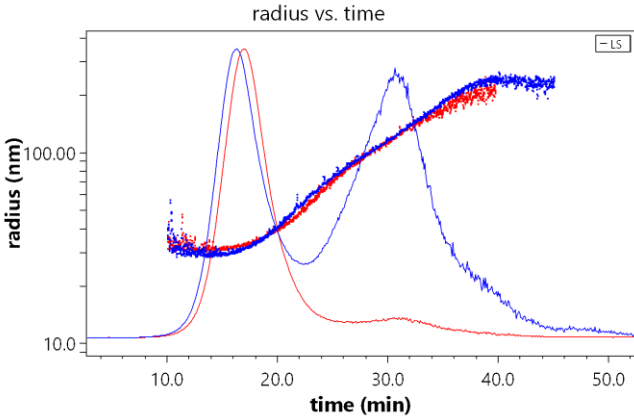
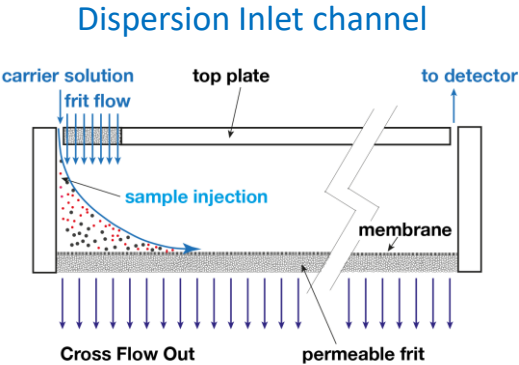




# RNA-LNP Long-Term Storage Stability



|               | Peak 1 rms radius (nm) | Peak 1 particle concentration (mL <sup>-1</sup> ) | Peak 2 particle concentration (mL <sup>-1</sup> ) |
|---------------|------------------------|---|---|
| Fresh sample  | 26.4                   | 5.55 e12  | 2.24 e09  |
| Stored sample | 24.7                   | 5.85 e12  | 2.01 e10  |



## Summary – FFF-MALS

- Orthogonal technique to SEC
- Less shear effects
- Suitable for sticky proteins, larger complexes, viruses, particles
- Retains aggregates for analysis sometimes removed by SEC
- Higher flexibility compared to SEC
  - Adjust separation range to different products without change of separation channel
  - Vast range for buffer compatibility

# Wyatt ProfloReal-Time Multi-Angle Light Scattering



Batch systems

DLS



HTP-DLS



Chromatography

SEC-MALS

IEX-MALS



AF4-MALS



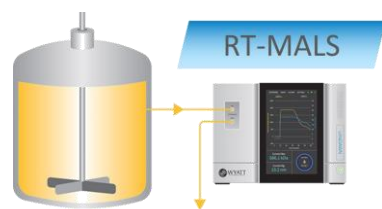
Process

RT-MALS



Dynamic Light  
Scattering (DLS)

Multi-Angle Light Scattering (MALS)



# Real-Time Multi-Angle Light Scattering

- Real-time measurements of molar mass, radius and particle concentration
- Triggers for fraction collection and process control

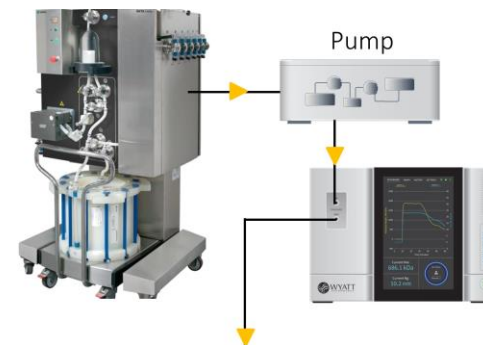
## In-line

- Lab- and pilot scale FPLC, UF/DF
- Short response time
- Flow rates up to 200 mL/min (depends on allowed backpressure)
- Soon: 800-1000 mL/min



## On-line

- For high flow rates or static processes
- Reactor vessel, homogenizer, fill-finish, chromatography, UF/DF



- **Traditional PAT measures *process or indirect parameters***

- Temperature, pressure, flow rate, feedstock (e.g. via Raman spectroscopy)
- UV signal (concentration of... something)
- Extensive modeling required

- **Real-time multi-angle light scattering (RT-MALS) measures *direct product attributes***

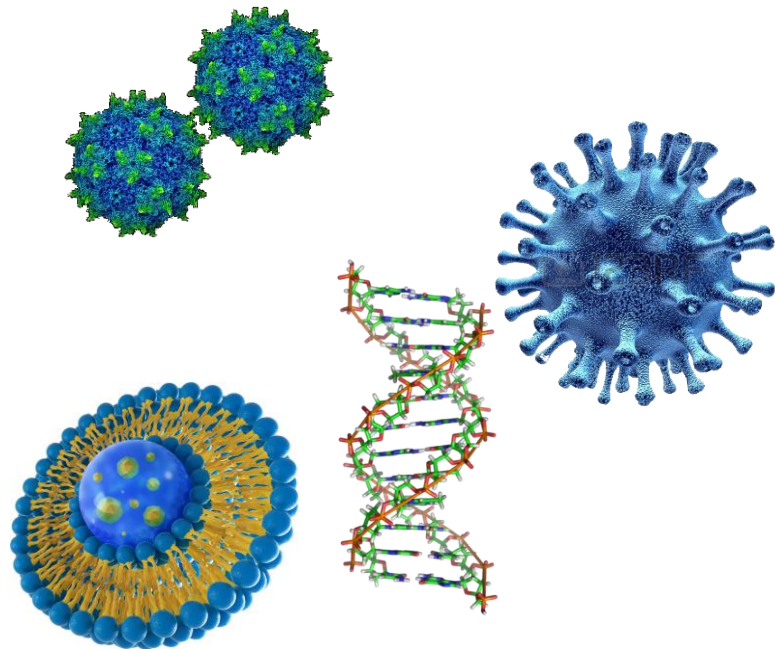
- Molar mass:  $10^3$  to  $10^9$  g/mol
- Size: radius from 10 to 250 nm
- Particle concentration (range depends on size)
- Molar mass and size inform on aggregation
- Payload: AAV full:total ratio (Vg/Cp)

## PAT:

*“a system for ...analyzing, and controlling manufacturing through **timely** measurements (i.e., during processing) of critical quality and **performance attributes** of ...materials and **processes**, with the goal of ensuring final product quality.” (FDA)*

# Gene vector attributes monitored in DSP by RT-MALS

|                         | $M_w$ | $R_g$ | $R$ | Part. Conc. | other              |
|-------------------------|-------|-------|-----|-------------|--------------------|
| Proteins, nucleic acids | ✓     | ✓     |     |             | Aggregate content  |
| AAVs, small VLPs        | ✓     |       | ✓   | ✓           | Vg/Cp, aggregation |
| Viruses, viral vectors  |       |       | ✓   | ✓           |                    |
| Lipid nanoparticles     |       |       | ✓   | ✓           |                    |



# RT-MALS Application Example

## Characterizing AAV





# AAV (and other small viral vectors): Vg/Cp, titer

## Attributes:

- Vg/Cp
- $N_{\text{capsid}}$
- $N_{\text{genome}}$
- $MW_{\text{capsid}}$
- $MW_{\text{genome}}$
- $R_g$

## AN8008: Real-time monitoring and control of AAV chromatographic enrichment with RT-MALS

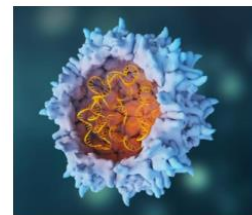
F. Michael Haller, Ph.D., Lonza Biologics and Dan Some, Ph.D. Waters | Wyatt Technology

### Summary

Downstream purification and enrichment of full AAV capsids for gene therapy products is typically accomplished by ion-exchange chromatography (IEX). While the ratio of UV260 to UV280 absorption is often used during IEX as a proxy for the full:total capsid ratio Vg/Cp, this method does not afford process developers deep insight into accurate empty and full titers, or the presence of product-related impurities. Only when detailed offline analysis of fractions is complete does that information make its way back to process developers or manufacturing teams.

Real-time multi-angle light scattering (RT-MALS) operates in-line with bench-scale FPLC systems to monitor and quantify critical quality attributes (CQA) and identify impurities. RT-MALS provides immediate results for pool

chloride or iodixanol density gradient, which has the benefit of being serotype-independent. However, ultracentrifugation is not suitable for capsid enrichment at commercial/GMP scales where chromatographic separations are preferred.



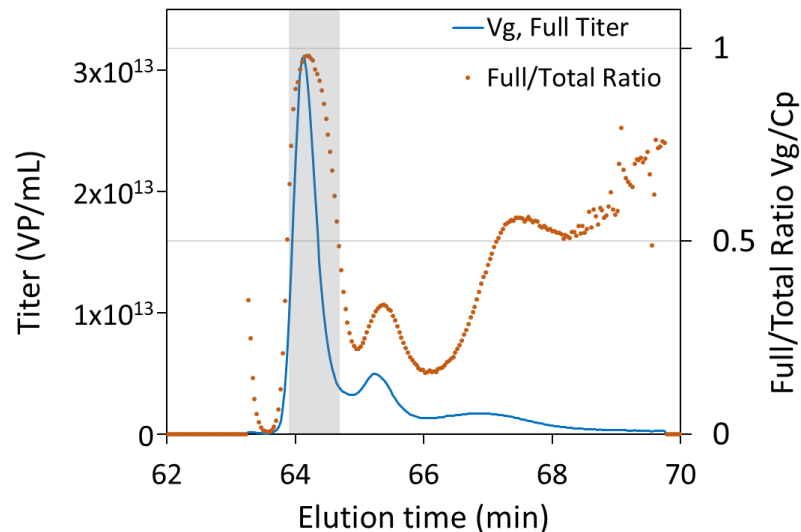
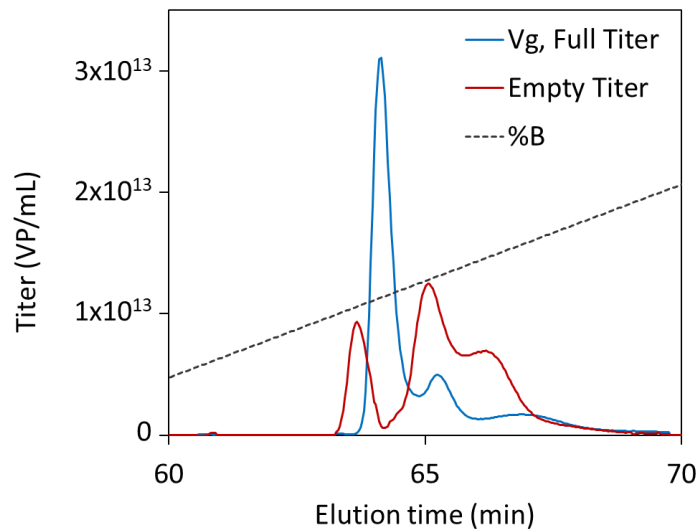
AAV enrichment by ion-exchange chromatography



# AAV (and other small viral vectors): Vg/Cp, titer during linear salt gradient

## Attributes:

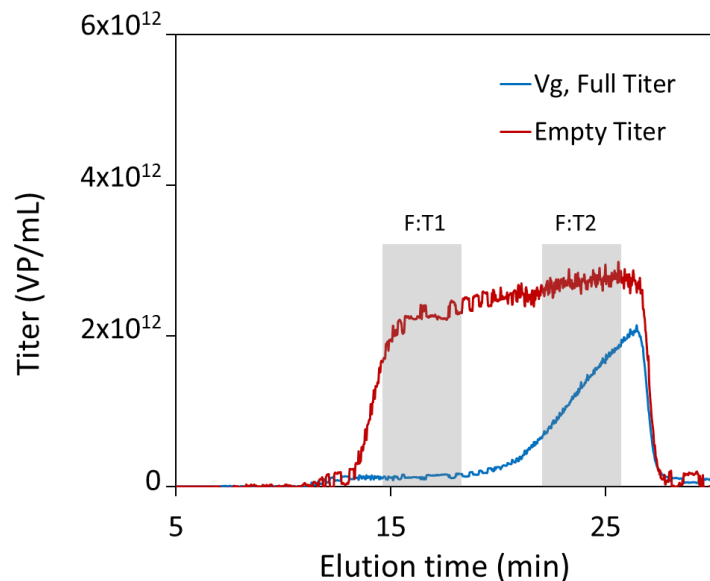
- Vg/Cp
- $N_{\text{capsid}}$
- $N_{\text{genome}}$
- $MW_{\text{capsid}}$
- $MW_{\text{genome}}$
- $R_g$



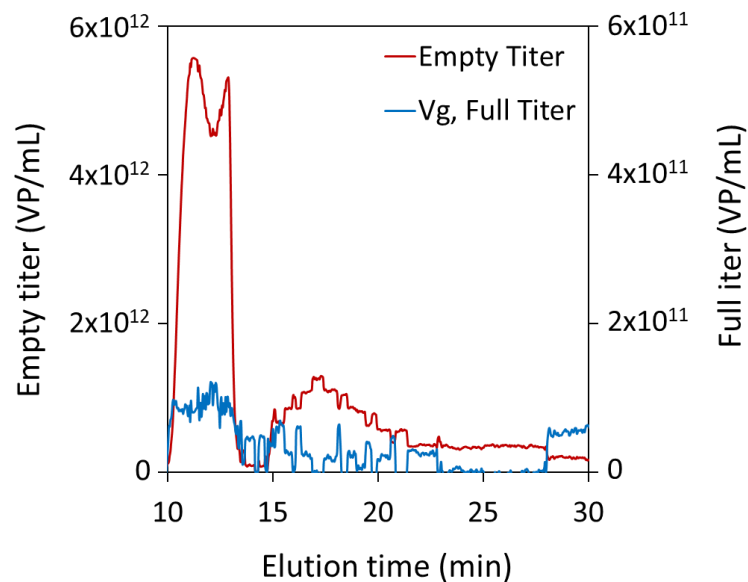


# AAV (and other small viral vectors): Vg/Cp, titer during column loading

Pre-optimal column loading



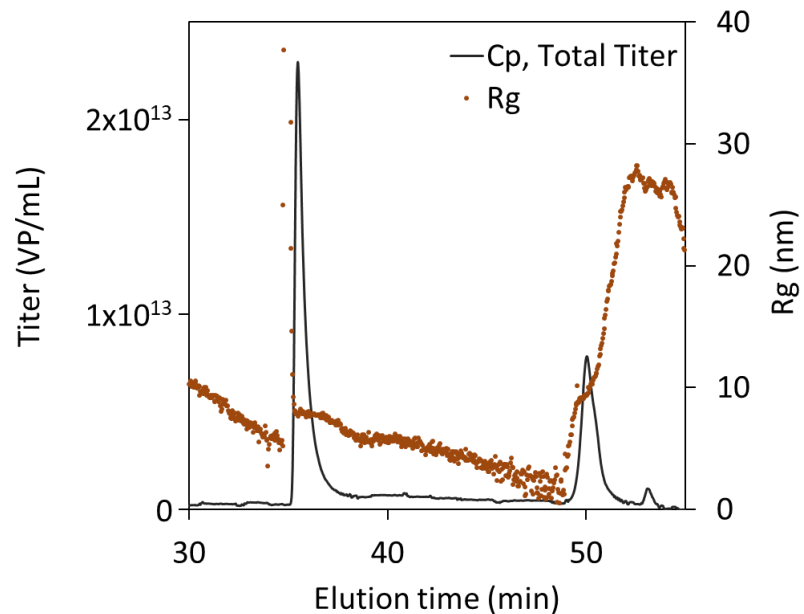
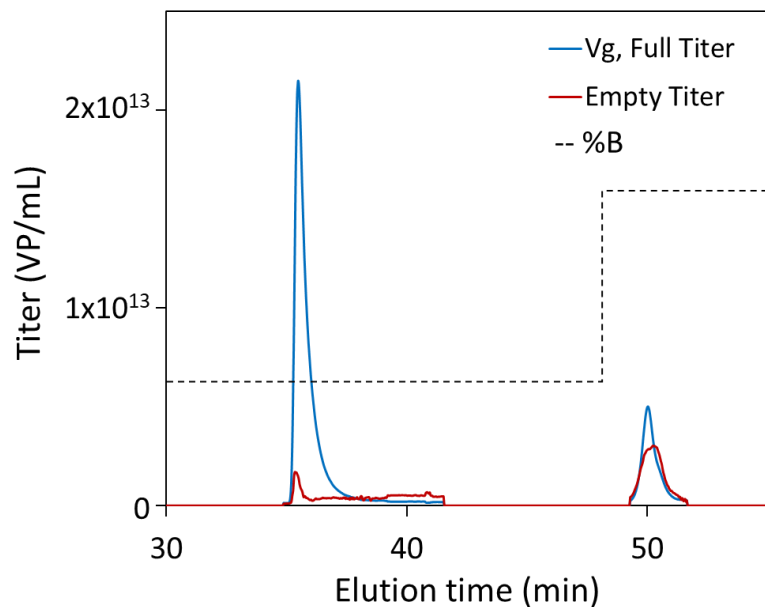
Optimized column loading



Slide courtesy of F. Michael Haller, Lonzac



# AAV (and other small viral vectors): Vg/Cp, titer during step elution & strip



Slide courtesy of F. Michael Haller, Lonzac

- Measurements of product parameters instead of secondary indicators
- No modelling involved
- Triggers for fraction collection and process control
- Applicable for FPLC, UF/DF, TFF and Fill-finish from scale-up to production
- Real-time molar mass, radius, particle concentration, and  $V_g/C_p$  (AAV)
  - Verify product quality in real time during production
  - Identify contaminations, HMW-species or fragments

# Summary: DLS & MALS for biologics

*Product quality attributes from research to production*



DLS &  
MALS

Identify  
formulation  
conditions for  
drug candidates in  
research by DLS

Perform in-depth  
characterization in  
development by  
SEC/FFF-MALS



(RT-)MALS

Increase  
efficiency in  
process  
development by  
SEC/FFF-MALS

Determine  
product attributes  
directly in process  
by RT-MALS



DLS &  
MALS

Perform in-line  
and at-line  
analytics in  
minutes by DLS &  
SEC/FFF-MALS

Real-time  
monitoring of  
product quality  
by RT-MALS



DLS &  
MALS

Detect  
aggregates in  
mere seconds  
with the help of  
DLS

Determine critical  
quality attributes  
for the product by  
SEC/FFF-MALS



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