One-stop stability

Cracking stability using a pile of one-trick, sample-hungry tools is a ton of work. Uncle combines 3 different measurement modes – fluorescence, SLS and DLS. So you can crank out all your data in just a few hours, and use way less precious sample. All the info you'll get makes picking the best formulation, protein, or viral vector a piece of cake.

- T_m & T_{agg}

- Isothermal stability

- Viral capsid stability

- T_m with SYPRO (DSF)

- Sizing & polydispersity

- Sizing with thermal ramp

- Thermal recovery

- Viscosity

- k_D

- B_{22}

- G_{22}

- ΔG

Unleash the Uni

Get more data with way less sample. The Uni only needs 9 µL, and you pick how you use it. Run 1 sample in the morning, 48 in the afternoon. Do a DLS read if that's all you need. Or, check DLS, then start a 3-day experiment to monitor real-time stability. Your samples are sealed airtight, so runs can be short or long – your call.

Full-spectrum

Biologics and gene vectors are special. With Uncle, you get the whole fluorescence spectrum, so you don't need to know ahead of time how your sample behaves. If you want to try out some new tricks with dyes, Uncle can pick up on those too. Uncle's SLS catches aggregation with two wavelengths – making it super sensitive and clutch for uncovering aggregates over a wide range of sizes.
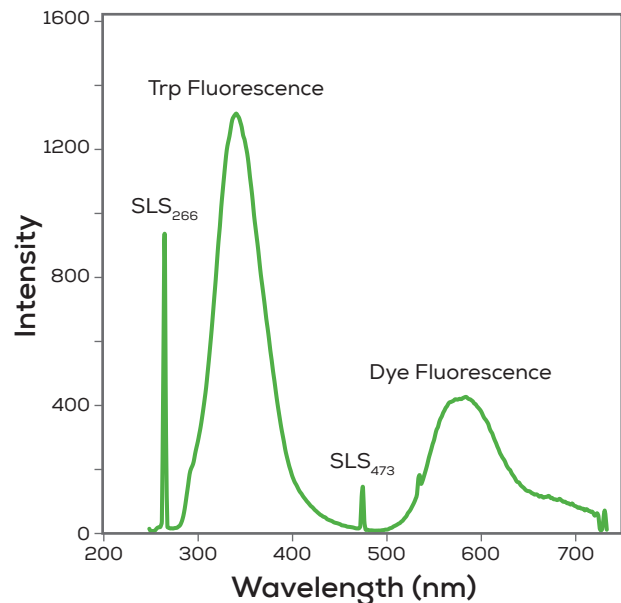
Uncover way more in one shot

Trying new formulations or constructs? Get answers for up to 48 samples in under 2 hours. Measure T_m and T_{agg} at the same time and know when unfolding leads to aggregation. Add a DLS read before the temp ramp to know if you've got aggregate trouble right out of the gate.
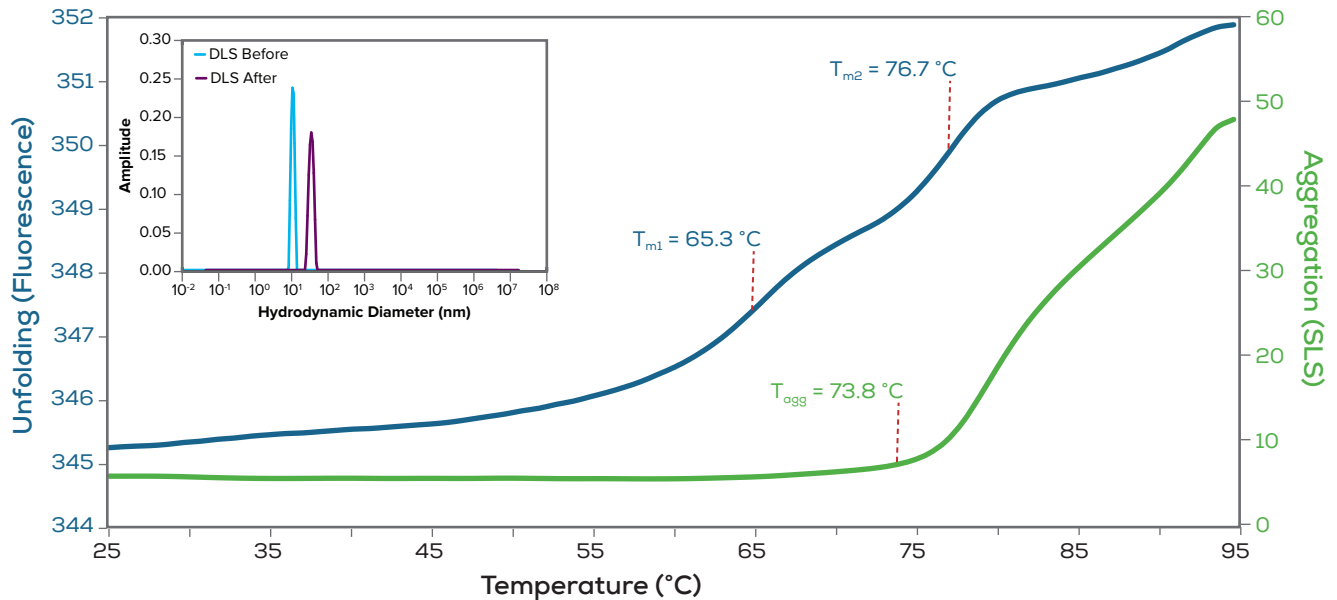
Let 'em simmer

Get a jump on testing long-term storage by tackling isothermal experiments early on – way before it becomes a problem down the line. Uncle is decked out with a set of tailormade apps that focus in on proteins, reporter dyes or vector payloads and how they handle stewing at static temps. Keep Uncle freed up for other stuff with its out-of-the-box isothermal applications – load your samples in Unis, stow them in an incubator, and then pop them back into Uncle to get eyes on who's acting up, whenever you want.
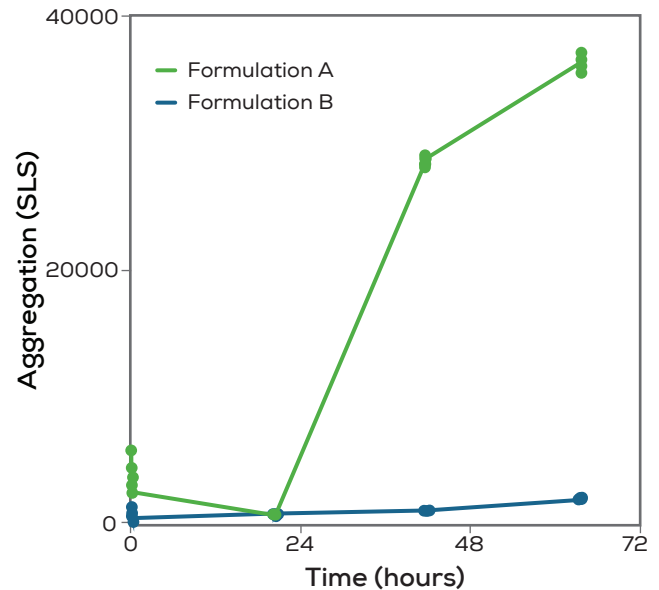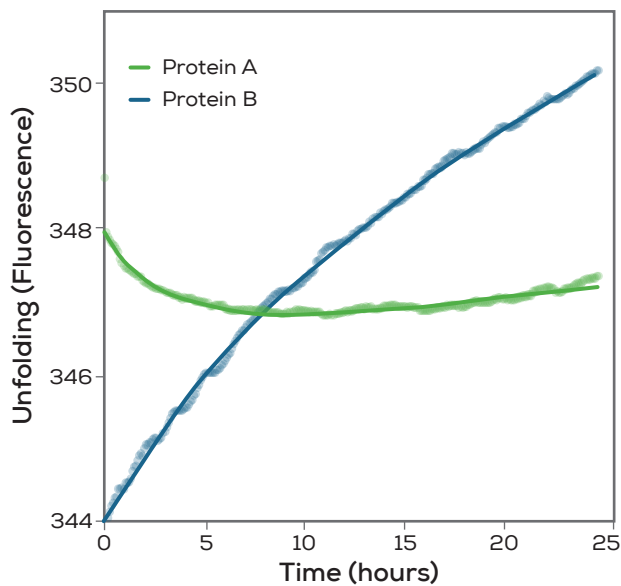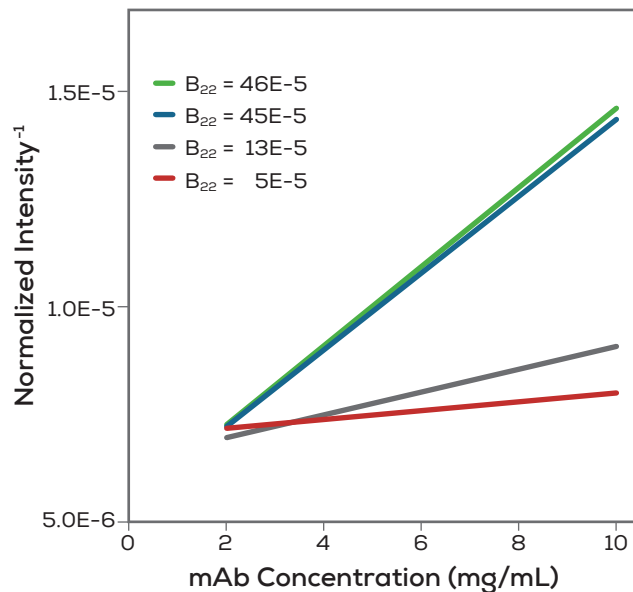
Heat until huge

Grab polydispersity, diameter, and size distribution on the spot using DLS. Then take the same samples and start a thermal ramp to measure which ones get bent out of shape and which keep their cool.
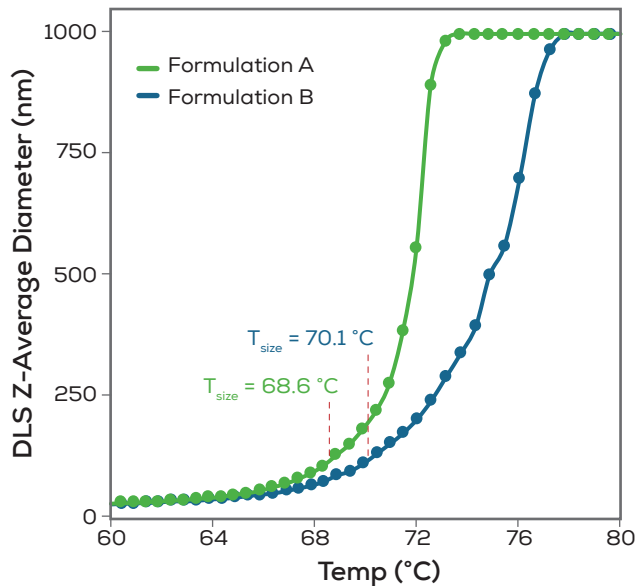
Feel the attraction

Get B_{22} and k_D at the same time in the same Uni. Change up excipients to see if your protein is better off or not – ASAP. Learn on the spot if your protein-formulation combo is good to go or risky for aggregation. For super high protein concentrations, G_{22} is ready to go.

Formulation A
Formulation B

T_{size} = 70.1 °C
T_{size} = 68.6 °C

DLS Z-Average Diameter (nm) vs Temp (°C)

B_{22} = 46E-5
B_{22} = 45E-5
B_{22} = 13E-5
B_{22} = 5E-5

Normalized Intensity^{-1} vs mAb Concentration (mg/mL)

Keep payloads on lock down

Uncle teams up with SYBR Gold to get a read on the temperature where your DNA starts to leak from your vector – way before the AAV capsid pops. Track initial free DNA and what's on the loose after a thermal ramp. Spot when aggregation gets out of hand with the help of SLS.
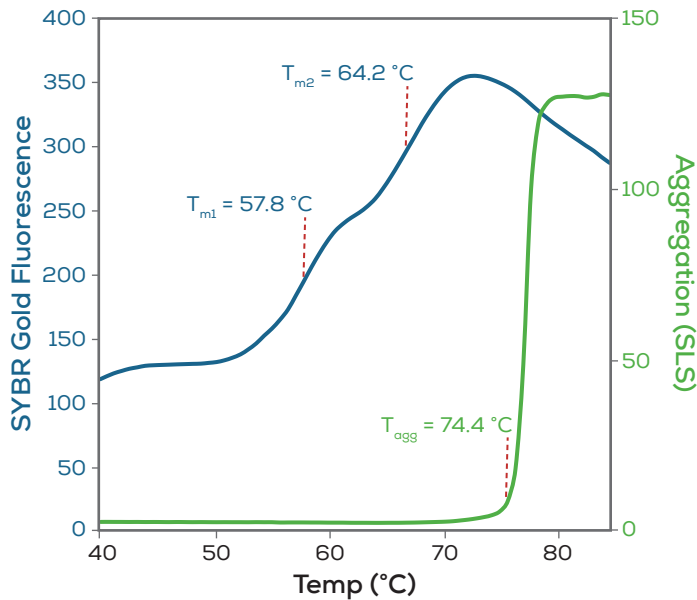
Spot genome jailbreaks

Make sure DNA or RNA isn't escaping from your vectors on the sly, over time. Uncle's full spectrum fluorescence and SYBR Gold isothermal app let you take an early, low volume look at accelerated, isothermal storage testing.

$T_{m2} = 64.2\ °C$

$T_{m1} = 57.8\ °C$

$T_{agg} = 74.4\ °C$

AAV9
AAV5
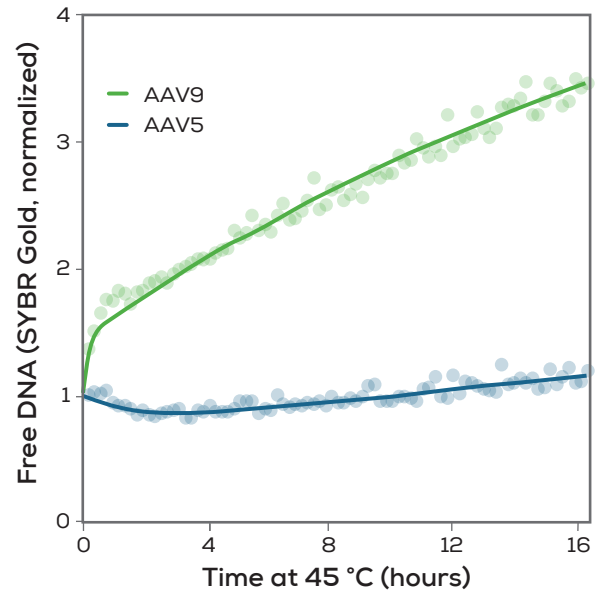
Specifications

Application	Full-spectrum Fluorescence	Static Light Scattering (SLS)	Dynamic Light Scattering (DLS)
T_m	●		
T_{agg}		●	
T_m with SYPRO (DSF)	●		
Isothermals	●	●	●
Sizing & polydispersity			●
Sizing with thermal ramp			●
k_D			●
B_{22} & G_{22}		●	
Thermal recovery	●	●	
Viscosity			●
ΔG	●		
Capsid stability	●	●	●

Instrument	
Minimum sample volume	9 µL, sealed capillaries
Simultaneous samples per experiment	48
Sample temperature range	15–95 °C
Sample concentration range	0.05 mg/mL – 300 mg/mL IgG (protein dependent)
Heating rate	0.1–10 °C/minute
Temperature accuracy	±0.1 °C
Physical	54 cm W x 50 cm D x 58 cm H, 50 kg
Electrical	Auto switching power supply, voltage 110–240 V AC, 50–60 Hz, single phase, fuse rating T6.3AL, 250V, max power 600 W
Regulatory compliance	Software has optional 21CFR11

Fluorescence and static light scattering	
Sample precision	<2% CV (T_m)
SLS resolution	~15 kDa change in mean molecular mass
AAV genome concentration	$\geq 5 \times 10^{11}$ viral genomes per mL
Excitation	266 nm and 473 nm laser
Detection	Fluorescence: CCD spectrometer at full 250–720 nm spectral range SLS: intensity at 266 nm and 473 nm

Dynamic light scattering	
Hydrodynamic diameter range	0.3–1000 nm
Size accuracy	±2%
Minimum sample concentration	0.1 mg/mL – lysozyme
AAV capsid concentration	$\geq 5 \times 10^{11}$ viral genomes per mL
Molecular weight range	192 Da – 25 MDa
Light source	660 nm laser diode
Detection	Avalanche photodiode module

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