

uncle



UNCHAINED  
LABS

## One-stop stability

Cracking stability using a pile of one-trick, protein-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 protein. All the info you'll get makes picking the best formulation, protein, or viral vector a piece of cake.

- $T_m$  &  $T_{agg}$
- $T_m$  with SYPRO (DSF)
- Isothermal stability
- Sizing & polydispersity
- Sizing with thermal ramp
- Thermal recovery
- Viscosity
- $k_D$
- $B_{22}$
- $G_{22}$
- $\Delta G$
- Viral capsid stability



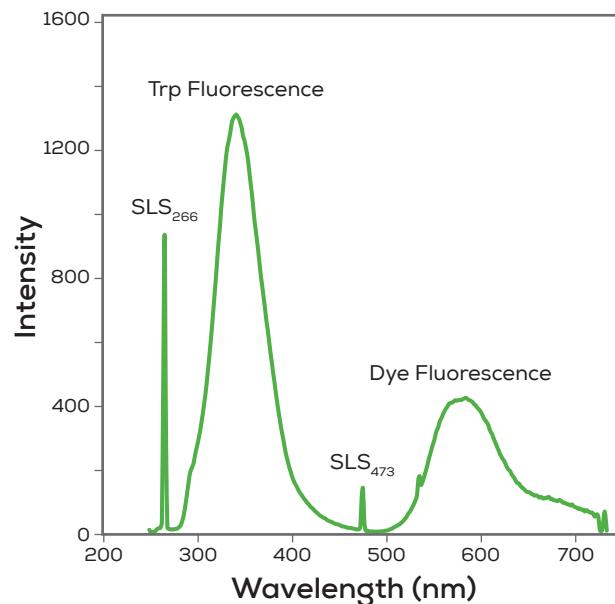
## Unleash the Uni

Get more data with way less protein. The Uni only needs 9  $\mu\text{L}$  of sample, 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.



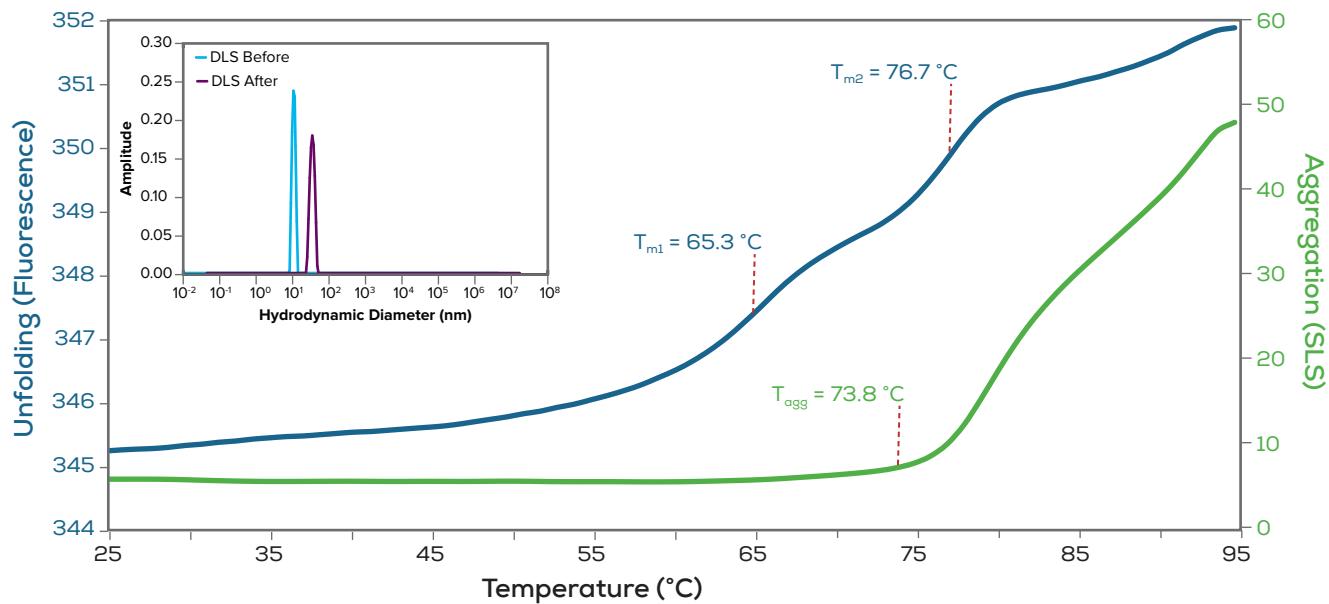
## Full-spectrum

Biologics behave differently. With Uncle, you get the whole fluorescence spectrum, so you don't need to know ahead of time how your protein behaves. If you want to try out some new tricks with dyes, Uncle can pick up on those too. Uncle catches aggregation with two wavelengths – so you'll see it no matter what.



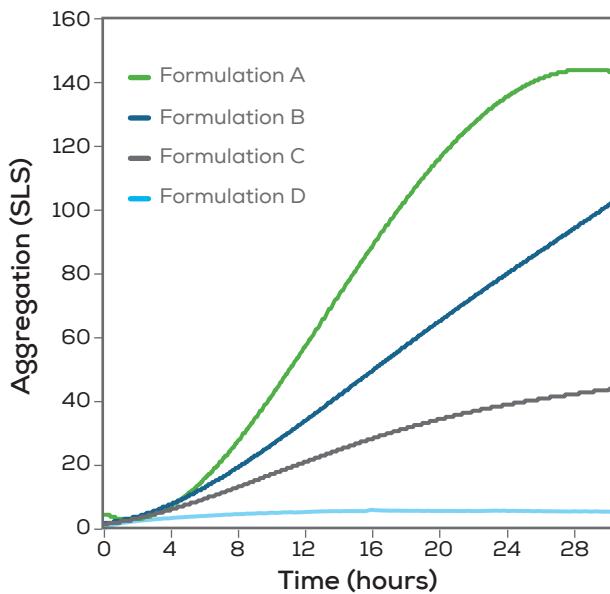
## Uncover way more in one shot

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.



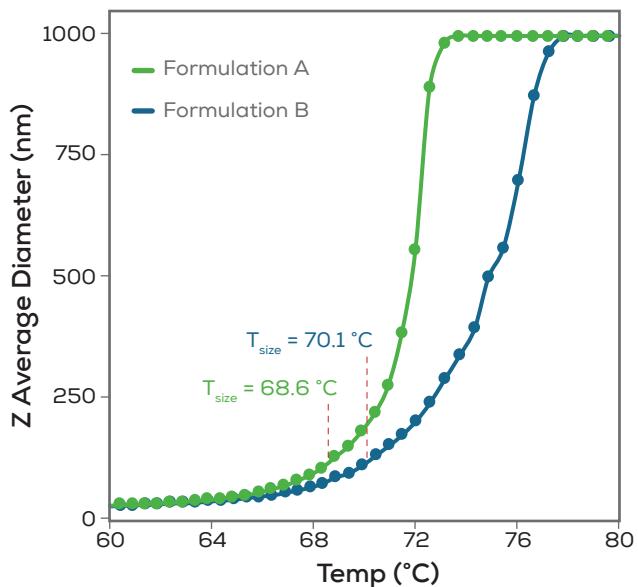
## Isothermal stability

Uncle handles reading DLS, SLS, or both for days with no sample evaporation. So set your temp and walk away. Get a heads-up on long-term stability with the conditions that matter most to you.



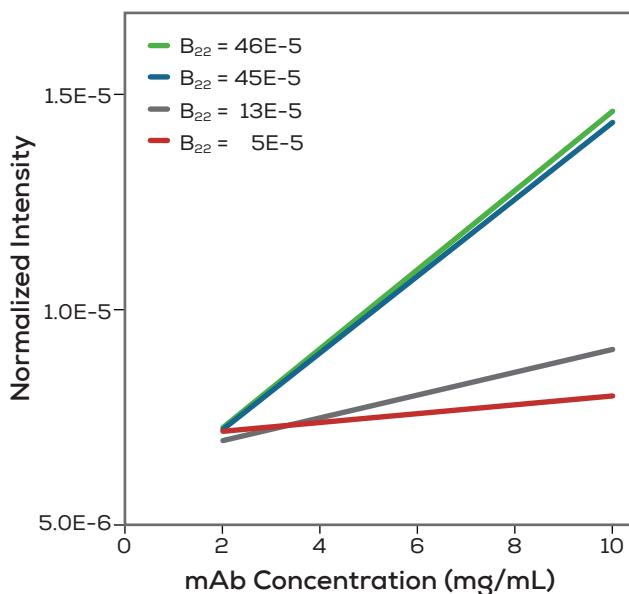
## Sizing with thermal ramp

Grab polydispersity, diameter, and size distribution with amped sensitivity. Then take the same samples and do a thermal ramp to measure which ones get bent out of shape and which keep their cool.



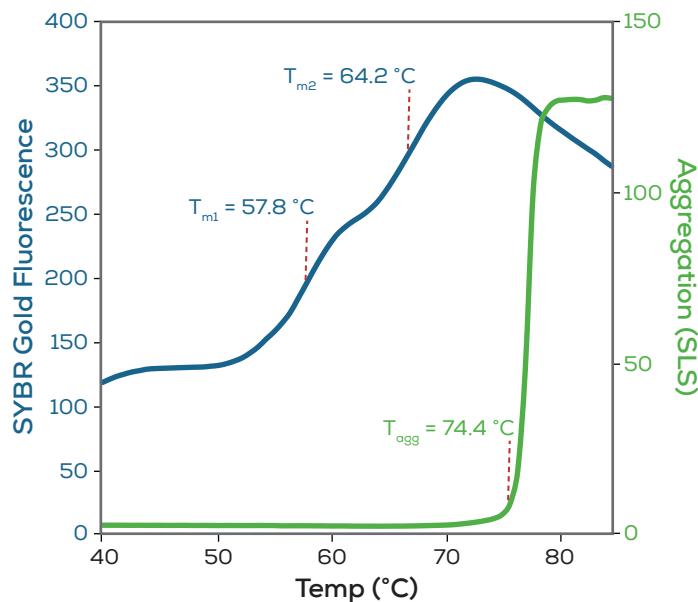
## B<sub>22</sub> & k<sub>D</sub>

Get B<sub>22</sub> and k<sub>D</sub> 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<sub>22</sub> is ready to go.



## Capsid stability

Uncle teams up with SYBR Gold to get a read on when your DNA starts to leak – way before the AAV capsid pops. Quantify initial free DNA and the amount that's on the loose after a thermal ramp. Know when aggregation gets out of hand and tackle particle titer with SLS and DLS.



# Specifications

Application	Full-spectrum Fluorescence	Static Light Scattering (SLS)	Dynamic Light Scattering (DLS)
T <sub>m</sub>	●		
T <sub>agg</sub>		●	
T <sub>m</sub> with SYPRO (DSF)	●		
Isothermal stability	●	●	●
Sizing & polydispersity			●
Sizing with thermal ramp			●
k <sub>D</sub>			●
B <sub>22</sub> & G <sub>22</sub>		●	
Thermal recovery	●	●	
Viscosity			●
ΔG	●		
Capsid stability & particle intensity	●	●	●
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 control accuracy	±1 °C (<70 °C), ±1.5 °C (>70 °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 <sub>m</sub> )		
SLS resolution	~15 kDa change in mean molecular mass		
AAV genome concentration	≥5 x 10 <sup>11</sup> 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	≥5 x 10 <sup>11</sup> 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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