

# HUNKY



**UNCHAINED**  
LABS

## See stability in hi-def

Months of stressing about what'll happen to your protein after one small formulation tweak is a royal pain – and a total waste of time. Hunky hands over the  $\Delta G$  info you can't get anywhere else. Quantify your protein's stability and know if it's going to aggregate now, not later. With 4 apps to choose from, automated liquid handling and full-on data analysis, Hunky is a gotta-have for measuring stability.

**$C_{1/2}$**  rank stability

**$\Delta G$**  quantify stability

**Agg Path** predict aggregation

**$\Delta G_{trend}$**  zoom in on aggregation



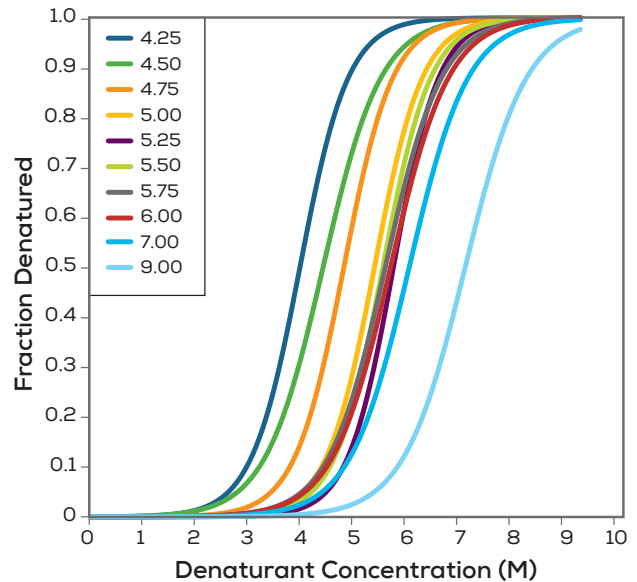
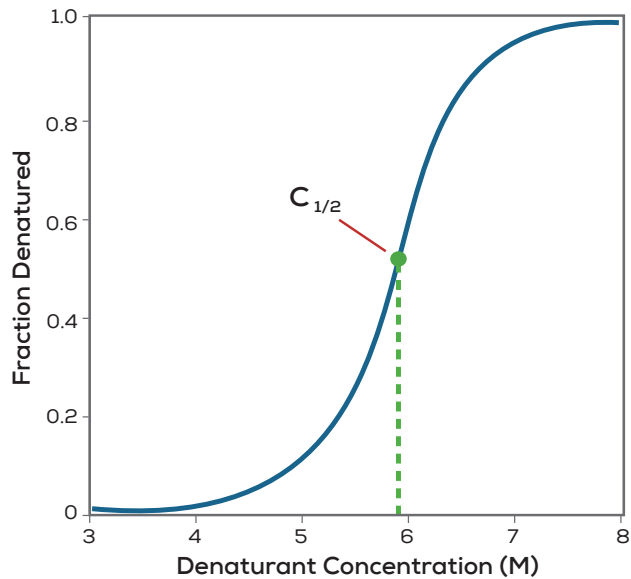
## Why $\Delta G$ rocks

Biologics hang between their native and denatured states.  $\Delta G$  is the only way to tell how much of each you've got at room temp. High  $\Delta G$ s mean your protein's mostly folded and good to go. A low  $\Delta G$  means it's more denatured, not as stable and needs extra TLC – or should get the boot altogether. Get quantitative, high-res differentiation on proteins that were too close to call with just  $T_m$ .

$\Delta G$ kcal/mol	Stability	Fraction denatured
9.6	Small amount of denatured protein	1/10,000,000
8.2		1/1,000,000
6.8		1/100,000
5.5	Moderate amount of denatured protein	1/10,000
4.1		1/1,000
2.7	Large amount of denatured protein	1/100
1.3		1/10
0		1/2

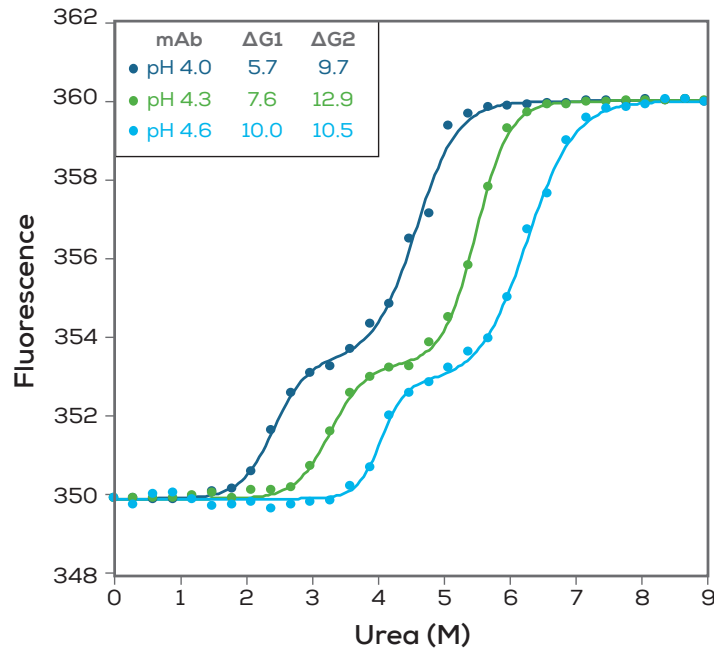
## Get a quickie

Hunky loads you up with massive amounts of stability info. It takes your protein, whips out denaturation curves and calculates the  $C_{1/2}$  – the concentration of denaturant needed to unfold one-half of your protein. Combine  $C_{1/2}$  with  $T_m$  values to double-check your results and bucket your good formulations and constructs from the bad.



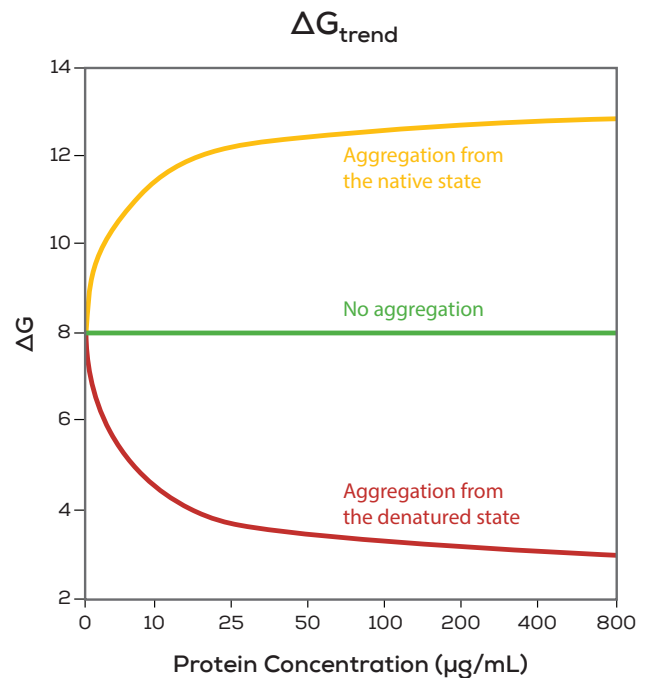
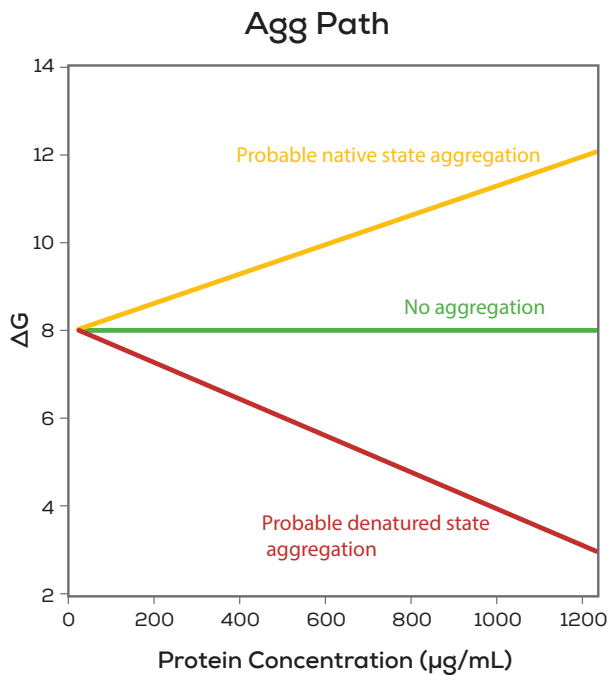
## Settle the score

Hunky's  $\Delta G$  values let you actually quantify how much denatured protein you've got in your sample. Automated data fitting shows you up to 3 unfolding transitions and lets you see small differences in your protein's stability – even in super tight pH or salt windows. There's no heat stress to mess up your curves either. Hunky does its thing at room temp to keep aggregation out of the equation so you get the rundown interference-free.



## Ditch the aggregators

Agg Path measures  $\Delta G$  at one high and one low protein concentration to predict aggregation propensity. If  $\Delta G$  stays constant, breathe easy. If not, throw it in the do-over pile. Use  $\Delta G_{\text{trend}}$  to monitor  $\Delta G$  over a range of concentrations for an even deeper dive into your aggregation situation. Get insight on whether your protein will aggregate, what pathway it will take and how bad it might get.



## Specifications

Description	Specification
Maximum unattended $\Delta G$ measurements	96
Maximum unattended $C_{1/2}$ screening conditions	288
Minimum stock protein concentration	25 $\mu\text{g}/\text{mL}$ IgG (protein dependent)
Minimum final protein concentration	2 $\mu\text{g}/\text{mL}$ IgG (protein dependent)
Typical protein stock volume required per $\Delta G$	0.5 mL
Time to measure each $\Delta G$	Average 30 mins (based on running full stacker)
Environmental conditions	Temperature range: 18–25 °C; Humidity: 40–60% RH (non-condensing)
Protein stock temperature	4 °C to ambient
Fluorescence excitation	280 nm LED
Fluorescence detection	CCD spectrometer, 300–720 nm spectral range
Fluorescence detection dynamic range	Five orders of magnitude
Physical	60 cm W x 63 cm D x 73 cm H, 80 kg
Electrical	Auto-switching power supply, voltage 100–240 V AC, 50–60 Hz



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Rev A