HUNK

UNCHAINED LABS

Make stability routine

What if you knew up front how a small tweak in formulation changed the stability of your biologic, or if it'll aggregate down the road? The only way to get your hands on that info is to know your ΔG, and the HUNK makes measuring it totally routine. So you'll know how changes in protein constructs, concentrations, and formulations affect stability now, not later.

ΔG measure stability

ΔG_{trend} predict aggregation

K_D small molecule affinity

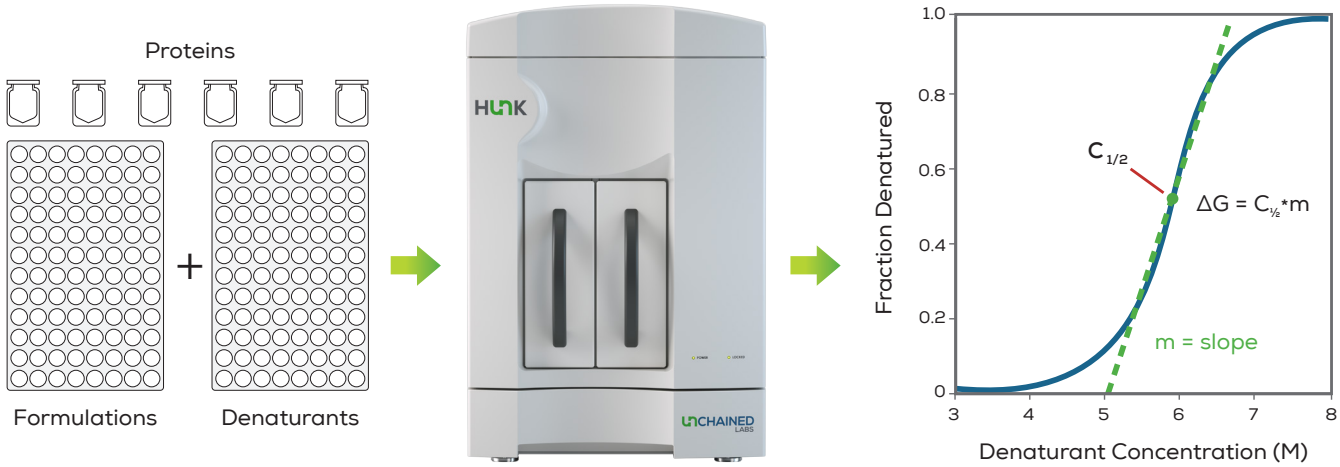
Why ΔG?

Biologics are in equilibrium between their native and denatured states and ΔG is the only way to know how much of each you've got at room temp. A high ΔG means your protein's less denatured, which is a good thing. A low ΔG means it's less stable and more denatured – a not so great thing. So figuring out if your biologic is good to go or needs extra work is a slam dunk.

ΔG 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

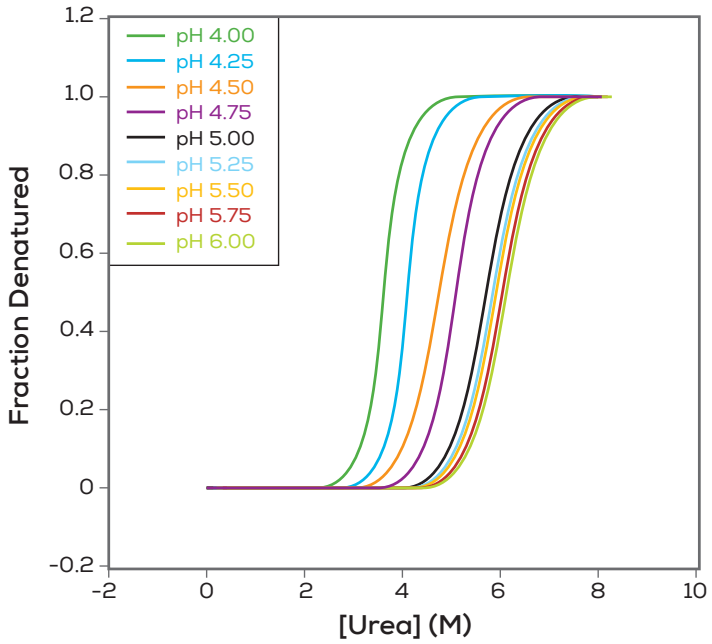
Walk away for hours or days

The only way to get ΔG before was a total pain – by hand – and why you probably skipped it altogether. That whole old-school process is completely hands-off with the HUNK. Pick a few conditions or max out on dozens. Add your protein samples, formulations and denaturant. The HUNK does all the work from there and kicks out your data automatically.



Get ΔG in about an hour

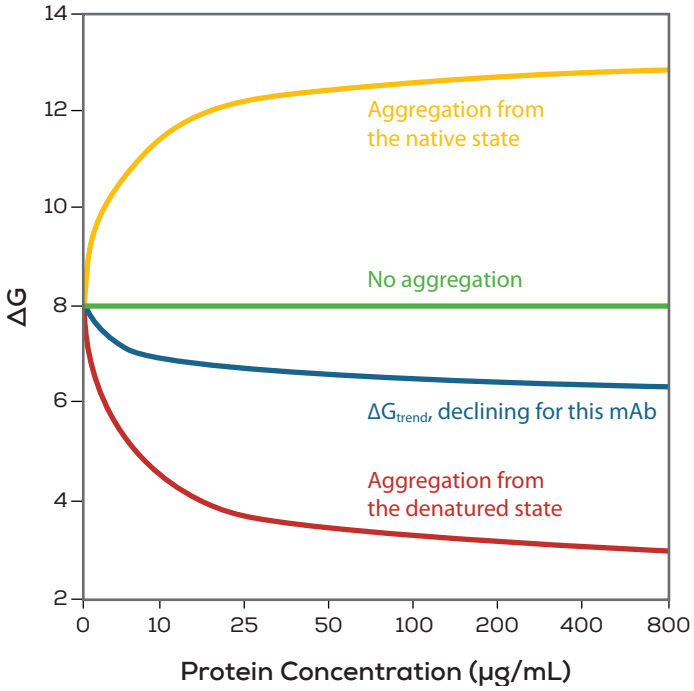
The HUNK cranks out ΔGs in about an hour per curve, no matter if you're comparing 2 conditions or up to 96 at once. Analysis is built in, so a few clicks lets you see what your additives, those tiny pH changes or that little bit of extra salt did to your biologic's stability. You pick the top conditions and motor on to optimization or aggregation prediction.



Predict aggregation

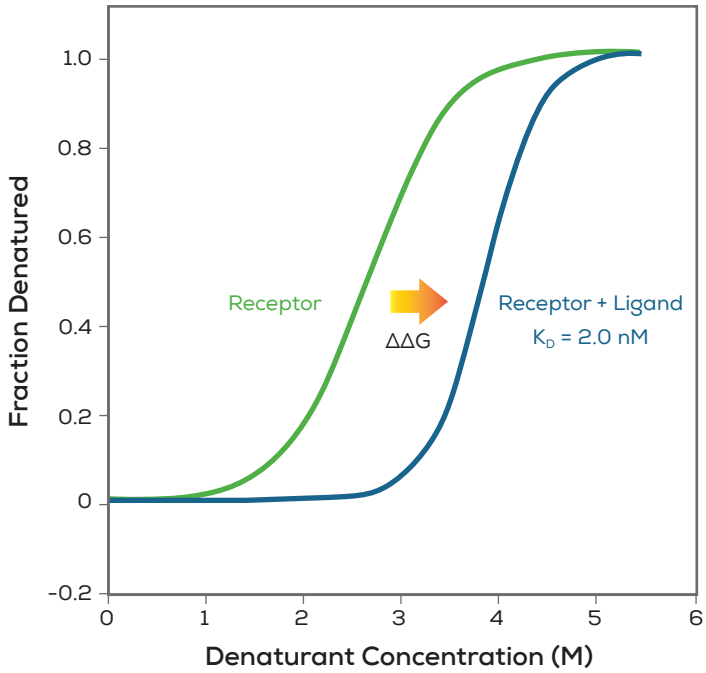
Tweak your formulation before long-term stability starts, not after. The HUNK's ΔG_{trend} method gives you the aggregation propensity and pathway. Monitoring ΔG_{trend} over increasing concentrations tells you if your protein will aggregate or not. If it does, you'll know if it happens in the native or denatured state, what fraction is denatured, how much is aggregated, and how much the denatured protein aggregates. Save your SEC time to rubber stamp the winning formulations.

mAb Concentration	ΔG
12 µg/mL	8.0
24 µg/mL	7.7
48 µg/mL	7.5
96 µg/mL	7.2
192 µg/mL	6.7
384 µg/mL	6.5
768 µg/mL	6.4



Add small molecule affinity

When you can't measure small molecule K_D with your existing platforms – try the HUNK instead. ΔGs on the HUNK also let you grab the affinity that small molecule ligands have for receptors. There's no dependence on mass. And because it's a totally solution-based assay, there's no need for immobilization or expensive consumables either.



Specifications

Description	Specification
Minimum protein concentration per ΔG	25 µg/mL IgG (protein dependent)
Typical volume required per ΔG	1 mL
Time to measure each ΔG	Average 1 hour
Maximum unattended ΔG measurements	96
Experiment temperature operating range	Constant 2 °C above ambient to 30 °C (+2 °C)
Protein stock temperature	4 °C to ambient
Fluorescence excitation and emission range	190–890 nm ex, 200–900 nm em photomultiplier
Fluorescence light source	Xe lamp
Fluorescence detection dynamic range	Five orders of magnitude
Environmental conditions	Temperature range: 18–28 °C
Physical	56 cm W x 71 cm D x 87 cm H, 91 kg
Electrical	Auto switching power supply, voltage 100–240 V AC, 50–60 Hz

UNCHAINED LABS

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Rev B