# When protein stability matters.

Precisely characterize thermal unfolding, chemical denaturation and aggregation with the most flexibility a system has to offer





# When flexibility matters.

Little to no experience is needed when it comes to measuring protein stability and protein aggregation on the Prometheus. Each system has a friendly lab footprint and is maintenance-free. The only tough decision is which throughput to choose.



# Start with the winner.

Take assumptions out of the equation — Get reproducible, quantitative results early on from discovery to validation and production. Use Prometheus to generate precise unfolding temperatures ( $T_m$  and  $T_{onset}$ ), critical denaturant concentrations ( $C_m$ ), free folding energy ( $\Delta G$  and  $\Delta \Delta G$ ), and aggregation onset ( $T_{agg}$ ) from start to finish. Be confident about moving forward with the right choice every step of the way.

### Measure under native conditions

No need to add a dye or modify buffer conditions. Run experiments on viscous samples too.

### Consume less sample

Requiring as little as 10  $\mu$ L in volume and 5  $\mu$ g/mL in concentration is always a plus.

### Prep samples... not

Wouldn't it be great to just quickly load samples and get a result in minutes? No sample prep needed, just load as-is.

### **Test more conditions**

Having flexibility to test multiple parameters in one run makes it easier to get to the end goal sooner.

### **Get precise results**

A high density of data points means better data quality and seeing details missed by other technologies.

### Choose any throughput

Run 1, 48 or any number of samples in between and do only what's necessary. Or, automate and do more.

### Do more simultaneously

Get  $T_m$ ,  $T_{onset}$  and  $T_{agg}$  results all in one run and end up spending time on other things.

### Use in regulated environments

Prometheus software complies with 21 CFR Part 11 requirements so feel free to use it wherever whenever.

# When precision matters.

Prometheus characterizes thermal and chemical unfolding under native conditions using nanoDSF technology. Absolutely label-free, nanoDSF precisely measures the intrinsic fluorescence of a protein while it's being subjected to either chemical or thermal denaturation.

nanoDSF uses high quality capillaries for a number of reasons — only microliters of sample are required, a wide range of concentrations are quickly measured in-solution, multiple conditions are assessed in one run, and hard-to-measure viscous samples are examined with ease.

Just dip a capillary into a sample, place it in Prometheus, and hit start to get  $T_m$ ,  $T_{onset}$  and  $T_{agg}$  results in minutes. And, if  $C_m$ ,  $\Delta G$  and  $\Delta \Delta G$  are needed, those can be done too with the same system.





Prometheus monitors the intrinsic fluorescence signal of proteins as a measure of its folding state. Fluorescence intensity at the single wavelength or F350/F330 ratio are plotted against increasing temperature or concentration of a chemical denaturant to determine the  $T_m$  or  $C_m$  of a protein.

## When quality matters.

Prometheus does it best when it comes to characterizing protein unfolding. In both thermal and chemical denaturation studies, even the most subtle unfolding events are easily seen that other traditional systems simply can't detect. Best of all, results are not compromised by aggregates in solution. Get higher quality results and gain the ability to make better decisions.

# When confidence matters.

Being confident in what to do next is key to doing great research. The formulation development group at Boehringer Ingelheim realized that having precise and high quality data for both thermal unfolding and aggregation is key to better predicting stability, developability and longer-term storage of their antibody candidates.

Prometheus provides comprehensive results for any type of protein — small or large proteins, biologics, enzymes, antibodies, ADCs and membrane proteins — and is especially good at screening buffer influences or testing formulation and storage conditions. Make better decisions based on more complete stability results.



Effects of pH on the thermal unfolding and aggregation of a mAb target protein



# When guidance matters.

It's so difficult to find a system that's easy to use these days. Prometheus uses PR.ThermControl, PR.ChemControl and PR.TimeControl software which make assays so painless to set up. From the moment samples are loaded, measurement settings are simply optimized and executed. While the experiment is running, quickly name or color code samples, and when it's done, results are instantly calculated. Choose to display the most important data at the end and easily export in one click to share with colleagues. Generating results can't get any easier.

# When options matter.

|   | NT.48  | NT.Plex                               | NT.Plex + NT.RA  |
|---|--|---------------------------------------|--|
| Samples per run   | Up to 48<br>(single capillaries)   | Up to 24<br>(capillary chip)          | Up to 1536 hands-off<br>(up to 64 capillary chips)       |
| Sample volume measured  | 10 µL  |                                       |  |
| Detected molecule<br>concentration range  | 0.005–250 mg/mL (standard IgG)   |                                       |  |
| Experiment time per run –<br>thermal unfolding (from<br>1 °C/min up to 7 °C/min ramp) | 18–75 minutes  |                                       | 4 hours to overnight<br>(384 samples)                    |
| Experiment time per run –<br>chemical unfolding                                       | 1 minute   |                                       | 27 minutes (384 samples)                                 |
| Precision of 1 °C/min thermal ramp  | ± 0.2 °C   |                                       |  |
| Temperature control   | Ramping options: 0.1 °C/min to 7 °C/min<br>Temperature range: 15 °C–95 °C (at 25 °C ambient temperature) |                                       |  |
| Fluorescence detection  | 330 nm and 350 nm  |                                       |  |
| Dimensions  | 35 cm W x 51 c   | cm H x 52 cm D                        | 110 cm W x 188 cm H x 90 cm D<br>(stand-alone enclosure) |
| Weight  | 30   | kg                                    | 200 kg   |
| Optional upgrades   | Aggregation detection optics   |                                       |  |
|   | High tempera<br>15 °C−110 °C (at 25 °C   | ature upgrade<br>ambient temperature) | Plate temperature control                                |

Visit nanotempertech.com to see the entire list of consumables.



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