



**SMARTFREEZCRYO**  
PRECISION CRYOSYSTEMS

# Cold Stability Accelerator

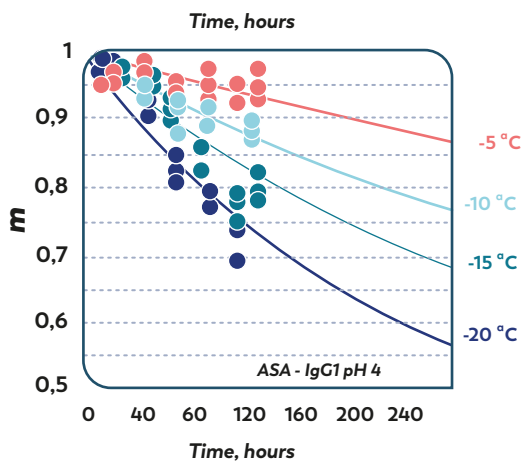
***A new approach to save time and hurdles related to poor understanding of the impact of cold-stresses on protein formulations***



- Runs **isothermal stability studies below 0 °C** to **clarify protein aggregation** mechanisms and to **optimize** the **product formulation process**.
- **Evaluates** directly the **influence of low-temperature** on protein stability, **avoiding** the uncertainty of **high-temperature modeling extrapolations**.
- Helps to develop **accurate degradation models** to predict in a few days, the long-term **cold stability of proteins**.

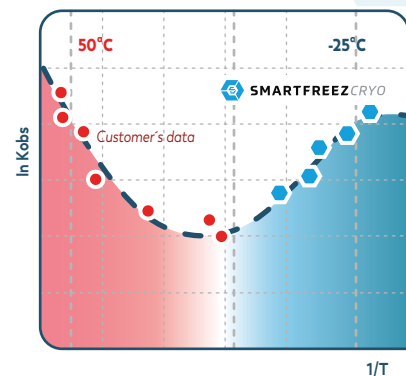
**B**iopharmaceutical stability studies for proteins are essential to assess sensitivity to factors that can cause aggregation and degradation that impact their biological activity, product safety, and quality.

The Cold Stability Accelerator (CSA) imposes isochoric conditions with stainless steel vials, to limit volume expansion, preventing ice growth. This method avoids the freezing of the solution, enabling to measure degradation kinetics and to evaluate in a few days the impact of temperature (**Fig.1**) and cryopreservatives on formulations.



**Fig. 1** - Small-volume stainless steel containers are used to measure protein's aggregation kinetics below the freezing temperature. When unfolding mediates aggregation, the rates increase with decreasing temperature, as shown in the example (IgG1 100 g/L).

The CSA measures cold aggregation of proteins, under accelerated conditions (by approaching cold denaturation temperature). These measurements complement high temperature data (e.g. customer's data) to anticipate cold stability by a few days and develop accurate degradation models (**Fig.2**), that can predict long term stability (months/years).



**Fig. 2** - Modelling protein stability using high temperature data (customer's data) and low temperature data (CSA's data).