Introduction

Differential scanning calorimetry (DSC) is used to measure heat flows associated with thermal transitions in materials. Applications include characterizing molecular thermodynamics, structure and stability through changes in entropy (ΔS), enthalpy (ΔH), Gibb's free energy (ΔG), heat capacity (ΔCp) and melting temperature (T_m).

Features of the Nano DSC:

Label-free
Samples are kept in a solution so they may be directly analyzed in their native state.

Low volume, capillary cells
The small cell volume reduces sample size and the coiled capillary cell shape prevents sample aggregation at higher temperatures.

Temperature and pressure range
Buffered samples up to 6 atm can be cooled to -10°C or heated to 130°C without boiling / freezing.

Information-rich data
A DSC experiment can determine thermodynamic properties of sample transitions including calorimetric entropy (ΔS) and enthalpy (ΔH), Gibb's free energy (ΔG), heat capacity (ΔCp), Van't Hoff (ΔH) and melting temperature (T_m).

Ultra high sensitivity
Protein samples of 2 µg minimum can be analyzed by the Nano DSC.

Nano DSC Autosampler

The Nano DSC autosampler enables fully automated operation for the Nano DSC for higher throughput and "start and walk away" use. Samples can be stored in two 96-well plates, at temperatures from 4 °C to ambient, with additional wash/rinse ports to minimize sample carry-over. The industry-proven HPLC - grade autosampler is programmable using the Nano DSC instrument software. The Nano-DSC can be used with or without the autosampler.

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Nano DSC - TA Instruments

Nano DSC with Autosampler, Differential Scanning Calorimetry

- Calorimetric Entropy (ΔS) and enthalpy (ΔH), Gibb's free energy (ΔG), heat capacity (ΔCp), Van't Hoff (ΔH) and melting temperature (T_m) determination
- Study protein domain stability and ligand binding, lipids, vesicles and polymers
- Characterize reaction mechanisms
- Pressure perturbation calorimetry for macromolecule hydration determination
- High instrument sensitivity and precision
- Manual or fully automated operation

Differential Scanning Calorimetry

Theoretical background

In a DSC protein experiment, the instrument heats or cools two cells, one cell containing the protein sample and the other cell containing the protein buffer alone as a reference, while maintaining an isothermal temperature between the two cells. As the sample is exposed to different temperatures, it may undergo transitions, such as unfolding or refolding, at certain temperatures. These types of events require energy since the protein will transition between two different states.

In general, a DSC instrument is capable of measuring any physical transition (e.g. a phase transition) where the transition is exothermic or endothermic.

Since an unfolding event requires energy, the temperature of the cell containing the unfolding sample will increase at a relatively slower rate while it is unfolding versus the buffer reference alone. The instrument compensates for this difference by increasing the power output slightly to the sample cell. As the experiment proceeds, the instrument continuously measures any temperature differences between the two cells. The raw output of a DSC experiment is a unit of power per unit time (µJ/s).

Data processing involves subtracting the data from the sample cell against the reference cell. In order to have a good baseline, the buffers in the sample and reference cells should be matched exactly.

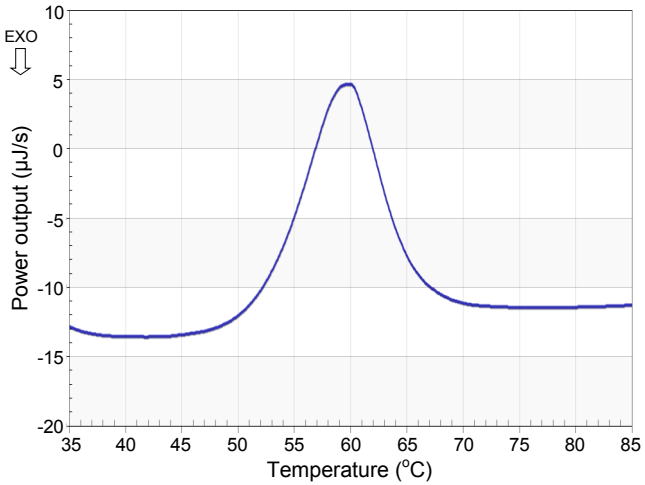
A DSC experiment determines the transition thermodynamics, including enthalpy (ΔH), entropy (ΔS), Gibb's free energy (ΔG), heat capacity (ΔCp) and transition temperature (T_m for melting temperature).

Lysozyme denaturation

Lysozyme denaturation using DSC

Protein sample: Lysozyme (1.0 mg/mL)
Buffer: 100 mM Glycine, pH 2.4
Temperature range: 25 to 95 °C
Scan rate: 1 °C / min
Pressure: 3 atm

Below is a representative curve of the raw data output from a DSC experiment. The peak represents a lysozyme denaturation transition event. Since the power output increases as the transition occurs (peak is "pointing up"), the transition is endothermic. Using the supplied data analysis software, the thermodynamic properties associated with the transition can be determined.

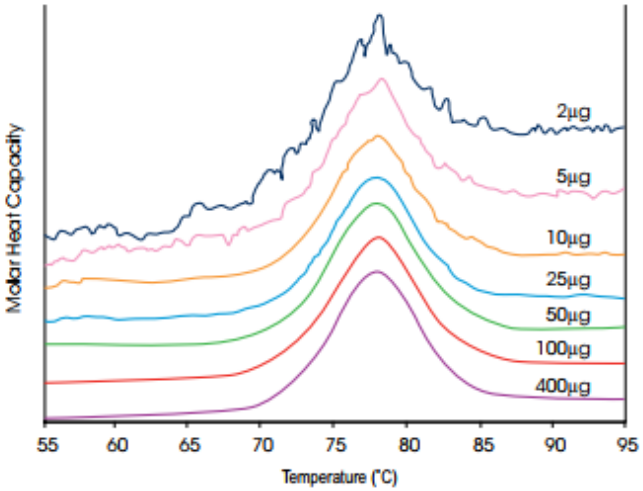


Instrument specifications	
Cell volume (300 µL)	Manual: 600 µL required Automated: 900 µL required
Temperature range	-10 °C to 130 °C
Scan rates	0.001 °C to 2 °C / min
Pressure control	Up to 6 atm
Cell composition	Platinum / Gold

Instrument sensitivity

Protein sample: Lysozyme (hen egg white)
Buffer: Glycine pH 4.0
Concentration range: 1.3 mg/mL (400 µg in cell) to 0.007 mg/mL (2 µg in cell)

Very little sample is required for a Nano DSC experiment as a result of the instrument's excellent sensitivity and baseline reproducibility. The data found below demonstrates that as little as 2 µg of protein is necessary to obtain high quality thermodynamic data, including melting temperature, enthalpy and entropy.



Lysozyme in cell (50µg)	Calorimetric ΔH (kJ mol^{-1})	Calorimetric ΔS (kJ K^{-1} mol^{-1})
400	512	1.46
100	512	1.46
50	517	1.47
25	513	1.46
10	515	1.47
5	490	1.40
2	503	1.43