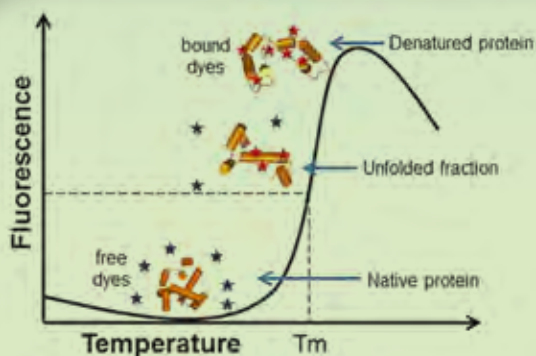


# JBScreen Thermofluor

## The protein stability screen



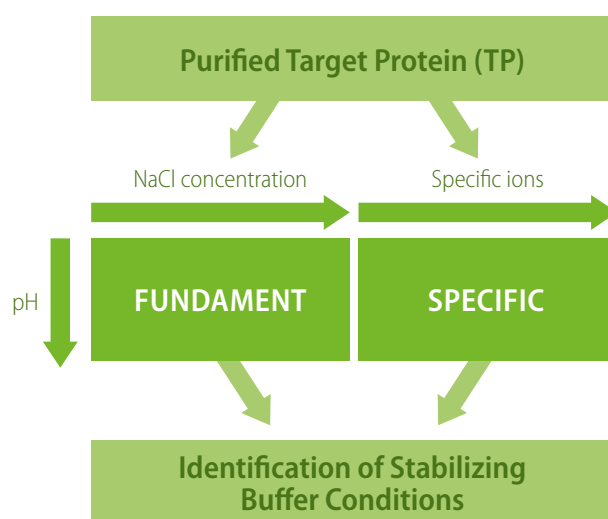
Identification of a buffer environment that enhances the protein's stability and homogeneity is crucial for the success in protein purification, characterization and crystallization [1 – 3].

The protein melting temperature ( $T_m$ ), determined by monitoring the protein unfolding in a temperature-dependent manner, is used as a reporter to assess protein thermostability. The higher the  $T_m$ , the higher is the thermostability of the protein in that specific environment.

JBScreen Thermofluor is a pre-crystallization screen for protein stability (and thus: protein crystallizability [4]) that eliminates the undesired overlay effects of traditional screening. Based on Super Buffers [5], the entire pH range from 4.0 to 10.0 is screened with one and the same buffer system thereby keeping the chemical environment constant. The optimum condition(s) are identified by focusing separately on each relevant parameter such as pH, ionic strength and specific ions [5,6].

JBScreen Thermofluor FUNDAMENT allows screening the pure pH effect at different ionic strengths without interfering additive effects, that would occur when changing the buffer system. pH and ionic strength are fundamental factors that influence the **whole protein molecule**.

JBScreen Thermofluor SPECIFIC screens for specific high-scoring mono-, di- and trivalent cations derived from the pdb [6]. These specific factors affect **energetically important hot spots on the protein**.



Product	Cat. No.	Amount	Price (EUR)
<b>JBScreen Thermofluor FUNDAMENT HTS</b> TSA for protein stability	CS-332	93 solutions (0,5 ml each)	227,00
<b>JBScreen Thermofluor SPECIFIC HTS</b> TSA for protein stability	CS-333	93 solutions (0,5 ml each)	227,00



Learn more about JBScreen Thermofluor on our website:



### References:

- [1] Boivin *et al.* (2013) Optimization of protein purification and characterization using Thermofluor screens. *Protein Expression and Purification* **91**:192.
- [2] Reinhard *et al.* (2013) Optimization of protein buffer cocktails using Thermofluor. *Acta Cryst. F* **69**:209.
- [3] Ericsson *et al.* (2006) Thermofluor-based high-throughput stability optimization of proteins for structural studies. *Anal. Biochem.* **357**(2):289.
- [4] Price *et al.* (2009) Understanding the physical properties that control protein crystallization by analysis of large-scale experimental data. *Nat. Biotech.* **27**:51.
- [5] Newman (2004) Novel buffer systems for macromolecular crystallization. *Acta Cryst. D* **60**:610.
- [6] <http://www.rcsb.org/pdb/home/home.do>

