

The Protein folding and Ligand Interaction Core facility

ProLinC

- a trans-national access site for



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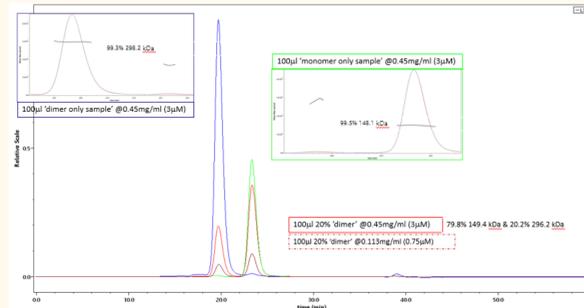
- ❖ Do you need access to Biophysical instrumentation;
- ❖ Or want (*help*) to characterise biological samples and their complexes?

- ProLinC (the PROtein folding and Ligand INteraction Core facility at Linköping University) has been established as a one-stop resource integrating a vast array of instruments and techniques ... for such needs.
- The facility provides an entry point to MOSBRI (the EU-program for biophysics: 'MOlecular-Scale Biophysics Research Infrastructure') offering international access with user support.
- The supporting staff have a diverse background with expertise in a number of different scientific areas ... facilitating experimental design and optimisation.

AUC SAXS
 NMR CD
 SEC-MALS DSC
 DLS Fluorescence microscopy
 Fluorescence spectroscopy Crystallization
 ITC nanoDSF MST
 SPR

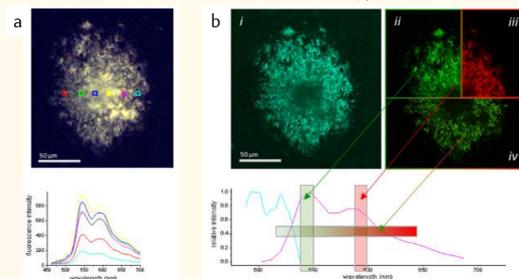
SEC-MALS ->

used as a robust benchmarking tool...
 ...samples with different IgG 'monomer' to 'dimer' ratios were used to calibrate new sensor technology in development



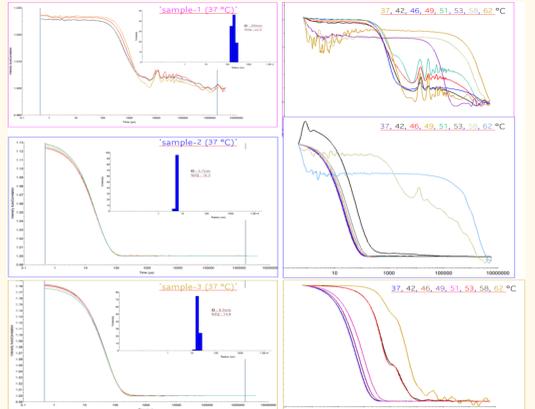
Fluorescence microscopy ->

successful development of aggregate/amyloid differentiating dyes... demonstrated through hyper-spectral fluorescence spectral analysis (a) combined with excitation/emission confocal microscopy (b)



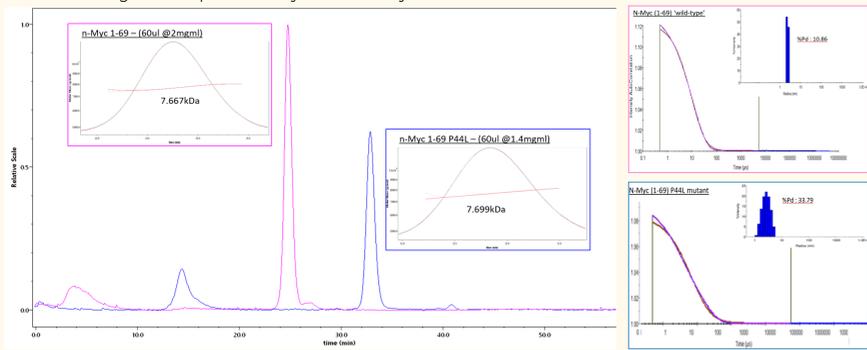
DLS ->

characterising the 'cloud-point' of different detergents (measurements recorded at intervals between 37-62°C)



SEC-MALS combined with DLS ->

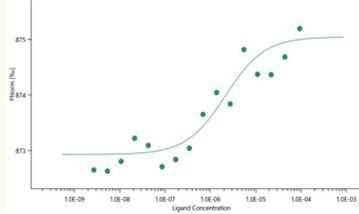
characterises the effect of the P44L mutation in N-Myc...
 ... change in shape and maybe flexibility!



MST ->

assessment of di-ubiquitin...

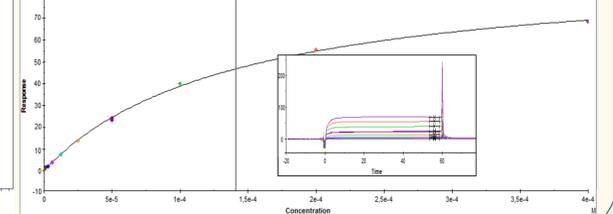
USP14 with K48 di-ubiquitin :: apparent k_d of 2.125 μ M



vs SPR ->

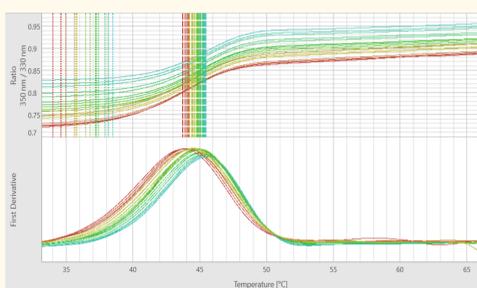
...mono-ubiquitin binding to 'His-tagged' USP14

USP14 with mono-ubiquitin :: apparent k_d of 141.1 μ M



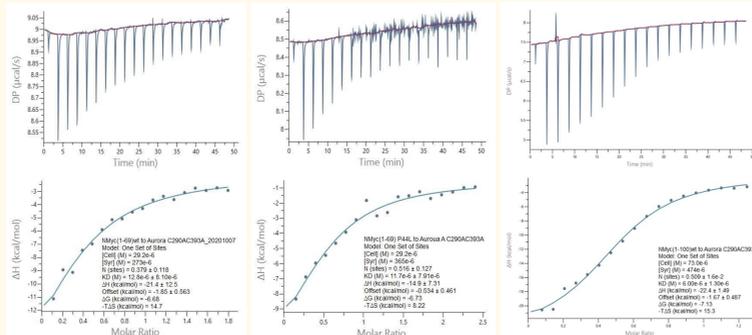
nanoDSF based 'thermal shift' assay ->

a stabilising interaction between N-myc and Aurora-A can be demonstrated.



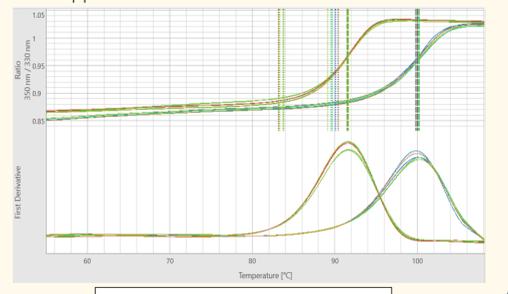
ITC ->

affinities of different N-myc constructs towards Aurora-A appear to be comparable (1-69, 1-100 and the P44L mutant forms of N-Myc were compared)



NanoDSF ->

highlight the effect of a de-stabilisation mutant...
 ...an approximate T_m shift from 100 to 91.5°C



- ❖ ProLinC is a major component of SMILE: an initiative to improve Small and Medium Enterprises (SME) access to experimental and computational laboratory infrastructures; as well as deepen collaboration between academia and business.

