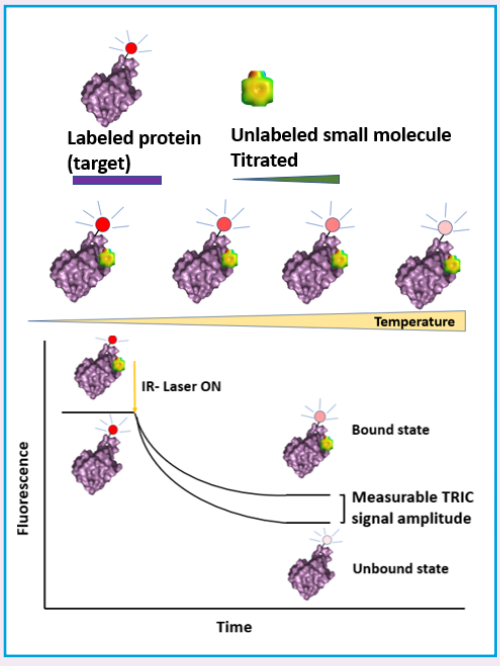
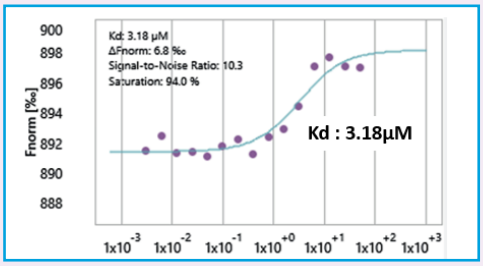
Temperature Related Intensity Change (TRIC) | Protein-Small Molecule Binding Affinity Studies

TRIC is the state-of-the-art technology that provides steady-state binding affinity (KD) in the millimolar-picomolar range in an immobilization free environment both rapidly and accurately. TRIC measures the change in fluorescence of your labeled target molecule in solution upon heating as a function of time. As long as the fluorophore is in a position that is sensitive to the binding of the small molecule, a measurement can be made. The protein biophysics and biochemical experts at **August Bioservices** have years of experience developing protein-based assays and can provide 1-on-1 support through every step of the assay development process, including optimization of target labeling strategies, custom assay buffer optimization, and steady-state binding affinity analysis.

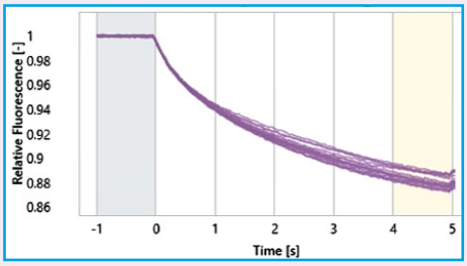
CASE STUDY:



BINDING AFFINITY DETERMINATION IN MINUTES AT MICROMOLAR / PICOMOLAR RANGE



SAMPLE OF PROTEIN-SMALL MOLECULE DOSE RESPONSE RAW DATA



] **Measurable TRIC signal amplitude**

TRIC binding affinity determination of Protein- small molecule was performed in a 384 well plate using Dianthus NT.23PicoDu. A 16-point dose response curve was performed by titrating the small molecule (189 Daltons) with a single point concentration of NHS labeled Protein target. Steady state binding affinity was determined to be 2.84(Kd) which agrees with SPR and ITC data orthogonally.

Key Takeaway...

With TRIC, up to 500 twelve-point dose-response curves can be performed in 10 hours with true steady-state affinity (Kd) determination.

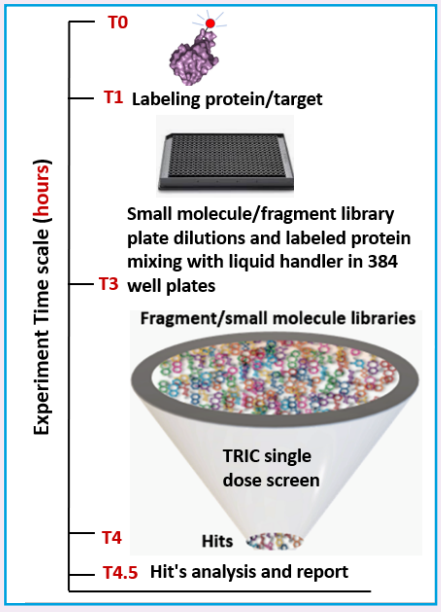
Temperature Related Intensity Change (TRIC) | Small molecule/fragment library screening

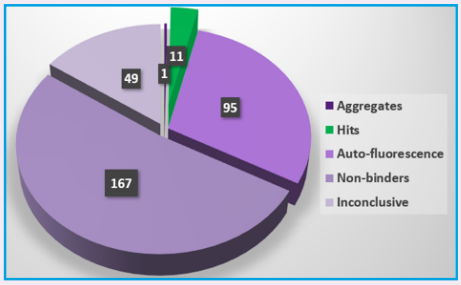
TRIC is an exciting and relatively new method that has become indispensable in small molecule and fragment-based drug discovery campaigns. This rapid, immobilization free, and reliable high-throughput screening approach requires a fluorescently labeled target sensitive to the binding event and measures the change in change in fluorescence upon heating as a function of time.

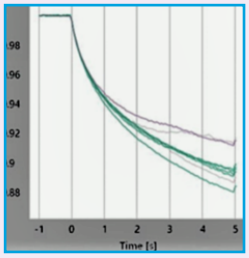
The experts at **August Bioservices** can help with all aspects of TRIC assay development for your drug discovery efforts by providing 1-on-1 support through every step of method development including optimization of target labeling strategies, custom buffer optimization for fragment-based library screening, the best choices of library screen for your system, hits analysis, hit validation, and beyond.

CASE STUDY:

FRAGMENT/SMALL MOLECULE LIBRARIES TO LIST OF HITS IN A FEW HOURS







Ligands categorized based on signal amplitude, fluorescence change, aggregation, scan quality and photobleaching.

Raw data of one of the 11 positive hits. Shown is the fluorescence intensity amplitude change with respect to time.

TRIC single dose affinity screening was performed in a 384 well plate using Dianthus NT.23PicoDu. A fragment-based library screen was performed on 323 different fragments. Histogram shows how ligands were categorized into hits (green in figure) or not based on the changes in the amplitude of TRIC target signal upon binding.

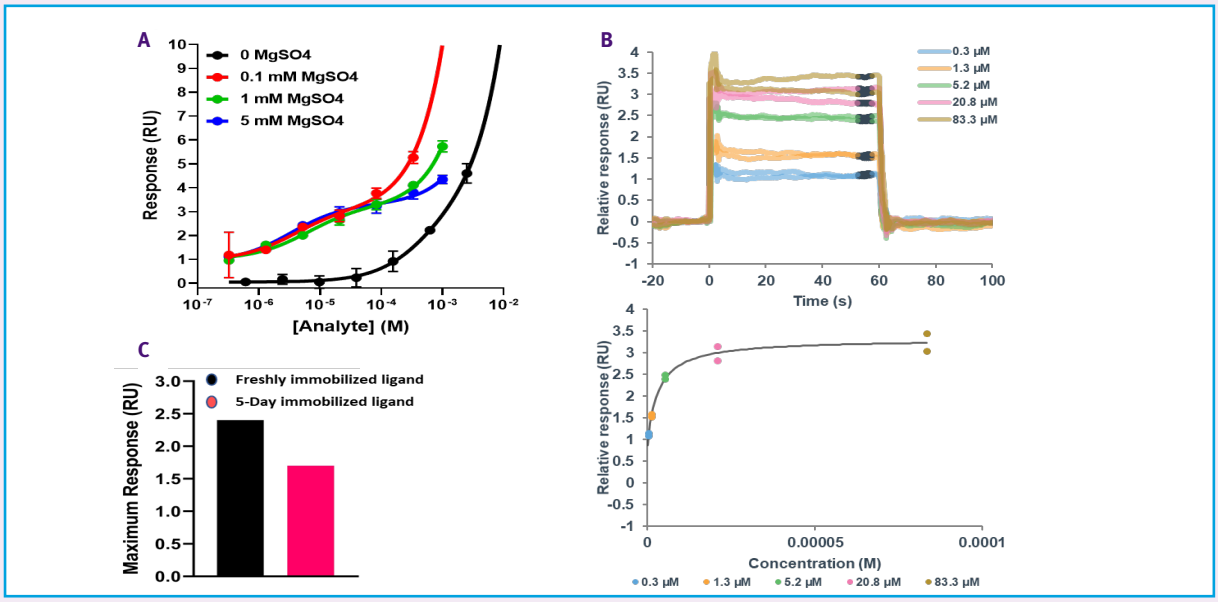
Key Takeaway...

TRIC is one of the fastest high-throughput screening methods, providing the ability to screen a 384 well plate in 30 minutes — which is about 15,000 compounds a day.

Small Molecule SPR-Based Assay Optimization

Surface plasmon resonance (SPR) is a proven label-free, in vitro tool that measures in real-time a variety of biomolecular interactions. A prime example is shown below where the SPR experts in August Bioservices designed and executed the optimization of the binding assay and ultimately the measurement of a small molecule (‹ 200 Da) to the macromolecule (~100 kDa). **August Bioservices** has both the state-of-the-art equipment and the years of know how to operate the sensitive Biacore S200 and the high throughput Biacore 8K systems. Our experts understand the complex nature of macromolecular systems and that sometimes the simple addition of an ion, the altering of the buffer composition, or the timing associated with how long a ligand is immobilized can all affect the outcome of an SPR experiment. **August Bioservices** can guide you through the optimization and set up for all your SPR needs, and more.

CASE STUDY:



SPR-based binding assay was developed to characterize binding of a small molecule Analyte (‹200 Da) to a large Protein ligand (MW = ~ 100 kDa). Protein was immobilized on a CM5 sensor chip via amine coupling. (A). Buffer screen was performed for optimal detection of Analyte binding. Strong non-specific binding signal was observed in the absence of MgSO4. Presence of MgSO4 was critical for detecting specific binding, while increasing MgSO4 concentrations resulted in decrease of the non-specific component. Data were fit using One-site-total model in GraphPad Prism 8. (B) Top: Reference and blank-subtracted sensograms showing Analyte binding to the Protein under optimized experimental conditions and Bottom: plot showing the steady state affinity (1 to 1 binding) fit of response vs. Analyte concentration data. Analysis was performed using Biacore Insight Evaluation software. (C). Analyte titrations were performed using 5-day old and freshly generated ligand surfaces. Bar graph shows a slight drop in Rmax for the 5-day immobilized ligand compared to the fresh ligand surface. Other parameters were unaffected, indicating a stable and active surface over a prolonged period.

Key Takeaway...

Optimizing biomolecular interactions is a delicate balance of buffer composition, the timing and length of ligand immobilization, and the potential addition of an ion.

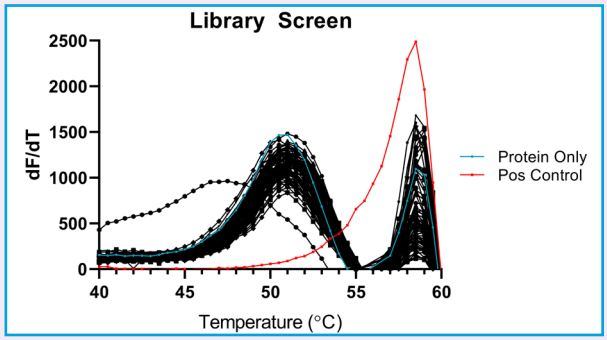
Differential Scanning Fluorimetry (DSF)

Differential Scanning Fluorimetry (DSF) requires no immobilization or labelling steps as interactions can be evaluated in solution giving way to quick assay set-up and optimization. Shown below are the results of a small library screen run with a protein. To determine potential binders, DSF was run with our protein of interest using a known positive control binder which shifts the temperature melting point (Tm) nearly 8 degrees to the right, showing apparent stabilization of the protein.

Of the 320 fragments tested, only two molecules shifted the Tm to the right and three molecules shifted the Tm to the left. With years of protein biochemistry experience, the industry leading experts at **August Bioservices** provide 1-on-1 support throughout the process, from custom-tailored assay development to fragment-based library screening.

CASE STUDY:

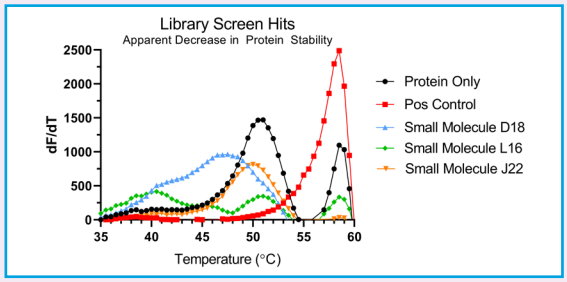
A



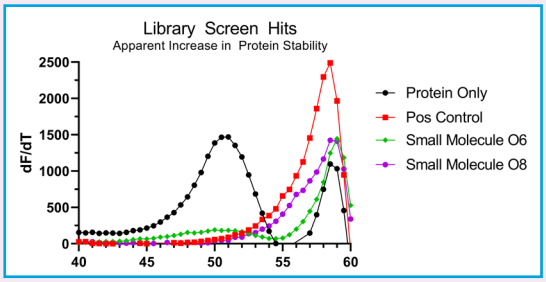
B

Condition	Temp. (°C)
Protein Only	50.5
Pos Control	58
Small Molecule (D18)	47
Small Molecule (L16)	40.5
Small Molecule (J22)	49.5
Small Molecule (o6)	58.5
Small Molecule (o8)	58

C



D



DSF was performed in a 384 well plate using Bio-Rad's CFX384 Real Time PCR Detection System.

A fragment-based library screen was performed on 320 different fragments (A). Hits were identified as being a 1°C shift or higher (B). Small molecules determined to show an apparent increase in stability shifted Tm peaks to the right (C) while molecules showing an apparent decrease in protein stability shifted Tm peaks to the left (D).

Key Takeaway...

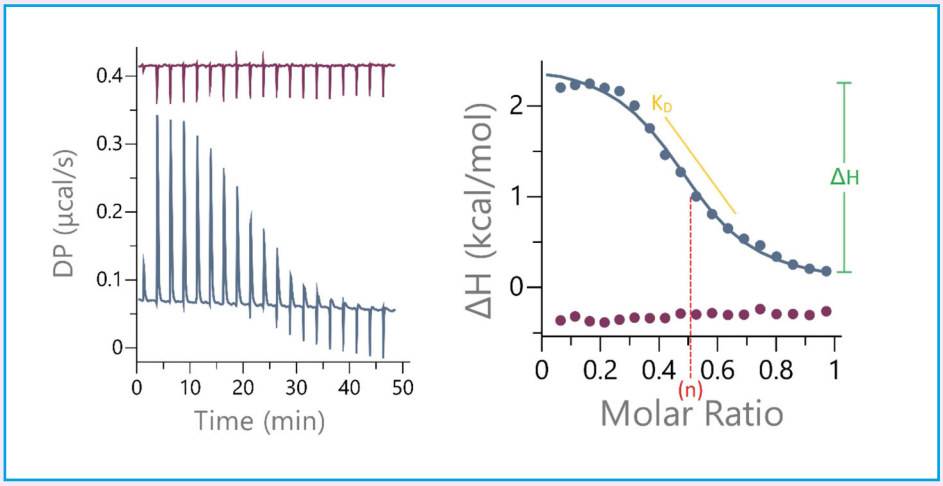
Differential Scanning Fluorimetry (DSF) is a proven method of modern drug discovery that is robust, low-cost, and high throughput.

Isothermal Titration Calorimetry (ITC)
Is your buffer killing your protein activity?

Isothermal Titration calorimetry (ITC) is a powerful biophysical characterization method that provides direct measurement of the heat of a biomolecular interaction and delivers label-free measurement of ΔH, ΔG, -TΔS, KD, and stoichiometry in a single experiment (Figure A). Proteins often need a very precise environment, aka buffer condition, to achieve their best activity. In some cases, without the proper buffer conditions, a protein will appear to be inactive even if it is properly folded. The experts at **August Bioservices** use the power of the Malvern PEAQ-ITC Automated instrument to screen for the best buffer conditions. The importance of buffer conditions show below (Figure B) demonstrates how very simple changes to a biological reaction, such as buffer and the addition of an ion, can mean the difference between measuring or missing a binding event.

CASE STUDY:

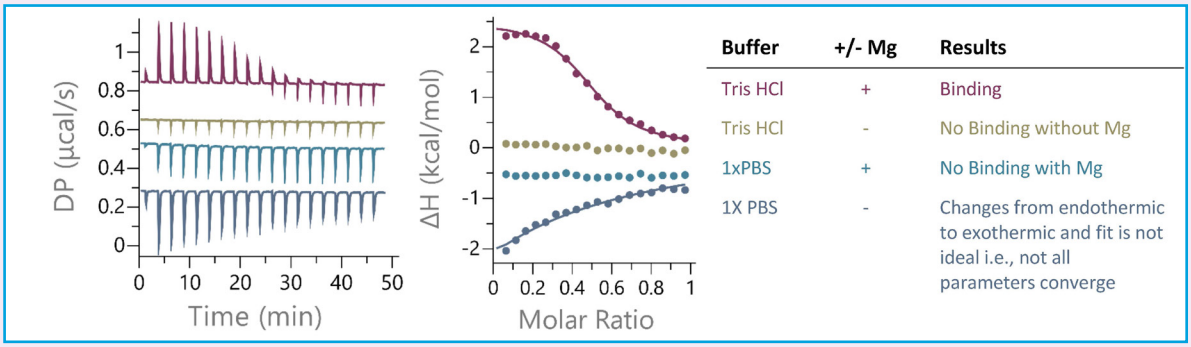
A



A. *Typical ITC experiment. The raw data on the left shows the heat change with each injection of ligand. The integrated heat plot on the right illustrates the plethora of data available from a single experiment.*

B. *Results of ITC experiments with the same Macromolecule and Ligand but differing buffer composition. Left is the raw data, middle is the integrated heat plot and fits and the table to the right highlights the results and the corresponding buffer compositions.*

B



Buffer	+/- Mg	Results
Tris HCl	+	Binding
Tris HCl	-	No Binding without Mg
1xPBS	+	No Binding with Mg
1X PBS	-	Changes from endothermic to exothermic and fit is not ideal i.e., not all parameters converge

Key Takeaway...

When using ITC, choosing the correct buffer can help prevent costly mistakes.