

# Small-Molecule Drug Target Identification/Deconvolution Technologies

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## Case-Studies



Advancing Technologies and Applications of Proteome Analysis

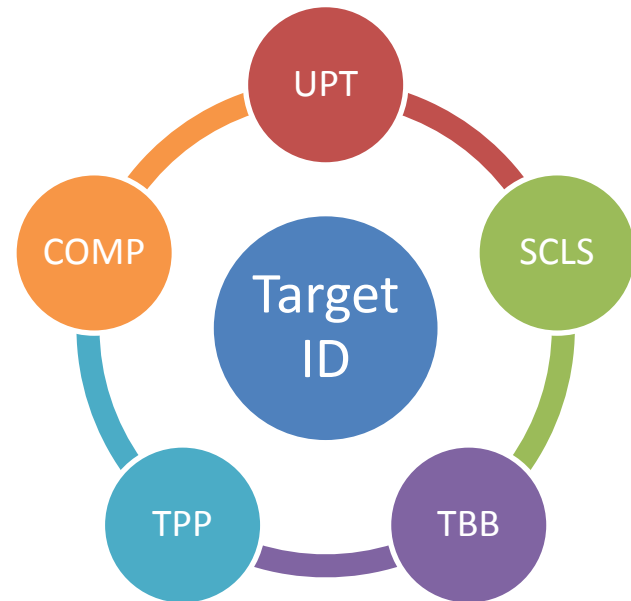


# Shantani Target ID Technology Tool Box

Target Deconvolution is not Trivial =  
A single Tool / Technology May Not necessarily solve the problem

## Our Focus = Target ID

We Utilize Several  
Proprietary and Generic  
Technologies for  
**Right Target**



1) **UPT** = Unique Polymer Technology, 2) **SCLS** = Subcellular Location Specific Target Capture Technology, 3) **COMP** = 'in-silico' target ID workflows, 4) **TBB** = Traditional Bead/Biotinylated Molecule Based Method, 5) **TPP** = Thermal Proteome Profiling



# Case Study # 1: A Drug Discovery Program from a Seattle, USA based Organization

## Scenario

- Phenotypically Screened 'Hit' compound, Target not known, 'Hit' can not be rationally optimized
- For Target ID Typical bead/biotinylation based affinity chromatography can not be performed because Molecule is not easy to derivatize

## Shantani's Solution

- Shantani's Proprietary Unique Polymer Technology that can immobilize underivatized molecule for affinity chromatography
- Eventually Target(s) that can be linked to observed phenotype were identified



# Unique Polymer Technology (UPT)

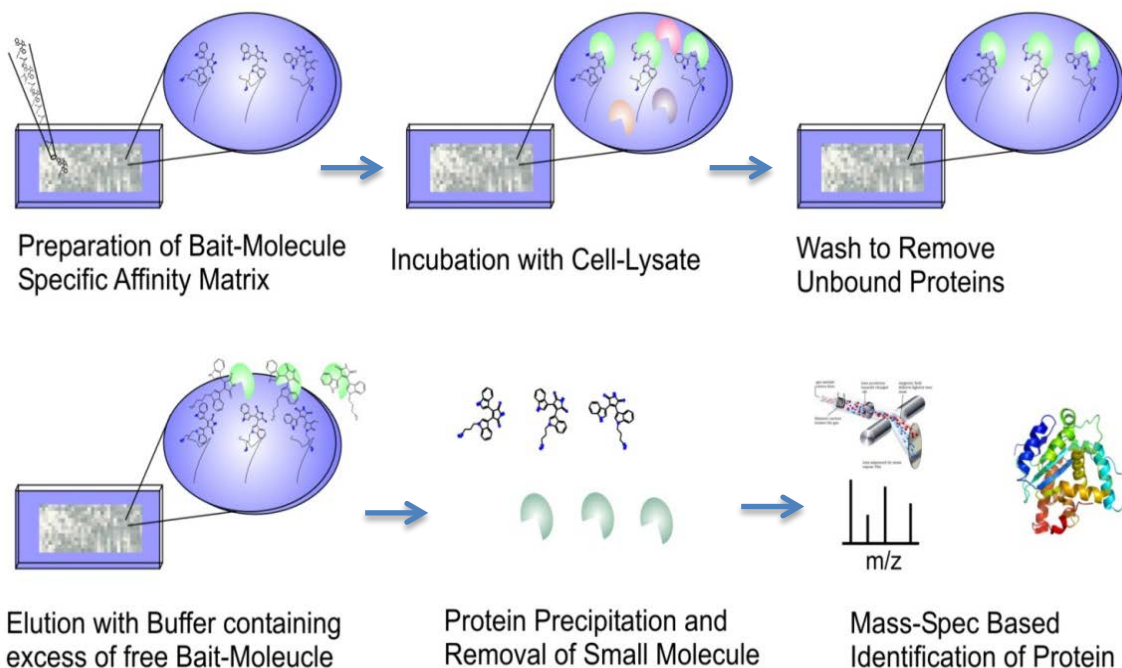
## Typical Target ID Workflow

### Uniqueness

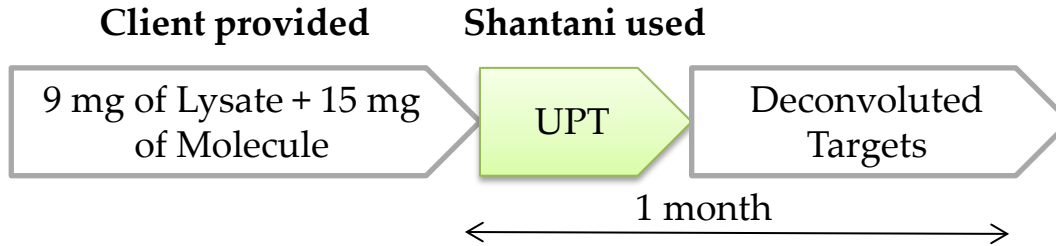
1. Molecule Derivatization not needed.
2. Target Identification can be completed in 2-3 weeks.

### Working Principle

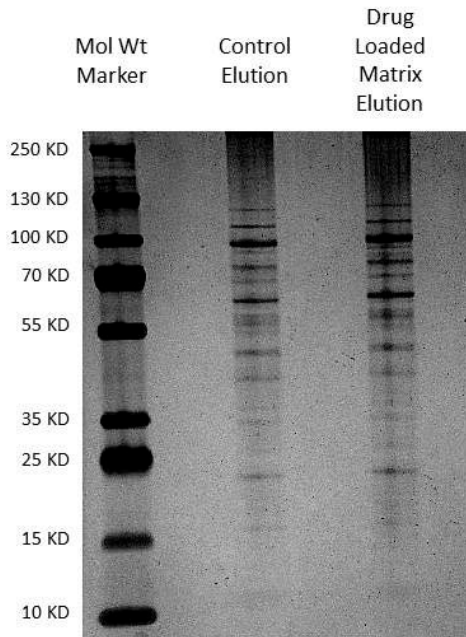
Molecule transiently get immobilized on Specifically Engineered Polymeric Surface through multiple non-covalent interaction with Polymer. Thus formed molecule specific affinity matrix is used in capturing the target from cell-lysates.



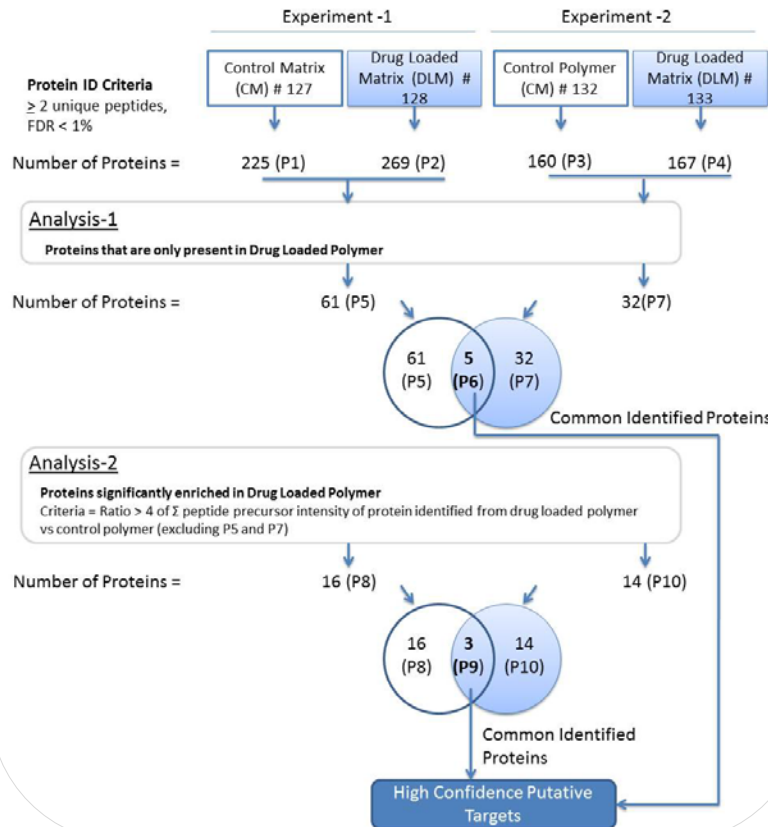
# Case # 1:



Typical SDS-PAGE Separated Protein Profile from Control and Molecule Loaded Matrix

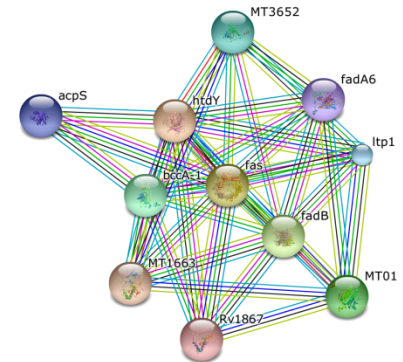


Typical Target Deconvolution Process



## Eventual Value and 'GO' Decision

Information of Target was used for Action Mechanism Analysis and few targets were shortlisted for validation



# Case Study # 2: A Large Indian Corporate looking for new regenerative medicine

## Scenario

- Bioactive compound, at lower concentration induces proliferation of cells but at 20X concentration induced cell death Target not known/MOA not clear 'Hit' can not be rationally optimized
- Some structure-activity relationship data available but no path forward.

## Shantani's Solution

- Shantani was consulted for Project
- Shantani used traditional bead based (TBB) methods and identified the targets
- 'in-silico' target validation was performed and targets were rank ordered based on predicted Kd values
- Identified targets with predicted lower affinity were linked with cell-death and higher affinity (strong affinity) with proliferation



# Traditional Bead Based Methodology (TBB)

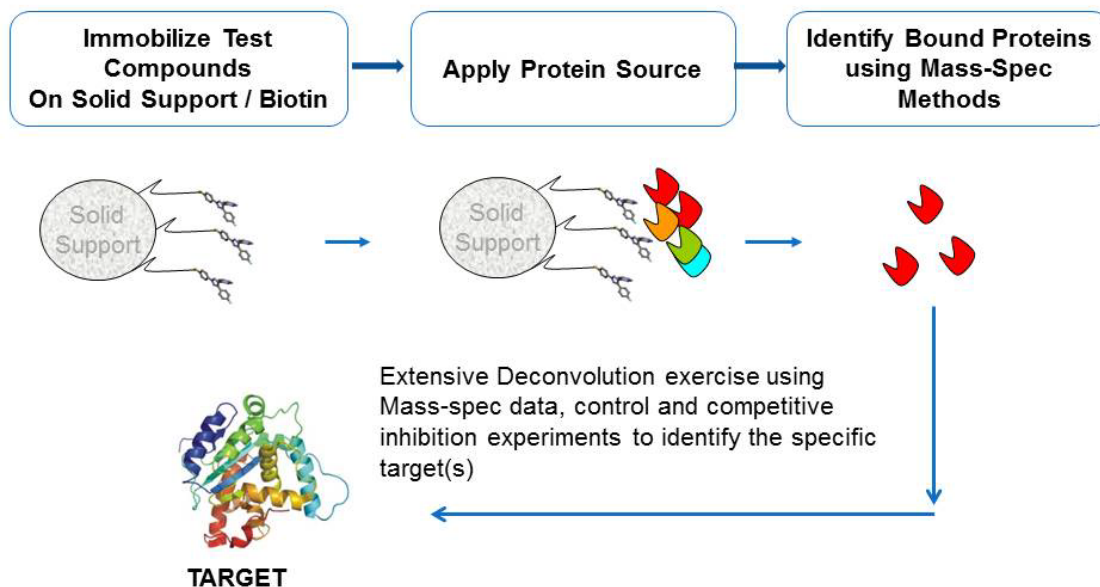
## Uniqueness

Can identify targets having broad range of affinity with molecule (Kd ~ nanomolar to micromolar)

## Working Principle

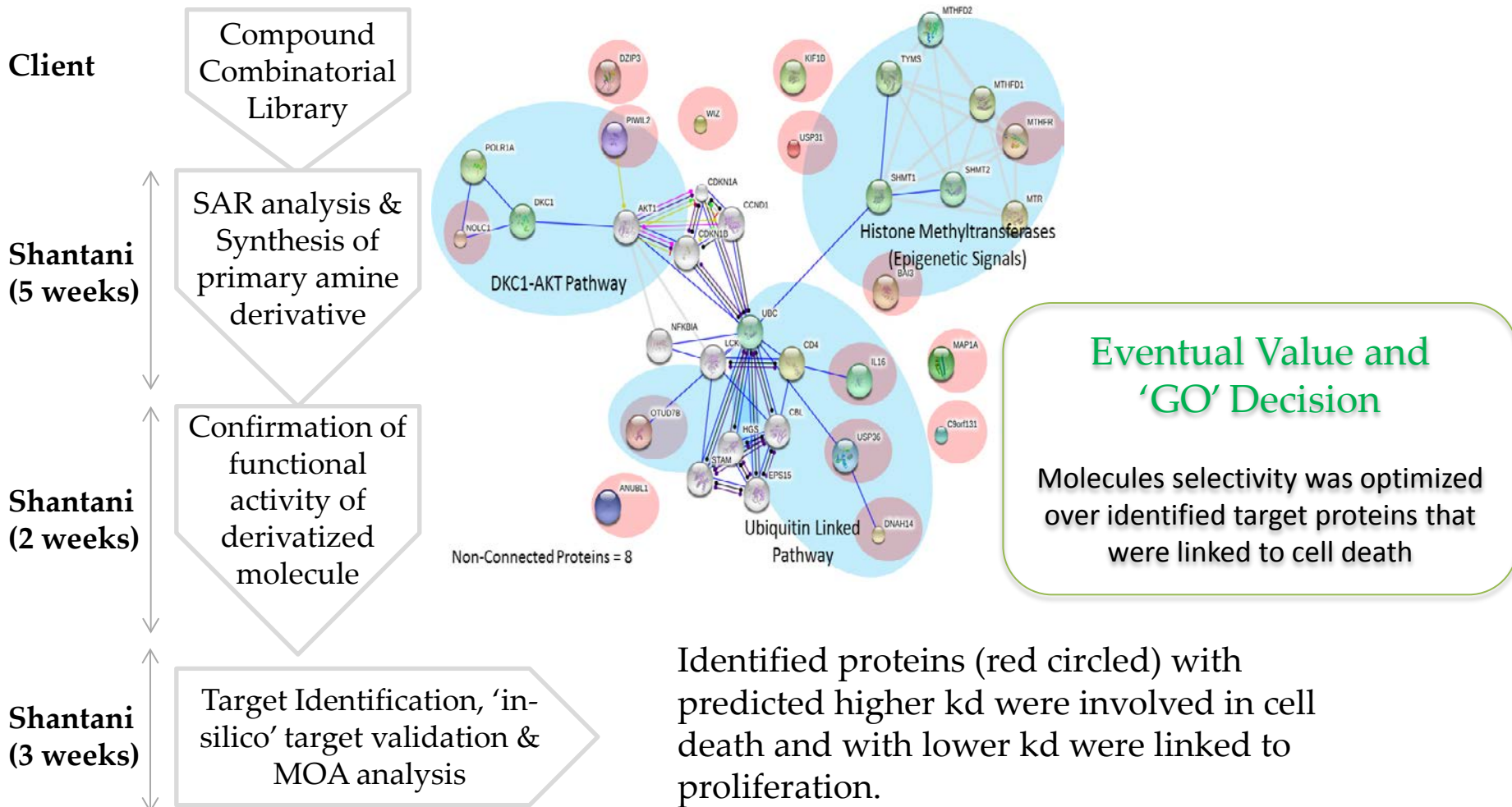
Molecules are immobilized on the solid support to prepare molecule specific affinity matrix. Affinity chromatography is carried out from relevant cell-lysate to capture the target proteins on solid support. Later captured proteins are identified using mass-spectrometry and deconvoluted.

## Typical Target ID Workflow





# Case # 2:





# Case Study # 3: A European SME

## Scenario

- Phenotypically Screened 'Hit' compound, Target not known, 'Hit' can not be rationally optimized
- For Target ID Typical bead/biotinylation based affinity chromatography can not be performed because a slight change in molecular structure loses the activity of the compound

## Shantani's Solution

- Shantani's Proprietary Unique Polymer Technology that can immobilize underivatized molecule for affinity chromatography
- Eventually Target(s) that can be linked to observed phenotype were identified



# Case # 3:

Client

'Hit' compound

Shantani  
(1 week)

Preparation of affinity matrix using UPT

Shantani  
(1 week)

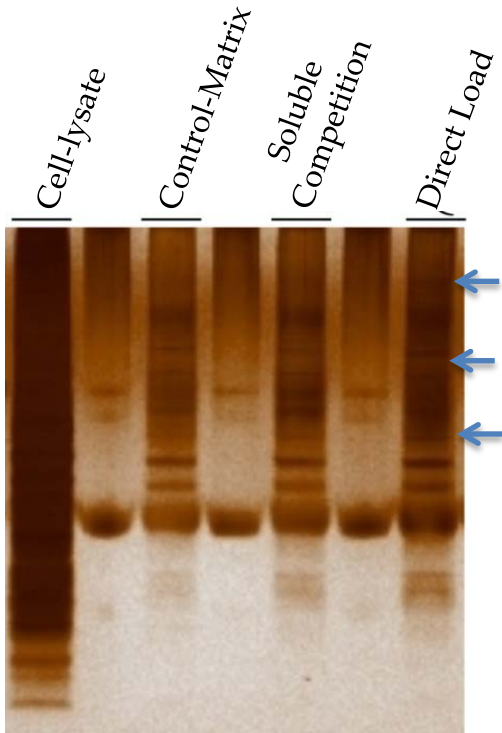
Affinity Chromatography and Target ID

Total Proteins Identified = 253

Shantani  
(1 week)

Target Deconvolution

Deconvoluted Specific Target = 5



Typical Enrichment of the Target in Direct Load Experiment – Silver Stain Profile

Protein Class / Name	Specificity Ratio
Methyl Transferase	1
Fibronectin Binding Protein	1
Mitochondrial Transport Protein	1
GTPase activating Protein	1
Adapter Protein for T-Cell Signalling	1

## Eventual Value and 'GO' Decision

Identified a Novel Epigenetic Target  
Target was validated by client using overexpression and Binding Studies



# Case Study # 4: A Internal Study

## Scenario

- Molecule Bisindolylmaleimide-III (Bis-III) interacts with GSK3- $\beta$  and induce apoptosis
- GSK3- $\beta$  is present both in cytoplasm and nucleus. For clarity on MOA and newer compound design location of target is needed
- SAR of the Bis-III molecule is well-established

## Shantani's Solution

- Shantani's Proprietary subcellular location specific target capturing target methodology
- Target location was identified and for conformation target was captured from specific sub-cellular location



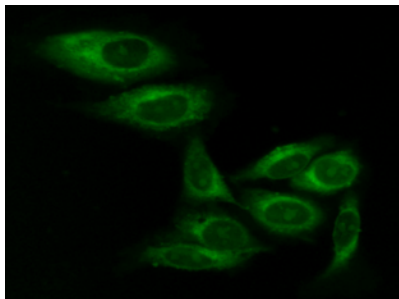
# Subcellular Location Specific Target Identification Technology (SCLS)

## Uniqueness

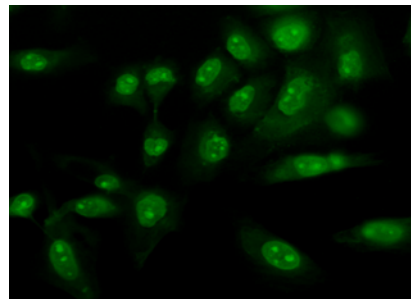
1. Very low false positive identification rate ~20%
2. Can identify targets in subcellular location specific manner in a live-cell set-up

## Working Principle

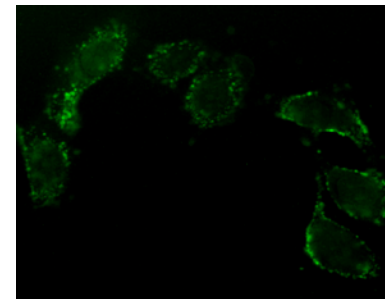
- 1) Bait –molecules are coupled to proprietary sub-cellular location specific probes
- 2) These probes in separate experiments drag the molecule in different specific sub-cellular locations and functional activity of the molecule is measured
- 3) Sub-cellular location that shows maximum activity is chosen as ‘target-rich’ compartment and target captures experiments are performed from ‘target-rich’ locations



**Cytoplasmic Probe**



**Nuclear Probe**



**Membrane Probe**

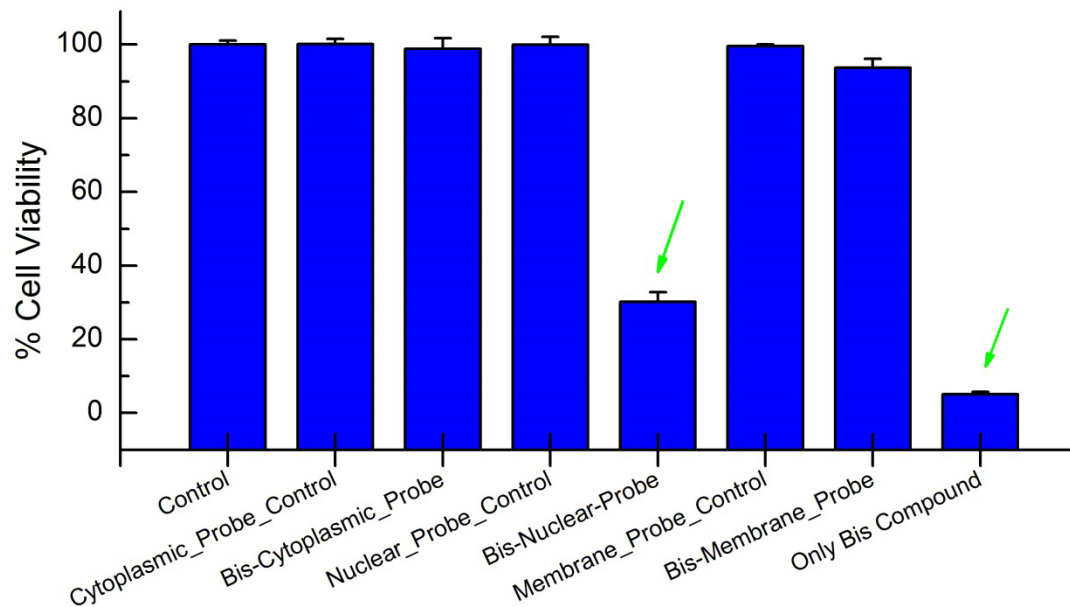


# Case # 4: Sub-cellular Location Specific Functional Activity of Bis-III Probes

Bis-III was coupled to three sub-cellular location specific proprietary peptides



Cytotoxic Assay in HeLa Cells



Bis-compound and all probes and control probes at 80  $\mu$ M concentration.

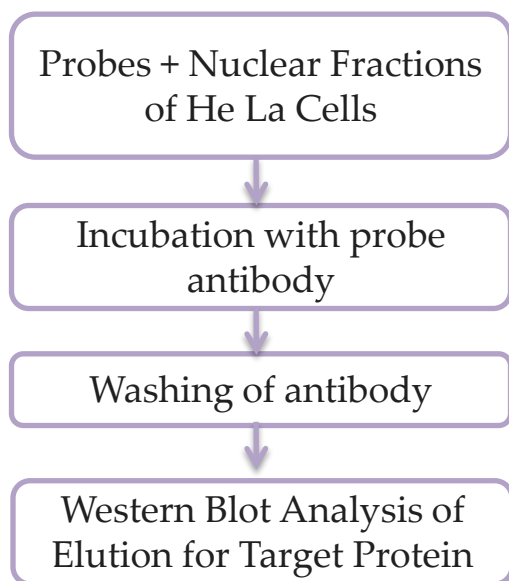
Bis-III probes that were targeted to the nucleus exhibited similar activity as the free Bis-III



Target located in nucleus is responsible for the activity

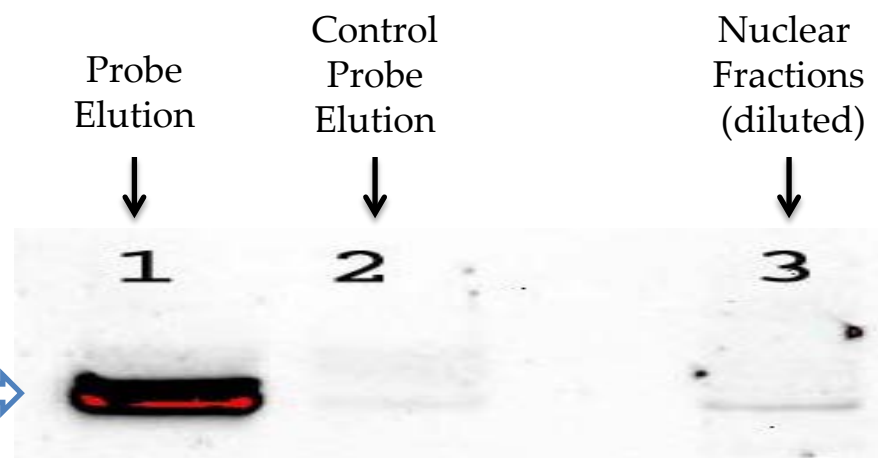


# Case # 4. Capture of Target from Nuclear Fractions



GSK3-beta →

Probes = Coupled with Bis-III



**Target was specifically captured with Probe.**

## Eventual Value and 'GO' Decision

Establishing sub-cellular location of the target clarified the MOA and new compound design included the additional parameters that molecule should target nucleus



# Case Study # 5 Identification of Target Using Computational Approaches

## Scenario

- Several Computational Approaches are available for identifying the Targets of Small Molecule that utilizes structural information of the molecule and compares it with the historical database (similar structure + Target)
- These approaches generate a long list of targets (most of them are false positive) and a few target for validation can not be prioritized

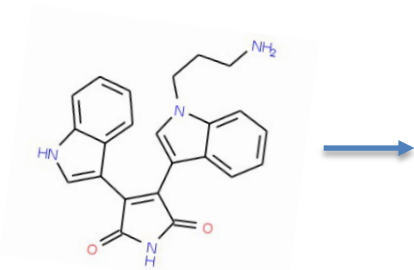
## Shantani's Solution

- Shantani's Proprietary computational approach identify a few but the rightful target



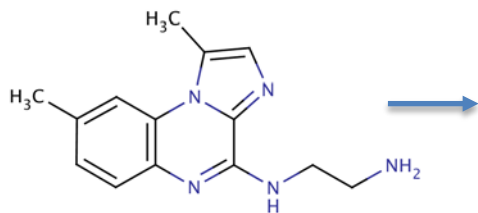


# Case # 5: Deconvolution of Targets of a Few Known Small Molecules using Shantani's COMP workflow



Bisindolylmaleimide-III

	# of Target Identified	# of Actual Target (Kd < 500 nm)	Success Ratio (Total / Actual Target)
Algorithm-1	26	1	4%
Algorithm-2	4	2	50%
Algorithm-3	16	2	13%
Shantani-Algorithm	2	1 (Identified Target =PKC-α)	50%



BMS-345541

	# of Target Identified	# of Actual Target (Kd < 500 nm)	Success Ratio (Total / Actual Target)
Algorithm-1	17	1	6%
Algorithm-2	8	2	25%
Algorithm-3	19	2	11%
Shantani-Algorithm	2	1 (Identified Target =IKK-β)	50%

## Eventual Value and 'GO' Decision

Shantani's COMP workflow allows identification of a few but rightful targets

Connect for further discussions

Saba Naaz Siddique

saba@shantani.com

Phone: +91-20-64103918

<http://www.shantani.com>



Advancing Technologies and Applications of Proteome Analysis