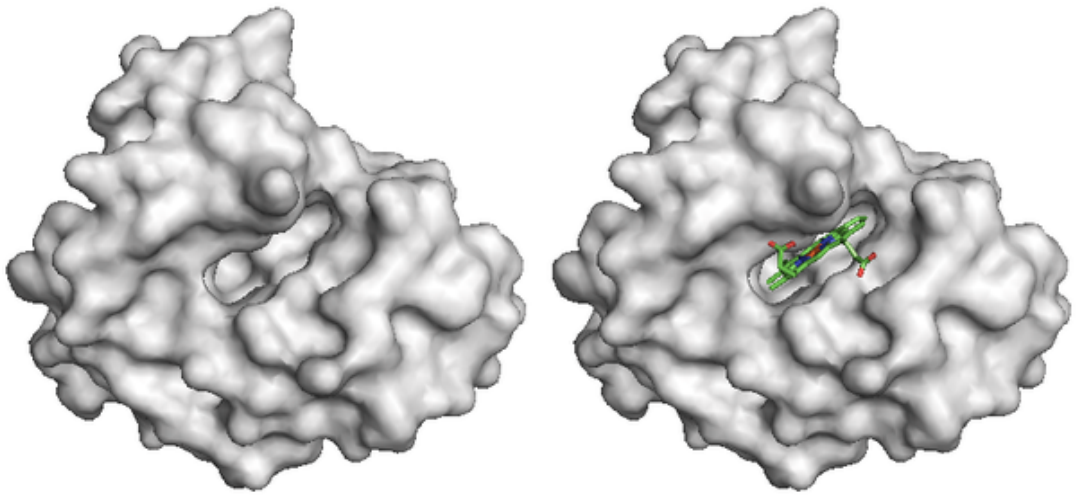


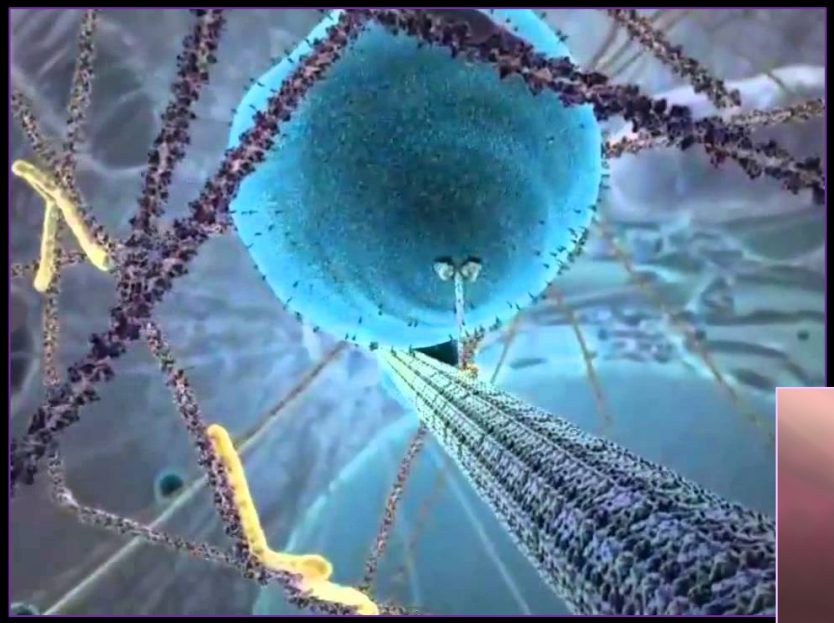
L4 – Quantitative Evaluation of Binding Interactions

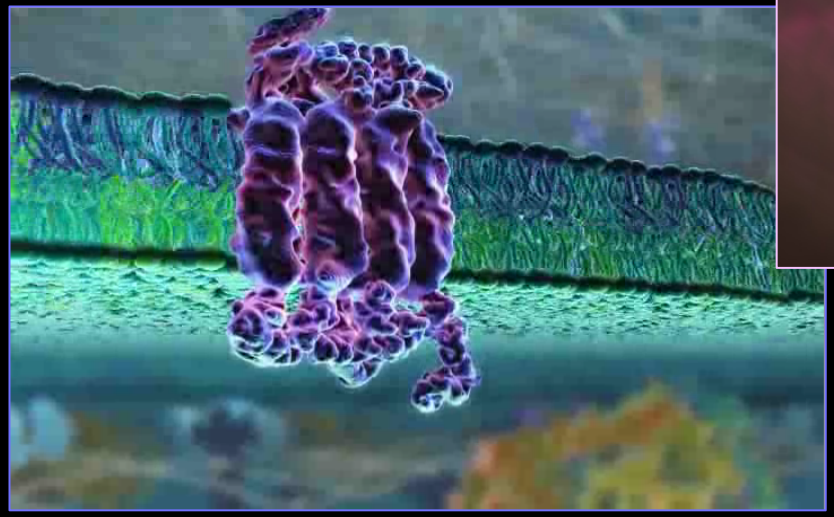
February 20, 2020

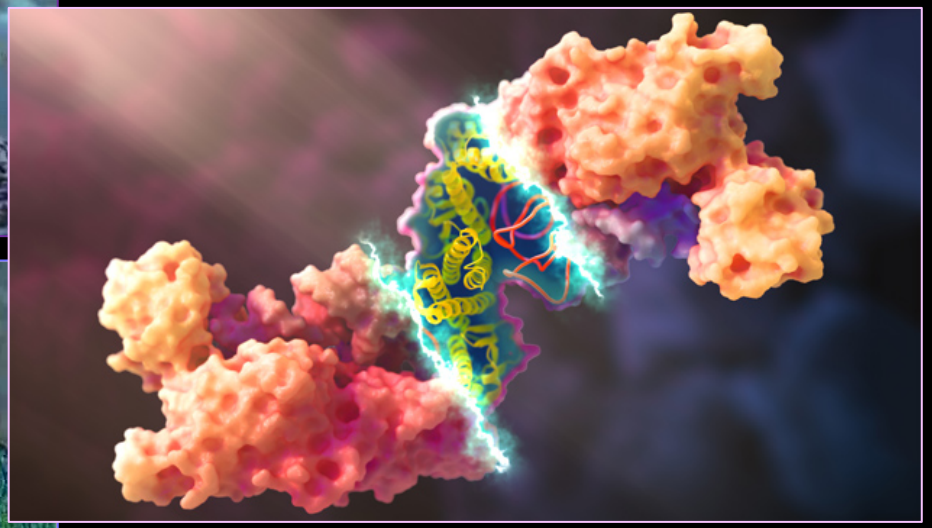
Molecular recognition is ubiquitous in biology

proteins, lipids, sugars, nucleic acids, metabolites, antibodies

The Inner Life of the Cell – Dr. Alain Viel, Harvard







https://www.youtube.com/watch?v=FzcTgrxMzZk

8 minute video – watch it while you are running an experiment

Basic language of binding interactions

from 20.110

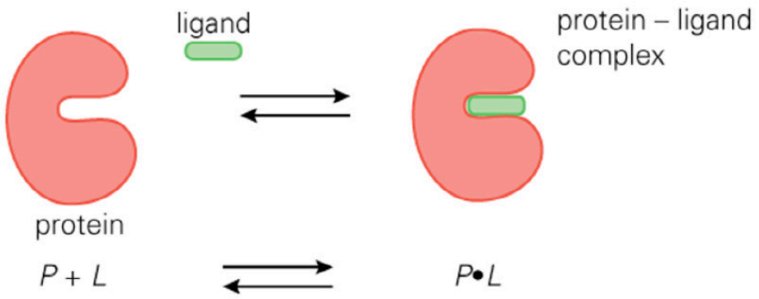
Affinity: strength of the interaction, measured by the corresponding decrease in free energy upon binding

Specificity: relative strength of interaction for a 'cognate' and 'non-cognate' receptor-ligand complex

There are two basic types of non-covalent interactions: simple binding and allosteric

Some binding interactions are 'simple' equilibria – each encounter is independent

simple interaction



Adapted from Kuriyan, The Molecules of Life, Chapter 12, Molecular Recognition

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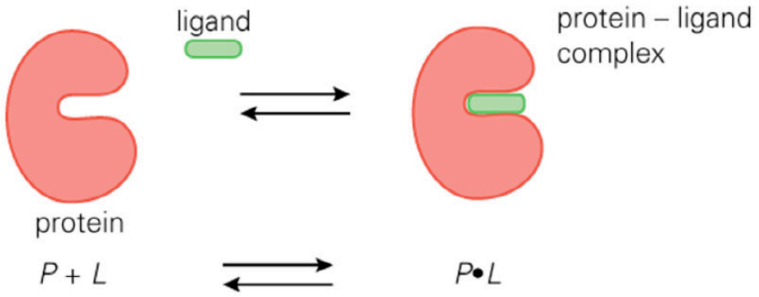
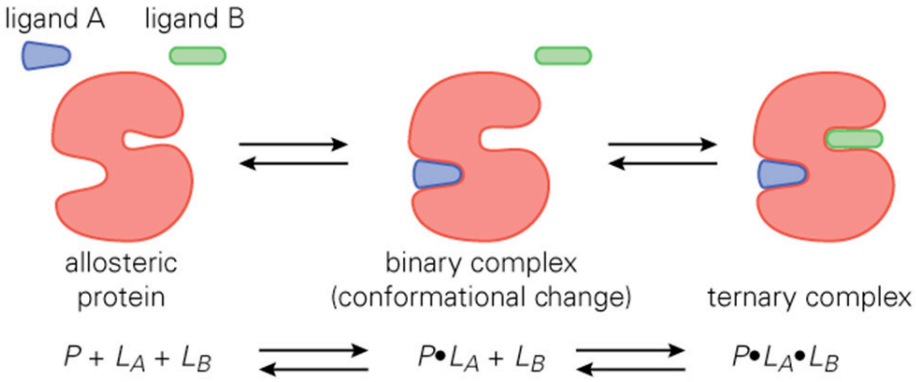


Others are more complex, involving allostery, where one ligand binding event alters the affinity for another ligand

allosteric interaction



Adapted from Kuriyan, The Molecules of Life, Chapter 12, Molecular Recognition

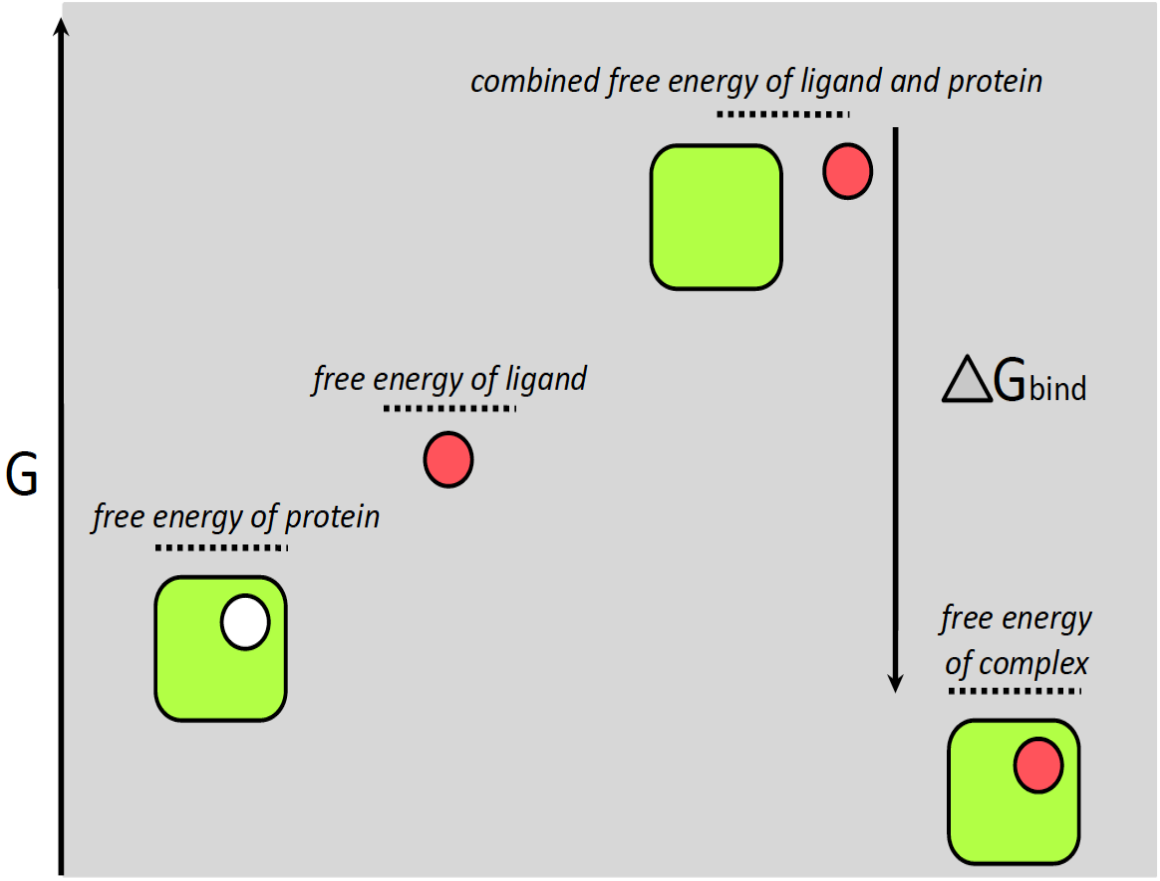
Thermodynamic analyses provide insight into molecular interactions

As you learned in 20.110, we can think about the following binding-related terms thermodynamically:

- affinity and specificity
- contribution of entropy and enthalpy
- dependence on temperature
- contributions of chemical groups on the ligand and/or the receptor

This information can in turn be used to understand a system and to alter the system (e.g. drug design)

Relationship of ligand binding free energy to association constants



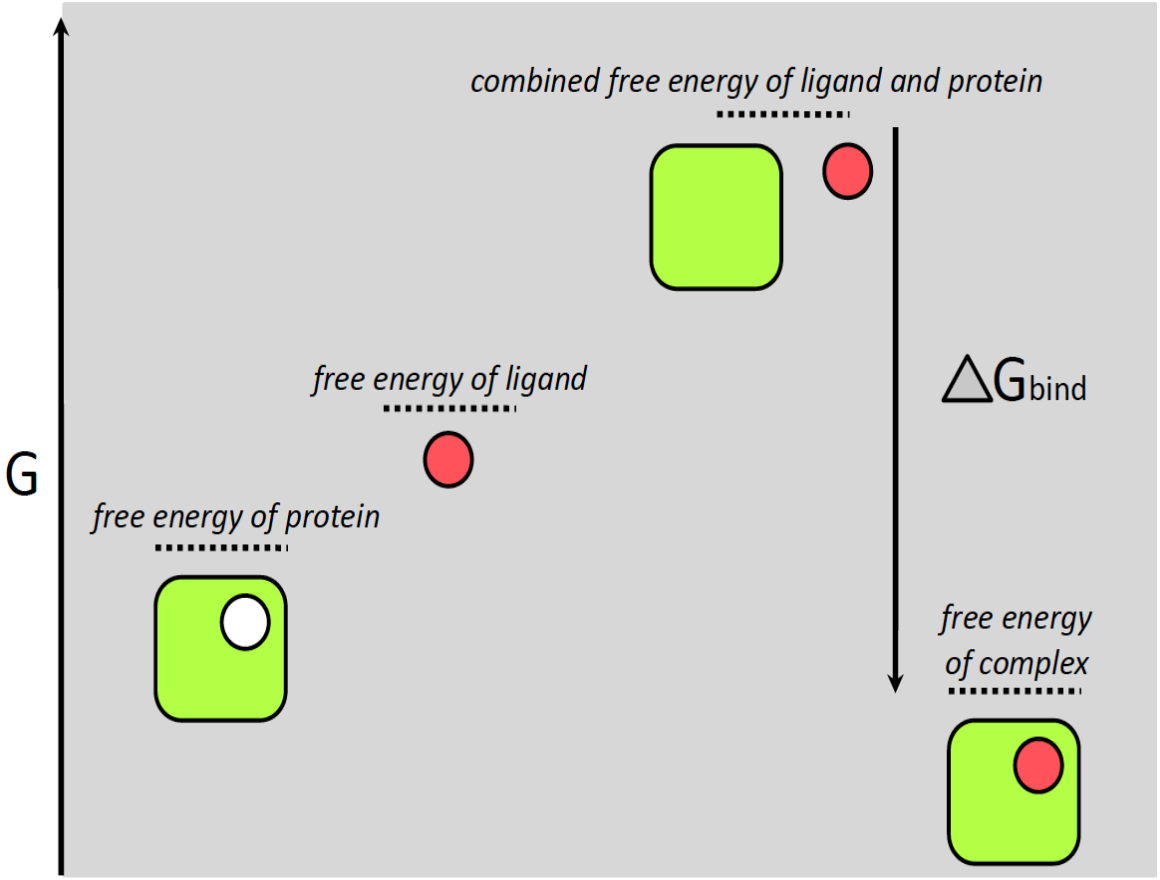
From 20.110:

$$\Delta G^{\circ}_{bind} = -RT \ln K_A$$

$$K_D \underset{\text{(dissociation constant)}}{} = \frac{[P][L]}{[P \cdot L]} = \frac{1}{K_A}$$

$$\Delta G^{\circ}_{bind} = +RT \ln K_D$$

Relationship of ligand binding free energy to association constants



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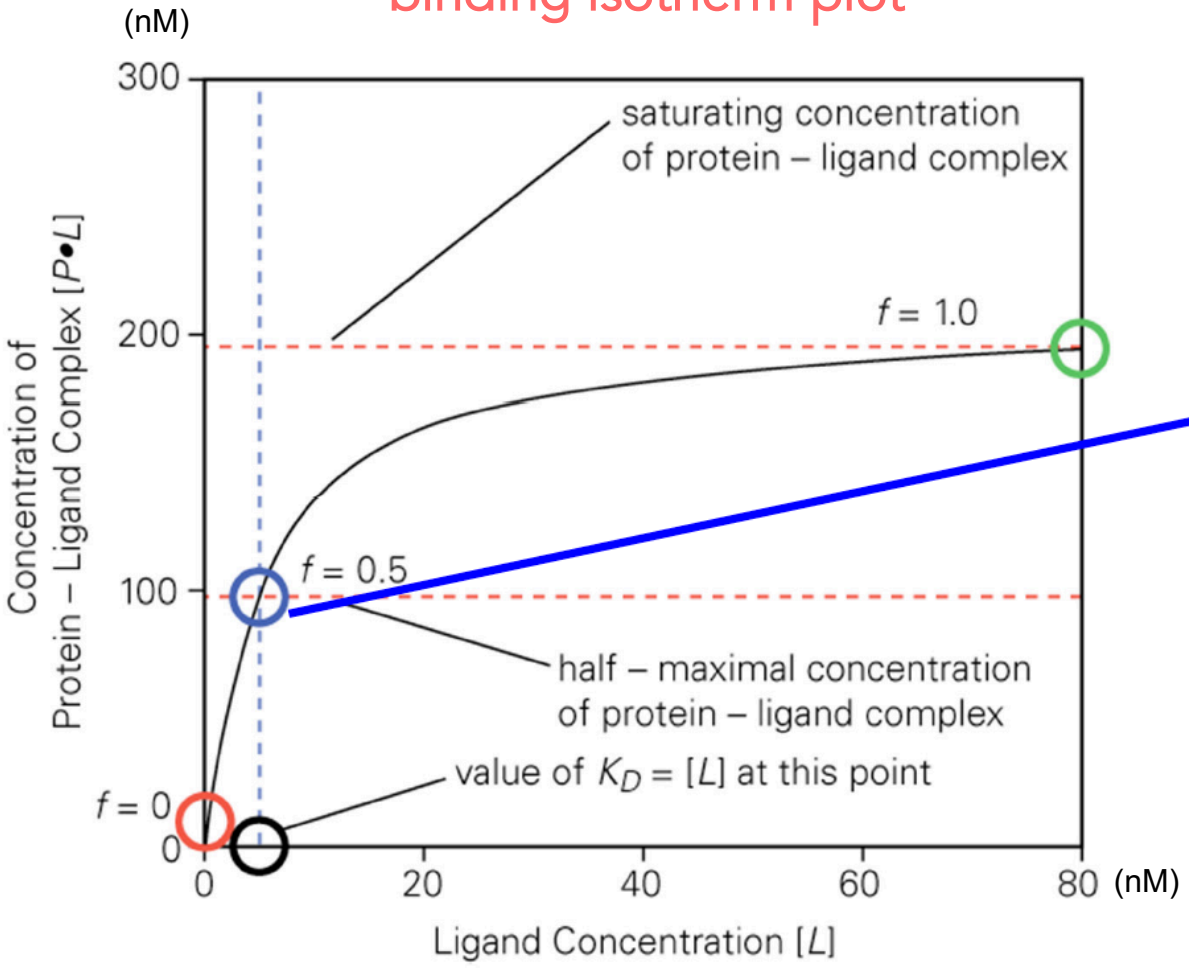
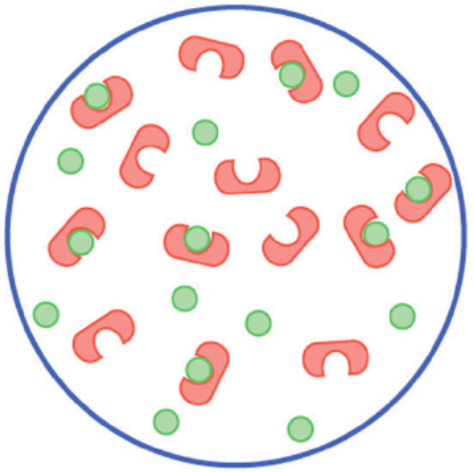
$$\Delta G^{\circ}_{bind} = +RT \ln K_D$$

Binding isotherms are half maximal at $[L] = K_D$

'binding isotherm plot'



$R \bullet L \leftrightarrows R + L$

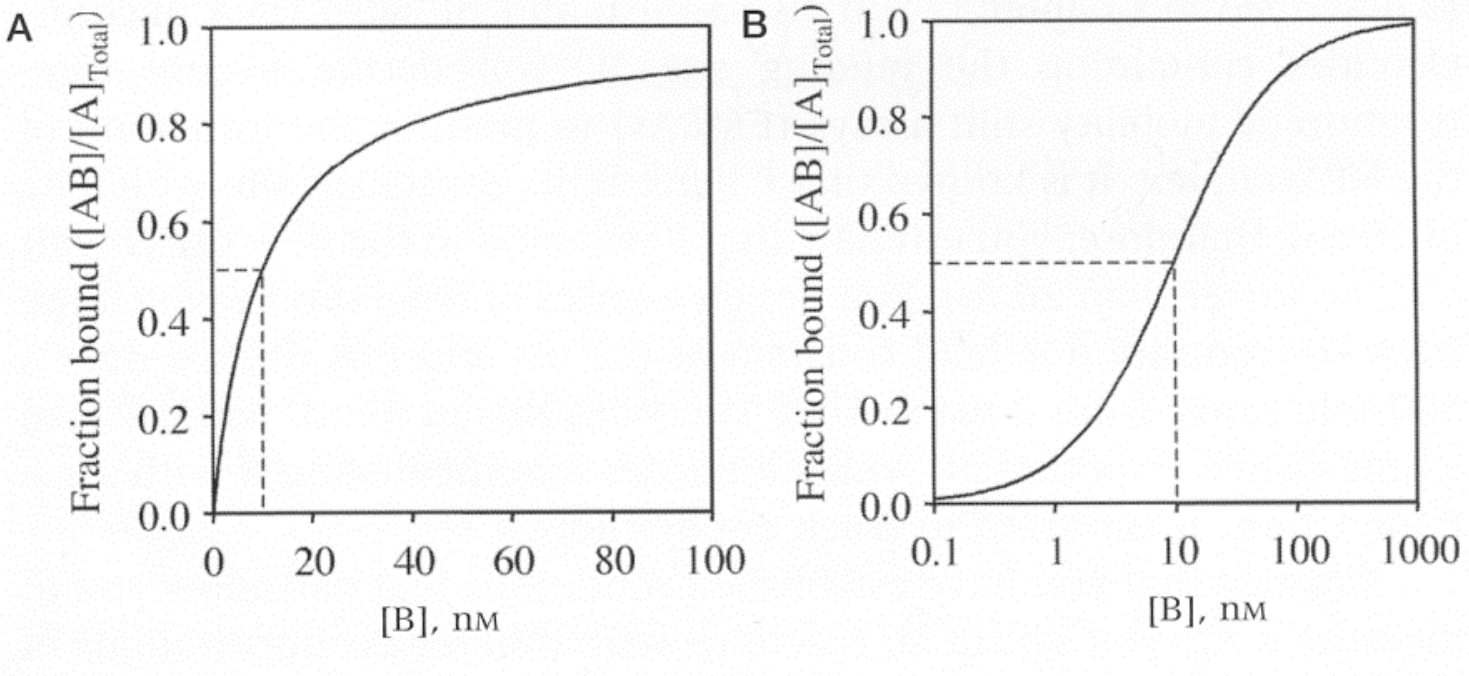


intermediate ligand concentration: $f = 0.5$
$K_D = [L]$ when $f = 0.5$

steady-state
equilibrium analysis

Logarithmic vs. Linear display of data

historic convention *current convention*



as a corollary, choose your concentrations wisely:

1, 3, 10, 30, 100, 300 nM

vs.

50, 100, 150, 200, 250, 300 nM

Range of biologically important interactions

Type of Interaction	K_D (molar)	ΔG^0_{bind} (at 300K) kcal/mol
Enzyme:ATP	~1×10^{-3} to ~1×10^{-6} (millimolar to micromolar)	**-4 to -8 kcal/mol**
signaling protein binding to a target	~1×10^{-6} (micromolar)	**-8 kcal/mol**
Sequence-specific recognition of DNA by a transcription factor	~1×10^{-9} (nanomolar)	**-12 kcal/mol**
small molecule inhibitors of proteins (drugs)	~1×10^{-9} to ~1×10^{-12} (nanomolar to picomolar)	**-12 to -17 kcal/mol**
biotin binding to avidin protein (strongest known non-covalent interaction)	~1×10^{-15} (femtomolar)	**-21 kcal/mol**

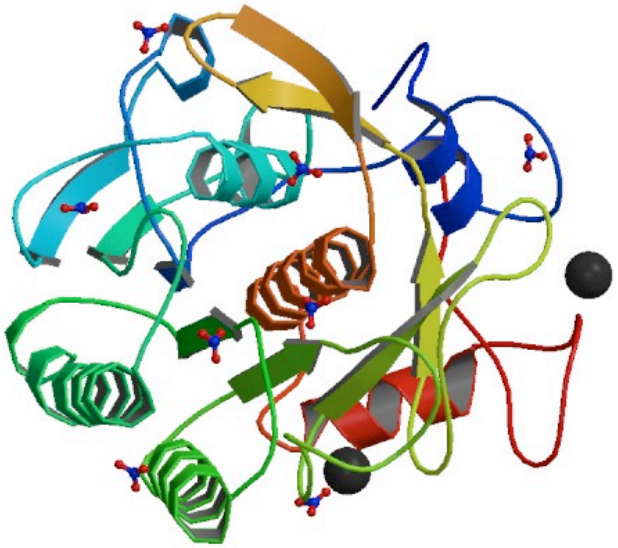
higher K_D value
weaker interaction

lower K_D value
stronger interaction

Adapted from Kuriyan, The Molecules of Life, Chapter 12, Molecular Recognition

Specificity in molecular recognition

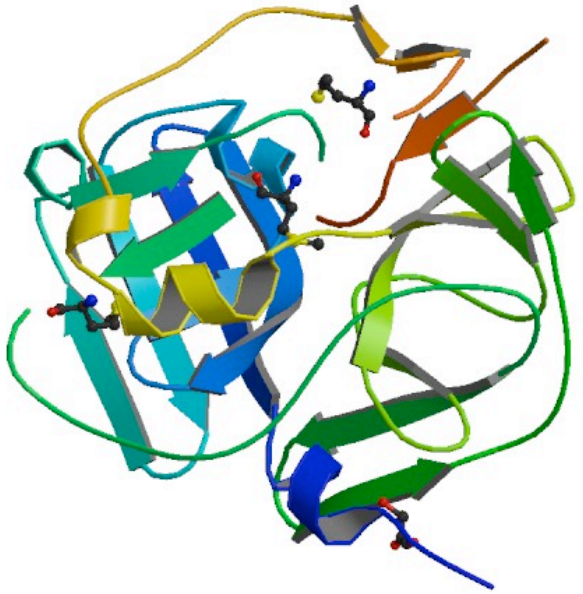
discrimination among targets



Proteinase K

low specificity

Aliphatic/X
Aromatic/X

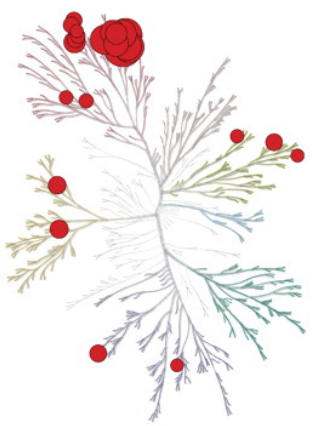


Tobacco Etch Virus (TEV) protease

high specificity

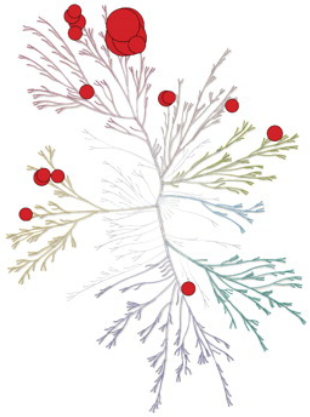
Glu-X-X-Tyr-X-Gln/Ser

Specificity in molecular recognition – kinase drugs



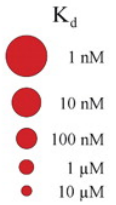
AC220

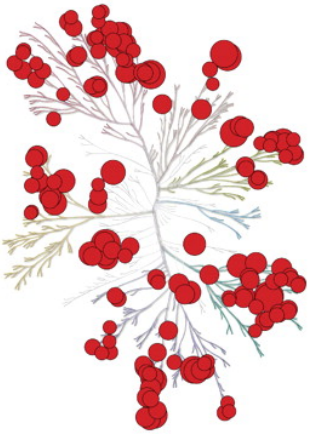
CEP-701



MLN-518

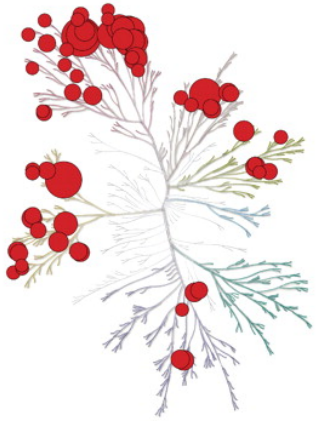
binding constants





PKC-412

CGP-52421



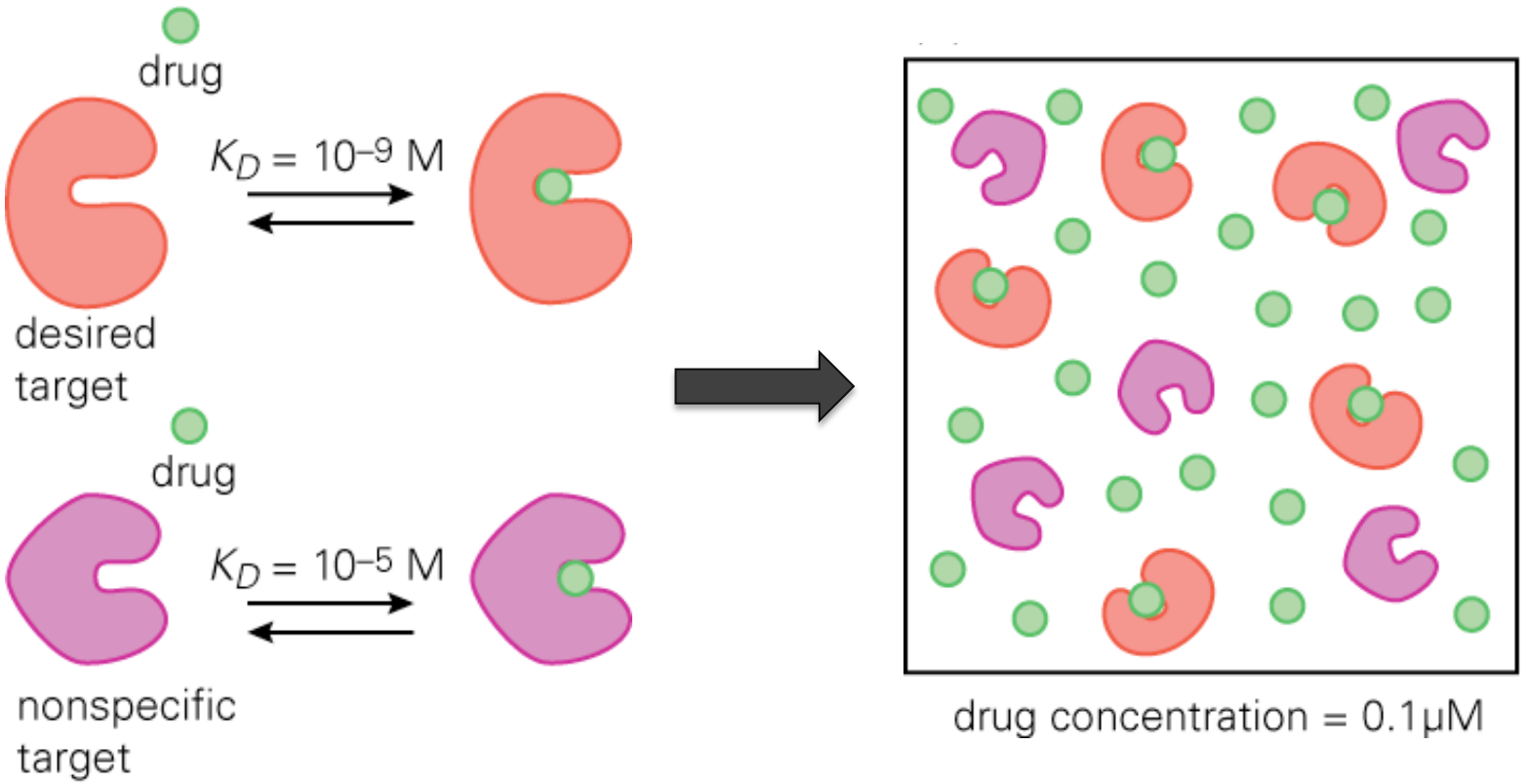
Sorafenib

Sunitinib

Adapted from Zarrinkar et al, Blood (2009), 114: 2984-2992

Specificity in drug binding – fractional saturation

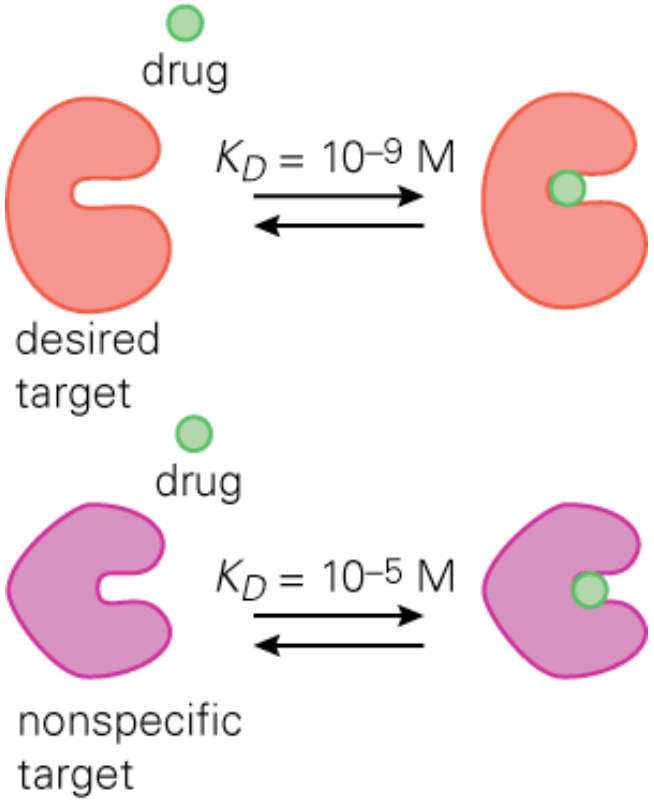
deliver the drug at a concentration below the K_D for non-cognate target



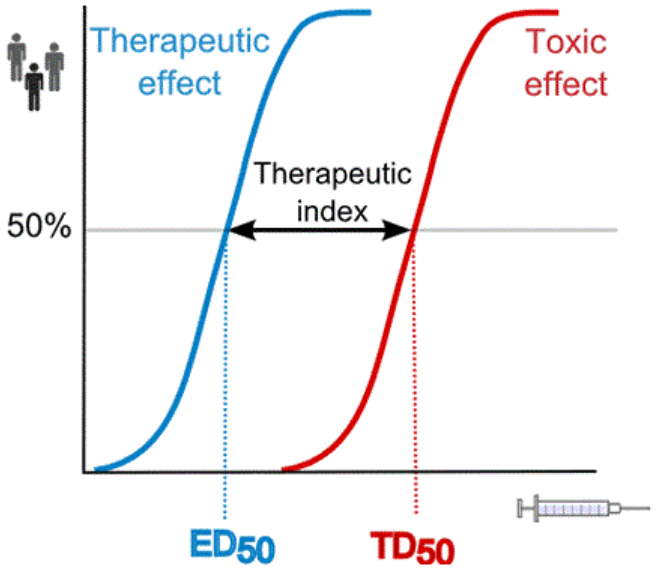
Adapted from Kuriyan, The Molecules of Life, Chapter 12, Molecular Recognition

Specificity in drug binding – fractional saturation

deliver the drug at a concentration below the TD_{50} in patients



impact therapeutic effects?



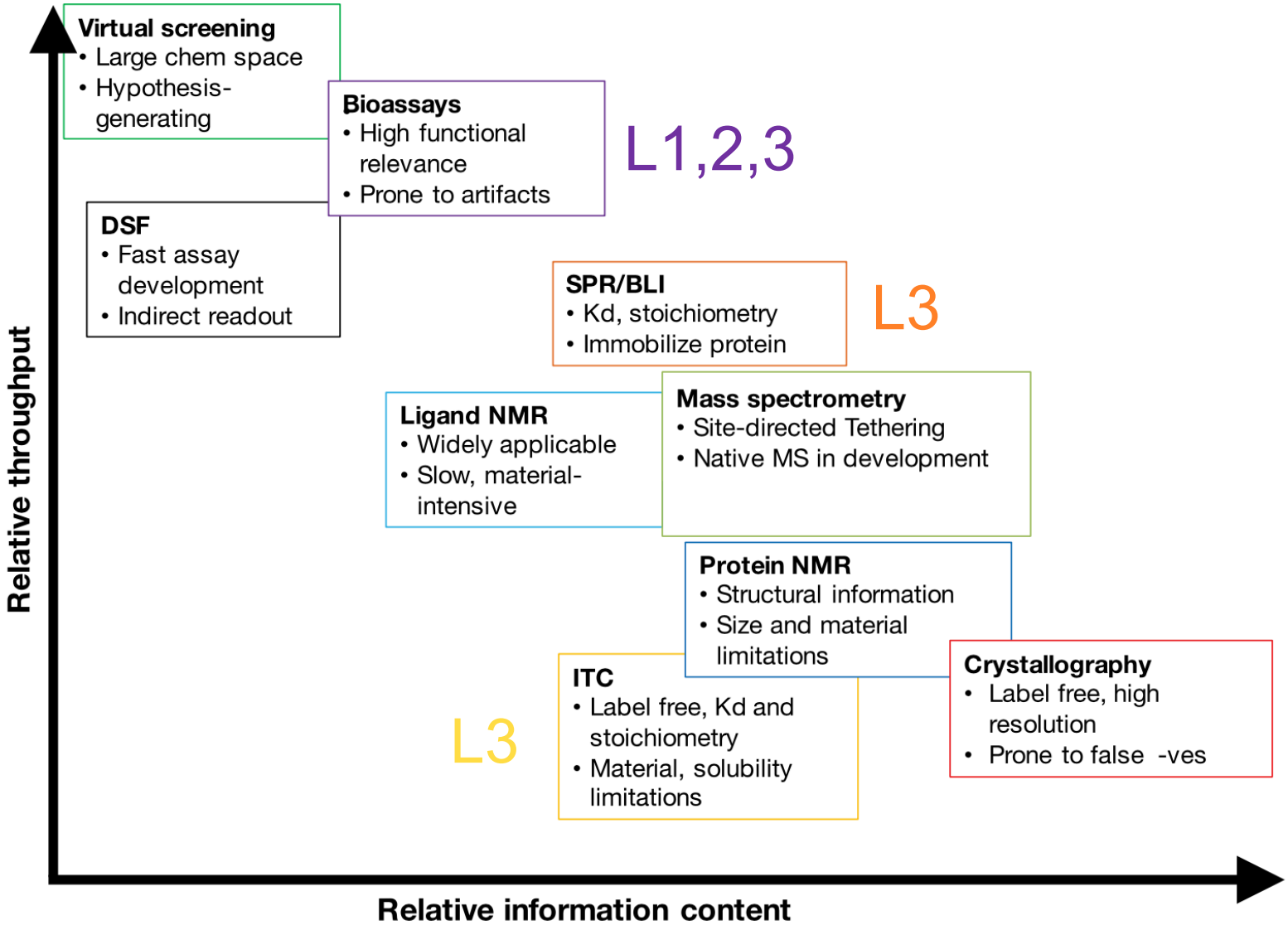
ED_{50} = effective in 50% patients

TD_{50} = toxic in 50% patients

Adapted from Kuriyan, The Molecules of Life, Chapter 12, Molecular Recognition

But how do we go about measuring these K_D values in a laboratory setting?

Methods to evaluate binding interactions



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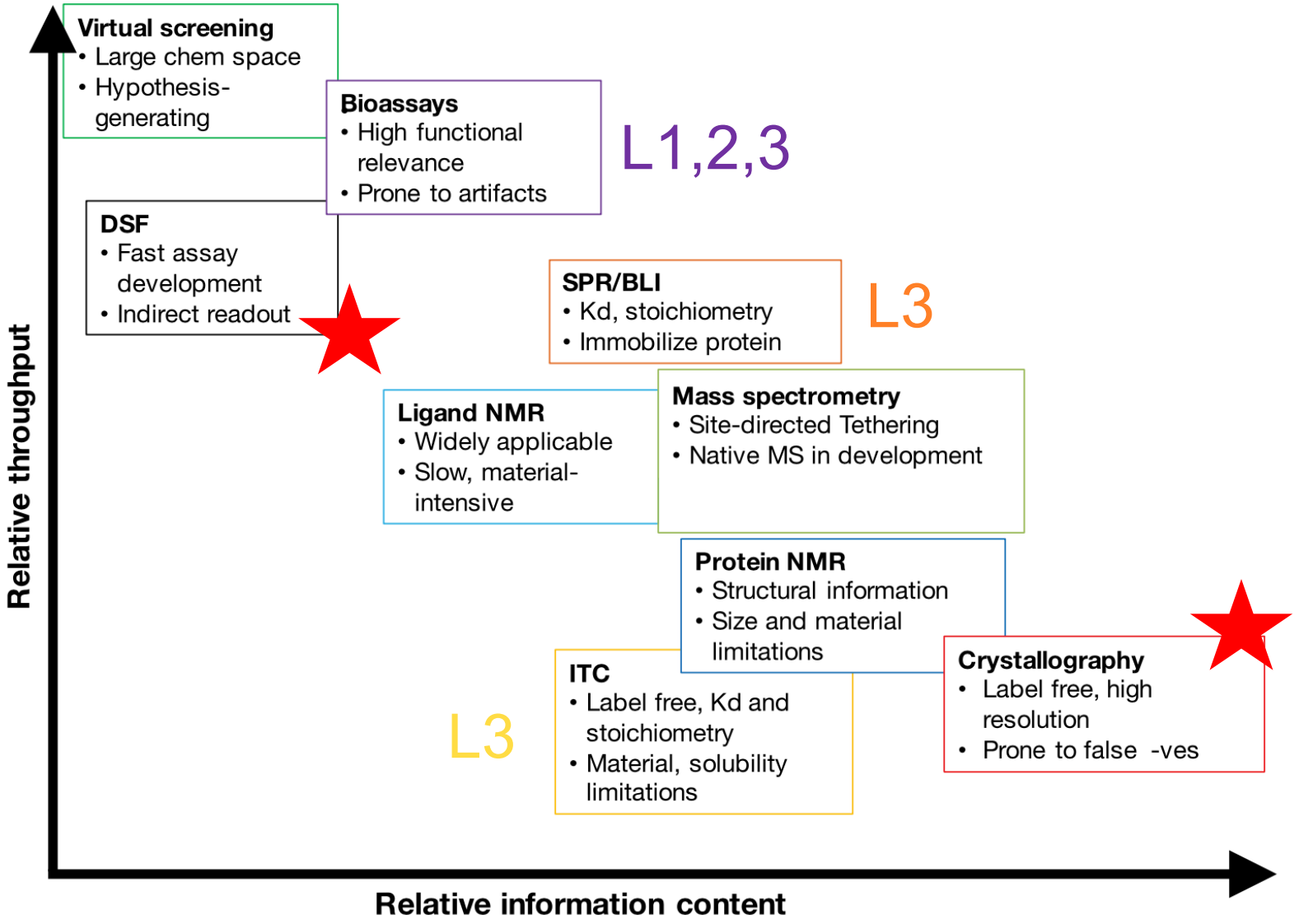
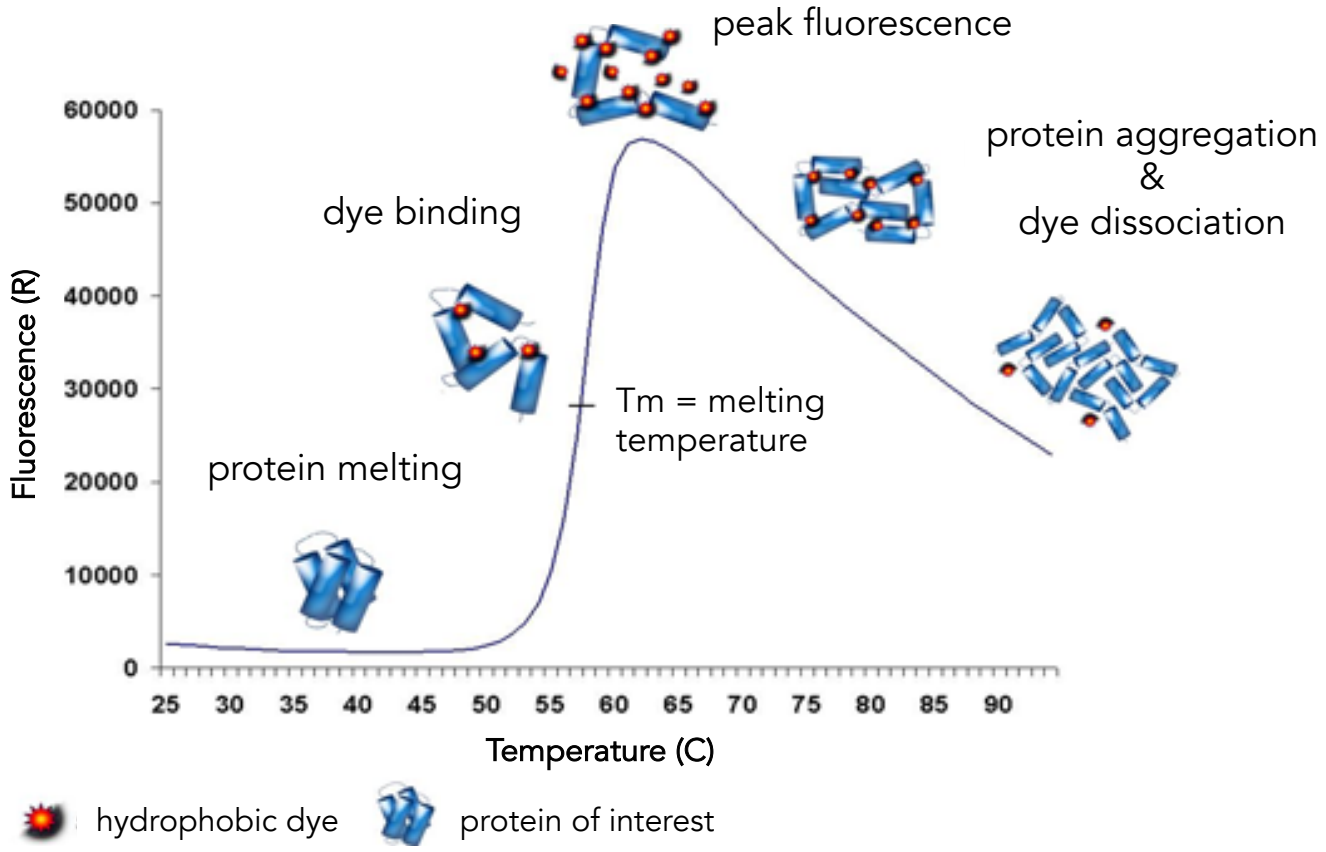
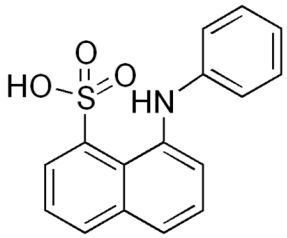


Measuring a thermal melt profile for a protein



Dyes used to detect protein unfolding

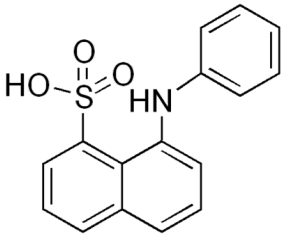


ANS

8-anilinonapthalene-1-sulfonic acid

(1965)

Dyes used to detect protein unfolding



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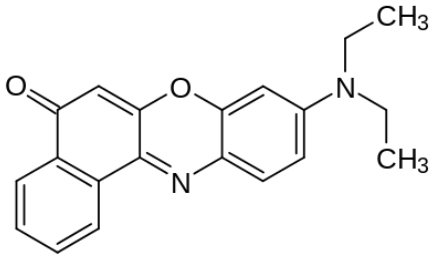


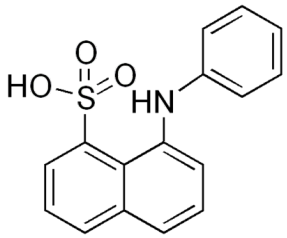
Nile Red

9-diethylamino-5-benzo[a]phenoxazinone
(1985)

solvatochromic

Nile Red under visible and
UV light in different solvents

Dyes used to detect protein unfolding



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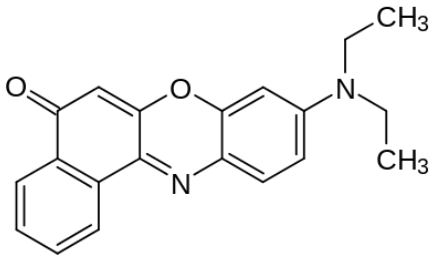

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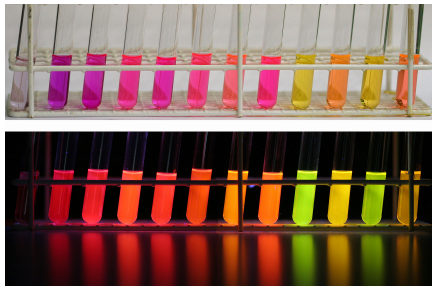

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Nile Red under visible and
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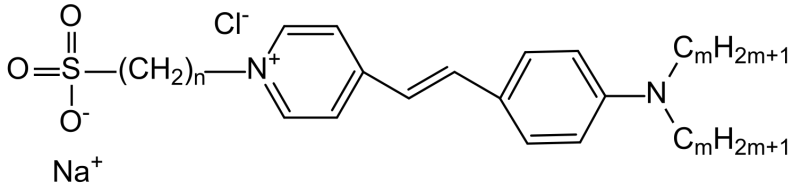
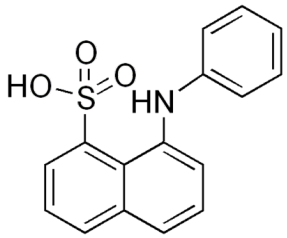


SYPRO® Orange

Most common dye for DSF/TS
(2004)

binds nonspecifically to hydrophobic surfaces;
water quenches fluorescence

Dyes used to detect protein unfolding



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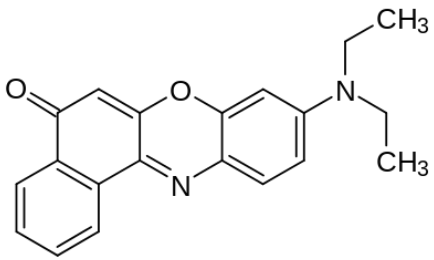

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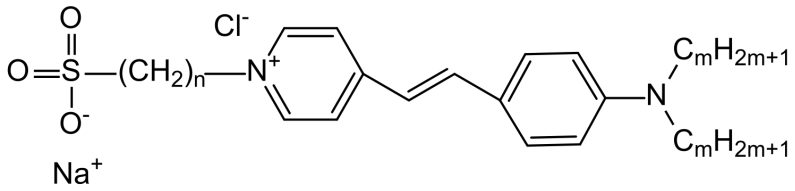

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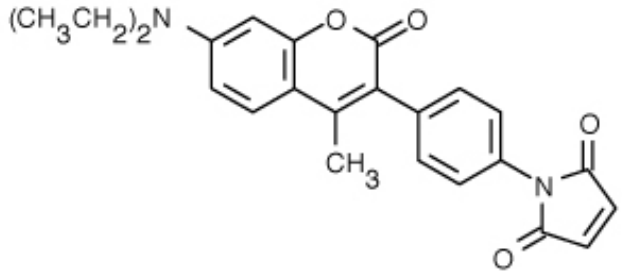
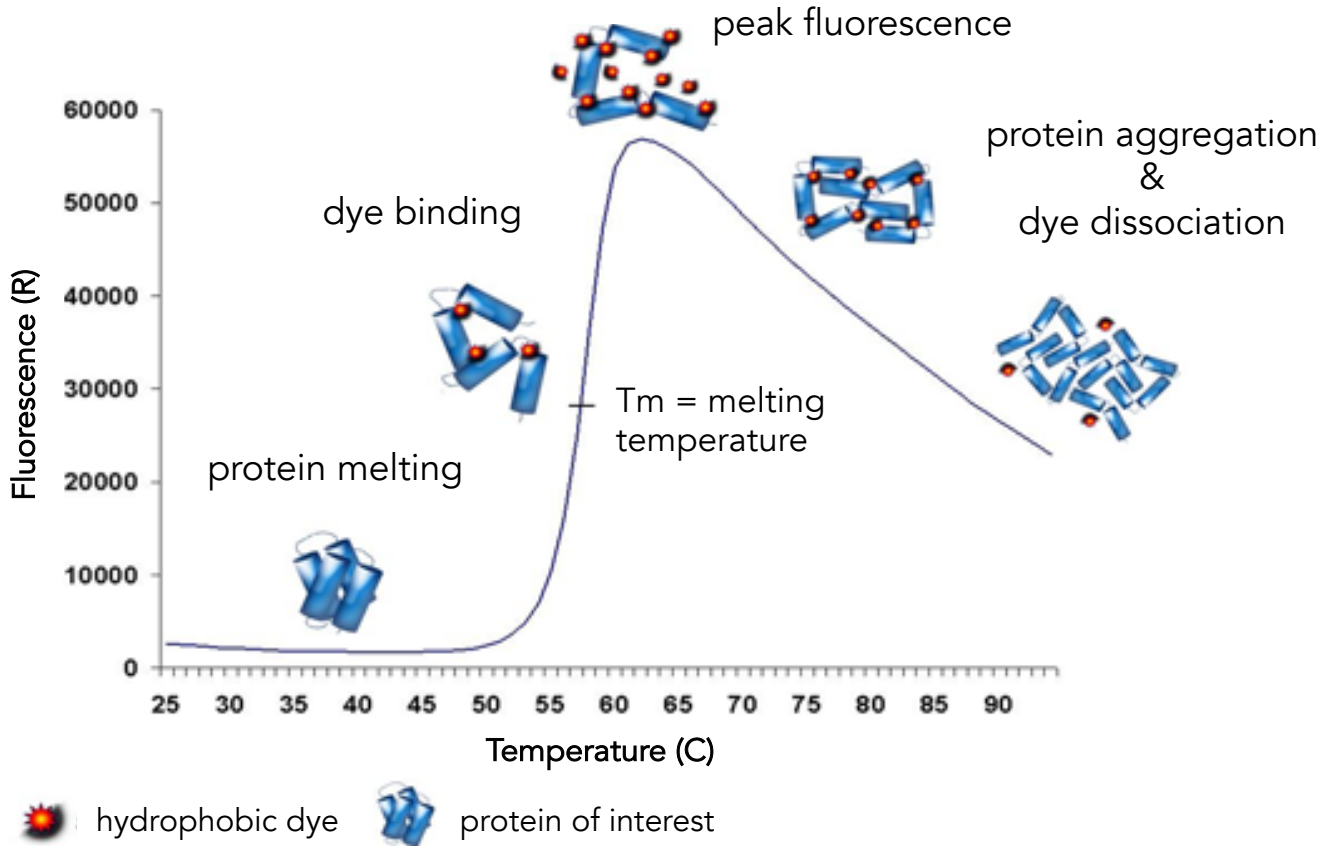


CPM

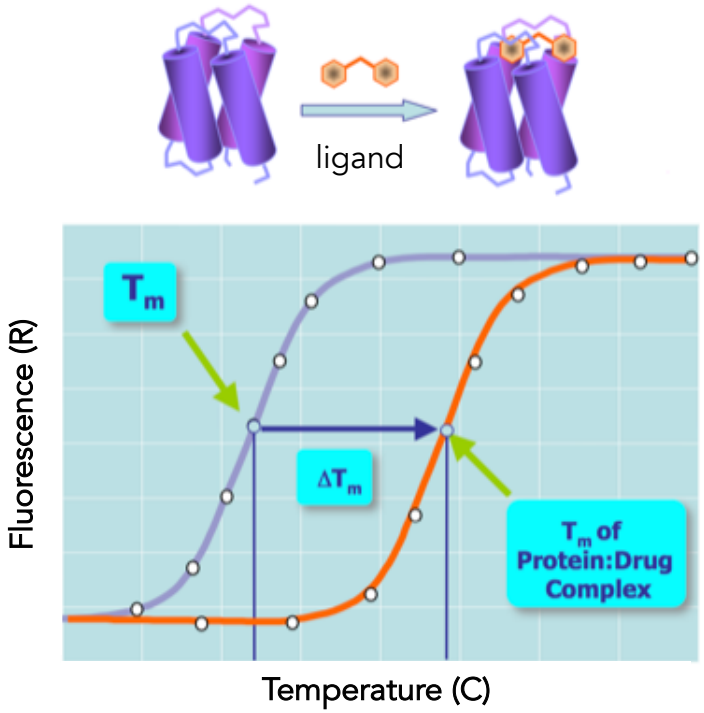
N-[4-(7-diethylamino-4-methyl-3-coumarinyl)phenyl]maleimide
(2008)

only fluoresces after reacting with Cys residues

What happens when you add a small molecule?

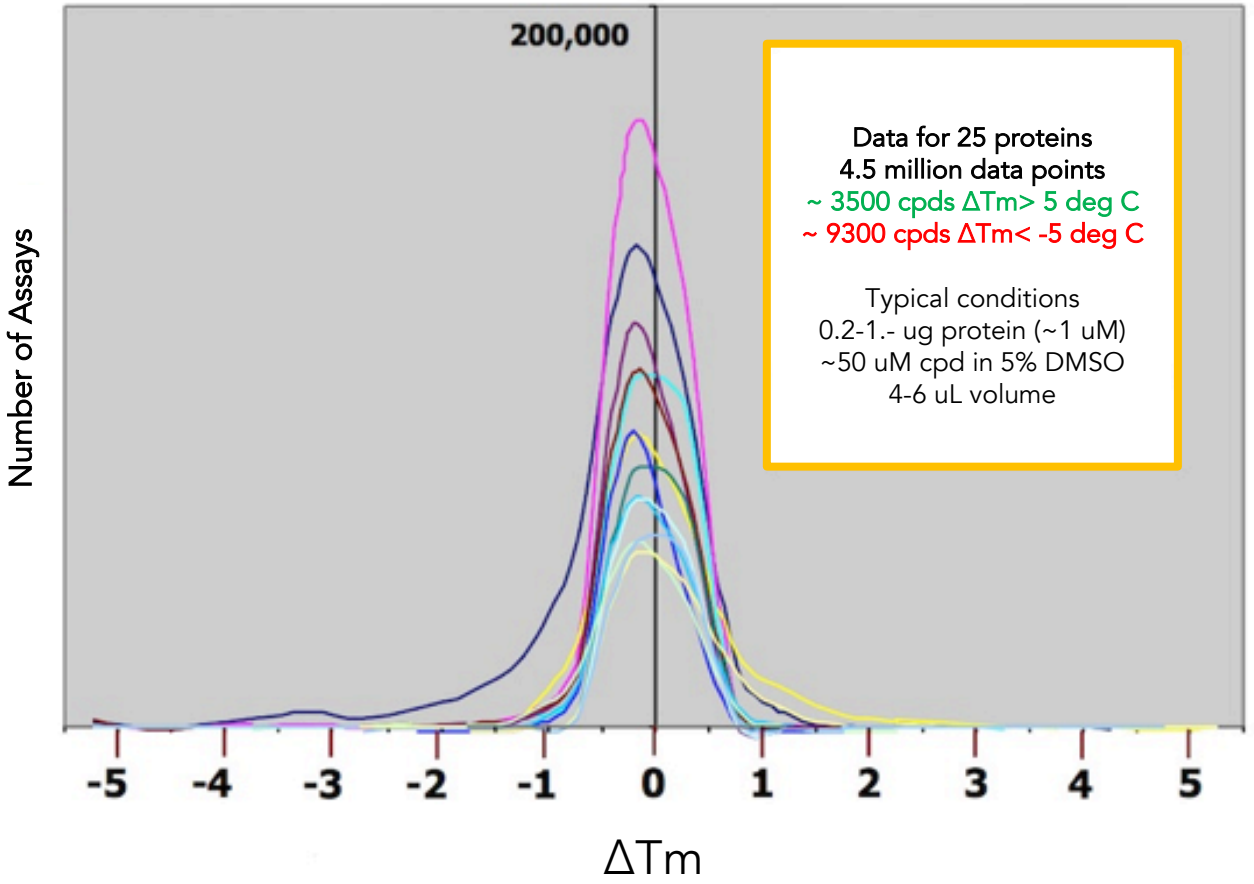


Thermal shift assays with small molecules



Adapted from Dr. Salemme at thermofluor.org

Real thermal shift screens with small molecules

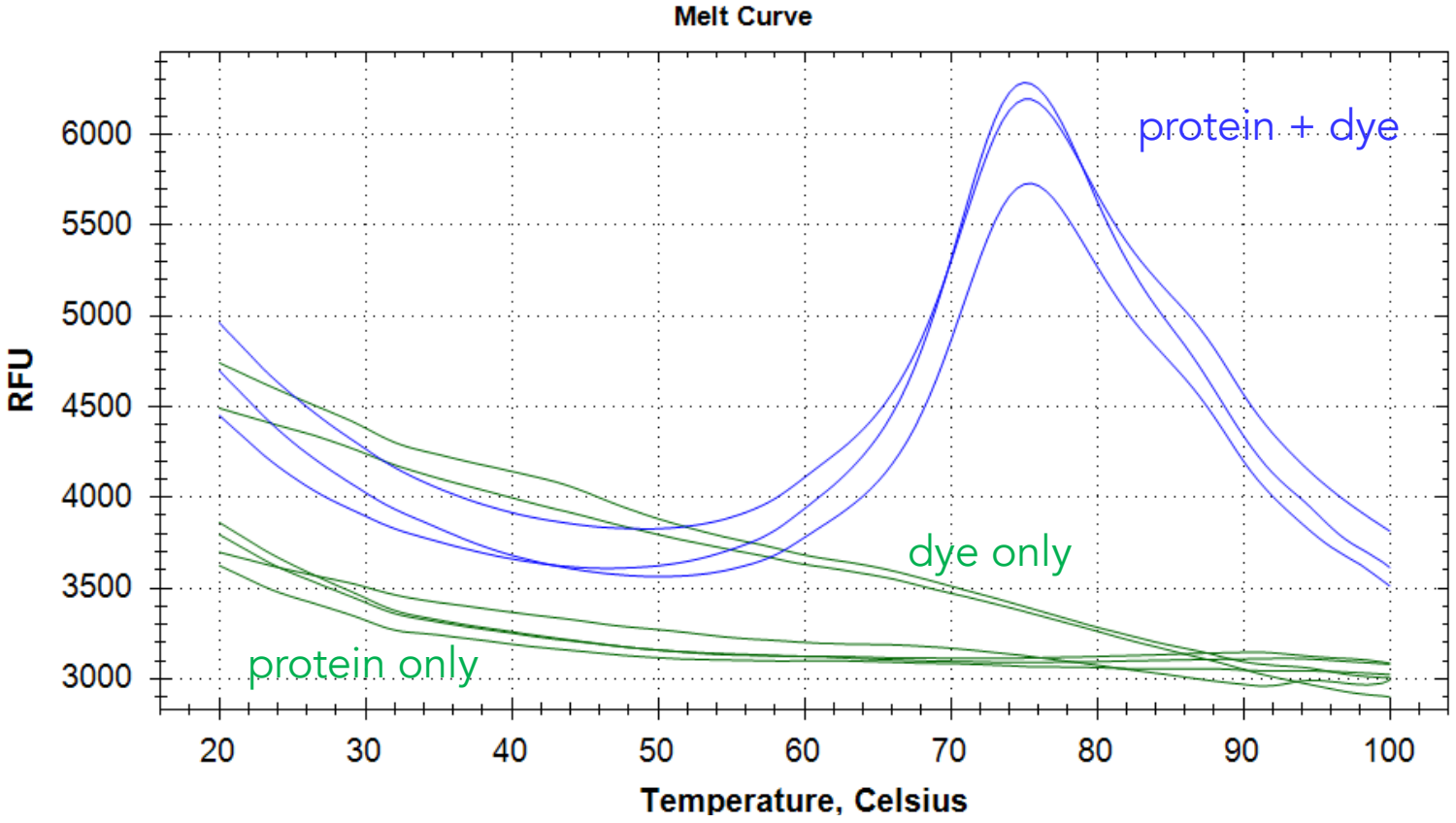


preferential ligand binding to unfolded states?

Adapted from Dr. Salemme at thermofluor.org

Real results from thermal shift studies

assay development

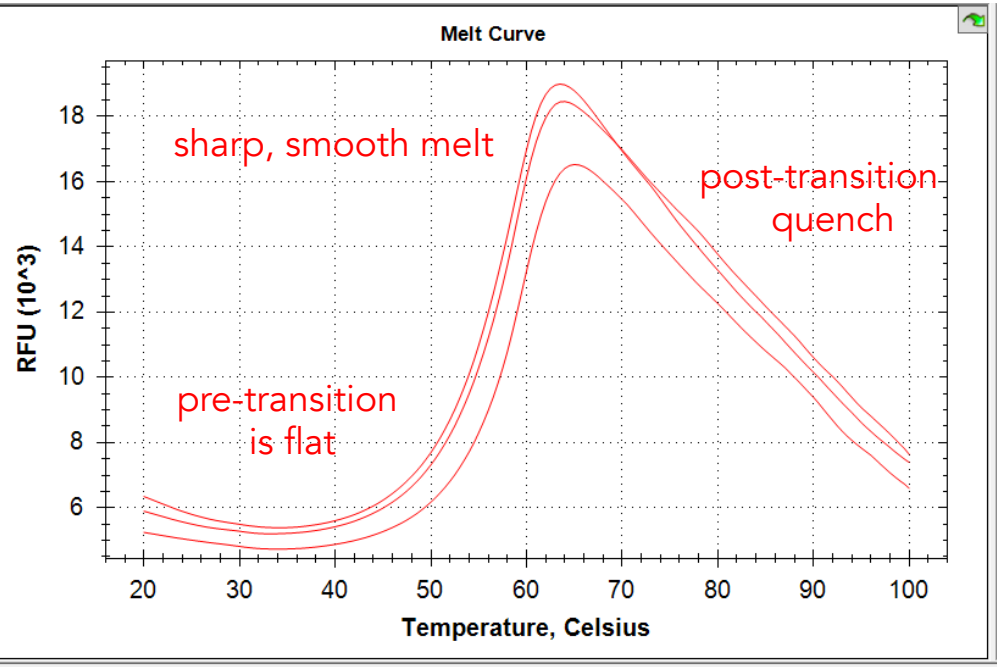


consider optimizing buffer conditions – pH, cofactors

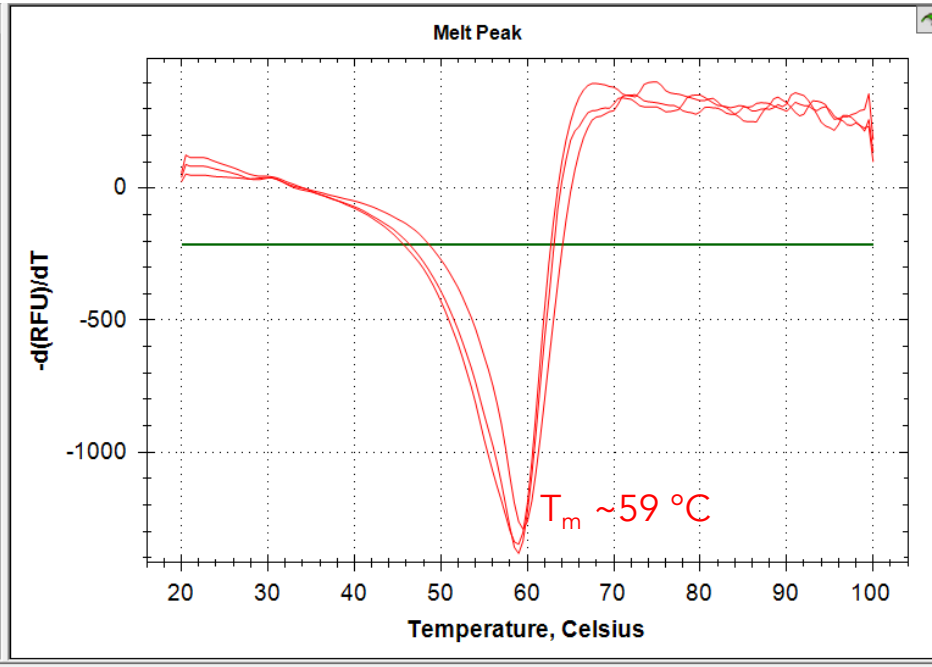
Adapted from Collaborative Crystallisation Centre

Real results with thermal shift assays

three replicates for a single experiment



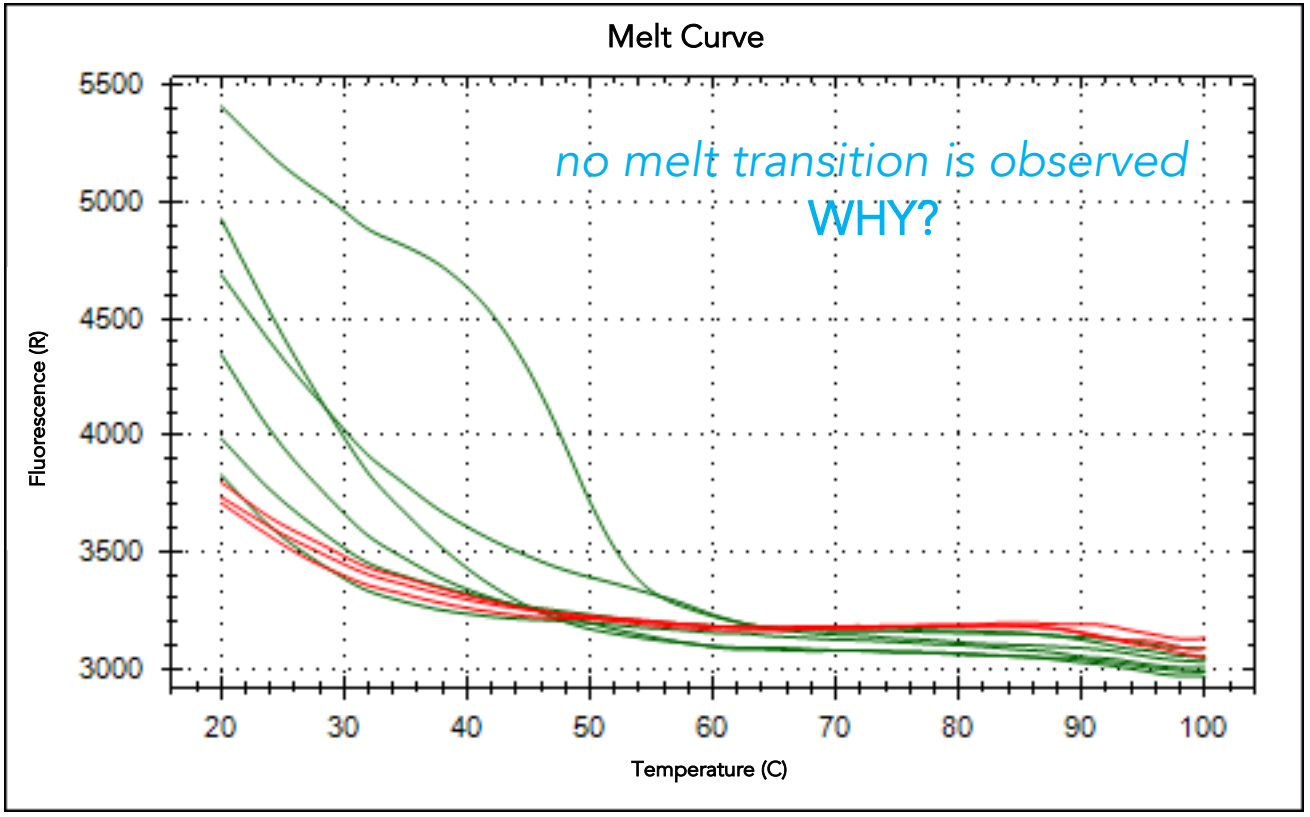
raw fluorescence thermal curves



first derivative representation

Adapted from Collaborative Crystallisation Centre

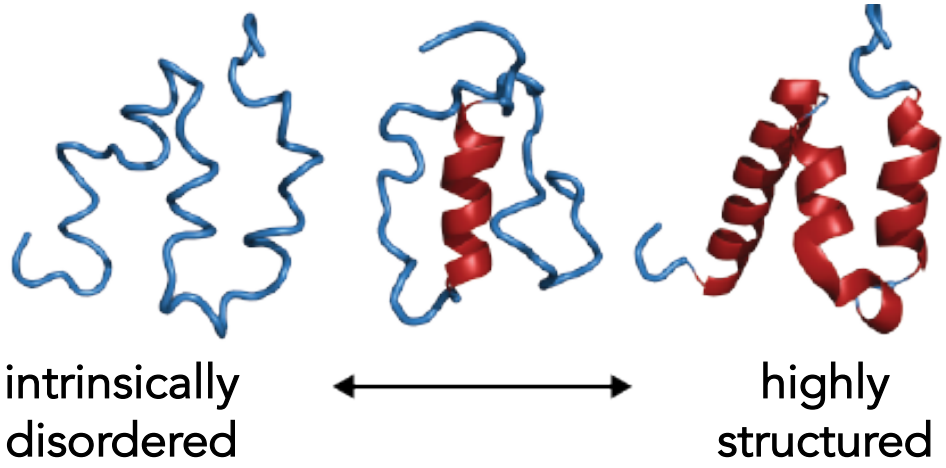
Real results with thermal shift assays



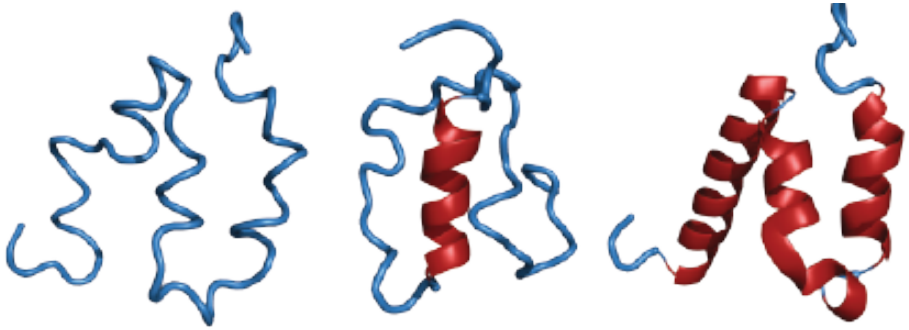
raw fluorescence thermal curves

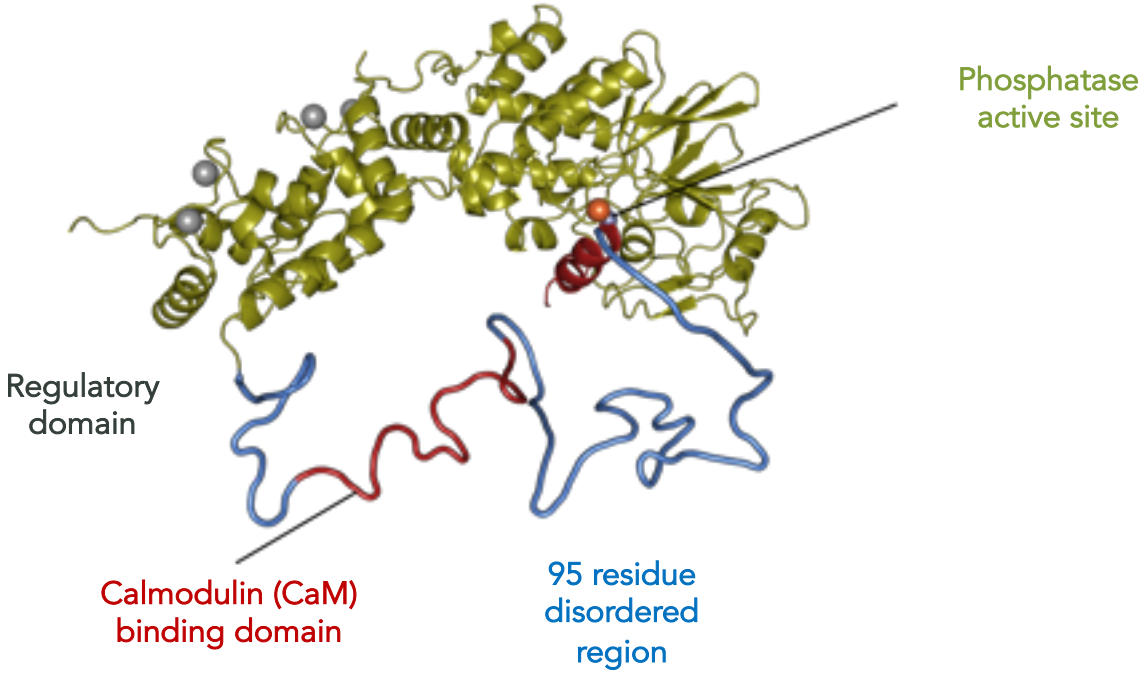
Adapted from Collaborative Crystallisation Centre

Protein disorder continuum



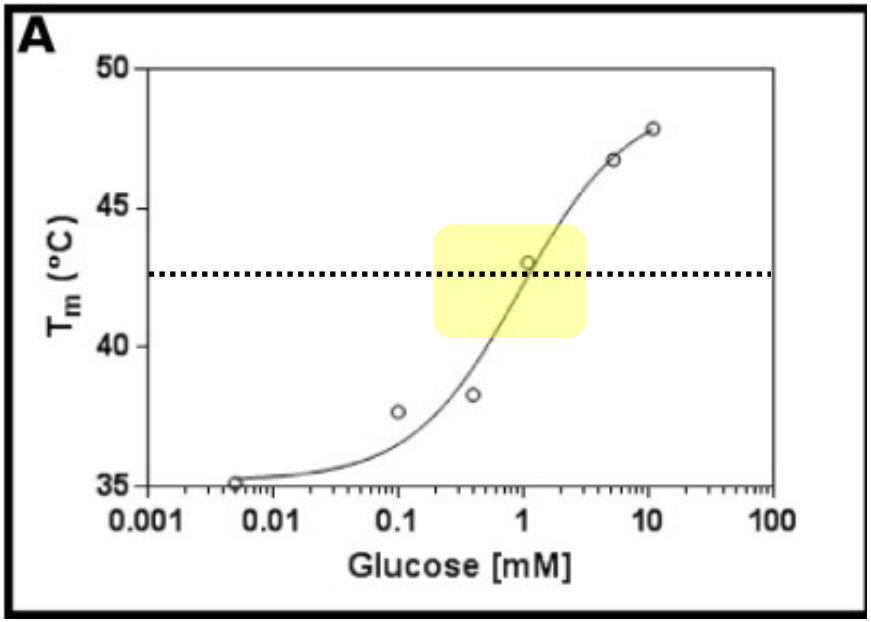
Protein disorder continuum





Determining apparent dissociation constants

hexokinase (receptor) and glucose (ligand)



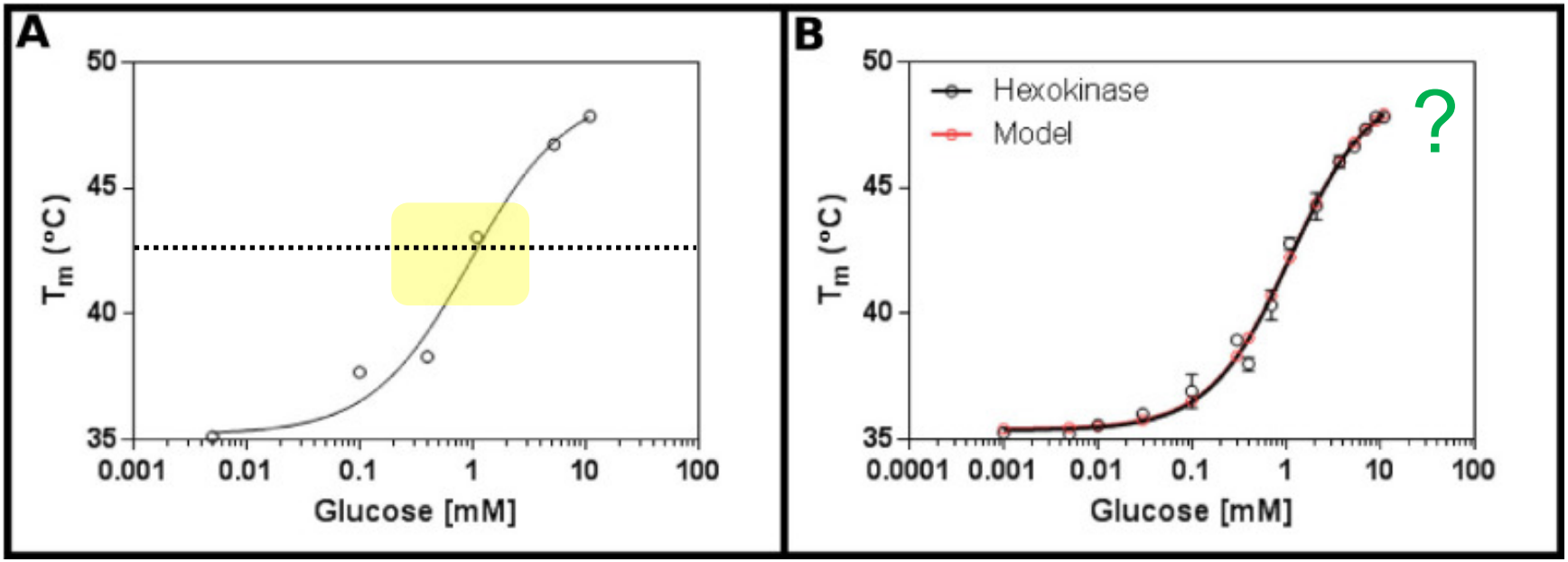
Experiment 1:

test a wide range of glucose concentrations

K_D is likely between 0.2 and 1.7 mM

Determining apparent dissociation constants

hexokinase (receptor) and glucose (ligand)



Experiment 1:

test a wide range of glucose concentrations

K_D is likely between 0.2 and 1.7 mM

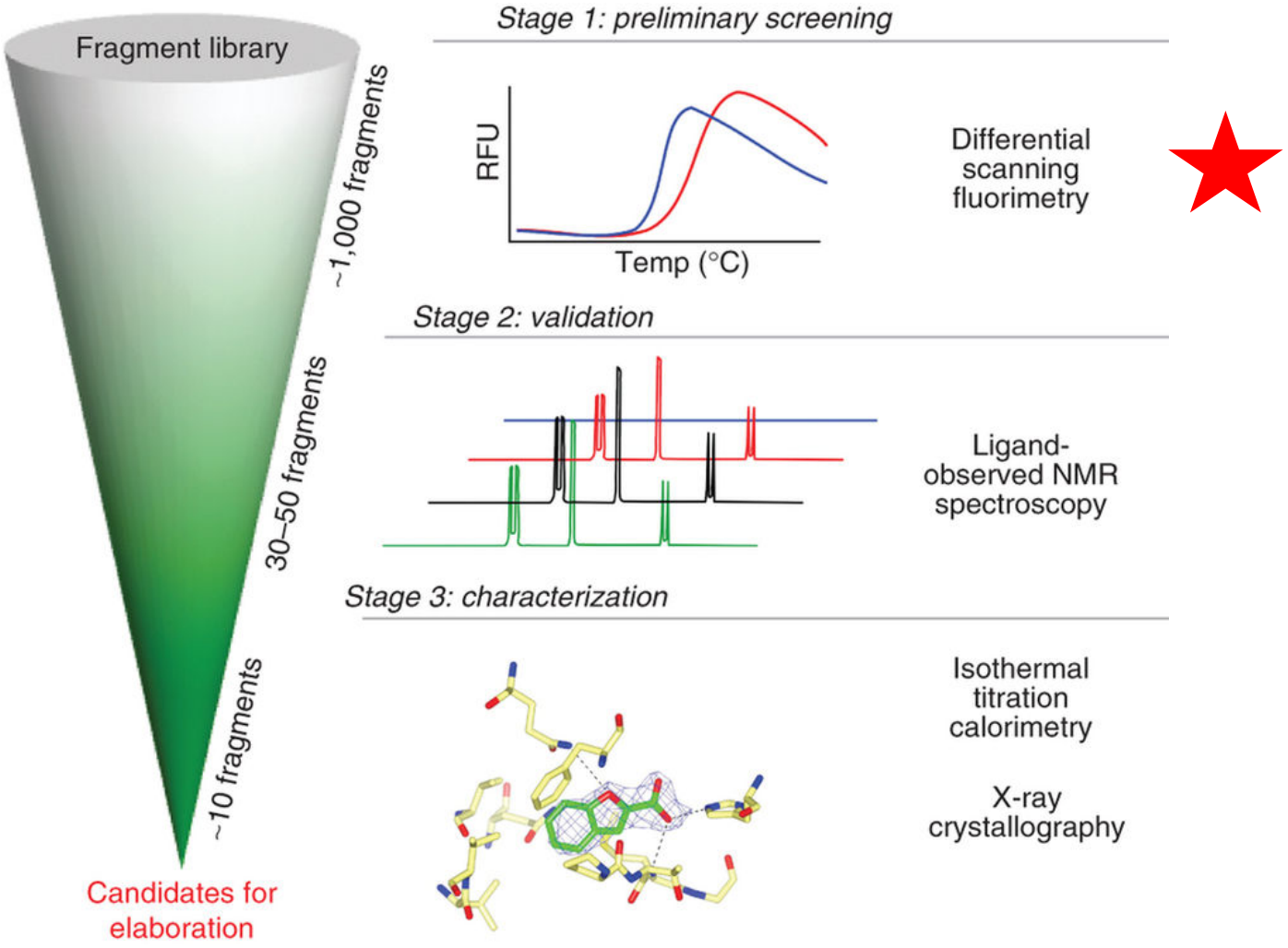
Experiment 2:

test 16 concentration of glucose
fit to single binding event model (red)

apparent K_D ~ 1.12 +/- 0.05 mM

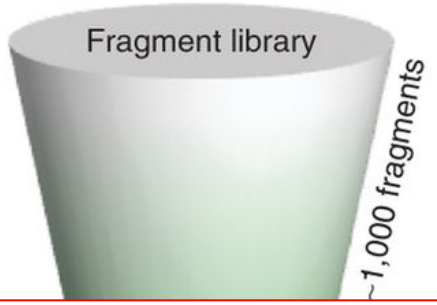
Small molecule stabilizers to aid crystallization

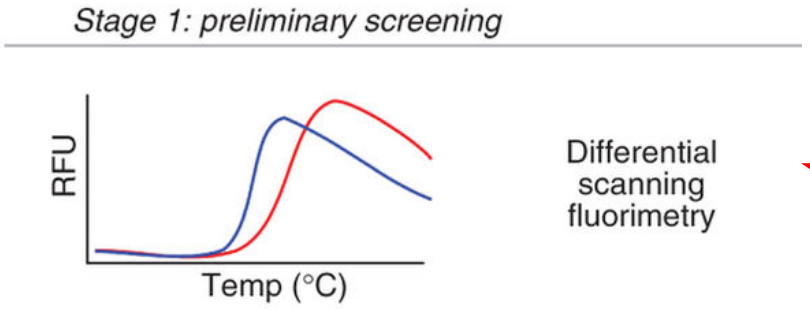
improving structural biology efforts



Small molecule stabilizers to aid crystallization

improving structural biology efforts





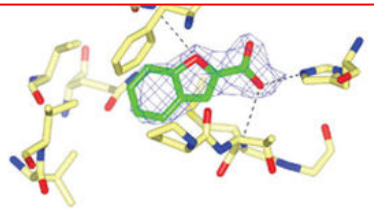
PNAS

Chemical screening methods to identify ligands that promote protein stability, protein crystallization, and structure determination

Masoud Vedadi*, Frank H. Niesen†, Abdellah Allali-Hassani*, Oleg Y. Fedorov†, Patrick J. Finerty, Jr.*, Gregory A. Wasney*, Ron Yeung*, Cheryl Arrowsmith*, Linda J. Ball†, Helena Berglund‡, Raymond Hui*, Brian D. Marsden†, Pär Nordlund‡, Michael Sundstrom†, Johan Weigelt‡, and Aled M. Edwards*§

*Structural Genomics Consortium, University of Toronto, 100 College Street, Toronto, ON, Canada M5G 1L5; †Structural Genomics Consortium, Botnar Research Centre, University of Oxford, Oxford OX3 7LD, United Kingdom; and ‡Structural Genomics Consortium, Karolinska Institutet, KI Scheeles vaeg 2 A1:410, 17177 Stockholm, Sweden

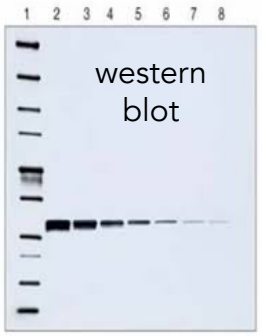
Candidates for elaboration

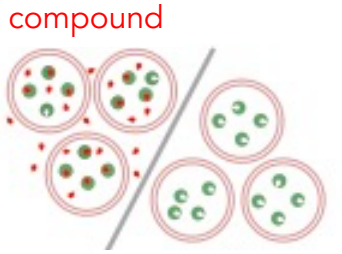


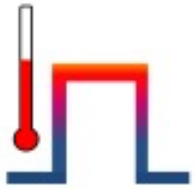
X-ray crystallography

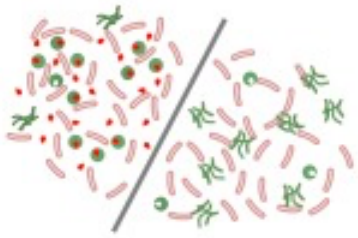
Target engagement in cells: cellular thermal shift assays (CETSA)

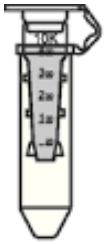
Monitor levels of soluble proteins

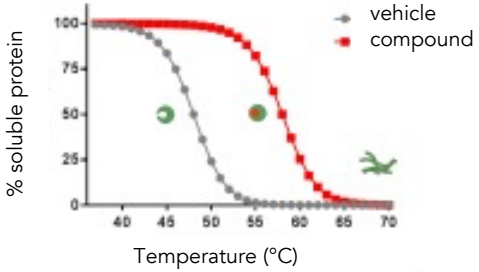








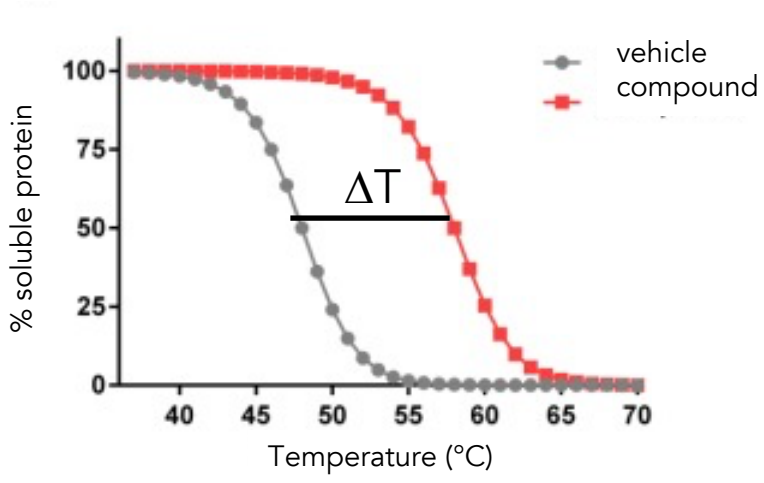




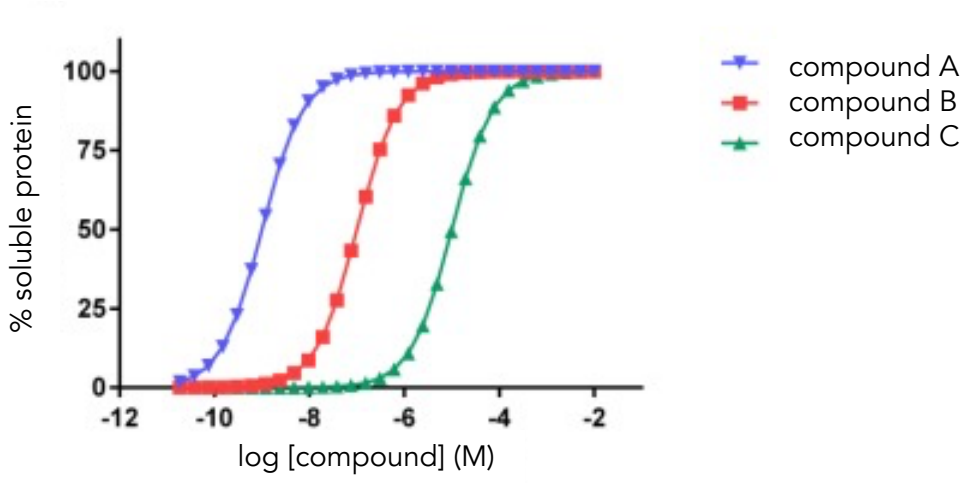
compound treatment in cells → heating and cooling → lyse cells → separation (optional) → detection

Anticipated results from CETSA assays

T_{agg} curve



ITDRF curves

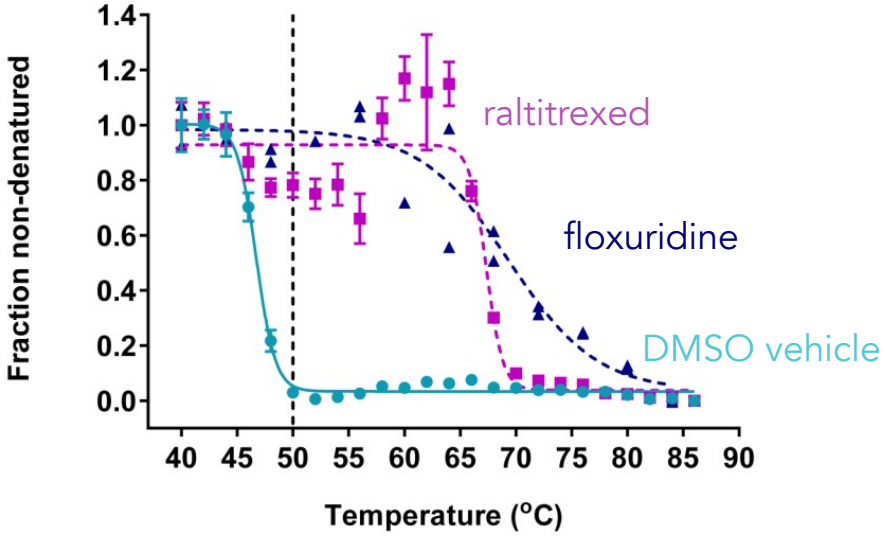


IsoThermal Dose Response Fingerprint
'apparent potencies' at single temp

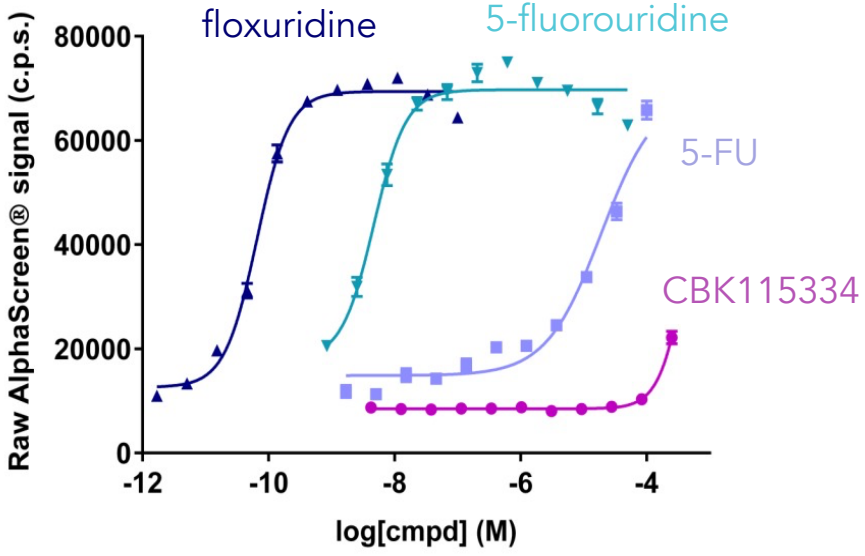
Real results from CETSA assays

thymidylate synthase drugs in K562 cells

T_{agg} curve

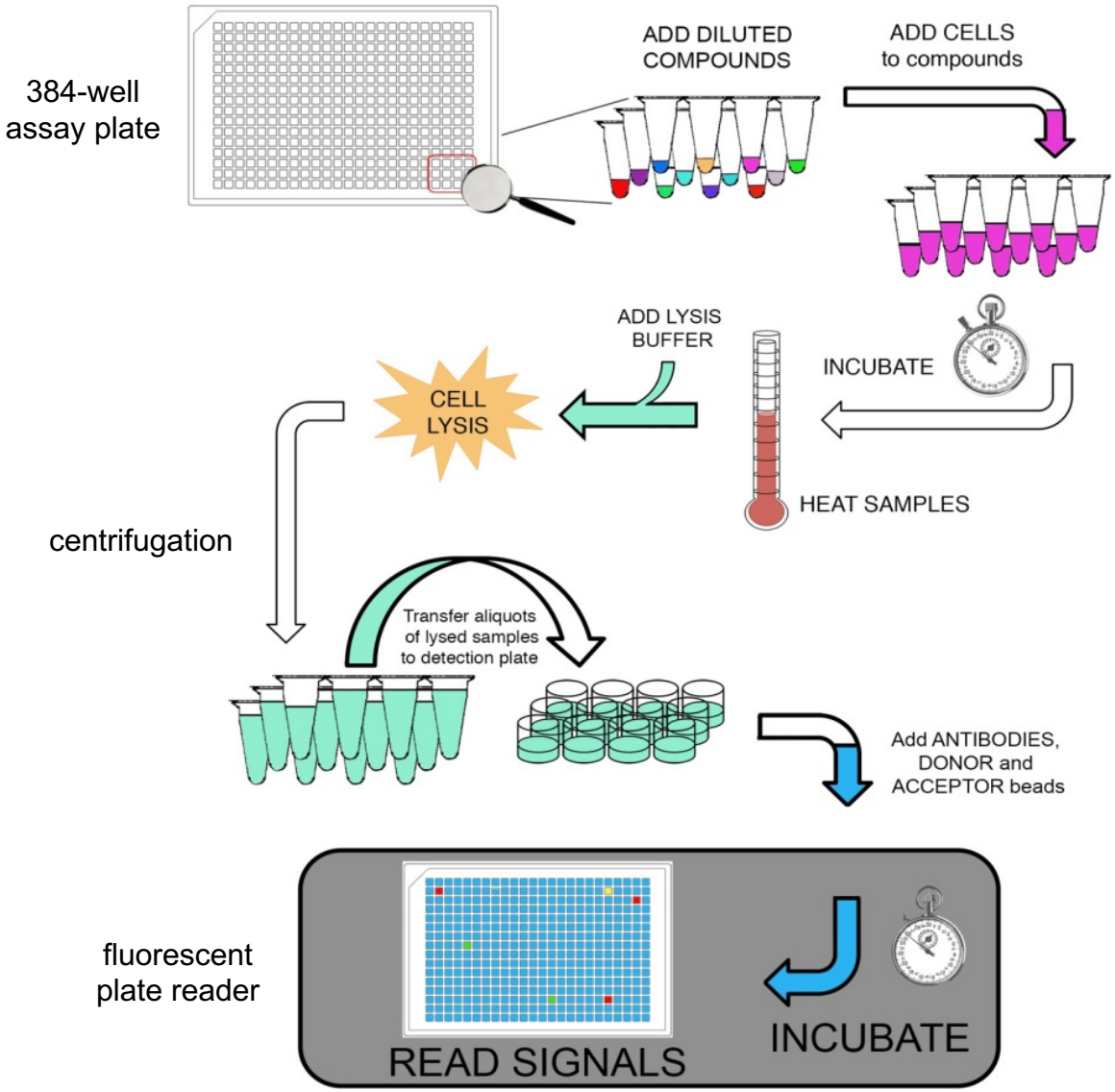


ITDRF curves at 50 °C



quadruplicate data from one independent experiment

CETSA for high-throughput screening



Adapted from the NIH Assay Guidance Manual

CETSA for target identification of drugs

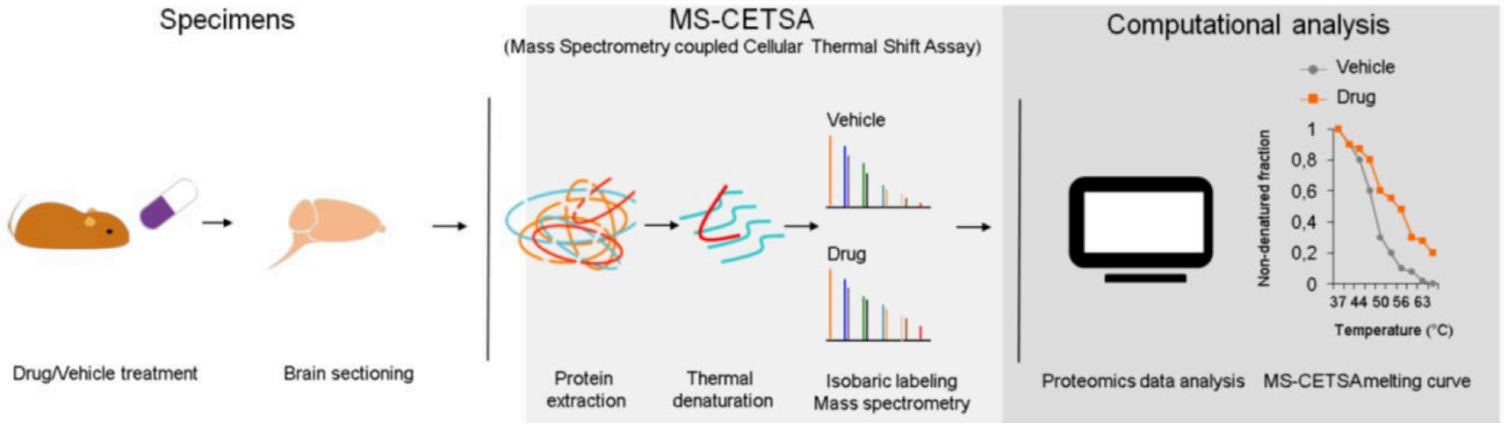
Cell Chemical Biology
Minireview

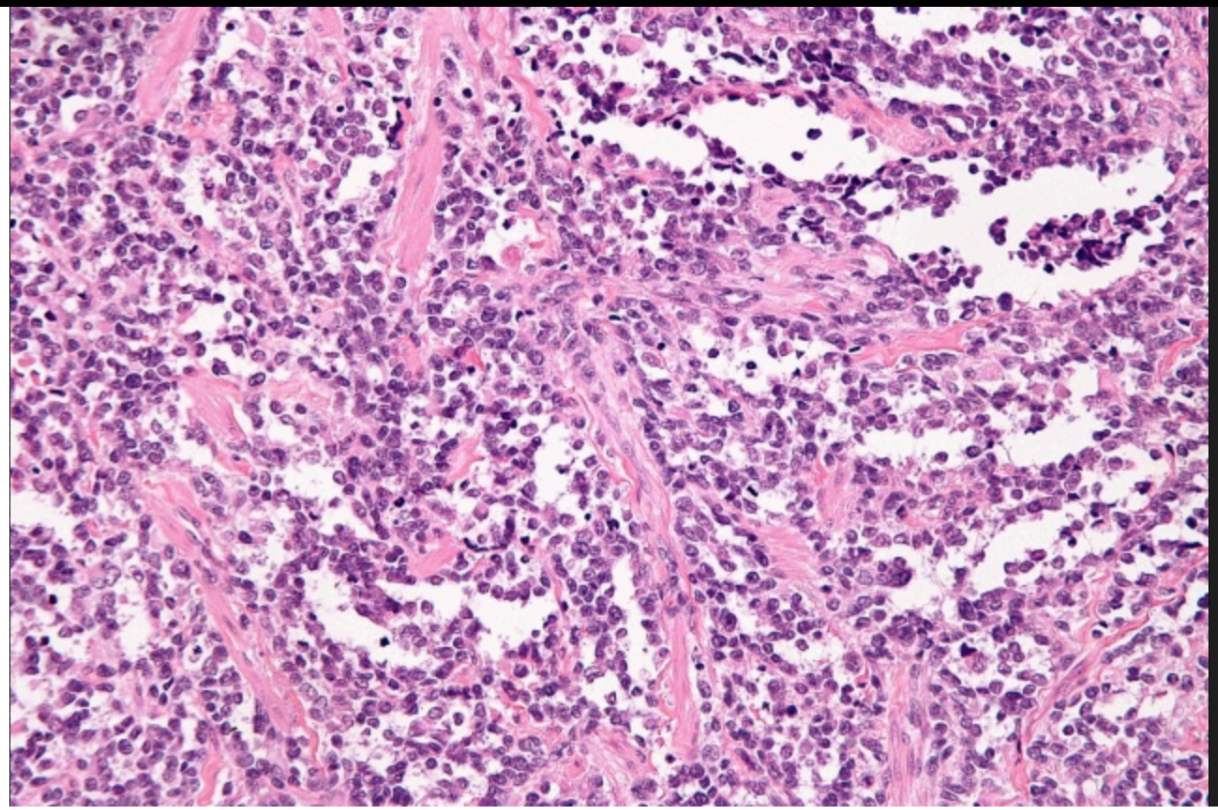
Small-Molecule Target Engagement in Cells

Marc Schürmann,[1] Petra Janning,[1] Slava Ziegler,[1] and Herbert Waldmann[1,2,*]
[1]Department of Chemical Biology, Max Planck Institute of Molecular Physiology, Otto-Hahn-Strasse 11, 44227 Dortmund, Germany
[2]Technical University Dortmund, Department of Chemistry and Chemical Biology, Otto-Hahn-Strasse 6, 44227 Dortmund, Germany
*Correspondence: herbert.waldmann@mpi-dortmund.mpg.de
http://dx.doi.org/10.1016/j.chembiol.2016.03.008

Monitoring how, when, and where small molecules engage their targets inside living cells is a critical step in chemical biology and pharmacological research, because it enables compound efficacy and confirmation of mode of action to be assessed. In this mini-review we summarize the currently available methodologies to detect and prove direct target engagement in cells and offer a critical view of their key advantages and disadvantages. As the interest of the field shifts toward discovery and validation of high-quality agents, we expect that efforts to develop and refine these types of methodologies will also intensify in the near future.

Workflow for novel drug target identification





Alveolar rhabomyosarcoma, a soft tissue cancer

Image: Michael Bonert/Wikimedia Commons

Taking a moonshot at a rare childhood cancer

Team of researchers including MIT Professor Angela Koehler obtains $5.8 million grant to study fusion-positive alveolar rhabdomyosarcoma.

CANCER MOONSHOT

Duke Cancer Institute

Fusion Oncoproteins in Childhood Cancers Consortium

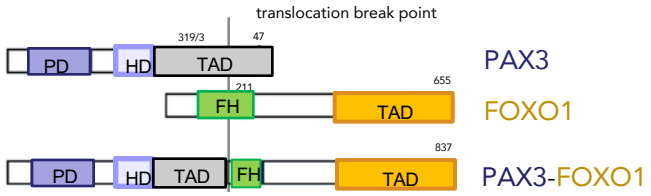
University of Zurich[UZH]

BROAD INSTITUTE

NATIONAL CANCER INSTITUTE

PAX3-FOXO1

pathognomic fusion in alveolar rhabdomyosarcoma



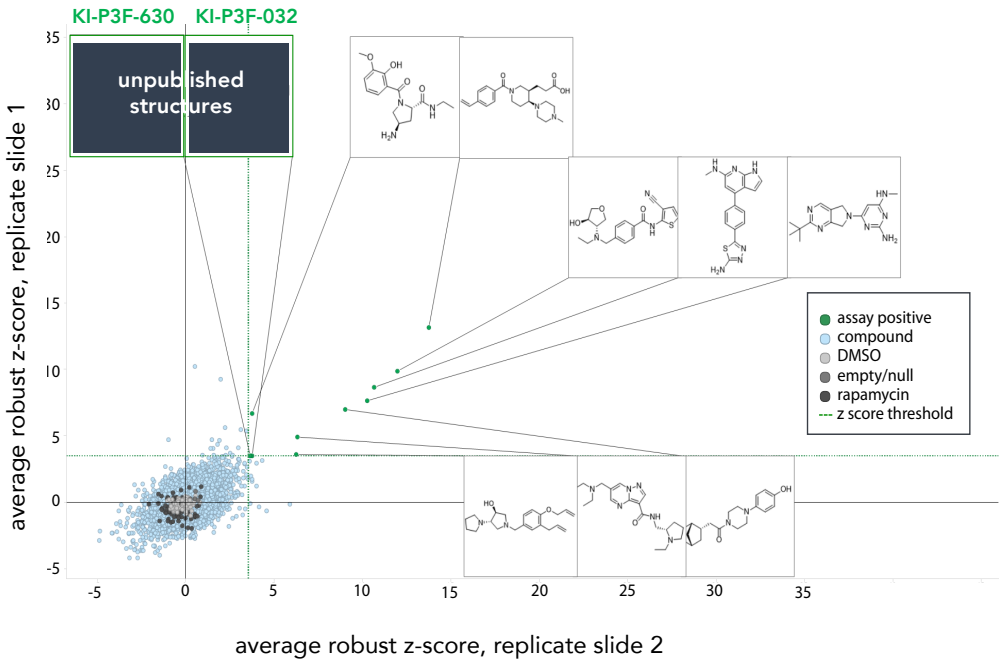
PAX3-FOXO1

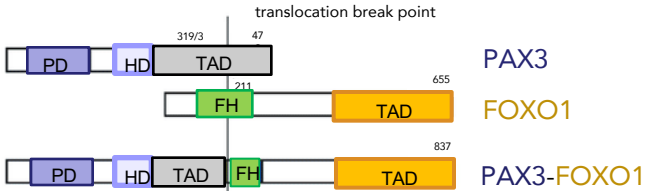
PAX3-FOXO1

pathognomic fusion in alveolar rhabdomyosarcoma

pathognomic fusion in alveolar rhabdomyosarcoma

SMM screening data for PAX3-FOXO1 from cell lysates



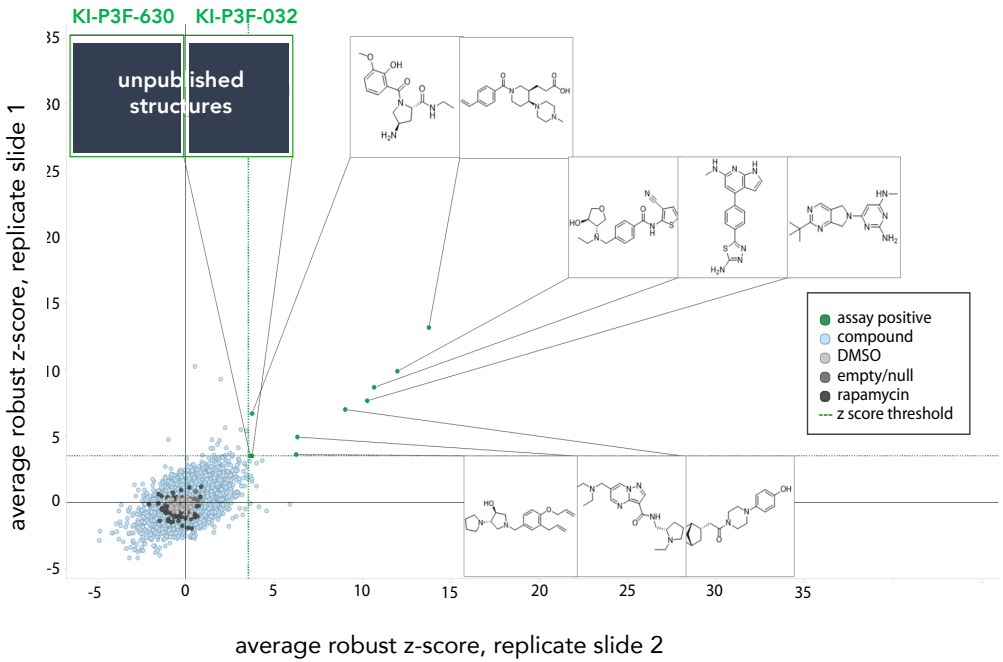


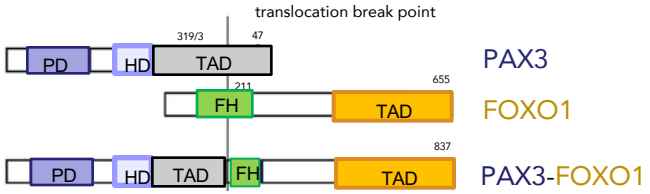
Shelby Doyle, Becky Leifer, Marco Wachtel, Beat Schaefer

PAX3-FOXO1

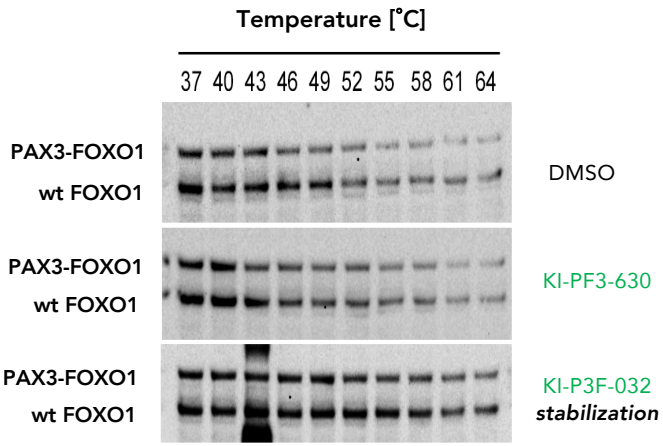
pathognomic fusion in alveolar rhabdomyosarcoma

SMM screening data for PAX3-FOXO1 from cell lysates





PAX3-FOXO1, FOXO1 CETSA



Shelby Doyle, Becky Leifer, Marco Wachtel, Beat Schaefer

Our path to finding ligands - lectures

2/5/20	Lecture 1	Intro to chemical biology: small molecules, probes, and screens
2/11/20	Lecture 2	Our protein target: TDP-43
2/13/20	Lecture 3	Small molecule microarrays
2/18/20	No Lecture	
2/20/20	Lecture 4	Quantitative evaluation of protein-ligand interactions
2/25/20	Lecture 5	A ligand discovery vignette: sonic hedgehog
2/27/20	Lecture 6	Engineering transcriptional responses with a small molecule
3/3/20	Lecture 7	Wrap up discussion: suggestions for how to report your findings