

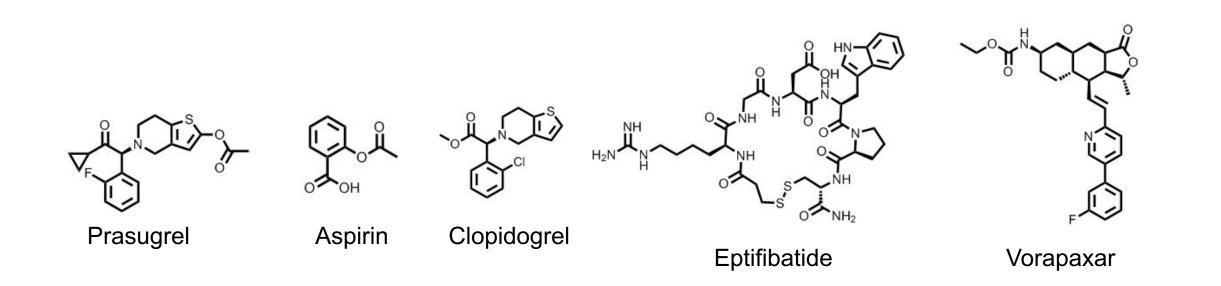
Miniaturization and Optimization of a Fluorescence Polarization Assay to Interrogate a Protein-Peptide Interaction

William Kuenstner¹, Adam Yasgar¹, Bolormaa Baljinnyam¹, Kyle Brimacombe¹, Ajit Jadhav¹, Kalyan Golla², Ulhas Naik², Anton Simeonov¹ ¹National Center for Advancing Translational Sciences, National Institutes of Health, Bethesda, MD 20892 ²Sidney Kimmel Medical College, Thomas Jefferson University, Philadelphia, PA 19107

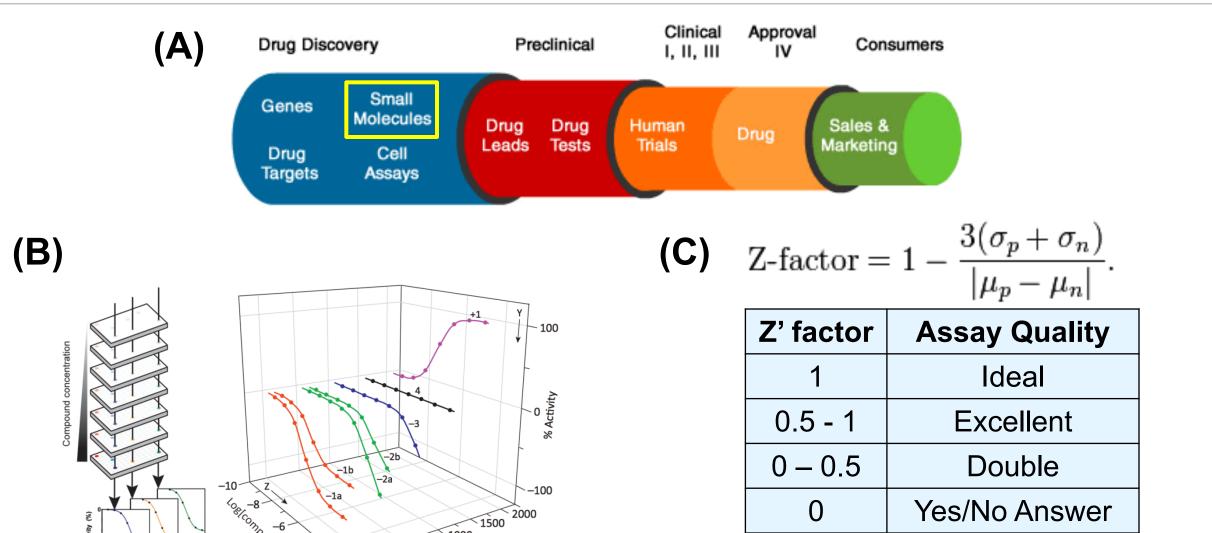
Therapeutic Significance

Cardiovascular diseases are the leading cause of death in America, accounting for 1 in every 4 deaths¹. Platelet plug formation has been implicated in many of these diseases, such as myocardial infarction and stroke. Current therapies (Prasugrel, Aspirin, Clopidogrel, Eptifibatide, Vorapaxar) are limited by drug side effects and resistance, as well as variability in patient response². Therefore, novel anti-platelet agents are needed. Our therapeutic target is a protein-peptide interaction (PPI) involved in modulating the formation of platelet plugs. Preventing this PPI with a small molecule holds promise as an anti-clotting therapy.

Current FDA Approved Anti-Platelet Drugs



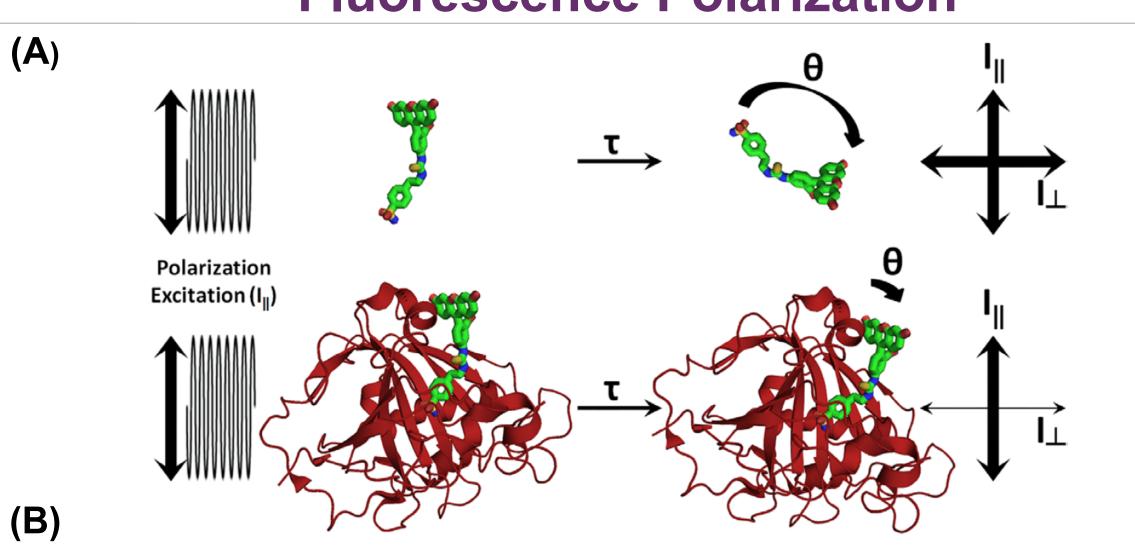
qHTS to Identify a PPI



(A) An overview of the drug discovery pipeline³. (B) A typical doseresponse curve generated from qHTS⁴. (C) A simple statistical parameter utilized in qHTS for assessing assay quality⁵.

Poor

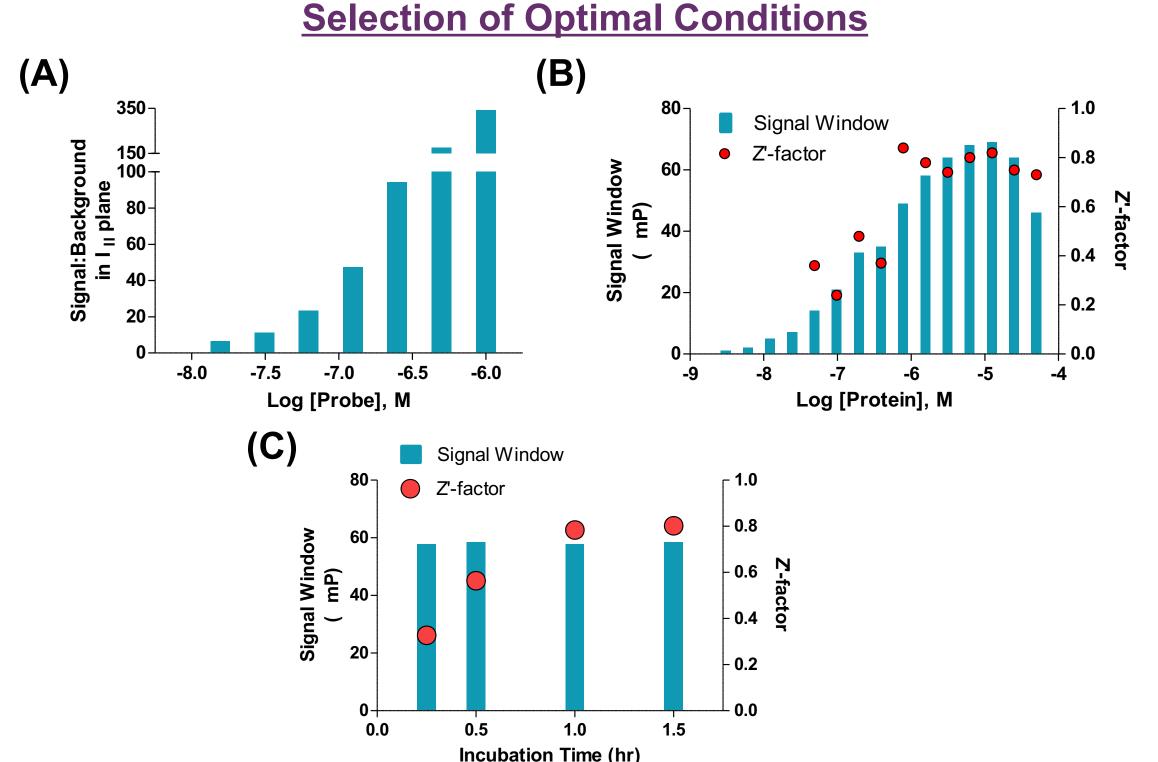
PPI Detection Method: Fluorescence Polarization



Molecular Weight of Probe	Rotational Speed of Probe	Predominant Emission Type
High	Low	Polarized
Low	High	Depolarized

(A) Polarized light excites a fluorescent probe whose emission intensity is measured parallel and perpendicular to the excitation plane. The degree of emitted fluorescence remaining polarized is indicative of a binding interaction⁶. (B) The conceptual relationship between the size of the probe complex and emission result.

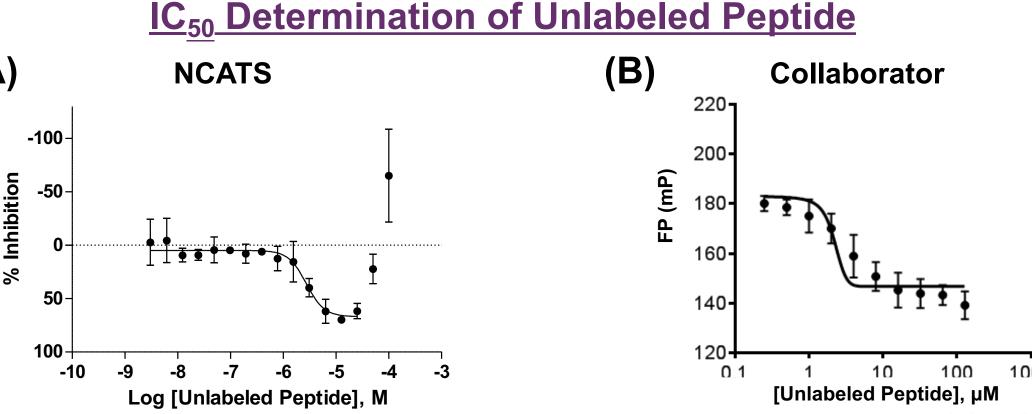
Assay Optimization in 384-well Format



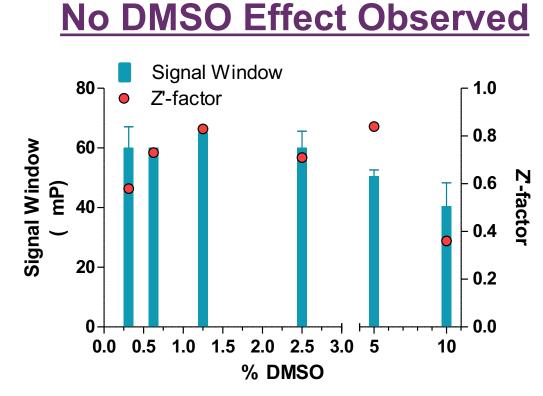
- (A) 25 nM [Probe] chosen due to exhibiting a strong S:B⁷.
- (B) 1 or 2 μM [Protein] selected to maximize Z' factor and signal window.
- (C) 1 hour incubation time (RT) selected to maximize Z' factor.

K_D Determination of the Protein-Peptide Interaction (D) Collaborator **NCATS** ◆ Scrambled Probe 175 │ ○ Scrambled Probe E 125-

- (D) To determine the K_D , protein was titrated against 25 nM probe (n = 3).
- (E) Collaborator K_D determination against 25 nM probe (n = 3).



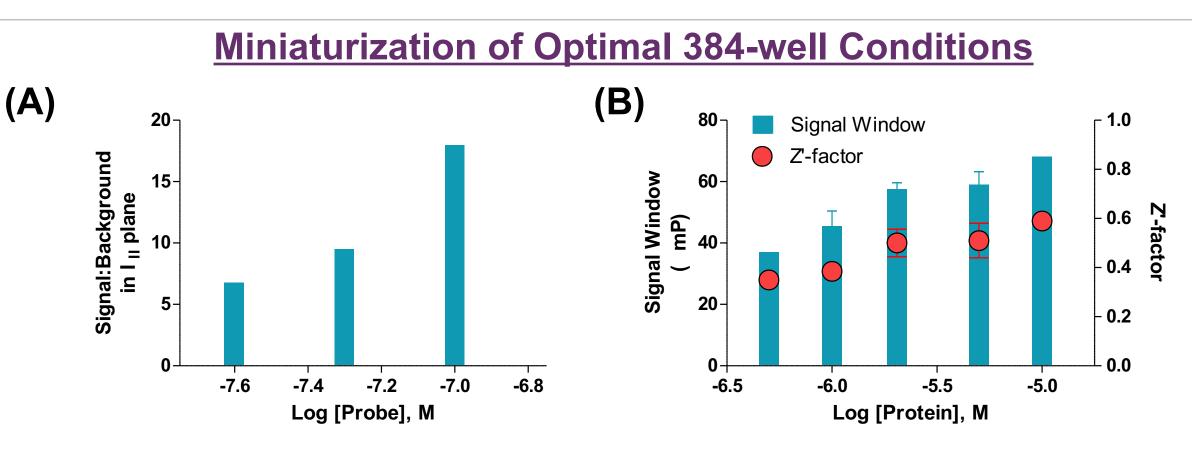
- (A) IC₅₀ value estimated at 2.7 μM due to artifacts seen at high concentrations (n = 3).
- (B) Collaborator IC_{50} determination of 2.2 μ M (n = 3).

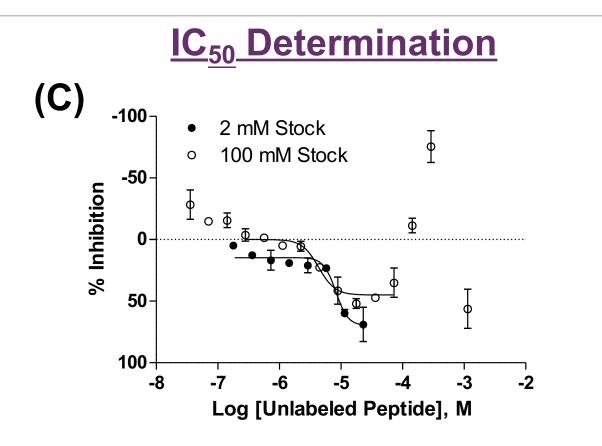


Comparison of Assay Parameters

	K _D Determination		Competition Assay	
Parameter	NCATS	Collaborator	NCATS	Collaborator
Assay Volume, µL	20	50	20	50
Incubation Time, hr.	1	0.25	1	0.25
[Probe], nM	25	25	50	100
[Protein], µM	Titration	Titration	1	2.5
[Unlabeled Peptide], µM	-	-	Titration	Titration
[IC ₅₀ Unlabeled Peptide], µM	-	-	2.72	2.20
[K _D Scrambled Probe], μM	1.63	5.68	-	-
[K _D Native Probe], μΜ	0.21	0.56	-	-
K _D Fold-Difference	8	10	-	-
			-	_

Assay Miniaturization to 1536-well Format





D)	Parameter	NCATS
	Assay Volume, µL	4
	Incubation Time, hr.	1
	[Probe], nM	100
	[Protein], µM	1.25
	[Unlabeled Peptide], µM	Titration
	[IC ₅₀ 2 mM Stock], µM	8.25
	[IC ₅₀ 100 mM Stock], μM	4.55

(A)-(B) Optimal conditions were selected using the same criteria described in 384-well format. (C) A competition assay similar to the experiment described in 384-well format. (D) Conditions of the competition assay.

Discussion and Next Steps

- Achieve full displacement of the probe in the 1536-well format competition assay.
- Perform overnight reagent stability tests for online robotic screen.
- Consider orthogonal methods to interrogate the PPI (e.g. AlphaScreen, Homogenous Time Resolved Fluorescence Assay).
- Screen small molecule libraries to identify small molecule inhibitors the PPI.
 - NCGC Pharmaceuticals Collection (~3,000 FDA approved drugs), Genesis Library (~70,000 compounds), MLSMR Library (~400,000 compounds).
- Utilize physiologically relevant cell-based assays to determine in vitro target engagement of small molecule inhibitors (e.g. Cellular Thermal Shift Assay).

References

1. CDC, NCHS. Underlying Cause of Death 1999-2013 on 2015. Data are from the Multiple Cause of Death Files, 1999-2013, as compiled from data provided by the 57 vital statistics jurisdictions through the Vital Statistics Cooperative Program. Accessed July 25, 2016. 2. Ferreiro, J.L. and Angiolillo, D.J. (2012). New Directions in Antiplatelet Therapy. Circ Cardiovasc Interv. 5,

- 3. http://tinyurl.com/zf8xdaj
- 4. Auld, D.S., et al. (2010) Understanding Enzymes as Reporters or Targets in Assays Using Quantitative High-Throughput Screening (qHTS). Experimental Standard Conditions of Enzyme Characterizations. Sept.
- 13-16, 2009. 5. Zhang, J.H. (1999) A Simple Statistical Parameter for Use in Evaluation and Validation of High Throughput Screening Assays. *J Biomol Screen*. 4, 67-73.
- 6. Hall, M.D., et al. (2016). Fluorescence polarization assays in high-throughput screening and drug discovery: a review. Methods Appl. Flouresc. 4, 022001
- 7. Banks, P. and Du, S. Understanding Fluorescence Polarization and Its Data Analysis. (2001). Perkin Elmer Life Sciences. Accessed July 25, 2016.