

ABSTRACT

Automated high throughput assessment of the kinase activity of lead compounds for optimization and selectivity assessment is essential for developing successful drug candidates. The typical high-throughput screen involves a primary assay of a huge number of compounds against a single target to determine lead hits that are then characterized further in selectivity and potency assays to validate and prioritize these hits as part of a drug discovery cascade. The primary assay and even the followup assays are typically run as an end point format to reduce the complexity. Determining the full-kinome selectivity profile for kinase inhibitors is a common need, but this can be very challenging since this requires the screening of lead compounds against hundreds of kinases run at different concentrations, with varying stability and that require different substrates or additives, as part of specific assay conditions including measuring inhibition at the ATP Km concentration for each kinase in the panel.

We will present the development of a semi-automated assay and then to fully automated assay workflow to address the complexity encountered with selectivity profiling. Using the PhosphoSens[®] continuous assay format for profiling provides a more robust and informative readout of the target biology (detection of any enzyme lag or instability) and inhibitor function (determination of initial and final reaction rates provides a more accurate assessment of inhibition and allows detection of time-dependent inhibition). This involves the automation of three types of samples: enzymes, substrates, compounds, and their individual properties and processing needs. It also involves new process development and the automation of unique liquid handling. New techniques for stability and solubility of the samples and reagents were paramount to achieve consistent and highly reproducible results. We will present data on full-kinase profiles of known specific and non-specific inhibitors validating the continuous assay format as well as the fully automated process.

THE PHOSPHOSENS[®] ASSAY – CONTINUOUS & ENDPOINT/RED FORMATS

A. Continuous (Kinetic), FI $\lambda_{ex max}$ = 360 nm

 $\lambda_{em max} = 485 \text{ nm}$ Cys

MANUAL



Add & Read Continuously

Peptide sequences are synthesized using solid-phase methods with the Sox fluorophore coupled through the sulfhydryl group of a cysteine residue proximal to a protein kinase phosphorylation site, such as a tyrosine, serine or threonine. Upon addition of a kinase, the peptide is phosphorylated. In the presence of magnesium ion, a chelation complex is formed with the phosphate group, resulting in fluorescence enhancement of the Sox fluorophore that can be monitored continuously as fluorescence intensity (A). Kinase inhibitors prevent phosphorylation and thus fluorescence. At any point, Europium ion can be added, to displace the magnesium ion, resulting in a long wavelength, time-resolved fluorescence (TRF) endpoint/Red format (B) that is useful for high-throughput or structure activity relationship (SAR) applications.

THE ASSAY

Reaction Conditions: 54 mM HEPES, pH 7.5						Reaction Set Up: 2 μL 10X Sox-based substrate												Reaction Conditions				
1 mM ATP 1 mM AMP ⁴ 1 μM t-RNA ⁶ 1X DNA-PK Activator ⁷ 1.2 mM DTT ⁹					2 1	 2 μL DMSO (10%) or Compounds (C μM in 10% DMSO) 12 μL Reaction Mix with ATP & DTT ⁹ 												1 mivi ATP 1.2 mM DTT ⁹ 0.012% Brii-35				
					<u>3</u> (4	<u>30-minute</u> pre-equilibrate at RT <u>4 μL 5X</u> Enzyme dilution buffer or 5X Kinase in EDB													0.5% 0.2	% glyce mg/m	erol I BSA	
0.012% Brij-35 0.5% glycerol							OR if	[:] nee 2 μL 1	ded LOX F	depe PS/D/	ndin AG/C	g on k a ³	kinas	5					0.5 10 r	mM E0 nM M	GTA ² gCl ₂	or
0.2 mg/ml BSA	2						• 2	2 μL 1		AMP	4 5								10 0	or 15 µ	M So	x-ba
10 mM MgCl ₂	or 2	20 MgC	21 ₂ 5				• 2	2 μL 1 2 μL 1	LOX I LOX t	rigCi _: RNA:	6								1% Νμ	M com	npoun	ıd, oı
10 mM KCl ¹ 140 µM Phosp	or 50 hatidv	mM K Iserine	Cl ⁸				• And	2 μL 1	LOX [DNA [:]	,								Kina	ase as	indica	ted
3.8 µM Diacylg	glycero) ³	-				2 μL	5X E	nzyn	ne dil	utior	า buff	er (El	DB)	adde	ed to	all					
10 or 15 μ M So	ox-bas	ed sub	strate	S			odd to al	numi Leve	bere n nu	a rov mbei	vs an red ro	a 10x ows	. Kina	ise II	n ed	B ad	aea					
1% DMSO N uM compou	nd. or	1% DN	/ISO																			
Kinase as indic	ated	_,			2	0 μL	Final	reac	tion	volui	ne rı	un at i	30°C	for 2	120	minu	tes.					
 Notes: Enzyme Dil 1 mg/ml Be 	ution ovine :	Buffer Serum	(EDB) Albun	: 20 m nin is a	nM HI addeo	EPES d to a	, pH ∄ all od	7.5 <i>,</i> 0 d nu).01% mbe	6 Brij red r	-35, s ows.	5% Gl	ycero	ol, 1	mM	DTT	9		<u>Not</u> •	<u>es:</u> Enzym 1 mg/	ne Dili ml Bo	utior ovine
Reactions	were r	un in P	Perkin	Elmer,	Prox	iPlate	e-384	l Plus	s, wh	ite s	nallo	w we	ll mic	ropl	lates	(Cat	•		•	Reacti	ons w	vere
#6008280) PerkinElme (360 nm) a	after er [Cat nd em	sealing . #6050 nission	g using 0185]) (485 r	; optic in a E nm) wa	ally-c Biotel avele	clear k Syn ength	adhe ergy s.	Neo	film 2 mi	(Top: crop	ate r	-Plus eadei	plate with	e sea n exc	al, citati	ion				NBS m plate s excita	hicrop seal, F tion (3	olates Perki 360 i
 Special Con PKC Family BCKDK ,⁹ 	n ditio , ⁴ Onl no DT	ns: ¹ O y for A T for N	nly for MPK F 1AP3K	PDHk amily 6 (ASK	<1-4 , , ⁵ Oi <2)	2 No nly fo	o EGT or RIF	<mark>А for</mark> РК1,2	[•] CaN ,3, 8	ИК Fa ٤5,6	mily for G	or PK iCN2,	C Far 7 for	nily, DN/	³ Oi A-PK	nly fo , ⁸ fo	or or		•	Specia PKC Fa BCKDI	al Con amily, < , ⁹ r	ditio ⁴ Or no D ⁻
Fig-1 Enzym	ie Posi	tion:	2	2		^	_	6		7	0	0		10	11		12	 T	he	diff	fere	٥nc
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The red squares above highlight 4 wells with 1 compound tested in two conditions in duplicate.

54 mM HEPES, pH 7.5	2 μL 1
1 mM ATP	2 μL D
1.2 mM DTT ⁹	2 μL V
0.012% Brij-35	
0.5% glycerol	
0.2 mg/m bsa	
10 mM MgCl ₂ or 20 MgCl ₂ ⁵	
10 or 15 µM Sox-based substrates	
1% DMSO	
N μ M compound, or 1% DMSO	
Kinase as indicated	
	10 uL
	<u>5-min</u>
	4 μL 5
	numb
	amun
Notos	20 µL
Enzyme Dilution Buffer (EDB): 20 r	nM HFF
1 mg/ml Bovine Serum Albumin is	added
Reactions were run in Corning, lov	v volum
NBS microplates (Cat. #3824) after	sealing
plate seal, PerkinElmer [Cat. #6050	J185]) (485 pm
	405 111
Special Conditions: ¹ Only for PDH DKC Family, ⁴ Only for AMBK Family	K1-4, ⁴
BCKDK ⁹ no DTT for MAP3K6 (AS	у, ^с Опі к2)
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he differences betwee	n ma
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Manual assay was ful	
micro-centrifuge vial	s. Fig
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Semi-automated assa	iy to
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anual and semi-automated: 384-w plates from strips of g-1 shows the plate layout. bok advantage of identical nts of the 384-w plate except for se and dilution buffer. An intermediate 96-w plate was used to combine the components of the assay including the compounds and then compressed into the 384-w assay plate. The final addition is then done from 96-w kinase and buffer plates nto the assay plate to start the reaction. Fig-2 shows a progress curve in every well. Odd rows are blanks with only EDB added and even rows are reactions with enzyme. The pre-equilibrate step was reduced from 30-min to 5min and temperature increase from RT to 30°C. This helped reduce the noise at the start of the reaction. The ProxiPlate Plus (10 - 20 μL working volume) was replaced with Corning (5 - 40 μ L working volume) improving the accuracy of the assay (final volume 20 μ L)

by reducing liquid overflow and sealing issues.

Automation of Full-Kinome Profiling Using a Continuous Kinase Activity Platform





ered rows Final reaction volume run at 30°C for 120 minutes PES, pH 7.5, 0.01% Brij-35, 5% Glycerol, 1 mM DTT to all odd numbered rows.

e 384-well, white flat round bottom polystyrene g using optically-clear adhesive film (TopSealA-Plus n a Biotek Synergy Neo 2 microplate reader with n) wavelengths. No EGTA for CaMK Family or PKC Family, ³ Only for

for RIPK1,2,3, & 5 , ⁶ for GCN2, ⁷ for DNA-PK , ⁸ for

The validation method involved using a full Kinome Profile with ~ 380 Wild-Type Kinases in 32 x 384-w assay plates. Staurosporine was used as a control at $1 \mu M$ final concentration. The manual assay was run directly into PE 384-w assay plates and the semi-automated assay was run using Biomek i7 Hybrid.

The method was run in a 96-w intermediate plate up to the Kinase addition step. Then the plate was compressed into a Corning 384-w assay plate and kinase was added to start the reaction. Each 4 wells (for example A1,A2,B1,B2) have the same compound. See Fig-1 and Fig-2. The manual assay was run N=2 and the semi-automated was run N=3. Both assays were read for 120 minutes in a kinetic continuous assay to monitor enzyme activity. The reading was done in Synergy Neo2 reader by **Solution** Regilent Technologies



Staurosporine will inhibit more than 200 of the ~380 tested wild-type kinases. % Inhibition was calculated and plotted in Fig-3 with average % Inh of N1 and N2 in the X-axis and both N1 & N2 in the Y-axis. The residual plot of both % Inh is below that. The data clearly show that manually, the kinome profiling assay was precise. The same was done to the % Inh data generated by the semi-automated system. Fig-4 showing average % Inh of N1, N2, & N3 and all replicates in the Y-axis. The residual plot of all % Inh replicates is below that. The semi-automated system is as precise as the manual run. Finally, the average % Inh of the manual run and the % Inh of the semi-automated run in Fig-5 show a very good correlation between the two systems, demonstrating the accuracy of the semi-automated system. All replicates were run on separate days.



Ziath Mirage 2D Tube Rack Barcode Scanner⁄ Agilent Vspin with auto-loader Micronic Screw-Cap Recapper CS700 A4S sealer on pull-out shelf -Multidrop Combi on pull-out shelf Multidrop Combi NL on pull-out shelf

- further by using full automation.
- projected AssayQuant Technologies growth.

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IMPROVED CURRENT THROUGHPUT AND FUTURE THROUGHPUT





Our current semi-automated capacity of 84 compounds/month (or an average of 20 plates/day) has been established by the automation team. While Fig-6 shows that we have completed a record 102 compounds in December 2022, that is only sustainable for the short term. The goal is also to provide full kinome results in 3 days which will require a multifaceted approach.

Fig-7 Shows three improvements to enable full automation:

Sample management and data analysis software provided by Scigilian's Store and Analyze. 2. Automated storage and retrieval managed by SPT Labtech's arktic[®] -80°C freezer. 3. Automated profiling run on Biosero's fully automated system with GBG dynamic scheduler. > But most important of all are the people at AssayQuant Technologies managing the automation. The theoretical throughput of 1 fully automated system assuming 3 assay plates/hour (due to liquid

handling limitation) is 260 compounds/month (60 assay plates/day). In order to achieve the estimated throughput of ~150 compounds/month in June 2023 as shown in Fig-8, we need to be able to run ~35 assay plates/day. To sustain this throughput, we need to run under 75% capacity and invest in redundancy and backup processes. The system also need to be scalable.

Investing in multiple fully automated systems, additional automated storage and retrieval capacity, more efficient processes that adhere with Lean Six Sigma principles, and highly skilled people will help the automation team meet AssayQuant Technologies projected growth. Additionally, investigating in new technologies like acoustic dispensing, 1536-w plate formats, assay miniaturization, and faster fluorescence readers, will help meet future needs in Kinase Profiling.

SUMMARY

✓ The information rich Full-Kinome Profiling assay was successfully converted to a semi-automated system including improved Full Kinome Profile of Staurosporine at 1 μM final concentration sample management and assay analysis. The semi-automated system and new assay was validated by using a promiscuous standard, Staurosporine, and comparing multiple manual runs to multiple semi-automated runs.

Y The manual assay was modified to allow for better and more efficient processing and automation.

✓ The manual throughout was increased from 14 to 84 compounds/month by using semi-automation and will be increased

Redundancy in automation, efficiency in processing, and adapting new technologies will improve the chances of meeting

✓ Most importantly, having the team's dedication and support at all levels helped achieve our automation goals.



