KinomeView™ to Serine/Threonine PhosphoScan® Proteomics

Step 1: KinomeView™ Study Design

KinomeView is western blot analysis with a set of 17 Phospho-Motif antibodies plus control antibodies to measure phosphorylation profiles in a kinome-centric manner and to guide PhosphoScan study design.

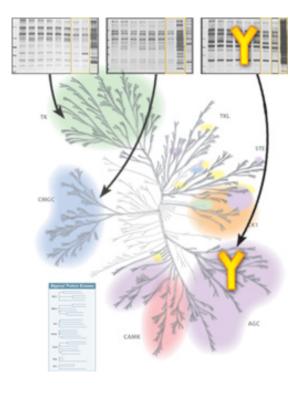
- 1. Study design begins with a teleconference or meeting with you to discuss how to apply KinomeView to the biology or chemistry under investigation.
- 2. KinomeView explores experimental parameters, including cell system, treatment doses and time points for PhosphoScan study design.
- 3. KinomeView control antibodies are included to measure experimental system-specific markers.

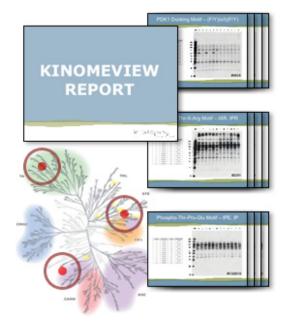
Step 2: KinomeView™ Analysis

- 1. For each of your sample sets, CST generates 19 western blots: one for each of 17 Phospho-Motif antibodies plus 2 positive control antibodies relevant to your experimental system.
- 2. KinomeView produces high-resolution western images.

Step 3: KinomeView™ Report and Consultation

- 1. KinomeView images are delivered as a report and as slides, along with specific recommendations for PhosphoScan studies and experimental parameters for analysis.
- 2. After you receive the report, CST scientists will review with you the KinomeView results, and discuss next-step PhosphoScan study design
- 3. KinomeView studies are completed in 2–4 weeks, and large comprehensive studies can be accommodated.





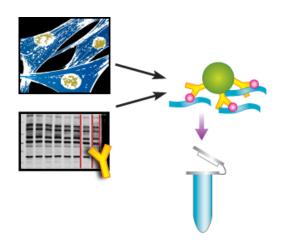


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Step 4: PhosphoScan® Proteomics Service Planning

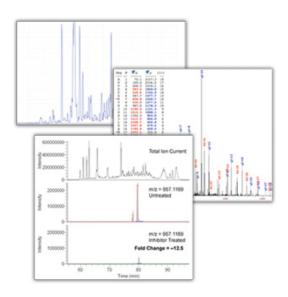
Next, the proteins and phosphorylation sites that showed pattern differences in KinomeView are identified by PhosphoScan, through immunoaffinity purification of phosphopeptides and mass spectrometry.

- 1. We will discuss with you the optimal PhosphoScan study design before you prepare samples.
- 2. We will also discuss with you and recommend quantification options to measure differences in phosphorylation resulting from sample treatments.
- 3. Planning includes coordinating our schedule for sample preparation and analysis with your project schedule and deadlines.



Step 5: PhosphoScan® Proteomics Analysis

- 1. Samples shipped to CST are validated by western blot with designated Phospho-Motif antibodies before starting PhosphoScan.
- 2. Samples are processed to protein extracts, which are digested with proteases and fractionated.
- 3. Whole proteome peptide samples are treated with the Phospho-Motif antibodies, chosen based on KinomeView, to enrich phosphorylation sites that caused pattern changes.
- 4. Enriched phosphopeptides and phosphorylation sites are identified by mass spectrometry (LC-MS/MS) analysis.
- 5. Treatment induced changes in phosphorylation levels are measured by either label-free or isotope-labeling (SILAC) quantification.



Step 6: PhosphoScan® Report and Consultation

- 1. PhosphoScan identification and quantification results are delivered as a report, which includes interpretation and recommendations by CST project scientists.
- 2. We provide a spreadsheet file listing peptide sequences and phosphorylation sites along with protein function and classification. We also provide detailed guidelines to help you mine the table.
- 3. After receiving the report, you will meet with CST scientists to review and discuss the PhosphoScan results.
- 4. PhosphoScan projects are completed in approximately 5 weeks. Preliminary results are sent at 2–3 weeks.



