

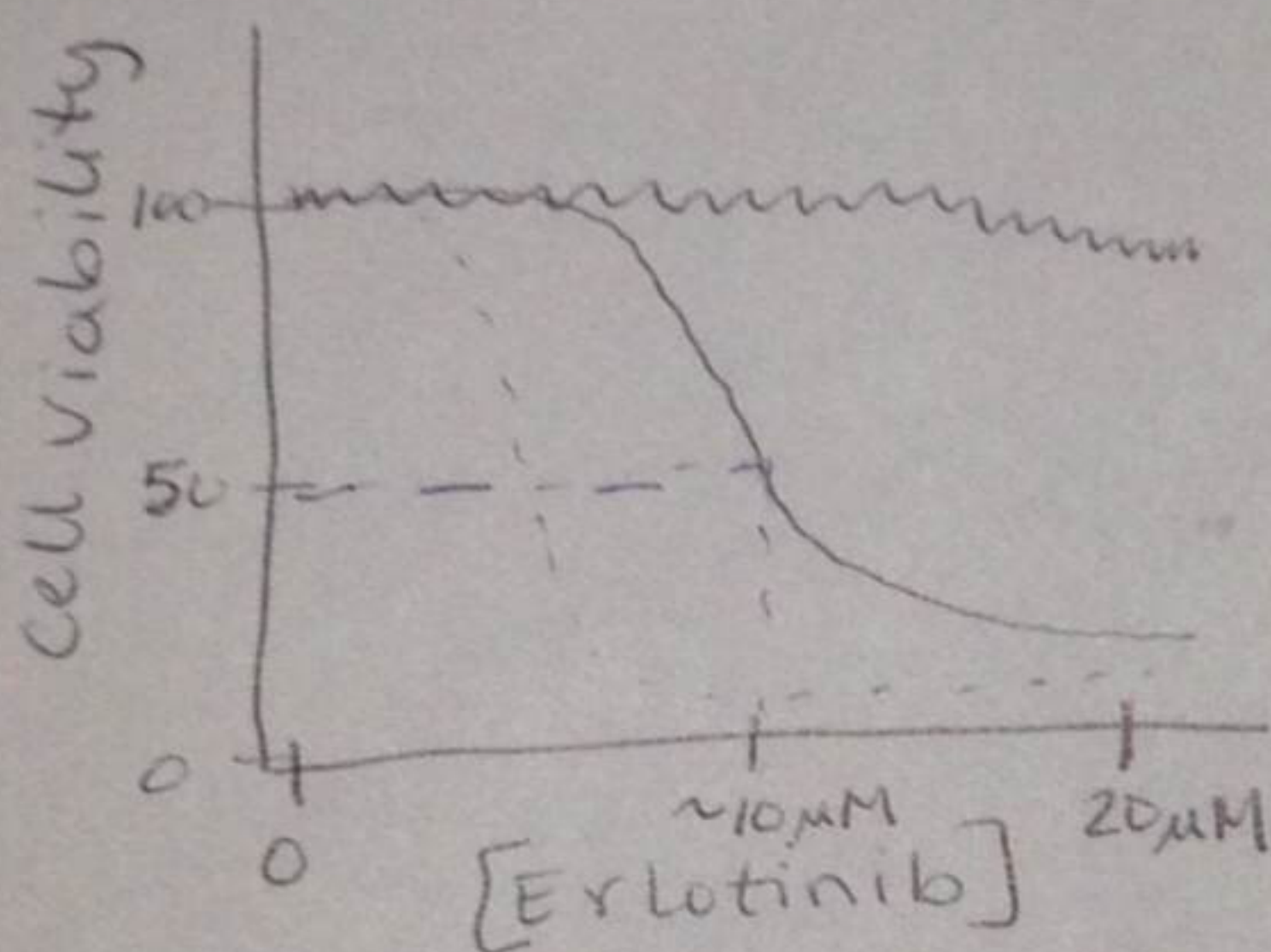
① System \rightarrow SKOV3 ovarian cancer

- Why? 60% o.c. EGFR

- EGFR inhibitors are unsuccessful in the clinic alone

- The mutation rate in ovarian cancer is low $< 5\%$ \Leftarrow "easy" to check

② Biological Question/Design challenge



----- "sensitive" cells

———— "normal" cells

~~~~~ SKOV3

@ 50%  $\left\{ \begin{array}{l} IC_{50}(\text{normal}) \approx 10 \mu\text{M} \\ * \text{could be lower} \end{array} \right.$   
EC<sub>50</sub>

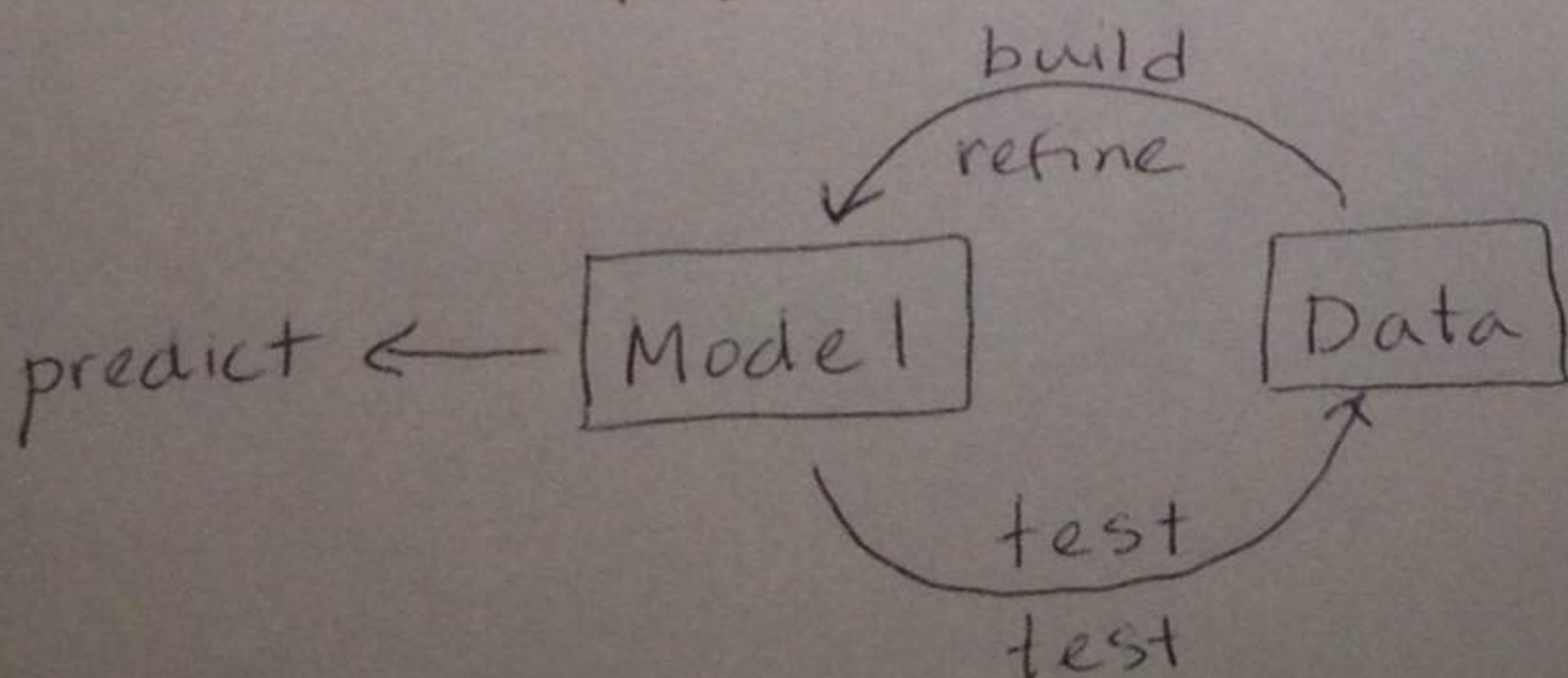
③ How can we use a "systems biology" approach to increase effectiveness of EGFR inhibitors?

What is "systems biology"?

- Network view vs. favorite protein/gene

- quantification/analysis  $\Rightarrow$  modeling

- lots of data needed





④ We use a "simple" ODE model to make a prediction  $\Rightarrow$  we will test our prediction on MZD7

⑤ In the ~~meat~~ meantime: Let's arm ourselves with more data?

What can facilitate resistance?

① Mutation ✓ (we tested for highest probability)  
↳ conclusion  $\rightarrow$  no mutation in EGFR

② Alternative signaling pathways

EGFR:  $\sim 260K$

HER2:  $1.4M$

HER3:  $\sim 14K$

} What do we know about this?

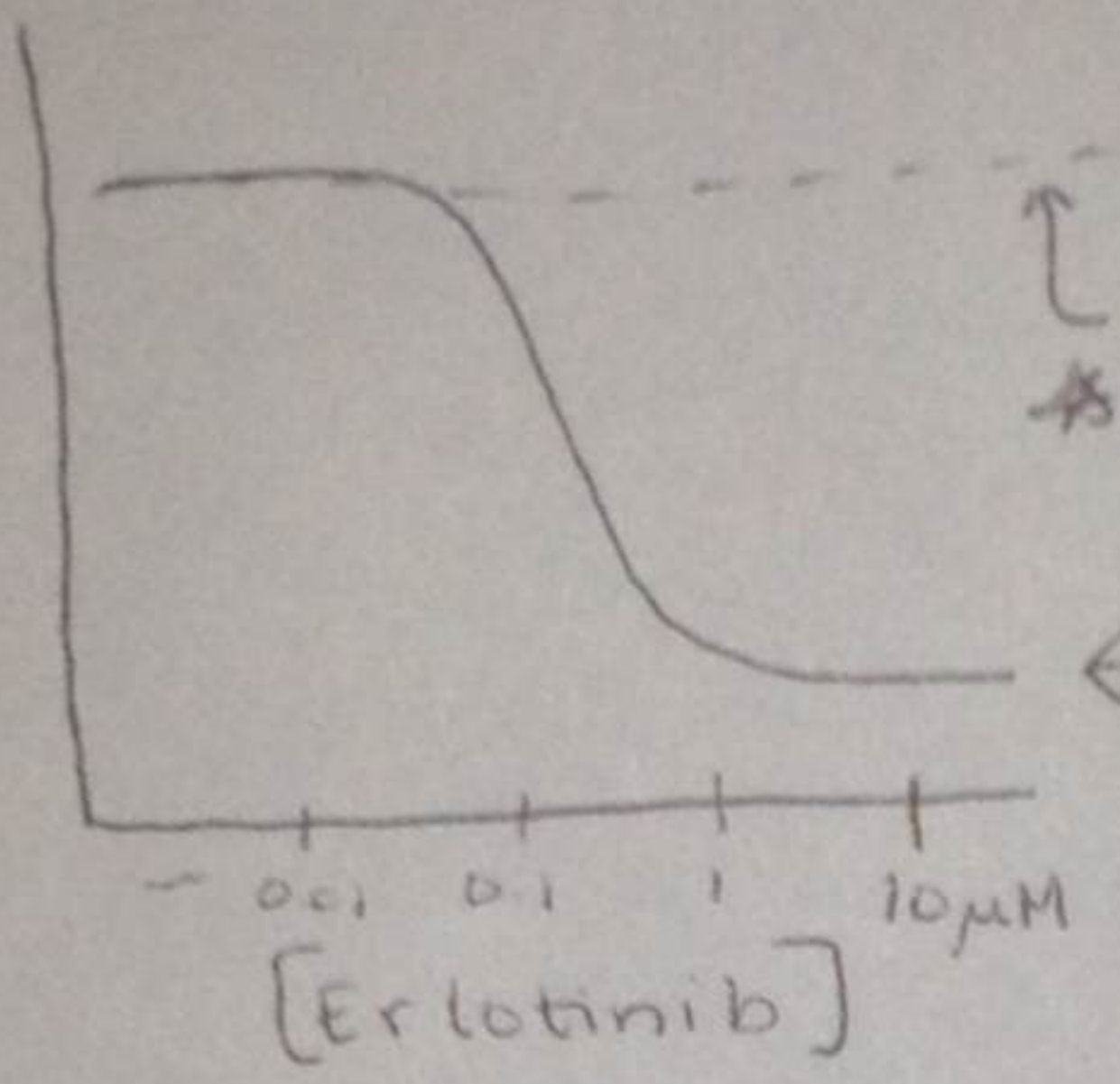
Look at pAKT, pErk & pSTAT3 after Erlotinib treatment

\* go to slide



⑥ Can we make predictions?

PY1068-EGFR

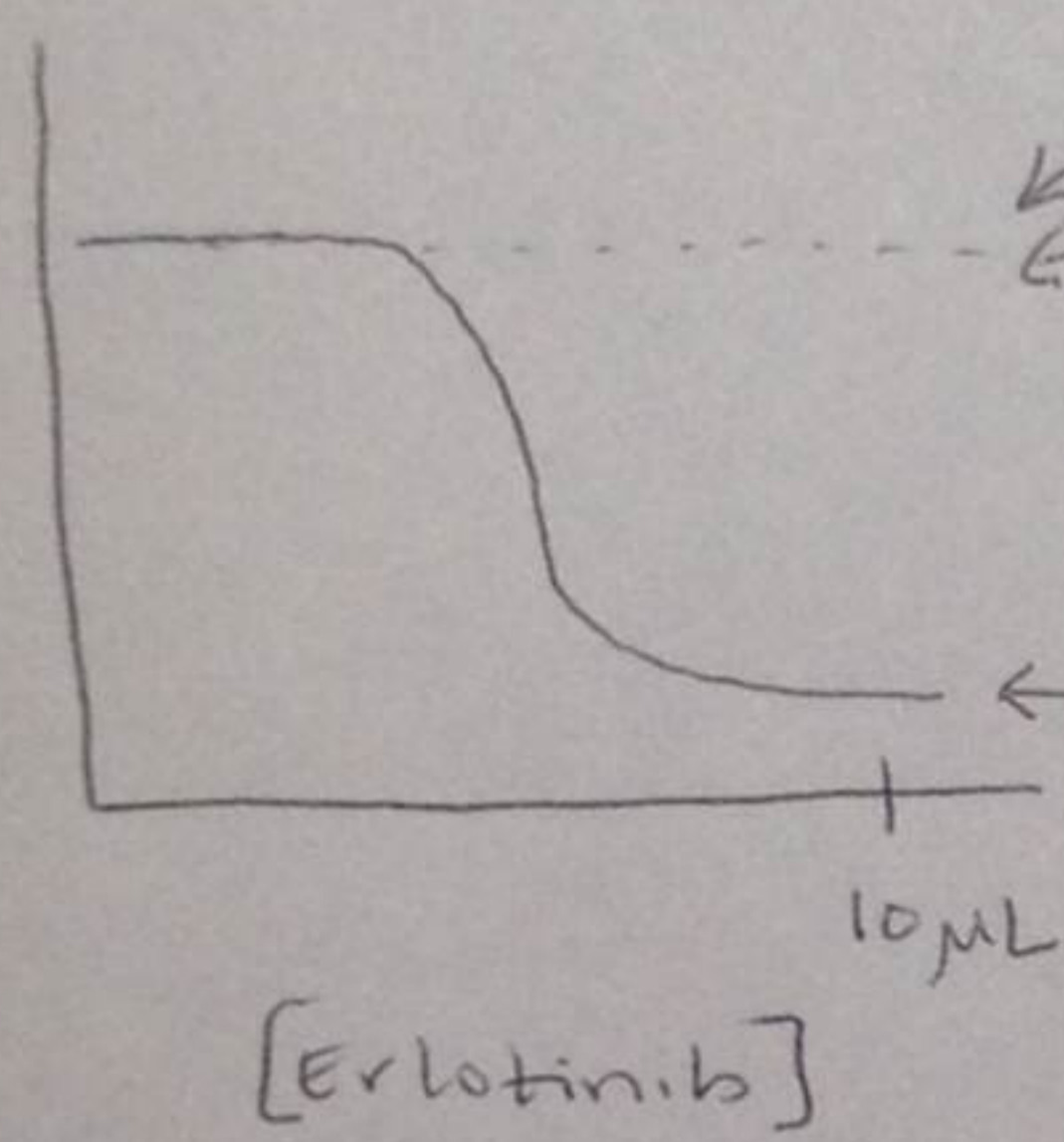


\*What do you think will happen?

Is this likely? } No

← "normal" response

pT202/Y204 Erk



← mutation in pathway? } compensatory signaling?

... and so on

← "normal" response

\* return to lecture here

⑦ What if they are all the same? ← Next time



# Module 2: Systems Engineering (M2D5)

- In-depth about goals of Module 2 -- how does it all fit together?
- Scale it up!
- Talk about next time in lab: wiki pages done Saturday.
- Journal club!



# Module 2 overview:



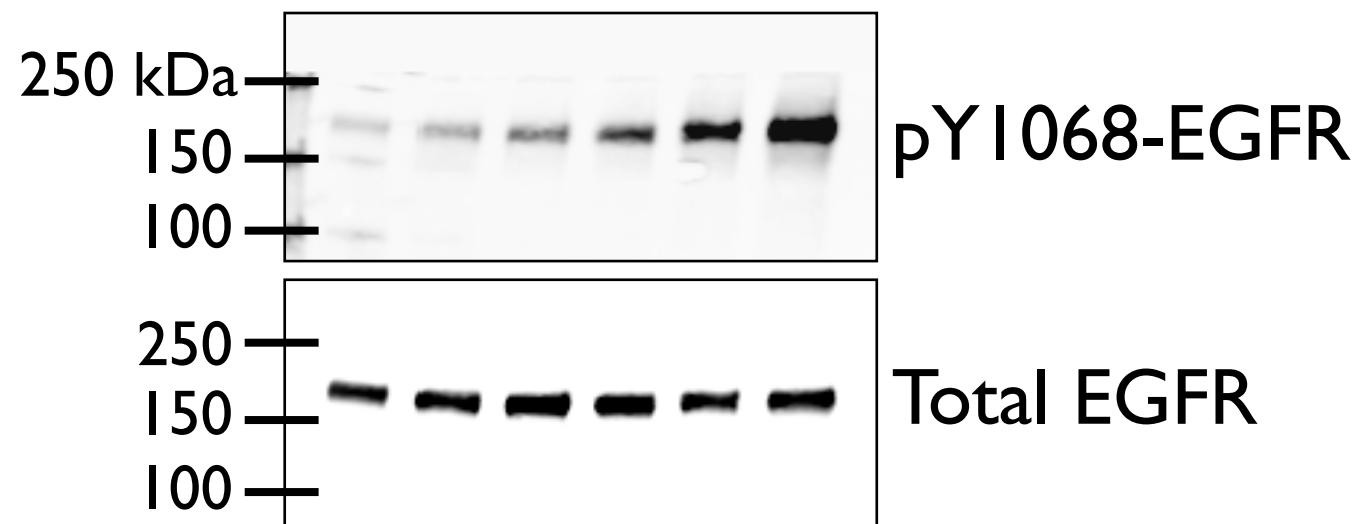
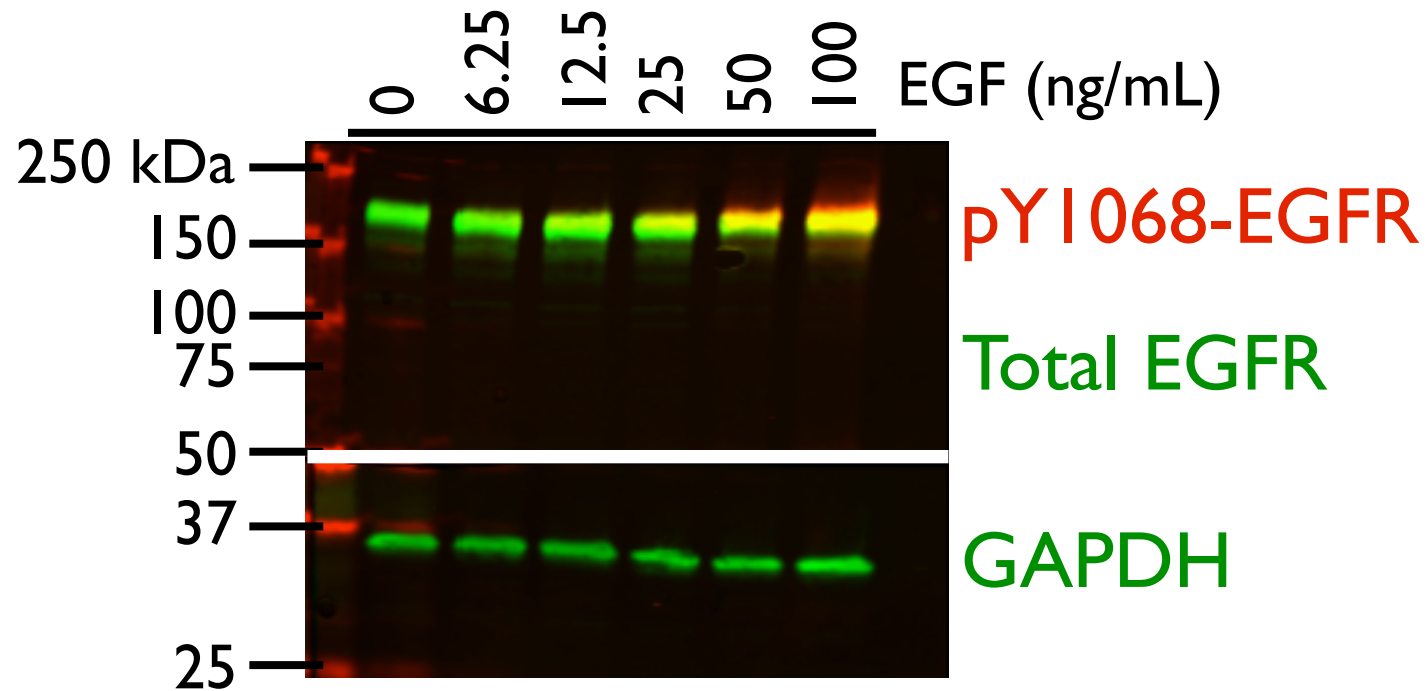
# Module 2 overview:



# Module 2 overview:



# Semi-quantitative analysis: Western blot

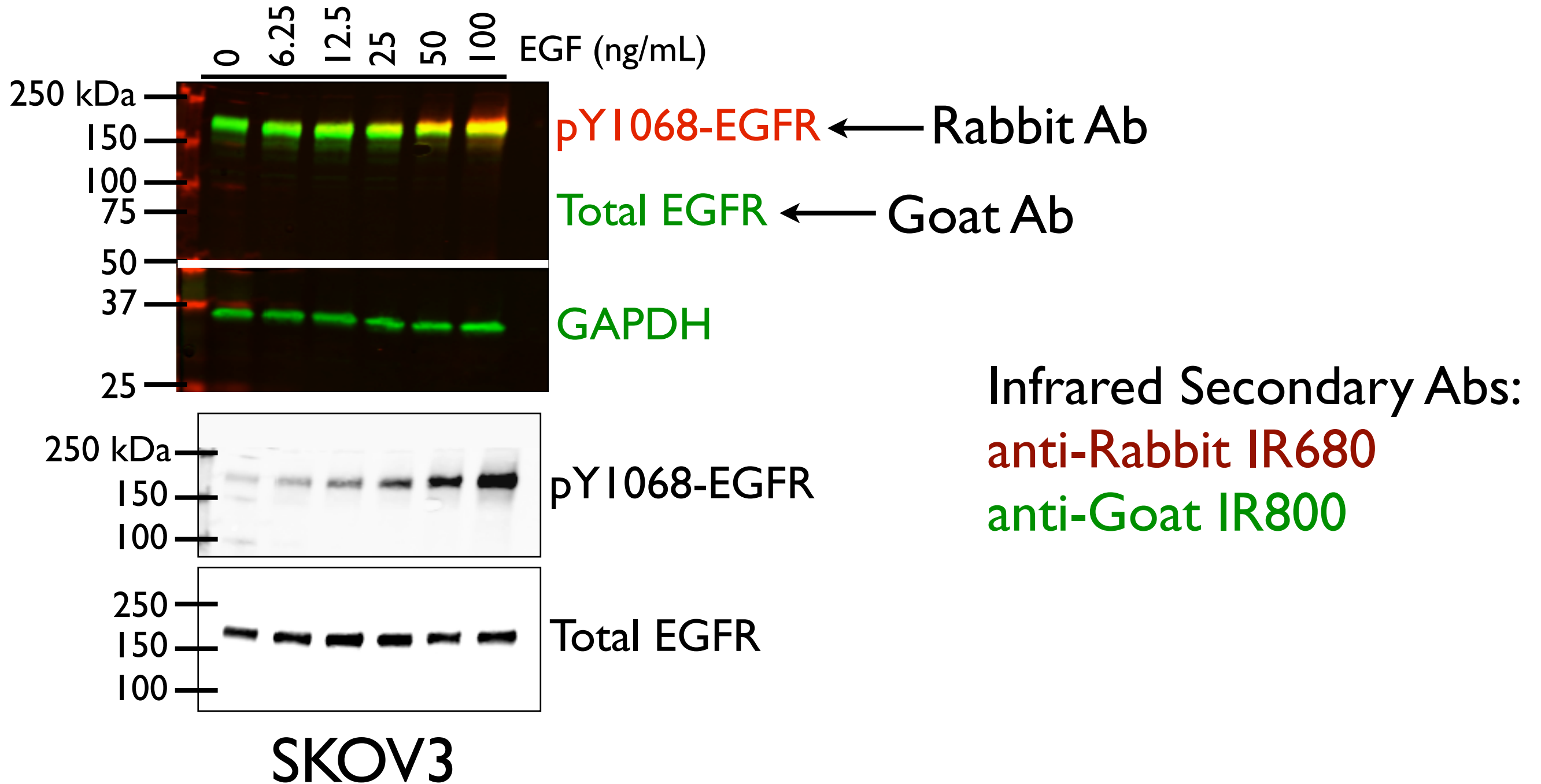


SKOV3

A few signals per lane -- up to ~17 lanes per mini gel.



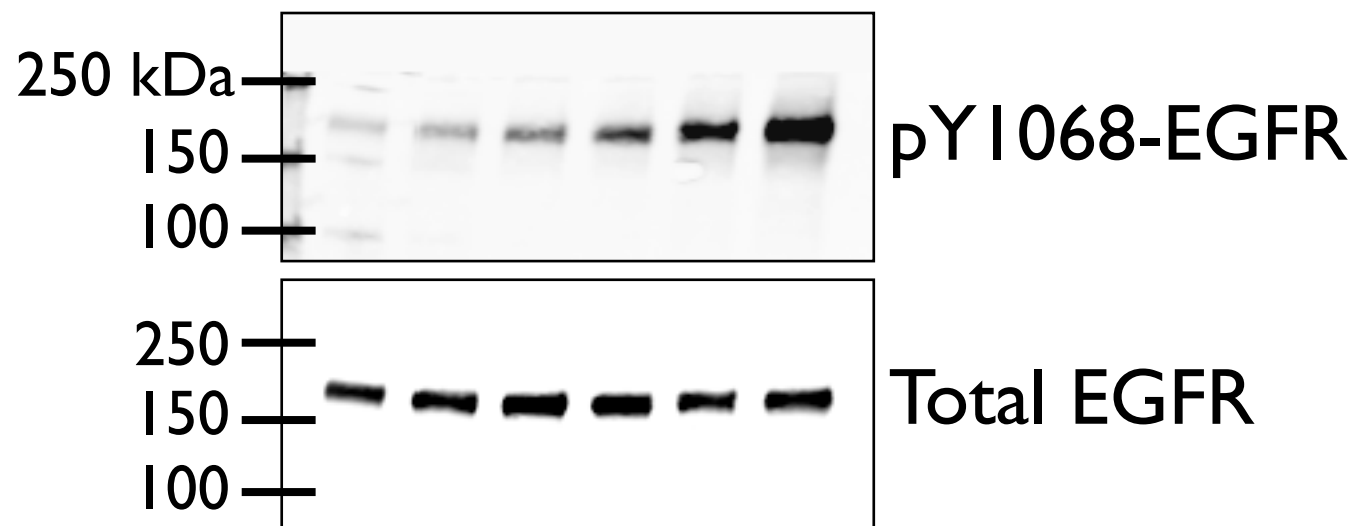
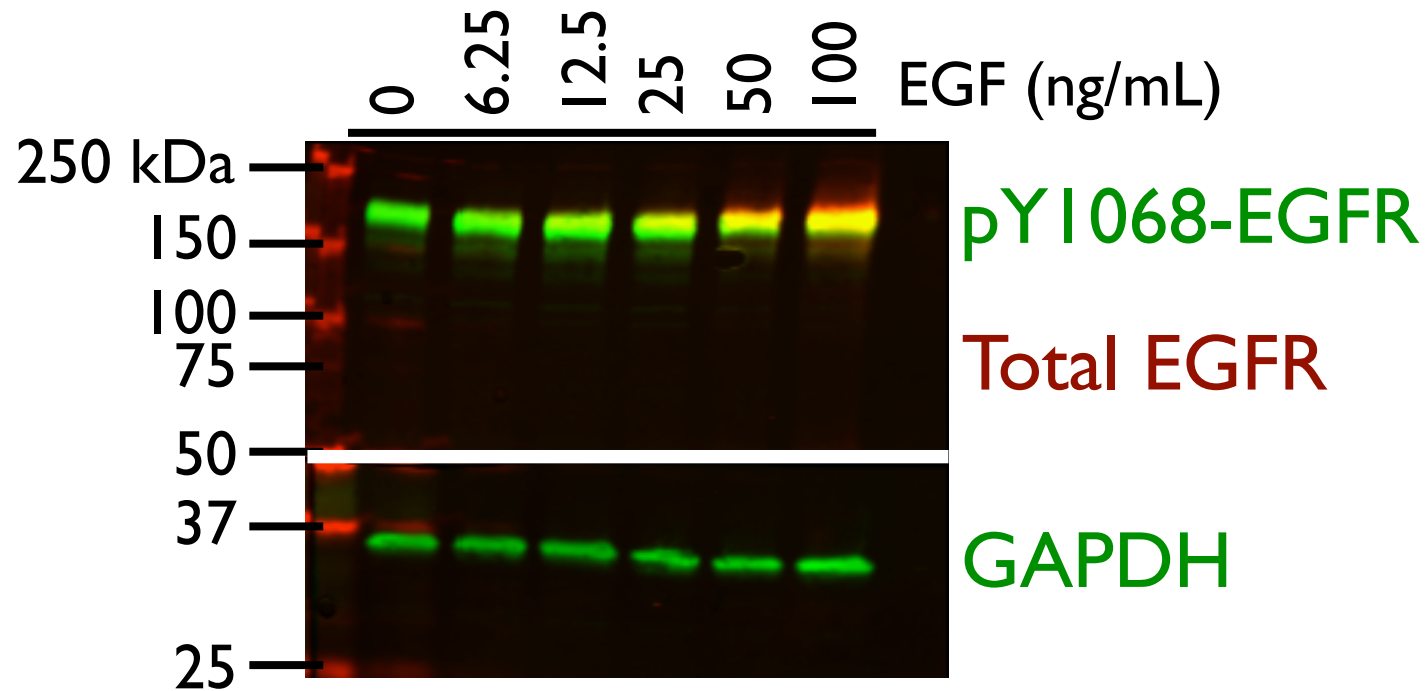
# Semi-quantitative analysis: Western blot



A few signals per lane -- up to ~17 lanes per mini gel.

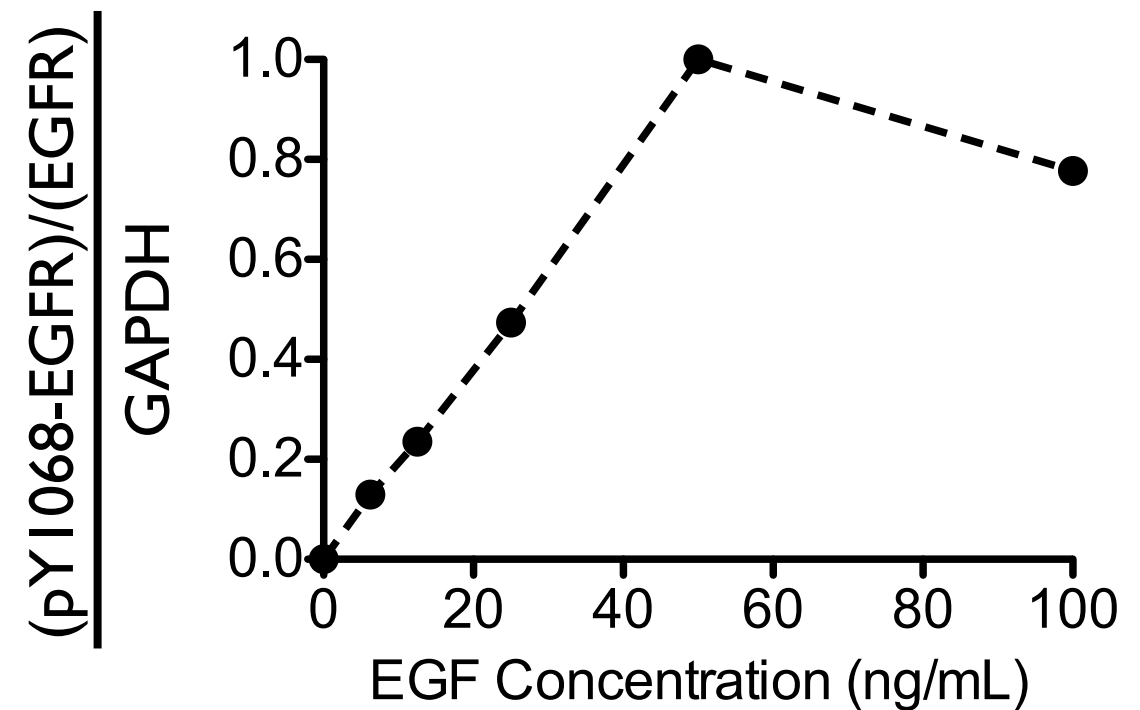


# Semi-quantitative analysis: Western blot



SKOV3

## Densitometric Analysis



A few signals per lane -- up to ~17 lanes per mini gel.



# Semi-quantitative analysis: Your experiment

1. All: pY1068-EGFR & Total EGFR

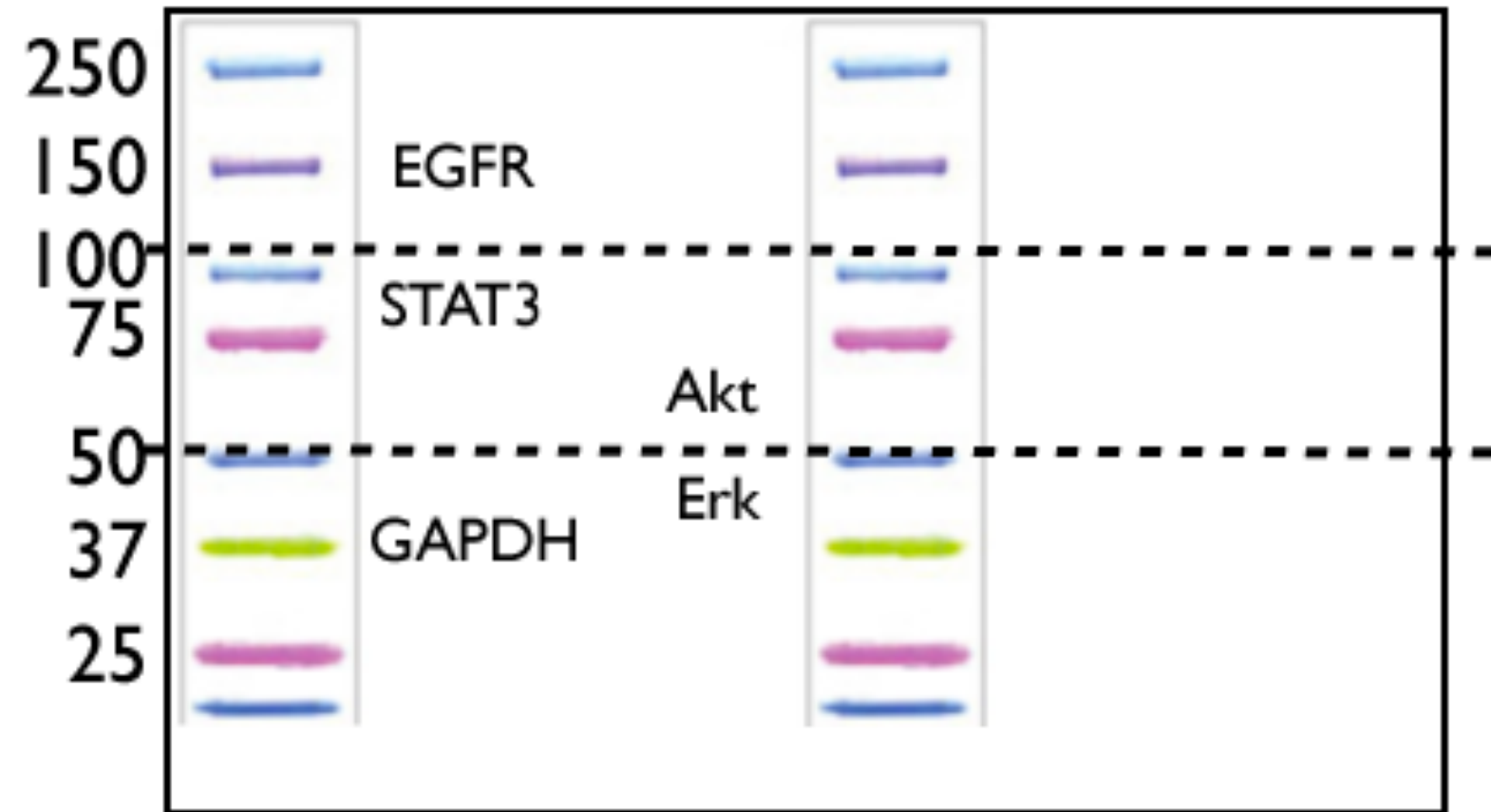
2. Pathway specific:

pERK & Total ERK

pAkt & Total Akt

pSTAT3 & Total STAT3

\*Last two + GAPDH

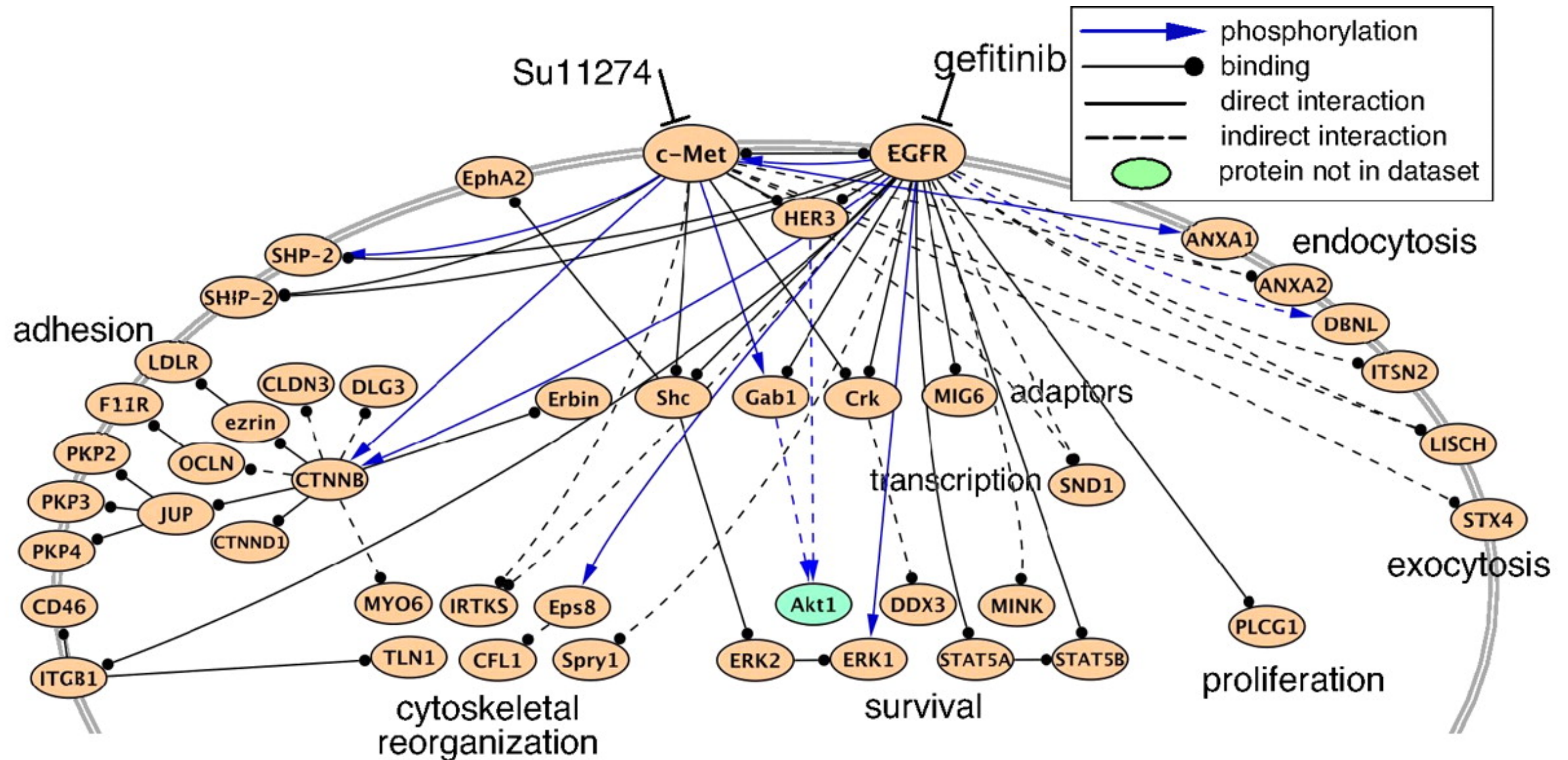




# Semi-quantitative analysis: Your experiment



# What if we wanted a broader network view?



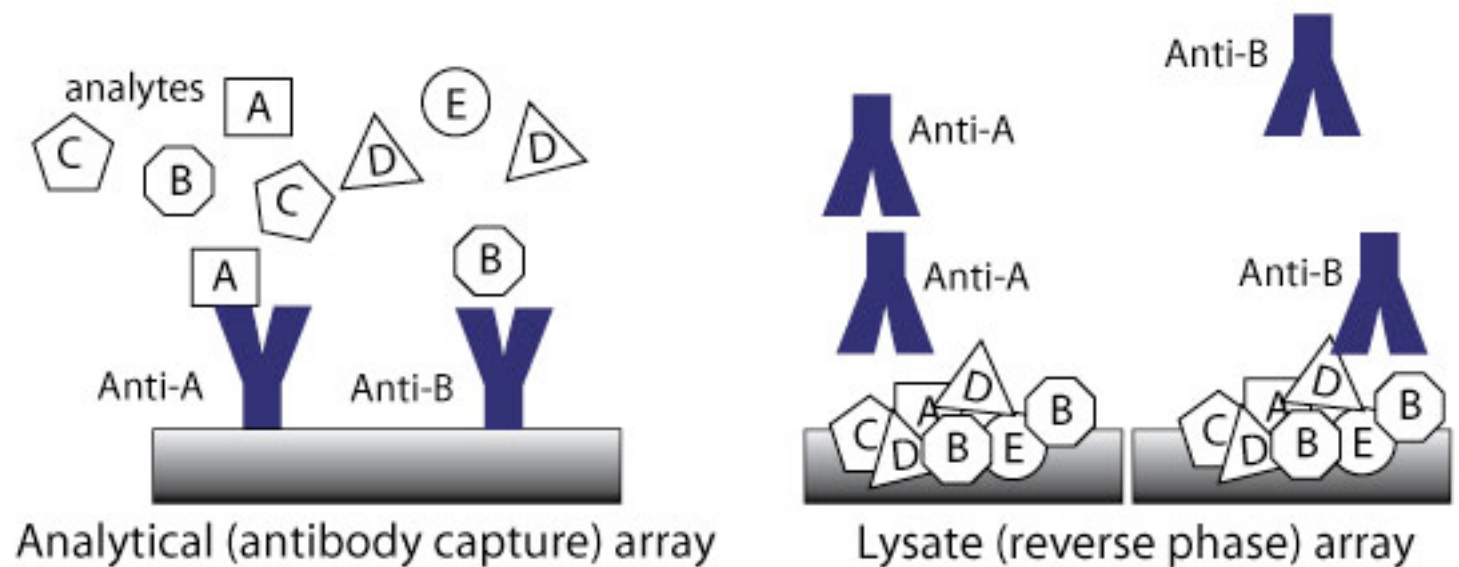
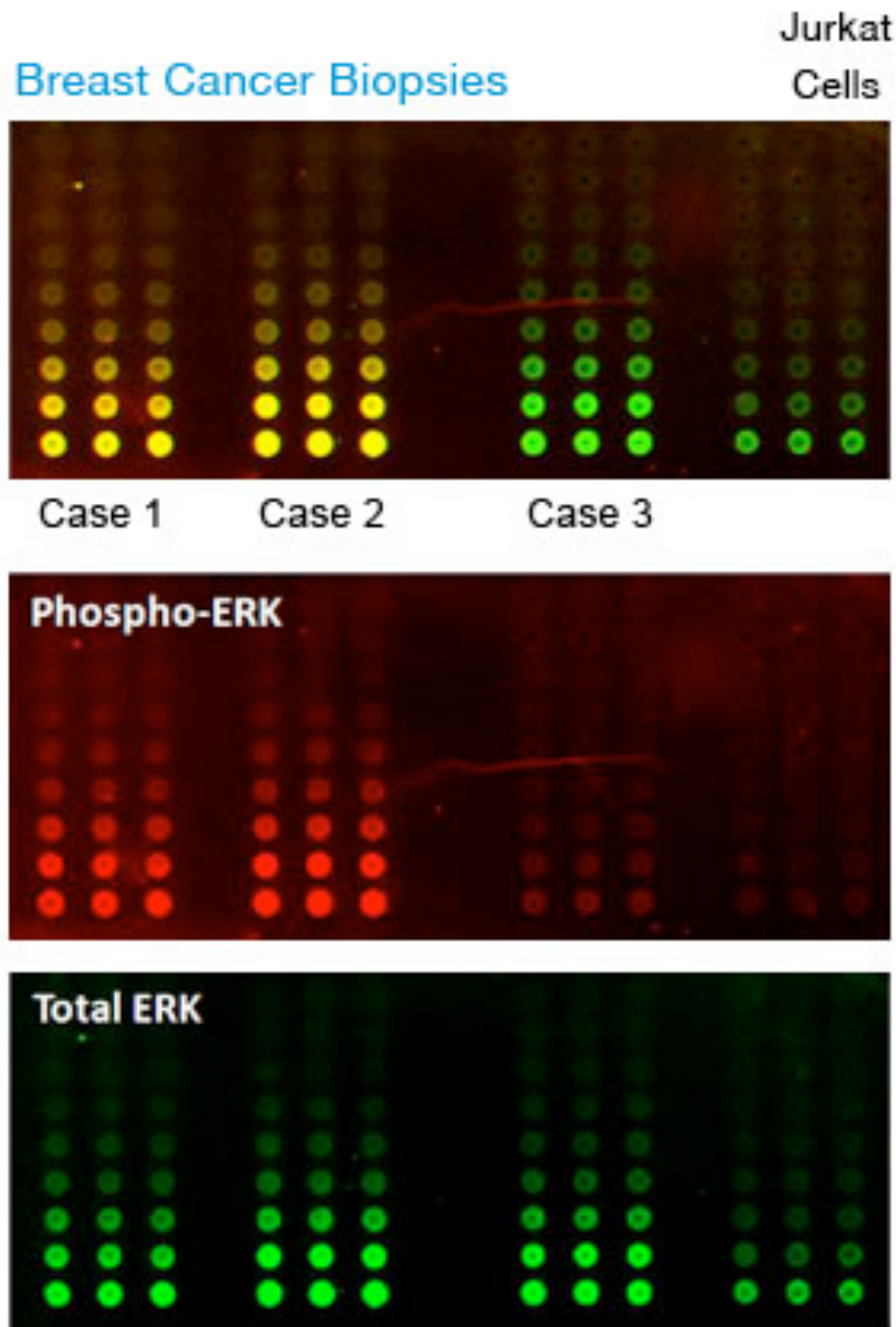
Regulatory networks sensitive to tyrosine kinase inhibitors in H3255 and MKN45 cells revealed by PhosphoScan-SILAC study.

Guo A et al. PNAS 2008;105:692-697

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PNAS

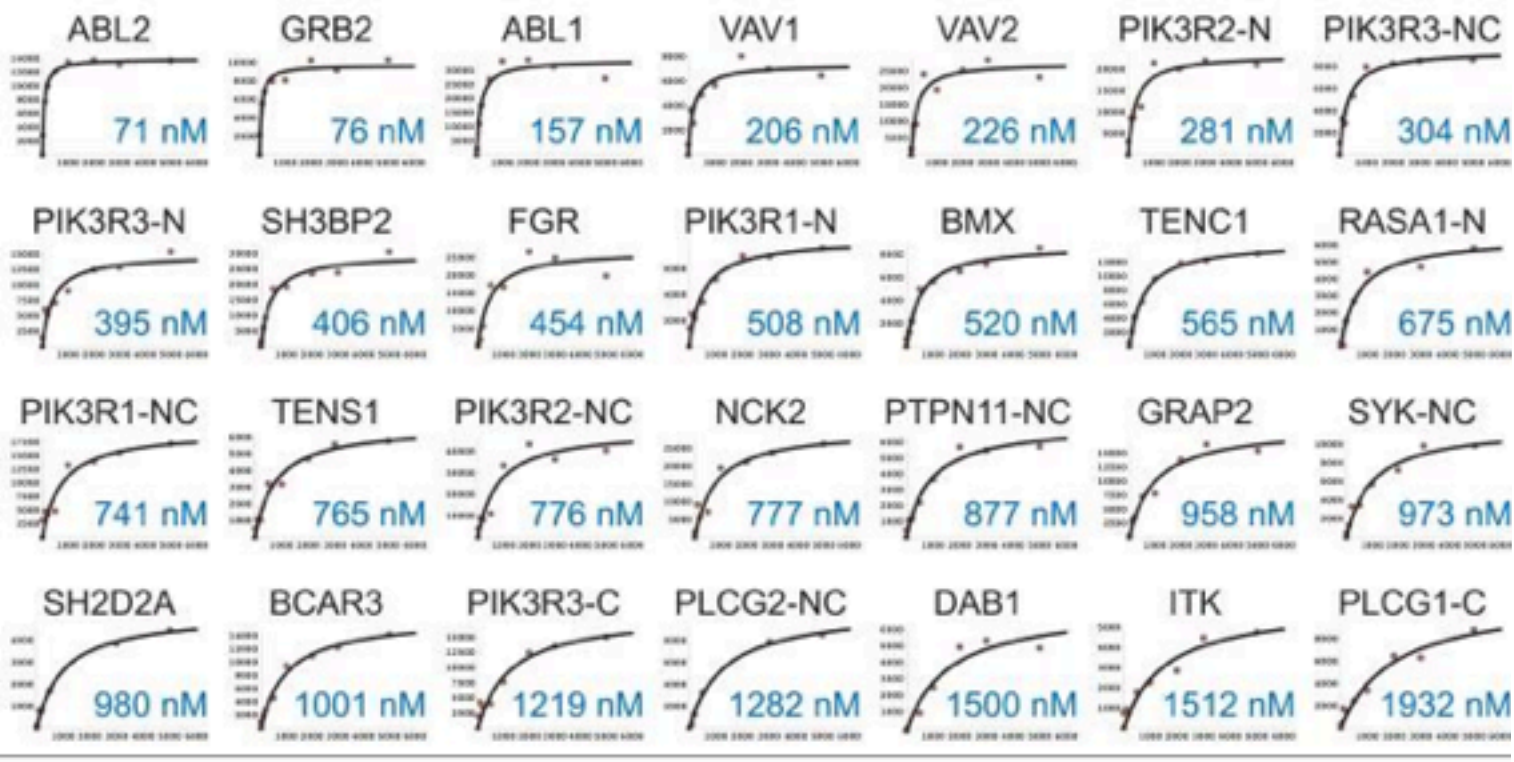
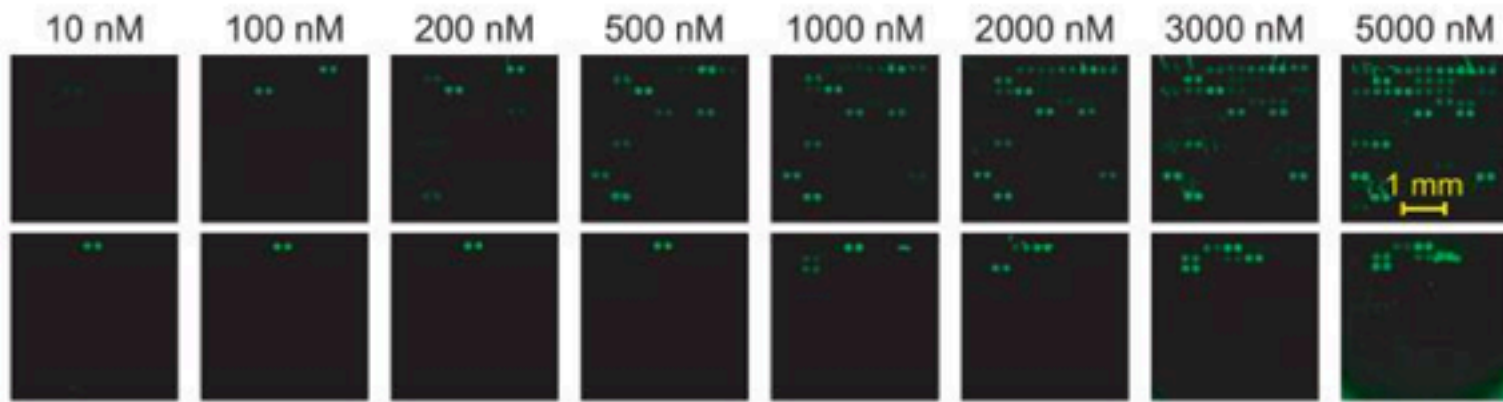
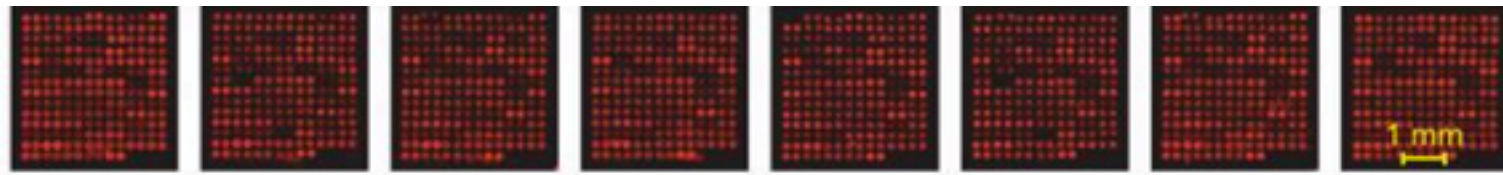
# Semi-quantitative analysis: Protein Microarray



A few signals per spot -- up to hundreds of spots per slide.



# Semi-quantitative analysis: Protein Microarray



Strength:

Multiplex -- many conditions can be screened

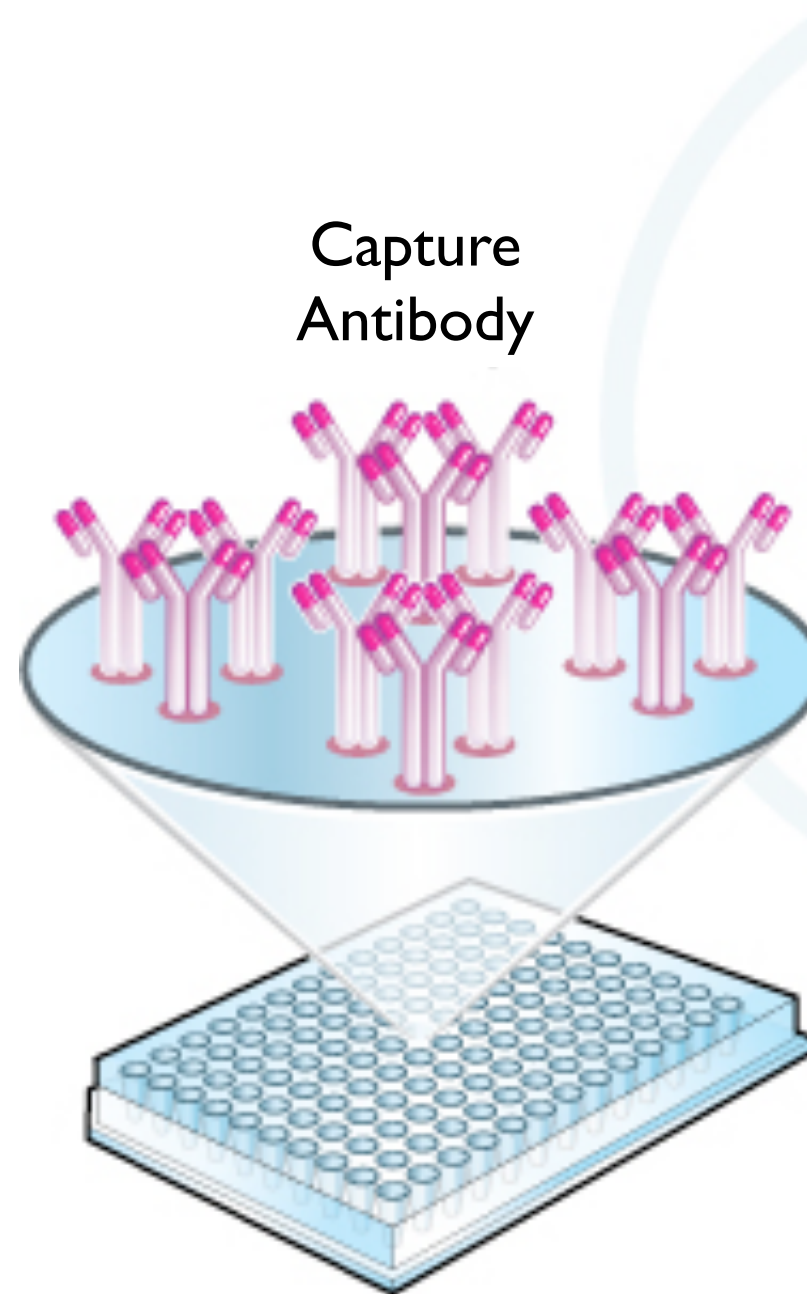
Weakness:

Non-specific interactions (also huge problem in WB)

Dissecting Protein Function and Signaling Using Protein Microarrays  
Curr Opin Chem Biol. 2009 October; 13(4): 398-405.

A few signals per spot -- up to hundreds of spots per slide.

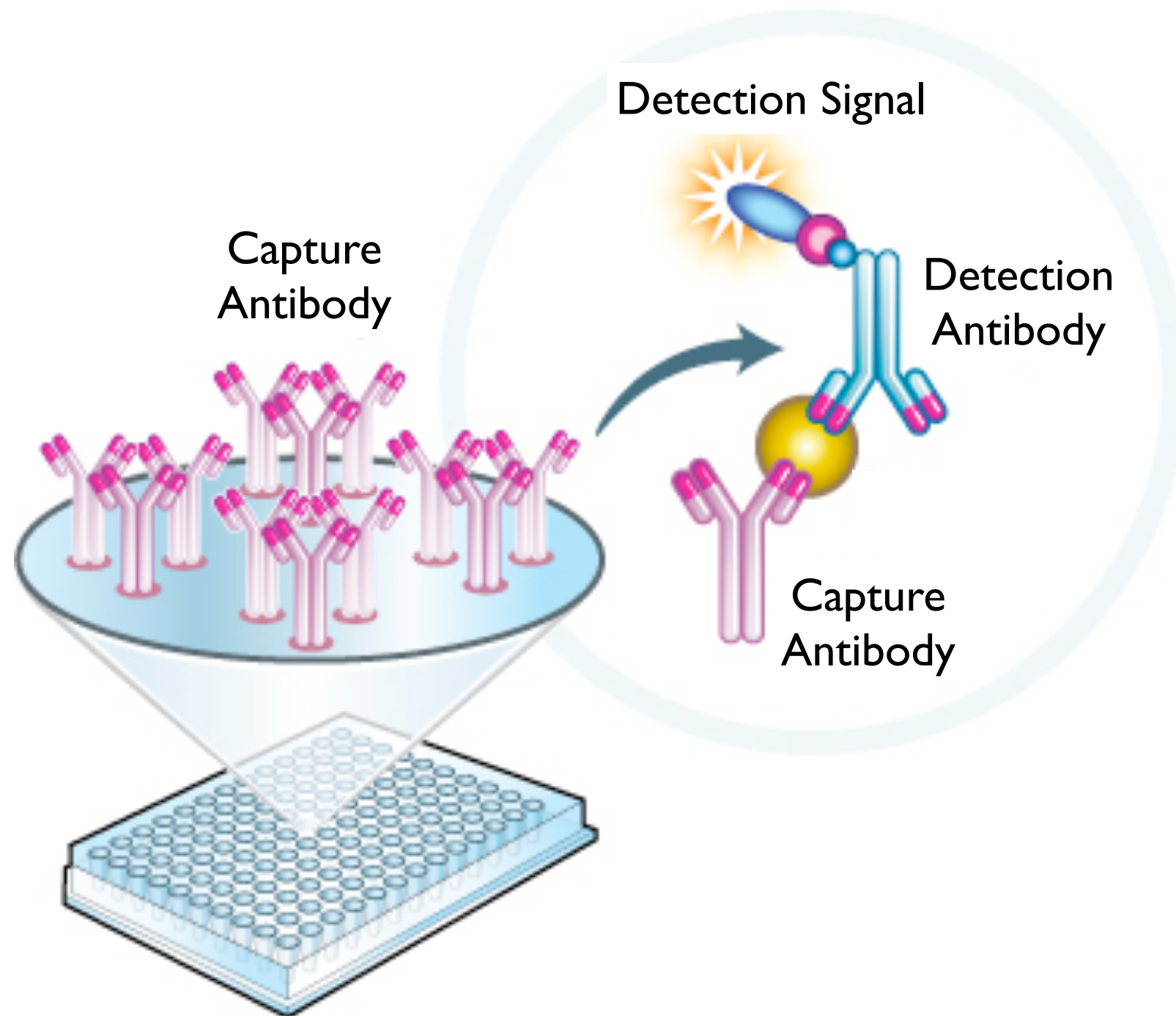
# Quantitative analysis: ELISA



One signal per well - but up to 384 wells/experiment.

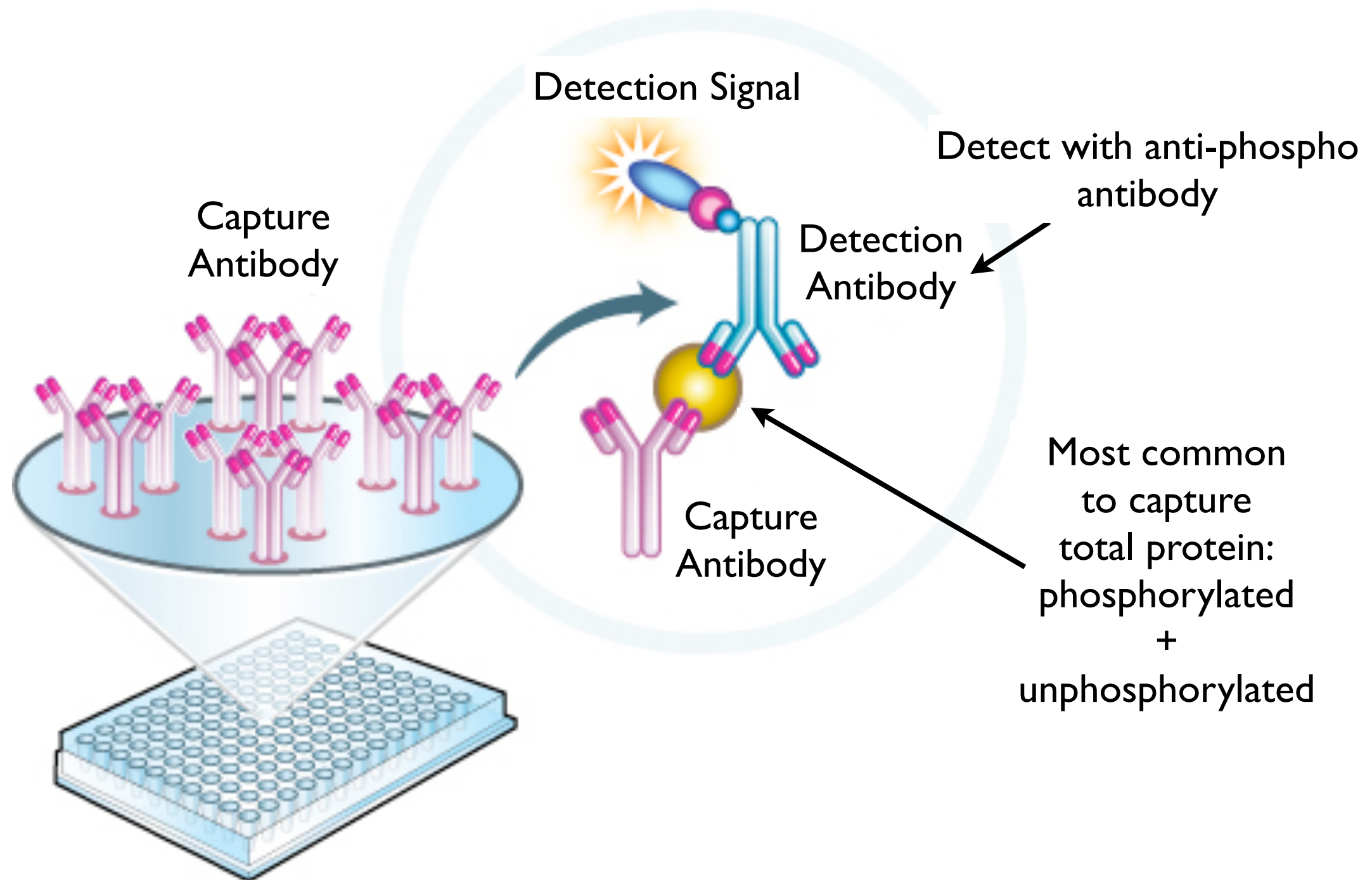


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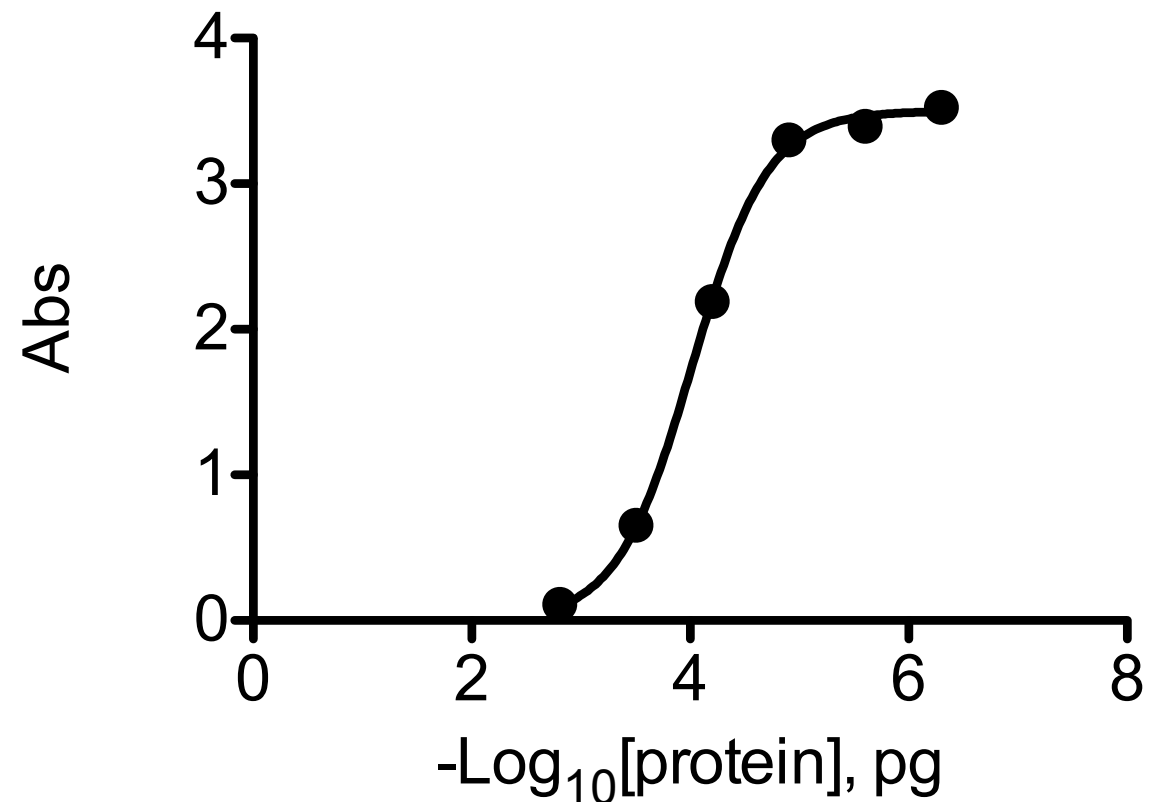


# Quantitative analysis: ELISA

How to quantify:

Very often not linear relationships

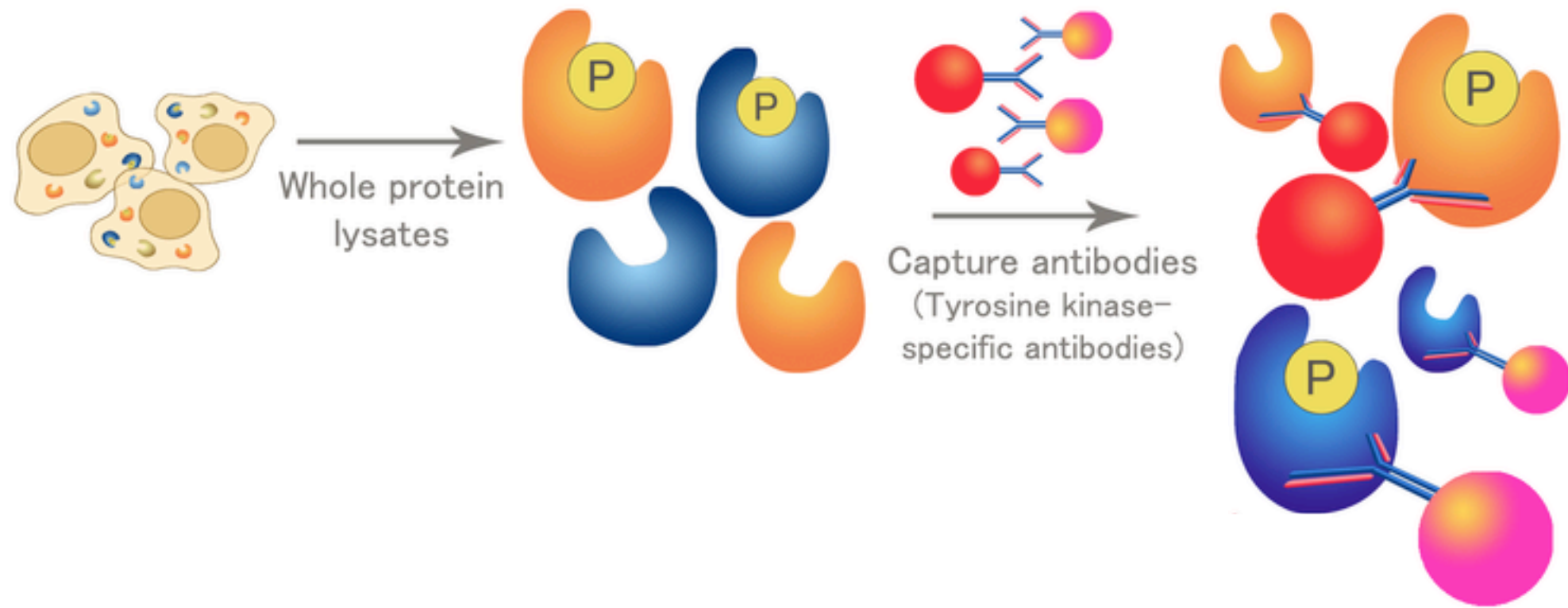
ELISA Standard Curve #2



$$Y = \text{Bottom} + (\text{Top} - \text{Bottom}) / (1 + 10^{((\text{LogEC50} - X) * \text{HillSlope}))})$$

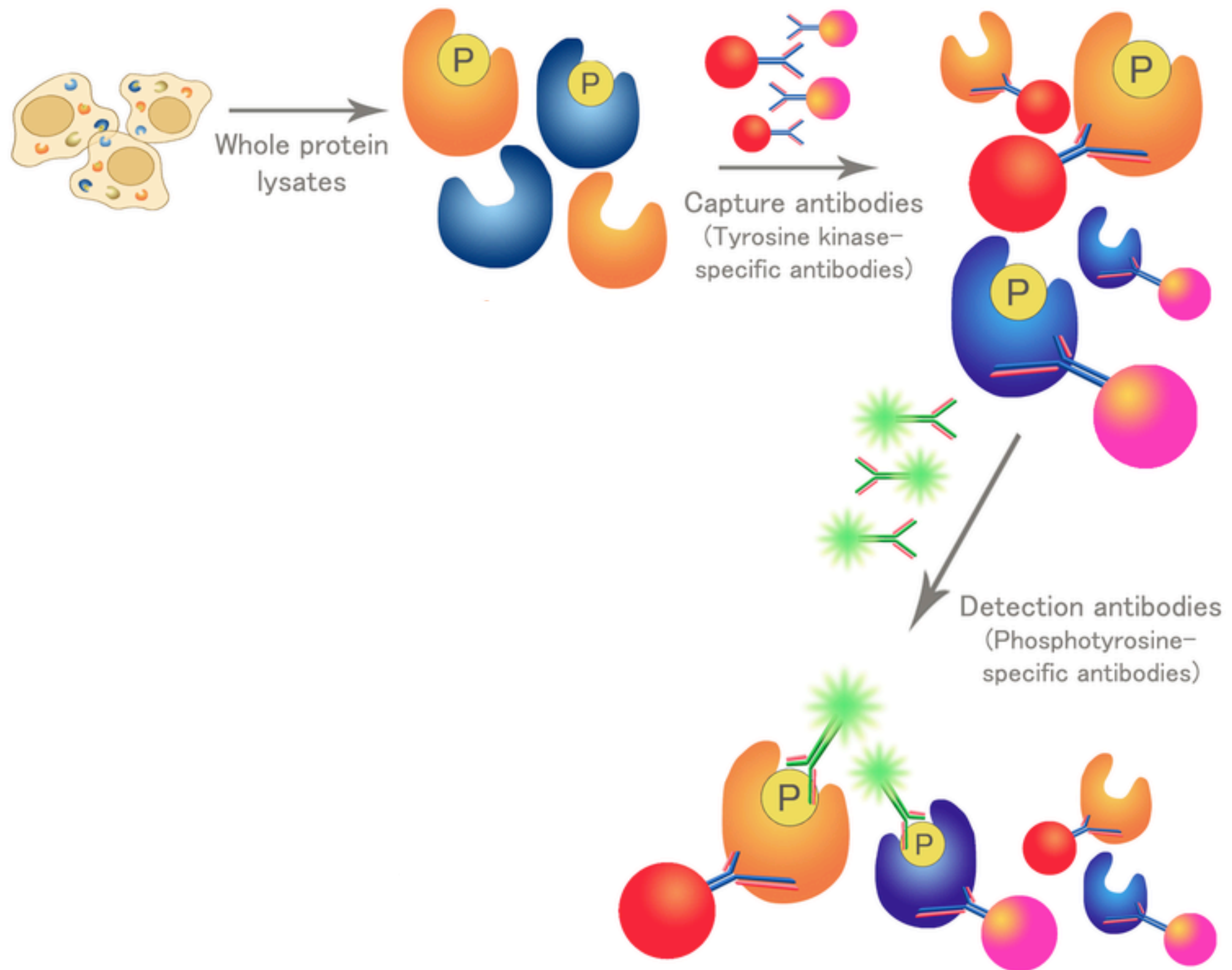
General protocol: Create a standard curve on each plate (usually supplied with kits or make your own)

# Quantitative analysis: Multiplexed bead based ELISA



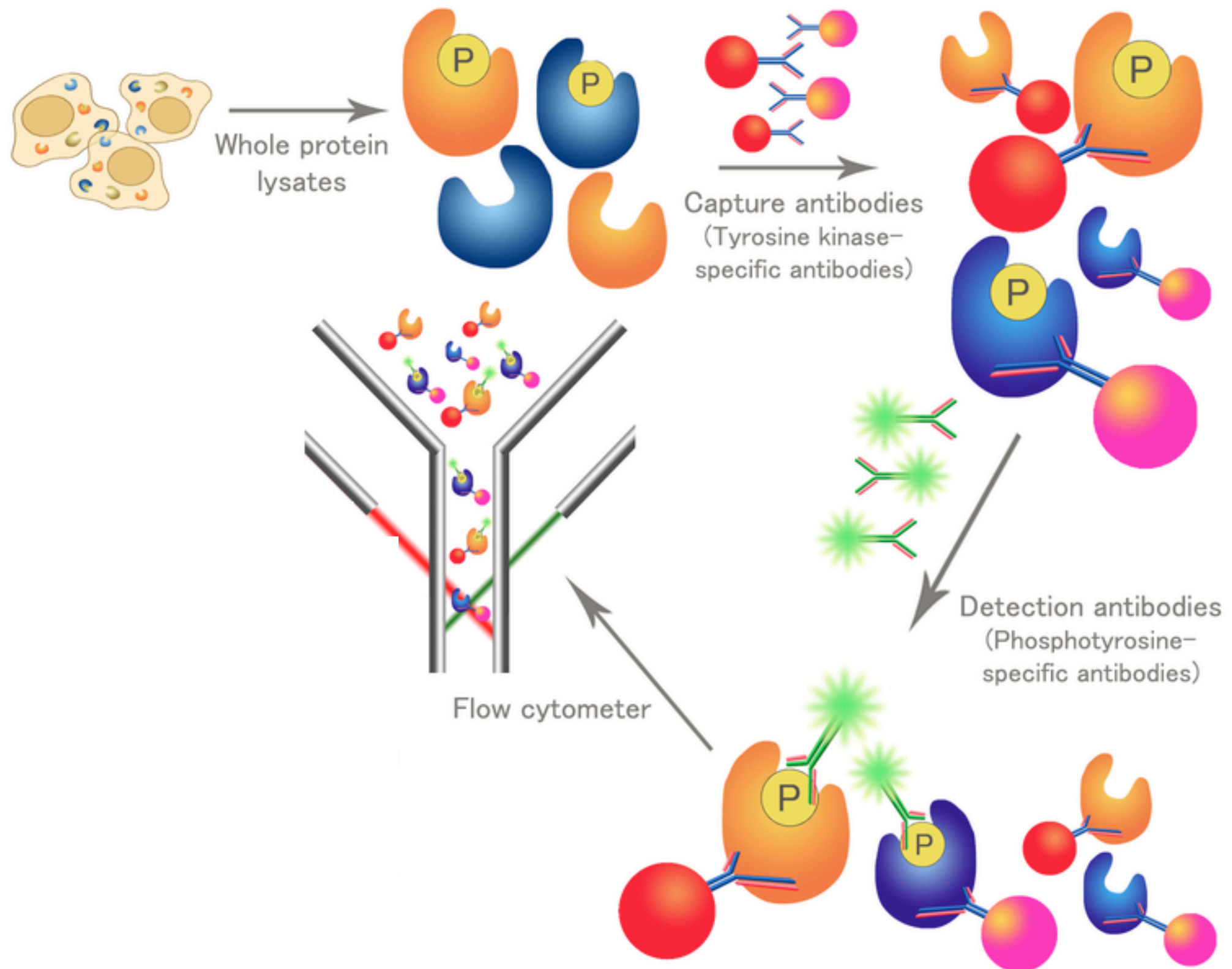


# Quantitative analysis: Multiplexed bead based ELISA



[http://commons.wikimedia.org/wiki/File:Workflow\\_IA.png](http://commons.wikimedia.org/wiki/File:Workflow_IA.png)

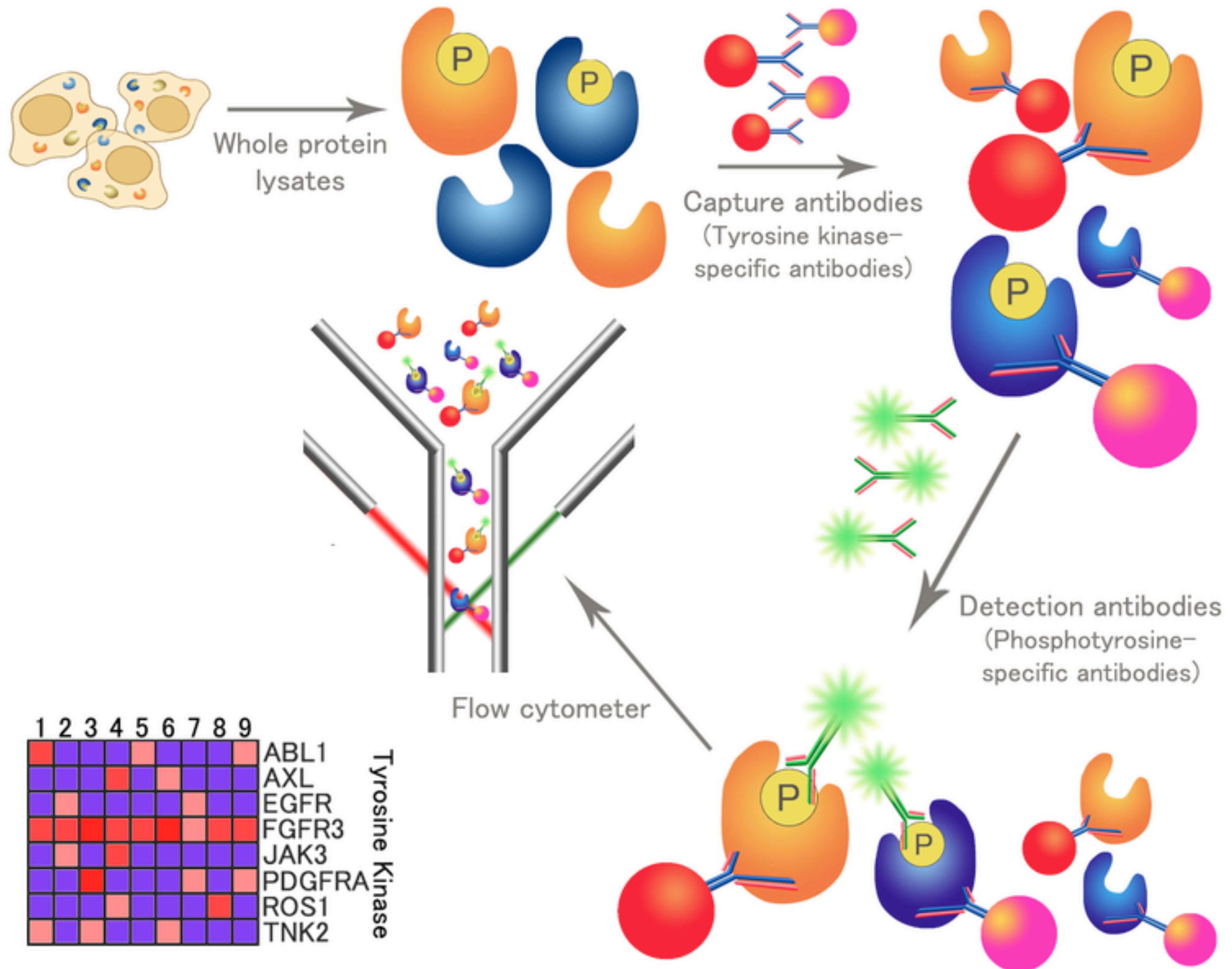
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# Quantitative analysis: Multiplexed bead based ELISA

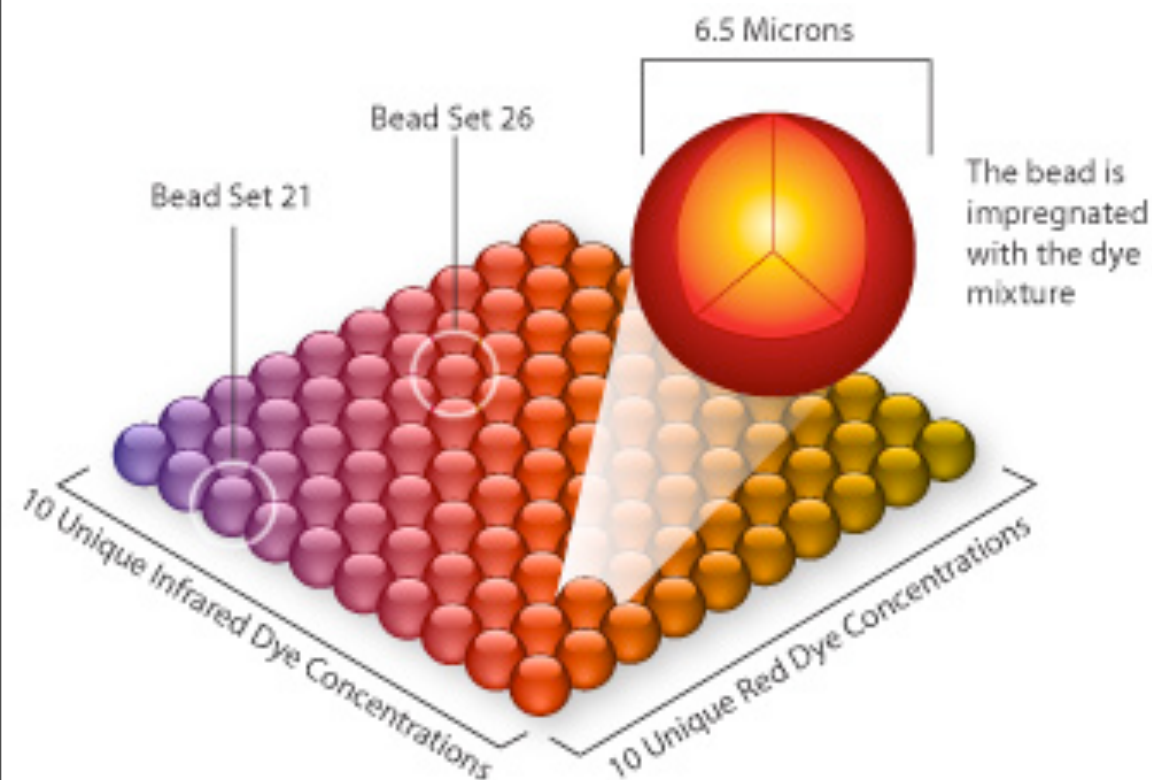
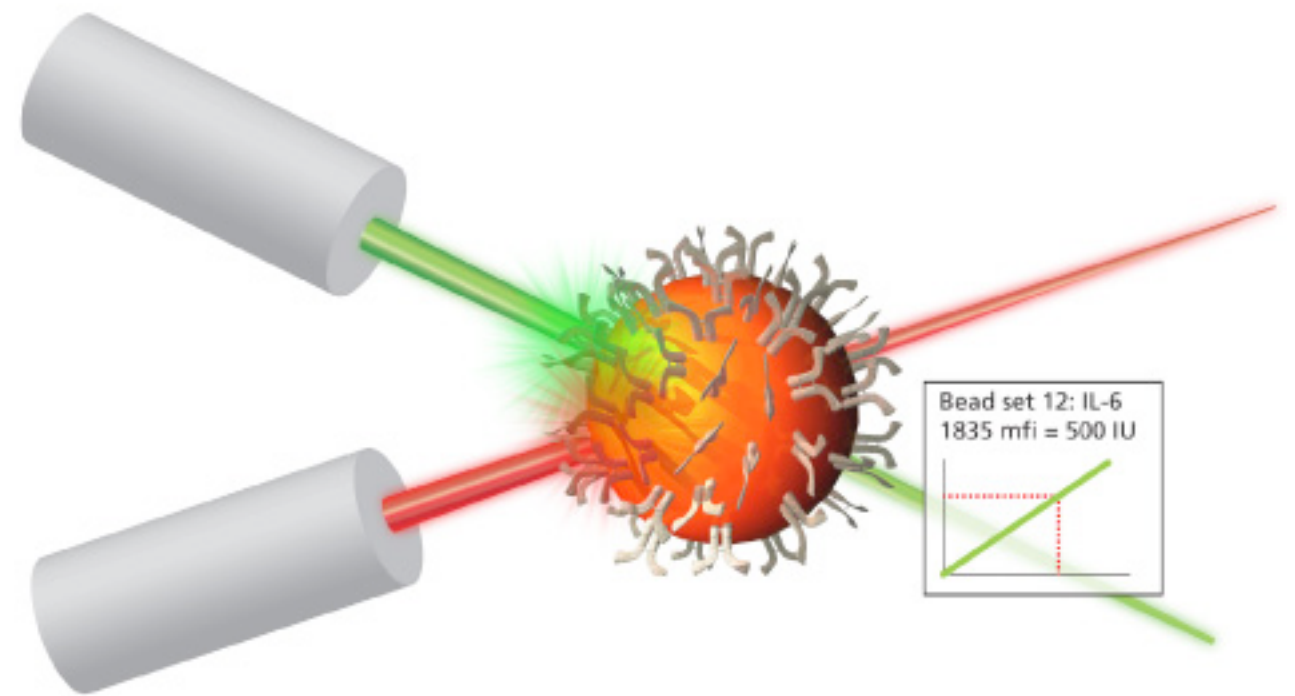


[http://commons.wikimedia.org/wiki/File:Workflow\\_IA.png](http://commons.wikimedia.org/wiki/File:Workflow_IA.png)

# Quantitative analysis: Multiplexed bead based ELISA

Theoretically up to hundreds of conditions per well -- 384 (sometimes > 1500!) wells per experiment

In reality: 20-30 different phosphoproteins / well max





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