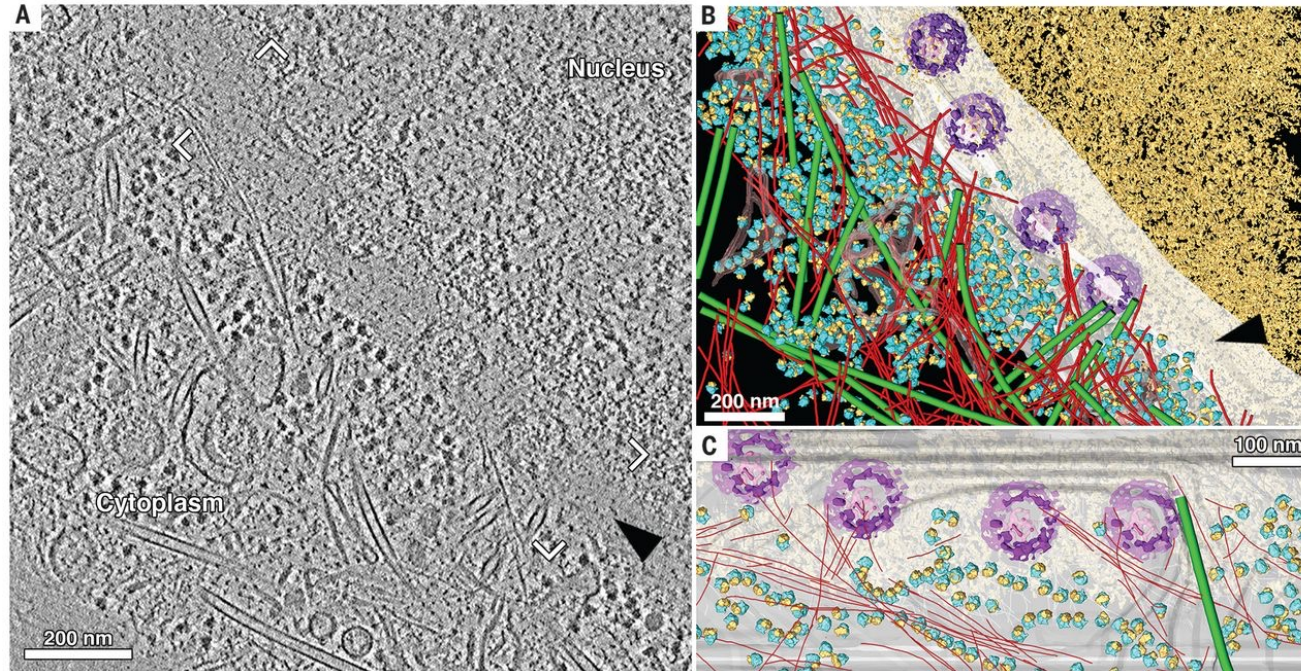


Chemo- proteomics

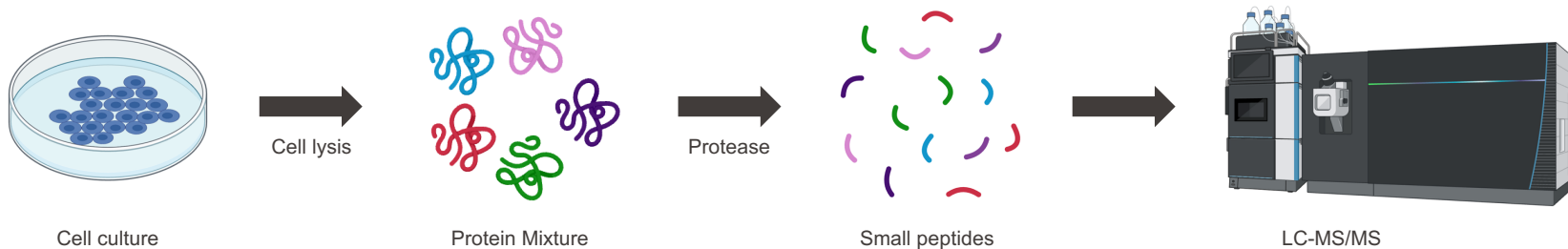
Target identification
Specificity profiling
Drug repurposing

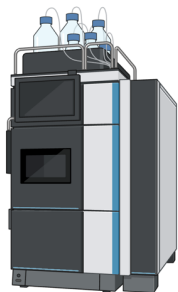
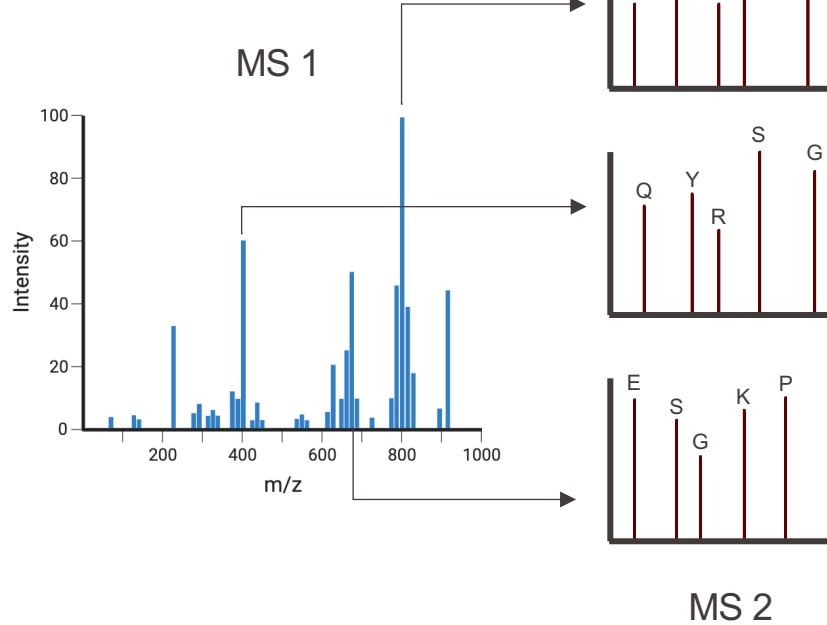
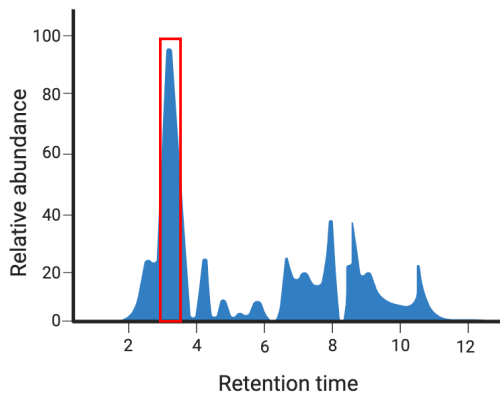
The Needle in the Haystack



How do you analyze all proteins in a cell at once?

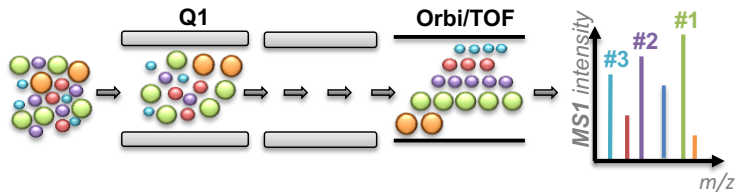
The science of turning an organized biological system into a soup of proteins.
(and sorting out the mess afterwards)





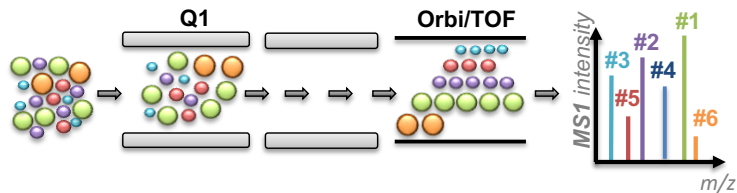
Data dependent acquisition

1. Precursor (MS1) full scan:



Data dependent acquisition

1. Precursor (MS1) full scan:



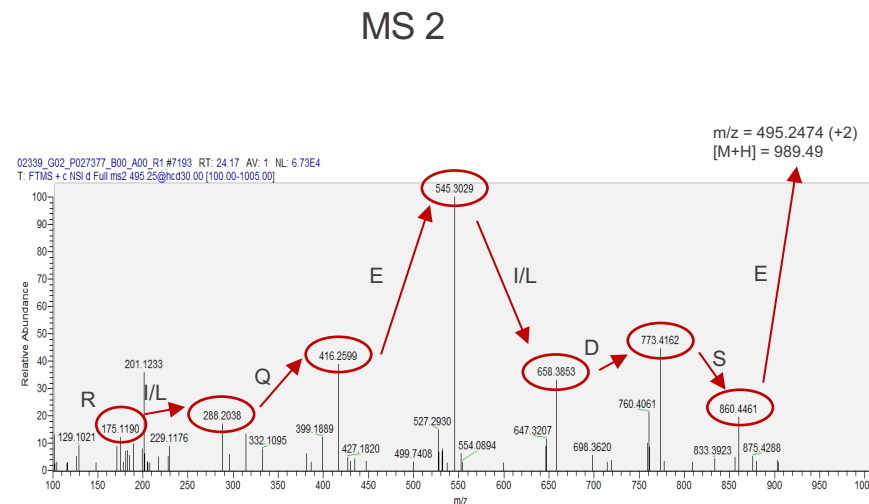
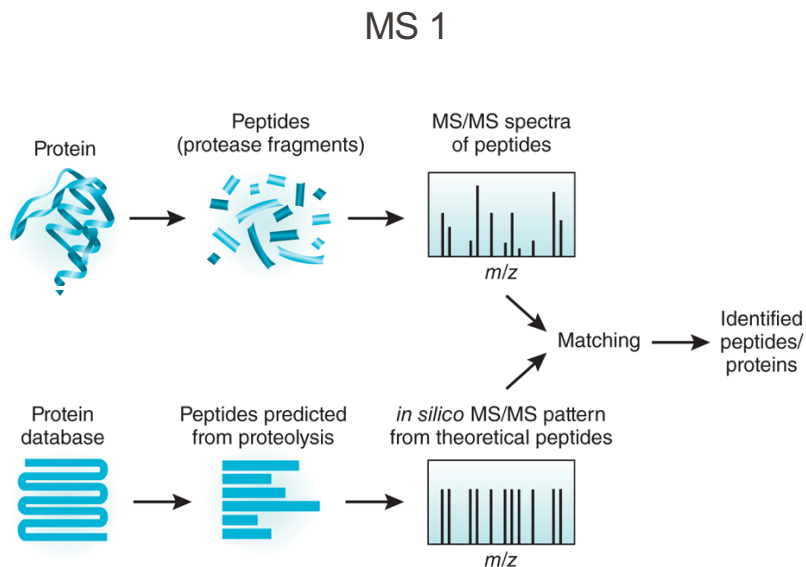
Exclusion list
for 30 seconds:

m/z #1

m/z #2

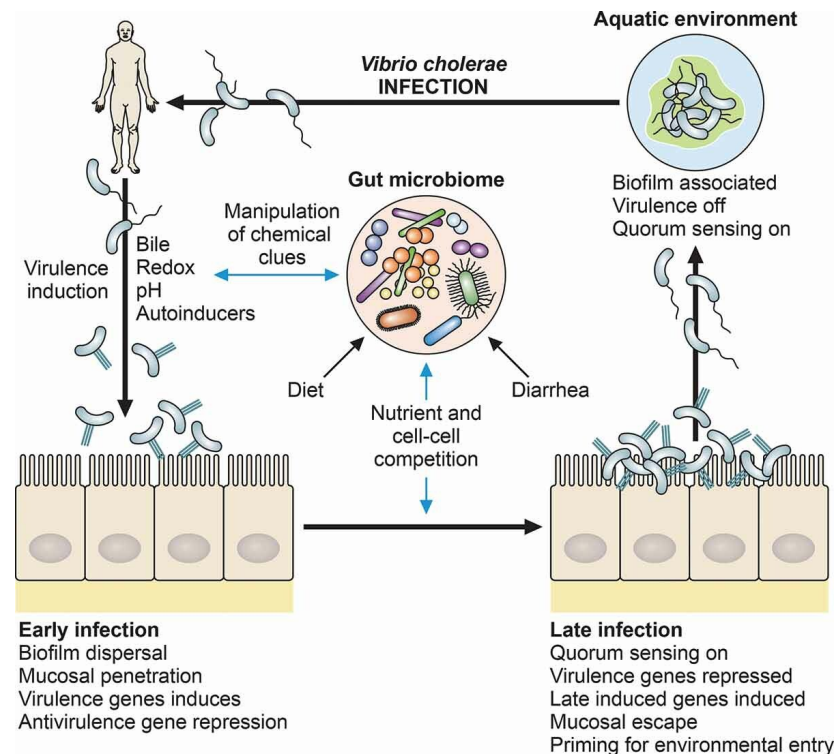
m/z #3

Data analysis: Sorting out the mess we made



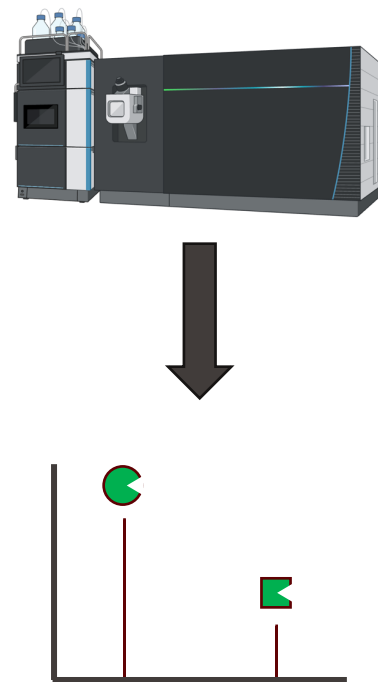
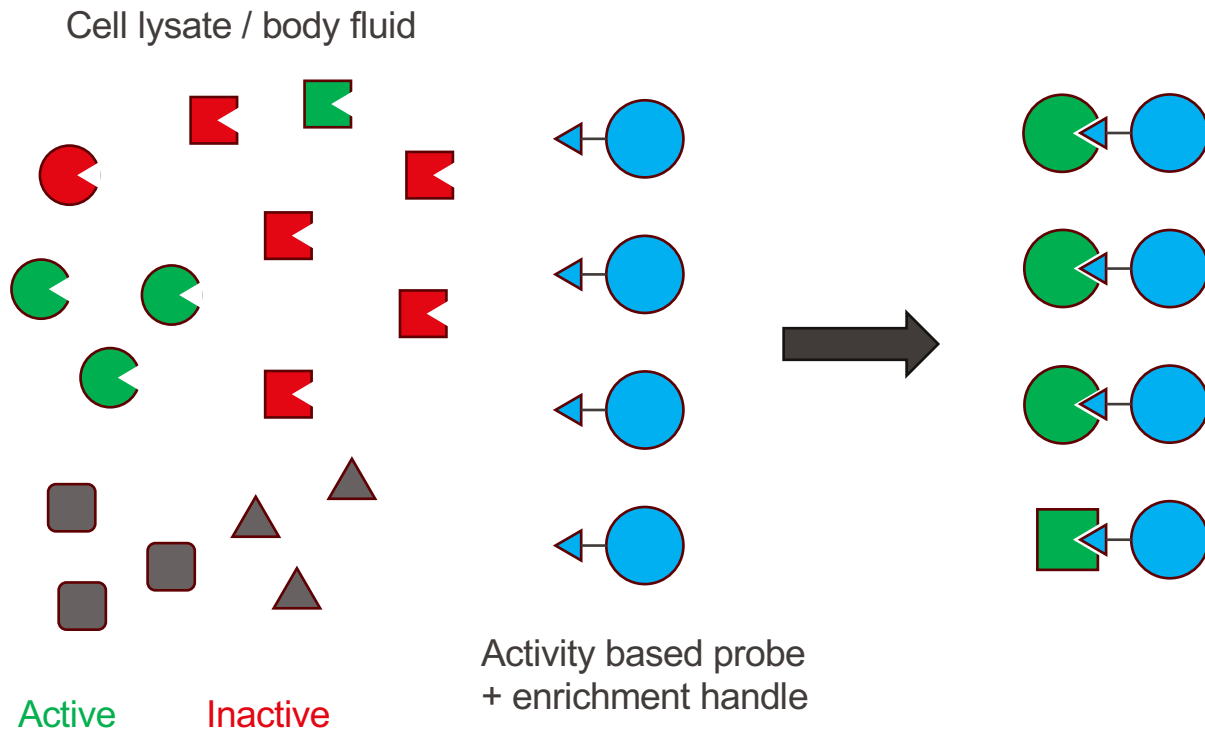
- Extracellular bacterium causing diarrhea
- Secretes serine hydrolases to shape its intestinal niche

Which properties would you require to identify a hydrolase as a promising drug target?



Activity-based Protein Profiling (ABPP)

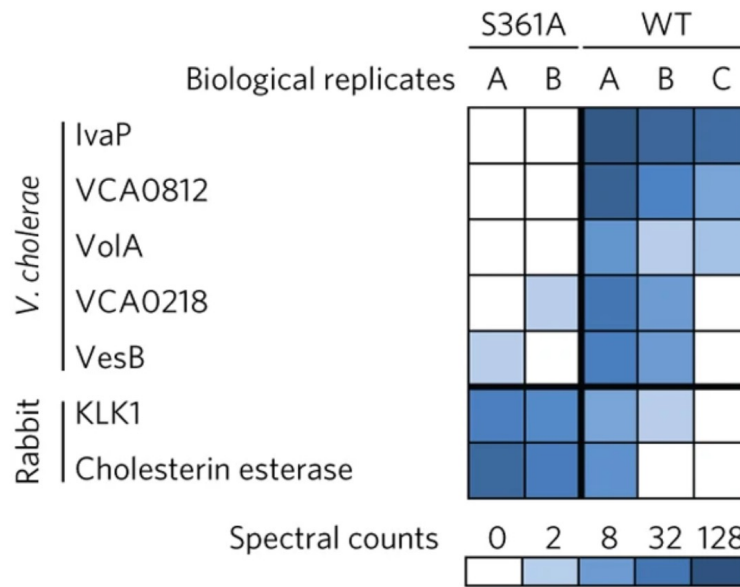
■ BIO698: Chemoproteomics for target deconvolution



V. Cholerae: Hydrolase targets

UniProt ID	<i>V. cholerae</i> Proteins in Rabbit Cecal Fluid	Sample A ^a		Sample B		Sample C	
		FPB	DMSO	FPB	DMSO	FPB	DMSO
Q9KVI8	Alkaline serine protease IvaP (VC0157)	76	0	128	0	30	0
Q9KLE3	Serine protease VesA (VCA0803)	13	0	4	0	6	0
Q9KSQ6	Trypsin-like serine protease VesB (VC1200)	12	0	7	0	4	0
Q9KLD4	Leucine aminopeptidase-related protein VCA0812	6	0	8	0	8	0
Q9KUF5	Protease DO VC0566	23	0	4	0	0	0
P01556	Cholera enterotoxin subunit B ctxB	4	0	2	0	0	0
Q9KMOV0	Thermolabile hemolysin VCA0218	8	0	0	0	7	0
Q9KUB9	Putative uncharacterized protein VC0603	11	0	0	0	0	0
Q9KLG1	Arylesterase VCA0783	6	0	0	0	0	0
Q9KQJ6	Putative uncharacterized protein VC2002	4	0	0	0	0	0
Q9KUG7	Protease, insulinase family VC0554	4	0	0	0	0	0
P01555	Cholera enterotoxin subunit A ctxA	3	0	0	0	0	0
P15493	Lipase lipA	0	0	5	0	0	0
Q9KLP3	Chitodextrinase VCA0700	0	0	0	0	2	0

IvaP: key modulator of infection

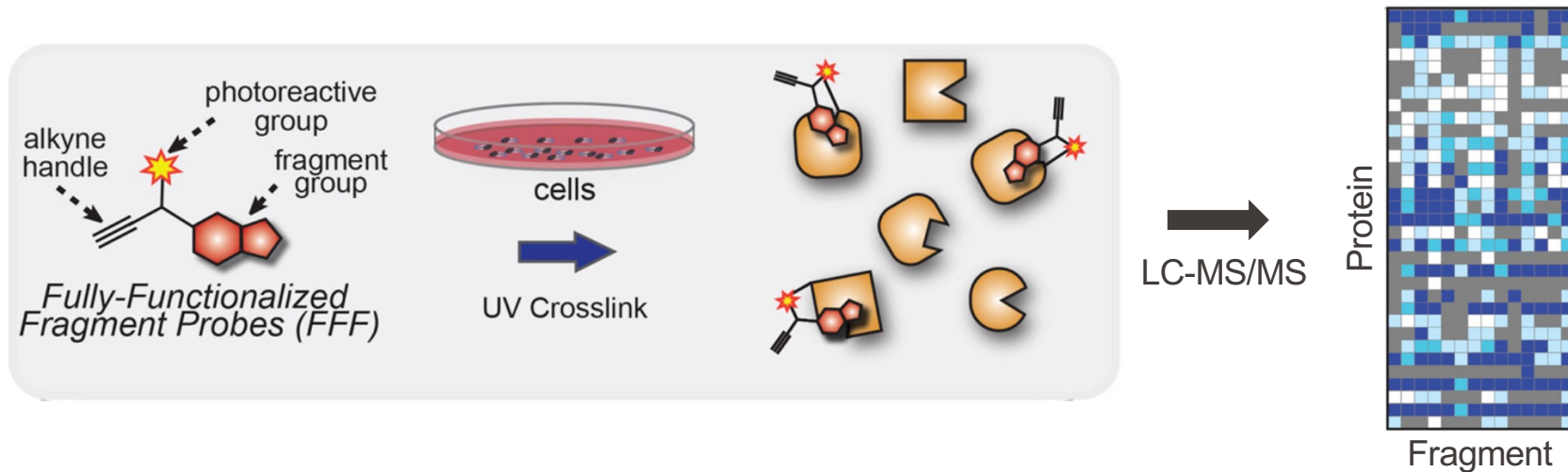


After identifying a promising drug target, how can we quickly identify a starting compound for preclinical research?

We can screen known drugs (or fragments thereof)
for binding to our target.

Proteomics aided Drug Discovery

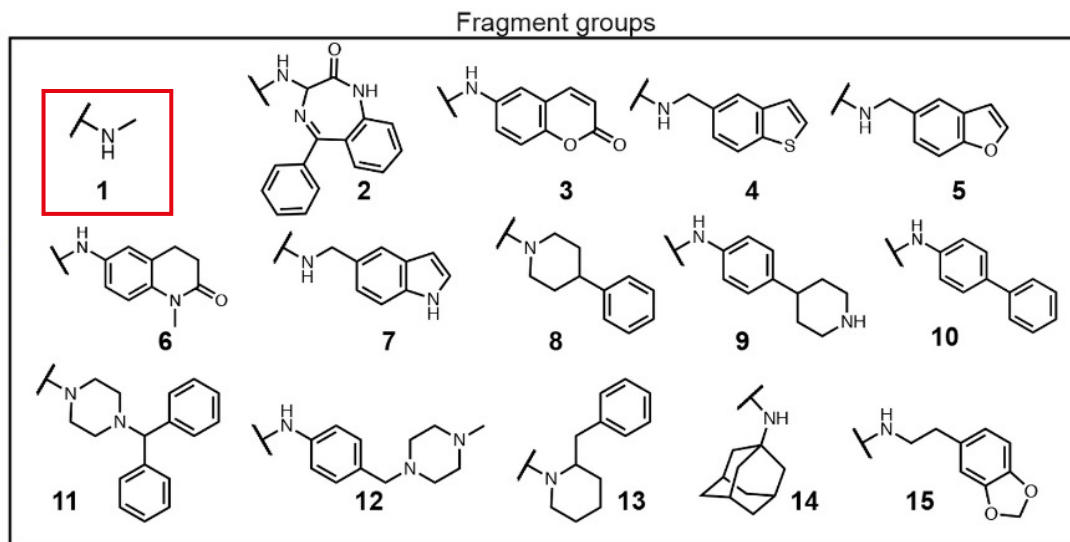
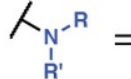
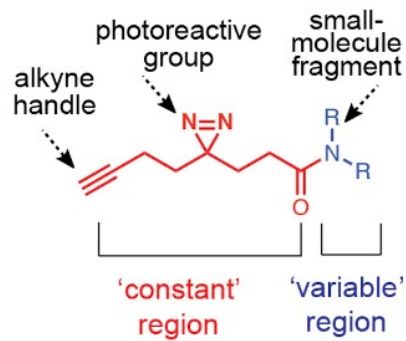
Can we search for drug-like fragments in a proteome-wide manner to identify drug candidates?



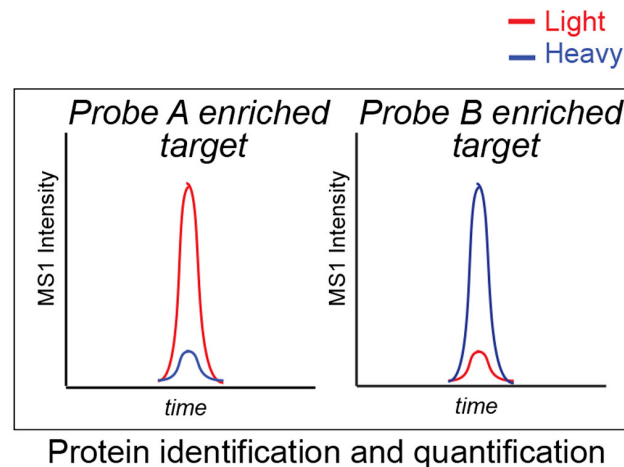
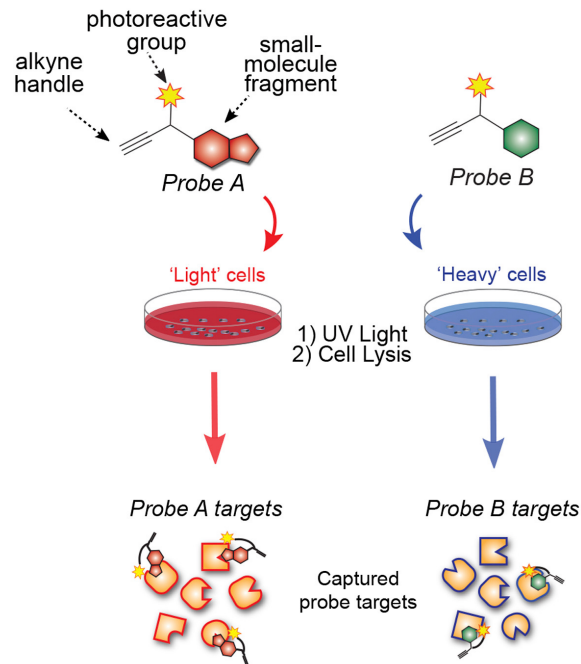
Why do you need to crosslink the fragment probes with the proteins?

To identify transient interactions, which would be disrupted during enrichment

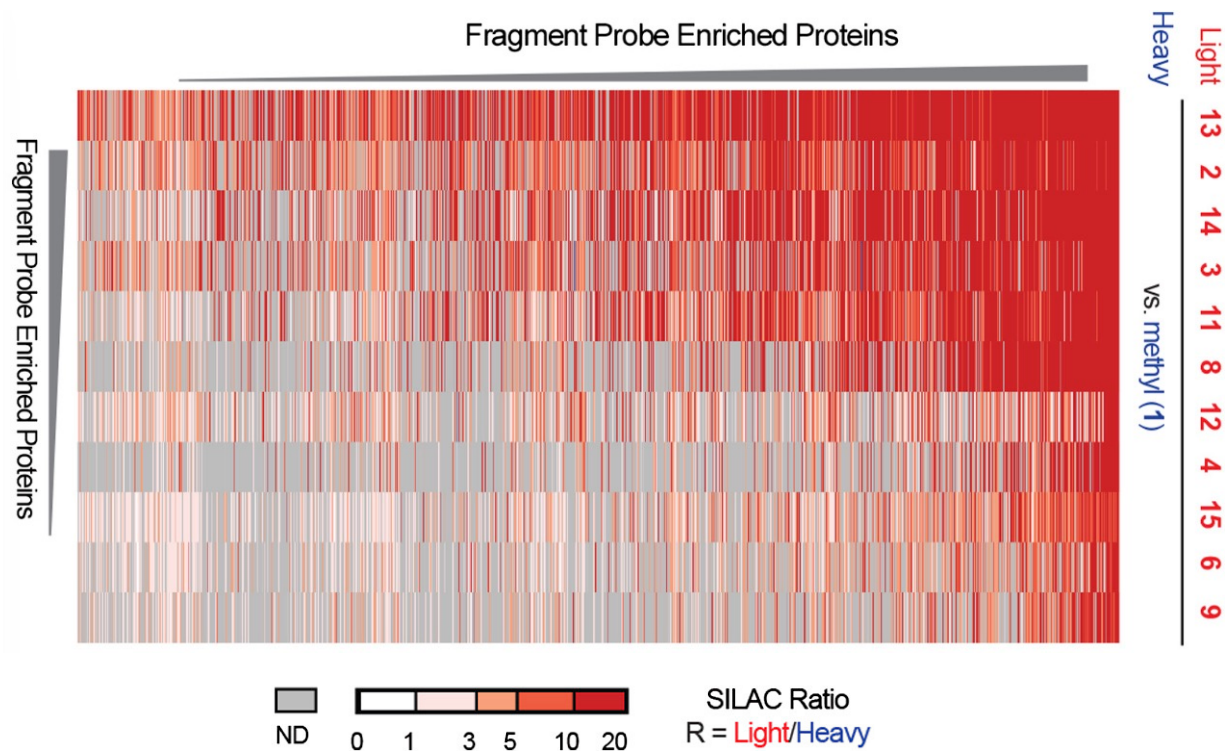
Proteomics aided Drug Discovery



stable isotope labeling by/with amino acids in cell culture



Targets enriched from HEK293T cells

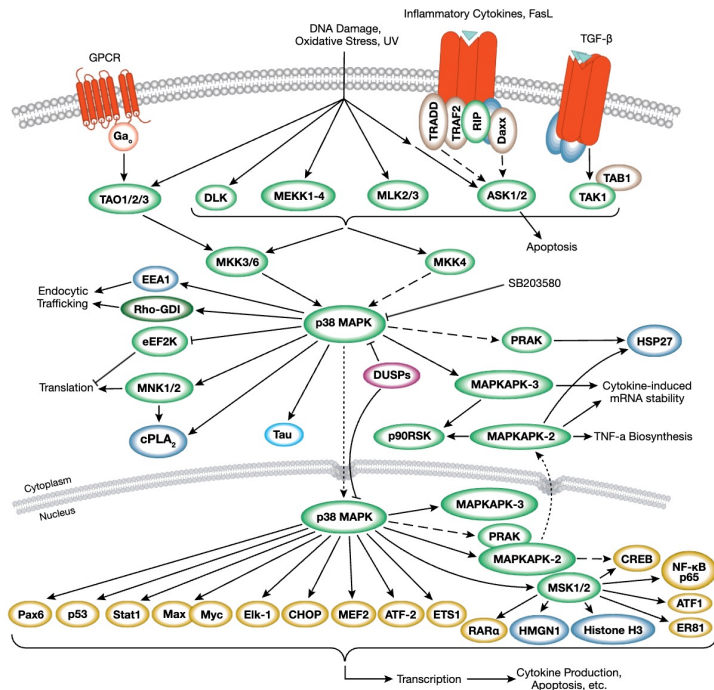


**Which information is crucial for early stage drug development?
(beside proof that the molecule binds the drug target)**

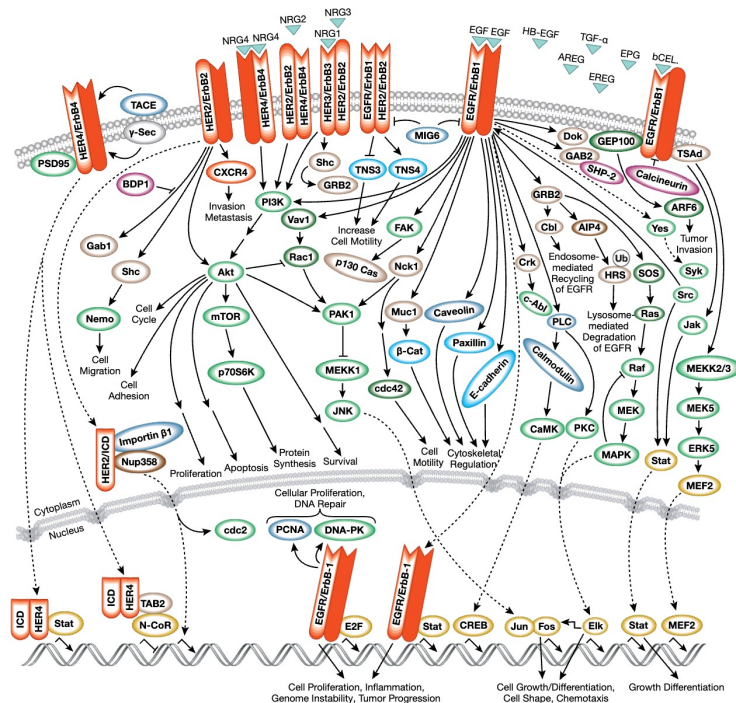
We need to identify potential off-targets to
determine the specificity of the candidate!

Kinases: Key players of cellular signal transduction

p38 MAPK



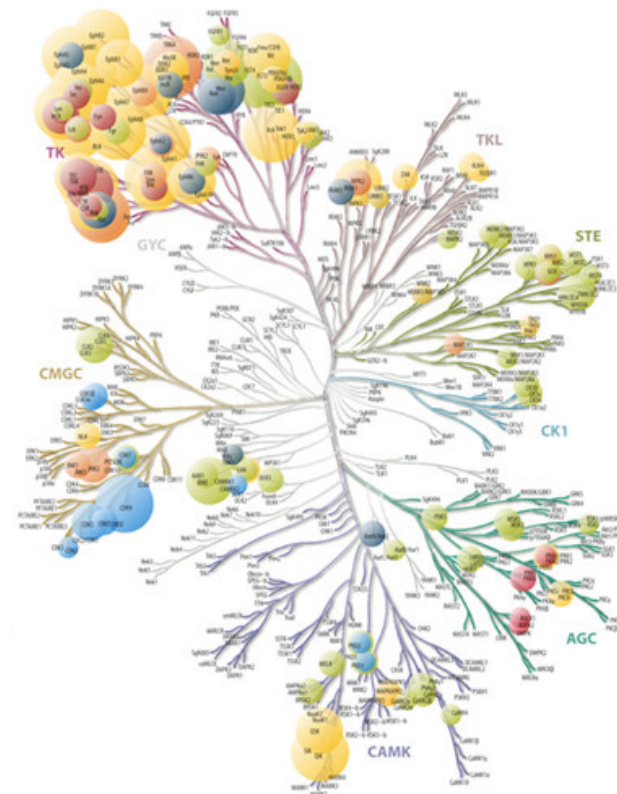
ErbB signaling



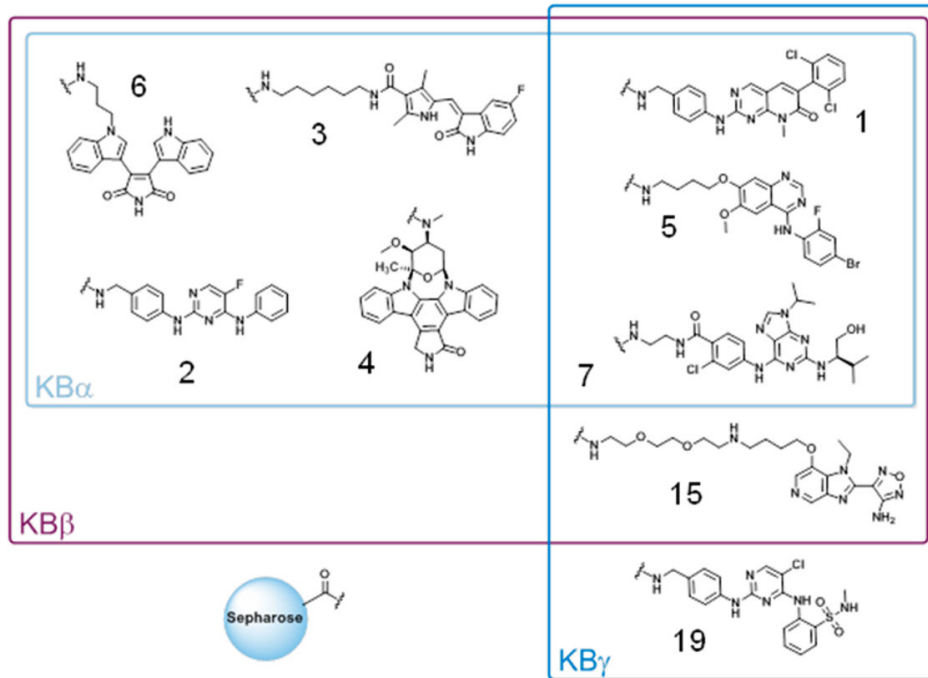
Kinase

- 50% of human kinases are linked to diseases
- About 120 kinase inhibitors approved to date, 30% R&D costs spent on kinase inhibitors
- Kinase inhibitors usually target the conserved ATP pocket causing severe side effects

We need a fast and reliable method to profile the target landscape of kinase inhibitors

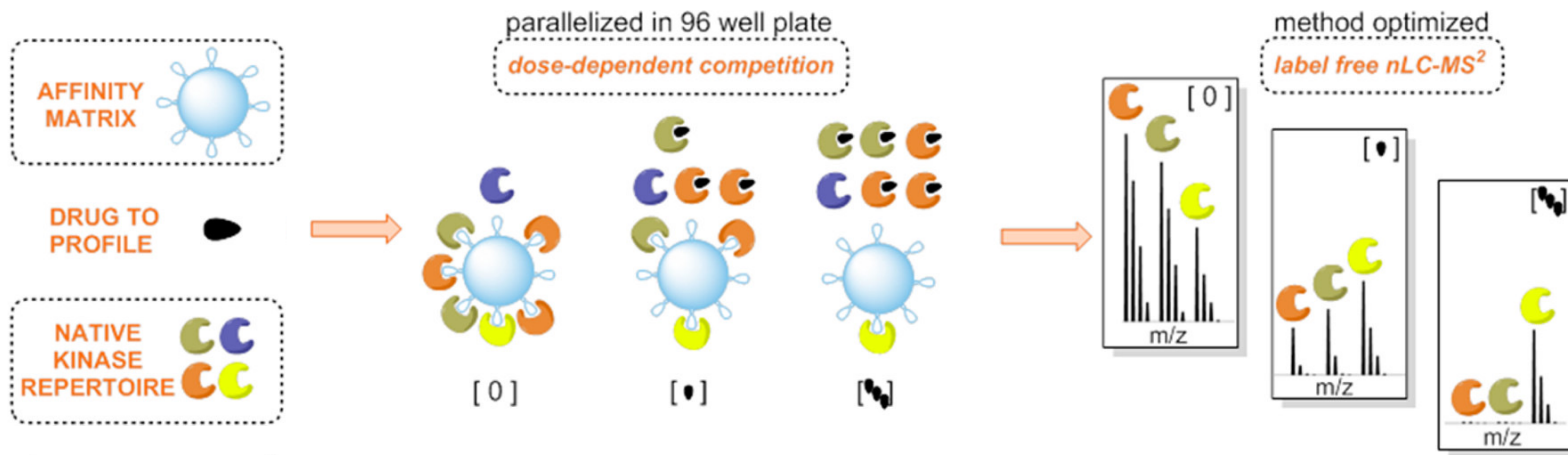


Kinobeads: affinity matrix to enrich the “kinome”

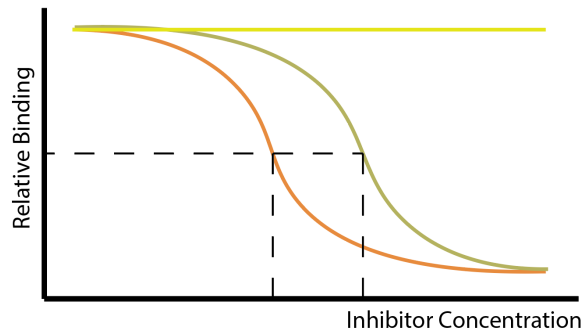


~ 260 kinases

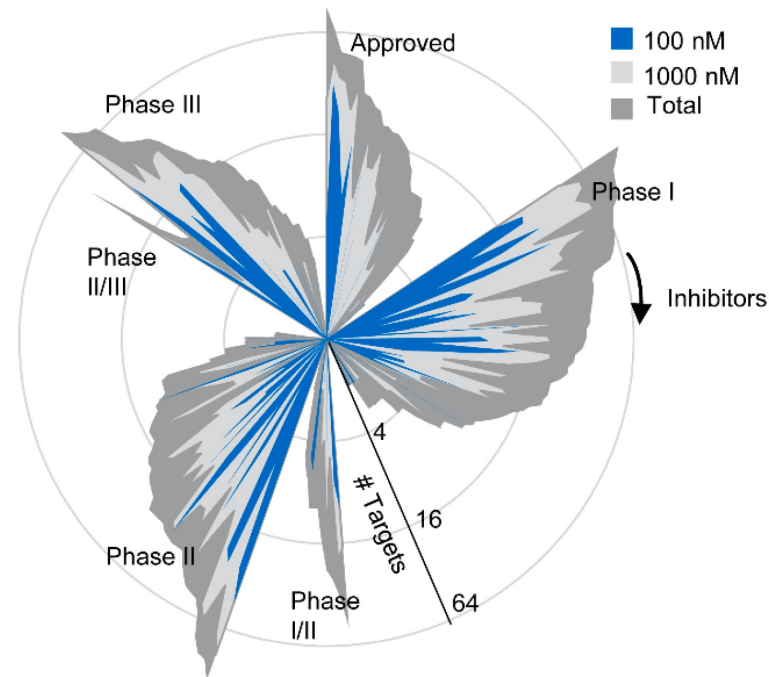
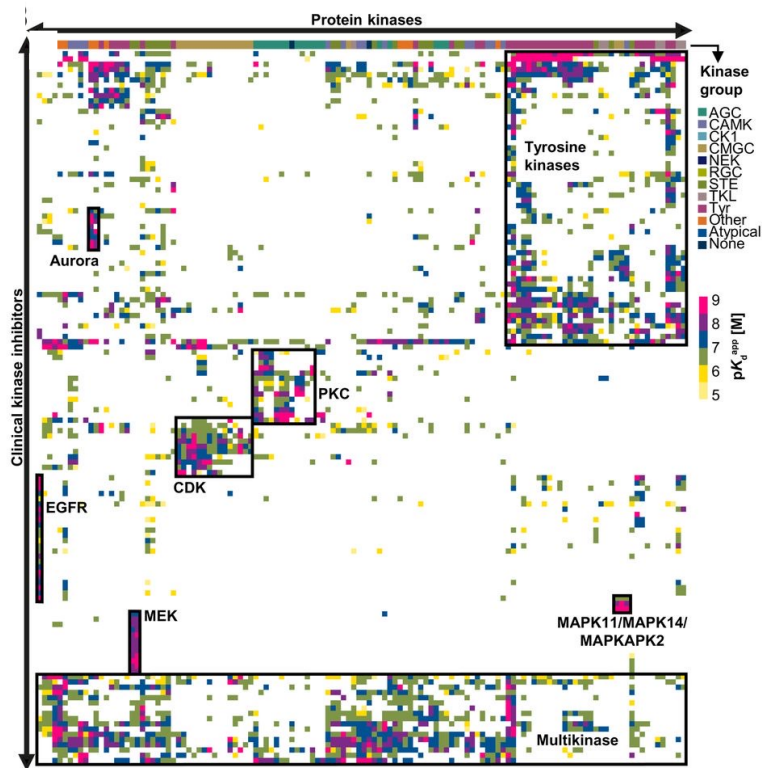
Selectivity Profiling with Kinobeads



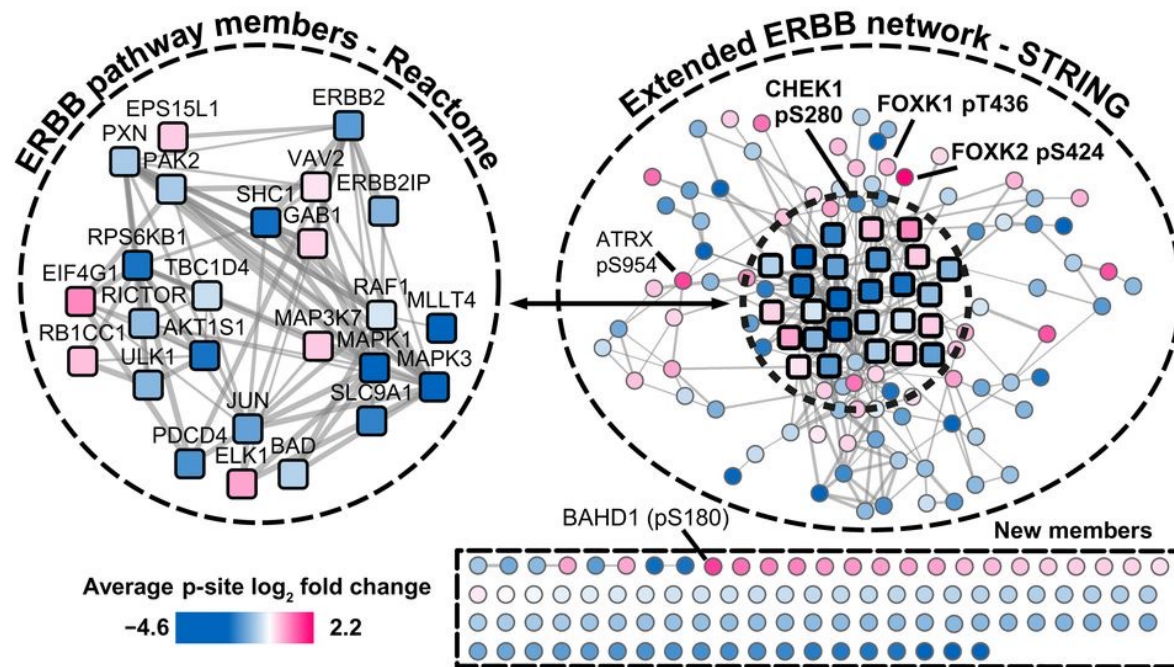
- Label-free
- Natively expressed kinases
- Cellular context



Selectivity Profiling with Kinobeads



Unravelling signaling pathways: Phospho-Proteomics



Data Accessibility: ProteomicsDB

