

*Proteomics
Standards Research
Group (sPRG)*

sPRG: yet another
phosphoproteomics standard?

sPRG working group members

Antonius Koller (Chair)	Northeastern University
Christopher Colangelo (ad hoc)	Primary Ion
David Hawke	UT MD Anderson Cancer Center
Anthony W. Herren	UC Davis
Gordana Isovev	Sciex
Kimberly A. Lee	Cell Signaling Technology
Ryan Leib	Stanford University
Bhavin Patel	Thermo Fisher Scientific
Brett Phinney	UC Davis
Brian C. Searle	University of Washington/Proteome Software Inc.
Allis Chien (EB Liaison)	Stanford University

Thank you!

PROTIFI

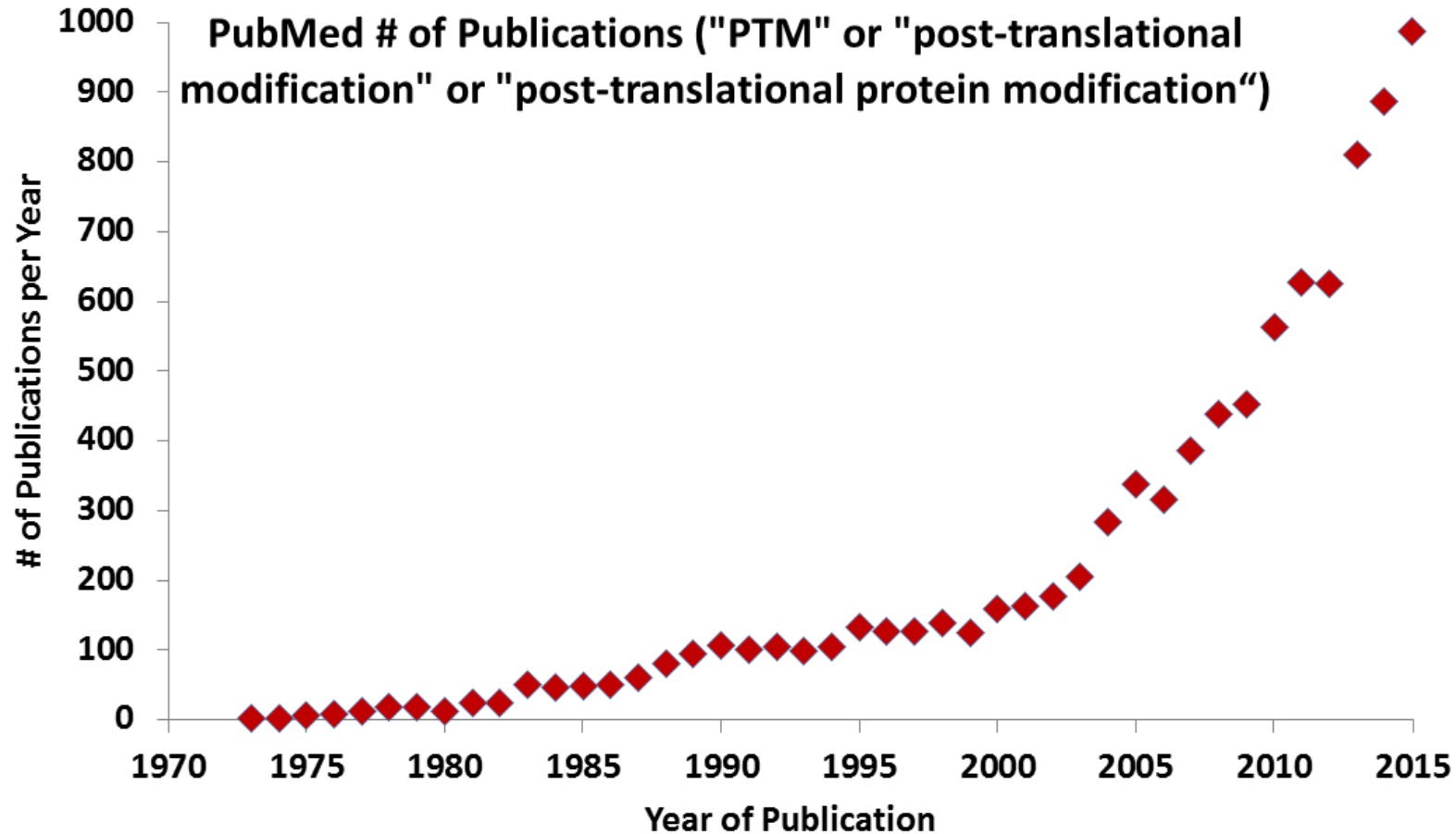


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Jenny Kim and Purvi Patel at Columbia University

PTMs continue to be a growing interest to proteomics



PRG 2003 phosphopeptide standard

- 2 digested proteins
- 2 synthetic phosphopeptides

Results:

- 54 labs returned data sets
- 5 identified 1 phosphopeptide
- 5 identified the other
- 3 identified both
- **Massive over reporting**

sPRG 2007 phosphopeptide standard

- Mixture of 7 phosphorylated proteins

Results:

- 44 labs returned data sets
- 50 “known” sites of phosphorylation
- 27 sites identified by multiple labs
- 8 “bonus” sites identified by multiple labs
- Only 5 sites identified by $\geq 50\%$ of labs
- **Over reporting? Interpretation hampered by unknowns**

sPRG 2010 phosphopeptide standard

- 6 digested proteins
- 23 synthetic phosphopeptides

Results:

- 43 labs returned data sets
- All 23 sites identified by multiple labs
- 16 sites identified by $\geq 50\%$ of labs
- Multiply phosphorylated peptides still a challenge

sPRG 2012 phosphopeptide standard

- 6 digested proteins
- 45 synthetic phosphopeptides
 - (including positional isomers)
- 41 synthetic modified peptides
 - sulfated tyrosine
 - nitrosylated tyrosine
 - acetylated lysine
 - mono- di- and tri-methylated arginine/lysine
 - sym/asymmetric di-methylated arginine
- 30 data sets returned

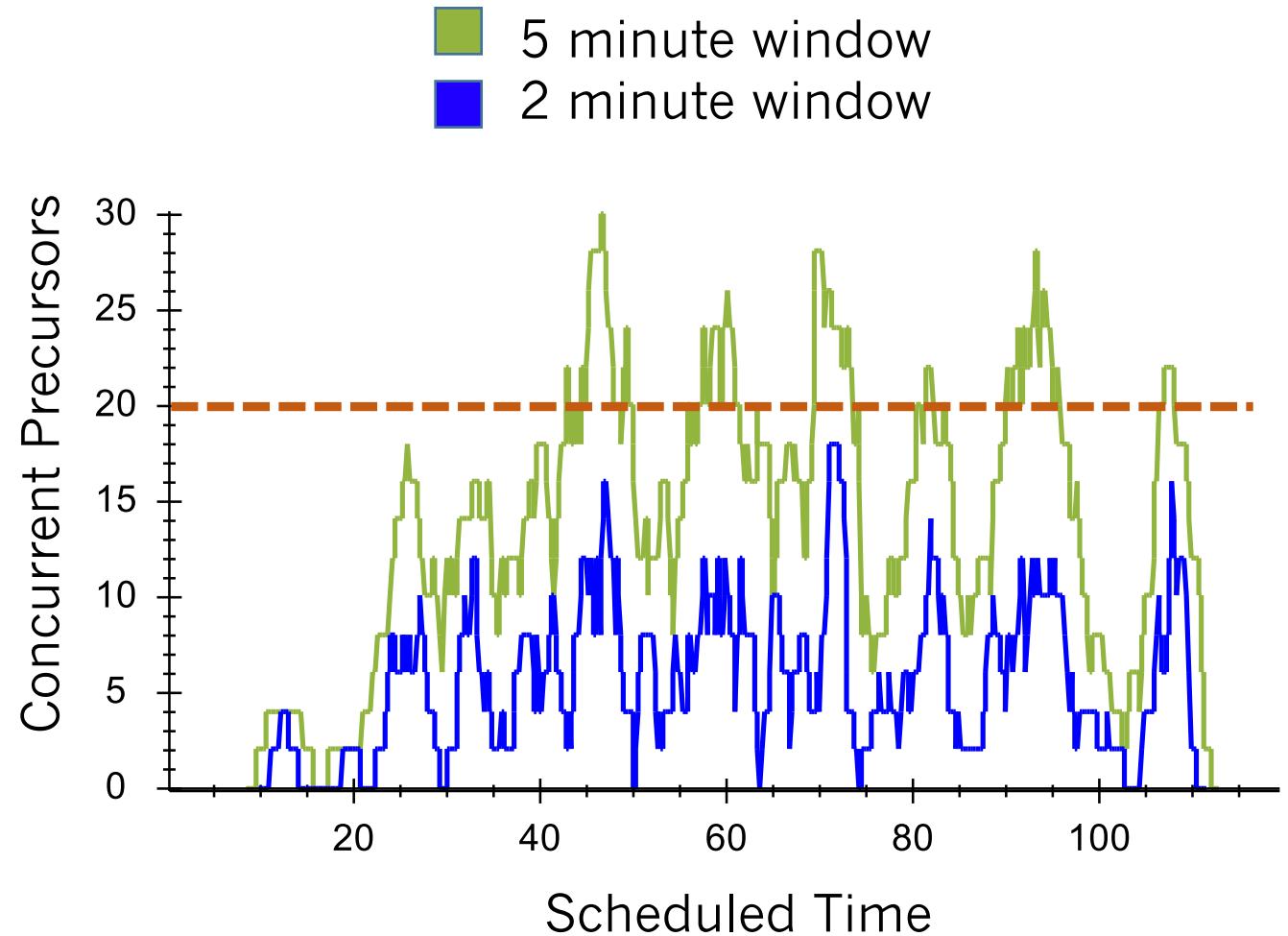
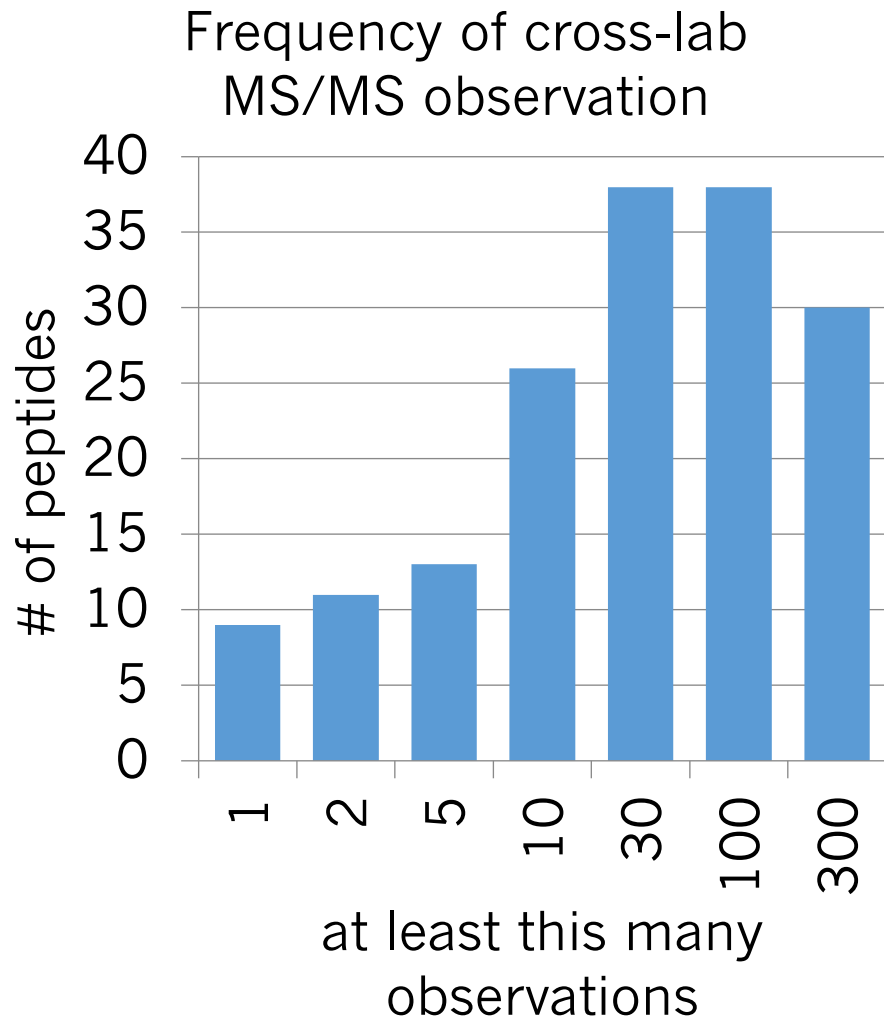
Cross study comparison shows general improvement

	PRG 2003	sPRG 2010	sPRG 2012
SV _p SDYEGK	15%	40%	80%
THILLFLPK _p SVSDYEGK	15%	62%	80%

sPRG 2018 phosphopeptide standard

- 147 biologically interesting synthetic phosphopeptides
- Chosen to cover seven different signaling pathways:
 - AMPK signaling
 - death and apoptosis signaling
 - EGFR/HER signaling
 - insulin/IGF-1 signaling
 - mTOR signaling
 - PI3K/AKT signaling
 - stress (p38/SAPK/JNK) signaling

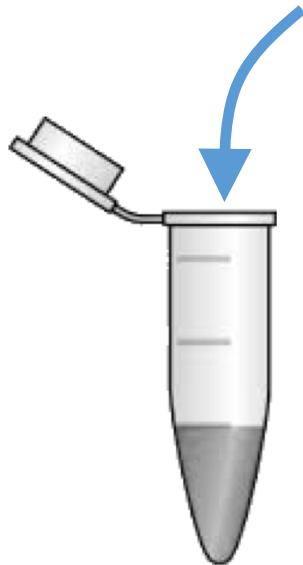
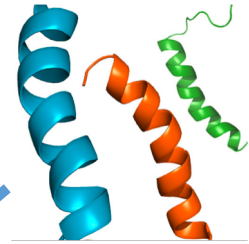
sPRG 2018 phosphopeptide standard



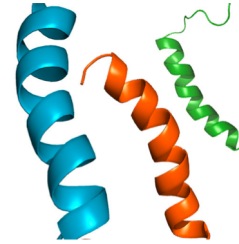
Our goal: to quantify endogenous phosphopeptides

- 60 laboratories requesting samples received two vials:

~5 pmol of
each standard
peptide mixed



~2 pmol peptides

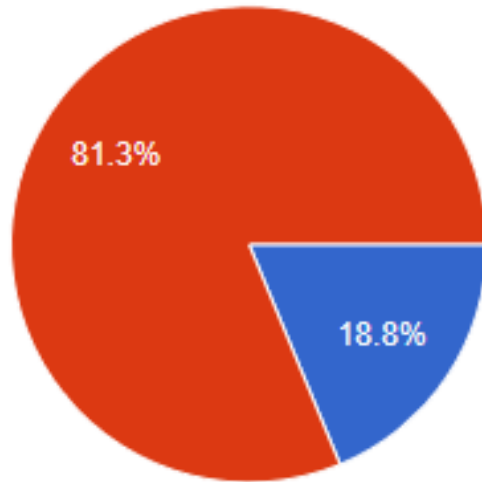


+ 1 mg EGF and
IGF activated
HeLa cell lysate



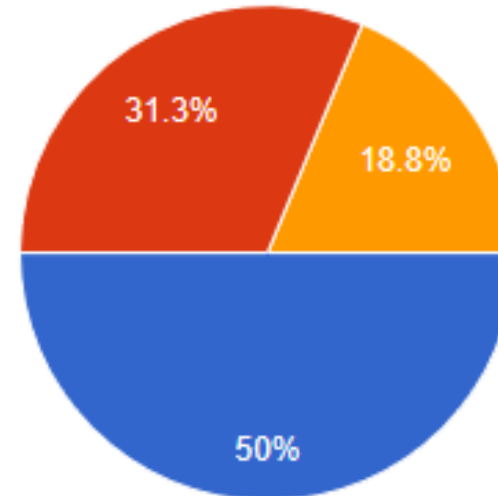
Participant demographics

ABRF membership: 19%



- Member
- Non-member

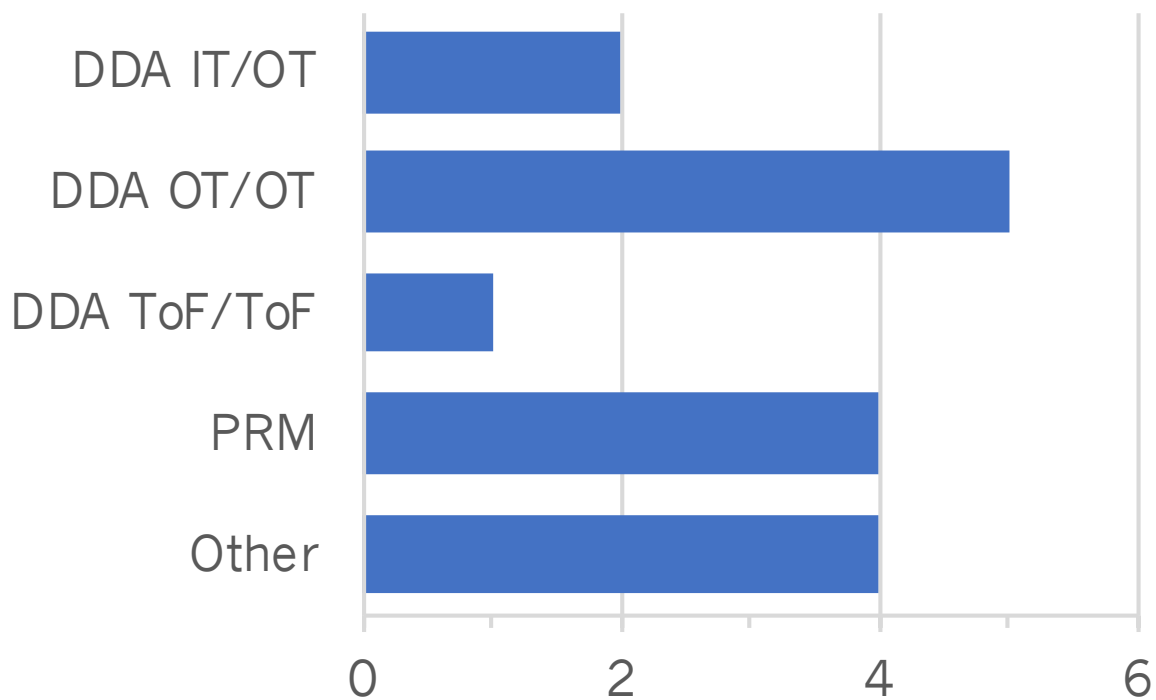
Core status: 69%



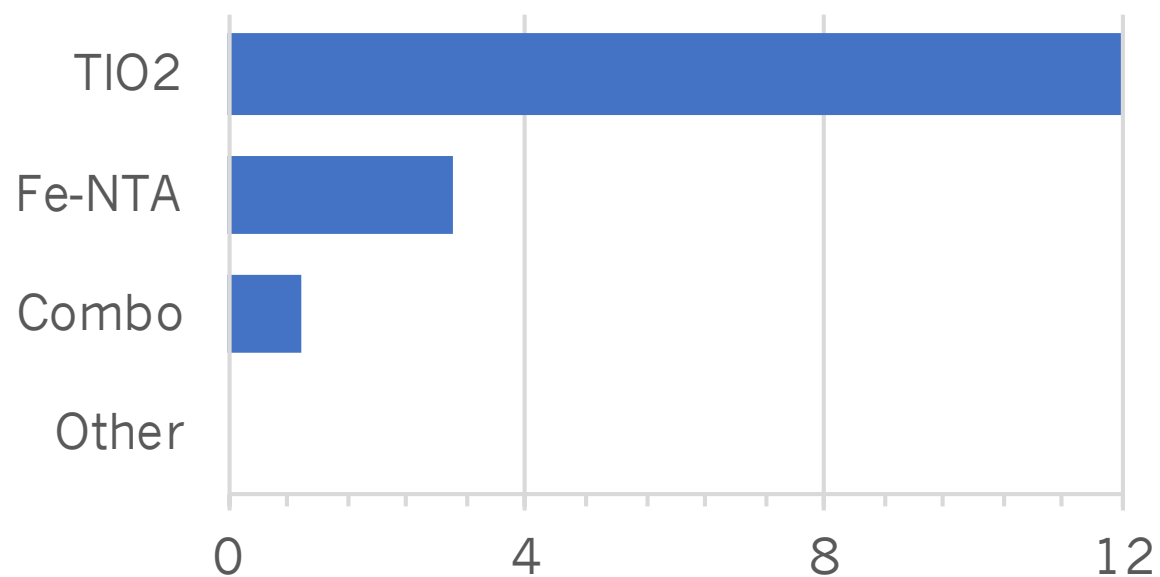
- Core only
- Non-core research lab
- Conduct both core functions and non-core lab research

Participant methods

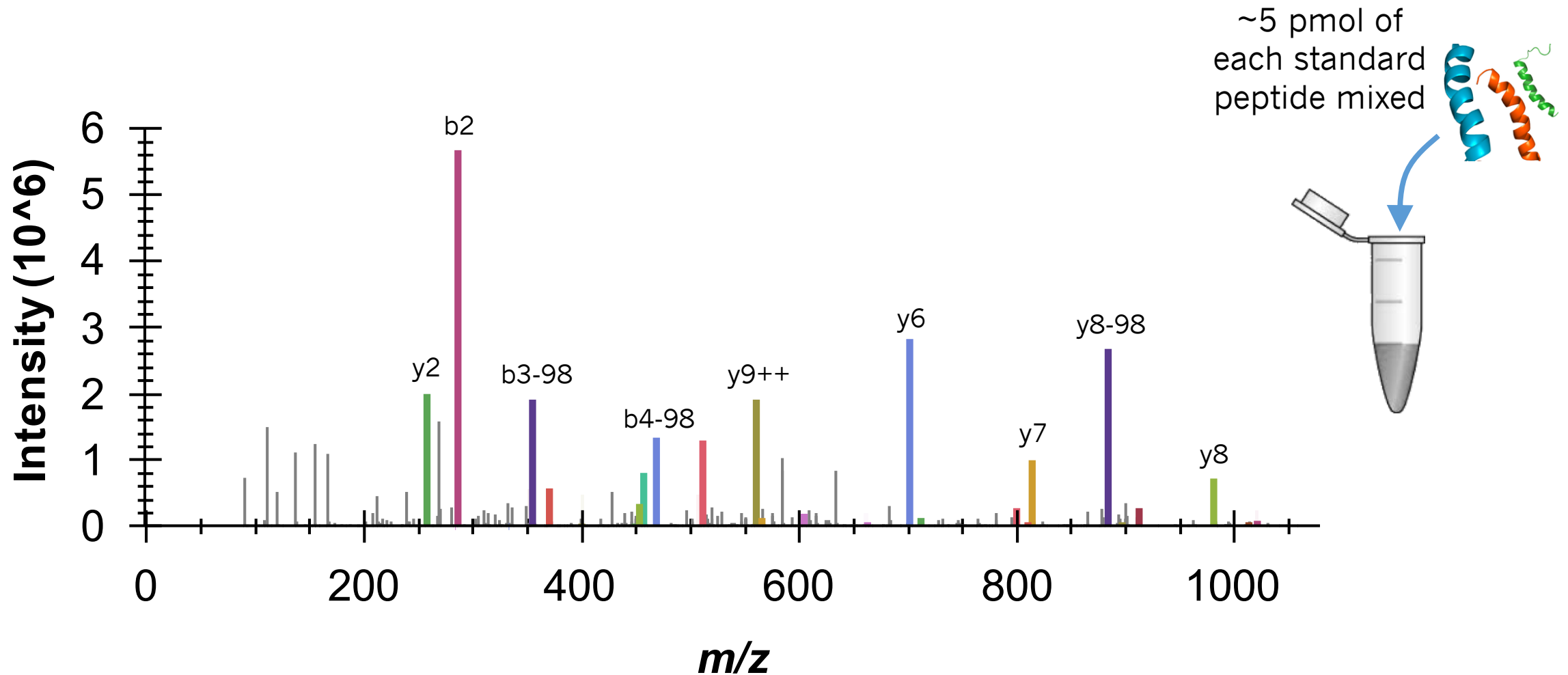
DDA=50%, PRM/SRM/DIA=50%



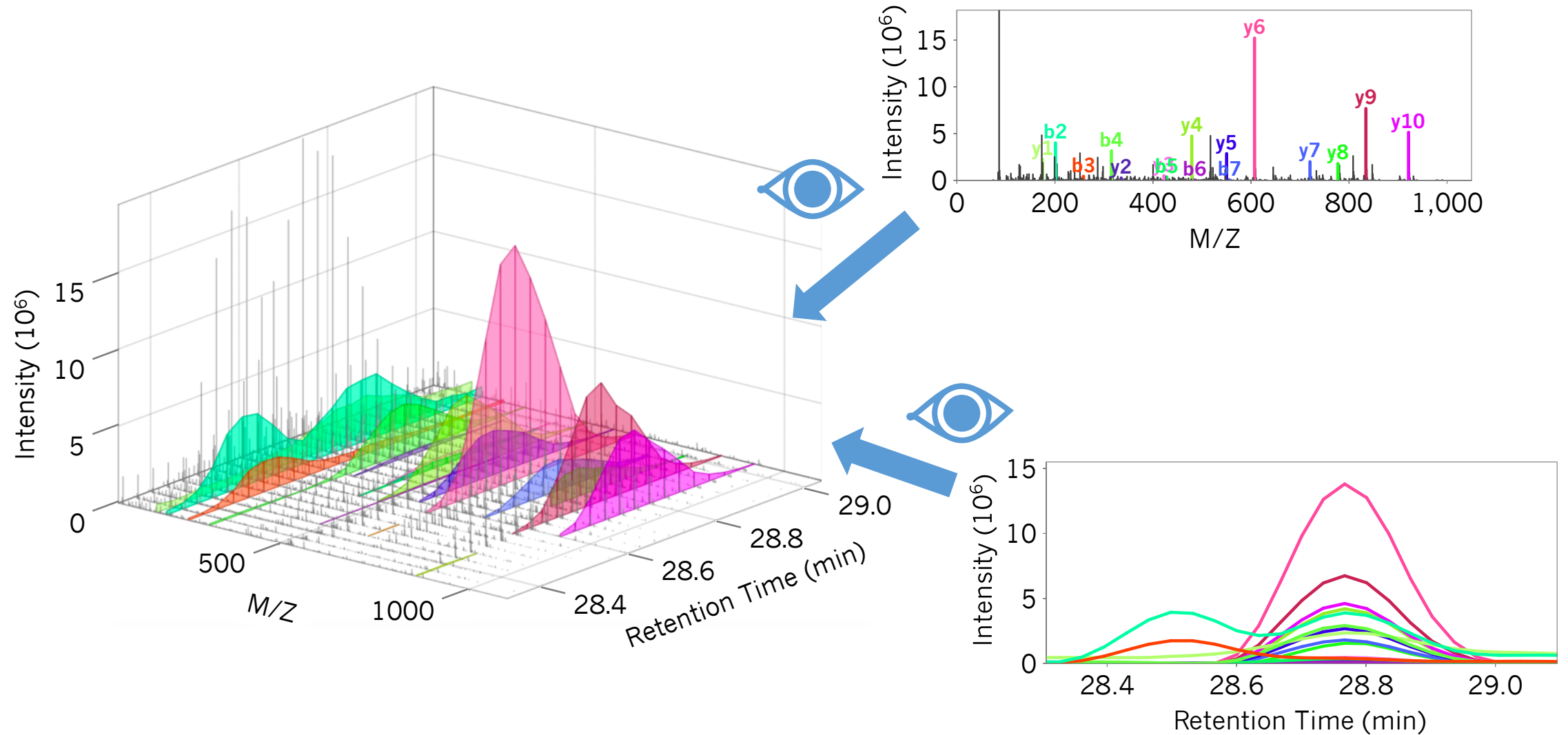
TIO₂=75%, Other=25%



Standard alone enables spectrum library building

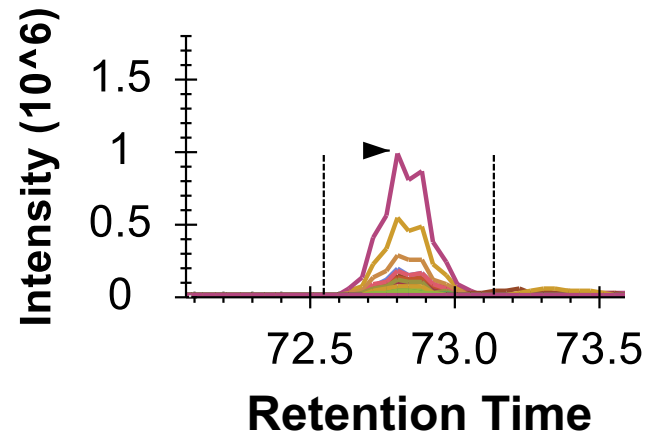


Multiple views of MS/MS data

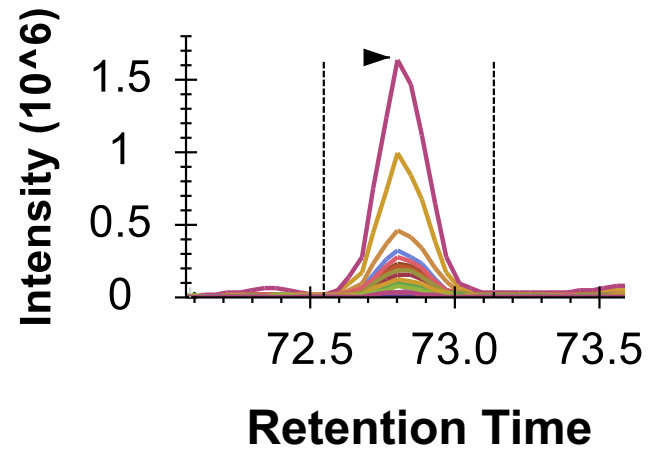


Using the standard to quantify phosphopeptides

Light (endogenous)

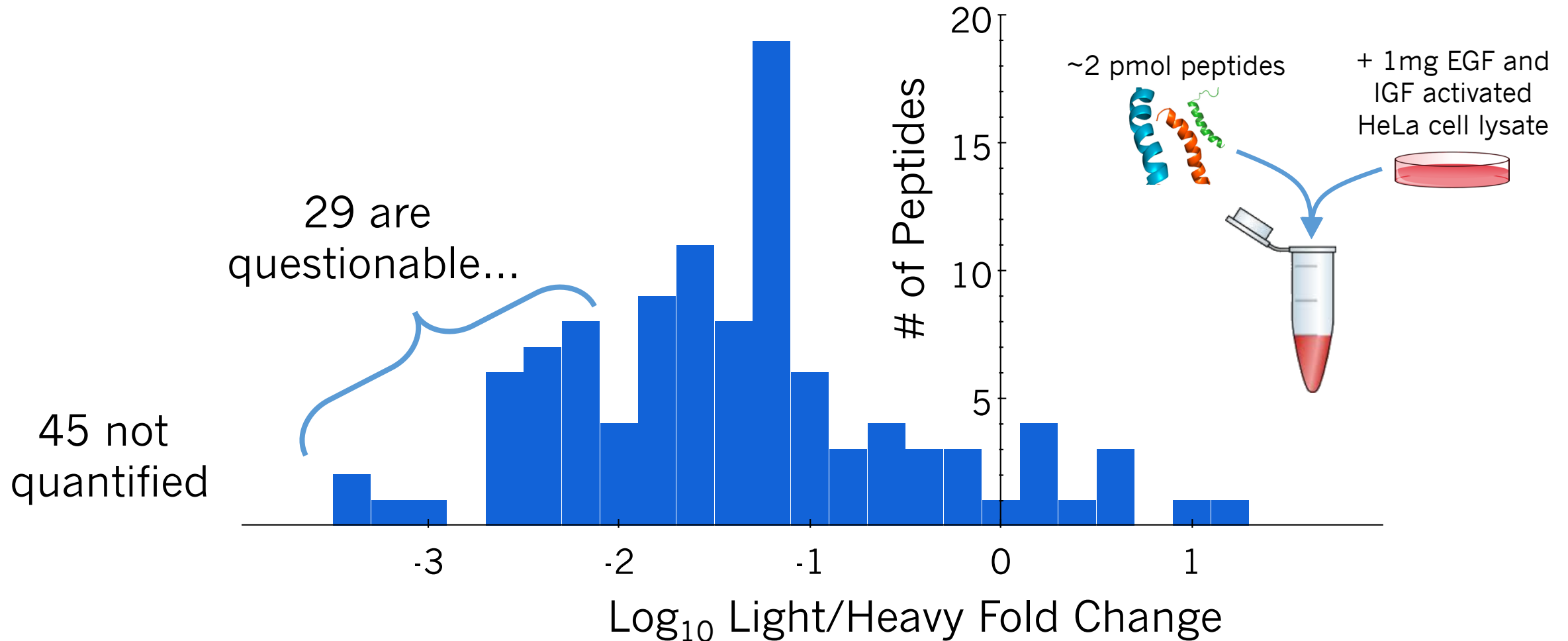


Heavy (standard)

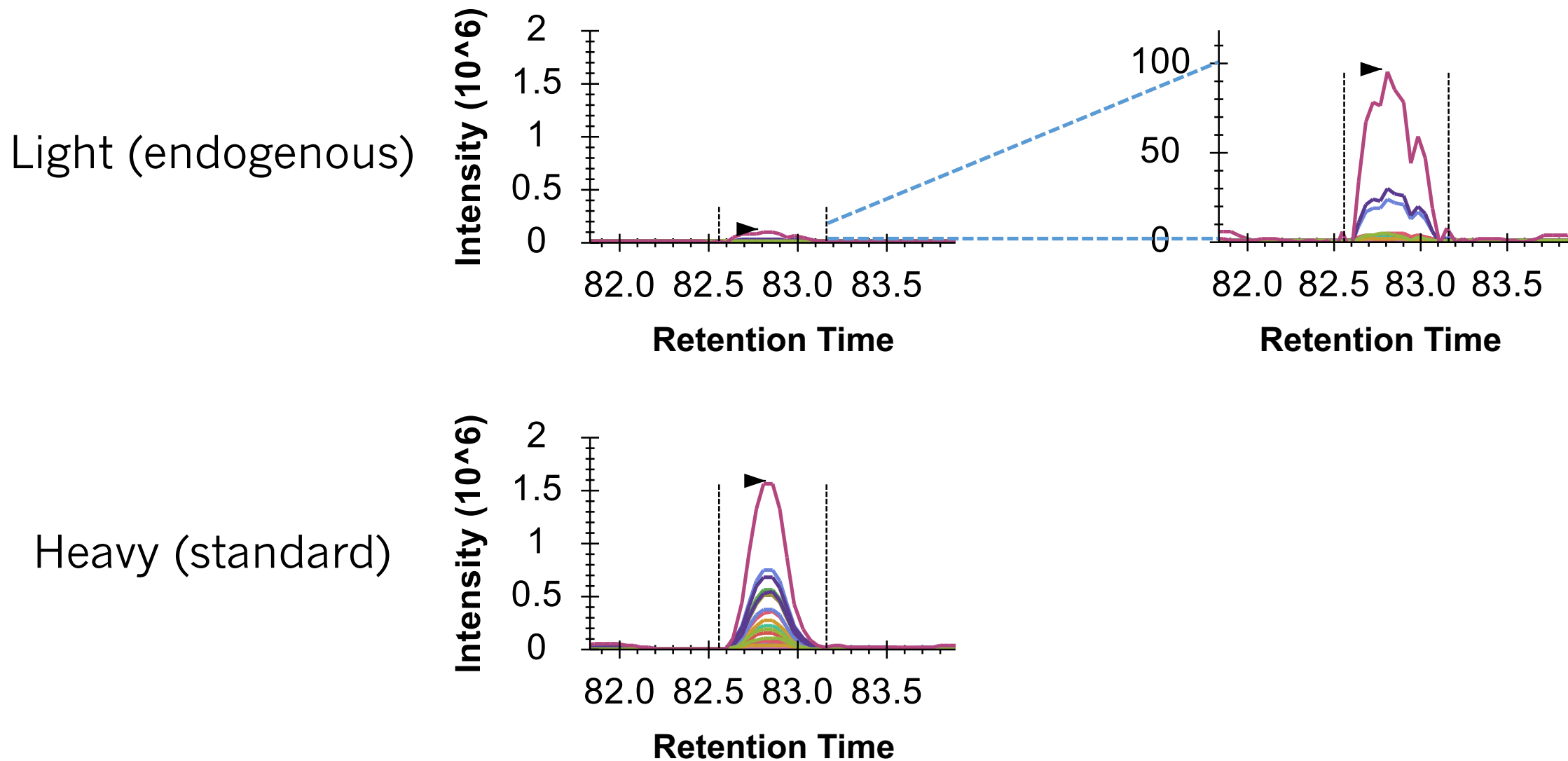


1:1.7 fold change

Many of our biologically interesting peptides are measurable *in vivo*

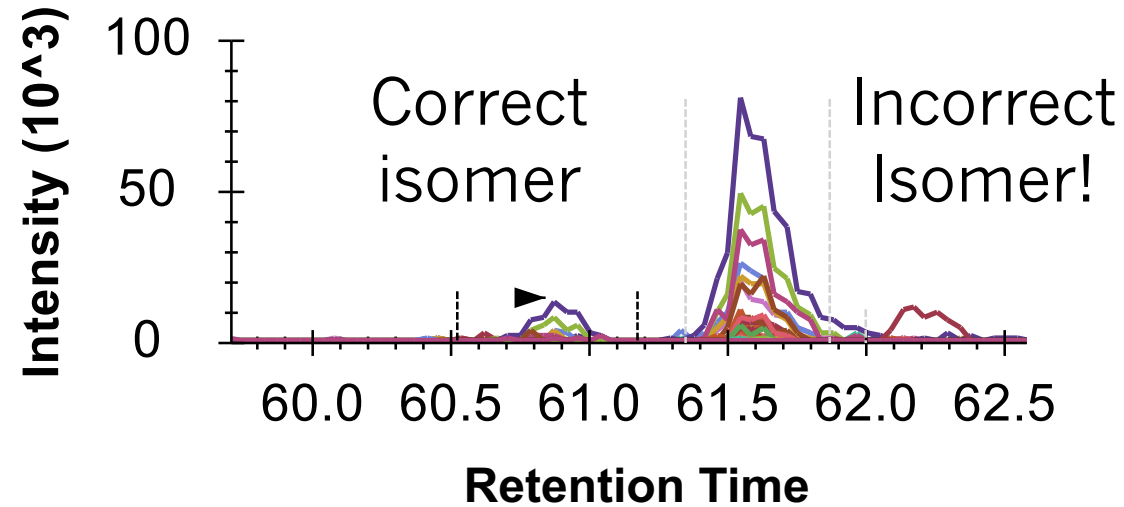


Many peptides are challenging without standards

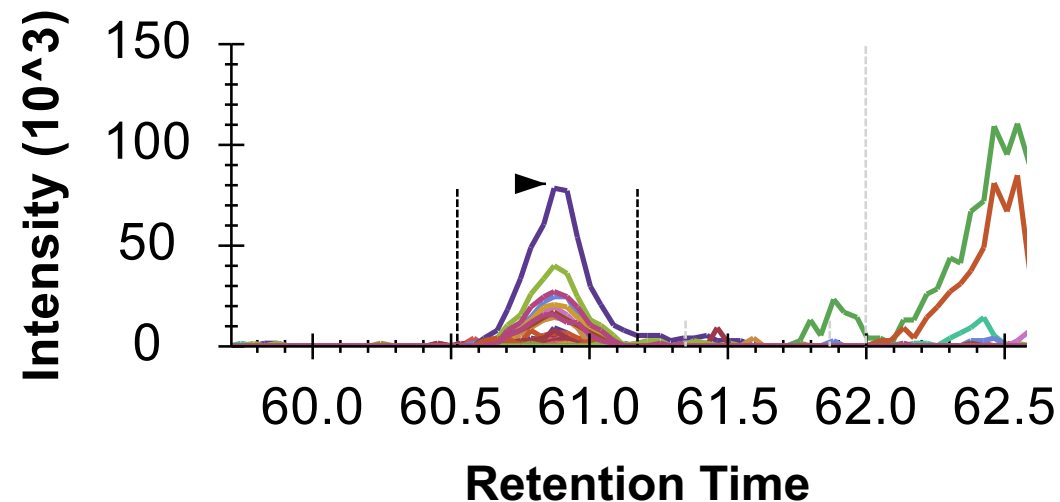


The standard helps determine positional isomers

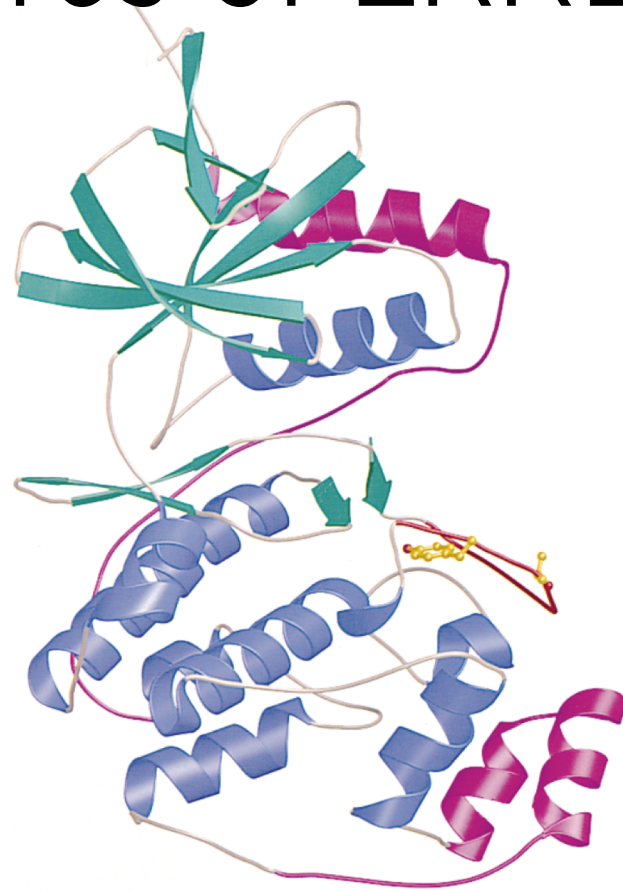
Light (endogenous)



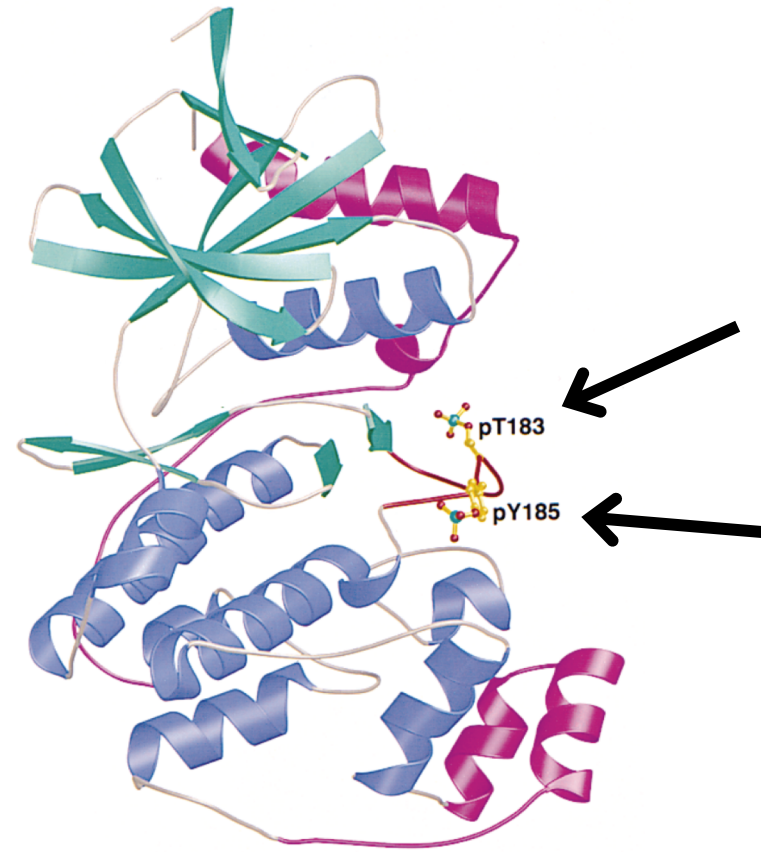
Heavy (standard)



Structures of ERK1/2

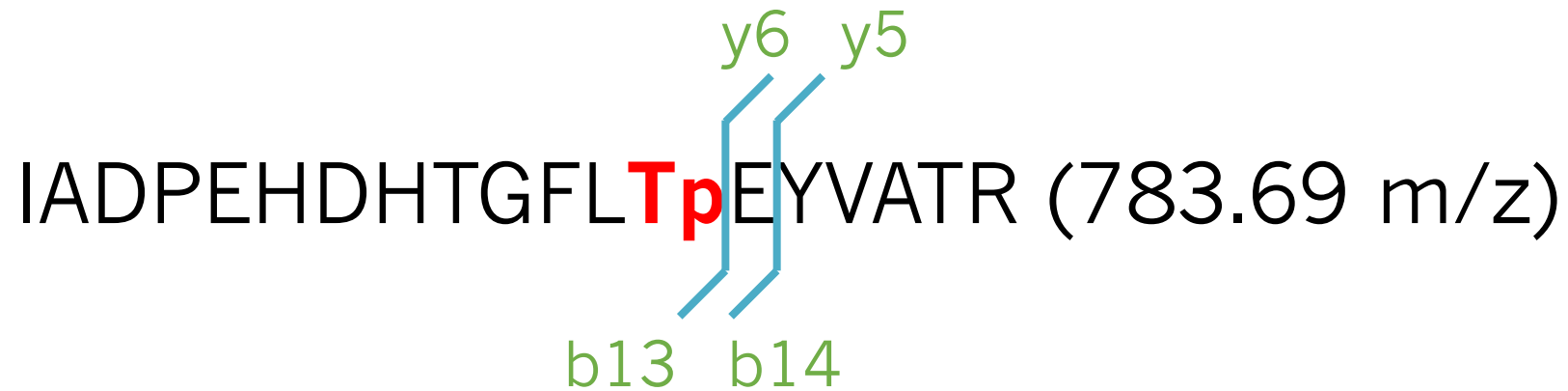


Inactive form

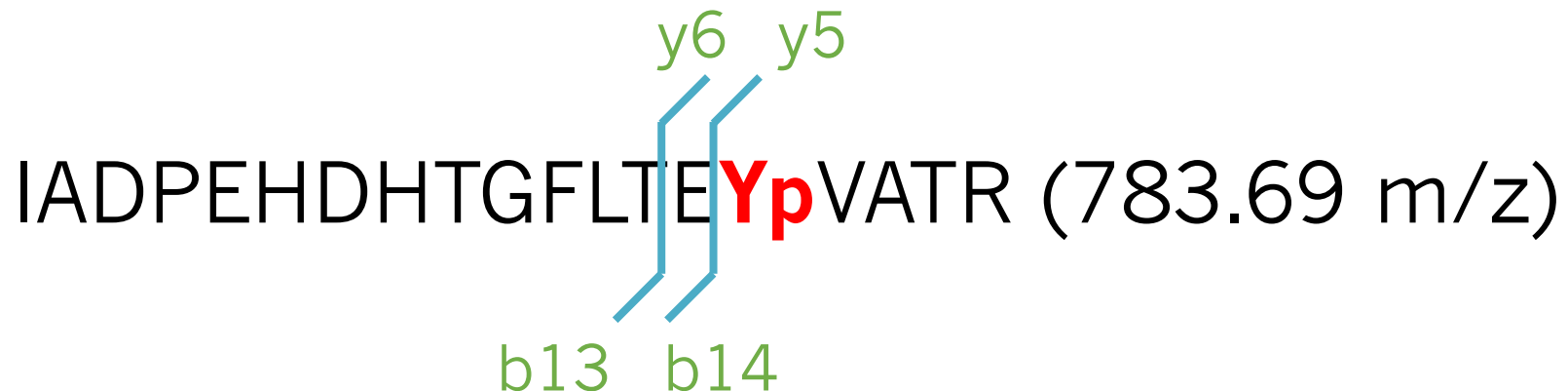


Active form

Differentiating two phosphosites in ERK1



versus

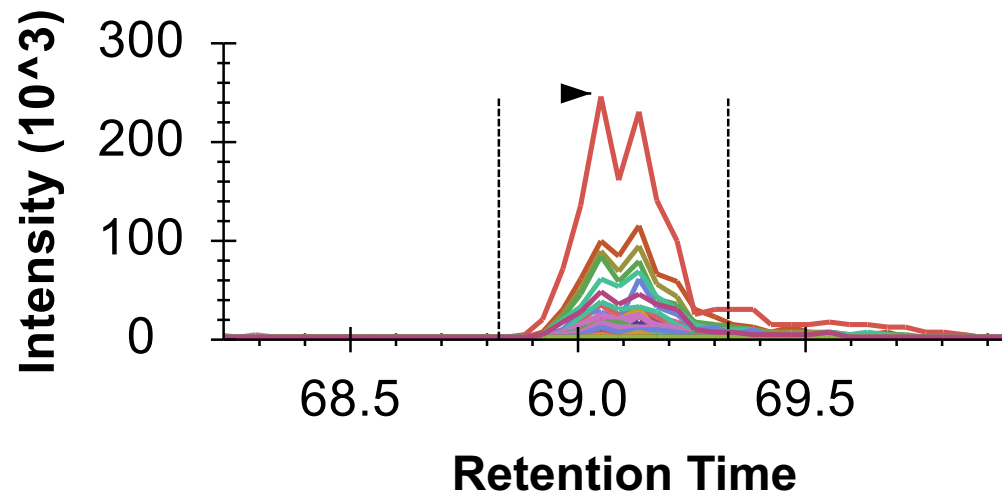


IADPEHDHTGFLTE

Y

VATR

Light
(endogenous)

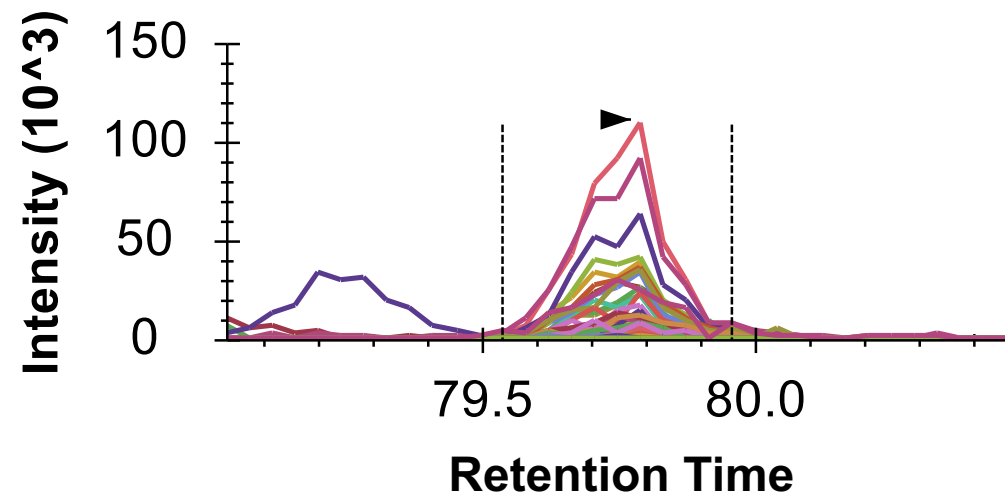


IADPEHDHTGFL

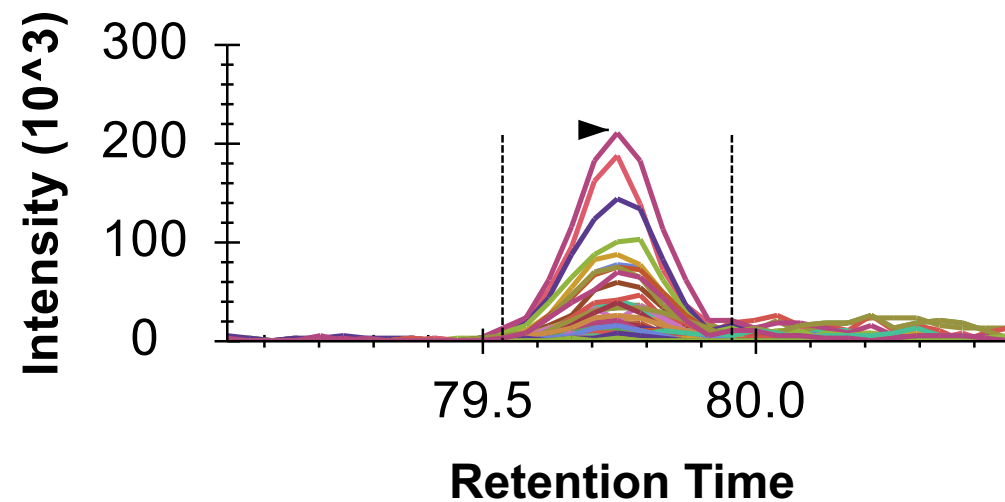
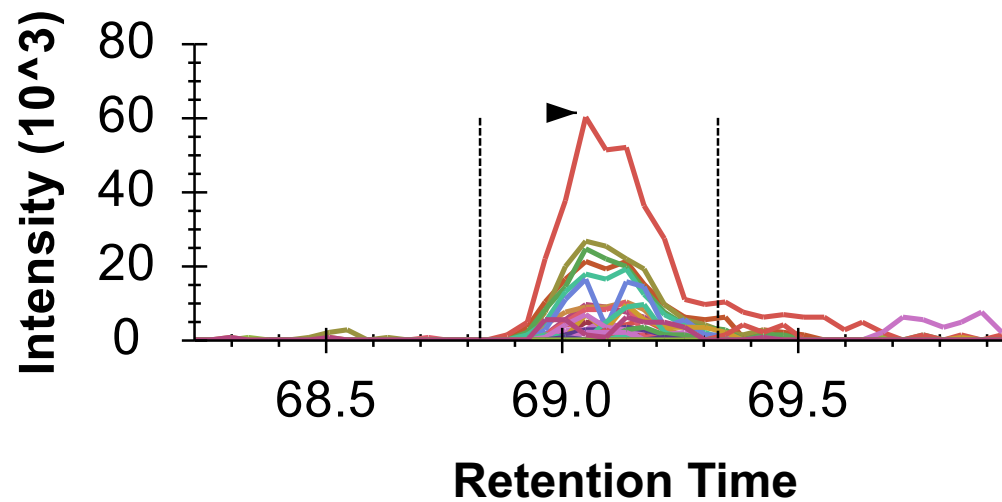
T

EVATR

Intensity (10^3)

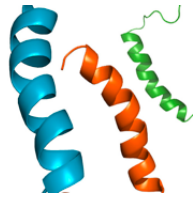


Heavy
(standard)

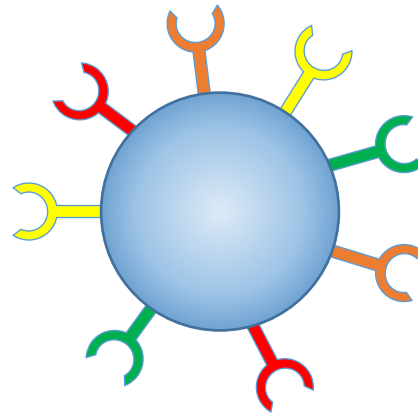
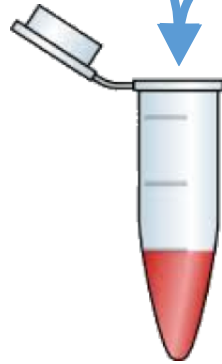


How do we derive an answer key?

~2 pmol peptides



+ 1mg EGF and
IGF activated
HeLa cell lysate

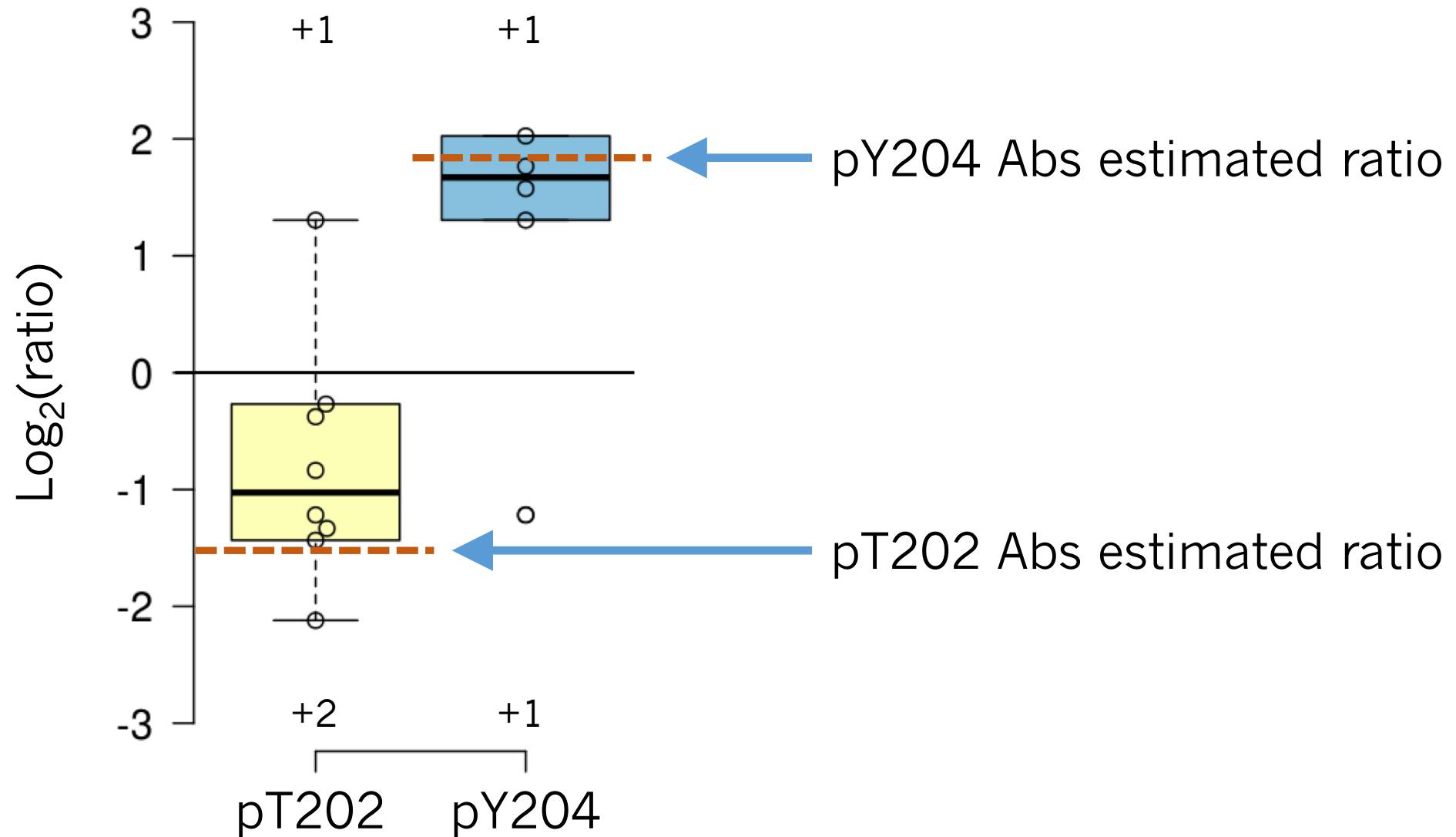


Site specific peptide antibodies
using PTMScan (CST)



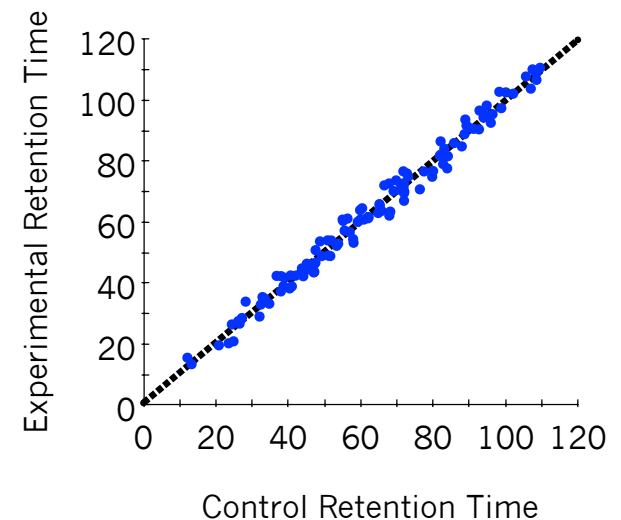
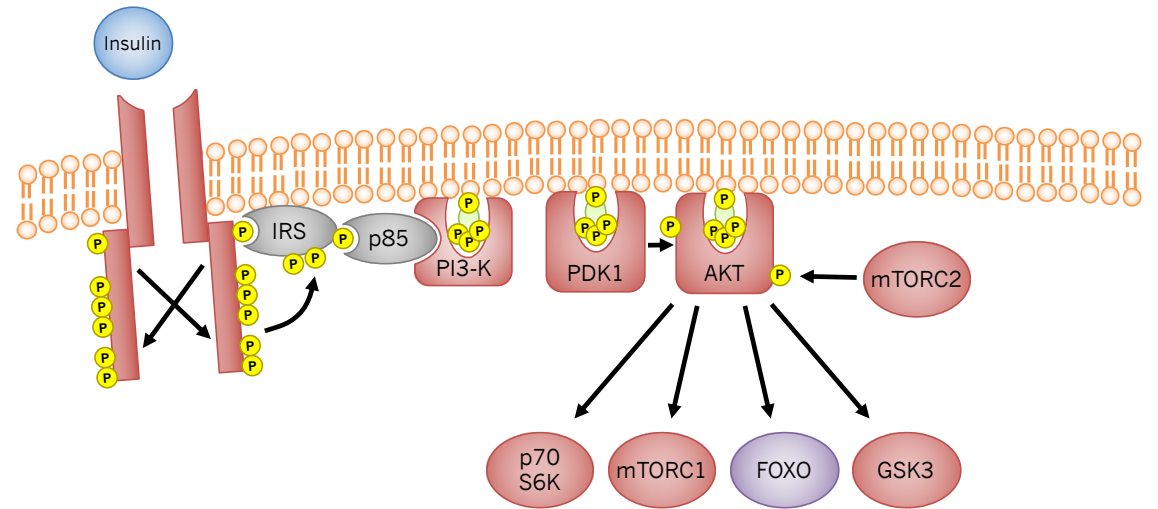
QQQ SRM analysis

How did participants do?



What is this standard good for?

- As a pre-built biological assay
- As an enrichment normalizer/benchmark
- As a phosphopeptide-based retention time standard (e.g. PRTC, iRT)



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Allis Chien (EB Liaison)	Stanford University

sPRG 2019?

Only 15 of 60 participants returned results...

We need more measurements returned!

New participants and new study ideas?

Thanks again!

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Questions? **Poster Board Number: 201**

- As a pre-built biological assay
- As an enrichment normalizer/benchmark
- As a phosphopeptide-based retention time standard (e.g. PRTC, iRT)

