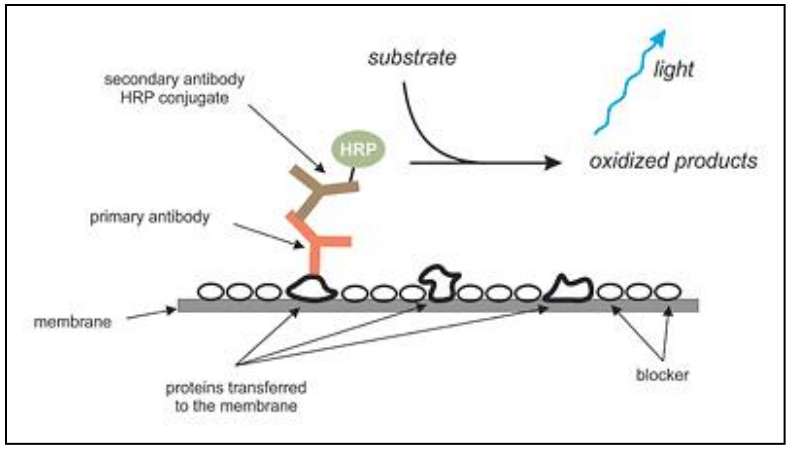
Protein Quantitation II: Multiple Reaction Monitoring

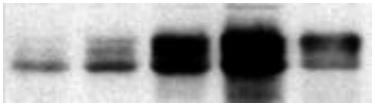
Kelly Ruggles
kelly@fenyolab.org
New York University

Traditional Affinity-based proteomics

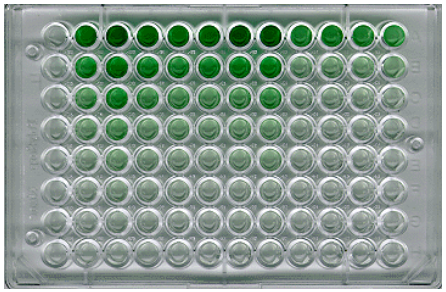
Use antibodies to quantify proteins



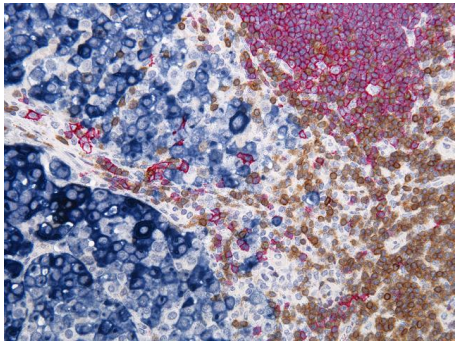
Western Blot



ELISA

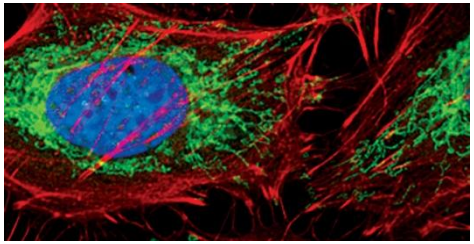


Immunohistochemistry



RPPA

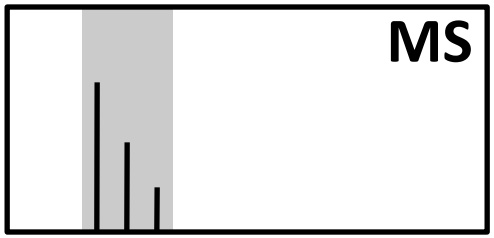
Immunofluorescence



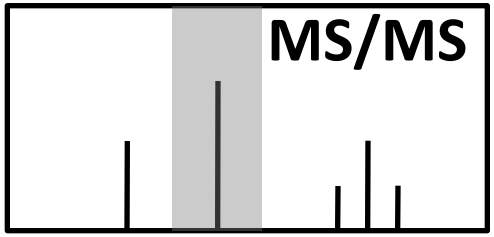
Mass Spectrometry based proteomic quantitation

Shotgun proteomics ← **LC-MS** → **Targeted MS**

1. Records M/Z



2. Selects peptides based on abundance and fragments



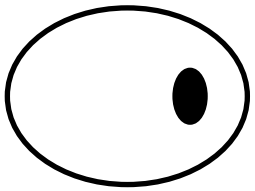
3. Protein database search for peptide identification

Data Dependent Acquisition (DDA)

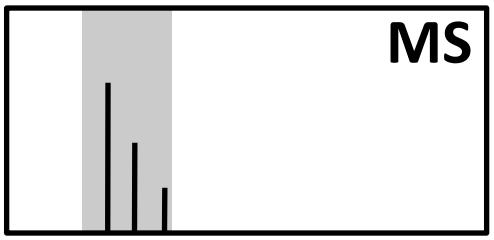
Digestion

Fractionation

Lysis



1. Select precursor ion



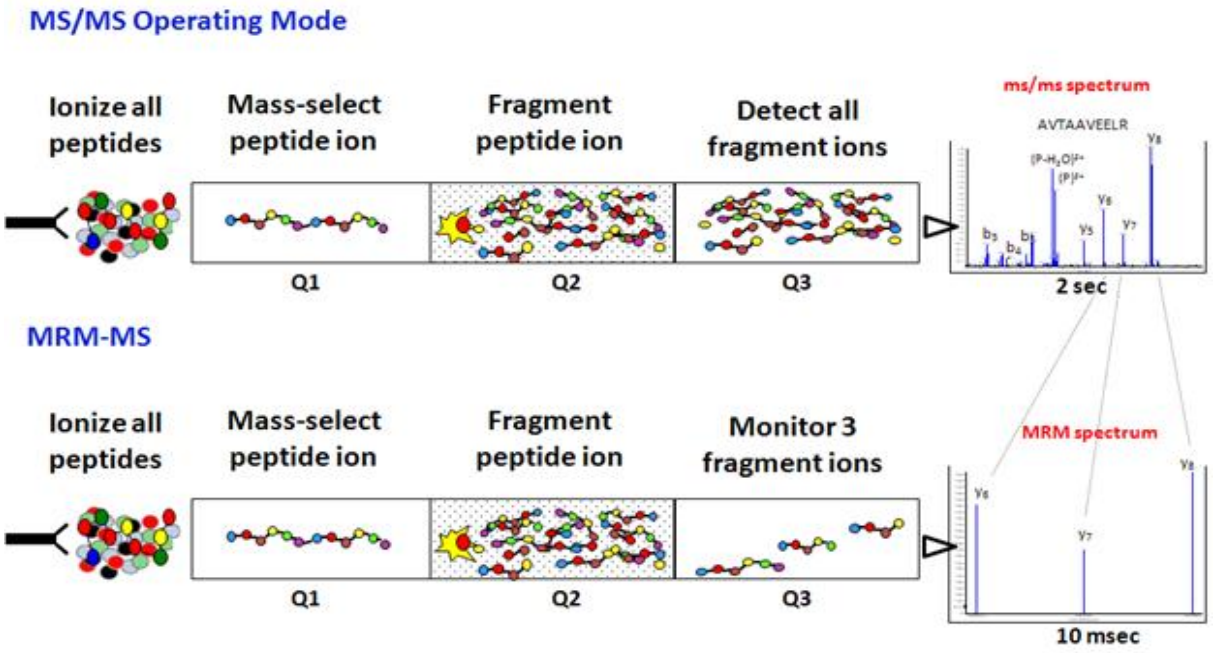
2. Precursor fragmentation

3. Use Precursor-Fragment pairs for identification

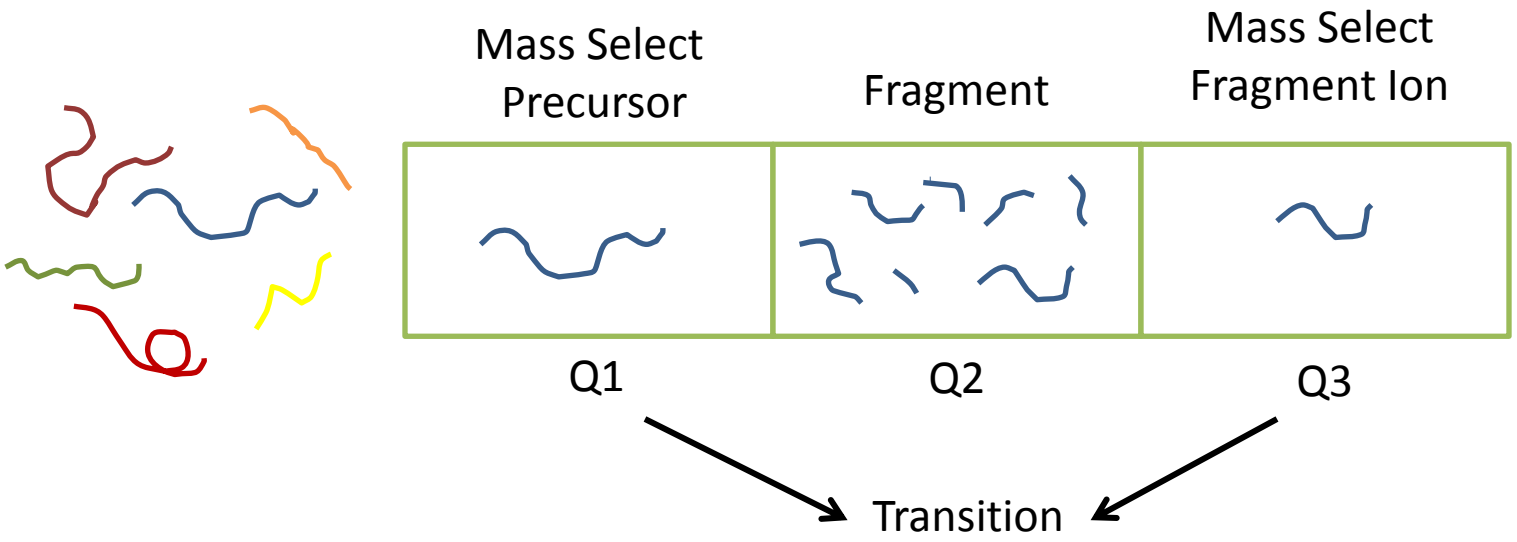
Uses predefined set of peptides

Multiple Reaction Monitoring (MRM)
Selected Reaction Monitoring (SRM)

- Triple Quadrupole acts as ion filters
- Precursor selected in first mass analyzer (Q1)
- Fragmented by collision activated dissociation (Q2)
- One or several of the fragments are specifically measured in the second mass analyzer (Q3)



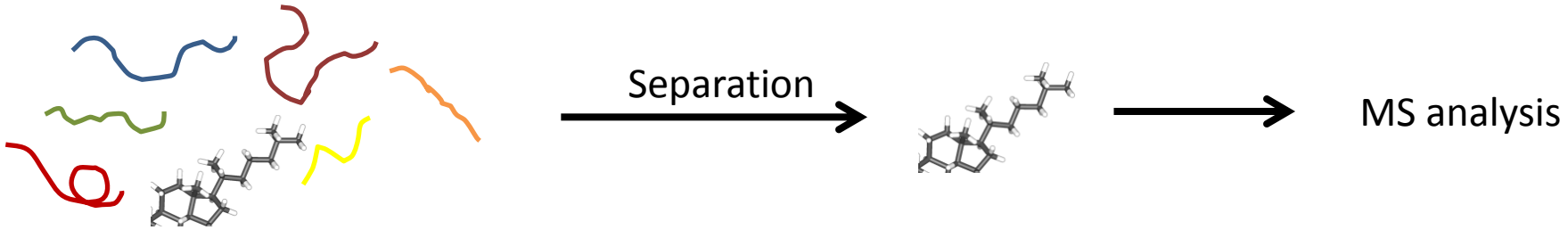
Peptide Identification with MRM



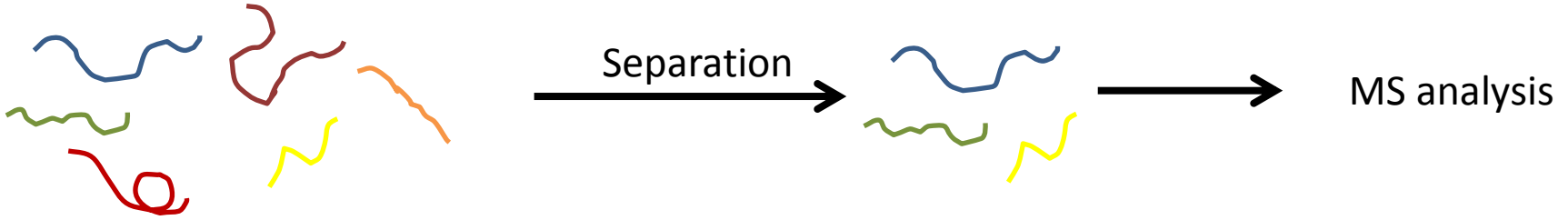
- Transition: Precursor-Fragment ion pair are used for protein identification
- Select both Q1 and Q3 prior to run
  - Pick Q3 fragment ions based on discovery experiments, spectral libraries
  - Q1 doubly or triply charged peptides
- Use the 3 most intense transitions for quantitation

Peptide Identification with MRM

- Used for to analyze small molecules since the late 1970s
- More recently, used for proteins and peptide quantitation in complex biological matrices
  - Particularly for biomarker discovery
- With small molecules, the matrix and analyte have different chemical natures so separation step is able to remove other components from analytes



- With proteomics, both the analytes and the background matrix are made up of peptides, so this separation cannot occur



Strengths of MRM

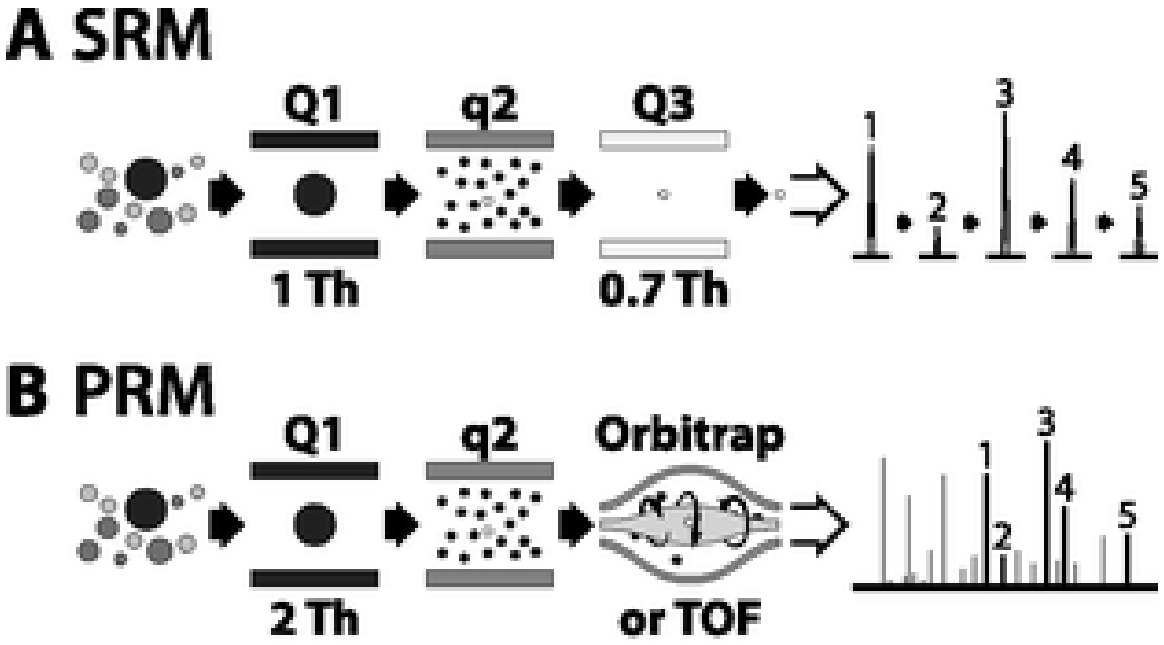
- Can detect multiple transitions on the order of 10msec per transition
- Can analyze many peptides (100s) per assay and the monitoring of many transitions per peptide
- High sensitivity
- High reproducibility
- Detects low level analytes even in complex matrix
- Golden standard for quantitation!

Weaknesses of SRM

- Focuses on defined set of peptide candidates
  - Need to know charge state, retention time and relative product ion intensities before experimentation
- Physical limit to the number of transitions that can be measured at once
  - Can get around this by using time-scheduled SRM, monitor transitions for a peptide in small window near retention time

Parallel Reaction Monitoring (PRM)

- Q3 is substituted with a high resolution mass analyzer to detect all target product ions
- Generates high resolution, full scan MS/MS data
- All transitions can be used to confirm peptide ID
- Don’t have to choose ions beforehand



Peterson et al., 2012

Applications of MRM

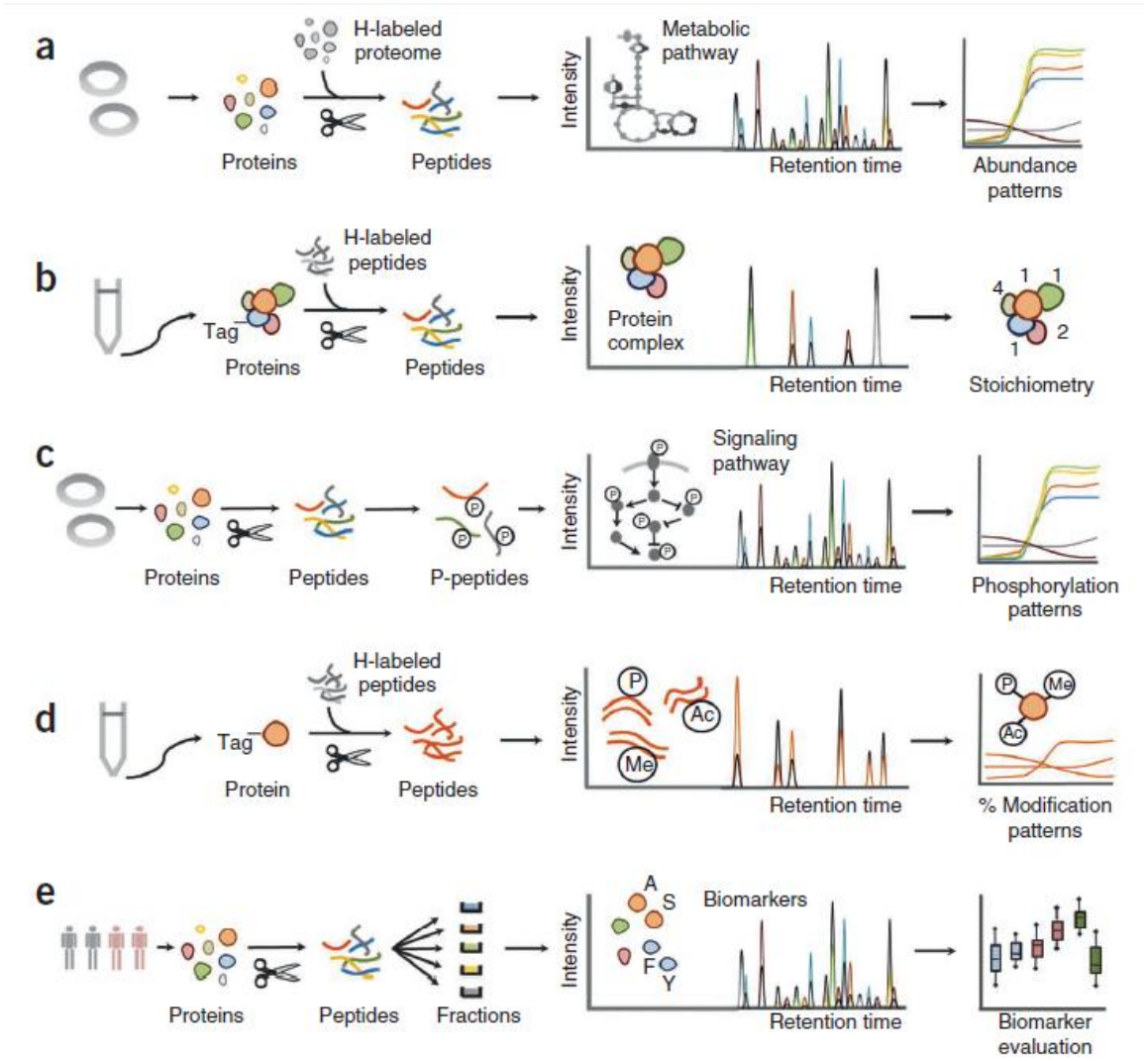
Metabolic pathway analysis

Protein complex subunit stoichiometry

Phosphorylation

Modifications within protein

Biomarkers: protein indicator correlating to a disease state

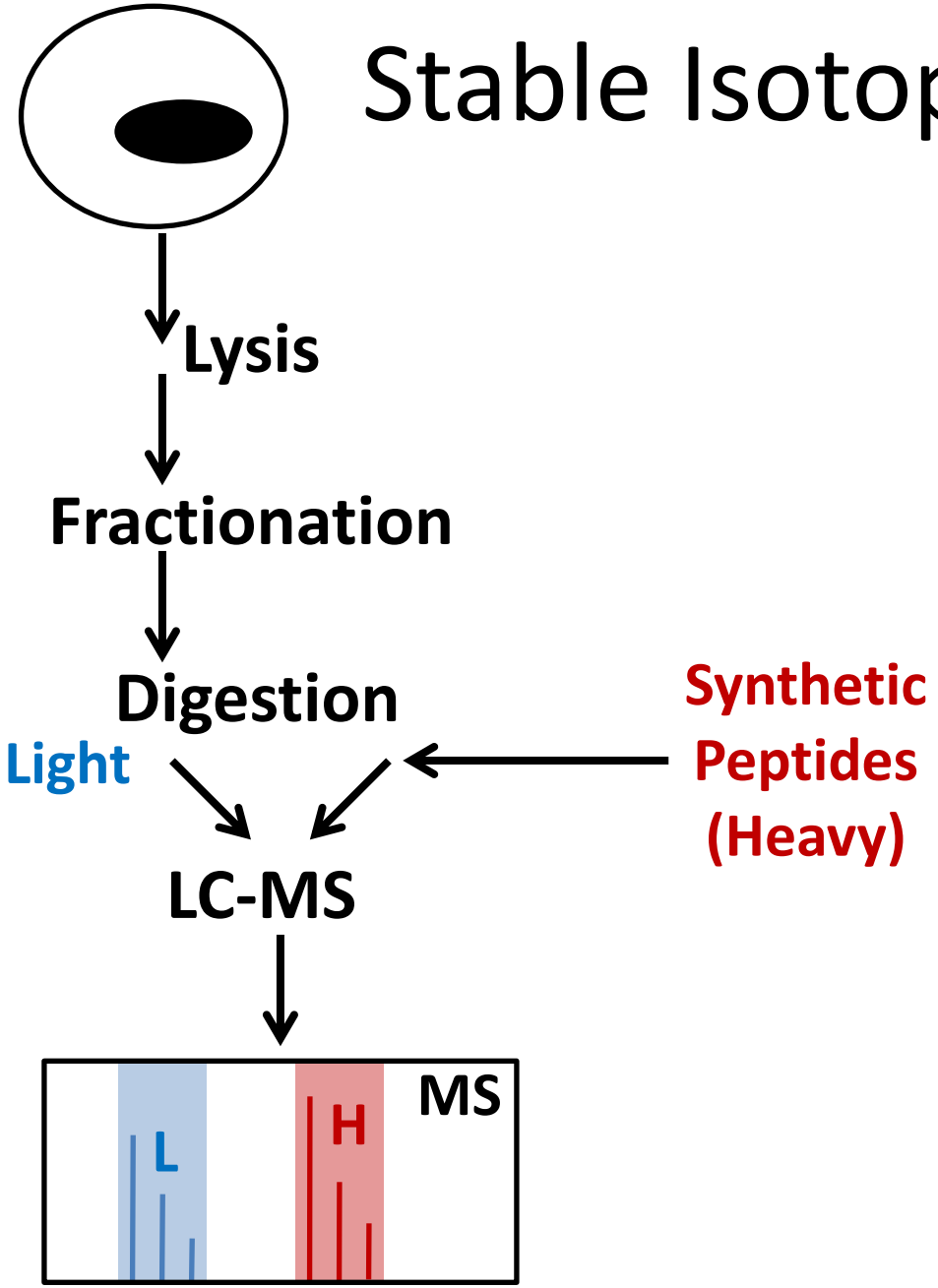


Can enrich for proteins/peptides using antibody

Label-free quantification

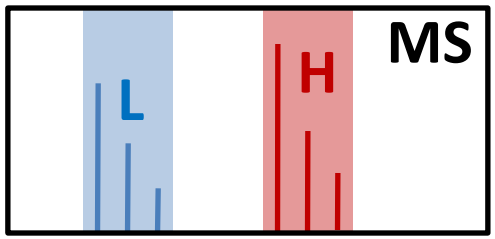
- Usually use 3 or more precursor-product ion pairs (transitions) for quantitation
- Relies on direct evaluation of MS signal intensities of naturally occurring peptides in a sample.
- Simple and straightforward
- Low precision
- Several peptides for each protein should be quantified to avoid false quantification

Stable Isotope Dilution (SID)



- Use isotopically labeled reference protein
- 13C and/or 15N labeled peptide analogs
- Chemically identical to the target peptide but with mass difference
- Add known quantity of heavy standard
- Compare signals for the light to the heavy reference to determine for precise quantification

Quantification Details



SIS: Stable Isotope Standard
PAR: Peak Area Ratio

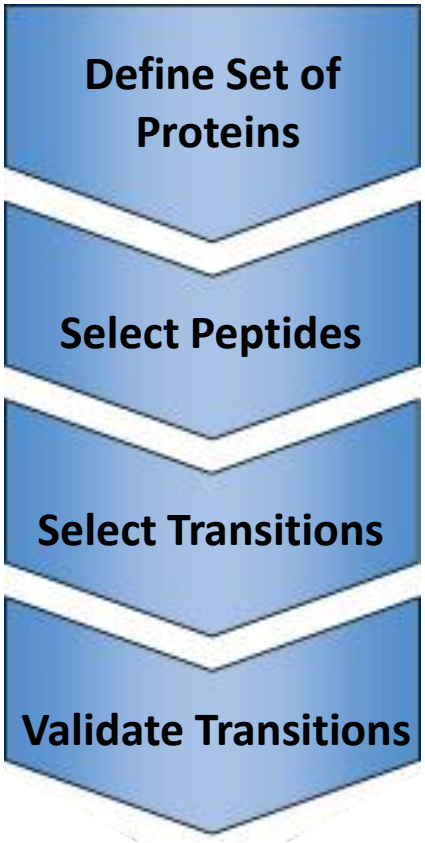
$$\text{PAR} = \frac{\text{Light (Analyte) Peak Area}}{\text{Heavy (SIS) Peak Area}}$$

Analyte concentration= PAR*SIS peptide concentration

-Use at least 3 transitions

-Have to make sure these transitions do not have interferences

Workflow of SRM proteomics



Clinical/Biological Question

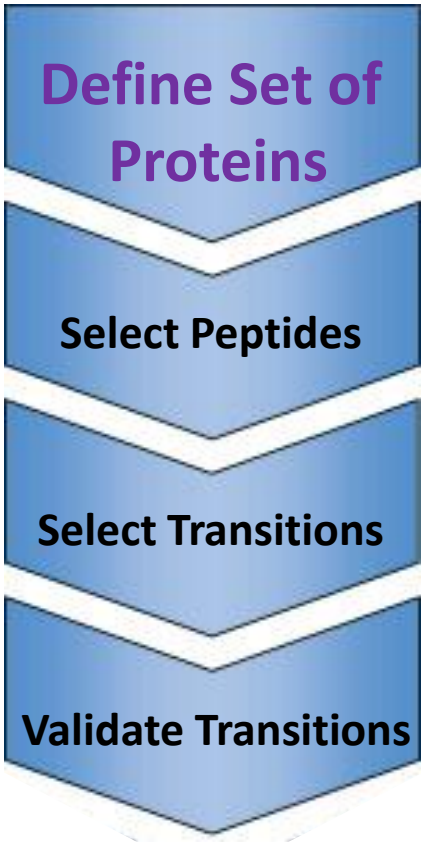
Proteotypic
LC and MS properties

Intensity of transitions
Interferences

Experimental Measurements

Protein Quantitation

Workflow of SRM proteomics



Clinical/Biological Question

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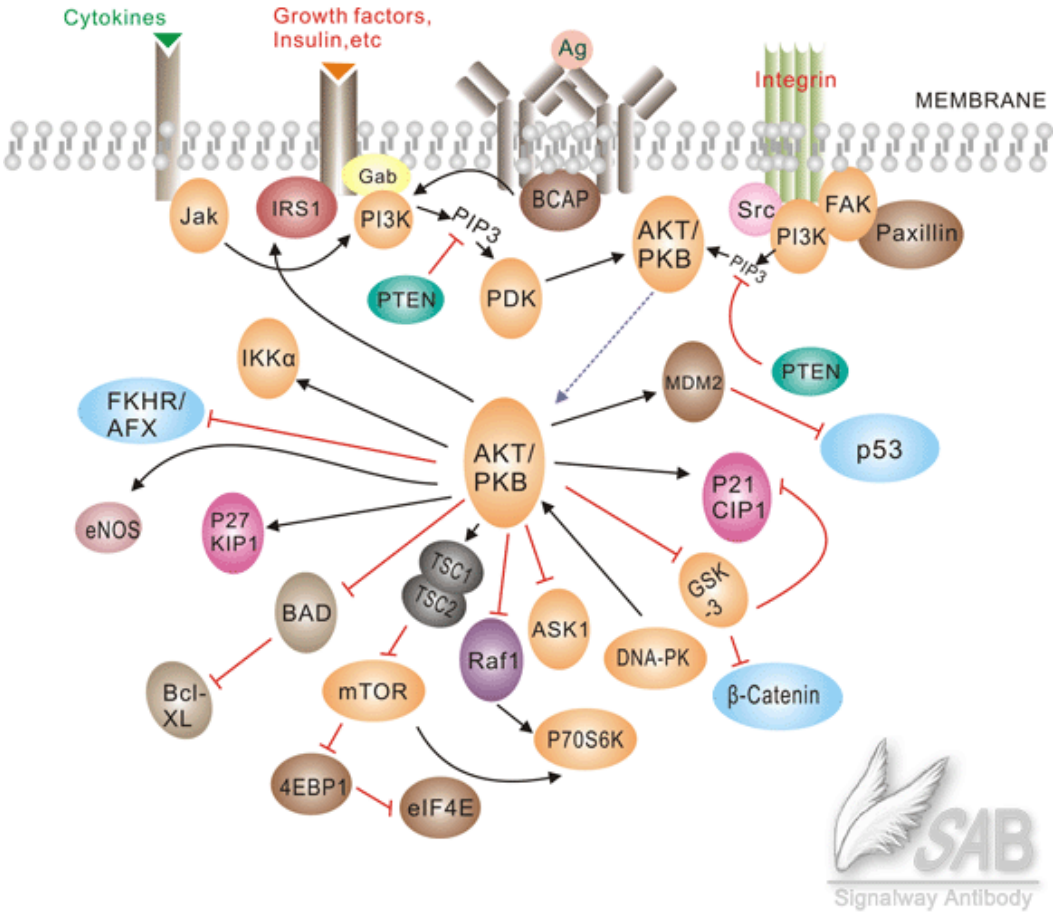
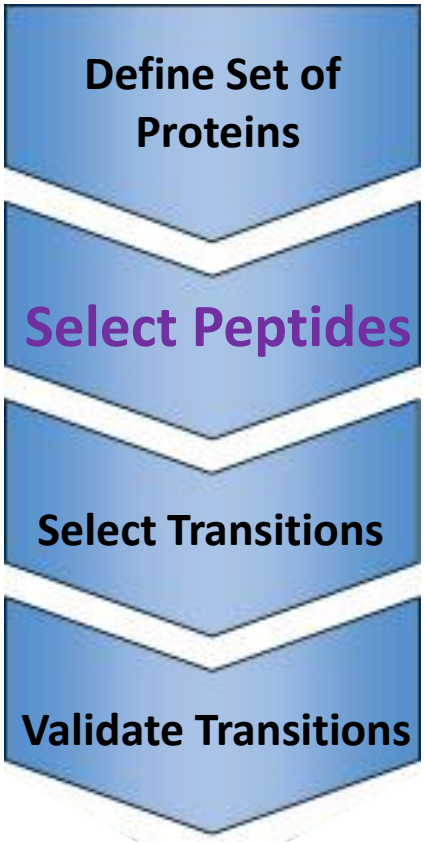
Motivating Example: AKT1 and Breast Cancer



Workflow of SRM proteomics



Clinical/Biological Question

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Protein Quantitation

Selecting Peptides

- A few representative peptides will be used to quantify each protein
- Need to fulfill certain characteristics
  - Have an unique sequence
  - Consistently observed by LC-MS methods
  - 8-25 amino acids
  - Good ionization efficiency
  - m/z within the range of the instrument
  - No missed cleavages
  - Not too hydrophillic (poorly retained) or hydrophobic (may stick to column)

Identifying Proteotypic Peptides

Set of Proteins

Trypsin

Peptides

RefSeq
Ensembl
Uniprot

Proteotypic Peptides

Step 1: Full protein sequence in FASTA format

```
MPKKKPTPIQLNPAPDGSAVNGTSSAETNLEALQKKLEELELDEQQRKRLEAFLTQKQKVGELKDDDFEK
ISELGAGNGGVVFKVSHKPSGLVMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFYSDGEIS
ICMEHMDGGSLDQVLKKAGRIPEQILGKVSIAVIKGLTYLREKHKIMHRDVKPSNILVNSRGEIKLCDFG
VSGQLIDSMANSFVGTRSYMSPERLQGTHYSVQSDIWSMGLSLVEMAVGRYPIPPPDAKELELMFGCQVE
GDAAETPPRPRTPGRPLSSYGMDSRPPMAIFELLDYIVNEPPPKLPSGVFSLEFQDFVNKCLIKNPAERA
DLKQLMVHAFIKRSDAEEVDFAGWLCSTIGLNQPSTPTHAAGV
```

Step 2: Tryptic Peptides

```
PTPIQLNPAPDGSAVNGTSSAETNLEALQK
LEAFLTQK
PSNIVLVNSR
LEELELDEQQR
DDDFEK.....
```

Step 3: Compare to human reference database
-Contain all peptide sequences
-Find all peptides that only map back to one gene

PTPIQLNPAPDGSAVNGTSSAETNLEALQK
LEAFLTQK
PSNIVLVNSR
LEELELDEQQR
DDDFEK.....

Match peptide to proteins
(Reference Protein DB)

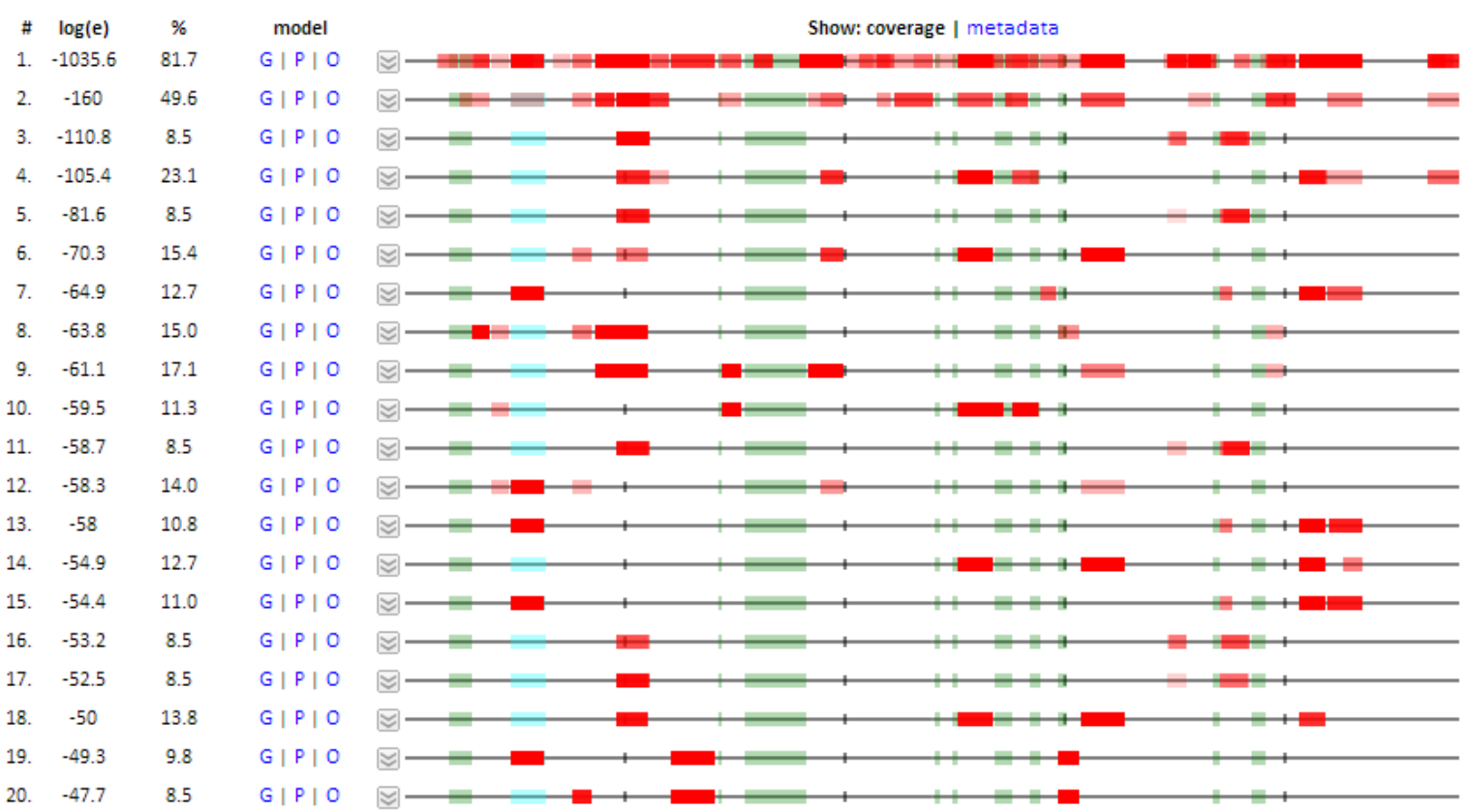
Match proteins to genes
(Using protein names and genomic DB)

LC/MS Properties: GPMDB

-Compares peptides to a collection of previously observed results

-Determines how many times the peptide has been observed by others

-<u>Most proteins show very reproducible peptide patterns</u>

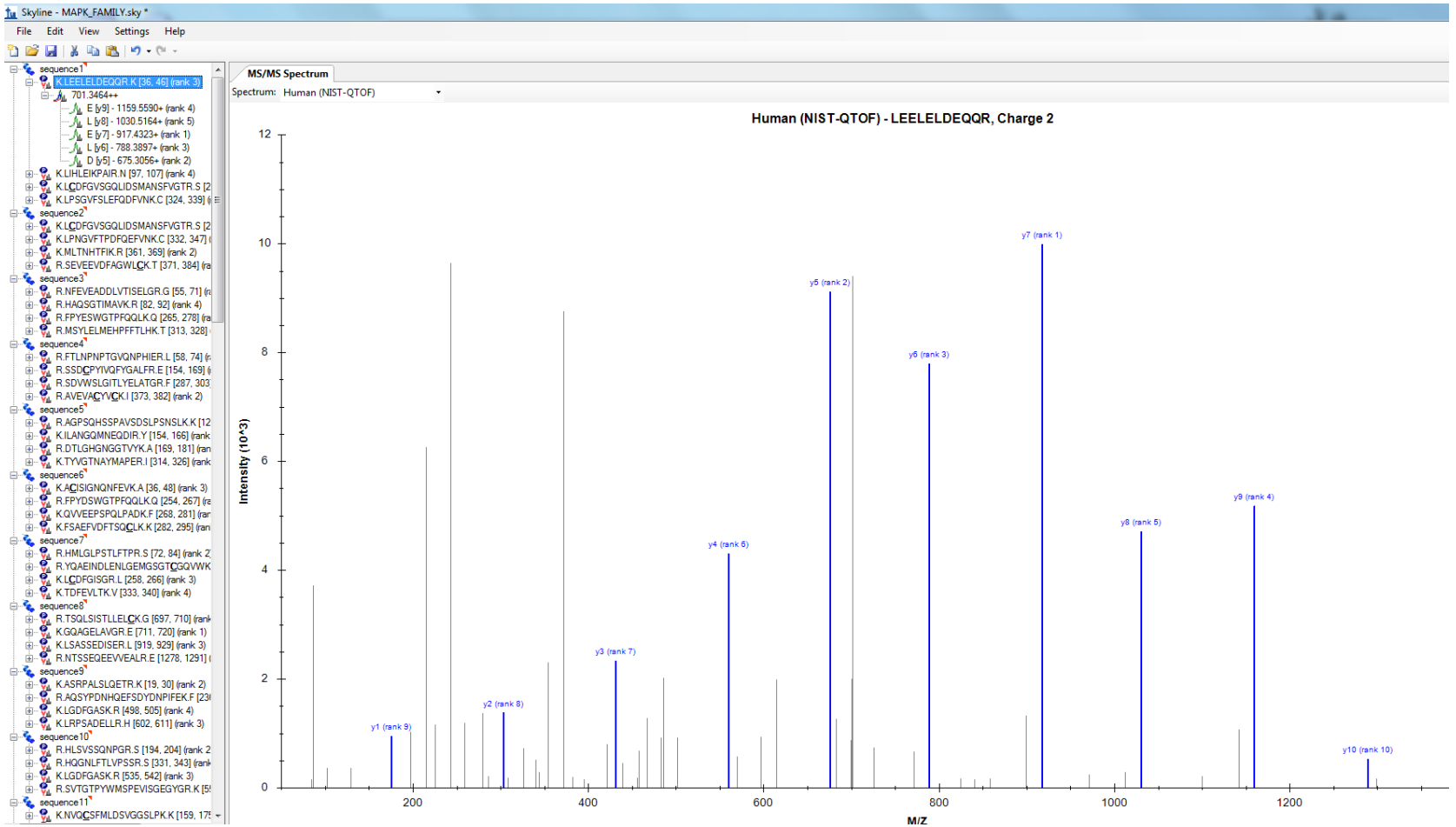


#	log(e)	%	model
1.	-1035.6	81.7	G | P | O
2.	-160	49.6	G | P | O
3.	-110.8	8.5	G | P | O
4.	-105.4	23.1	G | P | O
5.	-81.6	8.5	G | P | O
6.	-70.3	15.4	G | P | O
7.	-64.9	12.7	G | P | O
8.	-63.8	15.0	G | P | O
9.	-61.1	17.1	G | P | O
10.	-59.5	11.3	G | P | O
11.	-58.7	8.5	G | P | O
12.	-58.3	14.0	G | P | O
13.	-58	10.8	G | P | O
14.	-54.9	12.7	G | P | O
15.	-54.4	11.0	G | P | O
16.	-53.2	8.5	G | P | O
17.	-52.5	8.5	G | P | O
18.	-50	13.8	G | P | O
19.	-49.3	9.8	G | P | O
20.	-47.7	8.5	G | P | O

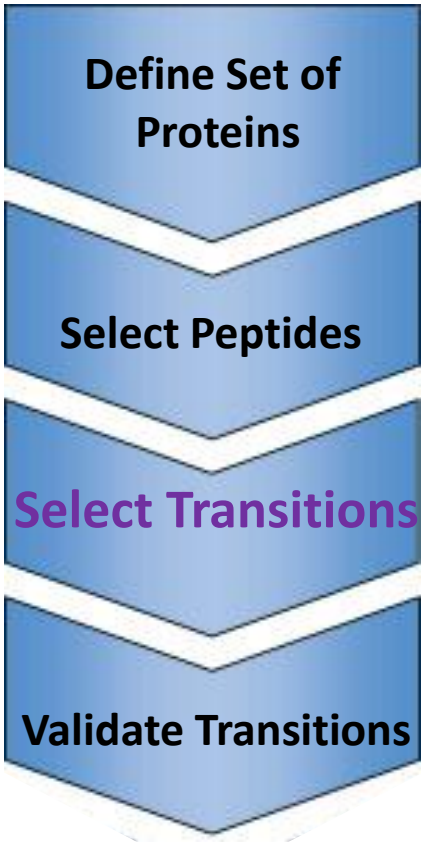
LC/MS Properties: Skyline

-Compares peptides to MS/MS spectral library

-Predicts most abundant transitions



Workflow of SRM proteomics



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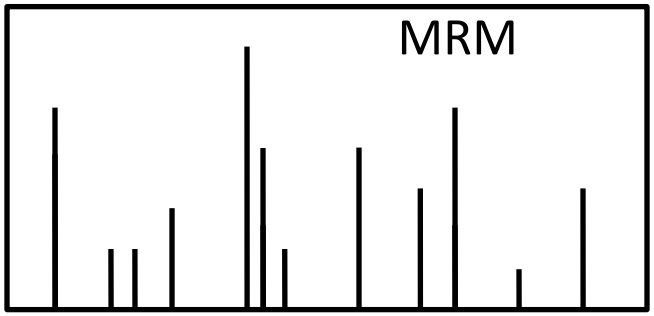
Protein Quantitation

Selecting Transitions

- Limitation of MRM-MS: ~1-2 m/z unit window for precursor and fragment ion occasionally let in interfering peptides with similar characteristics
- If we want to use these transitions for quantitation, we need to be confident there are no interferences
- Largest always largest, smallest always smallest etc.
- b-fragments of high m/z are less represented on QqQ



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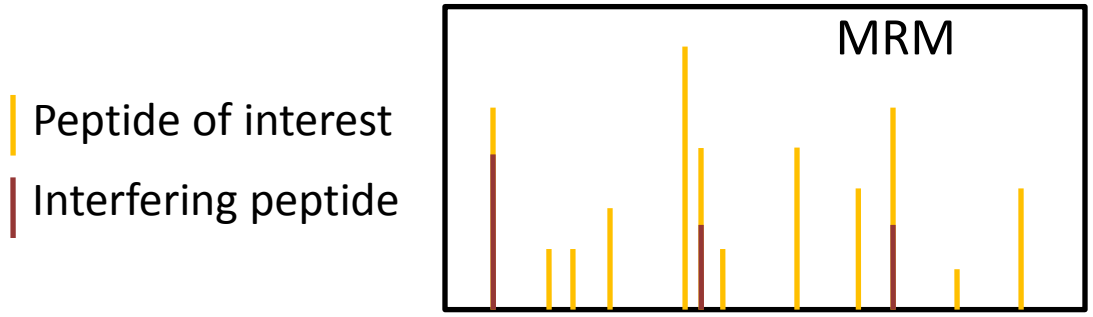
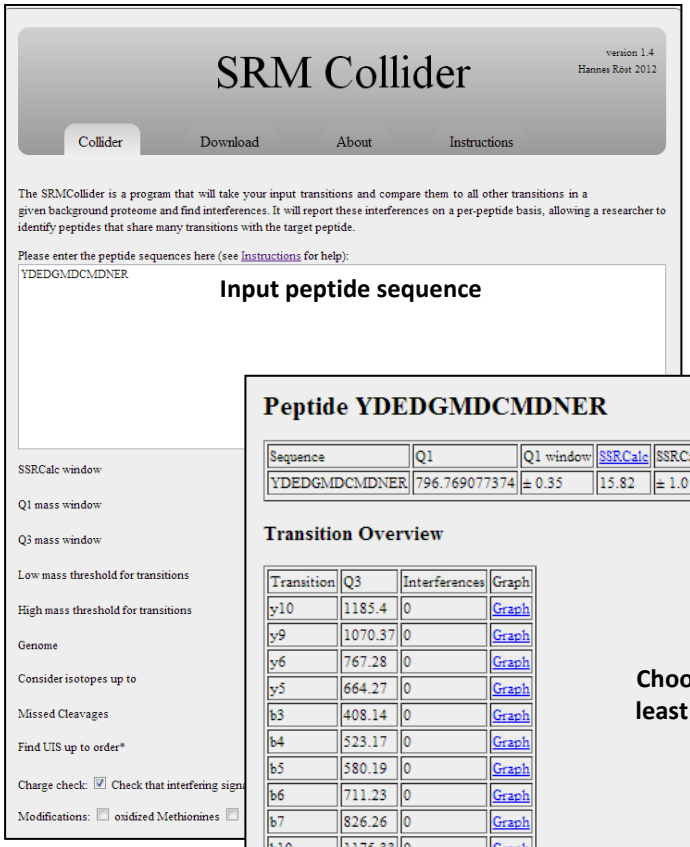


Selecting Transitions: SRMCollider

- Input peptides of interest
- Determines the m/z values for transition pair
- Simulates a typical SRM experiment
- Predicts fragment intensities and retention time information for input peptide
- Compares the transition to all other transitions in a background proteome
- Outputs the number of predicted interferences for each transition for that peptide



Peptide YDEDGMDCMDNER

Sequence	Q1	Q1 window	SSRCalc	SSRCalc window	Interfering precursors	Background	Graph
YDEDGMDCMDNER	796.769077374	± 0.35	15.82	± 1.0	32	human	Graph

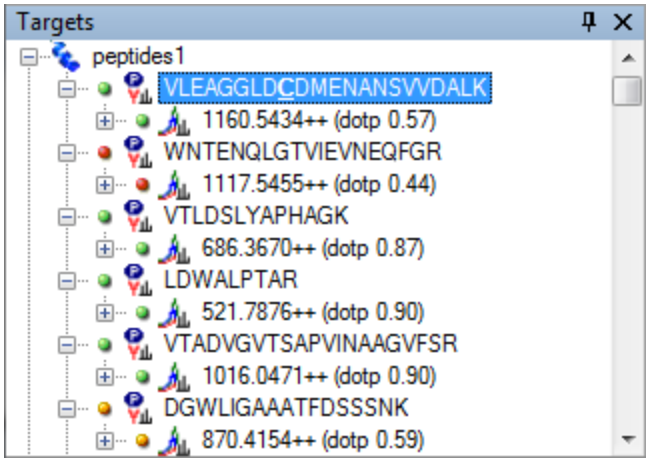
Transition Overview

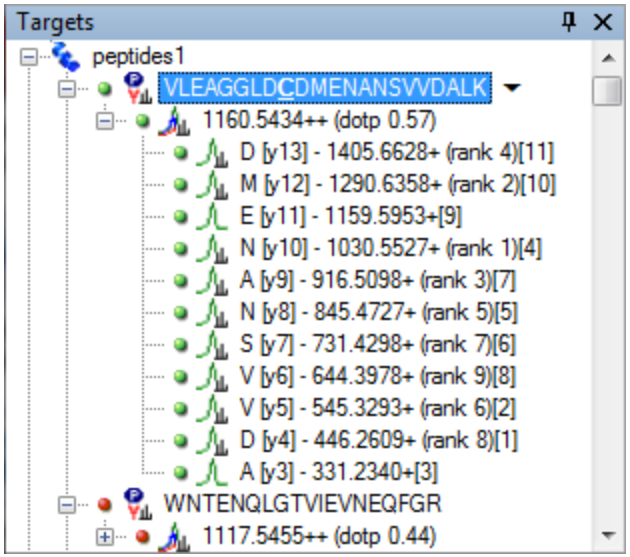
Transition	Q3	Interferences	Graph
y10	1185.4	0	Graph
y9	1070.37	0	Graph
y6	767.28	0	Graph
y5	664.27	0	Graph
b3	408.14	0	Graph
b4	523.17	0	Graph
b5	580.19	0	Graph
b6	711.23	0	Graph
b7	826.26	0	Graph
b10	1175.33	0	Graph
y11	1314.44	1	Graph
y8	1013.35	1	Graph
y7	882.31	1	Graph
y4	533.23	1	Graph
y3	418.21	1	Graph
y2	304.16	1	Graph
b8	929.27	1	Graph
b9	1060.31	1	Graph
y12	1429.47	2	Graph
b11	1289.38	3	Graph
b12	1418.42	3	Graph

Choose peptides that have at least one transition with zero interferences

Selecting Transitions: Skyline

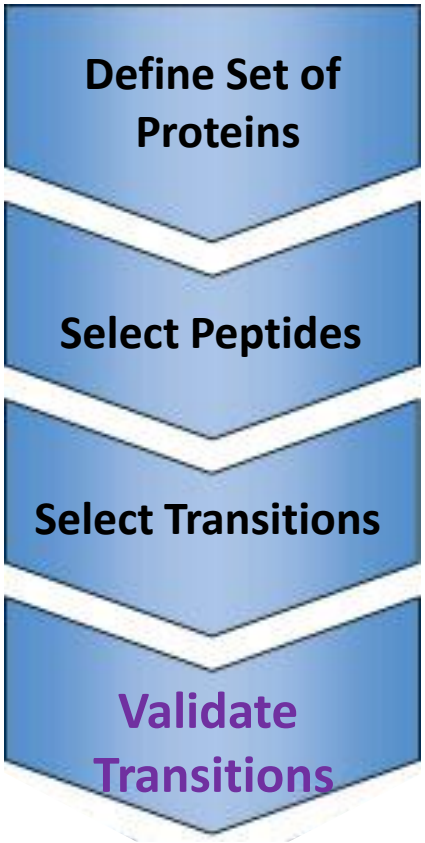
- Can use to find best transitions to pick
  - Intensity (rank)
  - Dot product (similarity to reference spectra)





Want high rank and dotp close to 1

Workflow of SRM proteomics



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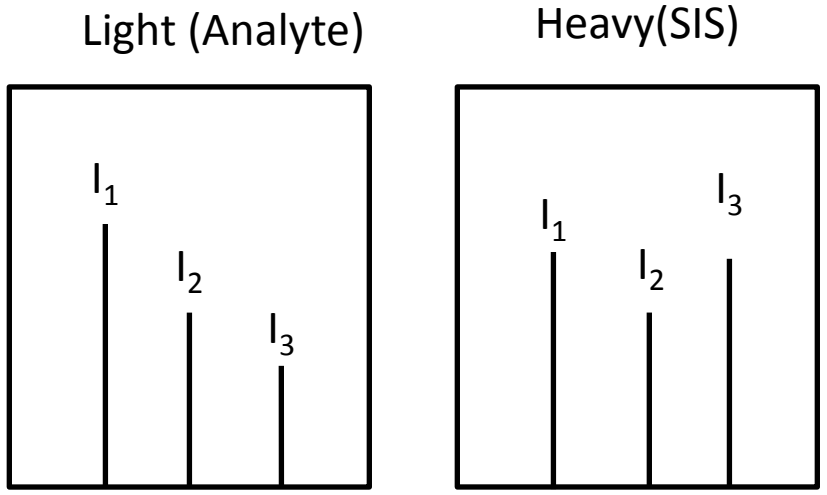
Protein Quantitation

Validating Transitions: "Branching ratio"

Branching Ratio (BR): ratio of the peak intensities

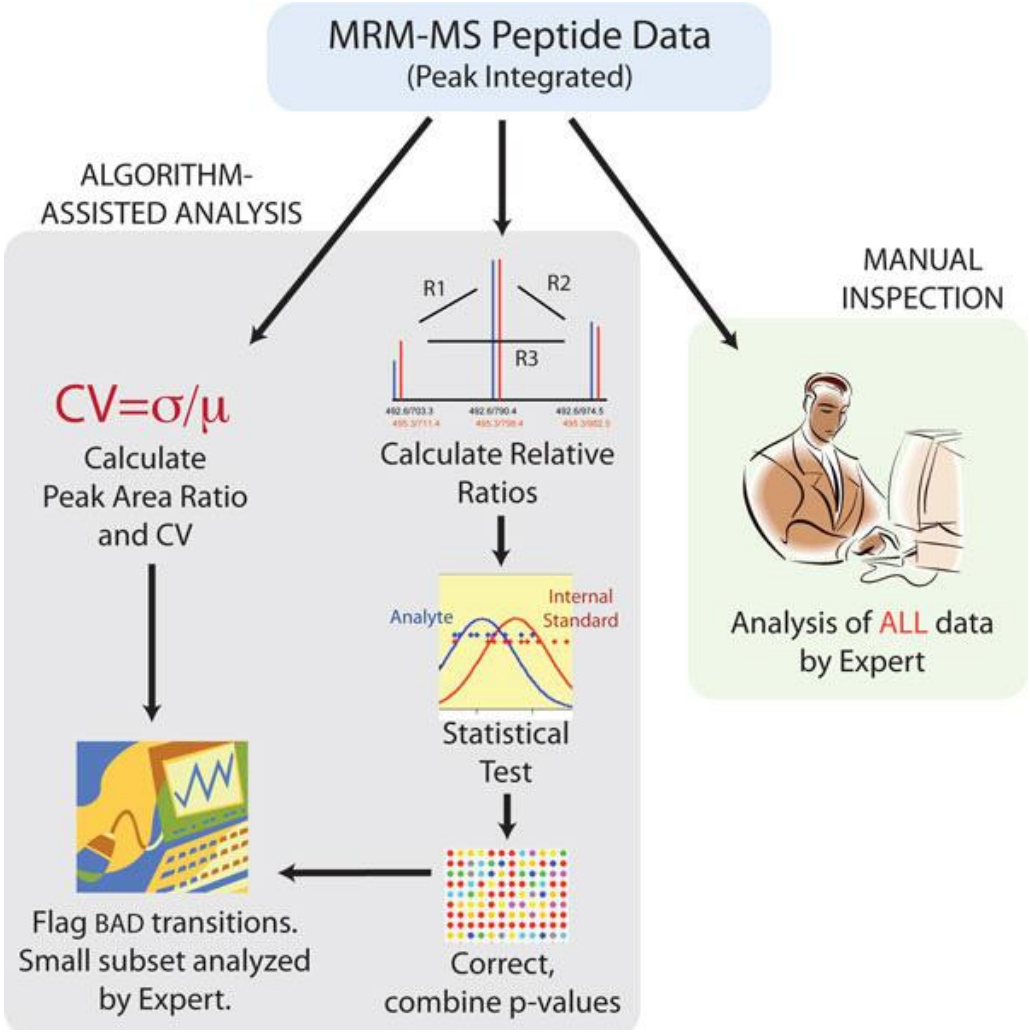
$$BR = ln\left\{\frac{\frac{I_{Ax}}{I_{Bx}}}{\frac{\sum\frac{I_{AxS}}{I_{BxS}}}{n}}\right\}$$



I_{Ax}, I_{Bx} : Peak areas of Analyte
I_{AxS}, I_{BxS} : Peak areas of SIS
n=number of SIS transitions

Kushnir, 2005

Validating Transitions: AuDIT

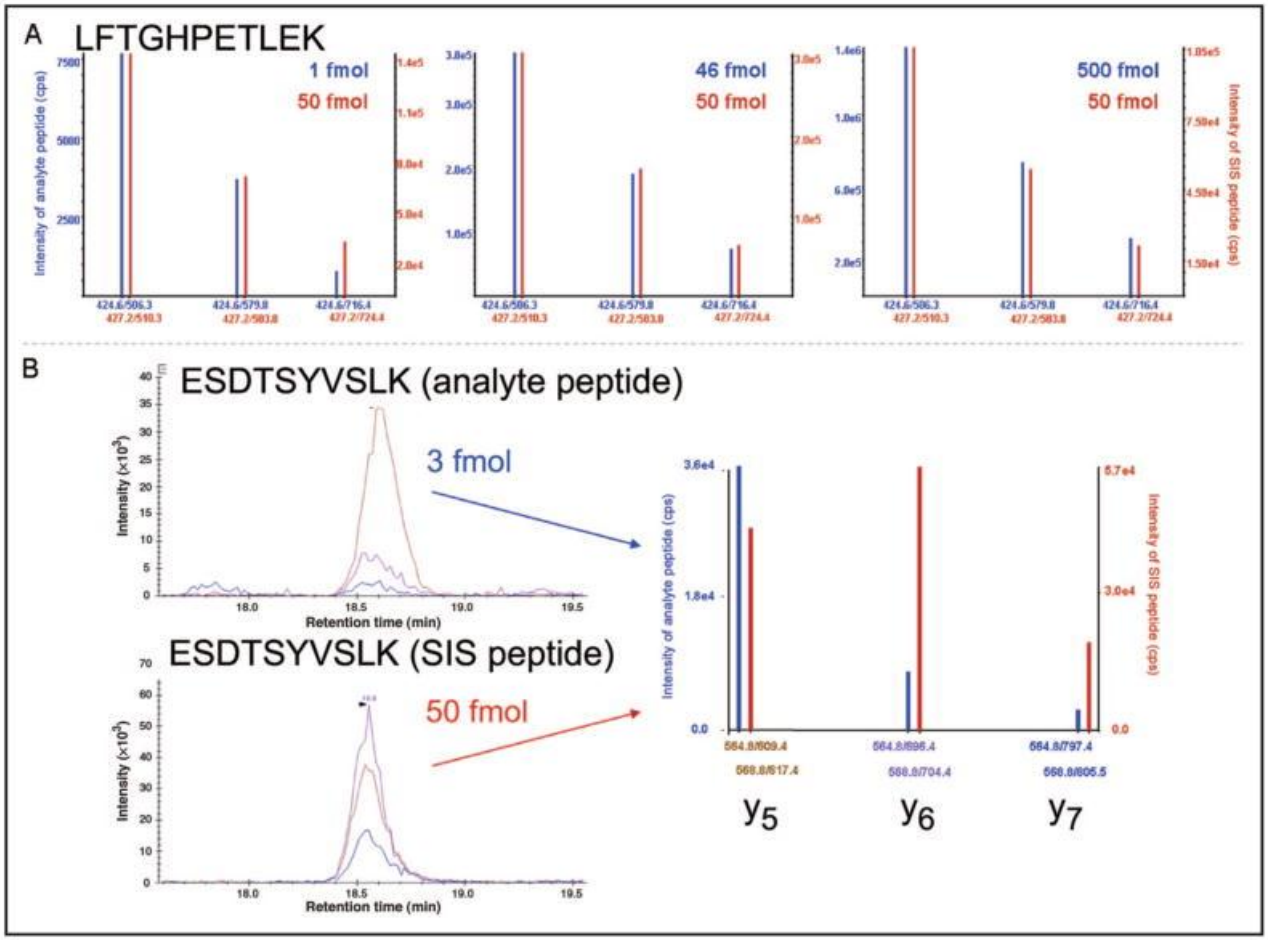


- AuDIT: Automated Detection of Inaccurate and imprecise Transitions
- Uses "branching ratio"

1. Calculate relative ratios of each transition from the same precursor
2. Apply t-test to determine if relative ratios of analyte are different from relative ratios of SIS

http://www.broadinstitute.org/cancer/software/genepattern/modules/AuDIT.html.

Validating Transitions: AuDIT



Blue: Light
Red: Heavy

Relative product ions should have a constant relationship

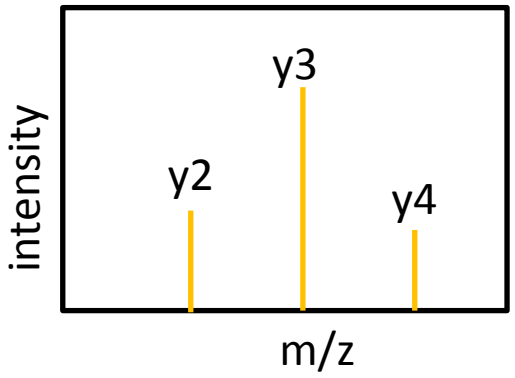
Abbatiello, 2009

Finding Interference: Simple vs Complex Matrix

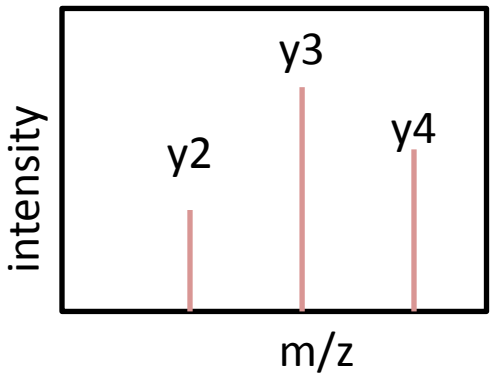
- PRM and MRM are most useful when quantifying protein in a complex matrix
  - Tumor lysate
  - Plasma
- Simple Matrix (buffer) should have no interferences
- Compare the transitions in complex to those in simple
- Ratio close to 1 indicates low interference

Simple Example of Complex v. Simple

Simple Matrix



Complex Matrix



Transition	Simple	Complex
y2	200	200
y3	400	400
y4	100	300

Ratio of Transitions

	y2	y3	y4
y2	y2/y2	y2/y3	y2/y4
y3	y3/y2	y3/y3	y3/y4
y4	y4/y2	y4/y3	y4/y4

Simple Matrix

	y2	y3	y4
y2	1	0.5	**2**
y3	2	1	**4**
y4	**0.5**	**0.25**	1

Complex Matrix

	y2	y3	y4
y2	1	0.5	**0.67**
y3	2	1	**1.33**
y4	**1.5**	**0.75**	1

Transition Ratio Matrix
Complex/Simple

	y2	y3	y4
y2	1	1	**.335**
y3	1	1	**.333**
y4	**3**	**3**	1

y2 and y3 are “good” transitions with no interference

Finding Interference: Simple vs Complex Matrix

Heavy

Complex

Simple

Ratio of Ratios -Matrix

Complex/Simple

Heatmaps

List of “good” and “bad” transitions based on 0.15 cutoff
Use these to make bar graphs

Light

Complex

Simple

Complex/Simple

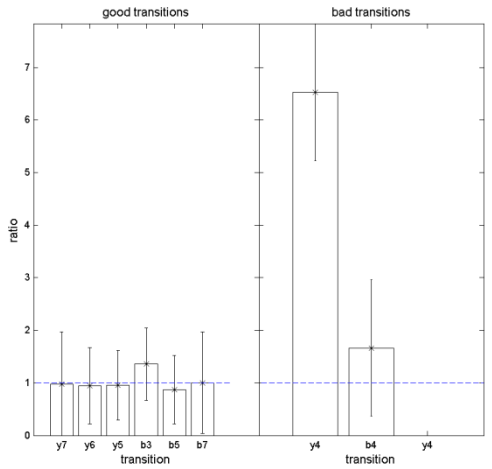
Finding Interference: Simple vs Complex Matrix

SIS Transition ratios

Complex

Simple

List of “good” and “bad” transitions based on 0.15 cutoff
Use these to make bar graphs



SIS Transition ratios

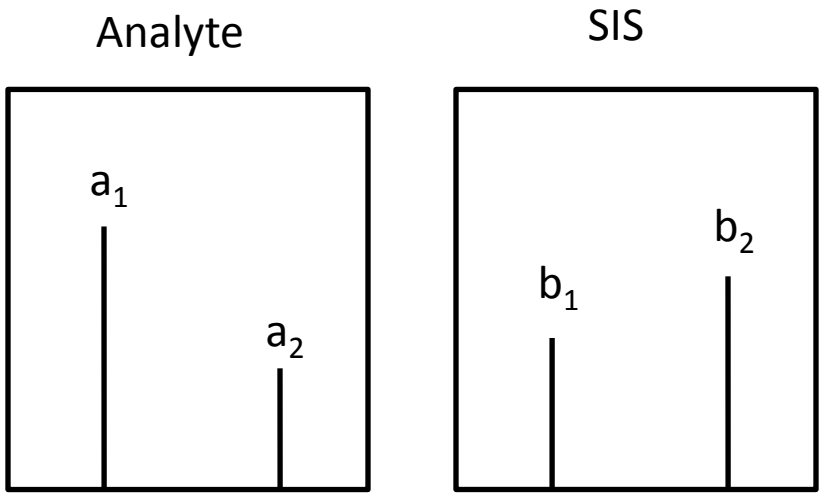
Complex

Simple

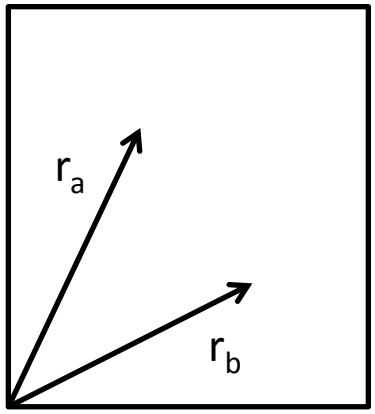
- Use the “good” transitions as a denominator to create ratios for every transition
- Find average ratio of both “good” and “bad” transitions using these denominators
- Graph Mean +/- Stdeviation
- The closer to 1 the lower the interference

Validating Transitions: Contrast Angle

- Spectral Contrast Angle: each spectrum represented as a vector in N-dimensional space
- Spectra that resemble each other have vectors pointing in the same direction (θ ~ 0°)



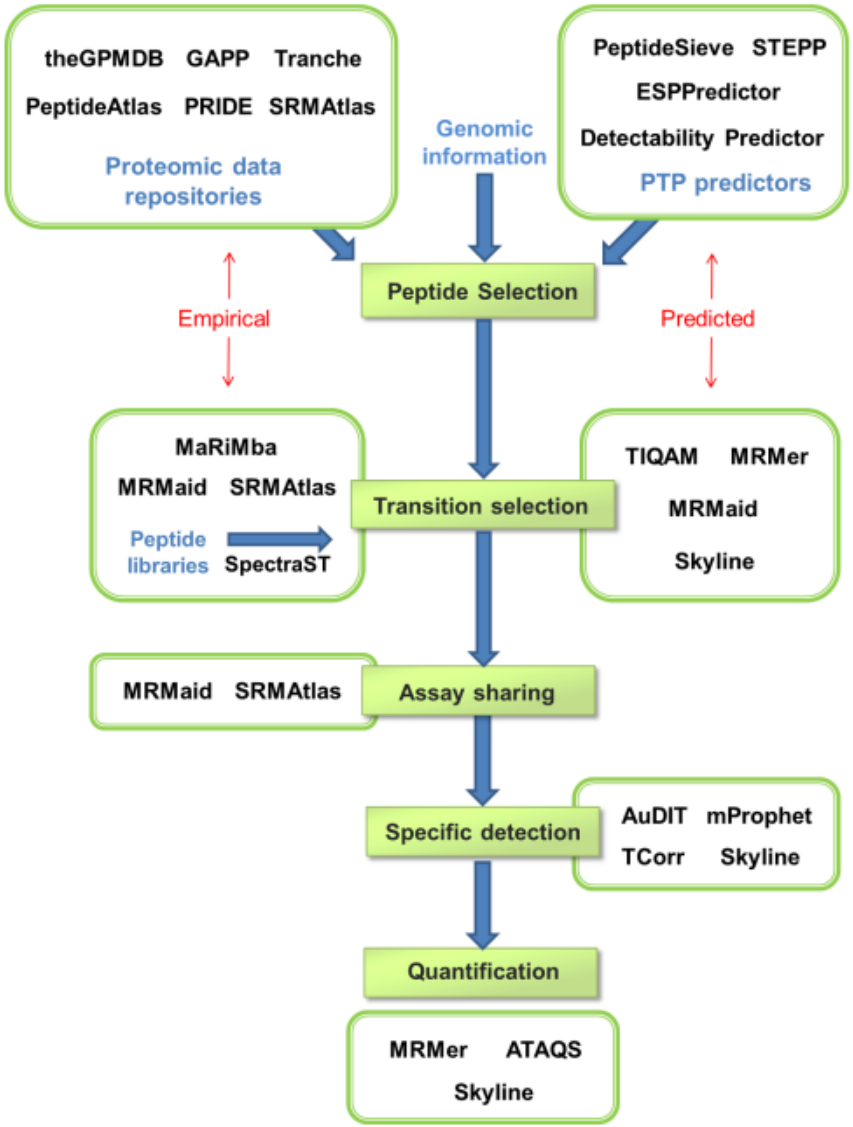
$$cos\theta = \frac{\sum a_i b_i}{\sqrt{\sum {a_i}^2 \cdot \sum {b_i}^2}}$$



$$r_a = \sqrt{{a_i}^2}$$

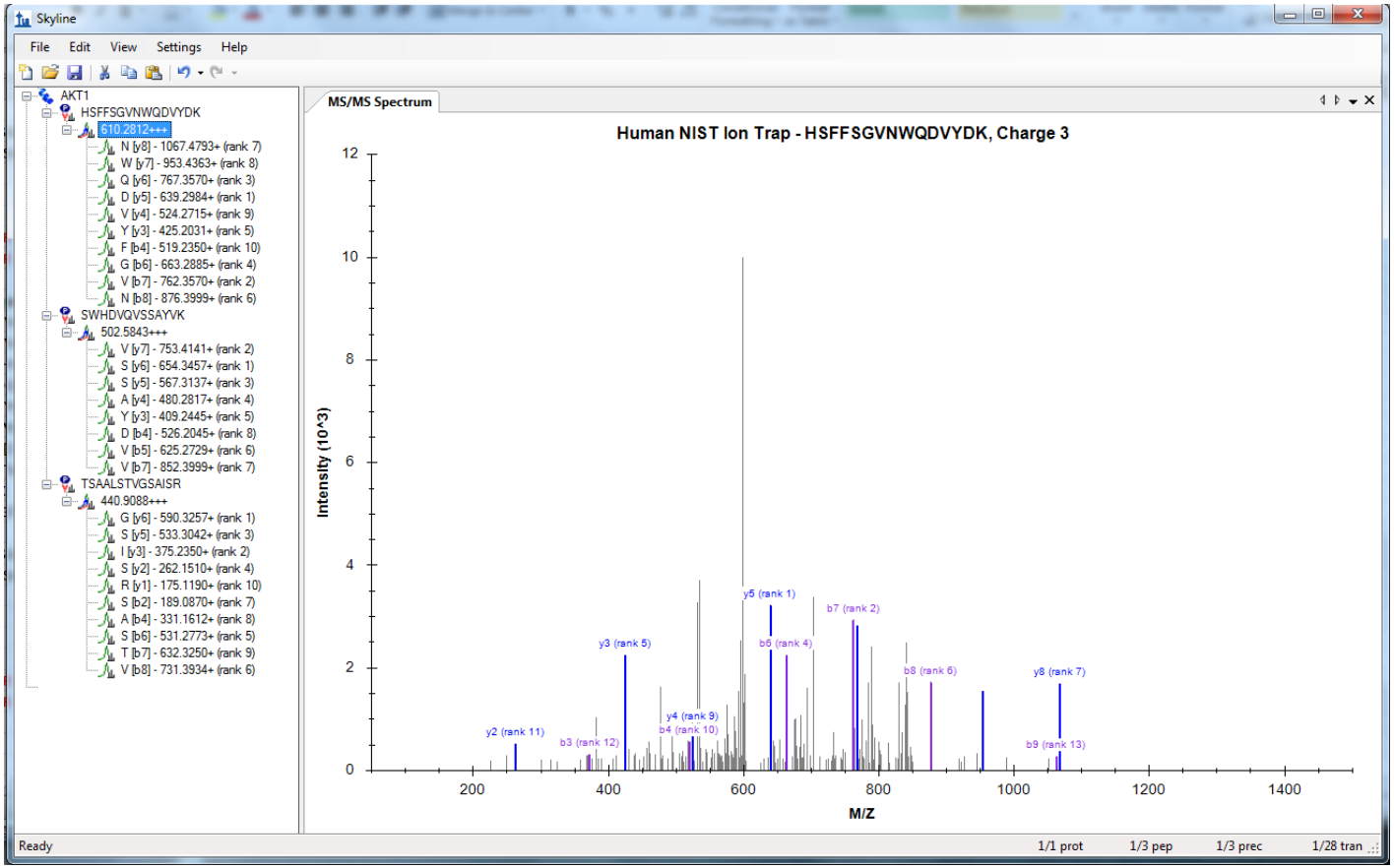
$$r_b = \sqrt{{b_i}^2}$$

Open Source MRM analysis tools

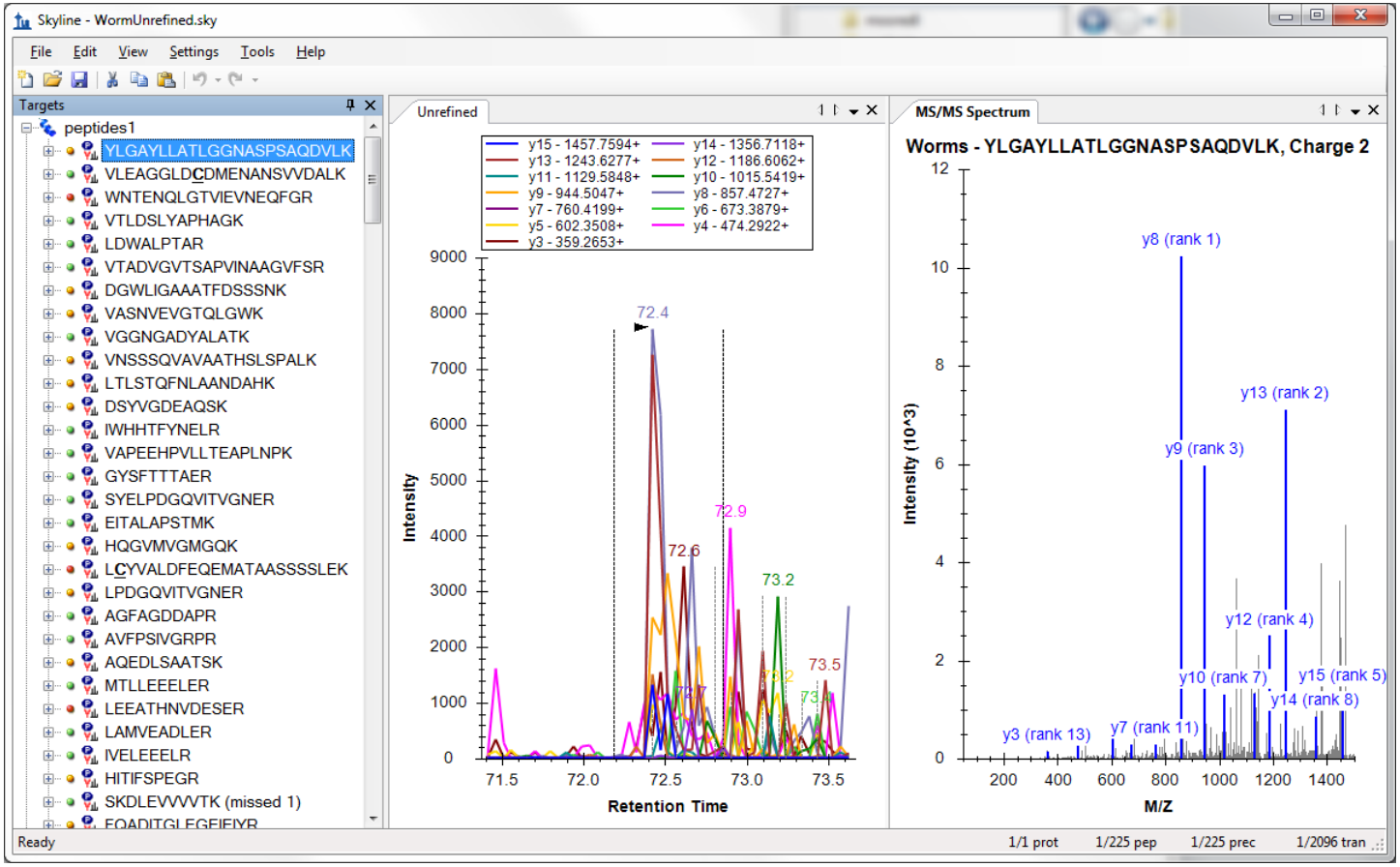


SKYLINE for creating targeted MS/MS methods

Skyline digests proteins and fragments peptides and uses spectral library to find transition intensity



Skyline for MRM: Method Building



Input all peptides of interest

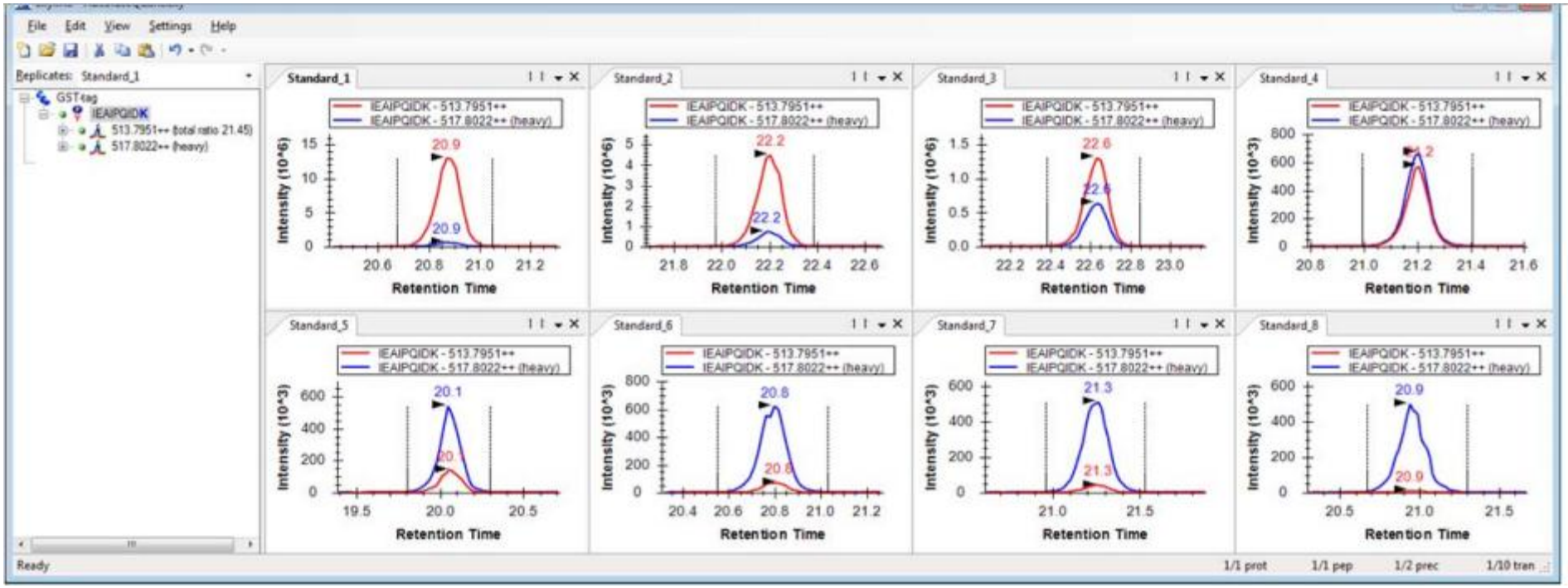
Shows graphs of MS/MS spectra from spectral library

Skyline for MRM: Method Building

- Helps generate protetypic peptide lists using MS/MS spectral libraries
- Find which peptides can be measured in specific matrix
- Find best transitions to measure for a peptide
- Creates transition lists and vendor-specific instrument methods for MRM experiements

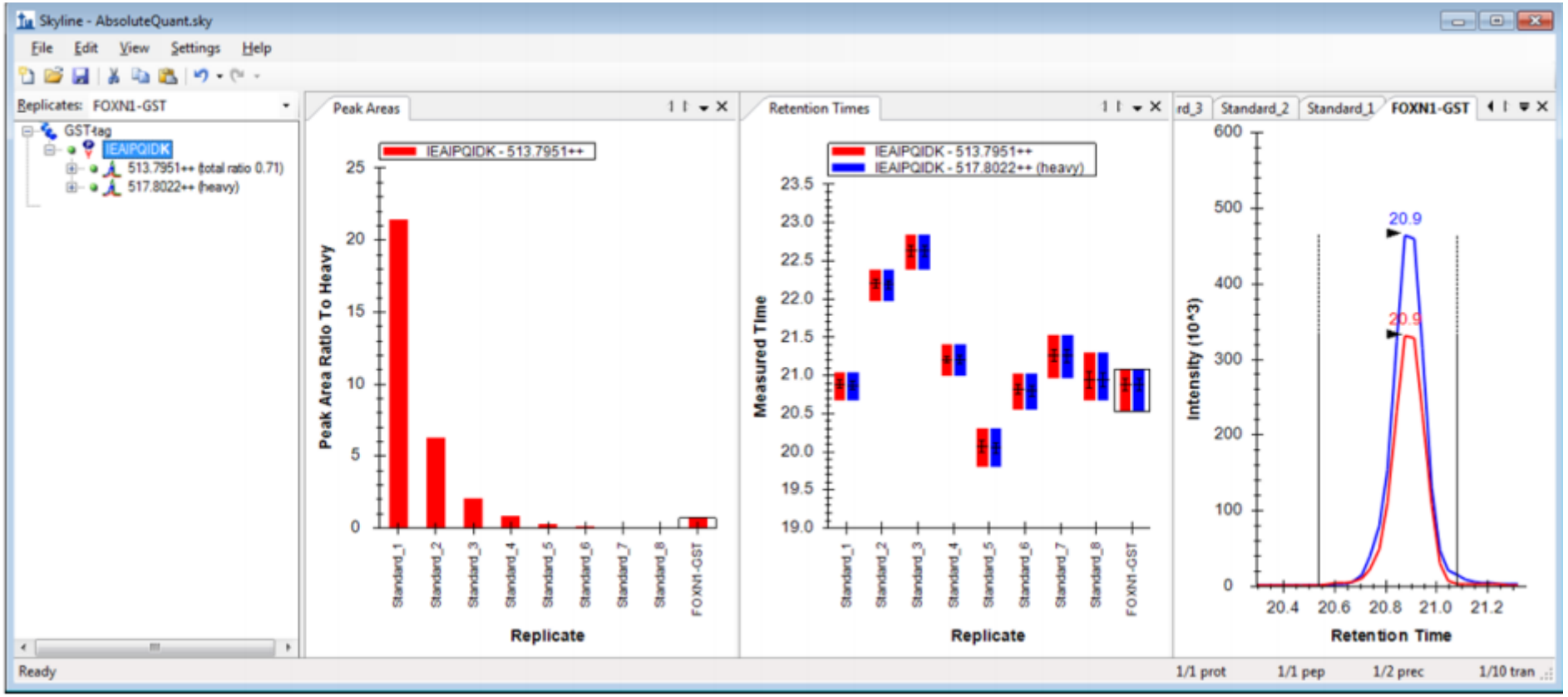
Skyline for MRM: Quantification

- Import raw files into skyline
- Pick peptide of interest
- Check standard peaks



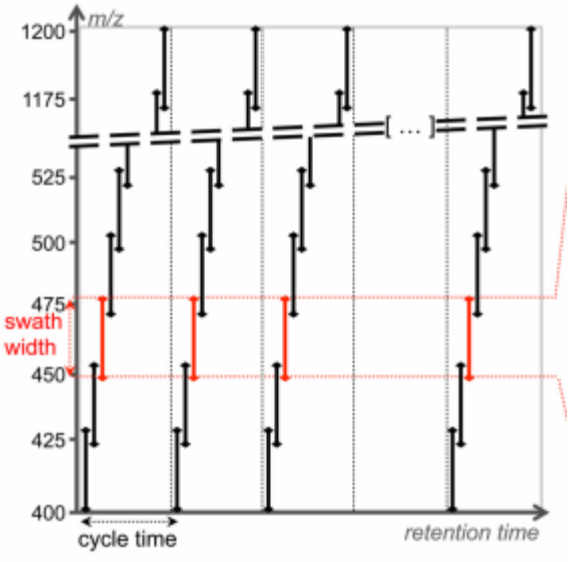
Skyline for MRM: Quantification

- Use the heavy standard PAR to make calibration curve
- Determine sample quantity based on curve



SWATH-MS: Data Collection

- Data acquired on quadrupole-quadrupole TOF high resolution instrument cycling through 32-consecutive 25-Da precursor isolation windows (swaths).
- Generates fragment ion spectra for all precursor ions within a user defined precursor retention time and m/z
- Records the fragment ion spectra as complex fragment ion maps

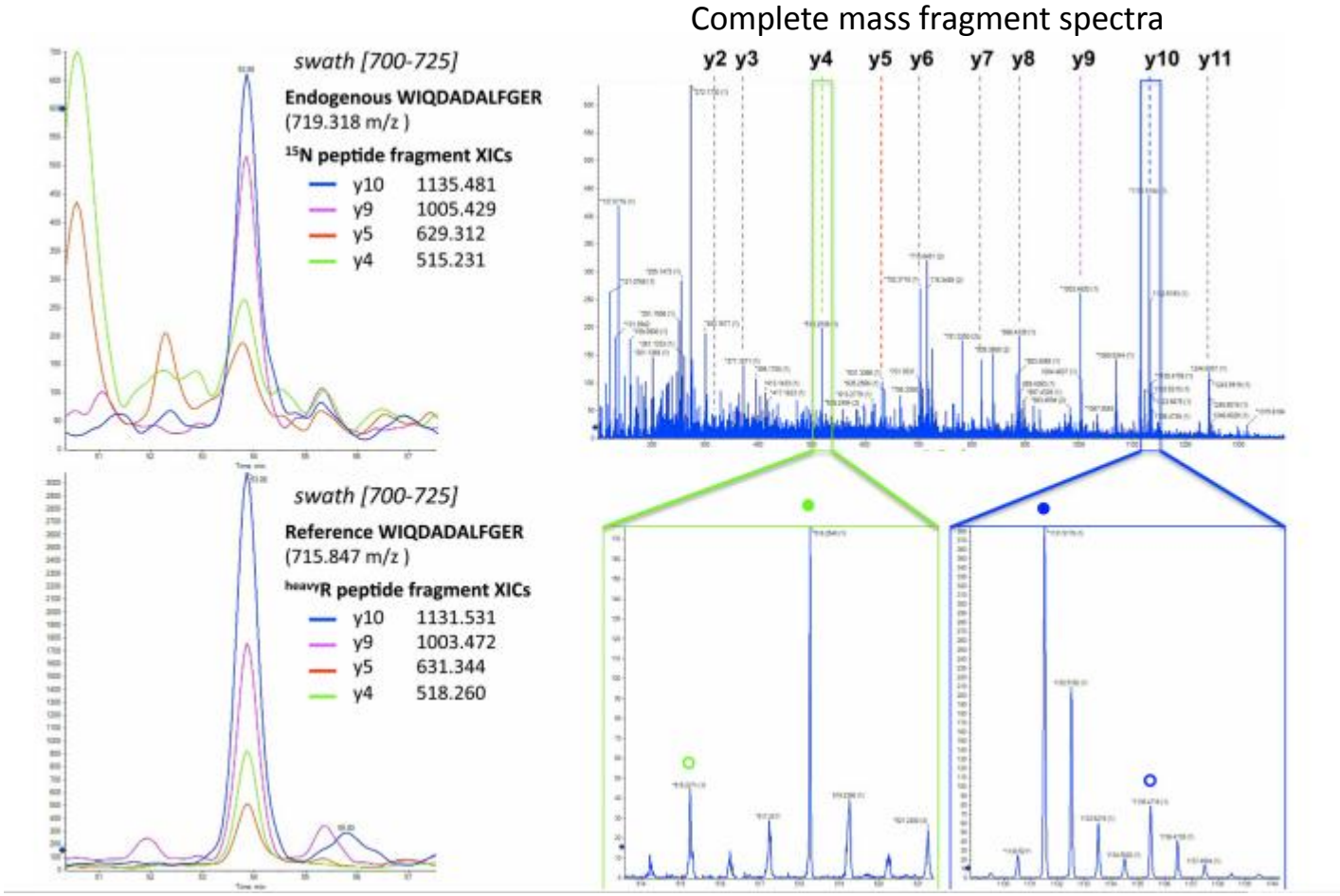


32 discrete precursor isolation windows of 25–Da width across the 400-1200 m/z range

Gillet et al., 2012

SWATH-MS: Data Analysis

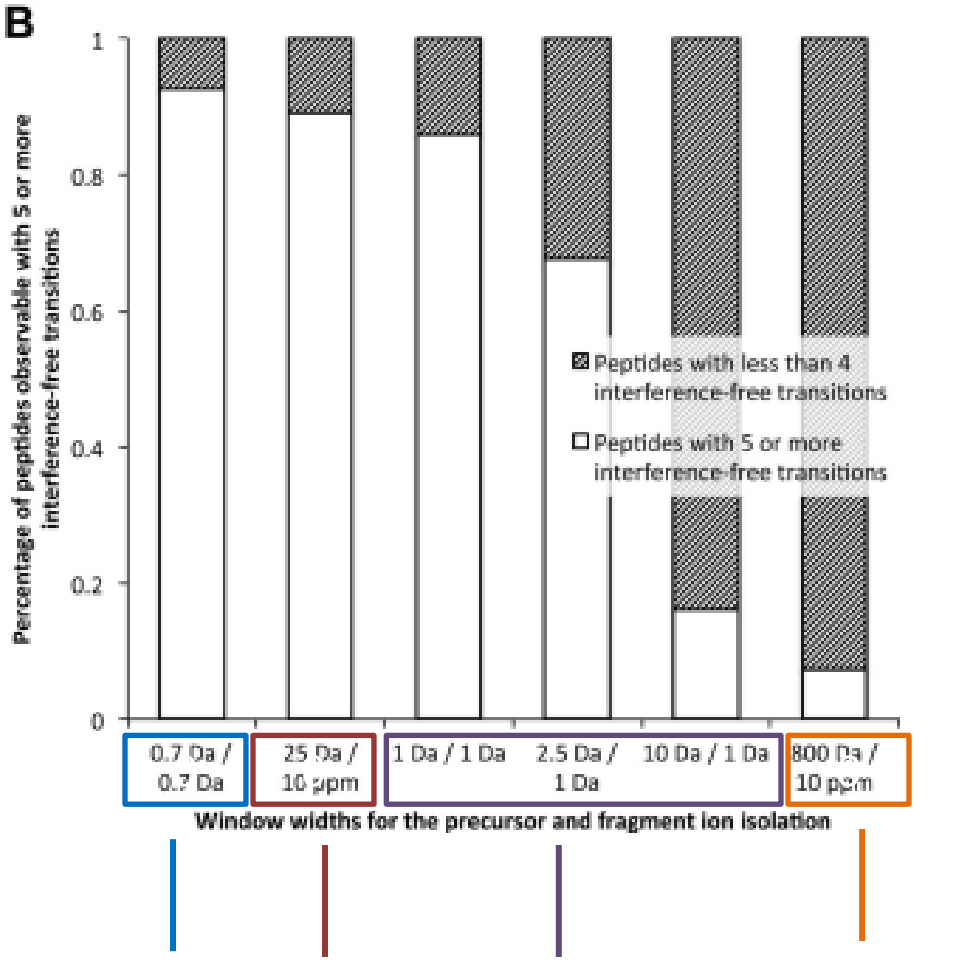
1. From spectral libraries, find fragment ion maps for peptides of interest
2. Mine the SWATH data for these spectra
3. Extract fragment ion traces for quantification



Endogenous (open) and reference peptide (closed) y4/y10 fragments

Gillet et al., 2012

SWATH-MS Fragment Ion Interferences



Gillet et al., 2012

Questions?


heh, mass spectrometry? i hate that crap... i'm more into indie analysis. the underground spectrometry scene is way better.
Toothpaste For Dinner.com