

PROTEOIQ



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General Manager US

**Enhancing label free quantification with the ProteoIQ
Proteomics Software Platform**



NuSep

Experts in protein discovery

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Experts in protein discovery



NuSep Global Locations



Experts in protein discovery



Our Mission: Empower Proteomic Data Analysis



Experts in protein discovery



ProteolQ Provides a Comprehensive Feature Set

Quantification	Label free - Spectral Counting	Yes	★
	Label free - Precursor Intensity	Yes	
	Label free - Total Ion Chromatograms	Yes	★
	Isobaric labelling - iTRAQ, TMT	Yes	
	Isotopic labelling - SILAC, iCAT	Yes	
Advanced Statistics	Analyze reproducibility	Yes	
	Onboard normalization procedures	Yes	
	Apply statistics to protein quantification	Yes	
Biological Annotation	Biological pathway analysis	Yes	
	View protein function and localization	Yes	
	Link to popular protein databases	Yes	
Validate Identifications	Peptide and protein probability	Yes	
	Peptide Protein False Discovery Rate	Yes	
Compatible With	Mascot, SEQUEST, Proteome Discoverer, X!Tandem, pepXML, mzXML	Yes	



ProteoIQ - Label-free quantification experimental workflows

Spectral Counting

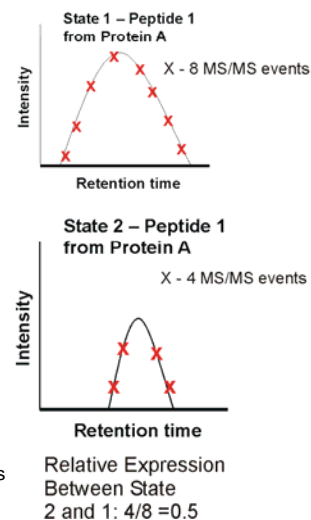
Liu *et al*¹ -linear correlation between spectral counts and relative protein abundance over 2 orders of magnitude. Spectral counting shows strong correlation with isotopic label² based approaches such as ¹⁴N/¹⁵N and precursor peak area intensity measurements³.

1. H. Liu, R. G. Sadygov, and J. R. Yates III, "A model for random sampling and estimation of relative protein abundance in shotgun proteomics," *Analytical Chemistry*, vol. 76, no. 14, pp. 4193–4201, 2004.

2. B. Zybailov, M. K. Coleman, L. Florens, and M. P. Washburn, "Correlation of relative abundance ratios derived from peptide ion chromatograms and spectrum counting for quantitative proteomic analysis using stable isotope labeling," *Analytical Chemistry*, vol. 77, no. 19, pp. 6218–6224, 2005.

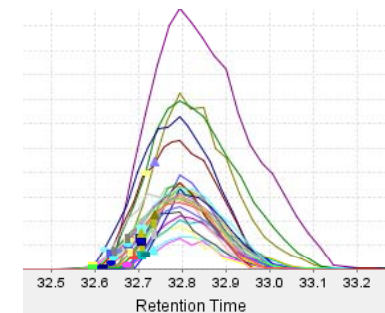
3. W. Old, K. Meyer-Arendt, L. Aveline-Wolf, K. Pierce, A. Mendoza, J. Sevinsky, K. Resing, N. Ahn "Comparison of label-free methods for quantifying human proteins by shotgun proteomics." *Molecular & Cellular Proteomics* vol. 4, pp. 1487-1502, 2005.

Quantitation by Spectral Counts



Intensity Based

Integrated measurement of precursor peak areas across multiple LC-MS/MS analyses⁴. Chelius *et al*⁴– demonstrated linear correlation for proteins over concentration ranges of 10fmol-1000pmol.



4. Chelius, D., Bondarenko, P. V., Quantitative profiling of proteins in complex mixtures using liquid chromatography and mass spectrometry. *J. Proteome Res.* 2002, 1, 317–323.

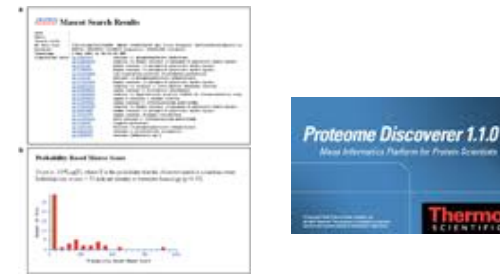
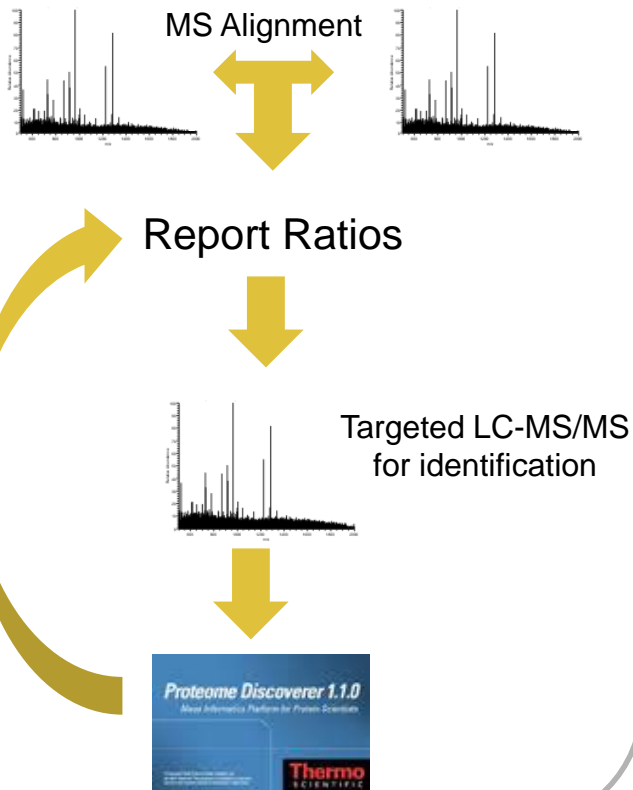
Advantages of label-free quantification

- Scalable for studies requiring large numbers of samples and replicates. Label based technologies (SILAC, iTRAQ etc.) are limited.
- High dynamic range
- Relatively inexpensive compared with traditional label based approaches
- Amenable to biological specimens from non-culture conditions

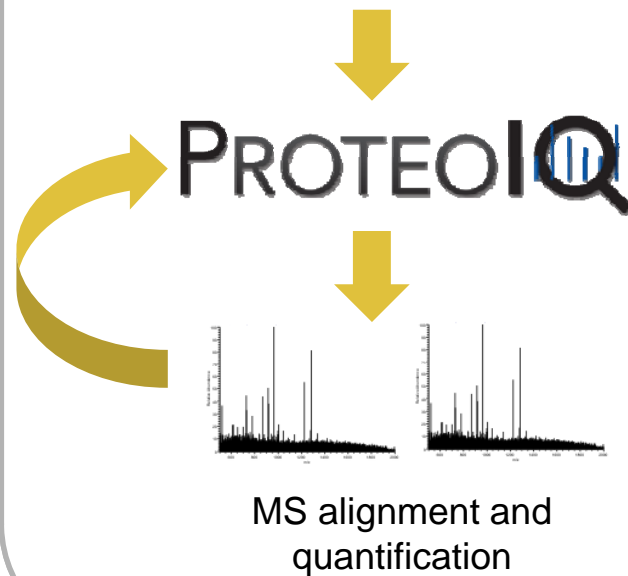


ProteoIQ – XIC Label Free Workflow

Traditional Label Free



PROTEOIQ



Label free quantification of human serum proteins

Results courtesy Dr. Kumar Kolli at Windber Research Institute

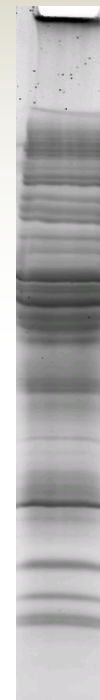
Biological specimens

- 3 patients
- Serum collected at one month, three months, and one year time points
- High abundance proteins depleted via an Agilent MARS column
- Enzymatic digestion with trypsin
- Peptides analyzed in triplicate via LC-MS/MS on an LTQ-FT (Thermo)

Data analysis

- 27 RAW files converted to mzXML
- Mascot search – Strict Trypsin and Semi Trypsin enzyme specificity
- Proteome Discoverer – Strict Trypsin and No Enzyme specificity
- Results assembled in ProteoIQ
- 1% Protein FDR, 0.9 Peptide Probability filter
- Quantification performed in ProteoIQ via spectral counting and XIC

30 ug
protein
load

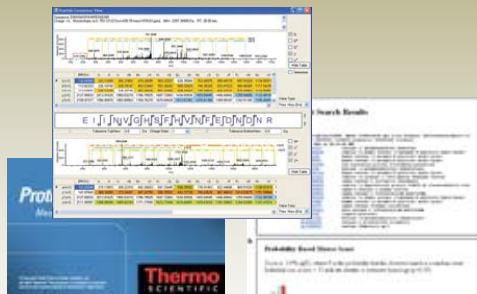


Deep
Purple



Robust data integration in ProteoIQ

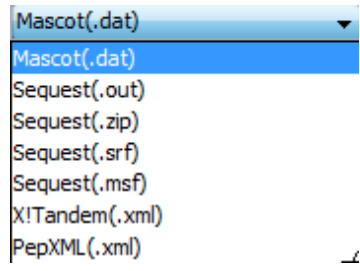
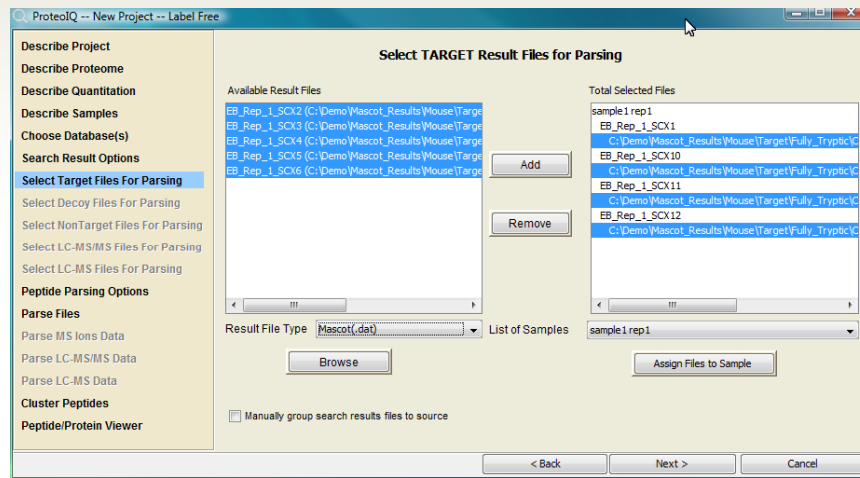
Combine search results from multiple search engines



PROTEOIQ

Robust data integration

- Combine multiple search engine and instrument results.
- Combine search parameters (enzyme, PTMs etc.)

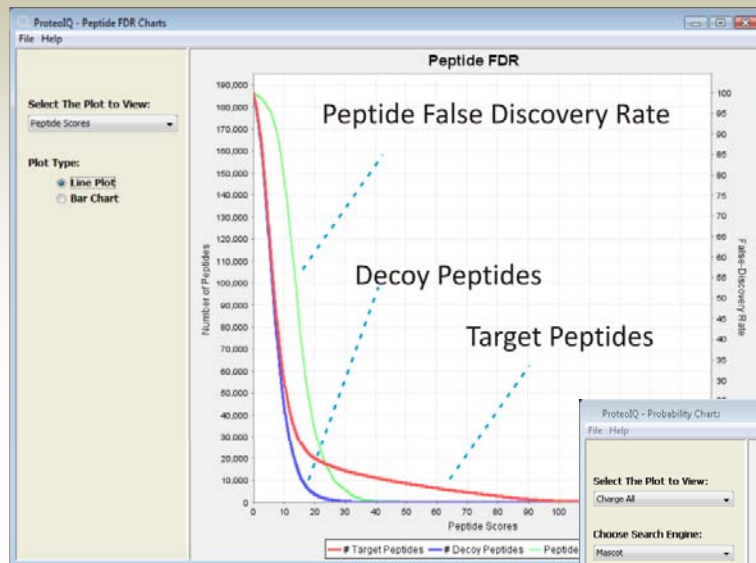


Experts in protein discovery

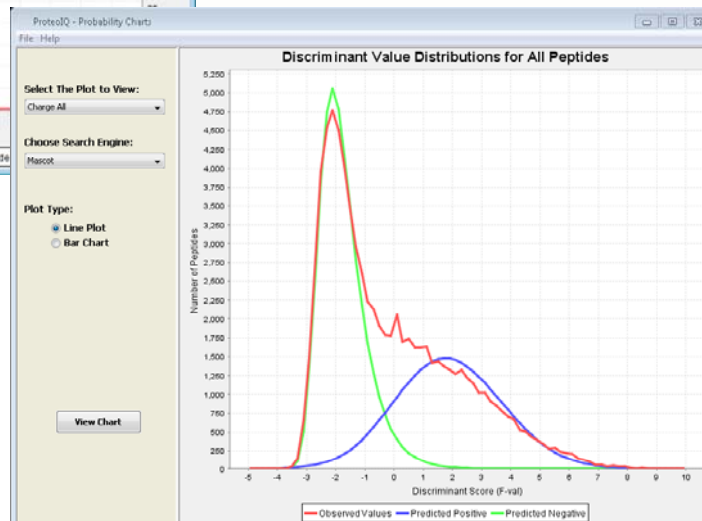


Identifications from multiple search engines independently validated

Validation via FDR¹



Validation via probability²



Control stringency via statistical filters

False-Discovery Rate Filters	
Metric to Use for FDR	Mascot ions score
Max Peptide FDR (%)	1.0
Max Protein FDR (%)	
Starting Pep Coverage for ProFDR	
Probability Filters	
Min Peptide Probability	
Min Protein Probability	
Min Protein Group Probability	



ProteolQ - Visualizing Multiple Search Results

Mascot IDs

SEQUEST IDs

Observed	Mr(expt)	Mr(calc)	Mass Delta	Charge	Mascot Ions Score	Mascot Prob	Sequest Xcorr	Sequest Prob	Peptide	344 One Month Intensity	344 One Month Log2 Relative Expression	344 One Year Intensity	344 One Year Log2 Relative Expression	344 Three Months Intensity	344 Three Months Log2 Relative Expression	371 One Month Intensity	371 One Month Log2 Relative Expression	371 In
643.808	1,285.602	1,285.583	15.292	2	24.21	0.998	1.382	0.936	ESLSSYWESAK	17,087.234	-0.612	13,706.694	-0.92	7,229.082	-1.848	28,232.503	0.115	47
643.804	1,285.592	1,285.583	7.695	2	46.56	1	1.92	0.996	ESLSSYWESAK	17,087.234	-0.612	13,706.694	-0.92	7,229.082	-1.848	28,232.503	0.115	47
643.805	1,285.596	1,285.583	10.164	2	44.04	1	1.631	0.97	ESLSSYWESAK	17,087.234	-0.612	13,706.694	-0.92	7,229.082	-1.848	28,232.503	0.115	47
643.81	1,285.606	1,285.583	17.856	2	34.93	1	1.228	0.967	ESLSSYWESAK	17,087.234	-0.612	13,706.694	-0.92	7,229.082	-1.848	28,232.503	0.115	47
643.806	1,285.596	1,285.583	10.734	2	23.98	0.998	1.235	0.969	ESLSSYWESAK	17,087.234	-0.612	13,706.694	-0.92	7,229.082	-1.848	28,232.503	0.115	47
850.123	2,547.347	2,547.241	41.492	3	59.62	1	2.085	0.961	STAAMSTYTGIFTDQVLSVLKGE	2,559.525	-0.893	2,790.807	-0.759	810.143	-2.564	1,608.504	-1.838	30
850.112	2,547.315	2,547.241	28.904	3	58.6	1	2.162	0.918	STAAMSTYTGIFTDQVLSVLKGE	2,559.525	-0.893	2,790.807	-0.759	810.143	-2.564	1,608.504	-1.838	30
850.129	2,547.364	2,547.241	48.249	3	40.79	1	1.667	0.535	STAAMSTYTGIFTDQVLSVLKGE	2,559.525	-0.893	2,790.807	-0.759	810.143	-2.564	1,608.504	-1.838	30
850.12	2,547.337	2,547.241	37.538	3	33.71	1	2.129	0.817	STAAMSTYTGIFTDQVLSVLKGE	2,559.525	-0.893	2,790.807	-0.759	810.143	-2.564	1,608.504	-1.838	30
850.115	2,547.323	2,547.241	32.146	3	29.92	1	2.406	0.998	STAAMSTYTGIFTDQVLSVLKGE	2,559.525	-0.893	2,790.807	-0.759	810.143	-2.564	1,608.504	-1.838	30
850.115	2,547.324	2,547.241	32.218	3	32.47	1	2.461	0.995	STAAMSTYTGIFTDQVLSVLKGE	2,559.525	-0.893	2,790.807	-0.759	810.143	-2.564	1,608.504	-1.838	30
850.097	2,547.27	2,547.241	11.085	3	31.66	1	3.038	0.998	STAAMSTYTGIFTDQVLSVLKGE	2,559.525	-0.893	2,790.807	-0.759	810.143	-2.564	1,608.504	-1.838	30
850.129	2,547.365	2,547.241	48.68	3	11.94	0.998	2.083	0.867	STAAMSTYTGIFTDQVLSVLKGE	2,559.525	-0.893	2,790.807	-0.759	810.143	-2.564	1,608.504	-1.838	30

Enzyme Specificity

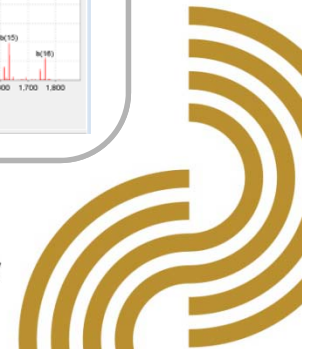
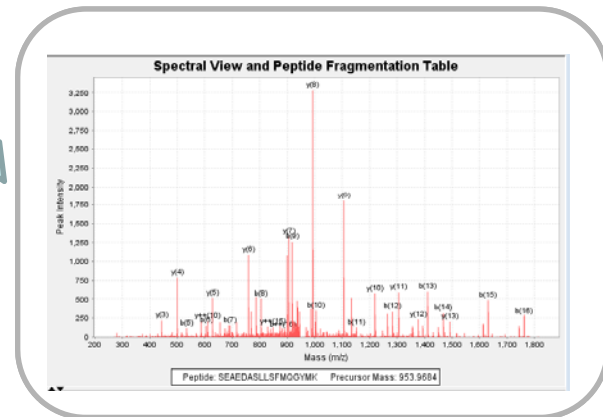
No_Enzyme
Trypsin
semiTrypsin

Modification Name

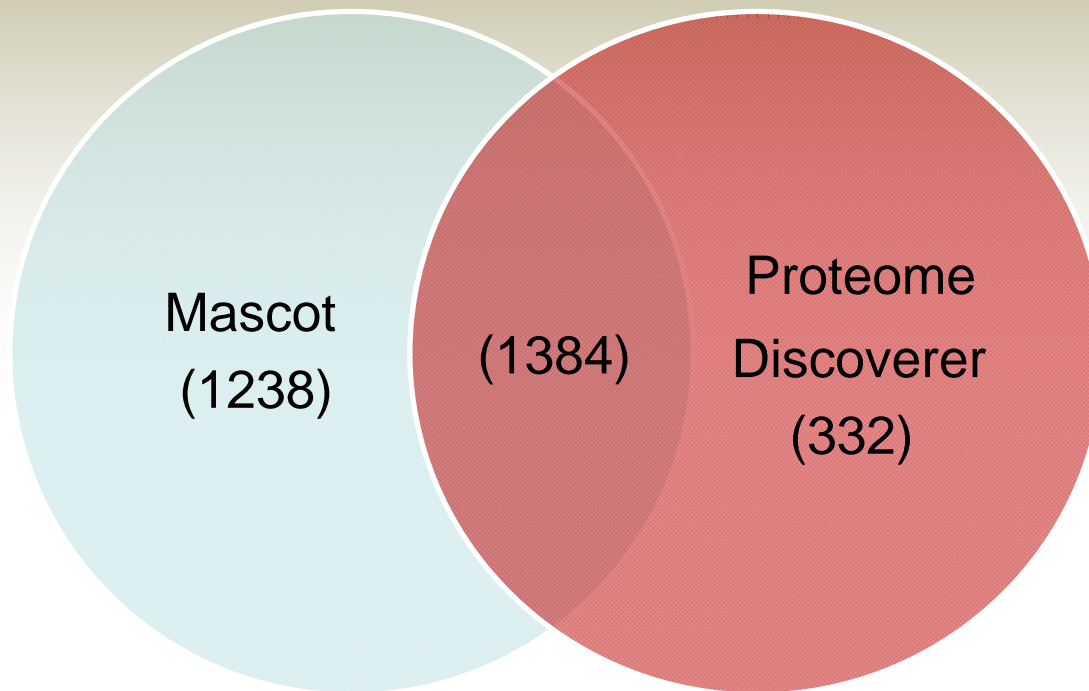
+0.98
+15.99
+57.02

DB Search Engine

Mascot
Sequest



Unique peptide assignments by search engine – fully tryptic



Validation Methods

1% Protein FDR
0.9 Peptide probability
2 peptides/protein

Result

Combining multiple search engines increases the number of **unique** peptide assignments

268 protein groups and 3530 unique peptides confidently identified



ProteoIQ – Combining search results using multiple search rules

- Biological samples are inherently complex
- Traditional workflows utilize a database search strategy in which there is strict adherence to enzyme rule searching using only the enzyme utilized for the experiment
- Such an approach ignores protein degradation, “non target” enzyme specificity and protein truncation
- A better approach is to search using “loose” enzyme specificity



Robust data integration in ProteoIQ

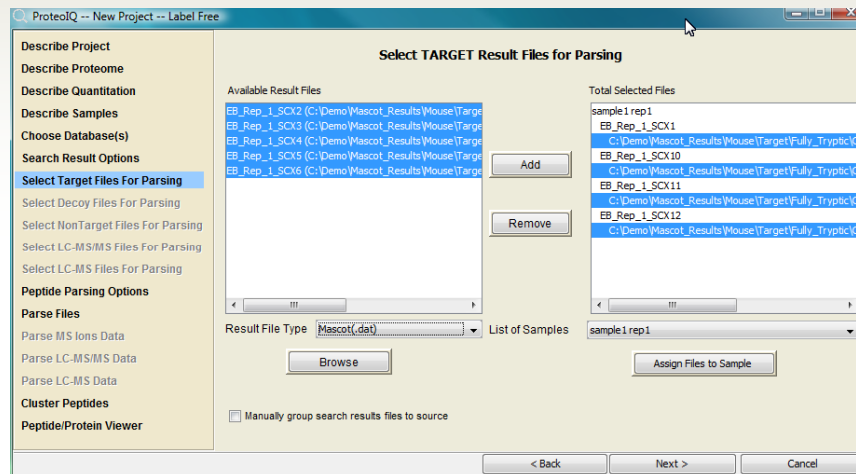
Combine search results from multiple search rules



Robust data integration

- Combine multiple search engine and instrument results.
- Combine search parameters (enzyme, PTMs etc.)

Strict Trypsin No Enzyme
Strict Trypsin Semi-Trypsin



- Mascot(.dat)
- Mascot(.dat)
- Sequest(.out)
- Sequest(.zip)
- Sequest(.srf)
- Sequest(.msf)
- X!Tandem(.xml)
- PepXML(.xml)



Experts in protein discovery



ProteolQ – visualization of search rules and resulting peptide IDs

Enzymatic Termini

Mass Delta	Charge	Mascot Ions Score	Mascot Prob	Sequest Xcorr	Sequest Prob	Peptide Sequence	Modification	Max Num Enzymatic Termini	Total Spectral Count
22.561	2	133.36	1	2.546	0.999	VTGEGCVYLQTSLK	+57.02 (C6)	2	6
46.075	2	114.86	1	3.308	1	MYYSAVDPTKDIFTGLIGPMK		2	8
45.451	2	114.82	1	3.448	1	FAHYVVTSQVVNTANEAR		2	6
21.723	2	114.24	1	1.77	0.997	HPNSPLDEENLTQENQDR		1	6
48.941	2	113.77	1	2.996	1	SLGECCDVEDSTTCFNAK	+57.02 (C5); +57.02 (C6); +57.02 (C14)	2	6
30.416	2	111.71	1	1.873	0.997	VLSLAQEQVGGSPK		2	7
23.154	2	109.8	1	3.013	1	SGMAIADVTLISGFHALR		1	5
0.29	2	109.03	1	3.794	1	SEAEDASLLSFMQGYMK		1	6

Enzyme Specificity

No_Enzyme
Trypsin
semiTrypsin

Modification Name

+0.98
+15.99
+57.02

DB Search Engine

Mascot
Sequest

Select for peptides identified by different search rules

Did the addition of multiple enzyme cleavage rules benefit proteome coverage and quantification?



The importance of multiple enzyme cleavage rules – Apolipoprotein C-III

ProteoIQ -- Protein Sequence Viewer

Group/Replicate	Mascot Protein Prob	Sequest Protein Prob	Total Protein Prob	Num Peptides	Spectral Count (SC)	Normalized SC (N-SC)	N-Int Log2 Relative Expression
344 One Month			1	2	8.0	2.67	-0.3
344 One Year			1	2	7.0	2.33	-0.36
344 Three Months			1	1	2.0	0.67	-0.34
371 One Month			1	3	5.0	1.67	-0.42
371 One Year			1	2	6.0	2	-0.45
371 Three Months			1	2	7.0	2.33	-0.6
427 One Month			1	5	13.0	4.33	0.45
427 One Year			1	1	1.0	0.33	0.34
427 Three Months			1	3	13.0	4.33	1.36
Total (Non-Redundant)	1	1	1	5	62		

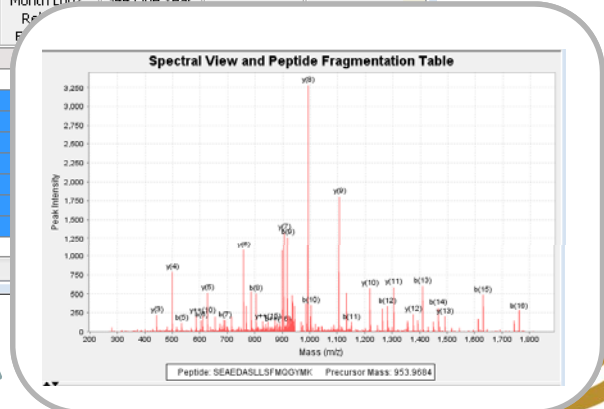
1	MQPRVLLVVALLLASARASEAEDASLLSFMQGYMKHATKTAKDALSSVQESQVAQQAR	60
61	GWVTDGESSLKDYWSTVKDKFSEFWDLDPVVRPTSAVAL	120

Sequence Id: NP_000031.1
 Sequence Name: apolipoprotein C-III precursor [Homo sapiens]
 Protein Length (AA): 99
 Protein Weight (kDa): 10.8275
 Hyperlinks: [NCBI Protein \(Entrez\)](#)
 GO: [GO:0010897](#) negative regulation of triglyceride catabolic process
[GO:0010903](#) negative regulation of very-low-density lipoprotein particle remodeling
[GO:0010987](#) negative regulation of high-density lipoprotein particle clearance

Single semi-tryptic peptide ID accounts for 20% of the protein sequence coverage and 62% of the total SpC (39).

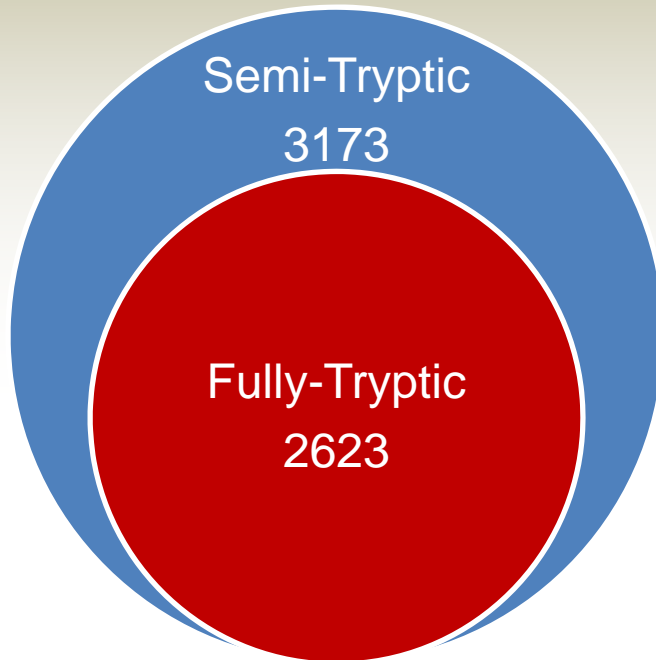
Spectral counts range from 2-13 across 9 samples. Difficult to quantify by SpC.

Observed	Mr(expt)	Mr(calc)	Mass Delta	Charge	Mascot Ions Score	Mascot Prob	Sequest Xcorr	Sequest Prob	Peptide	Total Spectral Count	344 One Month Intensity	344 One Month Log2 Relative Expression	344 One Year Log2 Relative Expression	344 Three Months Log2 Relative Expression
692.69	2,075.049	2,075	23.646	3	15.59	0.999	0	0	GWVTDGESSLKDYWSTVK	1	581.45			
953.968	1,905.921	1,905.849	0.285	2	109.05	1	4.188	1	SEAEDASLLSFMQGYMK	39	15,654.787			
953.958	1,905.901	1,905.849	0.287	2	94.97	1	3.948	1	SEAEDASLLSFMQGYMK	39	15,654.787			
953.96	1,905.905	1,905.849	0.288	2	81.13	0.999	3.646	1	SEAEDASLLSFMQGYMK	39	15,654.787			
953.972	1,905.929	1,905.849	0.287	2	98.4	1	4.126	1	SEAEDASLLSFMQGYMK	39	15,654.787			
953.962	1,905.91	1,905.849	0.286	2	95.93	1	3.931	1	SEAEDASLLSFMQGYMK	39	15,654.787			
953.968	1,905.922	1,905.849	0.286	2	103.61	1	3.581	1	SEAEDASLLSFMQGYMK	39	15,654.787			
636.307	1,905.9	1,905.849	0.574	3	43.61	0.972	2.962	1	SEAEDASLLSFMQGYMK	39	8,580.663			
636.301	1,905.88	1,905.849	0.575	3	46.6	0.986	2.084	0.997	SEAEDASLLSFMQGYMK	39	8,580.663			
953.967	1,905.92	1,905.049	0.29	2	109.15	1	3.469	1	SEAEDASLLSFMQGYMK	39	15,654.707			

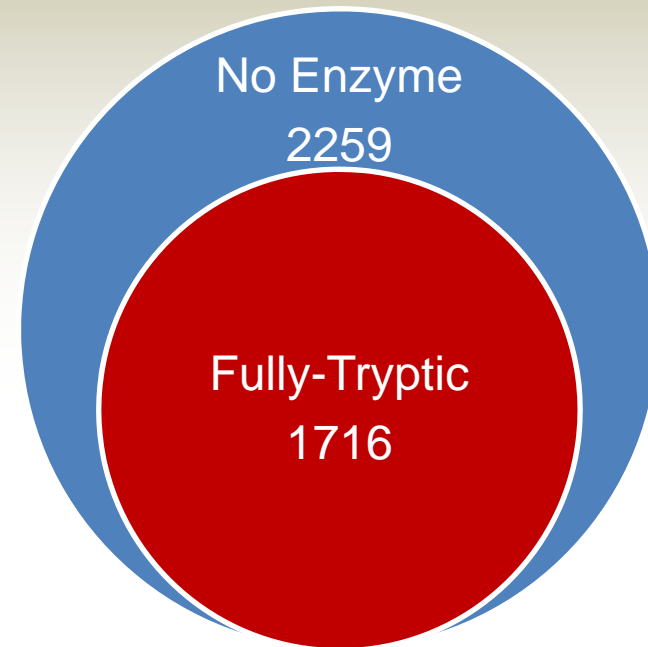


Unique peptide assignments by enzyme rule and search engine

Mascot



Proteome Discoverer



Validation Methods

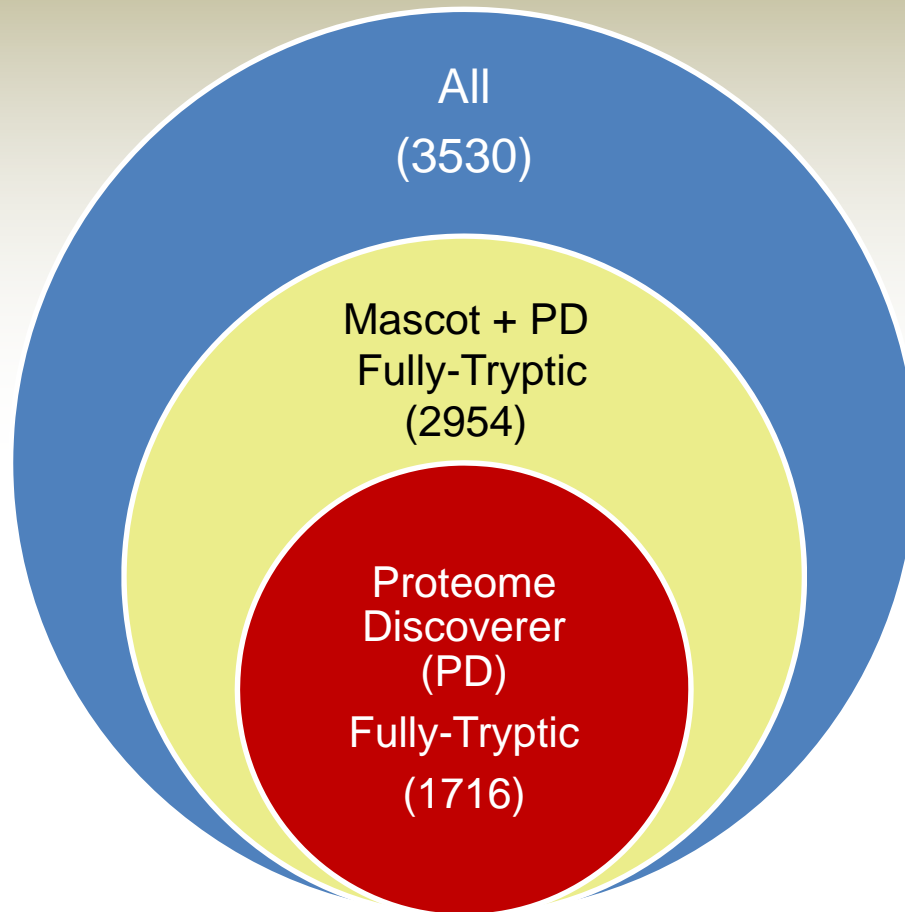
1% Protein FDR
0.9 Peptide probability

Result

Combining multiple enzyme cleavage rules yields an average 21% increase in the number of **unique** peptide assignments



Unique peptide assignments by enzyme rule and search engine



Validation Methods

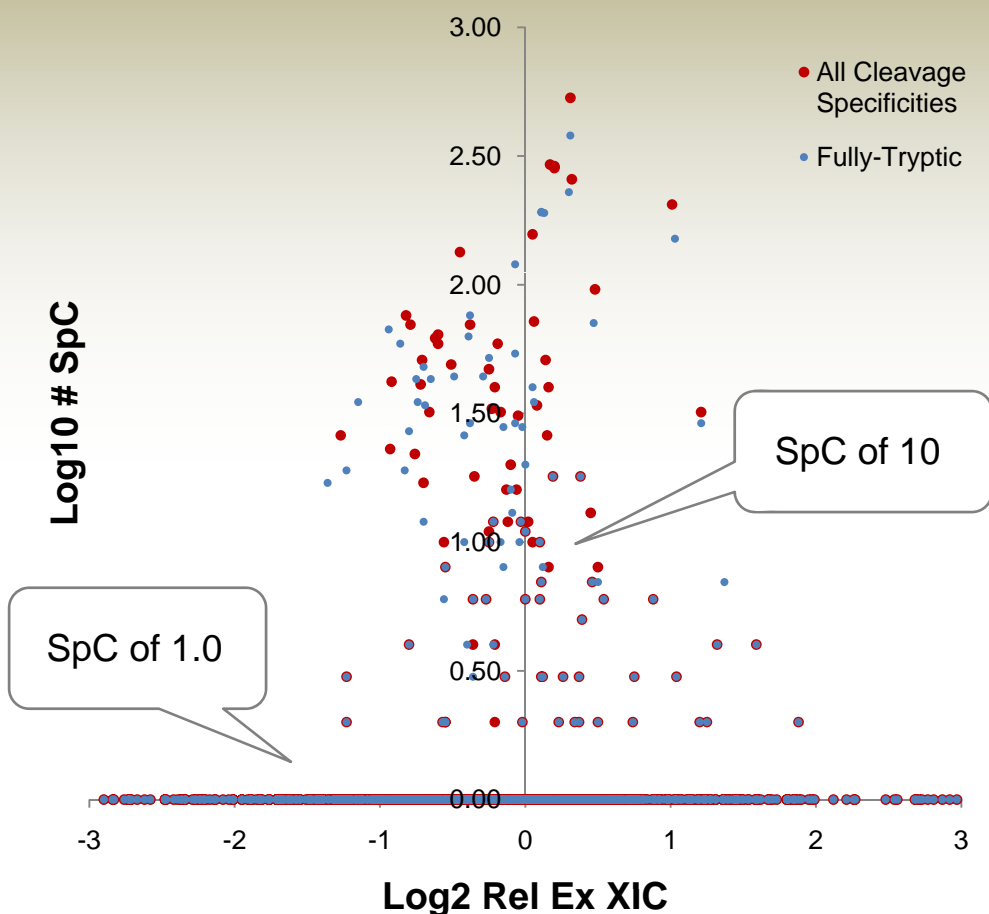
1% Protein FDR
0.9 Peptide probability

Result

Combining multiple search engines and enzyme cleavage rules yields a 48% increase in the number of **unique** peptide assignments



Increased protein sequence coverage adds confidence to label free quantitation



Spectral counting thresholds

Accurate quantification is not possible for proteins with very low spectral counts

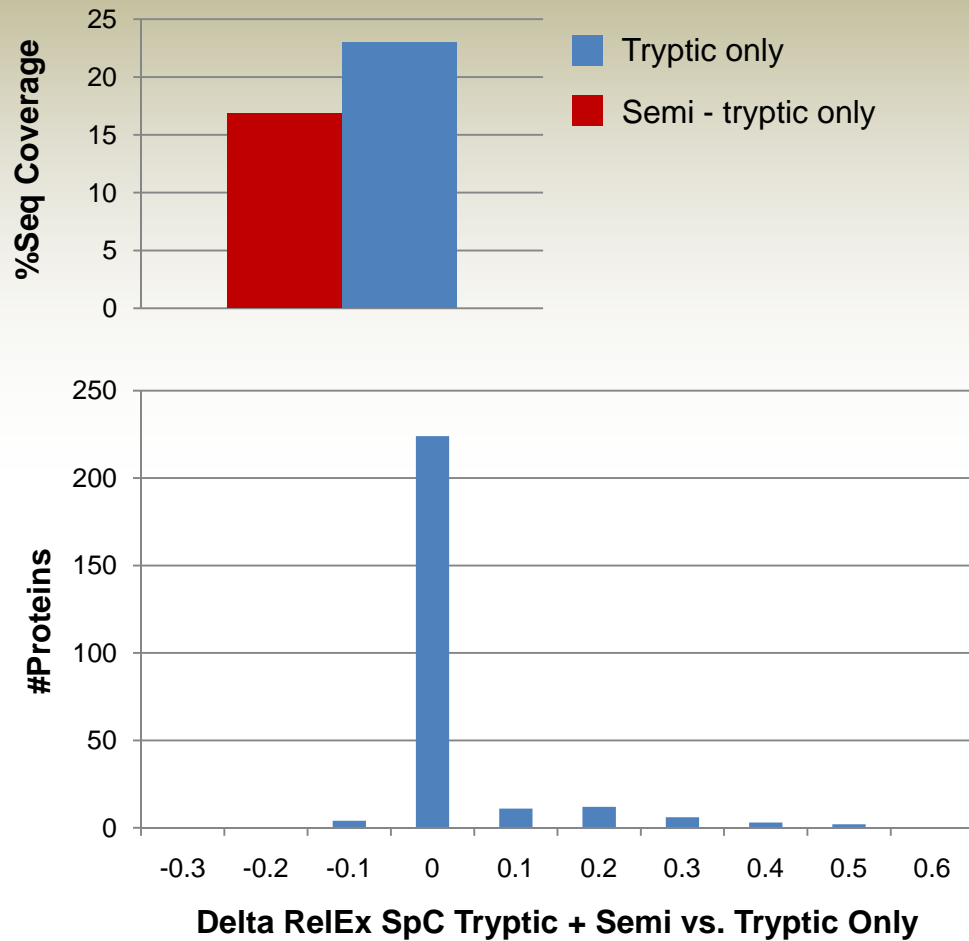
Typical thresholds for spectral filters are above 4 spectral counts for a single protein¹

Does this mean that a protein with 8 SPC is 2 fold over expressed when compared with the same protein with 4 SPC? Maybe or Maybe Not?

1. W. Old, K. Meyer-Arendt, L. Aveline-Wolf, K. Pierce, A. Mendoza, J. Sevinsky, K. Resing, N. Ahn "Comparison of label-free methods for quantifying human proteins by shotgun proteomics." *Molecular & Cellular Proteomics* vol. 4, pp. 1487-1502, 2005.



Increased protein sequence coverage adds confidence to label free quantitation



Validation Methods

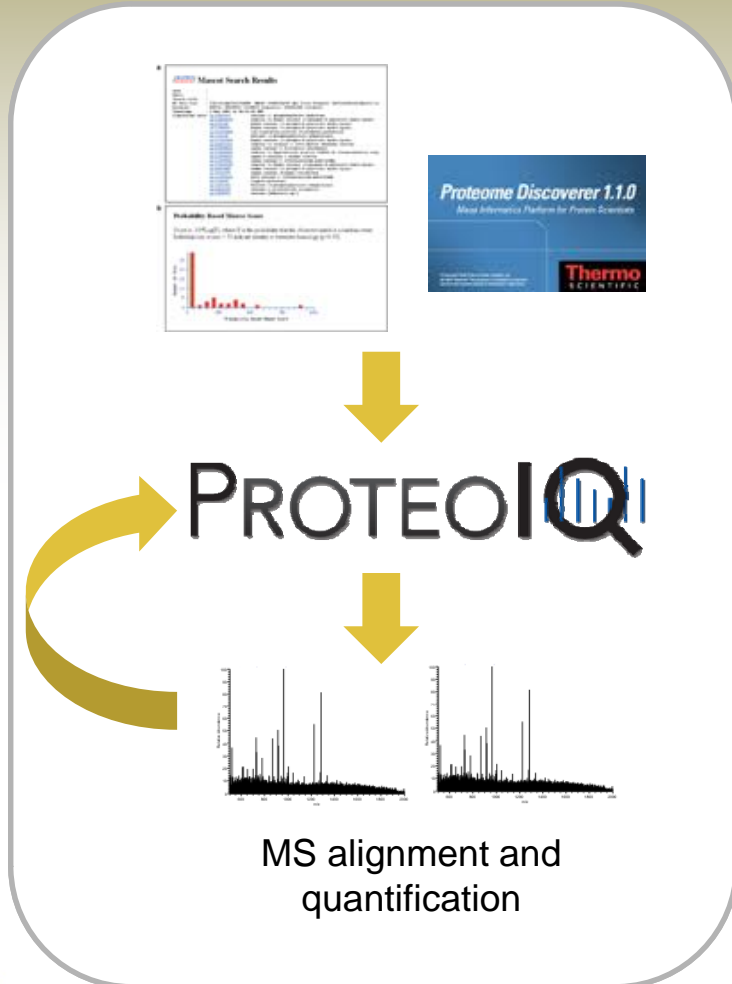
1% Protein FDR
0.9 Peptide probability
3 or more peptides/protein

Result

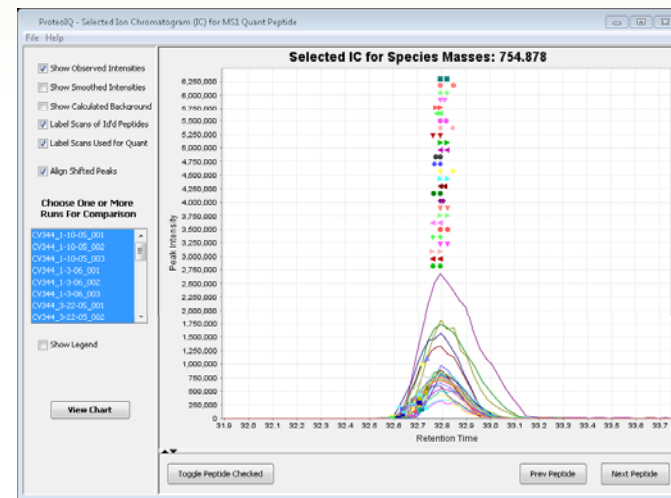
Addition of multiple enzyme rules
Does not effect RelEx on highly abundant proteins. Proteins with low #SpC exhibit a shift in RelEx.



ProteoIQ – XIC Label Free Workflow



Unlike spectral counting XIC based quantification only requires that a single precursor must have triggered and MS/MS event in order for a peak area to be calculated.



ProteoIQ - Visualizing XIC Quant

Protein Centric

RelEx

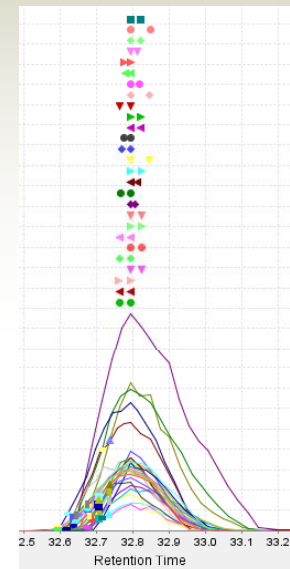
Select	Protein Group	Isoform Classification	Sequence Id	Sequence Name	427 One Month Normalized SC (N-SC)	427 One Month N-Int Log2 Relative Expression	427 One Year Normalized SC (N-SC)
<input type="checkbox"/>	1	Top	NP_000055.2	complement C3 precursor [Homo sapiens]	177	-7.659E-17	142.333
<input type="checkbox"/>	1	Other	XP_001719515.1	PREDICTED: similar to complement component C3, partial [...]	140	-3.375E-17	107.333
<input type="checkbox"/>	1	Other	XP_001724196.1	PREDICTED: similar to complement component 3 [Homo sap...]	35.667	-4.912E-17	32.333

Peptide Centric

Intensity

RelEx

Charge	Mascot Ions Score	Mascot Prob	Sequest Xcorr	Sequest Prob	Peptide Sequence	Modification	427 One Month Intensity	427 One Month Log2 Relative Expression	427 One Year Intensity
2	133.36	1	2.546	0.999	VTGEGCVYLQTSLK	+57.02 (C6)	25,899.557	2.313E-18	12,631.399
2	114.86	1	3.308	1	MYYSAVDPTKDIFTGLIGPMK		34,141.539	0	45,192.841
2	114.82	1	3.448	1	FAHYVVTSQVWNTANEAR		34,852.615	0	55,027.27
2	114.24	1	1.77	0.997	HPNSPLDEENLTQENQDR		25,773.66	4.626E-18	45,523.822
2	113.77	1	2.996	1	SLGECDDVEDSTTCFNAK	+57.02 (C5); +57.02 (C6...)	282,751.979	0	680,385.884



Experts in protein discovery



ProteoIQ – MS1 Quant Settings for the human serum proteome

MS1 Quant Settings

Please specify the MS1 quantitation settings:

Peptide Detection Settings: Lock Settings

Max Peak Width (# Scans) : 50

Mass Tolerance (ppm) 100.0

Data are Centroided

Chromatograms Aligned using Peptides Identified in all Runs

Samples Part of a Fractionation Num Contiguous Fractions 1

Quantitation Method:

Quantify Using Top Peaks within Elution Window

Number of Scans for Quant of Each Peptide: 2

Quantify Using Total Area within Elution Window

Use Smoothed Elution Curve

Elution Window Calculation Method:

User-defined Window

Peak Width (# Scans) 5

Automatically Determined by ProteoIQ

Percentage of Peak Height to Determine Peak Width 50.0

Use Same Scans for All Species

Max RT Variation of Precursors (s) 45.0

Minimum Signal-to-Noise for Inclusion of Peaks in Quantitation 2

Number of Most Intense Precursors to Use for Quantitation of Proteins 3

Perform Background Subtraction

Reference Group

* Note: These settings only affect protein sets created after the settings are applied.

Apply Close

Modify quantification settings on a global level or for individual peptides – get instant feedback

XIC Quant Methods

Precursor ppm tolerance = 100.00

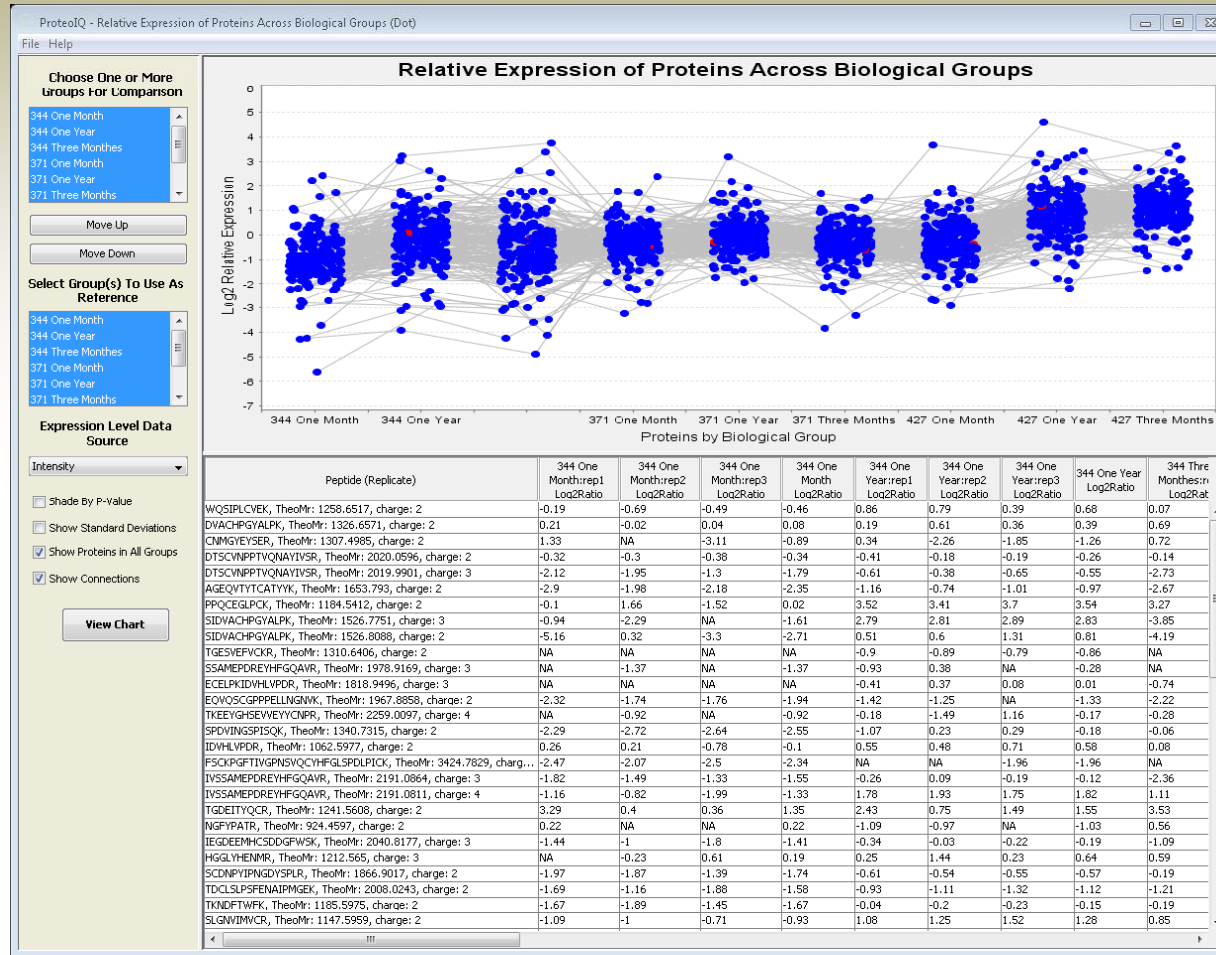
Prealignment performed
2 most abundant precursors within each XIC used for ratios calculations

Max RT variation = 45 scans

S/N filter = 2.0

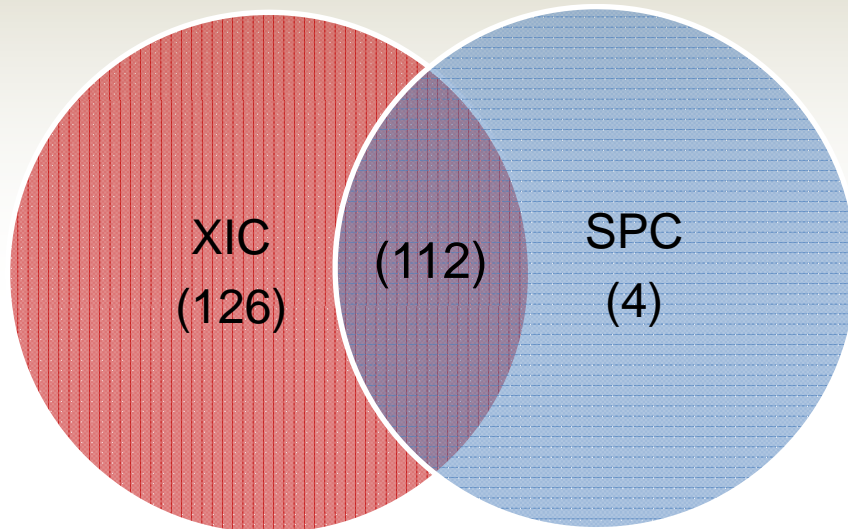


XIC based quantification across 3 patients and 3 time points



Correlation between SpC and XIC based quantification

Number of proteins quantified by either intensity based XIC or spectral counting (SPC)



Validation Methods

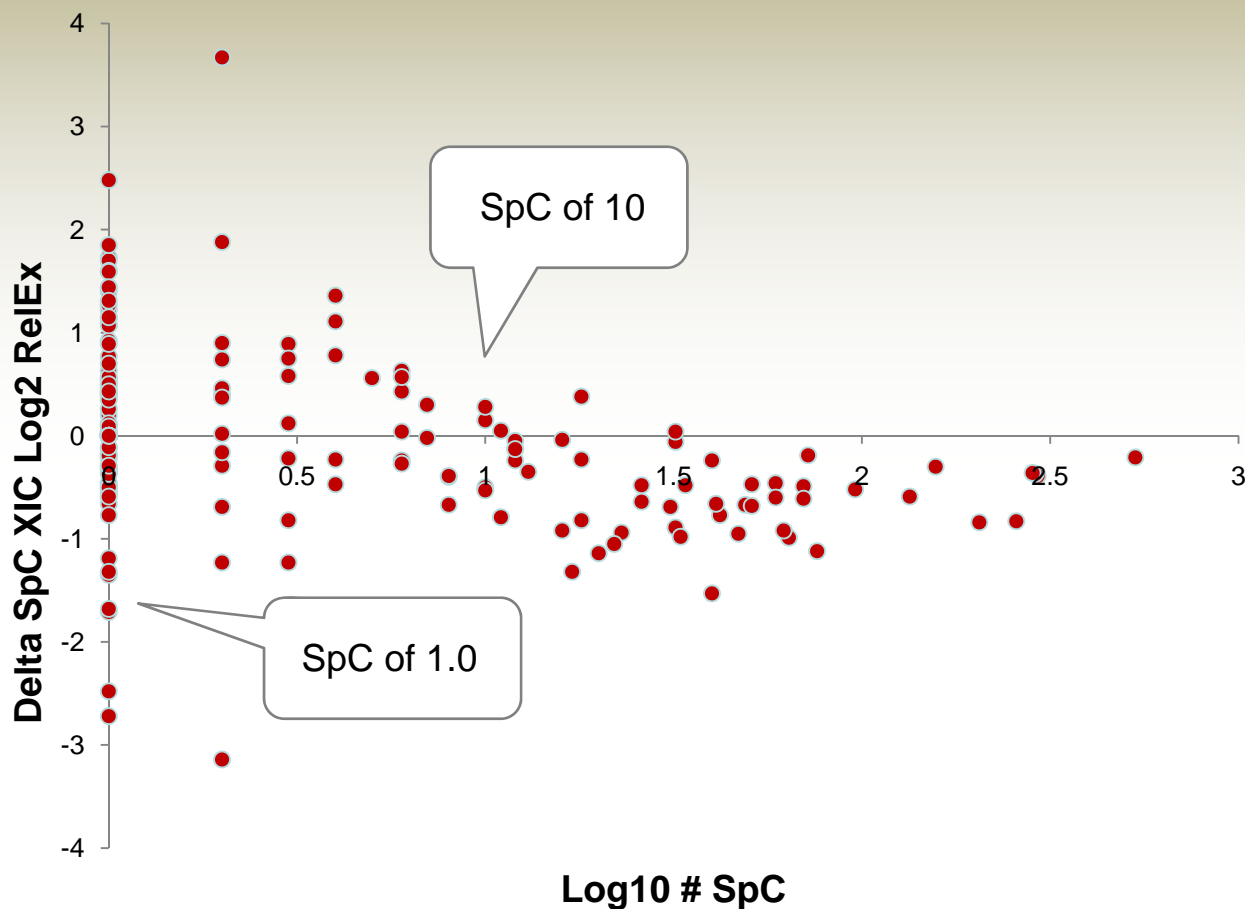
1% Protein FDR
0.9 Peptide probability
2 peptides/protein
5 or more SPC

Results

Significantly more proteins can be quantified by XIC approaches



Correlation between SpC and XIC based quantification



Validation Methods

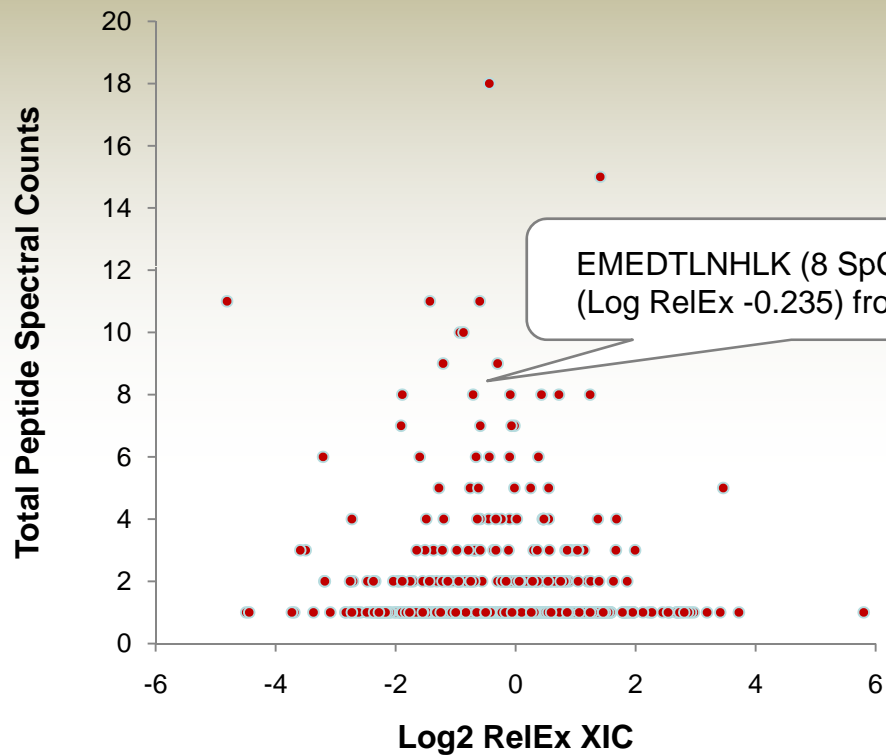
1% Protein FDR
0.9 Peptide probability
2 peptides/protein

Results

High degree of correlation between XIC and SpC for highly sampled proteins. XIC preferred below SpC of 5.



XIC quantitation for peptides from proteins with no spectral counts in patient 427

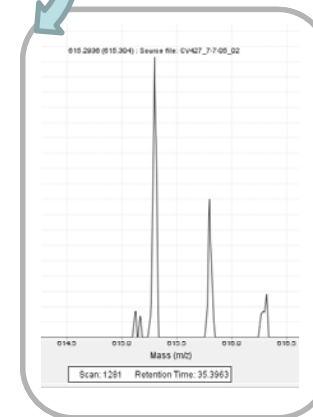
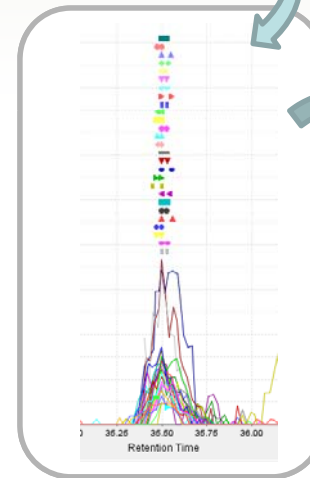


Validation Methods

1% Protein FDR
0.9 Peptide probability
2 peptides/protein

Results

1271 peptides were not identified in patient 427 that were identified in other samples and were quantified by XIC.



XIC quantification of IGFBP-3 (4-5 Log₁₀ pg/ml*)

ProteoIQ -- Protein Sequence Viewer

File View Help

Group/Replicate	Mascot Protein Prob	Sequest Protein Prob	Total Protein Prob	Num Peptides	Spectral Count (SC)	Normalized SC (N-SC)	N-Int Log2 Relative Expression
344 One Month		1	1	1	1.0	0.33	-1.4
344 One Year		1	1	1	3.0	1	-0.12
344 Three Months		1	2	2	4.0	1.33	-0.29
371 One Month		0	0	0	0.0	0	-0.5
371 One Year		0	0	0	0.0	0	0.17
371 Three Months		0	0	0	0.0	0	0.22
427 One Month		0	0	0	0.0	0	-0.58
427 One Year		0	0	0	0.0	0	1.7
427 Three Months		0	0	0	0.0	0	0.63
Total (Non-Redundant)	1	0.99	1	2	0		

1	MQRARPTLMAAALTLVLRLGPPVARAGASSAGLGPVVRCEPCDARALAQCAPPAVCAE	60
61	LVREPGGCCCLTCALSEGQPCGIYTERCGSLRCQSPDEARPLQALLDGRGLCVNASAV	120
121	SRLRAYLLPAPPAPGNASEEEDRSAGSVESPSVSSSTRVSDPKFPHLHSKI I I I KKGHA	180
181	KDSQRYKVDYESQSTDTQNFSSSEKRETEYGPCRR EMEDTLNHLKFLNLVLS PRGVHIPNC	240
241	DKKGFYKKKQCRPSKGRKRKGFMCVVDKYGQPLPGYTTKGEDVHCYSMQSK	300

Sequence Id: NP_000589.2

Sequence Name: insulin-like growth factor-binding protein 3 isoform b precursor [Homo sapiens]

Protein Length (AA): 291

Protein Weight (kDa): 31.8357

Hyperlinks:

[NCBI Protein \(Entrez\)](#)

GO

GO:biological_process

[GO:0014912](#) negative regulation of smooth muscle cell migration

[GO:0045663](#) positive regulation of myoblast differentiation

GO:molecular_function

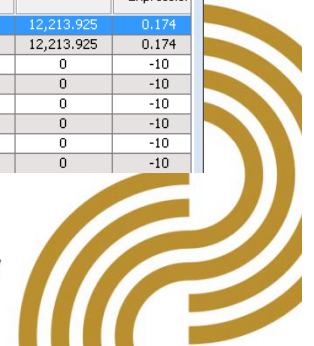
[GO:0018942](#) insulin-like growth factor binding protein complex

Two overlapping high confidence peptide assignments

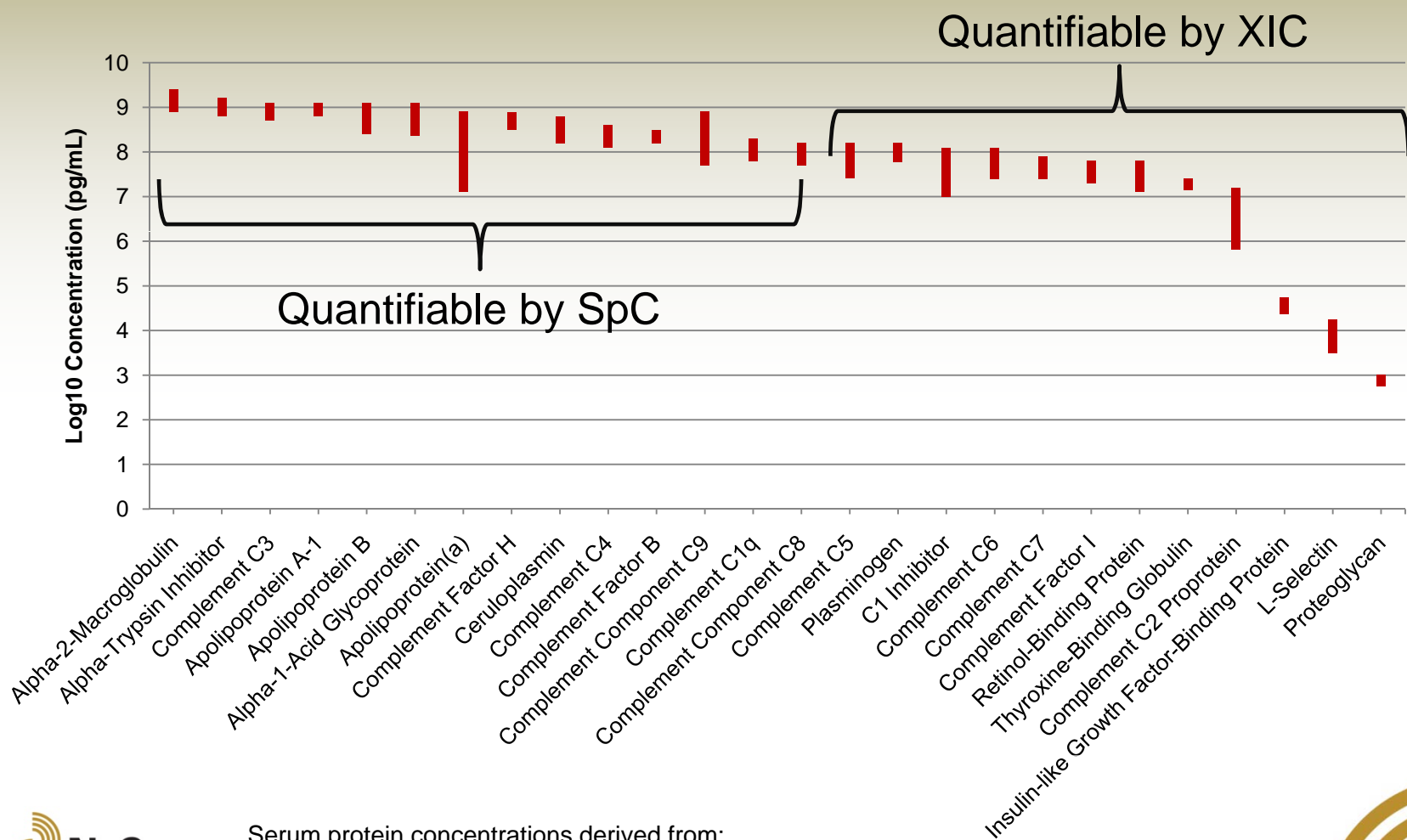
Zero SpC in patient 427.

Two peptides in patient 344 used for XIC

Observed	Mr(expt)	Mr(calc)	Mass Delta	Charge	Mascot Ions Score	Mascot Prob	Sequest Xcorr	Sequest Prob	Peptide	344 One Month Intensity	344 One Month Log2 Relative Expression	344 One Year Intensity	344 One Year Log2 Relative Expression	344 Three Months Intensity	344 Three Months Log2 Relative Expression	371 One Month Intensity	371 One Month Log2 Relative Expression	371 One Year Intensity	371 One Year Log2 Relative Expression
615.3	1,228.586	1,228.576	8.065	2	38.91	1	0	0	EMEDTLNHLK	4,336.831	-1.337	9,257.618	-0.244	8,784.3	-0.324	11,390.055	-0.118	12,213.925	0.174
615.307	1,228.599	1,228.576	19.094	2	20.48	0.995	0.791	0	EMEDTLNHLK	4,336.831	-1.337	9,257.618	-0.244	8,784.3	-0.324	11,390.055	-0.118	12,213.925	0.174
473.284	944.553	944.544	9.31	2	40.54	1	1.748	0.963	FLNLVLSR	3,463.387	-1.461	9,330.469	0.002	7,971.726	-0.248	990.183	-1.645	0	-10
473.283	944.551	944.544	6.596	2	38.01	1	1.588	0.839	FLNLVLSR	3,463.387	-1.461	9,330.469	0.002	7,971.726	-0.248	990.183	-1.645	0	-10
473.288	944.561	944.544	17.839	2	32.68	1	1.476	0.919	FLNLVLSR	3,463.387	-1.461	9,330.469	0.002	7,971.726	-0.248	990.183	-1.645	0	-10
473.283	944.551	944.544	6.725	2	38.18	1	1.803	0.985	FLNLVLSR	3,463.387	-1.461	9,330.469	0.002	7,971.726	-0.248	990.183	-1.645	0	-10
473.284	944.553	944.544	8.857	2	38.01	1	1.746	0.935	FLNLVLSR	3,463.387	-1.461	9,330.469	0.002	7,971.726	-0.248	990.183	-1.645	0	-10
473.282	944.549	944.544	4.851	2	33.97	1	1.764	0.968	FLNLVLSR	3,463.387	-1.461	9,330.469	0.002	7,971.726	-0.248	990.183	-1.645	0	-10



Increased quantitative dynamic range is achieved by XIC vs. SpC



Serum protein concentrations derived from:
 Anderson. Molecular Cellular Proteomics 1: 845-867, 2002
 Qian. Molecular Cellular Proteomics 7: 1963-1973, 2008

Experts in protein discovery



Conclusion

- ProteoIQ supports spectral counting and XIC based quantification
- Increased proteome coverage is achieved by combining multiple search engines and enzyme cleavage rules
- Spectral counting and XIC quantification correlate at high spectral counts
- XIC quantification provides reliable protein expression measurements for low abundance species



Learn More Today

Free Viewer

The screenshot shows the NuSep ProteoIQ Viewer software interface. The main heading is "ProteoIQ Viewer". Under "Software Info", it lists features like Statistical Validation, Proteome Identification, and Computational Proteomics. A "Download Now" button is prominent. The "Next Steps" section includes "Free Trial", "Download PROTEOIQ", and "Go To Demo Center".

Free Trial

The screenshot shows the NuSep Free Trial page. The main heading is "Free Trial". It includes a "Software Info" section with details about the ProteoIQ software. A "Contact Us" button is visible. The "Next Steps" section includes "Free Trial", "Download PROTEOIQ", and "Go To Demo Center".

Webinars and Videos

The screenshot shows the NuSep website featuring ProteoIQ Biological Annotation. The main heading is "ProteoIQ Biological Annotation". It includes a "GET YOUR FREE TRIAL SOFTWARE NOW!" button. The "Next Steps" section includes "Learn More", "Sign Up Now", "Learn More", and "Learn More".

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Q & A



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