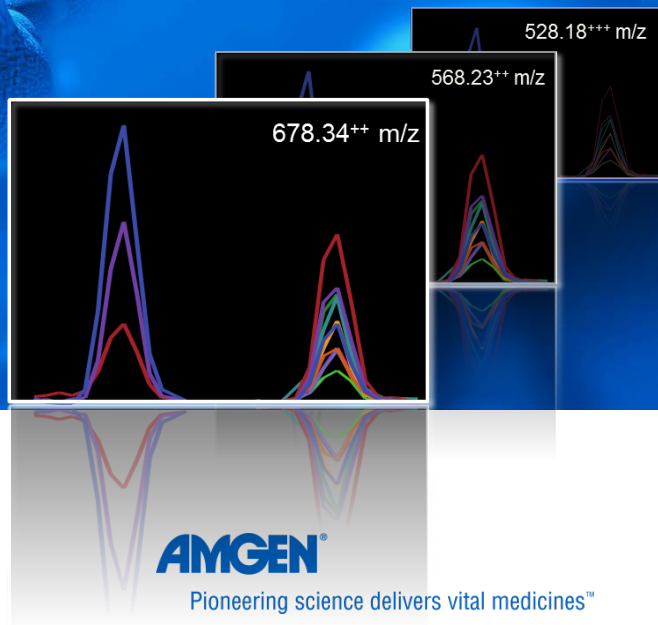


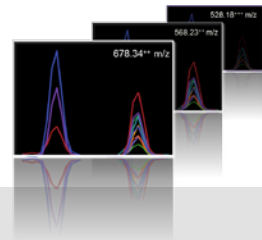
# Rapid Identification of Contaminants and Interferences using Skyline



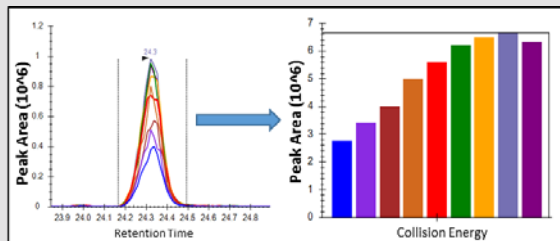
**MATT RARDIN**

ASMS SKYLINE USER MEETING, INDIANAPOLIS, IN  
JUNE 4TH, 2017

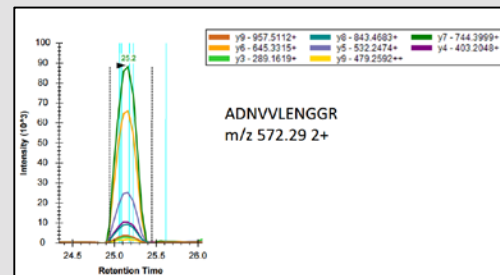
# SKYLINE APPLICATIONS AT AMGEN



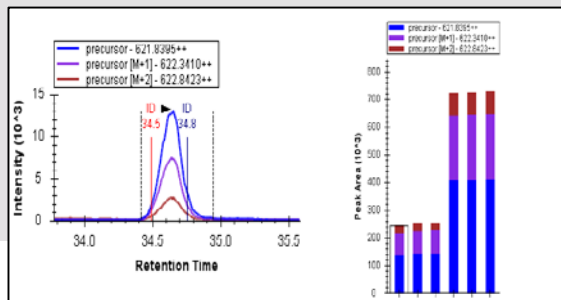
## SRM



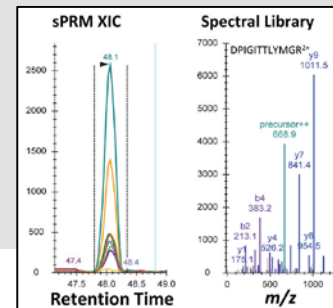
## DIA / SWATH



## MS1 Filtering

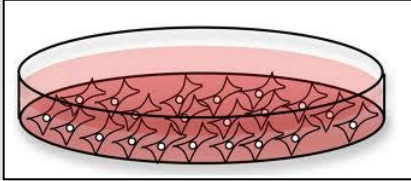


## PRM / MRM-HR



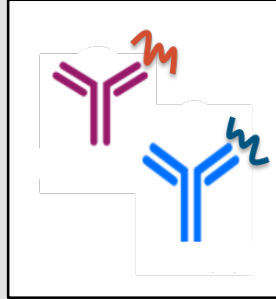
# WORKFLOW DEVELOPMENT

Tissue culture cells



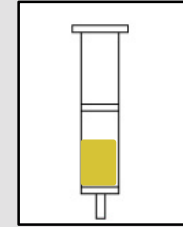
Lysis  
&  
Digestion

Affinity Enrichment



Acid elution

SPE

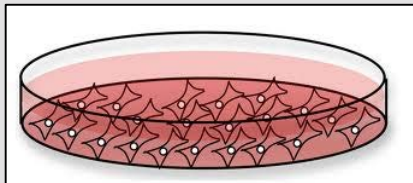


Orbitrap Fusion LC-MS/MS



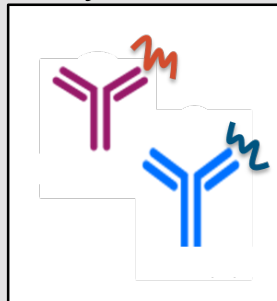
# WORKFLOW DEVELOPMENT

Tissue culture cells



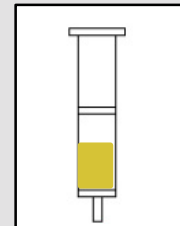
Lysis  
&  
Digestion

Affinity Enrichment

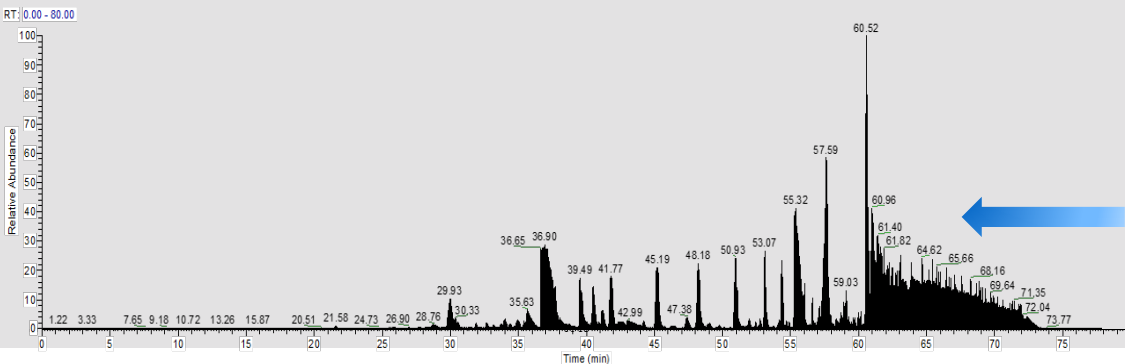


Acid elution

SPE

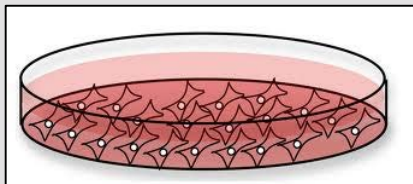


Orbitrap Fusion LC-MS/MS



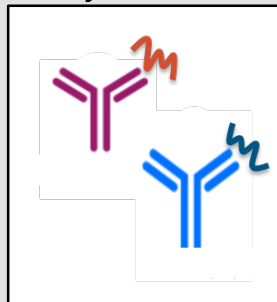
# WORKFLOW DEVELOPMENT

Tissue culture cells



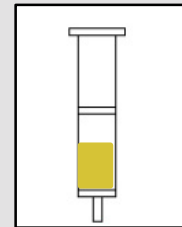
Lysis  
&  
Digestion

Affinity Enrichment



Acid elution

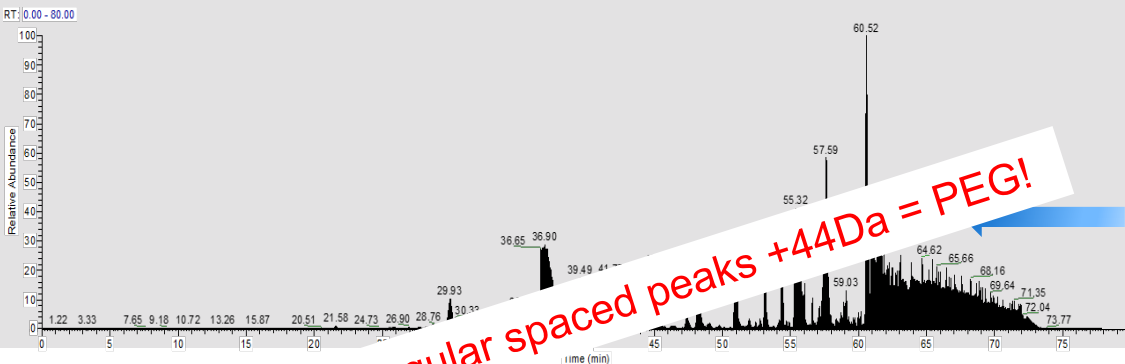
SPE



Orbitrap Fusion LC-MS/MS



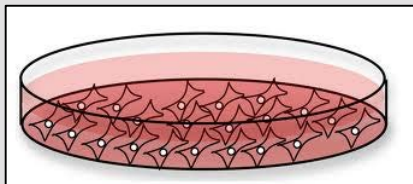
AMGEN



Regular spaced peaks +44Da = PEG!

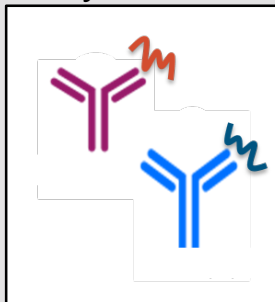
# TRACKING DOWN THE SOURCE

Tissue culture cells



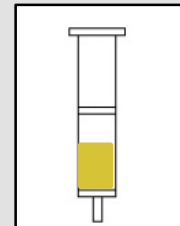
Lysis  
&  
Digestion

Affinity Enrichment



Acid elution

SPE



Orbitrap Fusion LC-MS/MS



Media?  
Buffers?  
Plastics?  
Antibodies?  
Reagents?  
Contaminated solvents?

# PROTEOMIC WORKFLOWS

**Sample handling/reagents – tissue, cells, biofluids, recombinant protein...**

*Homogenization, lysis, filtering...*

**Protein Matrix**

*Separation, enrichment, depletion, labeling...*

*Digestion*

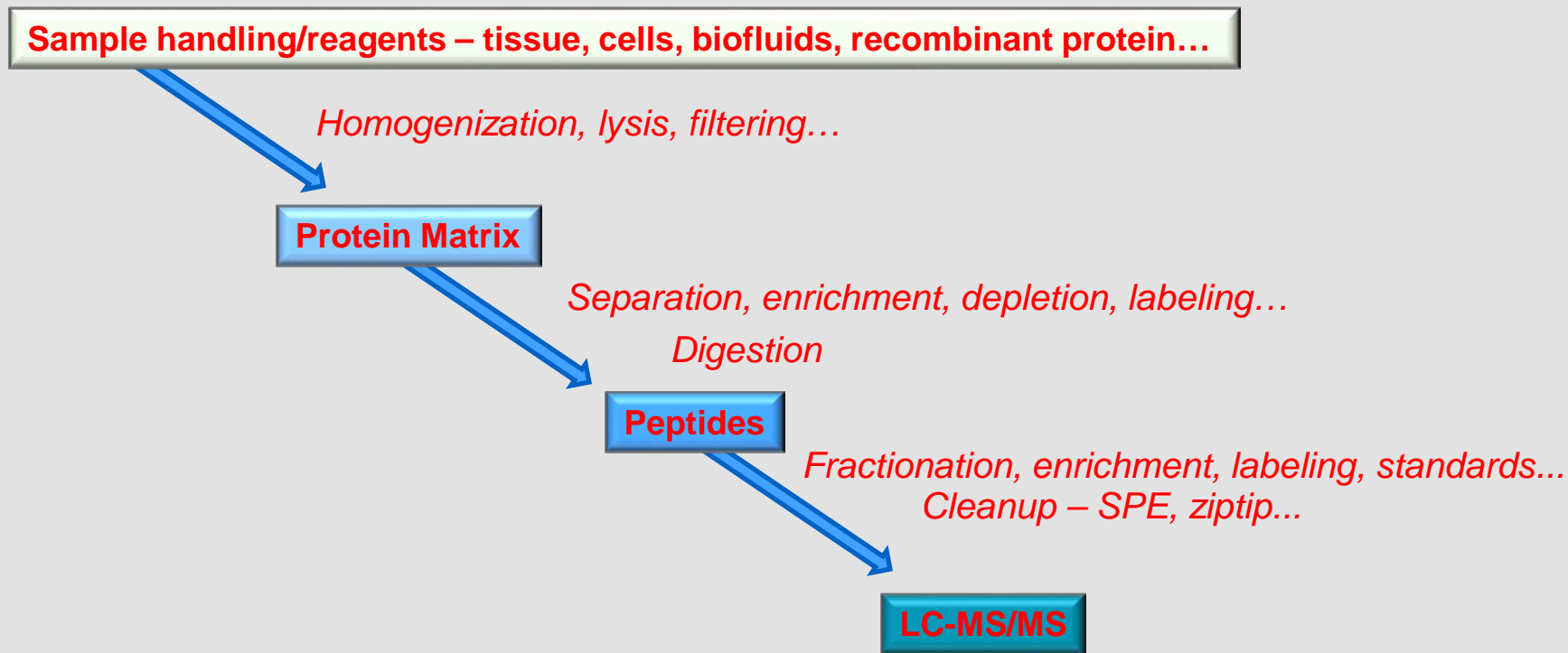
**Peptides**

*Fractionation, enrichment, labeling, standards...*

*Cleanup – SPE, ziptip...*

**LC-MS/MS**

# PROTEOMIC WORKFLOWS ARE A SOURCE OF CONTAMINATION





# RESOURCES FOR CONTAMINANTS AND INTERFERENCES



ELSEVIER

available at [www.sciencedirect.com](http://www.sciencedirect.com)



journal homepage: [www.elsevier.com/locate/aca](http://www.elsevier.com/locate/aca)



## Review article

### Interferences and contaminants encountered in modern mass spectrometry

Bernd O. Keller<sup>a,\*</sup>, Jie Sui<sup>b</sup>, Alex B. Young<sup>c</sup>, Randy M. Whittall<sup>d</sup>

14 April 2008

## UNIMOD

protein modifications for mass spectrometry

Unimod

Logged as **Guest** [Log out](#)

[Change password](#)

[Advanced search](#)

## Bioinformatics

[Issues](#)

[Advance articles](#)

[Publish](#) ▼

[Purchase](#)

[Alerts](#)

[About](#) ▼



**Volume 28, Issue 21**  
1 November 2012

### MaConDa: a publicly accessible mass spectrometry contaminants database FREE

Ralf J. M. Weber, Eva Li, Jonathan Bruty, Shan He, Mark R. Viant ✉

Bioinformatics (2012) 28 (21): 2856-2857.

DOI: <https://doi.org/10.1093/bioinformatics/bts527>

Published: 06 September 2012 [Article history](#) ▼

# DEVELOPING A SKYLINE LIBRARY OF CONTAMINATES AND INTERFERENCES USING MS1 AND SMALL MOLECULE FEATURES



**Skyline for small molecules: a flexible tool for cross-platform LC-MS/MS method creation and data analysis for metabolomics.**



J. Will Thompson<sup>1</sup>, Brian Pratt<sup>2</sup>, Max Horowitz-Gelb<sup>2</sup>, Laura G. Dubois<sup>1</sup>, Lisa St.John-Williams<sup>1</sup>, Giuseppe Astarita<sup>3</sup>, M. Arthur Moseley<sup>1</sup>, Michael MacCoss<sup>2</sup>, and Brendan MacLean<sup>2</sup>

<sup>1</sup>Duke Proteomics and Metabolomics Core, Center for Genomic and Computational Biology, School of Medicine, Duke University, Durham, NC; <sup>2</sup>Department of Genome Sciences, School of Medicine, University of Washington, Seattle, WA; <sup>3</sup>Waters Corporation, Milford, MA

## Recent Advances in Skyline: Small Molecule Targets and Ion Mobility Filtering

Brian Pratt<sup>1</sup>, Max Horowitz-Gelb<sup>1</sup>, J. Will Thompson<sup>2</sup>, Erin Baker<sup>3</sup>, J. Will Thompson<sup>4</sup>, Michael J. MacCoss<sup>1</sup>, Brendan MacLean<sup>1</sup>

<sup>1</sup>University of Washington, Seattle WA, <sup>2</sup>Duke University School of Medicine, Durham NC, <sup>3</sup>Pacific Northwest National Laboratory, Richland WA

Monoisotopic ion mass (singly charged)	Ion type	Formula for M or subunit or sequence	Compound ID or species	Possible origin and other comments	ESI	MALDI	References
33.03349	[M+H] <sup>+</sup>	CH <sub>3</sub> OH	Methanol	Acetonitrile, solvent	X		A
42.03383	[M+H] <sup>+</sup>	CH <sub>3</sub> CN	ACN	Acetonitrile, solvent	X		A
59.06037	[M+NH <sub>4</sub> ] <sup>+</sup>	CH <sub>3</sub> CN	ACN	Acetonitrile, solvent	X		A, F
63.04406	[A <sub>n</sub> B+H] <sup>+</sup>	[C <sub>2</sub> H <sub>4</sub> O] <sub>n</sub> H <sub>2</sub> O	PEG	Polyethylene glycol, ubiquitous polyether	X		D, K
64.01577	[M+Na] <sup>+</sup>	CH <sub>3</sub> CN	ACN	Acetonitrile, solvent	X		A, F
65.05971	[M <sub>n</sub> +H] <sup>+</sup>	CH <sub>3</sub> OH	Methanol	Methanol, solvent	X		A
74.06004	[M+H] <sup>+</sup>	C <sub>2</sub> H <sub>5</sub> NO	Dimethyl formamide	solvent	X		A, C, F
74.06004	[A <sub>n</sub> B <sub>n</sub> +H] <sup>+</sup>	(CH <sub>3</sub> CN) <sub>n</sub> (CH <sub>3</sub> OH) <sub>m</sub>	Acetonitrile/Methanol	ESI solvents	X		K
77.05971	[A <sub>n</sub> B+H] <sup>+</sup>	[C <sub>2</sub> H <sub>4</sub> O] <sub>n</sub> H <sub>2</sub> O	PPG	Polypropylene glycol, ubiquitous polyether	X		D, K
79.02121	[M+H] <sup>+</sup>	C <sub>2</sub> H <sub>5</sub> OS	DMSO	Dimethyl sulf oxide, solvent	X		A
83.06037	[M <sub>n</sub> +H] <sup>+</sup>	CH <sub>3</sub> CN	Acetonitrile	ESI solvents	X		A, C
85.02600	[A <sub>n</sub> B+Na] <sup>+</sup>	[C <sub>2</sub> H <sub>4</sub> O] <sub>n</sub> H <sub>2</sub> O	PEG	Polyethylene glycol, ubiquitous polyether	X		D, K
85.05887	[M+H] <sup>+</sup>	C <sub>2</sub> D <sub>2</sub> OS	d <sub>6</sub> -DMSO	d <sub>6</sub> -Dimethyl sulf oxide, solvent	X		A
88.03931	[A <sub>n</sub> B <sub>n</sub> +H] <sup>+</sup>	(CH <sub>3</sub> CN) <sub>n</sub> (HCOOH) <sub>m</sub>	Acetonitrile/Formic Acid	ESI solvents	X		A, C

## Expanding Skyline's Capabilities to Small Molecule Data Analysis

Laura G. Dubois

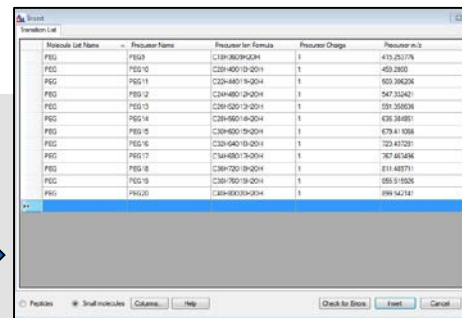
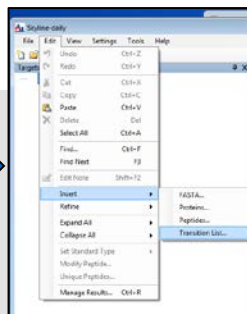
Duke Proteomics and Metabolomics Core Facility



## CREATING A MOLECULAR CONTAMINATION LIBRARY

Molecule List Name	Precursor Name	Precursor Formula	Precursor Charge	Precursor m/z
PEG	PEG9	C18H36O9H2OH	1	415.2538
PEG	PEG10	C20H40O10H2OH	1	459.2800
PEG	PEG11	C22H44O11H2OH	1	503.3062
PEG	PEG12	C24H48O12H2OH	1	547.3324
PEG	PEG13	C26H52O13H2OH	1	591.3586
PEG	PEG14	C28H56O14H2OH	1	635.3849
PEG	PEG15	C30H60O15H2OH	1	679.4111
PEG	PEG16	C32H64O16H2OH	1	723.4373
PEG	PEG17	C34H68O17H2OH	1	767.4635
PEG	PEG18	C36H72O18H2OH	1	811.4897
PEG	PEG19	C38H76O19H2OH	1	855.5159
PEG	PEG20	C40H80O20H2OH	1	899.5421

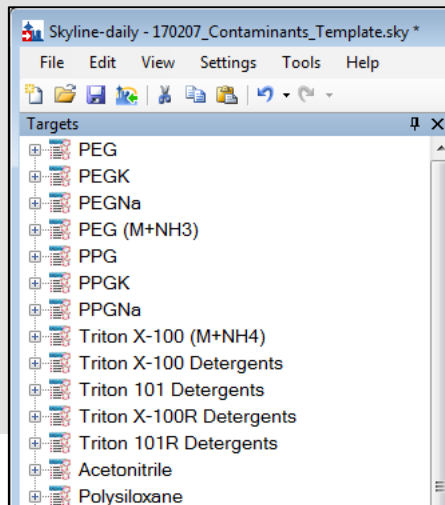
## Transition List



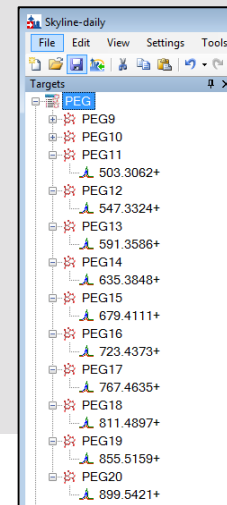
## Import List into Skyline

# Contamination Library

- 64 molecular groups
- 641 molecules



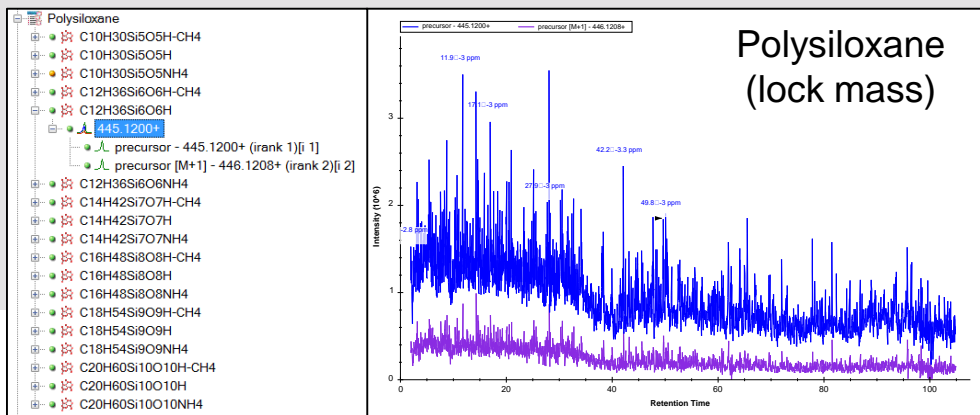
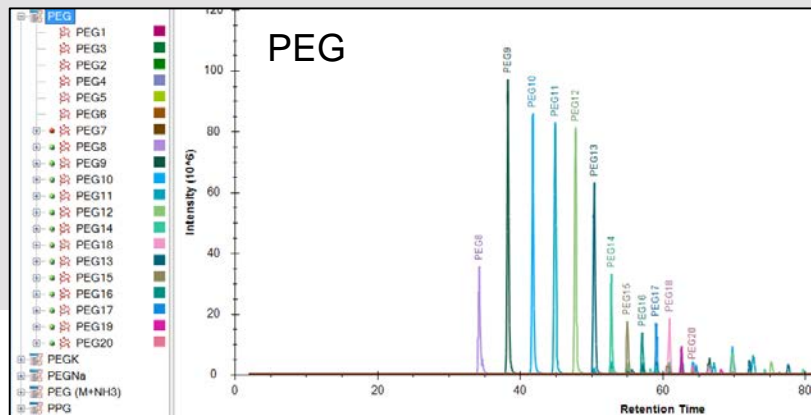
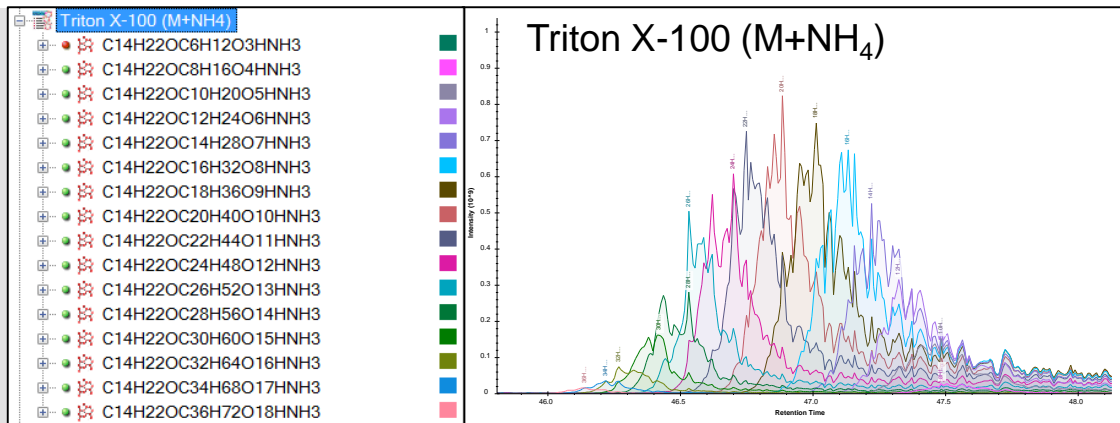
**Add additional groups to expand your library as needed**



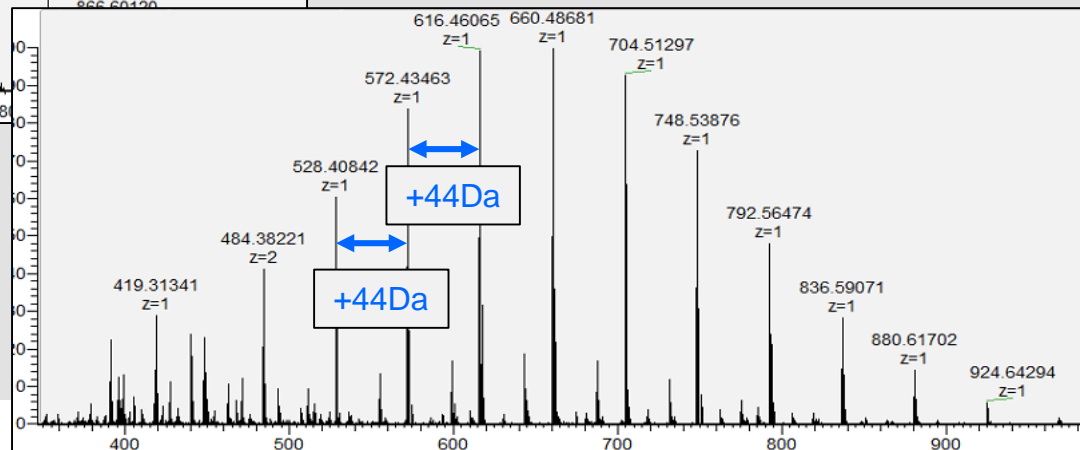
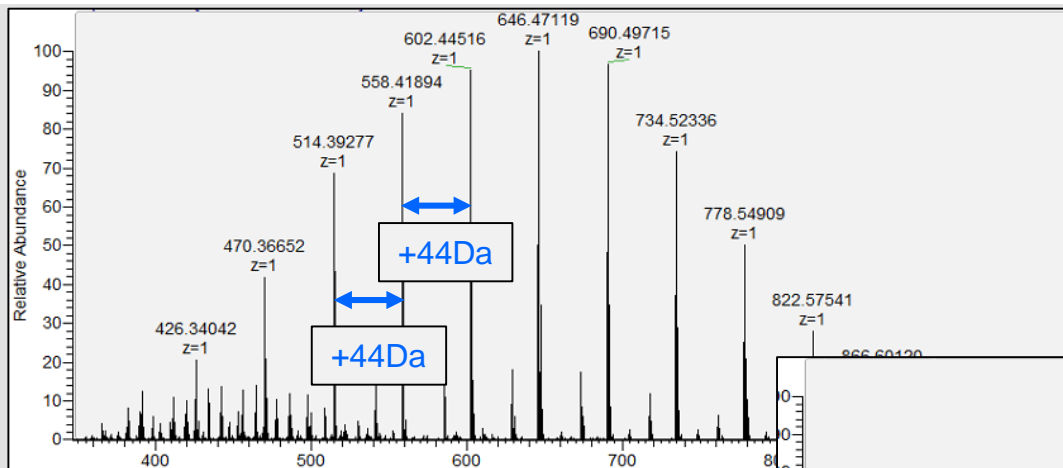
## Populate your molecular tree

# MONITORING COMMON CONTAMINANTS USING MS1 FILTERING

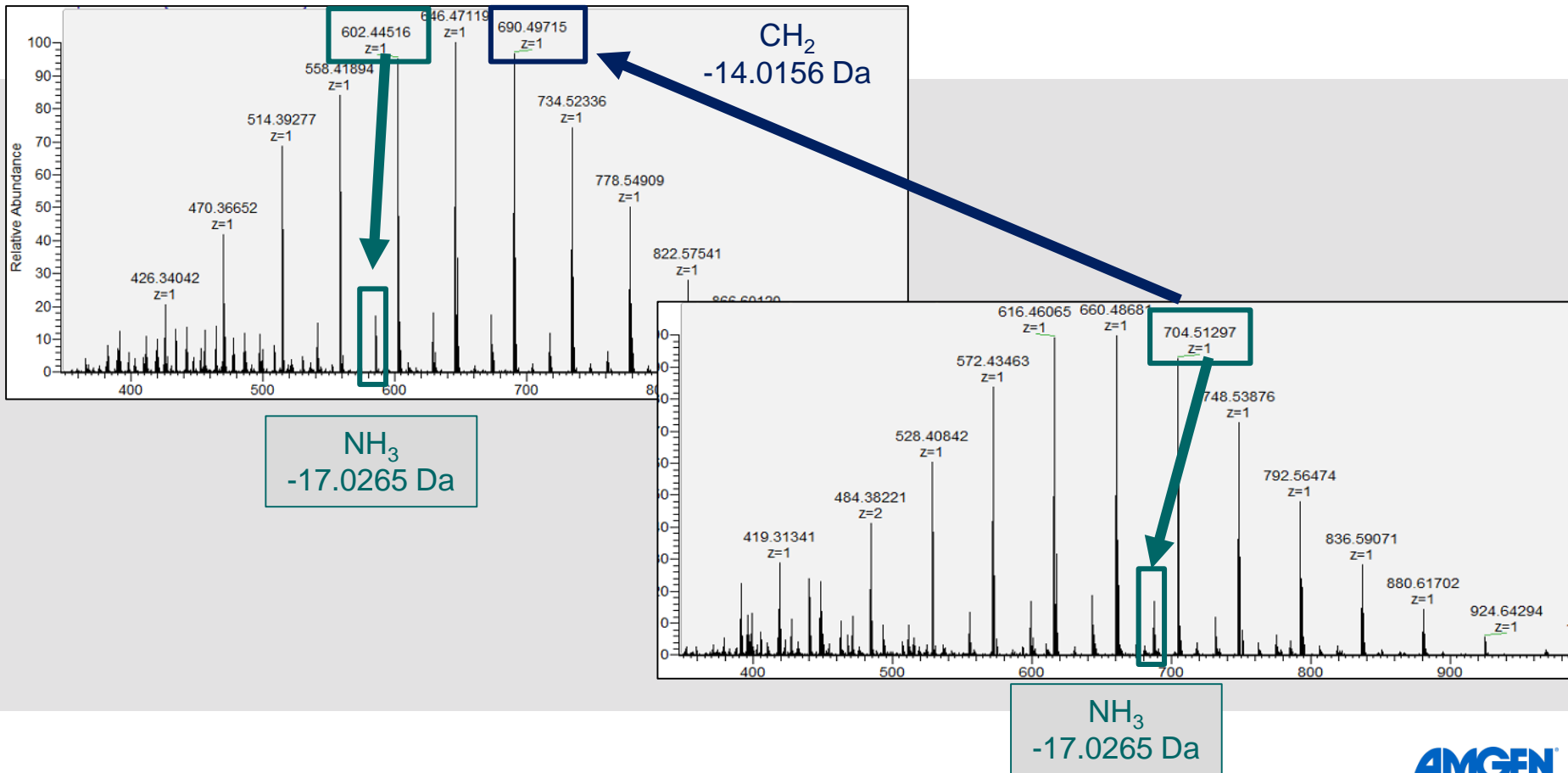
Contamination never  
looked so GOOD...



# IDENTIFYING AN UNKNOWN SPECIES OF (PEG)?



# IDENTIFYING AN UNKNOWN SPECIES OF (PEG)?



# IDENTIFYING UNKNOWN SPECIES USING mMASS



http://www.mmass.org/

Letter to the Editor

**mMass data miner: an open source alternative for mass spectrometric data analysis**

Martin Strohm, Martin Hassman, Bedřich Košata, Milan Količek

First published: 22 February 2008 Full publication history

DOI: 10.1002/rcm.3444 View/save citation

Cited by (CrossRef): 104 articles Check for updates Citation tools

## Mass to formula tool

File View Processing Sequence Tools Libraries Links Window Help

Mass To Formula

Mo. mass: 220.227653 Charge: 1 NH4+ Tolerance: 5 Da ppm Generate

Minimal formula: Maximal formula:

Composition rules: ☒ H/C ☒ NOPS/C ☒ NOPS ☒ RDBE ☒ Integer RDBE ☒ Check isotopic pattern

neutral formula	mass	m/z	error	H/C	rdbe	pattern
C12H26O2	202.1933	220.2271	2.5	2.2	0.0	n/a

- Show Isotopic Pattern
- Search in PubChem
- Search in ChemSpider
- Search in METLIN
- Search in HMDB
- Search in Lipid MAPS
- Copy Formula
- Copy List

## ChemSpider

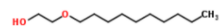
Search and share chemistry

Simple Structure Advanced History

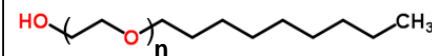
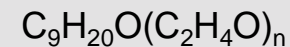
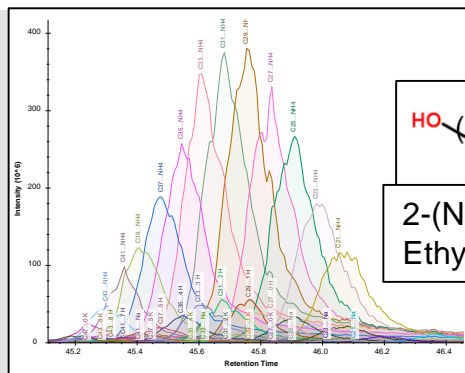
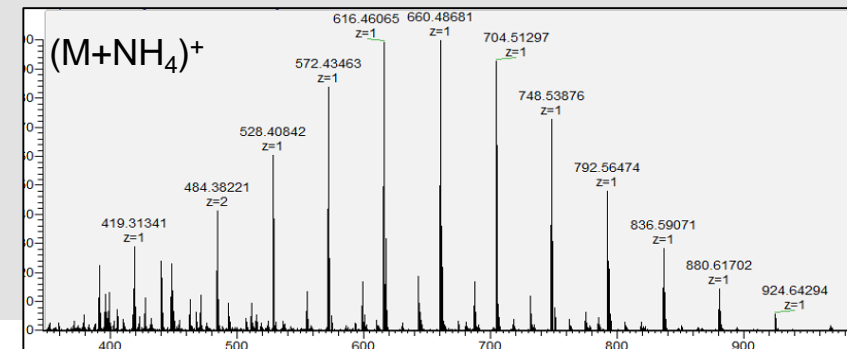
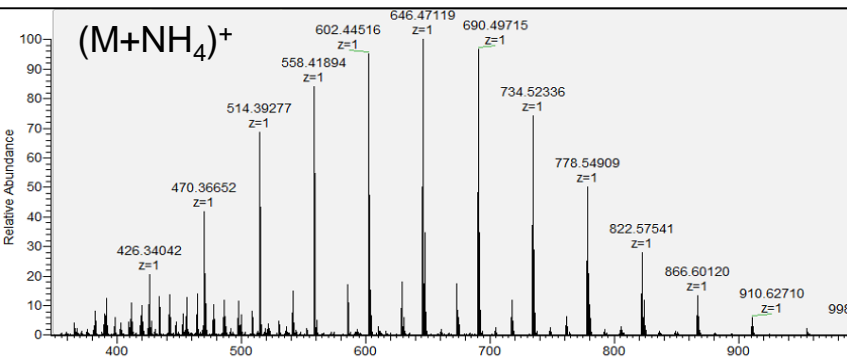
Found 386 results  
Search term: C12H26O2 (Found by molecular formula)

### 2-(Decyloxy)ethanol

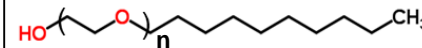
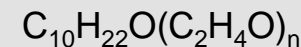
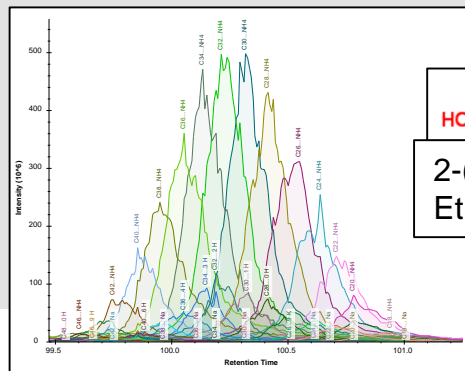
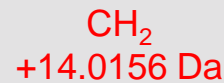
Molecular Formula C<sub>12</sub>H<sub>26</sub>O<sub>2</sub>  
Average mass 202.334 Da  
Monoisotopic mass 202.193283 Da  
ChemSpider ID 56542



## VISUALIZING NEW CONTAMINANTS IN SKYLINE



2-(Nonyloxy)ethanol  
Ethylene glycol mono-n-nonyl ether



2-(Decyloxy)ethanol  
Ethylene glycol mono-n-decyl ether



# SO WHAT WAS THE SOURCE OF CONTAMINATION?



Antibody columns were stored wrapped in parafilm...

# SO WHAT WAS THE SOURCE OF CONTAMINATION?



**Antibody columns were stored wrapped in parafilm...**

[Home](#) > [Proteomics Blog](#) > This is why you do not let artificially smelly people stand next to the Q-Exactive



## **This is why you do not let artificially smelly people stand next to the Q-Exactive**

Posted on [October 7, 2014](#) by [Brett Phinney](#) — [7 Comments](#) ↓

The Q-exactives seem to be much more sensitive to environmental contaminants than our previous instruments (LTQ's and LTQ-FT's). Here is an example of two BSA QC's run back to back. The only difference is that for one of them a HPLC service engineer with a lot of cologne was standing next to the Q-exactive. Notice the 371 background ion goes from  $10^5$  to  $10^8$  and totally swamps out the base peak ion chromatograms!

# ANOTHER SOURCE OF CONTAMINATION – MS STANDARDS?

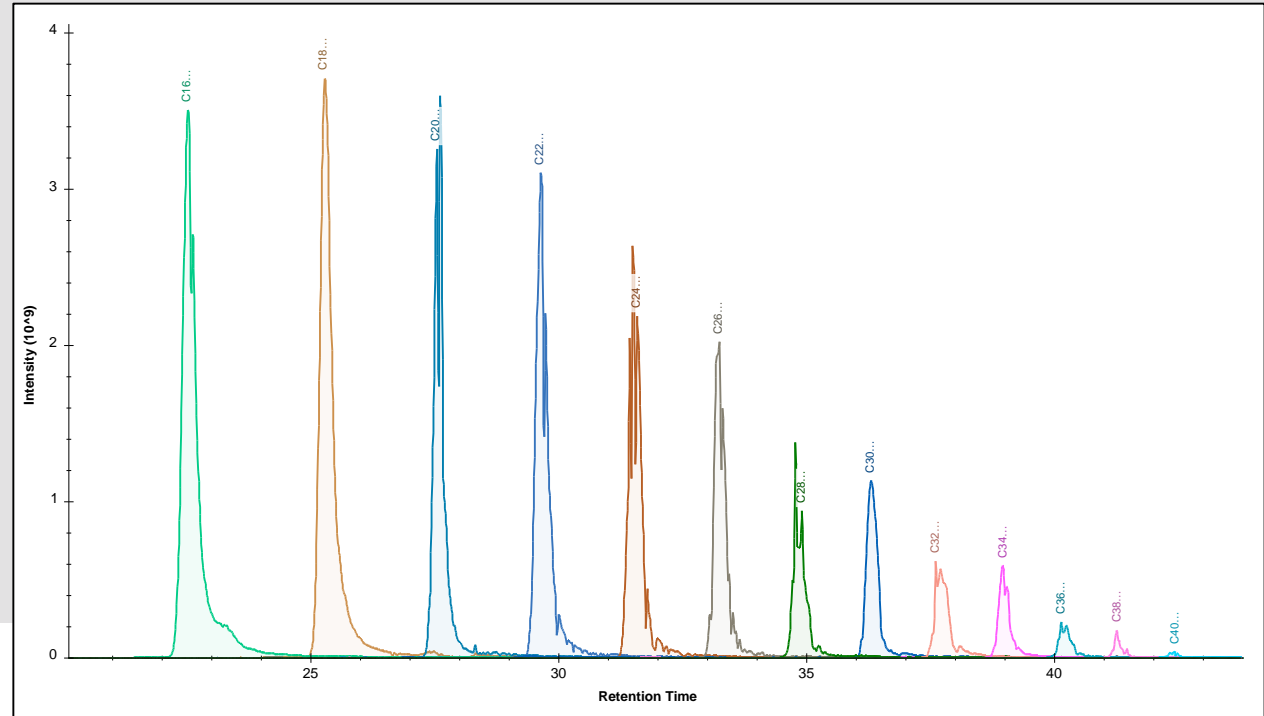
Many vendors now sell various mass spec standards... peptides, peptide mixture, proteins, antibodies, heavy labeled peptides and proteins

- We purchases 10ug of a heavy labeled (Lys+8, Arg+10) protein purified from HELA cells (~\$1500)

# ANOTHER SOURCE OF CONTAMINATION – MS STANDARDS?

Many vendors now sell various mass spec standards... peptides, peptide mixture, proteins, antibodies, heavy labeled peptides and proteins

- We purchased 10ug of a heavy labeled (Lys+8, Arg+10) protein purified from HELA cells (~\$1500)
- Peptide mapping of the protein standard revealed wide spread contamination with PEG
- Vendor was using 1% NP40 in their lysis and did not effectively remove associated PEG contamination nor did they even realize the problem...



# CONCLUSIONS

- **Using Skyline's small molecule tools we developed a library of common contaminants and interferences that can easily be monitored using MS1 Filtering**
- **Currently have a list of 64 molecular groups and over 641 molecules in our library**
- **Allows one to rapidly assess contamination of samples**
- **Provided an approach for identifying unknown molecular species**

# ACKNOWLEDGING THE CONTAMINATION CREW

- No one volunteered to be on this list...

