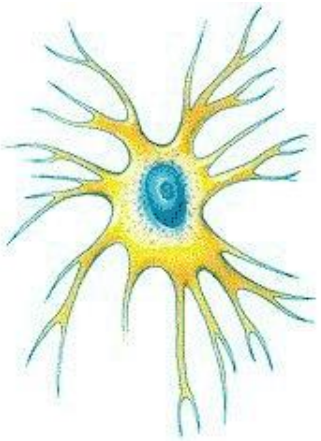
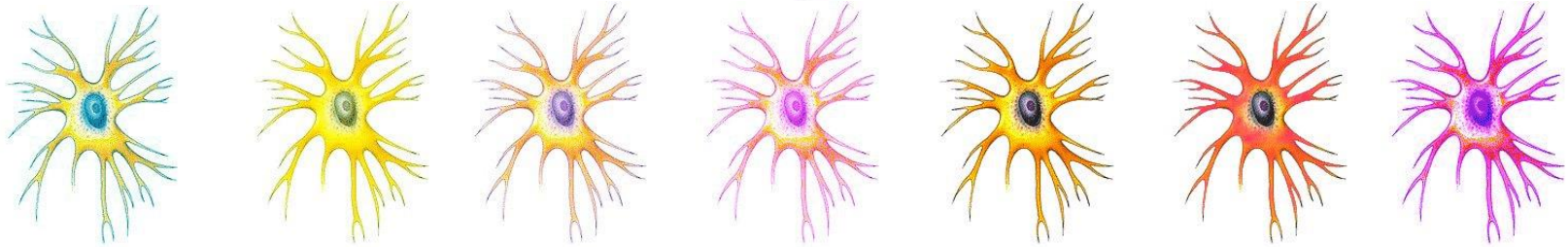


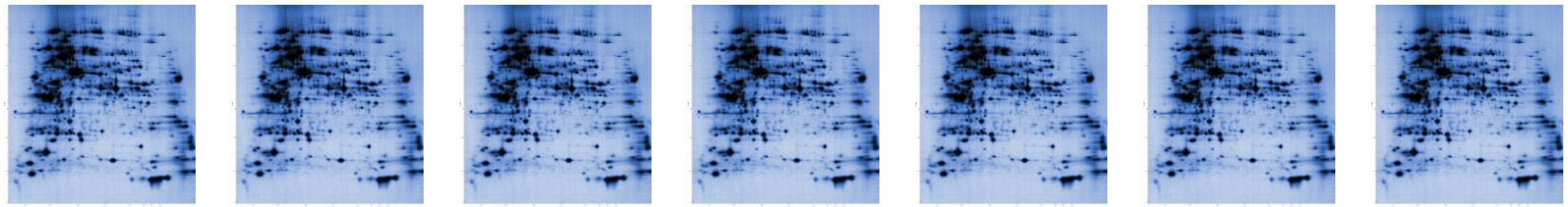
SWATH™: Recent advances in data-independent acquisition by mass spectrometry workflows and the creation of the OneOMICS™ cloud ecosystem

Volker Kruft, Business Development
volker.kruft@sciex.com

“omics”: sample complexity



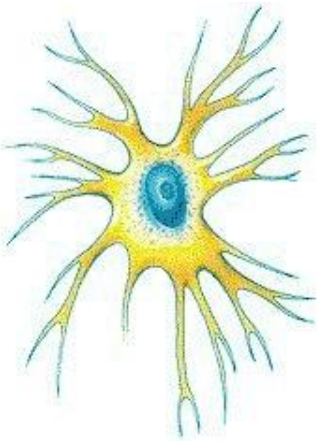


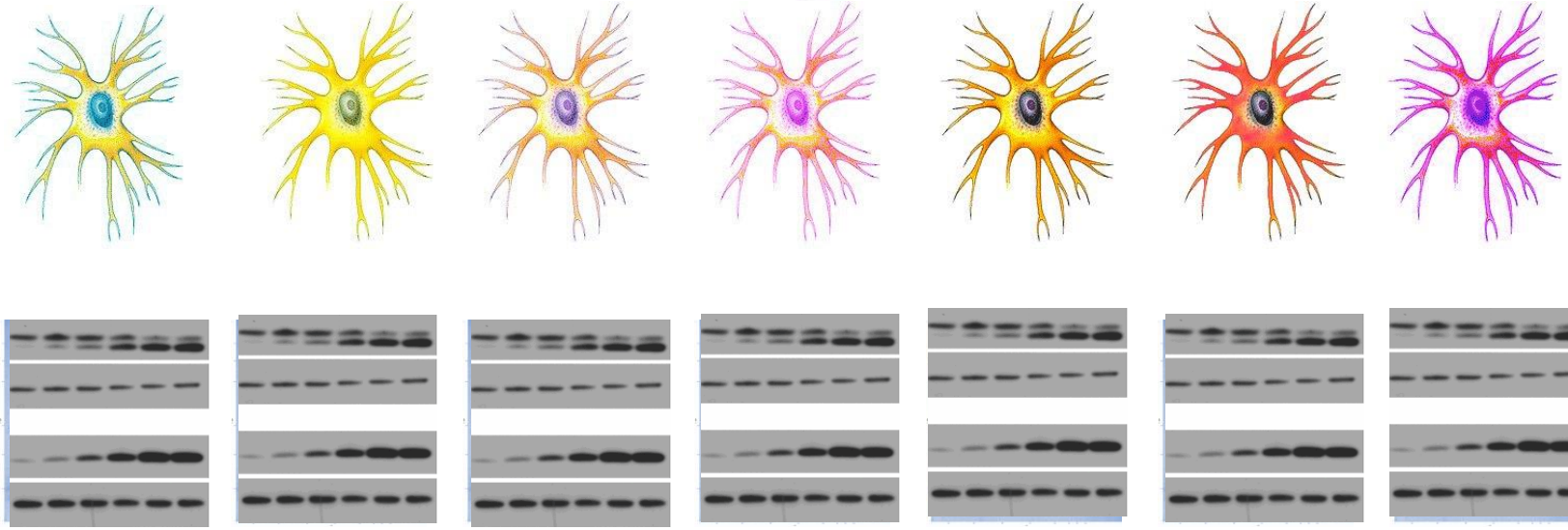


Proteome 1 Proteome 2 Proteome 3 Proteome 4 Proteome 5 Proteome 6 Proteome 7

SCIEX

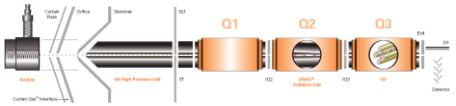
“omics”: sample complexity

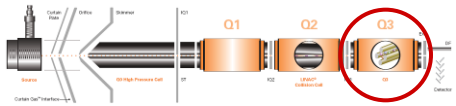


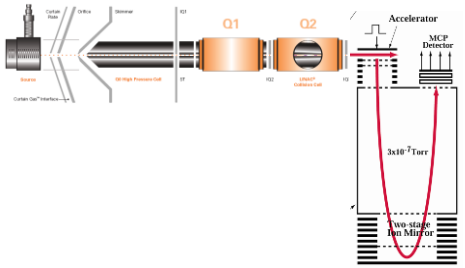


Proteome 1 Proteome 2 Proteome 3 Proteome 4 Proteome 5 Proteome 6 Proteome 7

Key Features of AB SCIEX LC/MS/MS Systems







Triple Quadrupole → Q TRAP® system → TripleTOF® system

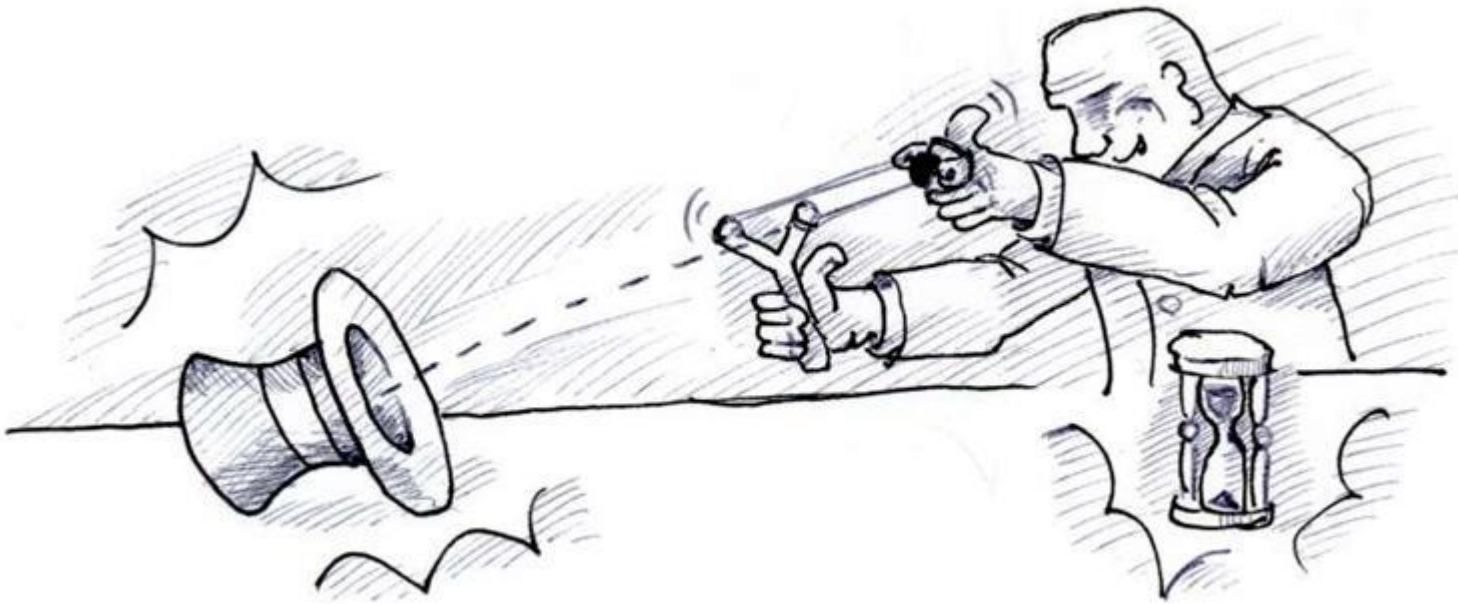
- **Quantitation**
- ID with MRM ratio

- Quantitation
- ID with MRM ratio
- **ID with MS/MS library searching**

- Quantitation
- ID with accurate mass
- ID with MS/MS library searching
- **ID true unknowns**
- **Retrospective data processing**

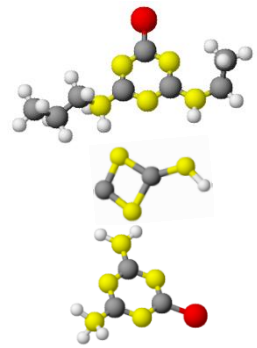
increasing confidence in compound ID

SCIEX

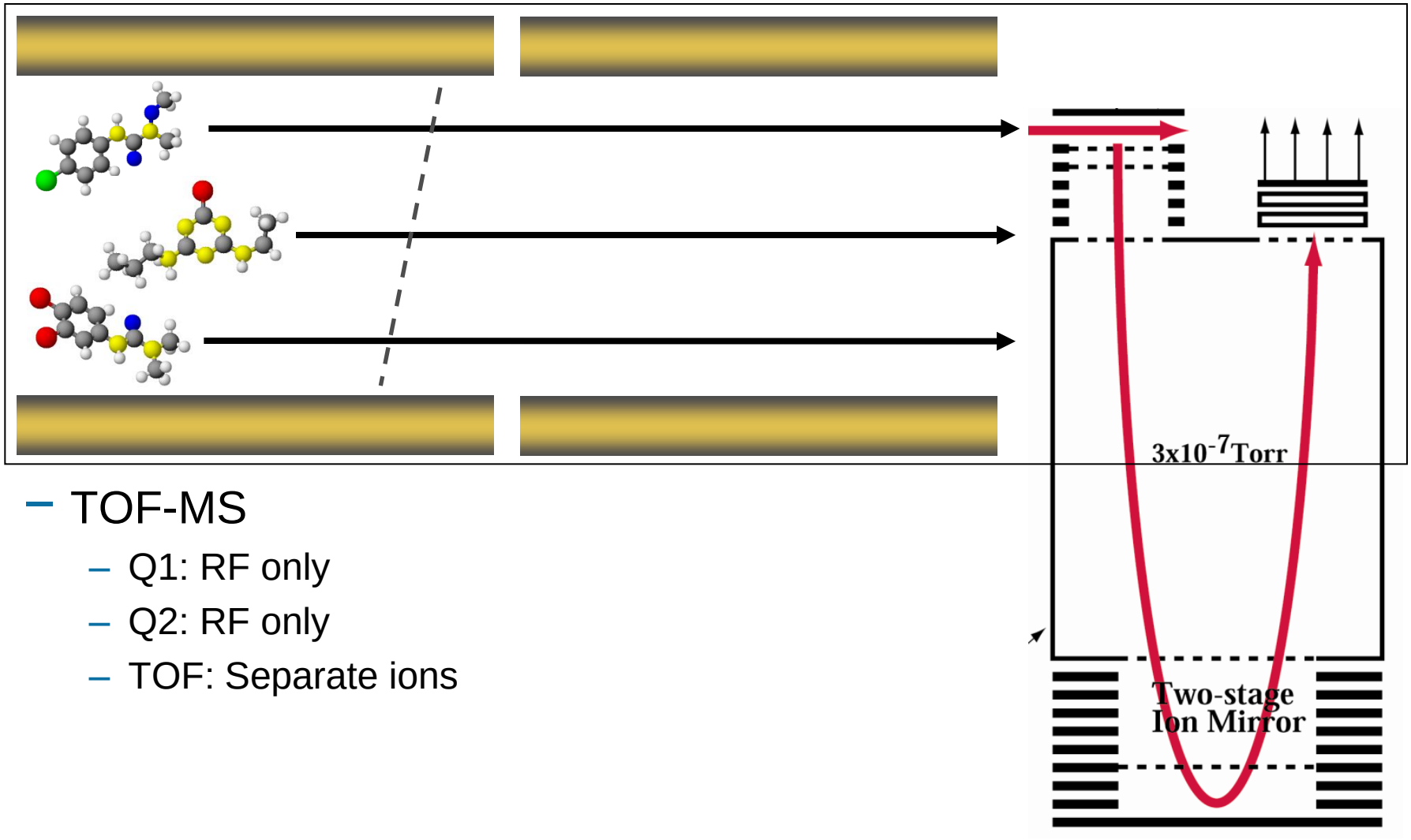


In Search of Greater Selectivity…
Principle of Time-of-Flight (TOF) Mass Spectrometry

- Ion packets are pulsed and accelerated into a TOF analyzer.
- Separation of ions is based on the time to traverse the flight tube, and arrive at the detector, on a nanosecond time scale.
  - Smaller *m/z* ions move faster than heavier *m/z* ions
- Higher resolution is achieved with longer flight path (longer TOF tubes, reflectors, faster acceleration).



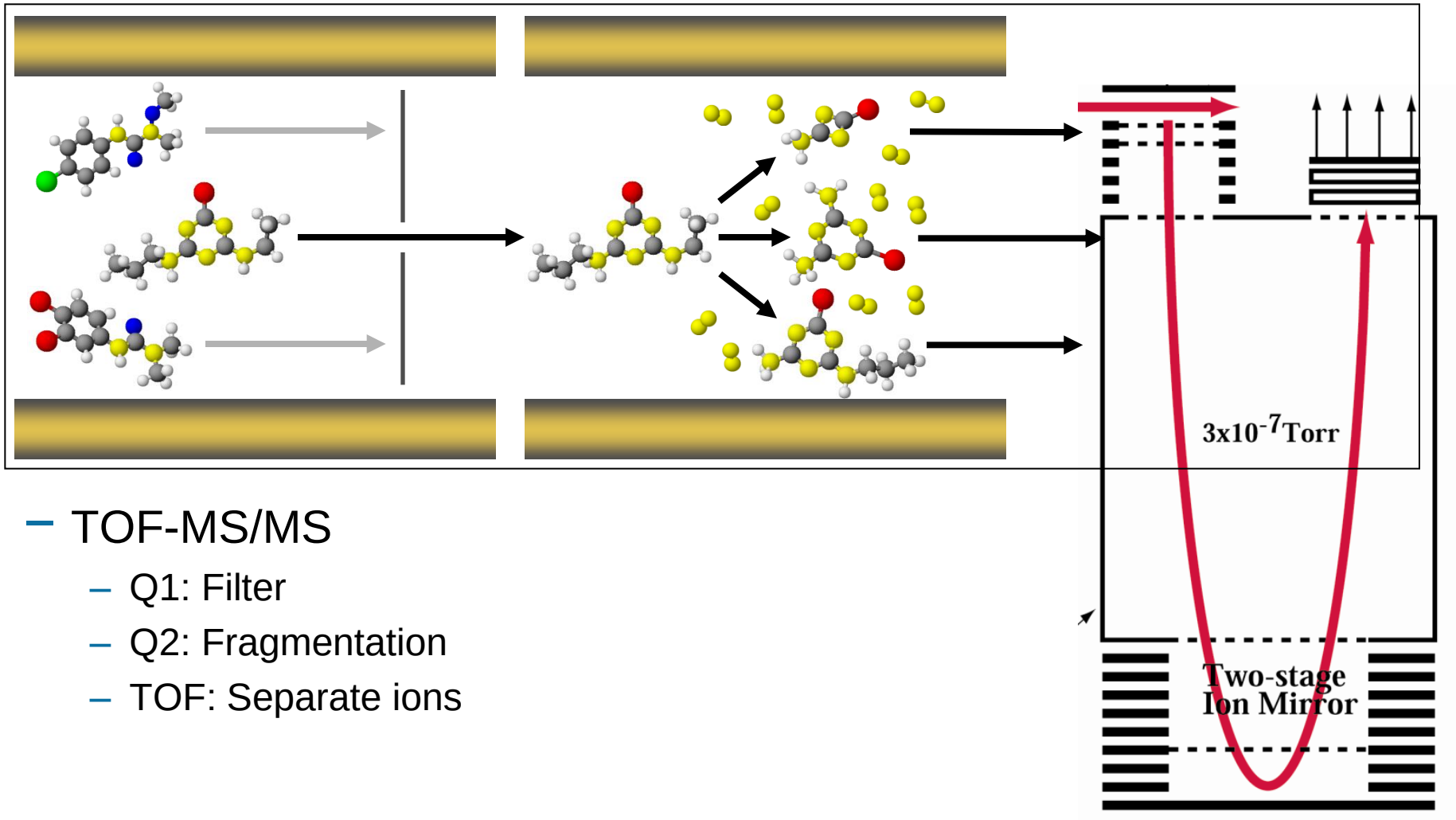
In Search of Greater Selectivity…
Principle of Time-of-Flight (TOF) Mass Spectrometry



- TOF-MS
  - Q1: RF only
  - Q2: RF only
  - TOF: Separate ions

SCIEX

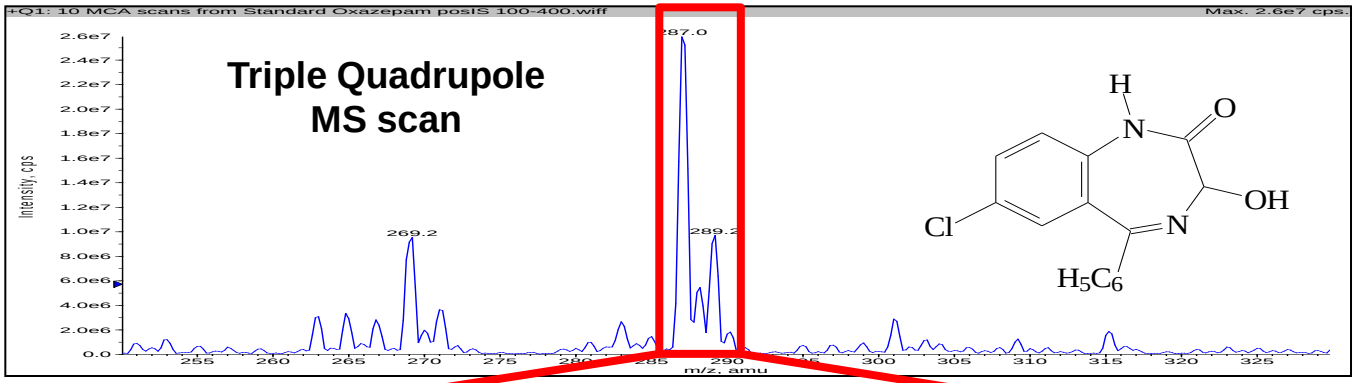
In Search of Greater Selectivity…
Principle of Time-of-Flight (TOF) Mass Spectrometry

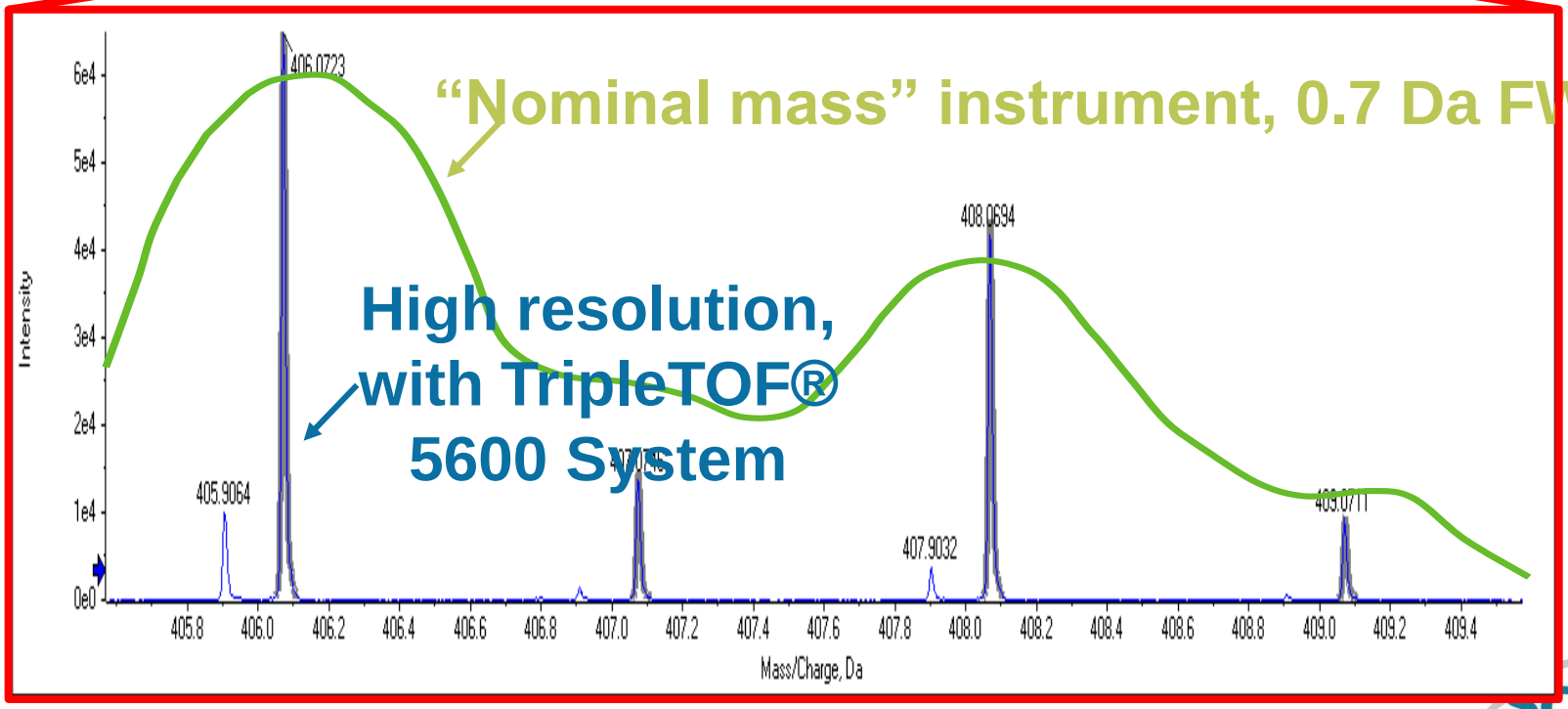


- TOF-MS/MS
  - Q1: Filter
  - Q2: Fragmentation
  - TOF: Separate ions

SCIEX

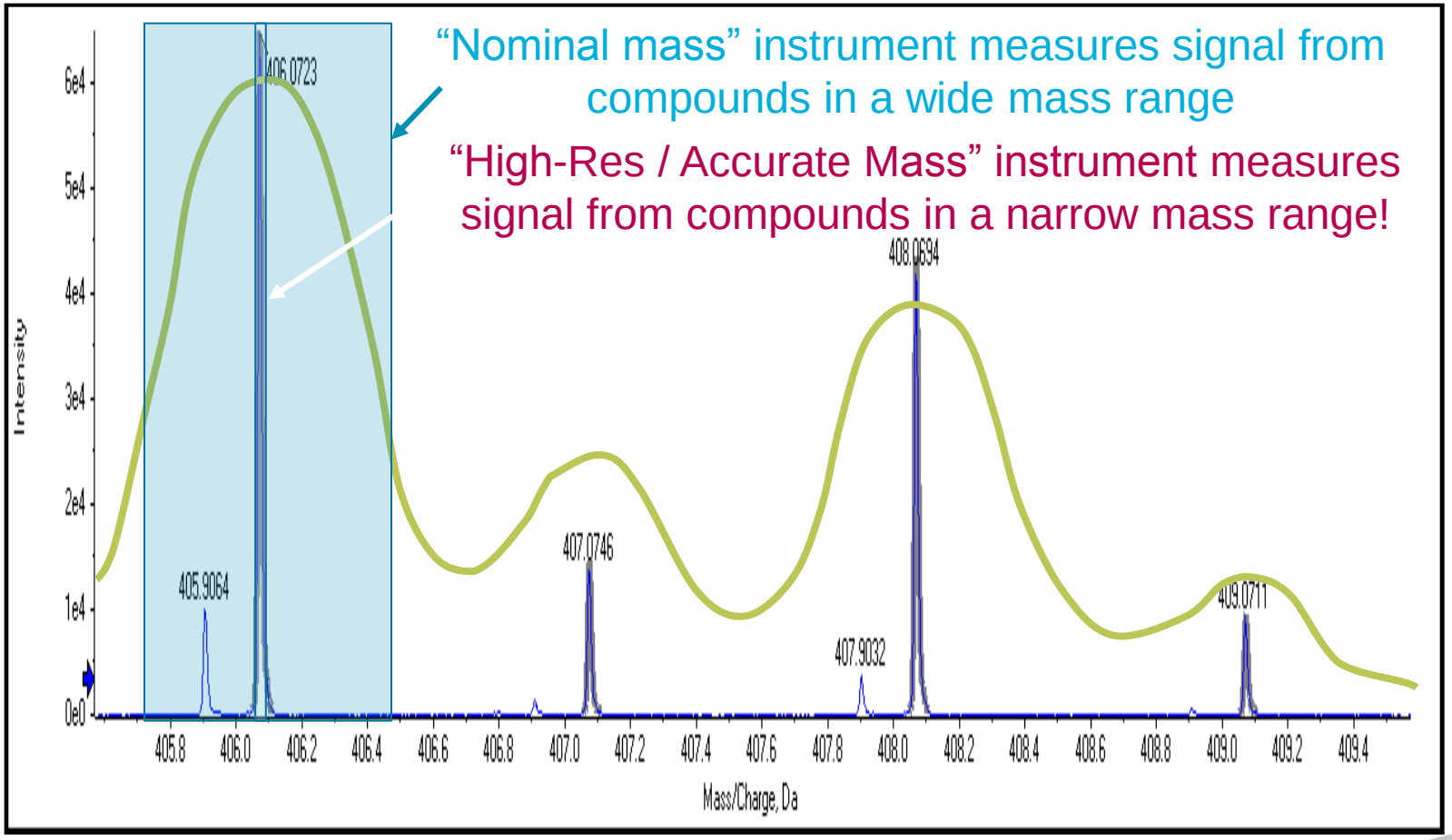
High Resolution Time-of-Flight (TOF) Mass Spectrometry





Why consider TOF technology?

- Greater specificity, with high-resolution measurements



Why consider TOF technology?

- Greater specificity, with high-resolution measurements

A simple example:

4 different molecular formulae with nominal mass = 28 Da

N_2	=	2 X 14.0031	= 28.0061
CO	=	12.0000 + 15.9949	= 27.9949
C_2H_4	=	(2 X 12.0000) + (4 X 1.0078)	= 28.0312
CH_2N	=	12.0000 + (2 X 1.0078) + 14.0031	= 28.0187

Cannot be distinguished by a “nominal mass” instrument

Accurate Mass Measurement
- aiding specificity of compound identification

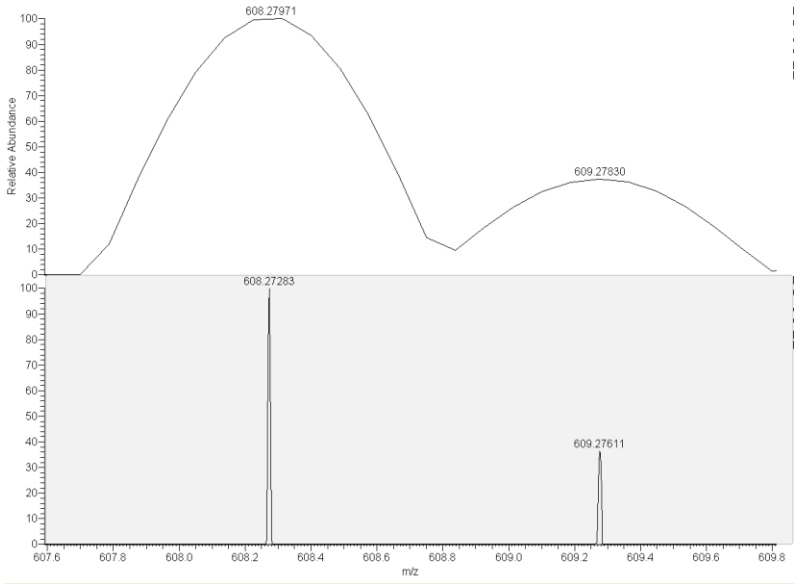
$C_{33}H_{40}N_2O_9$ has a protonated ion at 609.28066

Quadrupole MS reports mass to +/- 0.1Da = 165 ppm

High Resolution MS reports to <2ppm

Possible Formulas (C,H,N,O)

- 165 ppm 209
- 10 ppm 13
- 5 ppm 7
- 3 ppm 4
- 2 ppm 2

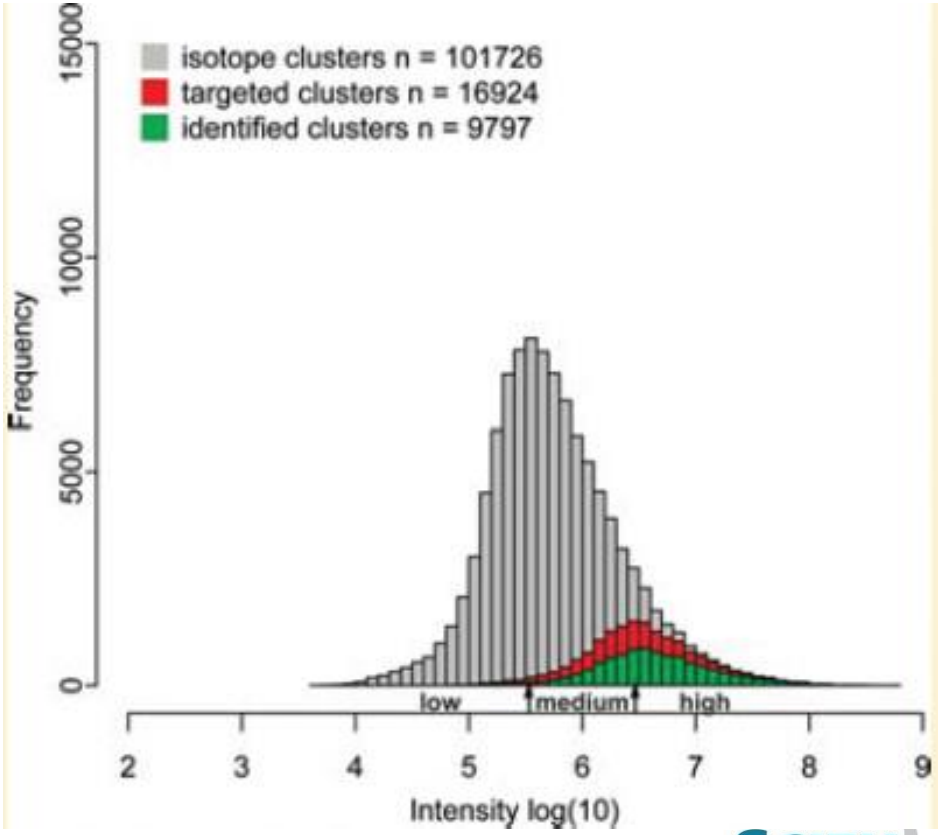


BUT – accurate MSMS provides higher confidence in identification

Journal of proteome research

More than 100,000 Detectable Peptide Species Elute in Single Shotgun Proteomics Runs but the Majority is Inaccessible to Data-Dependent LC−MS/MS

Annette Michalski, Juergen Cox, and Matthias Mann*



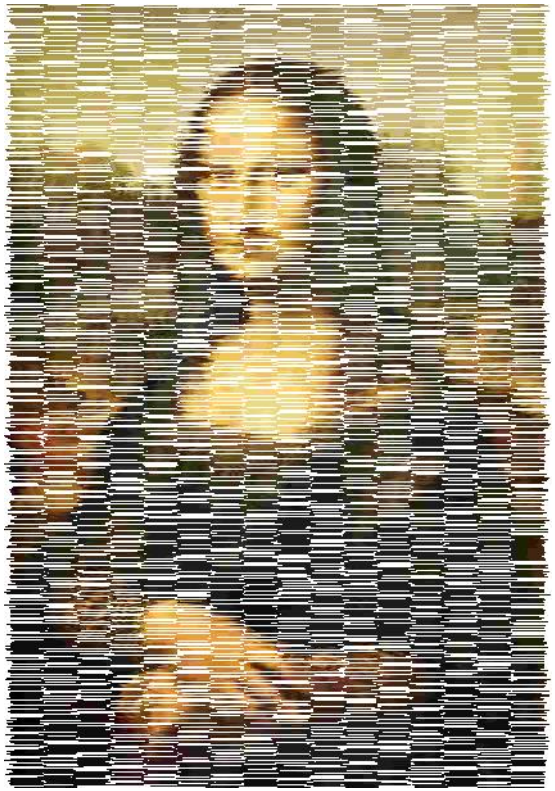
The goal: a complete picture



Jarrett Egertson, MacCoss Lab

SCIEX

Achieving the goal: data dependent acquisition?



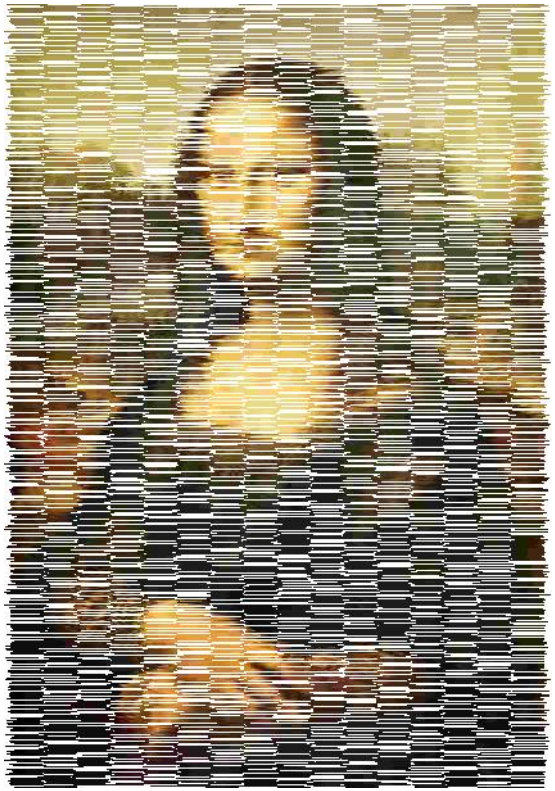


semi-random subsets

Jarrett Egertson, MacCoss Lab

SCIEX

Achieving the goal: MRM/SRM?







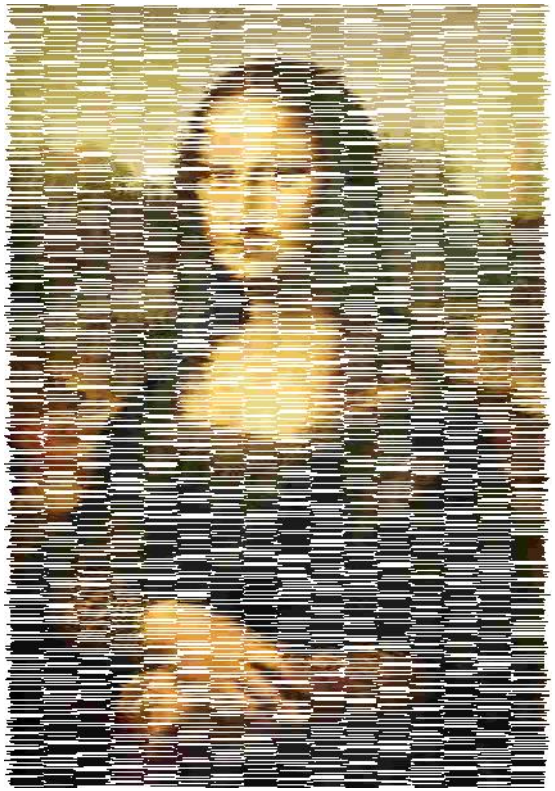
on semi-random subset

on targets

Jarrett Egertson, MacCoss Lab

SCIEX

Achieving the goal: MRM/SRM?









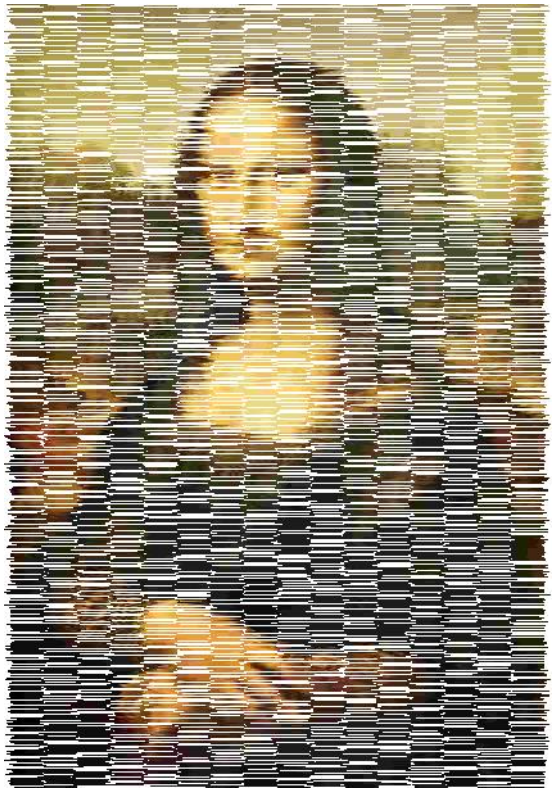
on semi-random subset

on targets

Jarrett Egertson, MacCoss Lab

SCIEX

Achieving the goal: data independent acquisition?



on semi-random subset



on almost everything

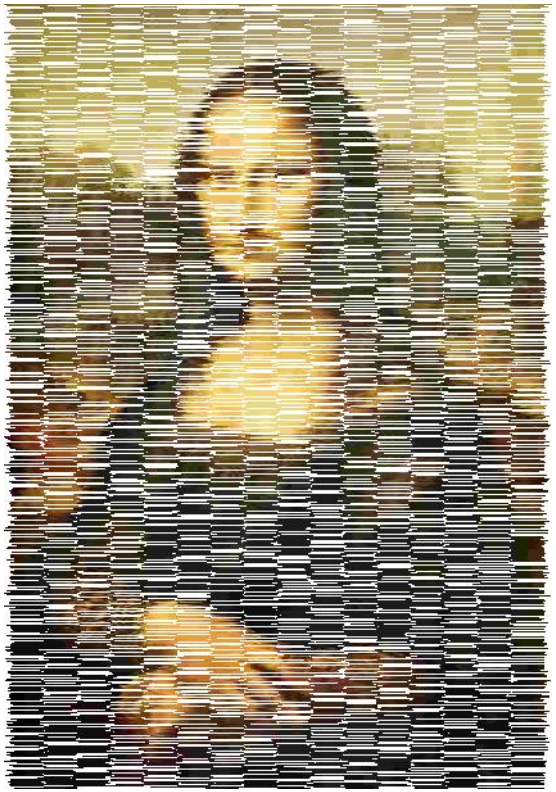


on targets

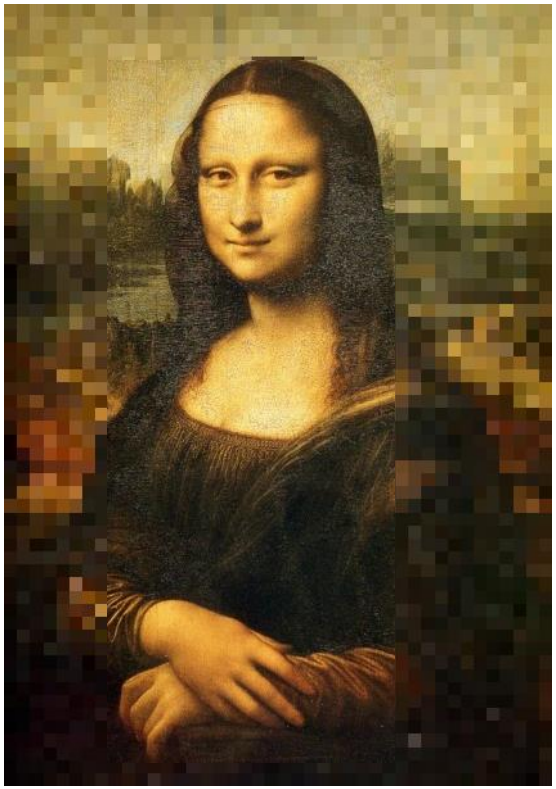
Jarrett Egertson, MacCoss Lab

SCIEX

Achieving the goal: data independent acquisition?



on semi-random subset



on almost everything



on targets

Jarrett Egertson, MacCoss Lab

SCIEX

Sequential Window Acquisition of all THeoretical Fragment Ion Spectra (SWATH™)

Conceived at Ruedi Aebersold's lab @ ETH Zürich
Implemented on SCIEX TripleToF™ systems
Data-Independent Acquisition (DIA)

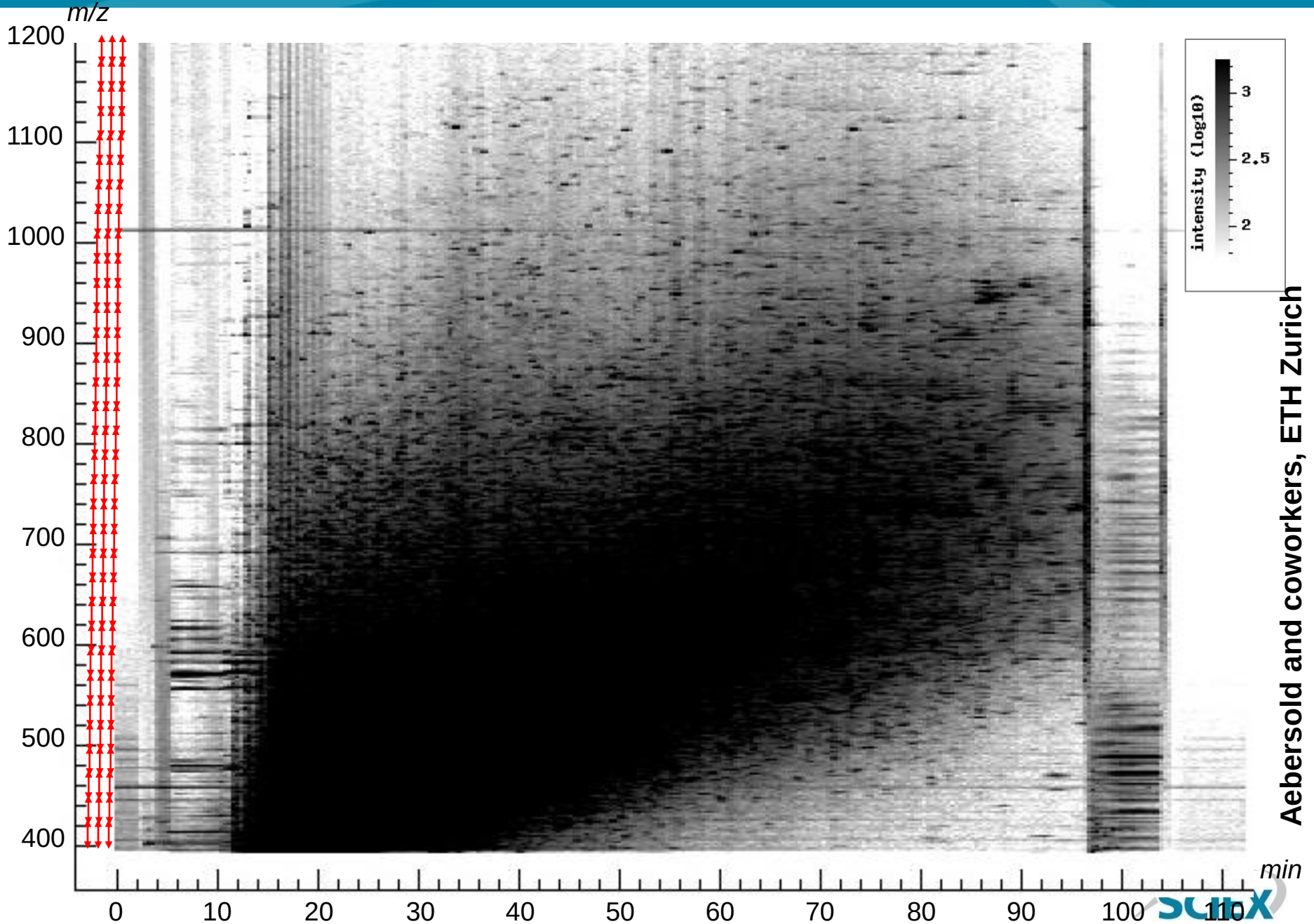




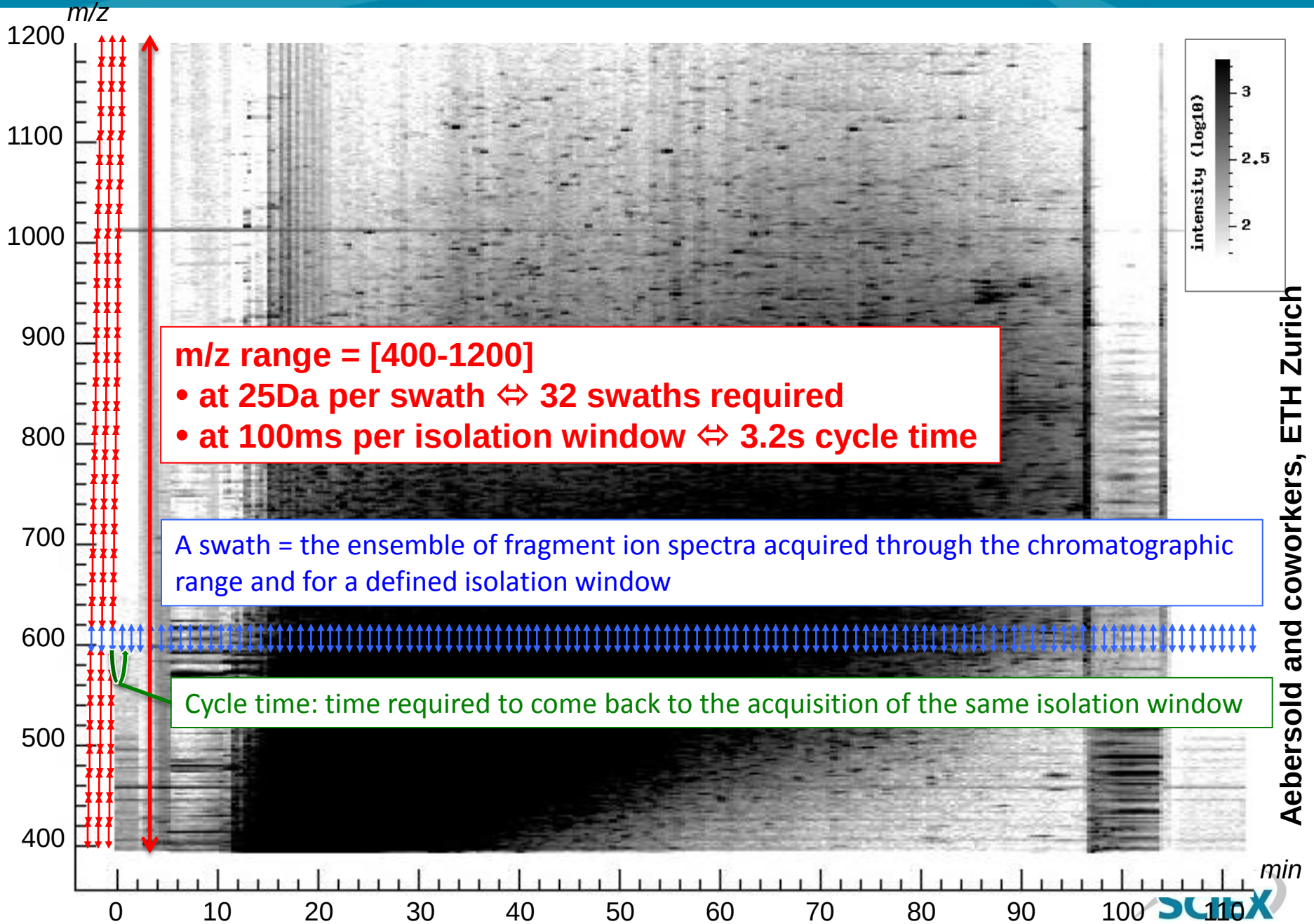




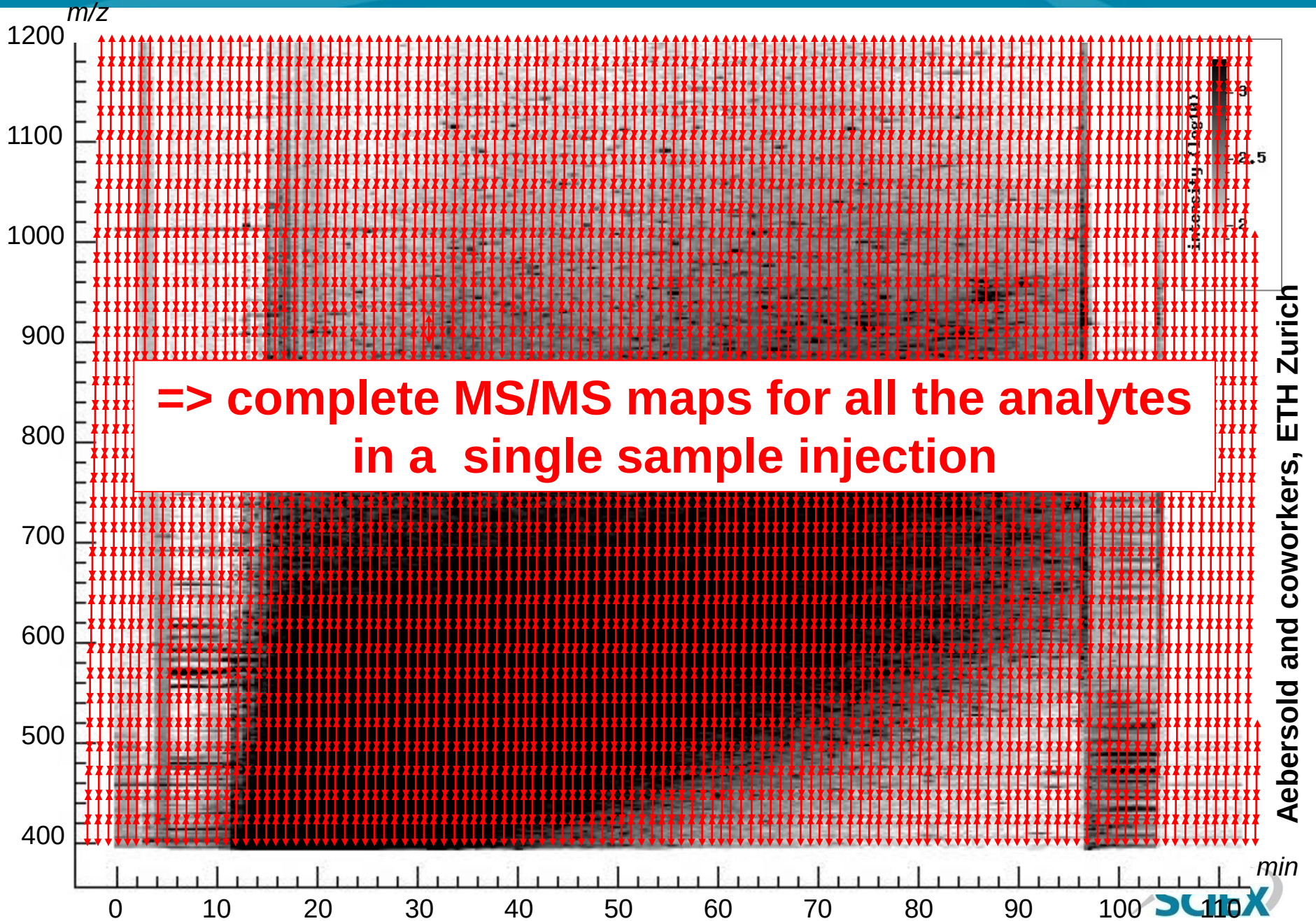
SWATH-MS Acquisition Principle



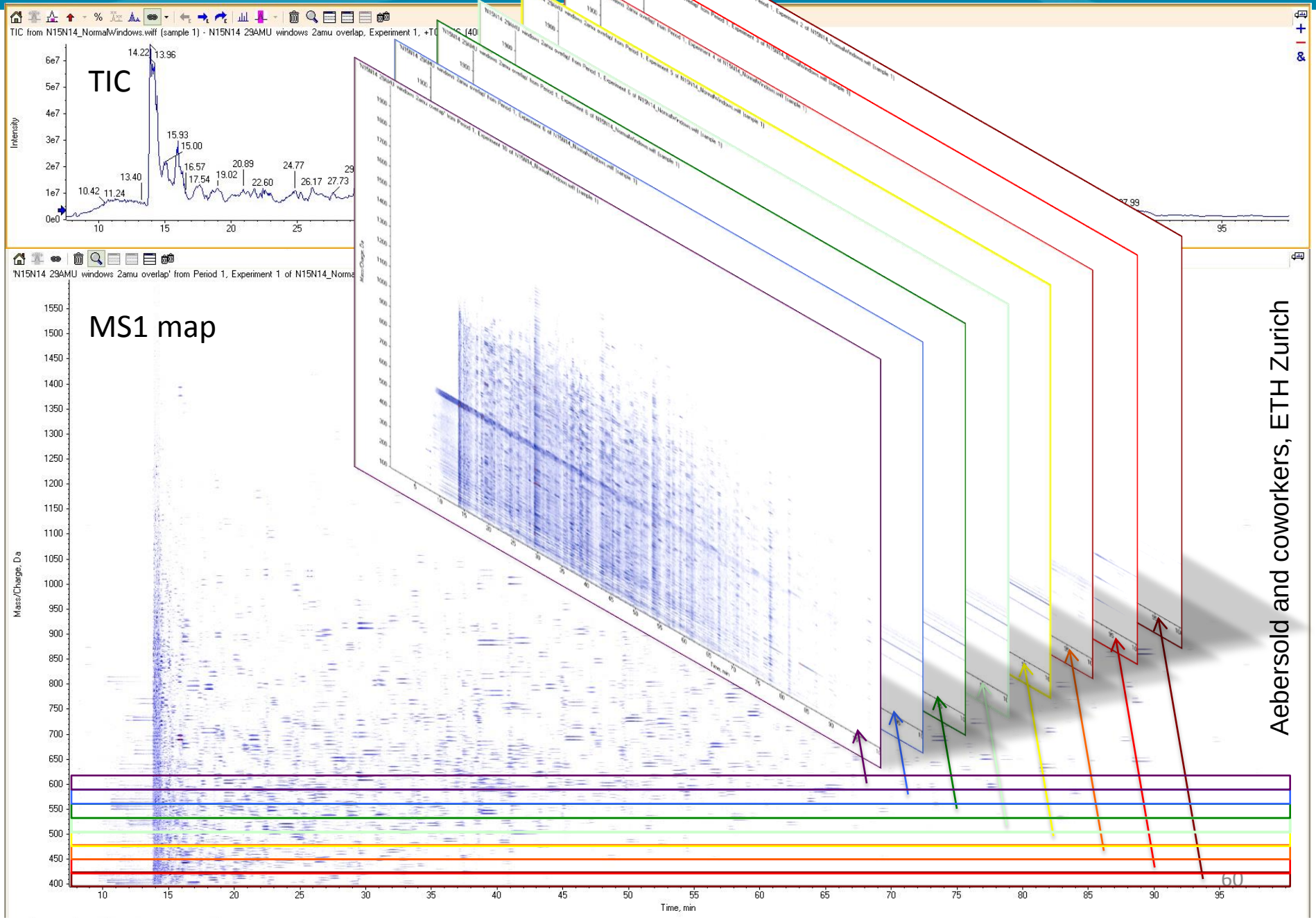
SWATH-MS Acquisition Principle



SWATH-MS Acquisition Principle



SWATH-MS principle: Acquisition & T[illegible]d analysis



Recent SWATH publications

MCP Papers in Press. Published on January 18, 2012 as Manuscript O111.016717

Targeted data extraction of the MS/MS spectra generated by data independent acquisition: a new concept for consistent and accurate proteome analysis

Anal Bioanal Chem
DOI 10.1007/s00216-011-5641-8

Ludovic C Gillet[1],

Lukas Reiter[1,3], R

ORIGINAL PAPER

High-resolution mass spectrometry for integrated qualitative and quantitative analysis of pharmaceuticals in biological matrices

Gérard Hopfgartner · David Tonoli · Emmanuel Varesio

Received: 31 July 2011 / Revised: 18 October 2011 / Accepted: 6 December 2011
© Springer-Verlag 2011

Recent SWATH publications

Quantitative Measurements of *N*-linked Glycoproteins in Human Plasma by SWATH-MS

Tpo1-mediated spermine and spermidine export controls cell cycle delay and times antioxidant protein expression during the oxidative stress response

Targeted Data Extraction of the MS/MS Spectra Generated by Data-independent Acquisition: A New Concept for Consistent and Accurate Proteome Analysis*

Quantifying protein interaction dynamics by SWATH mass spectrometry: application to the 14-3-3 system

Label-Free Quantitation and Mapping of the ErbB2 Tumor Receptor by Multiple Protease Digestion with Data-Dependent (MS1) and Data-Independent (MS2) Acquisitions

Interaction Domains of Sos1/Grb2 Are Finely Tuned for Cooperative Control of Embryonic Stem Cell Fate

Acquisition of protein signatures using SWATH-MS

SWATH MS delivers robust and consistent peptide and protein quantification from patient samples. Here, the concept and its advantages over former MS-based proteomic strategies are discussed

Mapping differential interactomes by affinity purification coupled with data-independent m spectrometry acquisition

SWATH publications – Mol Sys Biol

Article

TRANSPARENT PROCESS

OPEN ACCESS

molecular systems biology

Quantitative variability of 342 plasma proteins in a human twin population

Yansheng Liu[1,*,†], Alfonso Buil[2,†], Ben C Collins[1], Ludovic C J Gillet[1], Lorenz C Blum[1], Lin-Yang Cheng[3], Olga Vitek[3], Jeppe Mouritsen[1], Genevieve Lachance[4], Tim D Spector[4], Emmanouil T Dermitzakis[2] & Ruedi Aebersold[1,5,**]

PROOF

Abstract

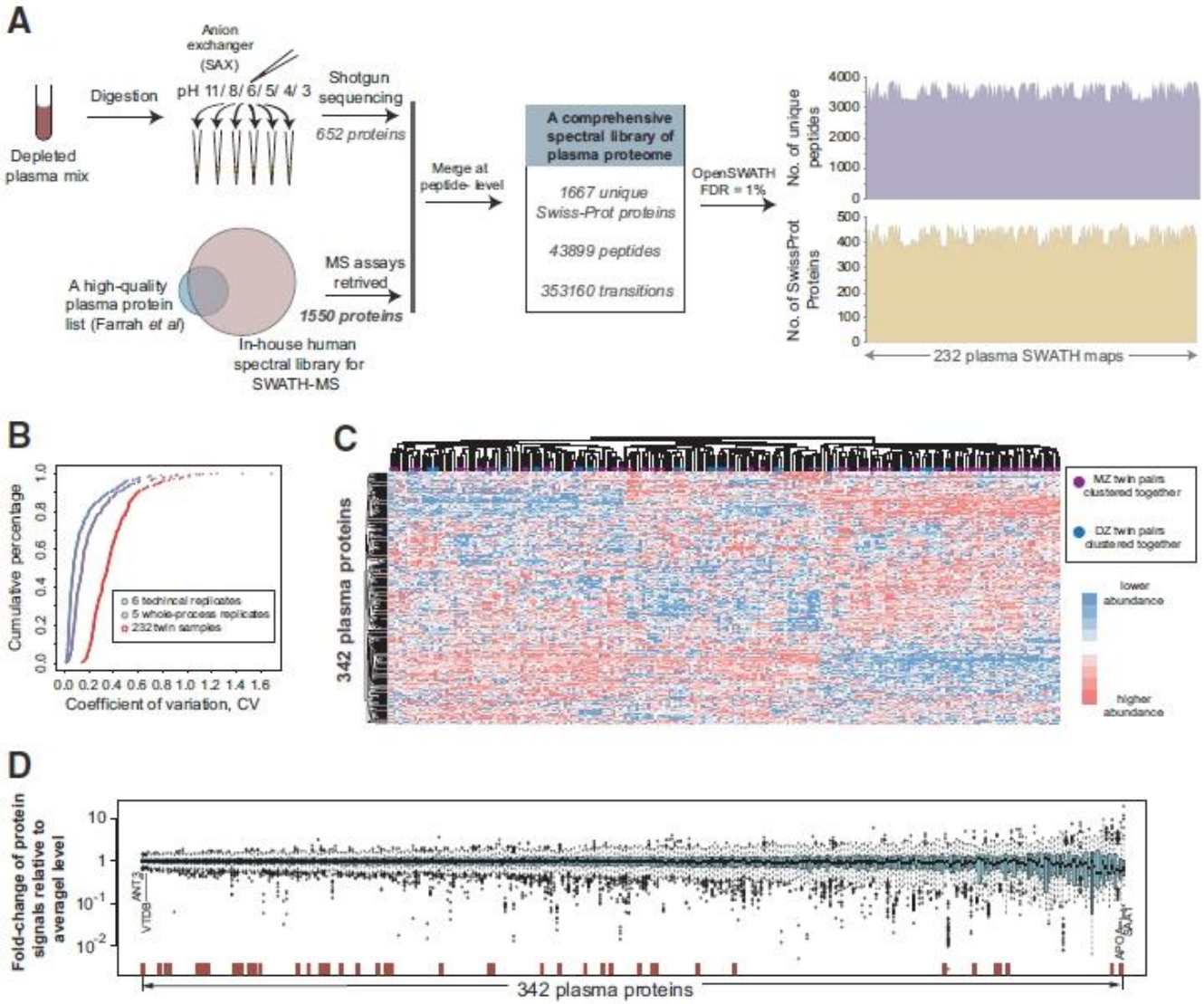
The degree and the origins of quantitative variability of most human plasma proteins are largely unknown. Because the twin

Introduction

The effects of genomic variation, modulated by lifestyle and environment, orchestrate the extensive phenotypic variability found in

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SWATH publications – Mol Sys Biol



Recent forensic publications

analytical chemistry

Subscriber access provided by MDS SCIEX

Anal Bioanal Chem
DOI 10.1007/s00216-014-8262-1

RESEARCH PAPER

Applying 'Sequential Windowed Acquisition of All Theoretical Fragment Ion Mass Spectra' (SWATH) for systematic toxicological analysis with liquid chromatography-high-resolution tandem mass spectrometry

Kathrin Arnhard · Anna Gottschall · Florian Pitterl · Herbert Oberacher

Received: 1 September 2014 / Revised: 3 October 2014 / Accepted: 8 October 2014
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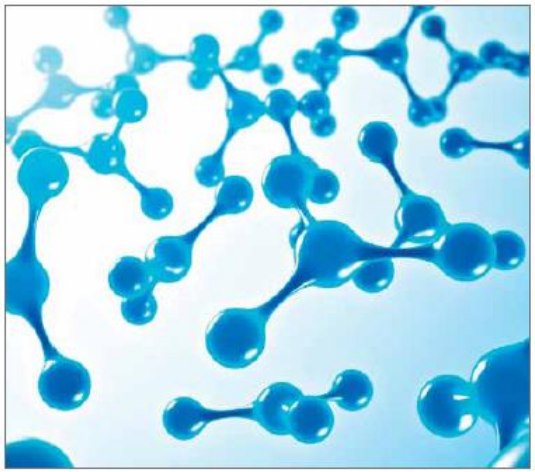
Abstract Liquid chromatography-tandem mass spectrometry (LC-MS/MS) has become an indispensable analytical technique and specific identification technique. SWATH is capable of identifying more compounds at lower concentration levels

SWATH publications - HHE

Acquisition of protein signatures using SWATH-MS

SWATH MS delivers robust and consistent peptide and protein quantification from patient samples. Here, the concept and its advantages over former MS-based proteomic strategies are discussed

Ludovic CJ Gillet
Yansheng Liu
Alexander H Ebhardt
Ruedi Aebersold
Department of Biology,
Institute of Molecular Systems Biology,
ETH, Zurich, Switzerland;
and Faculty of Science, University of Zurich,
Switzerland



Protein signatures are becoming increasingly prevalent in hospitals for the routine diagnosis and prognosis of diseases. Protein signatures are quantitative patterns of groups of proteins that distinguish biological samples. For example, the occurrence of prostate cancer is nowadays routinely screened by measuring the concentration of prostate-specific antigen (PSA), and a new multi-protein signature of glycosylated plasma proteins has been recently described that diagnoses and grades prostate cancer more sensitively

LABORATORIES

www.hospitalhealthcare.com/hhe

Which biomarker would you like to discover today?

A pilot study illustrating the feasibility of MS/MS^{ALL} with SWATH™ Acquisition on the AB SCIEX TripleTOF® 5600+ System for biomarker discovery in acute kidney injury is detailed

Peter Pichler MD
Research Institute of Molecular Pathology, Vienna, Austria
Ludwig Wagner MD
Department of Internal Medicine III, General Hospital of Vienna and Medical University of Vienna, Austria
Christian Baumann Dipl Ing
AB SCIEX, Darmstadt, Germany
Michael Schutzbier Dipl Ing
Research Institute of Molecular Pathology, Vienna, Austria
Volker Kruft PhD
AB SCIEX, Darmstadt, Germany
Karl Mechtler
Head of Protein Chemistry Facility (IMP Vienna) and President of the Austrian Proteomics Association (AuPA), Research Institute of Molecular Pathology, Vienna, Austria

Acute kidney injury (AKI) is one of many clinical challenges where new biomarkers would be highly desirable to help improve patient care and clinical outcome. The hypovolaemia, for example, due to cardiovascular disease or surgery, inflammatory diseases, renal or liver disease, diabetes mellitus, radiologic contrast media and age >75 years. Criteria for clinical assessment, such as RIFLE, allow stratification of AKI patients according to risk (Risk, Injury, Failure) and outcome (Loss, End Stage Renal Disease), based on the extent of decrease in the glomerular filtration rate (GFR) or the rise in serum creatinine level or the decrease in urinary output over prolonged duration.[2] However, these criteria are not perfect.[3] First, serum creatinine may require 48 hours to rise; by this time 50%

According to a report by the National Confidential Enquiry into Patient Outcome and Death (NCEPOD) in 2009, many deaths from AKI are still a result of delayed diagnosis, avoidable causes of AKI or inadequate risk assessment.[5] Recognition and risk assessment of AKI is important. First, the presence of AKI was shown to be an indicator of prolonged hospitalisation and increased mortality.[6] Second, RIFLE criteria were shown to correlate with mortality. For instance, mortality rates of 5%, 13% and 26% after cardiac surgery were reported for patients in RIFLE stages R, I and F respectively, with rates more than doubling from stage R to F.[7]

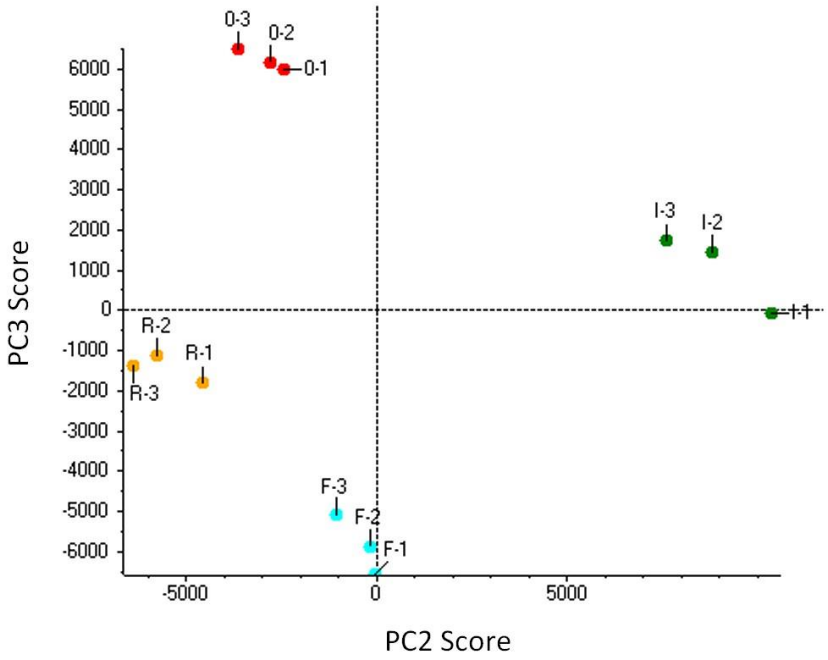
"Acute kidney injury is one of many clinical challenges where new biomarkers would be highly desirable to help improve patient care and clinical outcome"

SCIEX

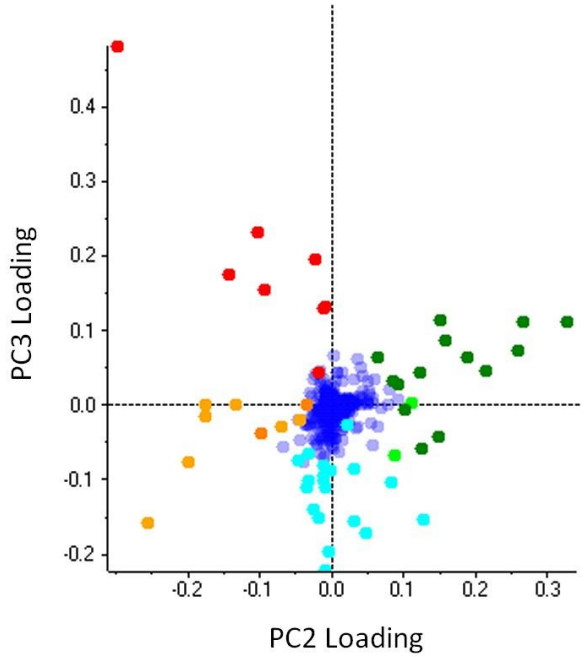
Recent SWATH publications - HHE



Scores for PC2 (29.7%) versus PC3 (18.8%)



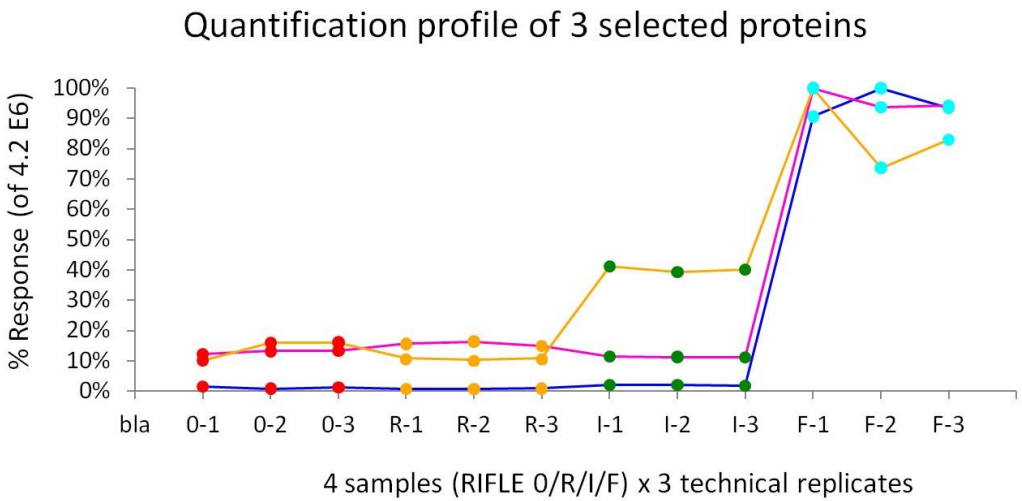
Loadings for PC2 (29.7%) versus PC3 (18.8%)



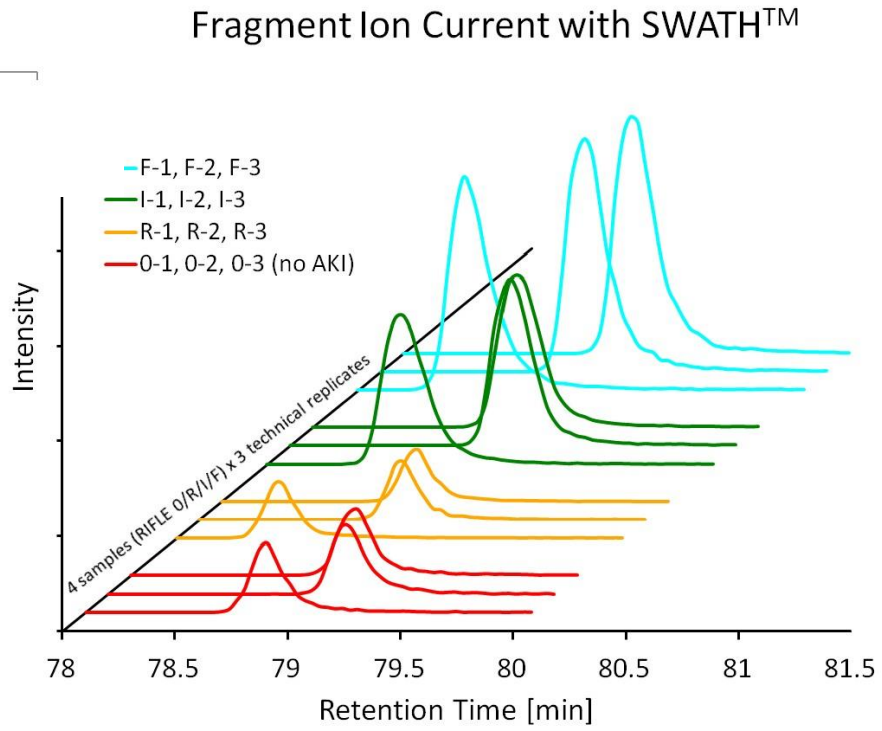
PCA analysis

SCIEX

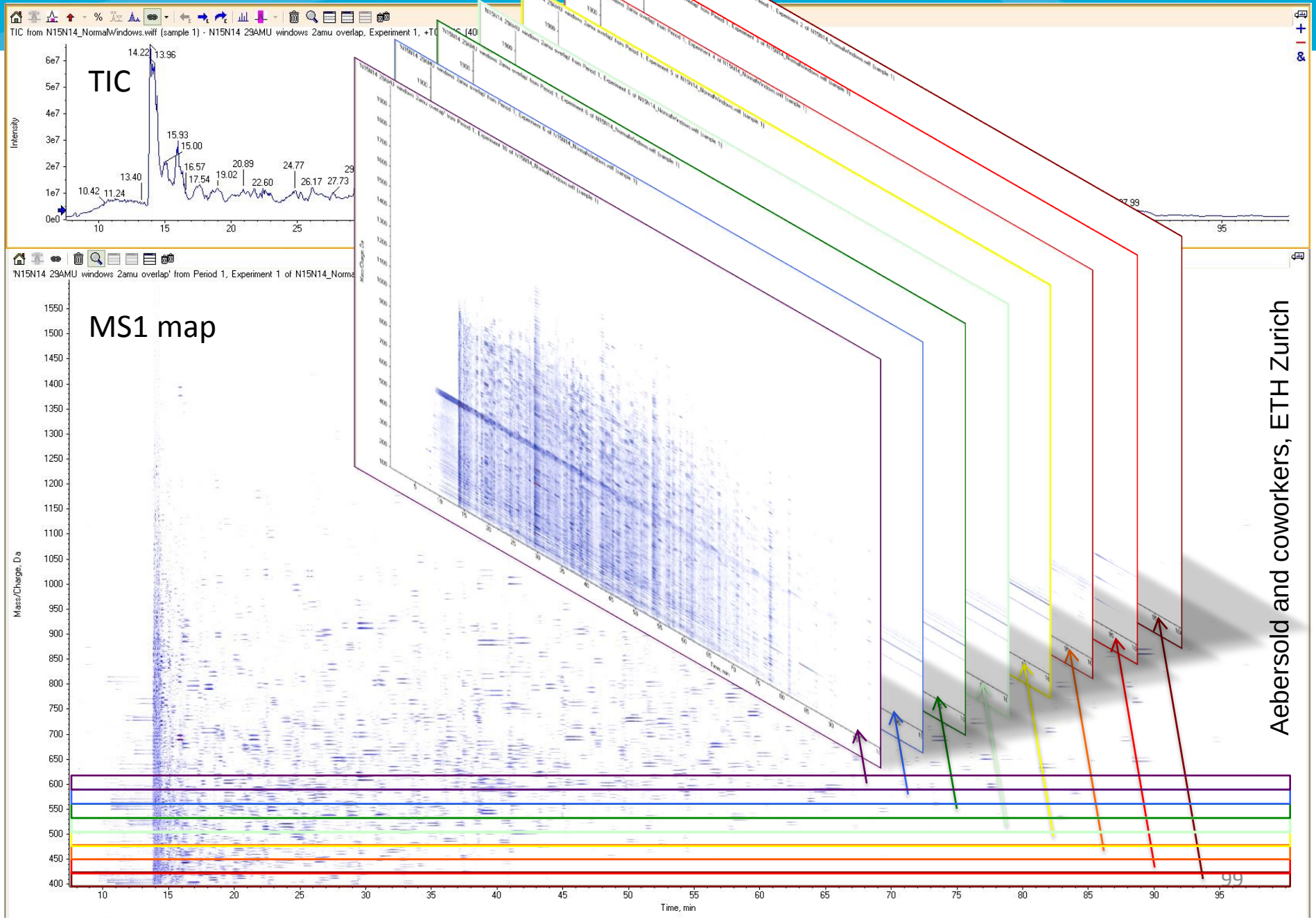
Recent SWATH publications - HHE



Protein/peptide candidates



SWATH-MS principle: Acquisition & T[illegible]d analysis



SWATH Initiatives

ISB Home

SWATHAtlas

SWATHATLAS HOME

DATA ACCESS

Current SWATH Libraries (View)

Library	Proteome Coverage	Contributors
H sapiens 10,000 protein 2014	51%, 10,316 of 20218 proteins	Rosenberger et al 2014
H sapiens HLA subtypes		
M tuberculosis comprehensive libra		
Methylobacterium extorquens PA1 2016		
Pseudomonas syringae DC3000 - (2016		
S cerevisiae synthetic peptide full		
Sphingomonas melonis Fr1 - comp		

Systems Biology

Revolutionizing science. Enhancing life.

Methylobacterium extorqu 2016

Pseudomonas syringae D 2016

www.openswath.org

kazan kremlin

OpenSWATH by ETH zürich

OpenSWATH | Tutorial | Data | IMSB@ETHZ

Description

OpenSWATH [1] is a proteomics software that allows analysis of LC-MS/MS DIA (data independent acquisition) data using the approach described by Gillet *et al.* [2]. The DIA approach described there uses 32 cycles to iterate through precursor ion windows from 400-426 Da to 1175-1201 Da and at each step acquire a complete, multiplexed fragment ion spectrum of all precursors present in that window. After 32 fragmentations (or 3.2 seconds), the cycle is restarted and the first window (400-426 Da) is fragmented again, thus delivering complete "snapshots" of all fragments of a specific window every 3.2 seconds.

The analysis approach described by Gillet *et al.* extracts ion traces of specific fragment ions from all MS2 spectra that have the same precursor isolation window, thus generating data that is very similar to SRM traces.

Libraries: Public Domain

Human Spectral Library

A repository of assays to quantify 10,000 human proteins by SWATH-MS

George Rosenberger, Ching Chiek Koh, Tiannan Guo, Hannes L. Röst, Petri Kouvonen, Ben C. Collins, Moritz Heusel, Yansheng Liu, Etienne Caron, Anton Vichalkovski, Marco Faini, Olga T. Schubert, Pouya Faridi, H. Alexander Ebhardt, Mariette Matondo, Henry Lam Samuel L. Bader, David S. Campbell, Eric W. Deutsch, Robert L. Moritz, Stephen Tate & Ruedi Aebersold

Affiliations | Contributions | Corresponding author

Scientific Data **1**, Article number: 140031 (2014) | doi:10.1038/sdata.2014.31

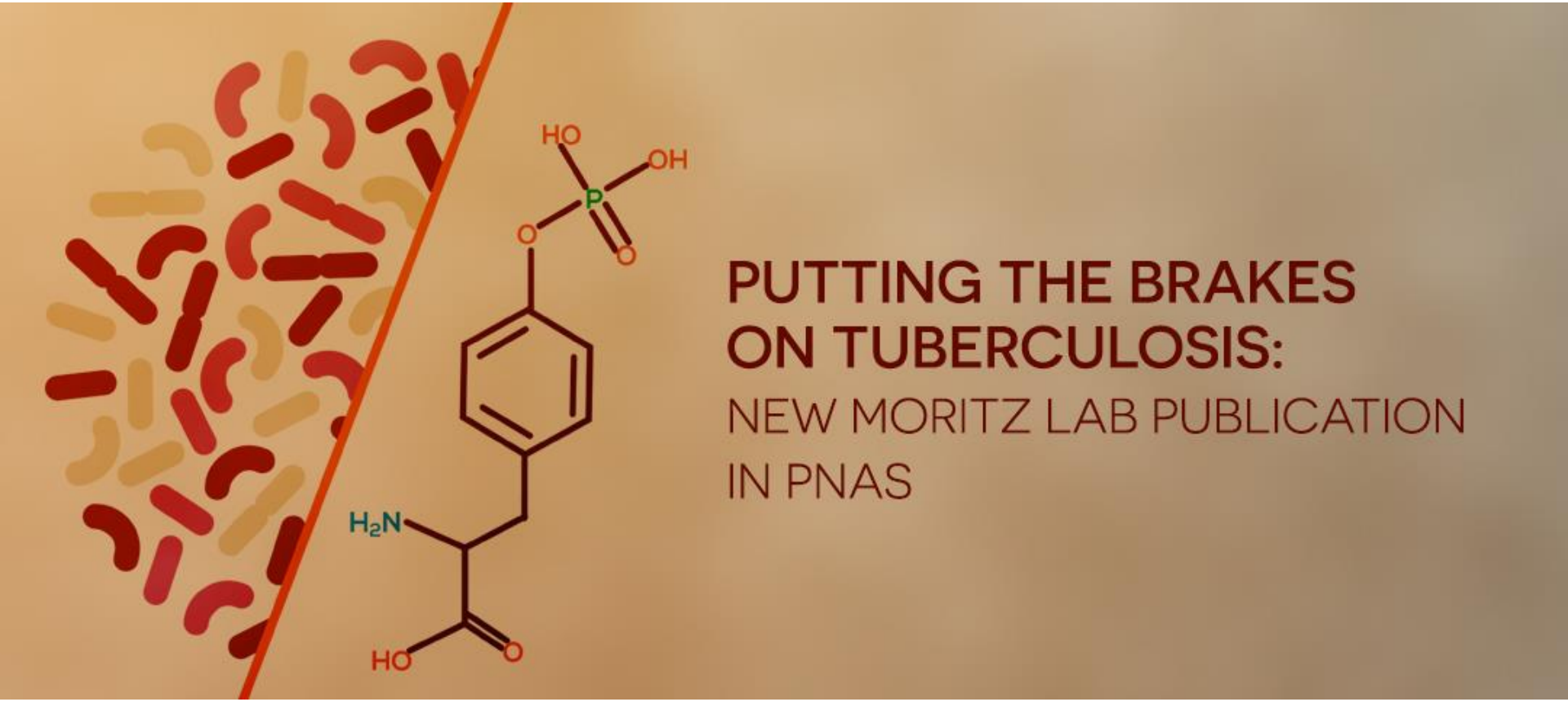
Received 11 June 2014 | Accepted 06 August 2014 | Published online 16 September 2014

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Libraries: Public Domain

M. tuberculosis Spectral Library

SRMAtlas



Libraries: from IDA experiments

nature protocols

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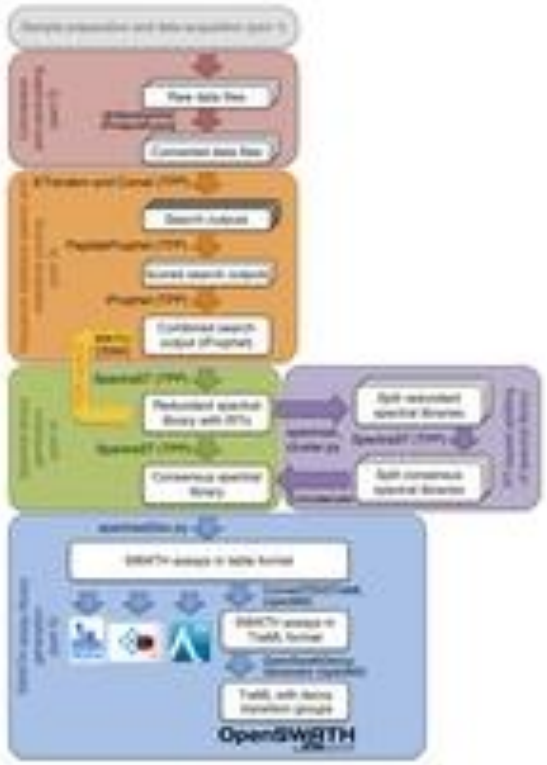
Building high-quality assay libraries for targeted analysis of SWATH MS data

Olga T Schubert, Ludovic C Gillet, Ben C Collins, Pedro Navarro, George Rosenberger, Witold E Wolski, Henry Lam, Dario Amodei, Parag Mallick, Brendan MacLean & Ruedi Aebersold

Affiliations | **Contributions** | **Corresponding author**

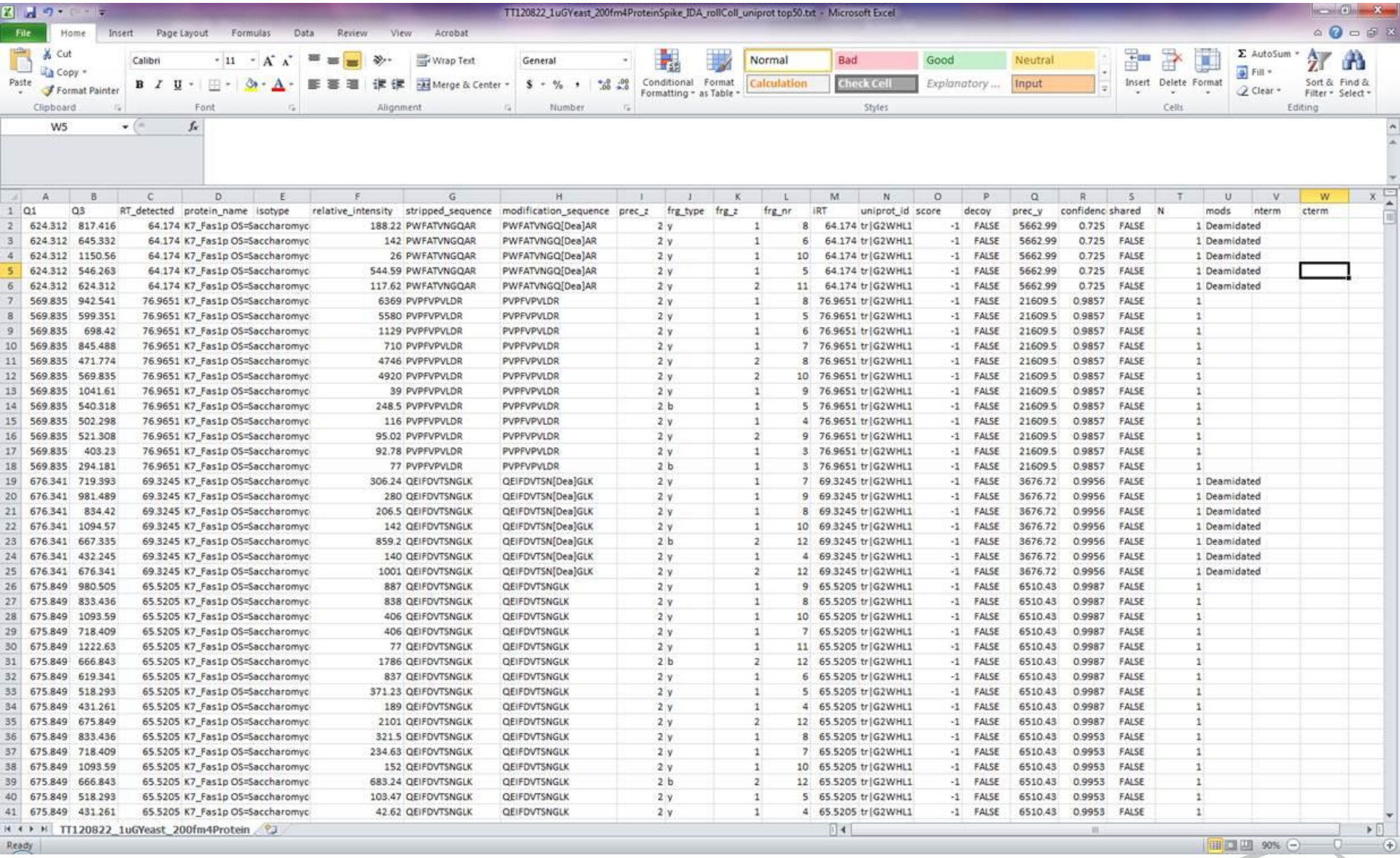
Nature Protocols **10**, 426–441 (2015) | doi:10.1038/nprot.2015.015

Published online 12 February 2015



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Libraries: Theoretical



TT120822_1uGYeast_200fm4ProteinSpike_IDA_rollColl_uniprot top50.txt - Microsoft Excel

Q1	Q3	RT_detected	protein_name	isotype	relative_intensity	stripped_sequence	modification_sequence	prec_z	frg_type	frg_z	frg_nr	iRT	uniprot_id	score	decoy	prec_y	confidenc	shared	N	mods	nterm	cterm
624.312	817.416	64.174	K7_Fas1p OS=Saccharomyc		188.22	PWFATVNGQAR	PWFATVNGQ[Dea]AR	2	y	1	8	64.174	tr|G2WHL1	-1	FALSE	5662.99	0.725	FALSE	1	Deamidated		
624.312	645.332	64.174	K7_Fas1p OS=Saccharomyc		142	PWFATVNGQAR	PWFATVNGQ[Dea]AR	2	y	1	6	64.174	tr|G2WHL1	-1	FALSE	5662.99	0.725	FALSE	1	Deamidated		
624.312	1150.56	64.174	K7_Fas1p OS=Saccharomyc		26	PWFATVNGQAR	PWFATVNGQ[Dea]AR	2	y	1	10	64.174	tr|G2WHL1	-1	FALSE	5662.99	0.725	FALSE	1	Deamidated		
624.312	546.263	64.174	K7_Fas1p OS=Saccharomyc		544.59	PWFATVNGQAR	PWFATVNGQ[Dea]AR	2	y	1	5	64.174	tr|G2WHL1	-1	FALSE	5662.99	0.725	FALSE	1	Deamidated		
624.312	624.312	64.174	K7_Fas1p OS=Saccharomyc		117.62	PWFATVNGQAR	PWFATVNGQ[Dea]AR	2	y	2	11	64.174	tr|G2WHL1	-1	FALSE	5662.99	0.725	FALSE	1	Deamidated		
569.835	942.541	76.9651	K7_Fas1p OS=Saccharomyc		6369	PVPFVPVLDR	PVPFVPVLDR	2	y	1	8	76.9651	tr|G2WHL1	-1	FALSE	21609.5	0.9857	FALSE	1			
569.835	599.351	76.9651	K7_Fas1p OS=Saccharomyc		5580	PVPFVPVLDR	PVPFVPVLDR	2	y	1	5	76.9651	tr|G2WHL1	-1	FALSE	21609.5	0.9857	FALSE	1			
569.835	698.42	76.9651	K7_Fas1p OS=Saccharomyc		1129	PVPFVPVLDR	PVPFVPVLDR	2	y	1	6	76.9651	tr|G2WHL1	-1	FALSE	21609.5	0.9857	FALSE	1			
569.835	845.488	76.9651	K7_Fas1p OS=Saccharomyc		710	PVPFVPVLDR	PVPFVPVLDR	2	y	1	7	76.9651	tr|G2WHL1	-1	FALSE	21609.5	0.9857	FALSE	1			
569.835	471.774	76.9651	K7_Fas1p OS=Saccharomyc		4746	PVPFVPVLDR	PVPFVPVLDR	2	y	2	8	76.9651	tr|G2WHL1	-1	FALSE	21609.5	0.9857	FALSE	1			
569.835	569.835	76.9651	K7_Fas1p OS=Saccharomyc		4920	PVPFVPVLDR	PVPFVPVLDR	2	y	2	10	76.9651	tr|G2WHL1	-1	FALSE	21609.5	0.9857	FALSE	1			
569.835	1041.61	76.9651	K7_Fas1p OS=Saccharomyc		39	PVPFVPVLDR	PVPFVPVLDR	2	y	1	9	76.9651	tr|G2WHL1	-1	FALSE	21609.5	0.9857	FALSE	1			
569.835	540.318	76.9651	K7_Fas1p OS=Saccharomyc		248.5	PVPFVPVLDR	PVPFVPVLDR	2	b	1	5	76.9651	tr|G2WHL1	-1	FALSE	21609.5	0.9857	FALSE	1			
569.835	502.298	76.9651	K7_Fas1p OS=Saccharomyc		116	PVPFVPVLDR	PVPFVPVLDR	2	y	1	4	76.9651	tr|G2WHL1	-1	FALSE	21609.5	0.9857	FALSE	1			
569.835	521.308	76.9651	K7_Fas1p OS=Saccharomyc		95.02	PVPFVPVLDR	PVPFVPVLDR	2	y	2	9	76.9651	tr|G2WHL1	-1	FALSE	21609.5	0.9857	FALSE	1			
569.835	403.23	76.9651	K7_Fas1p OS=Saccharomyc		92.78	PVPFVPVLDR	PVPFVPVLDR	2	y	1	3	76.9651	tr|G2WHL1	-1	FALSE	21609.5	0.9857	FALSE	1			
569.835	294.181	76.9651	K7_Fas1p OS=Saccharomyc		77	PVPFVPVLDR	PVPFVPVLDR	2	b	1	3	76.9651	tr|G2WHL1	-1	FALSE	21609.5	0.9857	FALSE	1			
676.341	719.393	69.3245	K7_Fas1p OS=Saccharomyc		306.24	QEIFDVTSNGLK	QEIFDVTSN[Dea]GLK	2	y	1	7	69.3245	tr|G2WHL1	-1	FALSE	3676.72	0.9956	FALSE	1	Deamidated		
676.341	981.489	69.3245	K7_Fas1p OS=Saccharomyc		280	QEIFDVTSNGLK	QEIFDVTSN[Dea]GLK	2	y	1	9	69.3245	tr|G2WHL1	-1	FALSE	3676.72	0.9956	FALSE	1	Deamidated		
676.341	834.42	69.3245	K7_Fas1p OS=Saccharomyc		206.5	QEIFDVTSNGLK	QEIFDVTSN[Dea]GLK	2	y	1	8	69.3245	tr|G2WHL1	-1	FALSE	3676.72	0.9956	FALSE	1	Deamidated		
676.341	1094.57	69.3245	K7_Fas1p OS=Saccharomyc		142	QEIFDVTSNGLK	QEIFDVTSN[Dea]GLK	2	y	1	10	69.3245	tr|G2WHL1	-1	FALSE	3676.72	0.9956	FALSE	1	Deamidated		
676.341	667.335	69.3245	K7_Fas1p OS=Saccharomyc		859.2	QEIFDVTSNGLK	QEIFDVTSN[Dea]GLK	2	b	2	12	69.3245	tr|G2WHL1	-1	FALSE	3676.72	0.9956	FALSE	1	Deamidated		
676.341	432.245	69.3245	K7_Fas1p OS=Saccharomyc		140	QEIFDVTSNGLK	QEIFDVTSN[Dea]GLK	2	y	1	4	69.3245	tr|G2WHL1	-1	FALSE	3676.72	0.9956	FALSE	1	Deamidated		
676.341	676.341	69.3245	K7_Fas1p OS=Saccharomyc		1001	QEIFDVTSNGLK	QEIFDVTSN[Dea]GLK	2	y	2	12	69.3245	tr|G2WHL1	-1	FALSE	3676.72	0.9956	FALSE	1	Deamidated		
675.849	980.505	65.5205	K7_Fas1p OS=Saccharomyc		887	QEIFDVTSNGLK	QEIFDVTSNGLK	2	y	1	9	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9987	FALSE	1			
675.849	833.436	65.5205	K7_Fas1p OS=Saccharomyc		838	QEIFDVTSNGLK	QEIFDVTSNGLK	2	y	1	8	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9987	FALSE	1			
675.849	1093.59	65.5205	K7_Fas1p OS=Saccharomyc		406	QEIFDVTSNGLK	QEIFDVTSNGLK	2	y	1	10	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9987	FALSE	1			
675.849	718.409	65.5205	K7_Fas1p OS=Saccharomyc		406	QEIFDVTSNGLK	QEIFDVTSNGLK	2	y	1	7	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9987	FALSE	1			
675.849	1222.63	65.5205	K7_Fas1p OS=Saccharomyc		77	QEIFDVTSNGLK	QEIFDVTSNGLK	2	y	1	11	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9987	FALSE	1			
675.849	666.843	65.5205	K7_Fas1p OS=Saccharomyc		1786	QEIFDVTSNGLK	QEIFDVTSNGLK	2	b	2	12	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9987	FALSE	1			
675.849	619.341	65.5205	K7_Fas1p OS=Saccharomyc		837	QEIFDVTSNGLK	QEIFDVTSNGLK	2	y	1	6	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9987	FALSE	1			
675.849	518.293	65.5205	K7_Fas1p OS=Saccharomyc		371.23	QEIFDVTSNGLK	QEIFDVTSNGLK	2	y	1	5	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9987	FALSE	1			
675.849	431.261	65.5205	K7_Fas1p OS=Saccharomyc		189	QEIFDVTSNGLK	QEIFDVTSNGLK	2	y	1	4	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9987	FALSE	1			
675.849	675.849	65.5205	K7_Fas1p OS=Saccharomyc		2101	QEIFDVTSNGLK	QEIFDVTSNGLK	2	y	2	12	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9987	FALSE	1			
675.849	833.436	65.5205	K7_Fas1p OS=Saccharomyc		321.5	QEIFDVTSNGLK	QEIFDVTSNGLK	2	y	1	8	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9953	FALSE	1			
675.849	718.409	65.5205	K7_Fas1p OS=Saccharomyc		234.63	QEIFDVTSNGLK	QEIFDVTSNGLK	2	y	1	7	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9953	FALSE	1			
675.849	1093.59	65.5205	K7_Fas1p OS=Saccharomyc		152	QEIFDVTSNGLK	QEIFDVTSNGLK	2	y	1	10	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9953	FALSE	1			
675.849	666.843	65.5205	K7_Fas1p OS=Saccharomyc		683.24	QEIFDVTSNGLK	QEIFDVTSNGLK	2	b	2	12	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9953	FALSE	1			
675.849	518.293	65.5205	K7_Fas1p OS=Saccharomyc		103.47	QEIFDVTSNGLK	QEIFDVTSNGLK	2	y	1	5	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9953	FALSE	1			
675.849	431.261	65.5205	K7_Fas1p OS=Saccharomyc		42.62	QEIFDVTSNGLK	QEIFDVTSNGLK	2	y	1	4	65.5205	tr|G2WHL1	-1	FALSE	6510.43	0.9953	FALSE	1			

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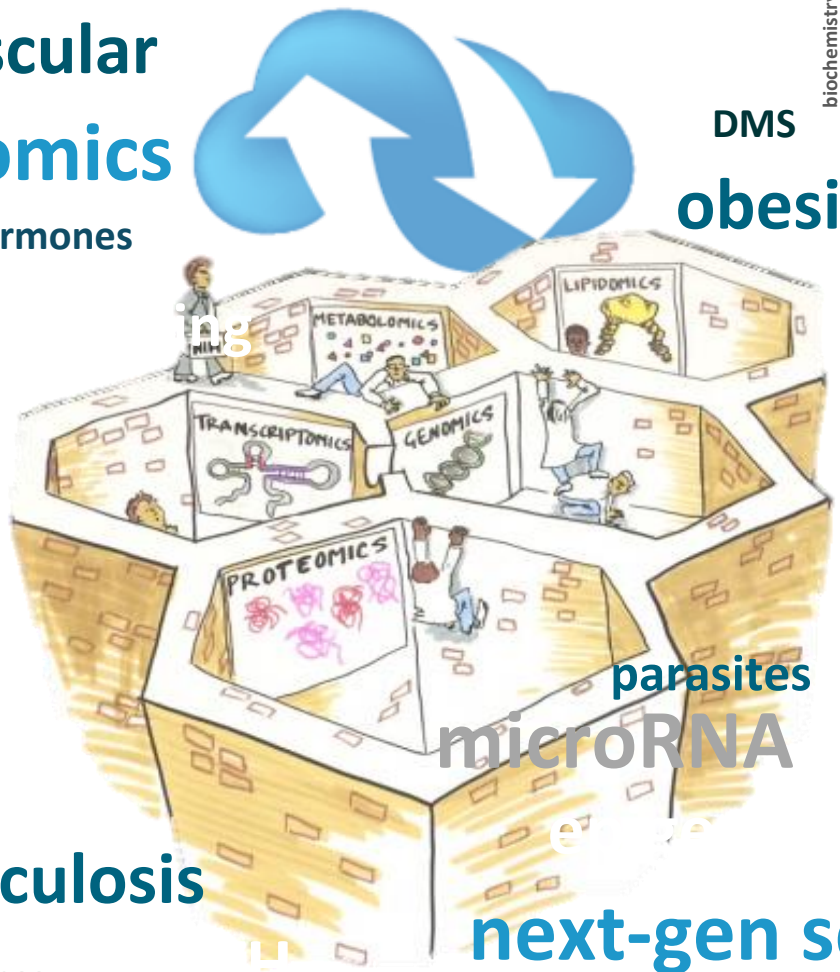
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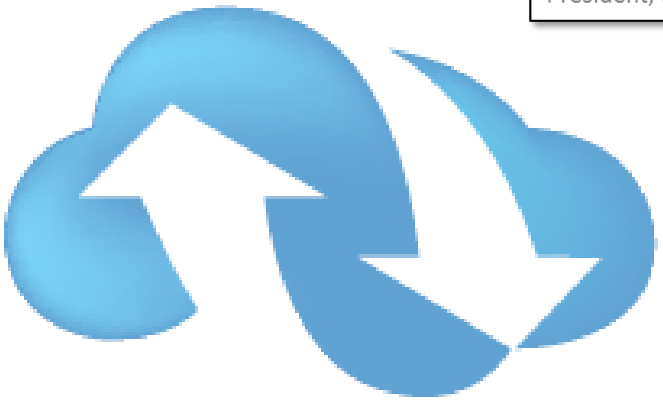
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1



Omics integration

2

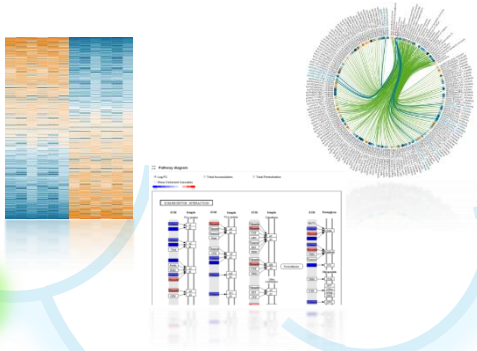


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3



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From Genomics to Proteomics and Beyond



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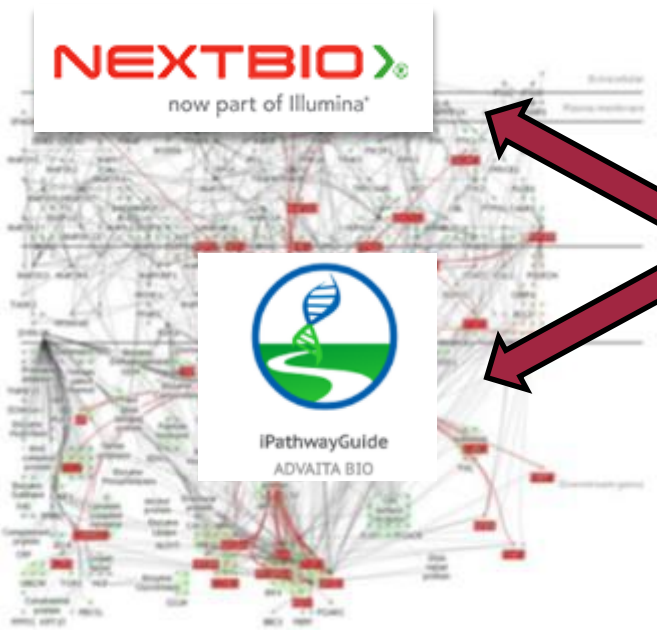
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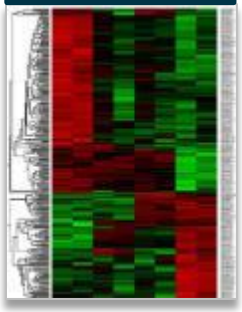
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SWATH
Ion library

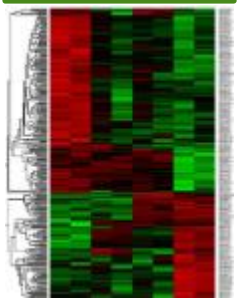




Gene Expression



Protein Expression



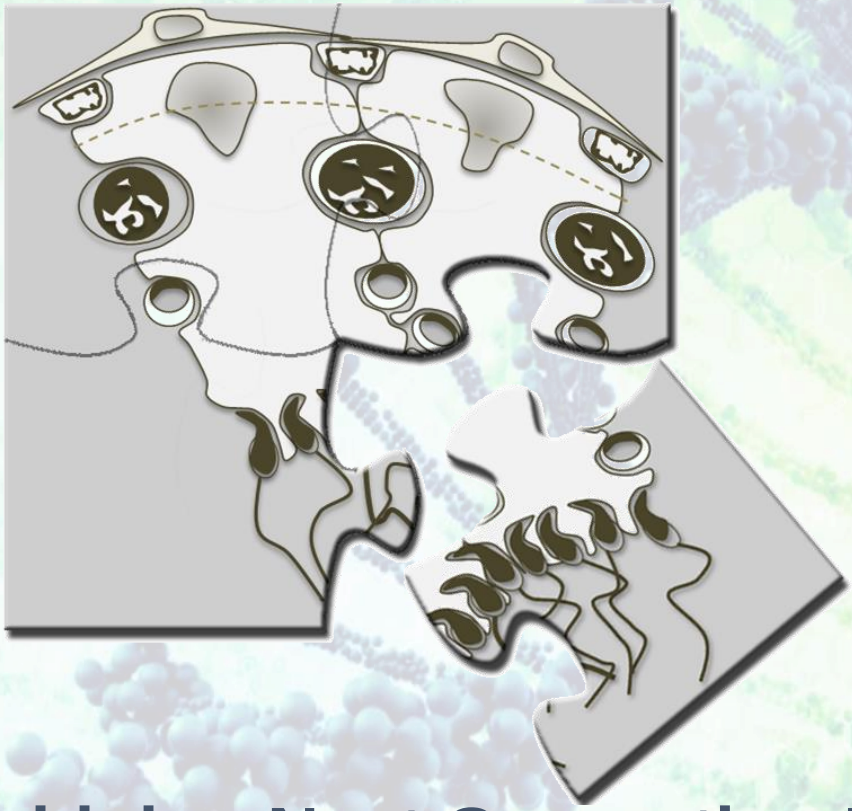


Protein Exp. Assembler
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Protein Exp. Extractor
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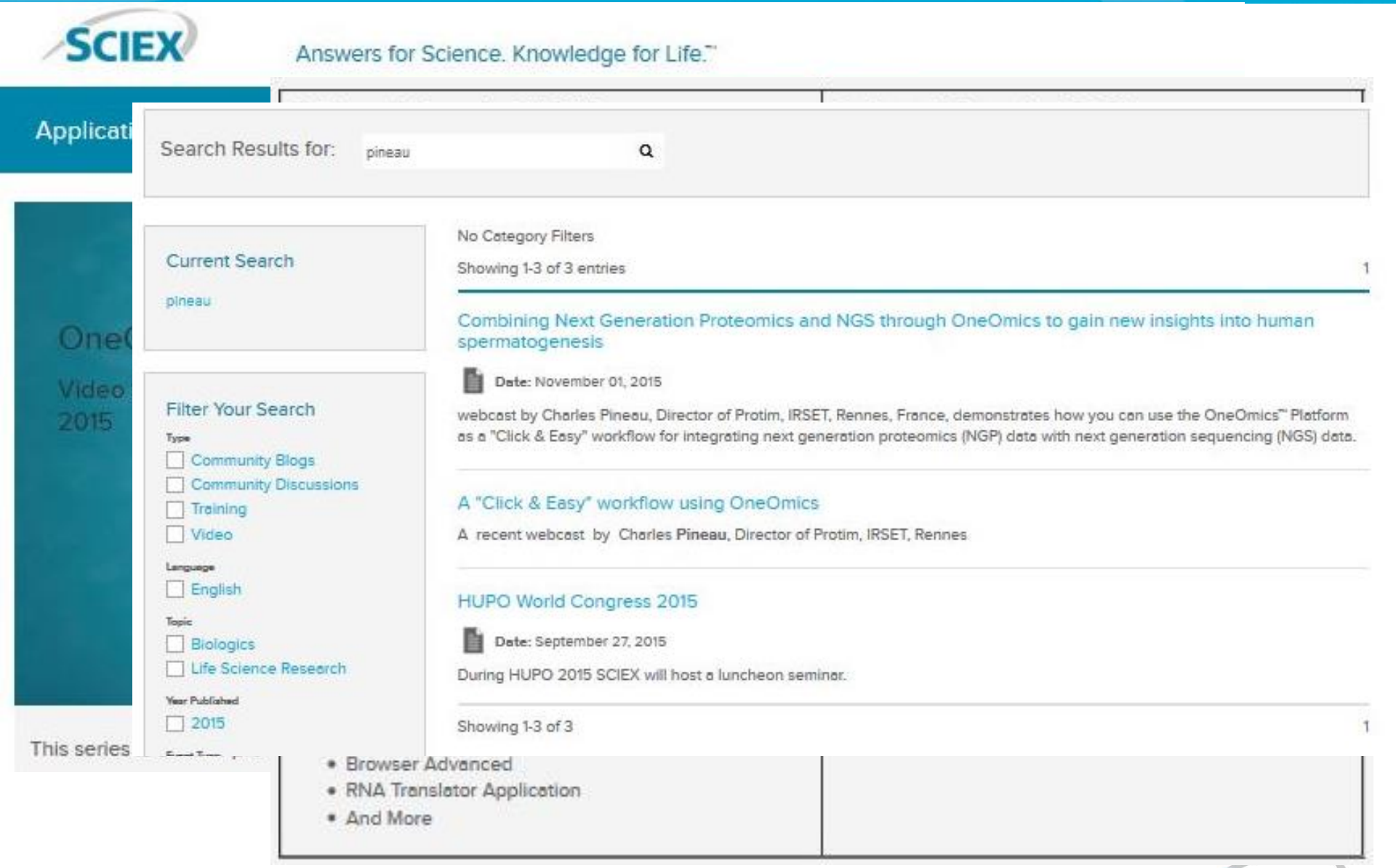
charles.pineau@inserm.fr

Multi-Omics Analysis of Primary Cytotrophoblasts from Second Trimester and Term Placentas

Katy Williams[1], Christie L. Hunter[2]; Andrew Olson[3]
[1]University of California San Francisco, USA; [2]SCIEX, USA; [3]Advaita Biosciences, USA

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Conclusions

- designing OMICS experiments needs careful planning
- we can now describe samples in (nearly) complete details
- identification and quantitation can be done on one system
- speed @ sensitivity @ resolution will be the key

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감사

ขอบคุณ

متشكرم

Благодаря!

Tesekkurler

Kiitos

Tak

Danke

Dziękuję

Thanks

Děkuji

Niżżik ħajr

Salamat po

Gracias

ありがとう

Спасибо

cảm ơn

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Thank you for your attention

谢谢

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תודה רבה

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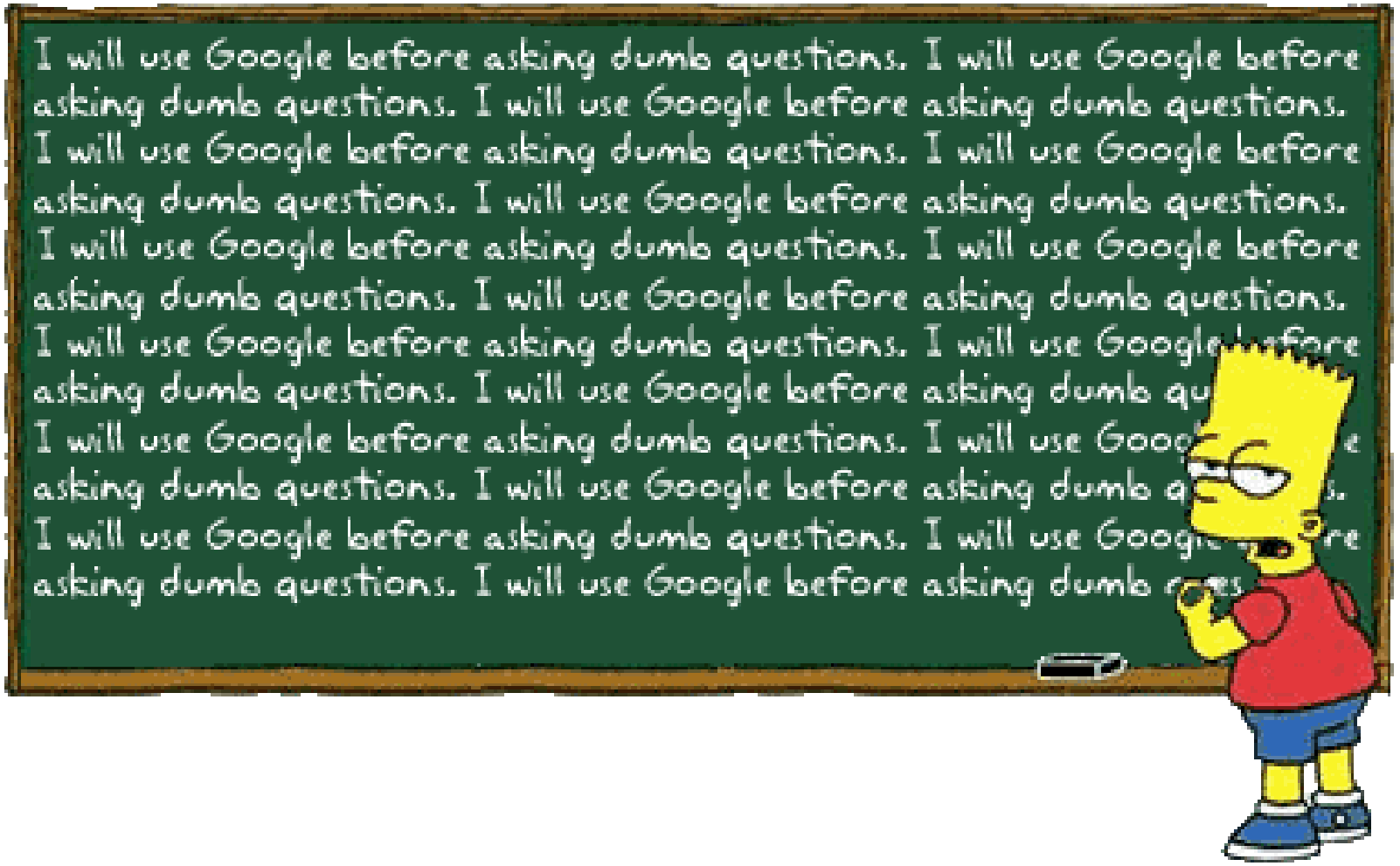
Děkuij

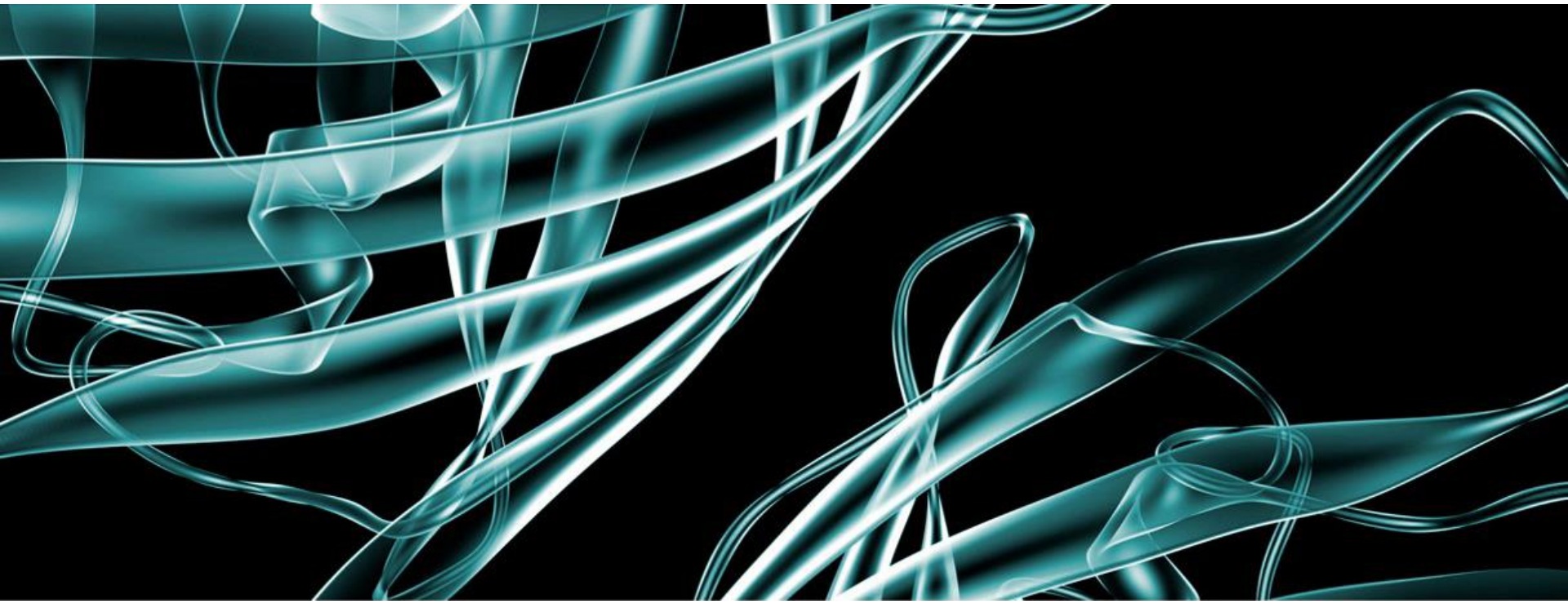
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Questions ?





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