QUALITY MEANS

RELIABILITY

MASS SPECTROMETRY PROTEOMICS

BIOMARKER DISCOVERY TO CLINICAL DIAGNOSTICS

SIGMA® | ALDRICH® | Fluka® | SUPELCO® | Cerilliant®

Optimize MS Proteomic Analysis with Sigma-Aldrich Quality

Sample Preparation

- Seppro® Protein Depletion Technology
- MS Safe Protease and Phosphatase Inhibitor Cocktail

Calibration and Standardization

- Universal Proteomics Standards
- Mass Spectrometry Performance and Retention Time Standards
- Phosphopeptide Mass Spectrometry Standards
- Stable Isotope Labelled Full Length Proteins

Digestion

- Proteomics Grade Trypsin
- Endoproteinases
- Protease Profiler Kit

Chromatographic Separation

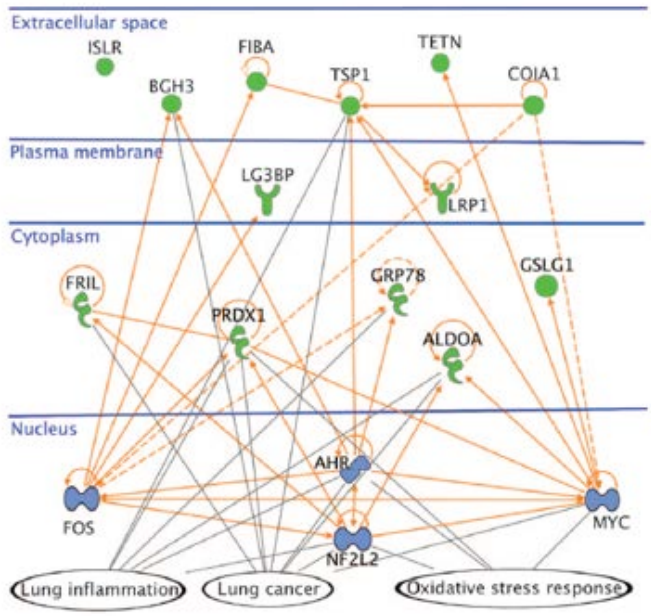
- BIOshell™ Fused-Core HPLC Columns
- LC-MS Grade Solvents

Groundbreaking MRM Diagnostics Enabled by Seppro®

Millions of patients annually are told that CT imaging results demonstrate the presence of pulmonary nodules, which may or may not be a sign of early stage cancer. Identification of malignancy at this stage could offer great benefits in theraputic invervention strategies. Currently, identification of malignancy in such a lung nodule is determined through invasive biopsies or surgery. Nearly 80% of the patients who undergo life threatening biopsy procedures are found to have benign pulmonary nodules. Therefore there is a tremendous need for a less invasive procedure to differentiate between benign lung nodules and early-stage cancer. Indi® (Integrated Diagnostics®), an emerging leader in molecular diagnostics, is helping physicians to assess pulmonary lung nodules through their development of a multiplexed proteomic serum analysis enabled by Seppro® protein depletion.

When developing their diagnostic, Xpresys® Lung, Indi utilized multiple reaction monitoring mass spectrometry (MRM-MS) and sophisticated bioinformatics to assess the diagnostic power of 371 potential protein biomarkers relevant to lung cancer. From the original 371 biomarkers, Indi uncovered an 11-protein blood-based classifier that can identify likely benign nodules with a high degree of probability. A multi-site, broad demographic clinical study suggested that when the classifier is detected and used to identify a patient's lung nodule as benign, the classifier result is correct more than 90 percent of the time. This breakthrough diagnostic tool provides physicians with an additional, objective tool that helps them to avoid unnecessary invasive procedures.

Seppro® has provided Indi with a unique sample preparation method which allows them to uncover these game-changing biomarkers. A combination Seppro IgY14/Supermix column provides an essential sample preparation step for plasma samples. This column is used to remove the 14 highest abundant proteins along with up to 200 medium abundant proteins to unmask key differential biomarkers of low relative abundance. This column depletes over 98% of the total protein content of human serum allowing our current analytical techniques to identify and quantify biomarkers that otherwise are invisible to the mass spectrometer. Utilization of common protein depletion methodologies remains inadequate in many instances, as the medium abundant proteins that are not included in the 14 most abundant still mask relevant indicators of human health. The high level of reproducibility and unique depth of depletion of Seppro IgY14/Supermix provides a powerful tool for uncovering the next set of serum biomarkers that can make a direct impact on disease diagnosis and monitoring today.



The 13 classifier proteins (green), 4 transcription regulators (blue), and 3 networks (orange lines) of lung cancer, oxidative stress response, and lung inflammation. All references are human UniProt identifiers.

Indi®
Integrated Diagnostics, Inc.

Science Translational Medicine 2013-10-16

A blood-based proteomic classifier for the molecular characterization of pulmonary nodules.

Xiao-jun Li, Clive Hayward, Pui-Yee Fong, Michel Dominguez, Stephen W Hunsucker, Lik Wee Lee, Matthew McLean, Scott Law, Heather Butler, Michael Schirm, Olivier Gingras, Julie Lamontagne, Rene Allard, Daniel Chelsky, Nathan D Price, Stephen Lam, Pierre P Massion, Harvey Pass, William N Rom, Anil Vachani, Kenneth C Fang, Leroy Hood, Paul Kearney

PMID 24132637

REVEAL THE UNSEEN:

Serum Protein Depletion Using Seppro®

- Unmatched depth of serum depletion – Unmask your proteins of interest
- Available in Spin and LC columns
- Available for Human, Mouse, Rat, and Plant sample depletion

The Seppro depletion technology allows for the removal of several highly abundant proteins from a variety of biological samples. The use of avian polyclonal IgY (Immunoglobulin Yolk) antibodies provides unique and advantageous features that allow highly-specific partitioning of protein mixtures. As a result, previously masked proteins become more accessible for investigation.

The Seppro Human IgY14 removes the 14 most abundant serum proteins, allowing detection of previously hidden targets of interest by either 2D Gel Electrophoresis or Mass Spectrometry.

The Seppro SuperMix technology delivers the most complete human depletion system available. When used in conjunction with the Human IgY14 resin, the protein mass removed includes 14 of the most abundant proteins from human serum or plasma, as well as other high abundance proteins (HAP) and medium abundance proteins (MAP). Overall, the result is removal of up to 99% of protein mass. To achieve this amount of protein mass removal, the system used is based on the IgY14 depletion column (LC5 or LC10 format) in conjunction with the SuperMix column (LC2 or LC5 format). For details regarding proteins or antibody classes depleted, see figures on page 5.

Seppro® Protein Depletion Technology

Easily isolate and identify your target protein by removing up to 99% of protein mass (dependent on resin selection).

Sample Source

Plasma or Serum

- Human
- Rat
- Mouse
- Additional species available

Plant

- Rubisco removal

Convenient Formats

Spin Columns

- 2 columns/kit
- 200 runs (100 runs/column)

LC Column

- LC2, LC5 or LC10
- 100 injections/column

Custom Options

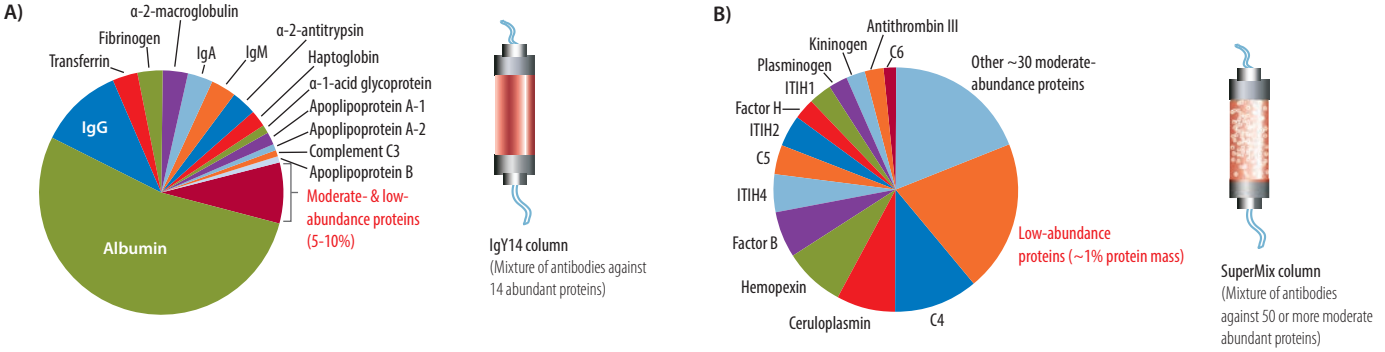
- Unique resin blends
- Bulk resin (single or blends)

Seppro Product	Ordering Info	Undiluted Sample Capacity	Proteins Depleted
IgY14 Human	Remove 14 highly abundant proteins in human plasma or serum		
IgY14 Spin Columns	SEP010-1KT	15-20 µl	HSA, IgG, Fibrinogen, Transferrin, IgA, IgM, Haptoglobin, α_2-Macroglobulin, α_1-Acid Glycoprotein, Apo A-I HDL, α_1-Antitrypsin, Apo A-II HDL, Complement C3, LDL (Apo B)
IgY14 LC2	SEP020-1KT	40-50 µl	
IgY14 LC5	SEP030-1KT	100 µl	
IgY14 LC10	SEP040-1KT	200-250 µl	
Supermix	Additional removal of moderately abundant human proteins		
Supermix Human LC2	SEP050-1KT	Flow through from IgY14 LC5	Further protein depletion resulting in 99% total protein removal
Supermix Human LC5	SEP060-1KT	Flow through from IgY14 LC10	
Rat	Remove 7 highly abundant proteins in rat plasma or serum		
Rat Spin Columns	SEP130-1KT	15-20 µl	Rat serum albumin, IgG, Fibrinogen, Transferrin, IgM, Haptoglobin, α_1-Antitrypsin
Rat LC10	SEP120-1KT	200-250 µl	
Mouse	Remove 7 highly abundant proteins in mouse plasma or serum		
Mouse Spin Columns	SEP110-1KT	15-20 µl	Mouse serum albumin, IgG, Fibrinogen,Transferrin, IgM, Haptoglobin, α_1-Antitrypsin
Mouse LC10	SEP090-1KT	200-250 µl	
Mouse Supermix LC5	SEP100-1KT	Flow through from mouse LC10	Further partitions complex mouse plasma/serum samples
Rubisco	Remove Rubisco protein in plant samples		
Rubisco Spin Columns	SEP070-1KT	15-20 µl	RuBisCO (Ribulose-1,5-bisphosphate carboxylase/oxygenase)
Rubisco LC2	SEP080-1KT	40-50 µl	

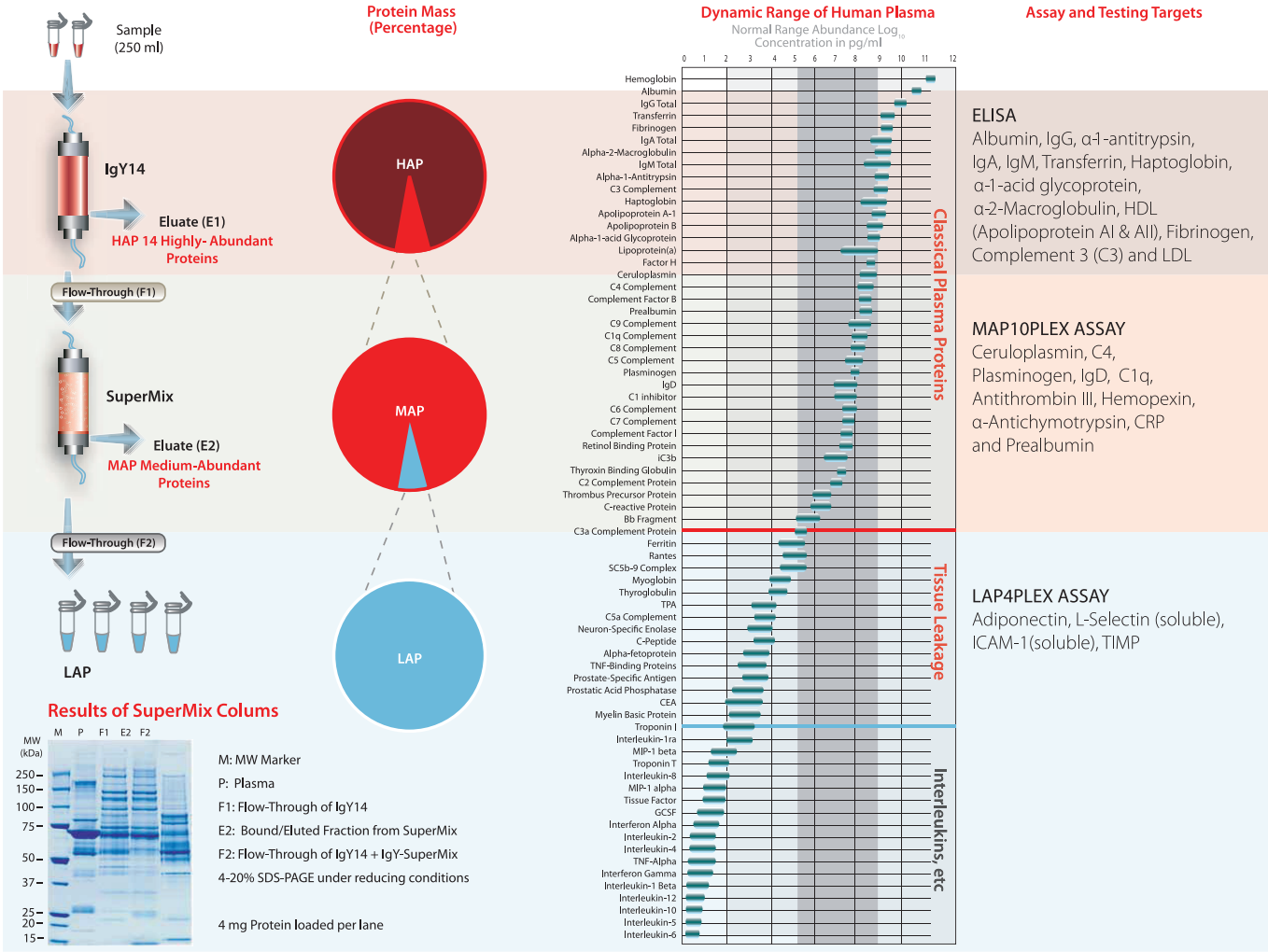
To learn more about the Seppro Human IgY14/Supermix depletion approach, visit **sigma.com/seppro**

* Please also ask about our Custom Capabilities including IgY14/Supermix Combination Columns.

Greatest Depth Depletion in the Market



The HAP and MAP distributions in the human blood plasma proteome. The top 14 HAP are targeted by the IgY14 column (A) and 50 MAP are targeted by the SuperMix column. The percentage of protein abundances are based on spectral count data from LC–MS/MS experiments. In this context, HAP are defined as 14 proteins captured by the IgY14 column, and MAP are those 50 proteins captured by the SuperMix column as listed in Table 1 except C3. All other proteins are considered as LAP.



Preserve the Integrity of your Sample

MSSAFE: MS-SAFE PROTEASE AND PHOSPHATASE INHIBITOR COCKTAIL

- The MS-SAFE Protease and Phosphatase Inhibitor Cocktail (Cat. No. MSSAFE) is Sigma's new combination protease inhibitor and phosphatase inhibitor cocktail that is designed to be totally compatible with downstream mass spectrometry applications.
- MSSAFE is the only commercial inhibitor cocktail completely free of any inhibitors that can potentially modify proteins.
- MSSAFE is also fully compatible with IMAC, as MSSAFE completely omits any metal chelators.
- Available in 1VL and 5 × 1VL quantities

MSSAFE Inhibitor Components

Protease Inhibitor	Specific Inhibitory Target of Component
Bestatin hydrochloride	Aminopeptidases (e.g. leucine aminopeptidase, alanyl aminopeptidase)
Leupeptin	Serine & cysteine proteases (e.g. trypsin, plasmin, trypsinogen, urokinase, kallekrein)
Phosphoramidon sodium salt	Thermolysin, collagenase
Pepstatin A	Acid proteases (e.g. pepsin, renin, cathepsin D, many microbial aspartic proteases)
Elastatinal	Elastase
Aprotinin	Serine proteases (e.g. chymotrypsin, trypsin, elastase)
Nafamostat mesylate	Serine proteases, kallikrein
Antipain	Serine/cysteine proteases, some trypsin-like serine proteases
Phosphatase Inhibitor	**Specific Inhibitory Target of Component**
Okadaic acid	Type 2A protein phosphatases
Sodium fluoride	Serine phosphatases, threonine phosphatases
Sodium orthovanadate	ATPases, protein tyrosine phosphatases, other phosphate-transferring enzymes
Bromotetramisole oxalate	L-isoforms of alkaline phosphatases

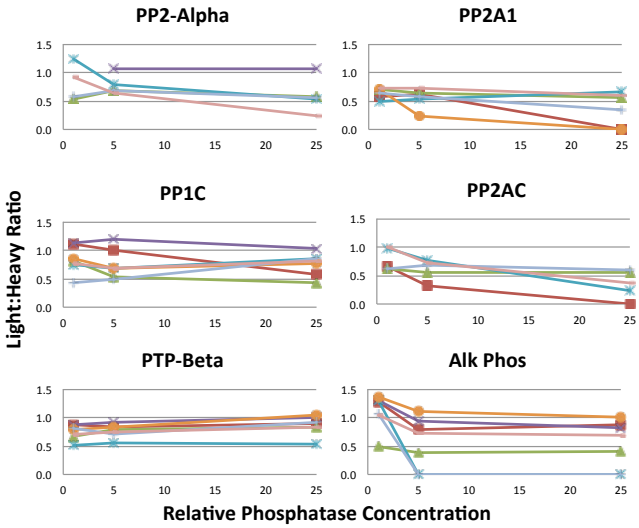


Figure 1. Demonstration of phosphatase specificity and inhibition with the Sigma PhosphoMix phosphopeptide standard against different phosphatases. A decrease in the light:heavy ratio of the phosphorylated peptide at higher phosphatase concentrations indicates that the phosphopeptide is a substrate for the phosphatase, and additionally that MSSAFE is properly inhibiting the phosphatase in question.

For more information, visit
sigma.com/mssafe

Standardize Your MS Proteomics Research

PEPTIDE AND PROTEIN CALIBRATION STANDARDS FOR MASS SPECTROMETRY

Universal Proteomics Standards (UPS)

Complex mixtures of 48 proteins ranging from 6,000 to 83,000 Daltons, for standardization and evaluation of mass spectrometer conditions prior to the analysis of complex protein samples.

- Troubleshoot and optimize your analytical protocol
- Confirm system suitability before analyzing critical samples
- Normalize your analytical results day-to-day or lab-to-lab
- Each protein is HPLC purified and AAA quantified prior to formulation

UPS1: Universal Proteomics Standard Set Protein Mass Spectrometry Calibration Standard

- 5 pmol of each of the 48 proteins

UPS2: Proteomics Dynamic Range Standard Set Protein Mass Spectrometry Calibration Standard

- 48 proteins formulated into a dynamic range from 50 pmoles to 0.5 fmoles

LC-MS Performance Standards

MSQC1: MS Qual/Quant QC Mix Proteomics MRM LC-MS Calibration Standard

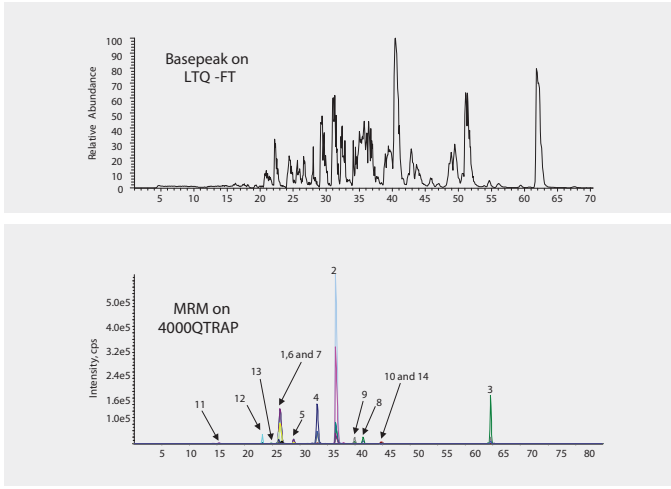
- Injection-ready LC-MS standard to benchmark and monitor daily performance of both qualitative and quantitative proteomics platforms
- Mixture of 6 tryptically digested HPLC purified human proteins

MSRT1: MS RT Calibration Mix Proteomics Retention Time Standard for LC-MS

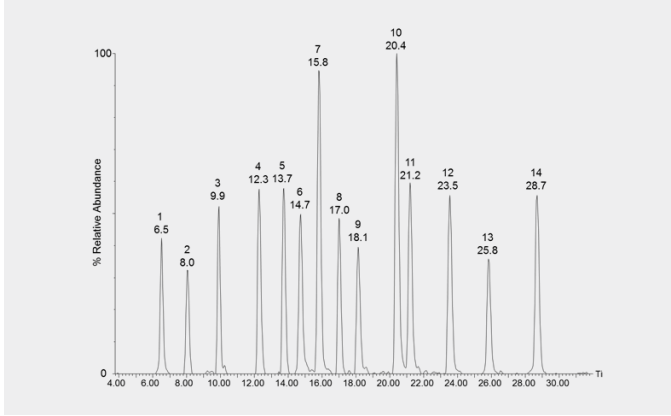
- Injection-ready LC-MS platform standard to test properties such as LC resolution, peptide elution profiles, and retention time prediction
- Mixture of 14 stable isotope-labeled peptides spanning the normal elution profile of complex proteomics samples

Protein	Peptide #	Peptide Sequence*
Carbonic Anhydrase I	1	GGPFSDSY[R]
	2	VLDALQAI[K]
Carbonic Anhydrase II	3	AVQQPDGLAVLGIF[K]
	4	SADFTNFDP[R]
NAD(P)H dehydrogenase	5	ALIVLAHSE[R]
	6	EGHLSPDIVAEQ[K]
C-reactive Protein	7	ESDTSYVSL[K]
	8	GYSIFSYAT[K]
Peptidyl-Prolyl cis-trans isomerase A	9	FEDENFIL[K]
	10	VSFELFAD[K]
	11	TAENF[R]
Catalase	12	FSTVAGESGSADTV[R]
	13	NLSVEDAA[R]
	14	GAGAFGYFEVTHDIT[K]

* Amino acid in [brackets] denotes site of heavy label incorporation



Top: Full-scan LC-MS chromatogram of MSQC1 on a LTQ-FT mass spectrometer.
Bottom: Chromatogram of MRM analysis of MSQC1 on a 4000QTRAP mass spectrometer.



Peaks are labeled with Peptide # and retention time. LC-MS was performed on an Acquity-LCT platform with ~8 pmols injected onto a 1 mm I.D. Ascentis Express Peptide ES C18 column (**Cat. No. 53561-U**) at 90 µL/min, using a linear organic gradient modified with 0.1% formic acid.

Standardize Your MS Proteomics Research

STABLE ISOTOPE – LABELED PROTEIN STANDARDS

PhosphoMix™ Phosphopeptide MS Standards

- For phosphopeptide analysis and workflow verification
- Available in matched pairs of natural (Light) and stable isotope-labeled (Heavy) mixtures

MSP1L: MS PhosphoMix 1 Light Phosphopeptide Standard for MS

MSP1H: MS PhosphoMix 1 Heavy Phosphopeptide Standard for MS

MSP2L: MS PhosphoMix 2 Light Phosphopeptide Standard for MS

MSP2H: MS PhosphoMix 2 Heavy Phosphopeptide Standard for MS

MSP3L: MS PhosphoMix 3 Light Phosphopeptide Standard for MS

MSP3H: MS PhosphoMix 3 Heavy Phosphopeptide Standard for MS

SILu™ Mab Stable Isotope-Labeled Universal Monoclonal Antibody Standard

SILuMab is a highly purified stable isotope-labeled IgG1 monoclonal antibody expressed in a proprietary Sigma-Aldrich CHO cell line grown in serum-free $^{13}C6\ ^{15}N_4$ Arg / $^{13}C_6\ ^{15}N_2$ Lys enriched media.

SILuMab design is optimized to be used as an internal standard for quantitation of monoclonal antibodies as well as Fc-fusion therapeutics.

SILuMab yields reproducible, linear curves from 0.1 µg/mL to 1000 µg/mL without enrichment or depletion.

Quantitative LC/MS assays utilizing SILuMab offer advantages over traditional ELISA-based methods because of their superior specificity, sensitivity, and reduced matrix effects.

- Label incorporation: >98% by mass spectrometry
- Sequence confirmed by peptide mapping and intact mass analysis
- Purity ≥90% by SDS-PAGE

Ordering Information

Product Description	Pk. Size	Cat. No.
SILuMab Stable-Isotope Labeled Universal Monoclonal Antibody Standard	100 µg	MSQC3
Monoclonal Antibody Standard (Unlabeled)	1 mg	MSQC4

Inquire about custom packaging

Contact us to inquire about the rest of our Stable Isotope Labelled Protein offering at silu@sial.com

For more information or to place an order, contact your Sigma-Aldrich Sales Representative or visit sigma-aldrich.com/silumab

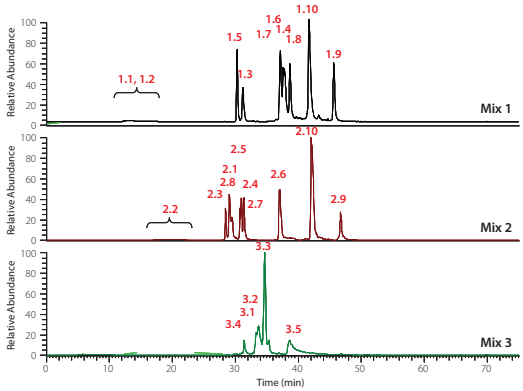
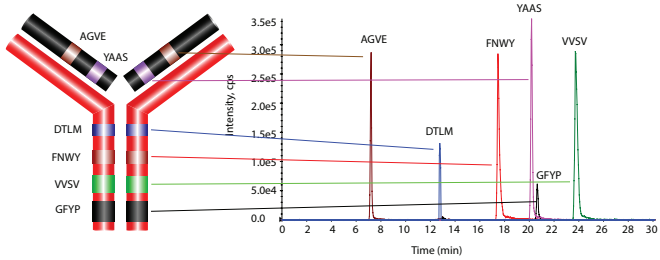


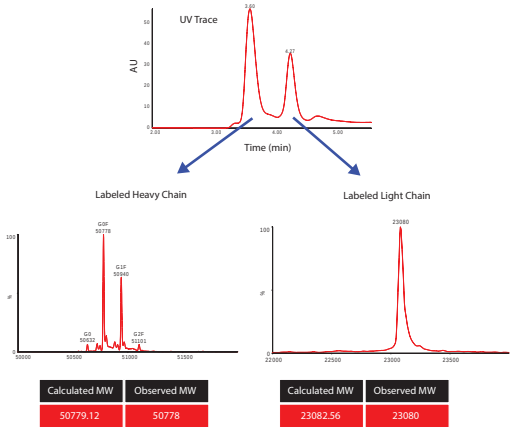
Figure 1. HPLC chromatograms of the 3 phosphopeptide mixtures using reverse phase (C18) stationary phase. The broad range of elution times as well as signal strength following electrospray (shown) or MALDI ionizations were taken into account during product design.

Universal MRM Utility



Extracted ion chromatogram (XIC) of representative peptides from the digested SILuMab. Using optimized overlap with common sequences in the Fc region of candidate antibodies, SILuMab provides universal utility, thus eliminating the need for production of candidate-specific internal standards.

Highly Characterized



SEC-UV and deconvoluted spectra resulting from intact mass analysis of the SILuMab standard. Calculations were based on the assumption that 99% label incorporation was achieved. Excellent agreement was seen between the calculated and observed molecular weight values.

Sigma-Aldrich is the Primary Source for High Quality Proteases

	Trypsin Proteomics Grade	Trypsin Singles Proteomics Grade	Trypsin Spin Column Proteomics Grade
			
Features and Benefits	• Reductively methylated to minimize autolytic activity • TPCK treated to quench chymotryptic activity • Highly purified	• All the advantages of Proteomics Grade Trypsin in a convenient, single-use 1 µg package • Eliminates repetitive pipetting	• 15 minute protein digestion • Eluted peptides are ready for MS analysis – no additional sample preparation required
Catalog Number	**T6567**	**T7575**	**TT0010**
Package Size	• 20 µg (sufficient to digest 400 µg – 2 mg of sample) • 5 × 20 µg (sufficient to digest 2–10 mg of sample)	96 × 1 µg (sufficient to digest 96 samples, 20–100 µg each)	10 columns (sufficient to digest 10 samples, 10–100 µg each)

	Protease Profiler Kit
	
Features and Benefits	• Five proven proteases for detailed characterization of proteins of interest • Perform double enzymatic digests
Catalog Number	**PP0500** (Individual components also available separately, see below)
Package Size	1 kit (sufficient to digest up to 5,900 µg of sample)
Components	• Trypsin, Proteomics Grade (**T6567**) • Asp-N Protease (**P3303**) • Lys-C Protease (**P3428**) • Glu-C Protease (**P6181**) • Arg-C Protease (**P6056**) • Enzyme Solublization Reagent • Enzyme Reaction Buffer

Other Endoproteinases

Cat. No.	Product Description
A6362	Alpha-lytic protease
A6487	Alpha-Lytic Protease M190A Mutant
P6056	Endoproteinase Arg-C from mouse submaxillary gland suitable for protein sequencing, lyophilized powder
P3303	Endoproteinase Asp-N from Pseudomonas fragi mutant strain suitable for protein sequencing, lyophilized powder
P6181	Endoproteinase Glu-C from Staphylococcus aureus V8 suitable for protein sequencing, lyophilized powder
P3428	Endoproteinase Lys-C from Lysobacter enzymogenes suitable for protein sequencing, lyophilized powder
45167	45167 Endoproteinase Pro-C, recombinant from E. coli ~3 U/mg
C6423	α-Chymotrypsin from bovine pancreas suitable for protein sequencing, salt-free, lyophilized powder
P3125	Papain from papaya latex buffered aqueous suspension, 2× Crystallized, 16-40 units/mg protein
P5380	Subtilisin from Bacillus licheniformis Type VIII, lyophilized powder, 7-15 units/mg solid

For a complete listing of proteomics grade proteases, visit
sigma.com/proteasefinder

Chromatographic Separations

SUPELCO BIOshell™ COLUMNS

Faster Peptide and Protein Reverse Phase Liquid Chromatography

BIOshell columns are the most recent innovation in Fused-Core® particle technology: high efficiency reversed-phase columns for protein and peptide separations. BIOshell columns can be operated in HPLC or UHPLC instrumentation equipped with a mass spectrometer or any other detector.

Features and Benefits

- The efficiency of core-shell particles is about 40% higher than that of fully porous particles of the same size
- Dialkyl silane reagents provide extra bonded phase stability
- High operating temperatures increase throughput and improve peak shape and efficiency of strongly hydrophobic peptides and proteins
- Each column type was tested up to 600 bar pressure to allow operation at high flow rate
- Narrow particle size distribution allow the use of 2 micron porosity frits, even for 2.7 micron particles
- BIOshell Fused-Core columns are rugged, robust and reliable

Featured Products

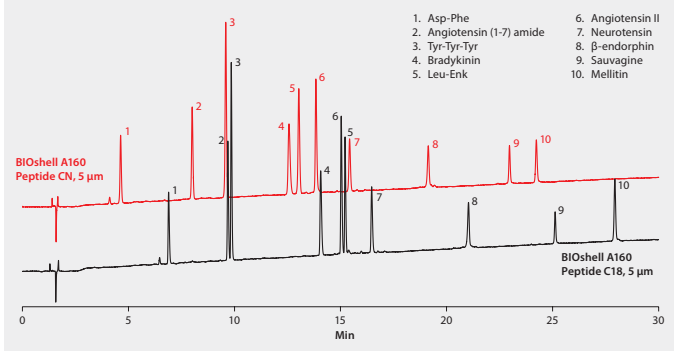
Pore Size	Particle Size	I.D. (mm)	L (cm)	C4	C18	CN
BIOshell Fused-Core Peptide and Protein Columns						
400 Å	3.4 µm	2.1	5	66824-U	—	—
400 Å	3.4 µm	2.1	10	66825-U	—	—
400 Å	3.4 µm	2.1	15	66826-U	—	—
400 Å	3.4 µm	4.6	5	66827-U	—	—
400 Å	3.4 µm	4.6	10	66828-U	—	—
400 Å	3.4 µm	4.6	15	66829-U	—	—
160 Å	2.7 µm	2.1	3	—	66901-U	66965-U
160 Å	2.7 µm	2.1	5	—	66902-U	66966-U
160 Å	2.7 µm	2.1	7.5	—	66903-U	66967-U
160 Å	2.7 µm	2.1	10	—	66904-U	66968-U
160 Å	2.7 µm	2.1	15	—	66905-U	66969-U
160 Å	2.7 µm	3.0	3	—	66906-U	66970-U
160 Å	2.7 µm	3.0	5	—	66907-U	66971-U
160 Å	2.7 µm	3.0	10	—	66908-U	66972-U
160 Å	2.7 µm	3.0	15	—	66909-U	66973-U
160 Å	2.7 µm	4.6	5	—	66913-U	66974-U
160 Å	2.7 µm	4.6	10	—	66915-U	66975-U
160 Å	2.7 µm	4.6	15	—	66917-U	66976-U
160 Å	5 µm	2.1	3	—	67001-U	67061-U
160 Å	5 µm	2.1	5	—	67002-U	67062-U
160 Å	5 µm	2.1	7.5	—	67003-U	67063-U
160 Å	5 µm	2.1	10	—	67004-U	67064-U
160 Å	5 µm	2.1	15	—	67006-U	67065-U
160 Å	5 µm	3.0	3	—	67007-U	67066-U
160 Å	5 µm	3.0	5	—	67008-U	67067-U
160 Å	5 µm	3.0	10	—	67011-U	67068-U
160 Å	5 µm	3.0	15	—	67012-U	67069-U
160 Å	5 µm	4.6	5	—	67013-U	67071-U
160 Å	5 µm	4.6	10	—	67014-U	67080-U
160 Å	5 µm	4.6	15	—	67015-U	67081-U
BIOshell Fused-Core Peptide and Protein Guard Columns						
400 Å	3.4 µm	2.1	1	66830-U	—	—
400 Å	3.4 µm	4.6	1	66831-U	—	—
160 Å	2.7 µm	2.1	1	—	66918-U	66977-U
160 Å	2.7 µm	3.0	1	—	66919-U	66978-U
160 Å	2.7 µm	4.6	1	—	66921-U	66979-U
160 Å	5 µm	2.1	1	—	67016-U	67082-U
160 Å	5 µm	3.0	1	—	67017-U	67083-U
160 Å	5 µm	4.6	1	—	67018-U	67084-U

Related Product

Description	Cat. No.
BIOshell Guard Cartridge Holder	66841-U

Rapid, Efficient HPLC Analysis of Peptides on BIOshell™ A160 Peptide C18 and Peptide CN Columns

column: BIOshell A160 Peptide C18 (67015-U) or BIOshell A160 Peptide CN (67081-U), both 15 cm x 4.6 mm I.D., 5 µm particles
mobile phase: [A] water/0.1% TFA [B] acetonitrile/0.1% TFA
gradient: 5-50% B in 30 minutes
flow rate: 1.0 mL/min
column temp.: 40 °C
detector: UV, 215 nm
injection: 10 µL of each compound, 0.01 mg/mL in water/0.1% TFA



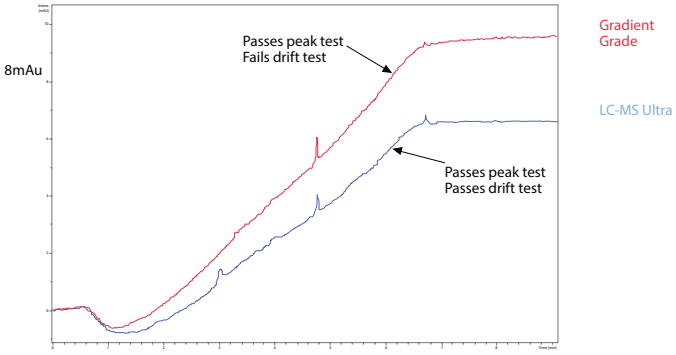
LC-MS Ultra CHROMASOLV® Grade Solvents

SOLVENTS OF THE HIGHEST PURITY PACKAGED IN SUPERIOR MATERIALS TO ENSURE THE QUALITY OF YOUR LC-MS RESULTS

- High purity for extremely low detection limits under any detection mode together with UHPLC
- Excellent Lot-to-lot reproducibility
- Suitability tested by UHPLC-MS and UHPLC-MS TOF
- Microfiltered (0.1µm)
- Packaged in clear borosilicate glass containers

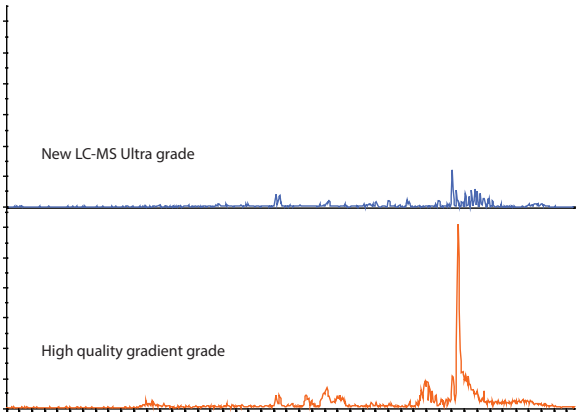
UHPLC Application Test

– Low UV drift for LC-MS ultra solvent (specification limit is 8 mAu)

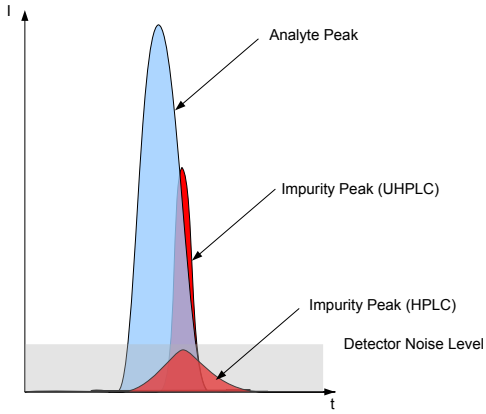


Impurity Profiling in ESI (+) Mode

– Clean and insignificant impurity level



The major m/z impurity of LC-MS Ultra is much lower than that for a high quality gradient grade solvent



Impurities which are not detected by HPLC may be detected by UHPLC

High-purity solvents and additives support UHPLC performance

New LC-MS Ultra CHROMASOLV solvents and LC-MS Ultra eluent additives

Cat. No.	Brand	Name	Description	Package Size
14261	Fluka	Acetonitrile	LC-MS Ultra CHROMASOLV, ≥99.9%, gradient tested for UHPLC, UV & MS	1 L, 2 L
14262	Fluka	Methanol	LC-MS Ultra CHROMASOLV, ≥99.9%, gradient tested for UHPLC, UV & MS	1 L, 2 L
14263	Fluka	Water	LC-MS Ultra CHROMASOLV, gradient tested for UHPLC	1 L, 2 L
14264	Fluka	Trifluoroacetic acid	LC-MS Ultra eluent additive, ≥ 99.0% suitable for UHPLC-MS	1 mL, 2 mL
14265	Fluka	Formic acid LC-MS	Ultra eluent additive, ≥ 98% suitable for UHPLC-MS	1 mL, 2 mL
14266	Fluka	Ammonium formate	LC-MS Ultra eluent additive, suitable for UHPLC-MS	25 g
14267	Fluka	Ammonium acetate	LC-MS Ultra eluent additive, suitable for UHPLC-MS	25 g

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Safety-related Information

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