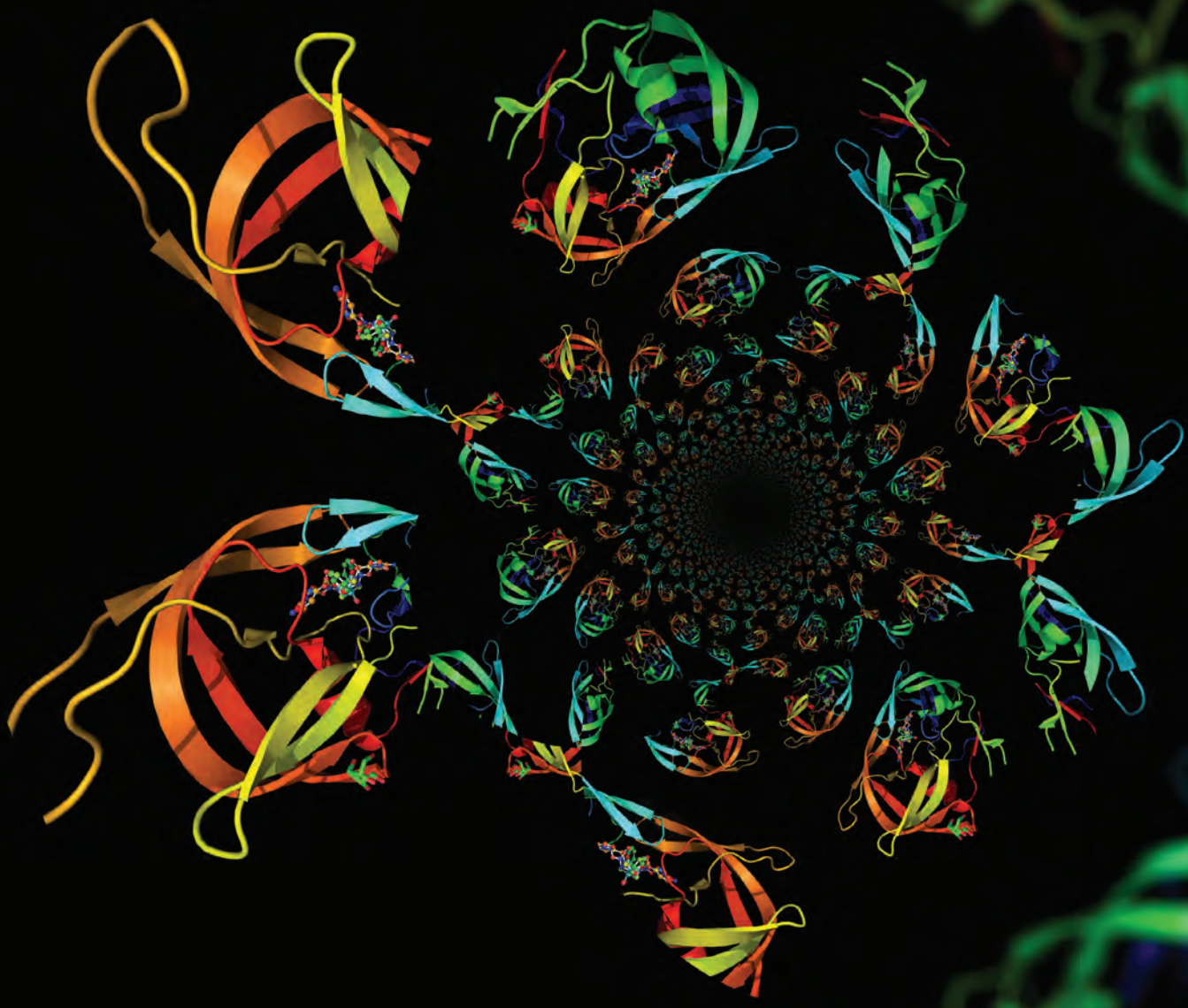
TOOLS FOR MASS SPECTROMETRY

PROTEOMICS AND METABOLOMICS



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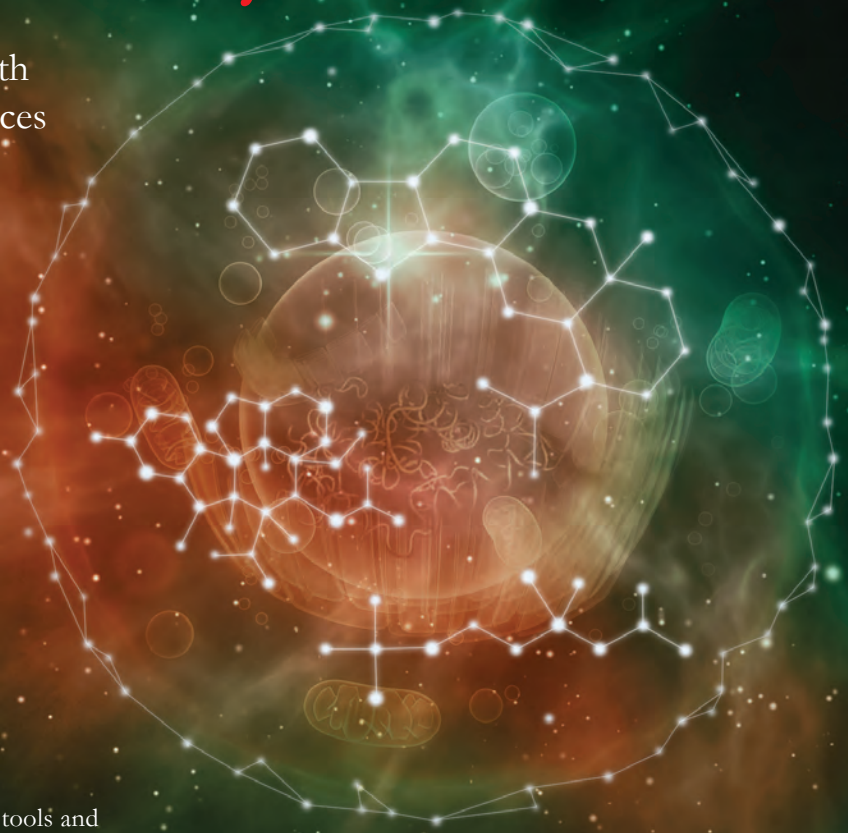
SIGMA-ALDRICH®

SIGMA Life Science Where bio begins™

Navigate toward Metabolomic discovery.

Target your metabolism research with comprehensive metabolomic resources from Sigma® Life Science.



Bionavigate.

Sigma Life Science metabolites, enzymes, separation tools and technologies help you navigate the metabolic pathways to biomarker discovery. Our comprehensive offering of unique isolated and synthetic metabolites includes the amino acid, carbohydrate, lipid and TCA Cycle metabolite libraries.

Now featuring tandem mass spectrometry data from The Scripps Center for Metabolomics METLIN Metabolite Database for several metabolites.

Find metabolites for your research needs
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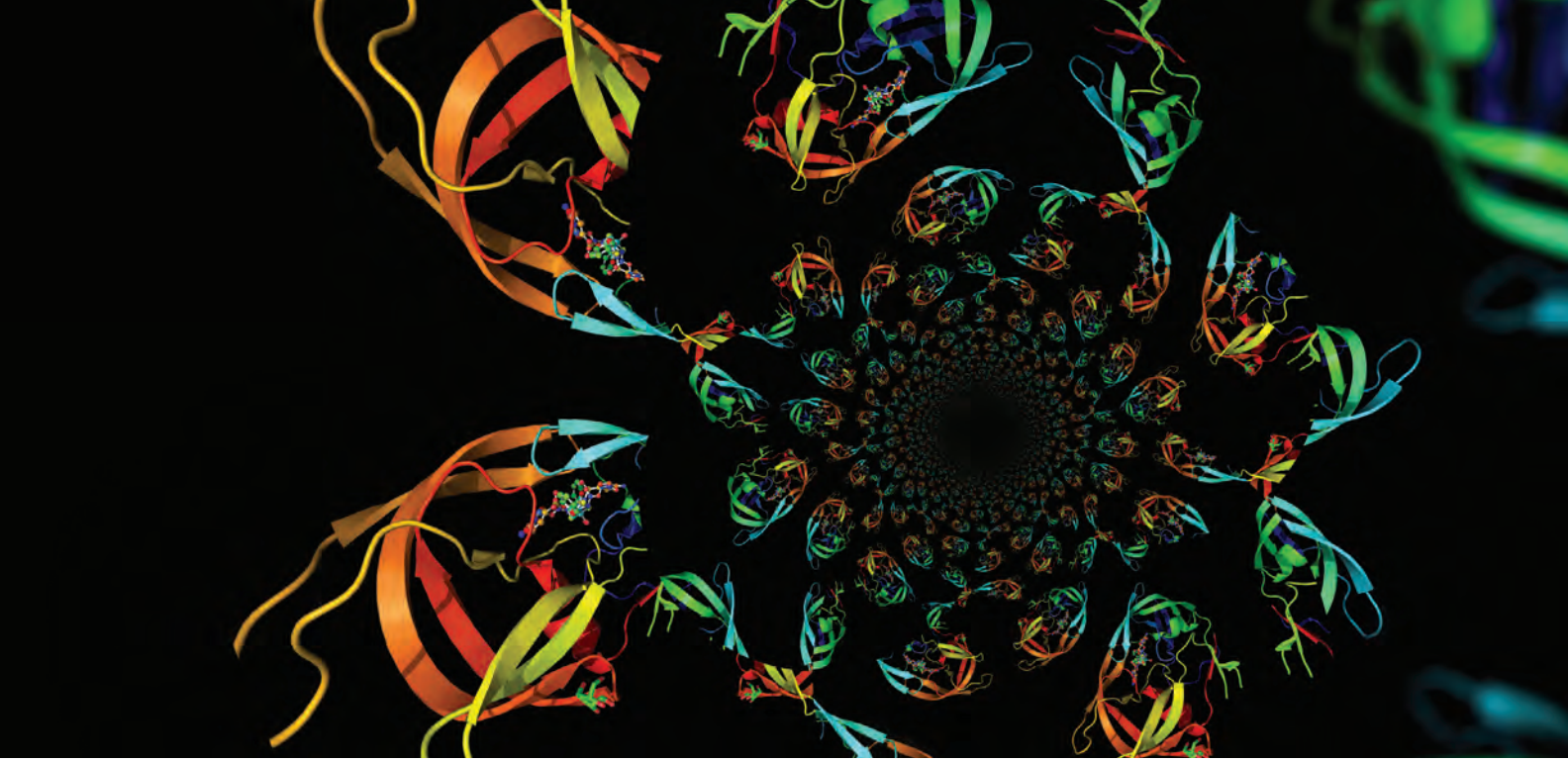

As your partner in discovery, we are here to provide you with the products and information that you need to stay on the leading edge of mass spectrometry (MS) research in proteomics and metabolomics. Our MS portfolio covers workflows from sample preparation to downstream analysis, and allows you to probe biological systems and analyze prospective biomarkers in depth. We are committed to providing you with the broadest range of advanced products for MS workflow applications, backed by unrivaled scientific knowledge, customer service and technical service.

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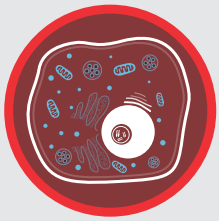
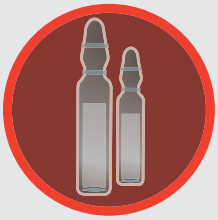
SOLUTIONS ACROSS THE ENTIRE MS WORKFLOW



SAMPLE PREPARATION

DIGESTION/LABELING



STANDARDIZATION/CALIBRATION

CHROMATOGRAPHIC SEPARATION

DETECTION & ANALYSIS

SIGMA | ALDRICH | ISOTEC | SUPELCO

PROTEOMICS TOOLS

- SILAC Metabolic Labeling Materials (Aldrich | ISOTEC)
- Seppro® Depletion Technology (Sigma)
- CelLytic™ (Sigma)
- MSSAFE™ Inhibitor Cocktail (Sigma)

- Proteases (MS Grade) (Sigma)
- SCIEX iChemistry™ Solutions

- Universal Proteomics Standards (UPS1/UPS2) (Sigma)
- MS Qual / Quant QC Mix (Sigma)
- MS RT Calibration Mix (Sigma)
- MS PhosphoMix Phosphopeptide Standards (Sigma)
- AQUA Peptides™ (Sigma)
- SigmaProt Intact Protein LC-MS Standard (Sigma)
- SILu™Mab and SILuLite Antibody Standards (Sigma)
- PEPscreen® (Sigma)

- LC/MS & UHPLC Columns (SUPELCO)
- TSKgel HPLC Columns (SUPELCO)

- ProteoMass™ MALDI-MS Calibrants (Sigma)
- MALDI Matrices (Sigma-Aldrich)

METABOLOMICS TOOLS

- ZipTip®
- HybridSPE®-Phospholipid (SUPELCO)
- Supel™-Select for SPE (SUPELCO)
- SupelMIP® (SUPELCO)

- SCIEX Amplifex™

- Stable Isotope Labeled Bioactive Compounds (Aldrich | ISOTEC)
- Mass Spectrometry Metabolite Library of Standards (Sigma)

- LC/MS & UHPLC Columns (SUPELCO)
- GC columns/Tools (SUPELCO)

- MALDI Matrices (Sigma-Aldrich)
- METLIN Metabolite Database (Sigma®)

PRODUCTS FOR METABOLIC LABELING

ISOTEC® has the Products and Materials You Need for Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC)

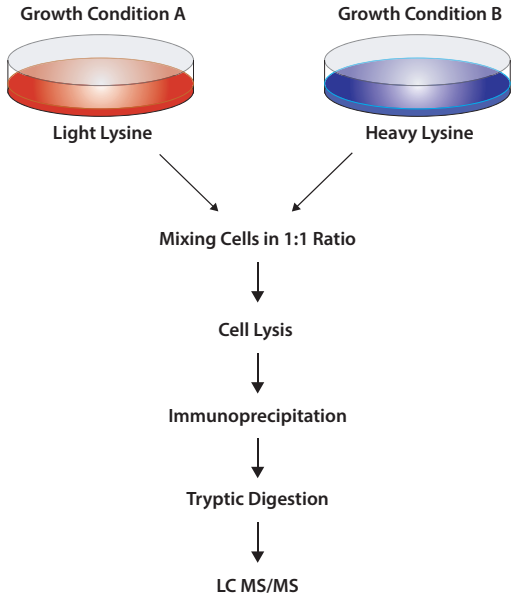
ISOTEC Stable Isotopes offers a complete line of SILAC labeling materials to facilitate your quantitative proteomics experiments.

- **99% enriched amino acids** – ^{13}C and/or ^{15}N Arginine and Lysine to improve overall quantification accuracy
- **DMEM or RPMI-1640 media** – Depleted media to gain the greatest labeling flexibility and sequence coverage
- **Dialyzed Fetal Bovine Serum (FBS)** – Maintains a 10 kDa molecular mass cutoff for a defined environment of small molecules

Isotopically Labeled Amino Acids

Cat. No.	Description
608033	L-Arginine-$^{13}C_6$, $^{15}N_4$ hydrochloride
643440	L-Arginine-$^{13}C_6$ hydrochloride
600113	L-Arginine-$^{15}N_4$ hydrochloride
608041	L-Lysine-$^{13}C_6$, $^{15}N_2$ hydrochloride
643459	L-Lysine-$^{13}C_6$ hydrochloride
608092	L-Isoleucine-$^{13}C_6$, ^{15}N
605239	L-Leucine-$^{13}C_6$
608068	L-Leucine-$^{13}C_6$,^{15}N
608106	L-Methionine-$^{13}C_5$, ^{15}N
299154	L-Methionine-*methyl*-^{13}C, d_3
300616	L-Methionine-*methyl*-d_3
749915	L-Leucine-$^{13}C_6$, ^{15}N, 2, 3, 4, 4, 5, 5, 5-d_7, 4-*methyl*-d_3
609021	L-Lysine-$^{15}N_2$ hydrochloride
643459	L-Lysine-$^{13}C_6$ hydrochloride
608041	L-Lysine-$^{13}C_6$, $^{15}N_2$ hydrochloride
749907	L-Lysine-$^{13}C_6$, $^{15}N_2$, 2, 3, 3, 4, 4, 5, 5, 6, 6-d_9 monohydrochloride
609242	L-Methionine-^{15}N
749893	L-Methionine-$^{13}C_5$, ^{15}N, 2, 3, 3, 4, 4-d_5, *methyl*-d_3
608114	Proline-$^{13}C_5$, ^{15}N
750018	L-Arginine-$^{13}C_6$, $^{15}N_4$, 2, 3, 3, 4, 4, 5, 5-d_7 hydrochloride
749915	L-Leucine-$^{13}C_6$, ^{15}N, 2, 3, 3, 4, 5, 5, 5-d_7-4-*methyl*-d_3
609021	L-Lysine-$^{15}N_2$ hydrochloride
643459	L-Lysine-$^{13}C_6$ hydrochloride
608041	L-Lysine-$^{13}C_6$, $^{15}N_2$ hydrochloride
749907	L-Lysine-$^{13}C_6$, $^{15}N_2$, 2, 3, 3, 4, 4, 5, 5, 6, 6-d_9 monohydrochloride
609242	L-Methionine-^{15}N
749893	L-Methionine-$^{13}C_5$, ^{15}N, 2, 3, 3, 4, 4-d_5-*methyl*-d_3
608017	L-Phenylalanine-$^{13}C_9$,^{15}N
607770	L-Threonine-$^{13}C_5$,^{15}N
492868	L-Tyrosine-$^{13}C_9$
600148	L-Valine-$^{13}C_5$ ^{15}N

SILAC Workflow



SILAC Depleted Media and Dialyzed Serum

Cat. No.	Description
F0392-100ML F0392-500ML	Fetal Bovine Serum – Dialyzed by ultrafiltration against 0.15 M NaCl, USA origin, sterile-filtered, cell culture tested
D9443-500ML	Dulbecco's Modified Eagle's Medium – Low glucose, with 1000 mg/L of L-glucose, L-glutamine, and sodium bicarbonate. Without arginine, leucine, lysine, sodium pyruvate, and phenol red. Liquid, sterile-filtered, cell culture tested.
R1780-500ML	RPMI-1640 Medium with L-glutamine and sodium bicarbonate. Without arginine, leucine, lysine, and phenol red. Liquid, sterile-filtered, cell culture tested.

For a complete list of SILAC products, visit
sigma-aldrich.com/silac

Protected Amino Acids

Protected amino acids provide researchers with the ability to create their own unique peptide standards for MS-based applications. Using a synthetic peptide standard enables researchers to quantify and study the characteristics of proteins across a multitude of applications, including disease biomarkers.[1]

ISOTEC Stable Isotopes offers a wide selection of both Fmoc and t-Boc protected labeled amino acids for the synthesis of peptide standards.

Cat. No.	Description
489905	Fmoc-Ala-OH-^{15}N
605131	Fmoc-Ala-OH-$^{13}C_3$
667064	Fmoc-Ala-OH, $^{13}C_3$, ^{15}N
485888	Fmoc-Ala-OH-3, 3, 3-d3
653659	Fmoc-Arg(Pbf)-OH-$^{13}C_6$, $^{15}N_4$
668753	Fmoc-Asn(Trt)-OH-$^{13}C_4$, $^{15}N_2$
683639	Fmoc-Asp(OtBu)-OH-$^{13}C_4$, ^{15}N
663956	Fmoc-Gln-(Trt)-OH-$^{13}C_5$, $^{15}N_2$
605182	Fmoc-Gly-OH-1-^{13}C
578622	Fmoc-Ile-OH-^{15}N
597228	Fmoc-Ile-OH-$^{13}C_6$, ^{15}N
485950	Fmoc-Leu-OH-^{15}N
653632	Fmoc-Lys(Boc)-OH-$^{13}C_6$, $^{15}N_2$
651443	Fmoc-Phe-OH-$^{13}C_9$,15_N
651451	Fmoc-Pro-OH-$^{13}C_5$, ^{15}N
609145	Fmoc-Ser(tBu)-OH-^{15}N
658928	Fmoc-Ser(tBu)-OH-$^{13}C_3$, ^{15}N
658162	Fmoc-Thr(tBu)-OH-^{15}N
658898	Fmoc-Tyr (t-Bu)-OH-$^{13}C_9$, ^{15}N
642886	Fmoc-Val-OH-$^{13}C_5$, ^{15}N
579890	Fmoc-Asn-OH-$^{15}N_2$
666009	Fmoc-Glu(OtBu)-OH-$^{13}C_5$, ^{15}N
489530	Fmoc-Glu(OtBu)-OH-$^{13}C_2$, ^{15}N
653640	Fmoc-Met-OH-$^{13}C_5$, ^{15}N
694274	Fmoc-Thr(tBu)-OH-$^{13}C_4$, ^{15}N
489913	Boc-Ala-OH-^{15}N
603449	Boc-Ala-OH-2-^{13}C, ^{15}N
596188	Boc-Ala-OH-2-^{13}C, ^{15}N
588407	Boc-Glu-OBzl-$^{13}C_5$, ^{15}N
587699	Boc-Glu-OH-^{15}N
489557	Boc-Gly-OH-2-^{13}C, ^{15}N
609161	Boc-Lys(Z)-OH-α-^{15}N
591092	Boc-Tyr-OH-^{15}N
604976	Boc-Val-OH-1-^{13}C

Reference

1. Ciccimaro, E. and Blair, I.A. Stable-isotope dilution LC-MS for quantitative biomarker analysis. *Bioanalysis*, **2(2),** 311-341(2010).

For a complete listing, visit
sigma-aldrich.com/protectedaa

Enzymatic Labeling with Water-^{18}O

Trypsin-mediated incorporation of ^{18}O remains an important technique for the exogenous isotopic enrichment of proteins for quantitative proteomics. Two ^{18}O atoms are introduced into the carboxy terminus of protein fragments during proteolytic cleavage in heavy water. The quantification of protein samples is achieved by combining natural abundance ^{16}O fragments and ^{18}O labeled peptide fragments then subjecting the mixture to mass spectrometric analysis to determine the ratio of $^{16}O/^{18}O$ labeled peak pairs.[1-2] ^{18}O enzymatic labeling has gained popularity in the examination of differential protein expression in pharmacological and cancer research.[3-4]

Cat. No.	Description	Isotopic Purity
487090	Water-^{18}O	99 atom % ^{18}O
329878	Water-^{18}O	97 atom % ^{18}O

References

1. Johnson, K.L., and Muddiman, D.C., (2004) A method for calculating $^{16}O/^{18}O$ peptide ion ratios for the relative quantification of proteomes. *J. Am. Soc. Mass Spectrom.*, **15**, 437-445.
2. Fenselau, C. (2007) A review of quantitative methods for proteomic studies. *J. Chromatography B*, **855**, 14-20.
3. Wang, J., et al., (2007) Integration of ^{18}O labeling and solution isoelectric focusing in a shotgun analysis of mitochondrial proteins. *J. Proteome Res.*, **6**, 4601-4607.
4. Lane, C.S., et al., (2007) Comparative cytochrome P450 proteomics in the livers of immunodeficient mice using ^{18}O stable isotope labeling. *Mol Cell Proteomics.*, **6**, 953-962.

Chemical Labeling

Stable Isotope coded labels enable researchers to perform NMR and mass spectrometric-based proteomics studies in the absence of metabolic labeling. Isotope labeling occurs by site-specific incorporation of labeled tags at cysteine residues or the general labeling of amines and carboxylic groups in protein samples. These techniques are particularly useful for applications where metabolic labeling is impractical or undesirable.

ISOTEC® offers a wide variety of labeled reagents that can be used as chemical labels in peptide and protein studies.

Cat. No.	Description
531227	Acetaldehyde-$^{13}C_2$
487821	Acetic anhydride-$^{13}C_4$
633259	N-Acetoxy-d_3-succinimide
607517	Acetyl chloride-1-^{13}C
485681	Benzoic acid-(phenyl-$^{13}C_6$)
366048	Benzyl chloride-d_5
283835	Bromoacetic acid-$^{13}C_2$
488232	Bromobenzene-$^{13}C_6$
488534	Chlorobenzene-$^{13}C_6$
485500	Dimethyl sulfate-$^{13}C_2$
457833	Ethylene-d_4 oxide
596388	Formaldehyde-$^{13}C,d_2$ solution 20 wt. % in D_2O
607312	Guanidine-^{13}C, $^{15}N_3$ hydrochloride
592668	Iodoacetamide-^{15}N
277185	Iodomethane-^{13}C
640492	2-Nitrobenzenesulfenylchloride-$^{13}C_6$
615692	Propionic anhydride-d_{10}
578517	Succinic anhydride-$^{13}C_4$
299359	Urea-^{13}C

For a complete list, visit **sigma-aldrich.com/chemtag**

SEPPRO®

Simplify Your Sample

- Depletion from a variety of sample types
- Spin-Column, LC, and 96-Well Plate
- Specific capture of target proteins
- Complete solution, reagents, and labware included

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 platform, incorporating Supermix technology, represents the most complete human protein depletion system available, removing 14 of the most abundant proteins from human serum or plasma, as well as other high and medium abundance proteins. Additional products are available for the depletion of mouse and rat samples, as well as the industry's only depletion system for the removal of Rubisco from plant samples.

The new HT Seppro® IgY14 Plate is specifically designed for high throughput removal of 14 highly abundant proteins from human serum or plasma. This product is based on the same avian antibodies (IgY) immobilized on a resin and incorporated into a 96-well plate. plate.incorporated into a 96 well plate.

Human Depletion Media

Cat. No.	Format	Size	Sample Capacity	Proteins Depleted
SEP010	Seppro IgY 14 Spin Columns	500 µL resin bed volume	15–20 µL (pooled normal human plasma or serum)	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)
SEP020	Seppro IgY14 LC2	6.4 × 63.0 mm (2 ml resin bed volume)	40–50 µL (pooled normal human plasma or serum)	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)
SEP030	Seppro IgY14 LC5	12.7 × 39.5 mm (5 ml resin bed volume)	100 µL (pooled normal human plasma or serum)	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)
SEP040	Seppro IgY14 LC10	12.7 × 79.0 mm (10 ml resin bed volume)	200–250 µL (pooled normal human plasma or serum)	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)
PROTIA	ProteoPrep Immunoaffinity Albumin and IgG Depletion Kit	350 µL resin bed volume	25–50 µL (pooled normal human plasma or serum)	Albumin and IgG

Isolate and identify your target protein at
sigma-aldrich.com/seppro

Human Supermix Media

Cat. No.	Format	Size	Sample Capacity	Proteins Depleted
SEP050	Seppro Human Supermix LC2	6.4 × 63 mm (2 mL resin bed volume)	Flow Through volume from IgY14 LC5	Further partitions complex human plasma/ serum samples
SEP060	Seppro Human Supermix LC5	12.7 × 39.5 mm (5 mL resin bed volume)	Flow Through volume from IgY14 LC10	Further partitions complex human plasma/ serum samples.

Mouse Depletion Media

Cat. No.	Format	Size	Sample Capacity	Proteins Depleted
SEP110	Seppro Mouse Spin Columns	500 µL resin bed volume	15–20 µL (pooled normal mouse plasma or serum)	Mouse serum albumin, IgG, Transferrin, Fibrinogen, IgM, Haptoglobin, α_1-Antitrypsin
SEP090	Seppro Mouse LC10	12.7 × 79.0 mm (10 mL resin bed volume)	200–250 µL (pooled normal mouse plasma or serum)	Mouse serum albumin, IgG, Transferrin, Fibrinogen, IgM, Haptoglobin, α_1-Antitrypsin

Mouse Supermix Media

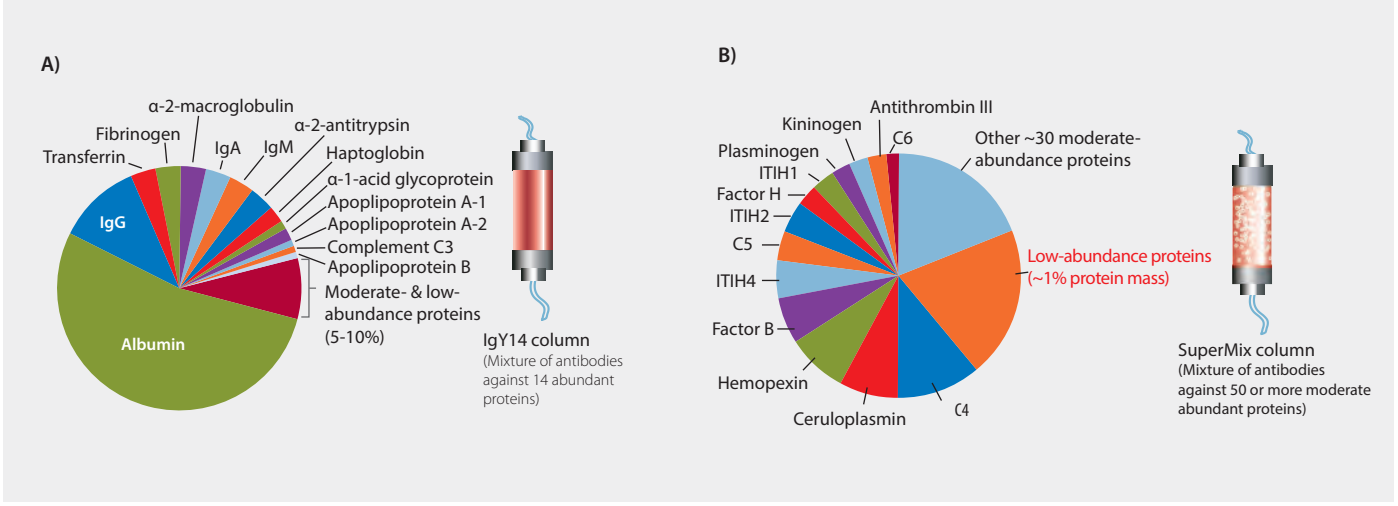
Cat. No.	Format	Size	Sample Capacity	Proteins Depleted
SEP100	Seppro Mouse Supermix LC5	12.7 × 39.5 mm (5 mL bed volume)	Flow Through volume from mouse LC10	Further partitions complex mouse plasma/ serum samples.

Rat Depletion Media

Cat. No.	Format	Size	Sample Capacity	Proteins Depleted
SEP130	Seppro Rat Spin Columns	500 µL resin bed volume	15–20 µL (pooled normal rat plasma or serum)	Rat serum albumin, IgG, Fibrinogen, Transferrin, IgM, Haptoglobin, α_1-Antitrypsin
SEP120	Seppro Rat LC10	12.7 × 79.0 mm (10 mL resin bed volume)	200–250 µL (pooled normal rat plasma or serum)	Rat serum albumin, IgG, Fibrinogen, Transferrin, IgM, Haptoglobin, α_1-Antitrypsin

Rubisco Depletion Media

Cat. No.	Format	Size	Sample Capacity	Proteins Depleted
SEP070	Seppro Rubisco Spin Columns	500 µL resin bed volume	15–20 µL (pooled normal plant sample)	RuBisCO (Ribulose-1, 5-bisphosphate carboxylase/oxygenase)
SEP080	Seppro Rubisco LC2	6.4 x 63.0 mm (2 mL resin bed volume)	40–50 µL (pooled normal plant sample)	RuBisCO (Ribulose-1, 5-bisphosphate carboxylase/oxygenase)



PROTEIN EXTRACTION

RECOMBINANT PROTEIN EXTRACTION

CelLytic™ Lysis Reagent

Cell lysis and high-yield protein extraction are important for quality recombinant protein purification. CelLytic formulations for bacterial, mammalian, yeast, or plant cell lysis result in higher protein yields than traditional physical disruption methods. CelLytic formulations are compatible with most affinity purification techniques, preserving protein function for downstream analysis.

Cat. No.	Product Description	Pack Size/Quantity
Bacterial Cell Lysis		
C8740	CelLytic B Cell Lysis Reagent, for bacterial cell lysis, 10 × concentrate	10 mL, 50 mL, 100 mL
B7310	CelLytic B Cell Lysis Reagent, for bacterial cell lysis, 10 × concentrate	50 mL, 250 mL
B7435	CelLytic B Cell Lysis Reagent, for bacterial cell lysis, standard strength	50 mL, 500 mL
CB0050	CelLytic B Plus Kit, for bacterial lysis	1 kit
C1990	CelLytic Express, for in-culture bacterial cell lysis	25 mL, 10 x 25 mL, 500 mL, 6 x 500 mL
C5491	CelLytic Express, 1 mL tablets, for direct lysis of bacterial cultures and for use in the HIS-Select® iLAP® column	25 each, 100 each
C5236	CelLytic Ib Inclusion Body Solubilization Reagent	25 mL, 100 mL
Mammalian Cell Lysis		
C2978	CelLytic M, Cell Lysis Reagent, suitable for mammalian cell lysis and protein solubilization	10 mL, 40 mL, 50 mL, 60 mL, 250 mL, 1L
CE0050	CelLytic MEM Protein Extraction Kit, for membrane proteins	1 kit
C3228	CelLytic MT Cell Lysis Reagent, for mammalian tissues	50 mL, 500 mL
NXTRACT	CelLytic NuCLEAR™ Extraction Kit, for mammalian tissue or cultured cells	1 kit
R0278	RIPA Buffer, for adherent and suspension cultured mammalian cells	50 mL, 500 mL
Plant Cell Lysis		
C2360	CelLytic P Cell Lysis Reagent, for plant lysis	50 mL, 250 mL
CELLYTPN1	CelLytic PN Isolation/Extraction Kit, for Plant Leaves	1 kit
Yeast Cell Lysis		
C4482	CelLytic Y Cell Lysis Reagent, for Yeast Cells	50 mL, 250 mL, 500 mL
CYP1	CelLytic Y Plus Kit, for Enzymatic Yeast Cell Lysis	1 kit

NATIVE PROTEIN EXTRACTION

ProteoPrep® Lysis Reagent

ProteoPrep kits and individual extraction reagents allow for selective or total protein extracts from cellular samples. The protein extracts obtained with each component can be optimized to meet your individual needs. The reducing and alkylating reagents produce protein samples that exhibit improved focusing and decreased streaking in 2D gels. Enough of each component is provided to process multiple protein samples. For researchers who have optimized an extraction protocol using one chaotropic extraction reagent, each kit reagent is also available as an individual product.

Cat. No.	Product Description	Pack Size/Quantity
PROTTOT	ProteoPrep Total Extraction Sample Kit	1 kit
PROTTWO	ProteoPrep Universal Extraction Kit	1 kit
PROTMEM	ProteoPrep Membrane Extraction Kit	1 kit
PROTDT	ProteoPrep Detergent Sample Kit	1 kit
PROTPR	ProteoPrep Protein Precipitation Kit	1 kit
PROTRA	ProteoPrep Reduction and Alkylation Kit	1 kit

ORGANELLE ISOLATION

Kits and Reagents for Organelle Isolation

For enrichment of functional mitochondria, chloroplasts, nuclei, golgi, and other important organelles.

To view all products in this range, visit
sigma-aldrich.com/organelle

Cat. No.	Product Description	Pack Size/Quantity
MITOISO1	Mitochondria Isolation Kit, sufficient for 10–20 g (animal tissue), sufficient for 50 assays (2 mL), isolation of enriched mitochondrial fraction from animal tissues	1 kit
MITOISO2	Mitochondria Isolation Kit, sufficient for 50 applications (2–5 x 10^7 cells), isolation of enriched mitochondrial fraction from cells	1 kit
NUC101	Nuclei Isolation Kit: Nuclei EZ Prep, sufficient for 25 nuclei preparations (~1-10 x 10^7 cells/preparation)	1 kit
NUC201	Nuclei Isolation Kit: Nuclei PURE Prep, sufficient for 15 nuclei preparations (~1–10 x 10^7 cells or 1 g of tissue per preparation)	1 kit
MITOISO3	Yeast Mitochondria Isolation Kit, sufficient for 40 applications (using 20 OD culture preparations), isolation of an enriched mitochondrial fraction of yeast cells	1 kit

For more information on Protein Extraction, visit
sigma-aldrich.com/extraction

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

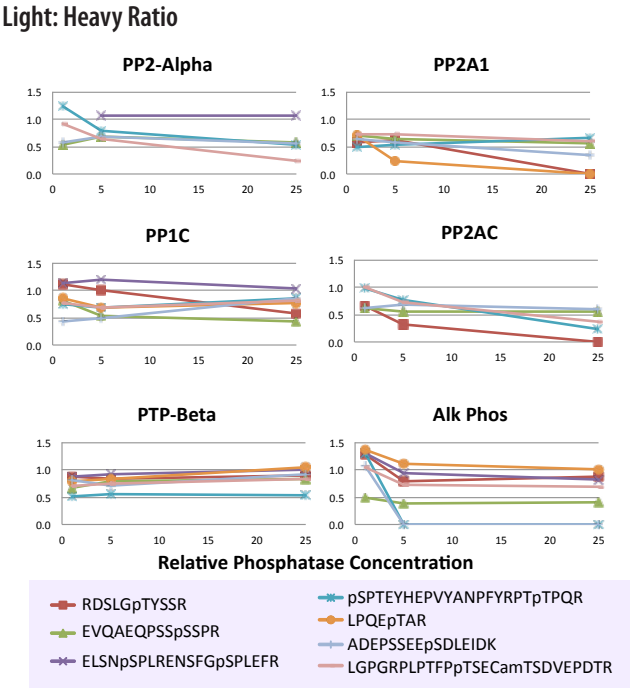


Figure 1. Demonstration of phosphatase specificity and inhibition with the Sigma PhosphoMix phosphopeptide standard against different phosphatases. A decrease in the light:heavy ratio of the phosphorylated peptide at higher phosphatase concentrations indicates that the phosphopeptide is a substrate for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

MSSAFE Inhibitor Components

Protease Inhibitor	Specific Inhibitory Target of Component
Bestatin hydrochloride	Aminopeptidases (e.g. leucine aminopeptidase, alanyl aminopeptidase)
Leupeptin	Serine and 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
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

For more information, visit
sigma-aldrich.com/mssafe

TRYPSIN AND PROTEASE SELECTION GUIDE

	Trypsin Proteomics Grade	Trypsin Singles Proteomics Grade	Trypsin Spin Column Proteomics Grade	Trypsin Profile In-Gel Digest Kit	Protease Profiler Kit
					
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	• Fast, efficient, complete in-gel tryptic digestion from PAGE to MALDI • Digested proteins are ready for MALDI-MS – no additional sample preparation required	• Five proven proteases for detailed characterization of proteins of interest • Perform double enzymatic digests
Cat. No.	T6567	T7575	TT0010	PP0100	**PP0500** (Individual components also available separately, see below)
Package Size	• 20 µg (sufficient to digest 400 µg – 2 mg of sample) • 5 × 20 µg (sufficient to digest 2–10 mg of sample) • 1 mg (sufficient to digest 20-200 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)	1 kit (sufficient for up to 100 excised protein spots)	1 kit (sufficient to digest up to 5,900 µg of sample)
Components	Trypsin, Proteomics Grade	• Trypsin, Proteomics Grade (**T6567**) • Trypsin Solublization Buffer • Enzyme Reaction Buffer • Biotech Grade Acetonitrile	• Trypsin Spin Columns containing 75 mg of solid support in a 50% acidic glycerol suspension • Collection Tubes • Enzyme Reaction Buffer	• Trypsin, Proteomics Grade (**T6567**) • Destaining Solution • Enzyme Reaction Buffer • Biotechnology Grade Acetonitrile • Trypsin Solublization Reagent • Peptide Extraction Solution	• 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
Suggested Sample Size	20–100 µg of sample per 1 µg of trypsin	20–100 µg of sample per 1 µg Trypsin Single	10–100 µg of sample per spin column	One excised protein spot or band	• 20–100 µg of sample per 1 µg of Trypsin • 50–200 µg of sample per 1 µg of Asp-N • 20–100 µg of sample per 1 µg of Lys-C • 20–100 µg of sample per 1 µg of Glu-C • 20–100 µg of sample per 1 µg of Arg-C
Digest Time	Overnight	Overnight	15 min	Overnight	Overnight
Digest Types	Solution or In-Gel	Solution or In-Gel	Solution	In-Gel	Solution or In-Gel
Enzyme Purity	>98%	95–98%	>98%	>98%	95–98%
Chymotryptic Activity	None Detected	None Detected	None Detected	None Detected	None Detected
Downstream Applications	HPLC-MS, MALDI-MS	HPLC-MS, MALDI-MS	HPLC-MS, MALDI-MS	HPLC-MS, MALDI-MS	HPLC-MS, MALDI- MS

Additional Proteases

Protease	Cat. No.	Package Size	Cleavage Specificity
Alpha-Lytic Protease (ALP)	**A6362**	20 µg, 5 × 20 µg	C-terminal to: Thr (T) Ala (A) Ser (S) Val (V)
Alpha-Lytic Protease (ALP) W190A Mutant	**A6487**	20 µg, 5 × 20 µg	C-terminal to: Met (M) Phe (F) Leu (L)
Endoproteinase Arg-C	**P6056**	1 VL	C-terminal to: Arg (R)
Endoproteinase Asp-N	**P3303**	1 VL	N-terminal to: Asp (D) Cysteic acid
Endoproteinase Glu-C	**P6181**	50 µg	C-terminal to: Glu (E) Asp (D)
Endoproteinase Lys-C	**P3428**	1 VL	C-terminal to: Lys (L)
Endoproteinase Pro-C	**45167** **E7656**	1 mg 1 mg	C-terminal to: Pro (P)

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

ZIPTIP PIPETTE TIPS

The ZipTip is a 10 µL (P-10) pipette tip with a bed of chromatography medium fixed at its end such that there is no dead volume. It is intended for purifying and concentrating femtomoles to picomoles of protein, peptide, or oligonucleotide samples prior to analysis, providing better data quality. The sample is aspirated and dispensed through the ZipTip to bind, wash, and elute. Recovered samples are contaminant-free and eluted in 0.5-4 µL for direct transfer to a MS target or vial.

ZipTip C18 is a 10 µL pipette tip with a ~0.6 µL bed of chromatography medium fixed at its end to avoid dead volume. ZipTip Micro-C18 is a 10 µL pipette tip with a ~0.2 µL bed of chromatography medium fixed at its end such that there is no dead volume. Both are ideal for concentrating and purifying peptides, proteins or oligonucleotides in seconds prior to MS, HPLC, capillary electrophoresis, and other analytical techniques.

Cat. No.	Description	Qty.
Millipore® ZipTip® Pipette Tips		
Z720038-8EA	C18	8 ea.
Z720070-96EA	C18	96 ea.
Z720046-960EA	C18	960 ea.
Z719986-8EA	Micro-C18	8 ea.
Z720003-96EA	Micro-C18	96 ea.
Z720011-960EA	Micro-C18	960 ea.

SCIEX iCHEMISTRY™ SOLUTIONS NOW AVAILABLE FROM SIGMA®

Tagging Chemistries For Quantitative Protein Mass Spectrometry

Sigma-Aldrich and SCIEX have commited to cooperate in the global distribution of SCIEX's iChemistry™ Solutions portfolio of products. This partnership enables global access to unique MS Reagents for Quantitation across a variety of applications.

SCIEX iChemistry Solutions are MS-based tagging reagents designed to improve sensitivity, productivity, and data precision. The synergy of SCIEX with Sigma-Aldrich products allows users to dig deeper into biological systems, analyze prospective biomarkers, and deliver results.

iTRAQ® REAGENTS (ISOTOPIC TAGS FOR RELATIVE AND ABSOLUTE QUANTIFICATION)

The iTRAQ Reagents are the first set of multiplexed, amine-specific, stable isotope reagents that can label all peptides in up to eight different biological samples, enabling simultaneous identification and quantitation, both relative and absolute, while retaining important post-translational modifications (PTMs).

Benefits

- Flexible – multiplex up to 8 different biological samples in a single experiment
- Simple workflow – no sample fractionation for reduced-complexity samples, such as affinity pull-downs
- Increased protein and proteome coverage – labels all peptides, including those with PTMs

Cat. No.	Description
4352135	iTRAQ Reagents Multiplex Kit
4352160	iTRAQ Reagents Methods Development Kit
4369561	iTRAQ Reagents 3-Assay Duplex Trial Kit
4370280	iTRAQ Reagents Application Kit – Plasma
4374321	iTRAQ Reagents Application Kit – Protein
4381664	iTRAQ Reagent – Multiplex Buffer Kit
4381662 (4390811)	iTRAQ Reagent – 8Plex One Assay Kit
4381663 (4390912)	iTRAQ Reagent – 8Plex Multiplex Kit
4390733 (4393528)	iTRAQ Reagent – 8Plex 25 U bulk pack
4390731 (4393529)	iTRAQ Reagent – 8Plex 50 U bulk pack
4466096	iTRAQ Reagent 25U Kit

mTRAQ® REAGENTS (MASS DIFFERENTIAL TAGS FOR RELATIVE AND ABSOLUTE QUANTIFICATION)

The mTRAQ Reagents are amine-specific, stable isotope-labeled reagents, available in duplex or triplex format, designed for high-confidence protein and peptide biomarker verification using multiple reaction monitoring (MRM) analysis.

Benefits

- Established chemistry – >95% labeling efficiency
- High selectivity – MRM-based relative quantitation of proteins/peptides/PTMs
- Supports reproducible quantitative MRM assays in biomarker verification
- Compatible with fractionation
- Easy transition from iTRAQ reagent-based discovery to verification
- Economical compared to stable isotope-labeled synthetic peptide approaches when larger numbers of peptides need to be monitored

Cat. No.	Description
4374771	mTRAQ Reagent 10 Assay Kit (10 assays of each reagent Δ0, Δ4, and Δ8)
4381664	iTRAQ Reagent-Multiplex Buffer Kit
4427698	mTRAQ Reagent Δ4 50 Unit Pack
4427700	mTRAQ Reagent Δ8 50 Unit Pack
4440015	mTRAQ Reagent Δ0 50 Unit Pack

CLEAVABLE ICAT® REAGENTS (ISOTOPE CODED AFFINITY TAG)

Cleavable ICAT reagents are a cysteine-specific, protein-based labeling strategy designed to compare two different sample states.

Benefits

- Provides more complete protein identification and quantification data than is possible with 2-D gels
- Simplifies the peptide pool for MS analysis
- Enables analysis of larger peptides

Cat. No.	Product Description
4339035	Cleavable ICAT Reagent – Methods Development Kit
4339036	Cleavable ICAT Reagent – 10 Assay Kit
4339038	Cleavable ICAT Reagent – Bulk Kit (10 Units)
4339039	Cleavable ICAT Reagent – Bulk Kit (100 Units)

CYP450 PROTEIN ASSAY – (CYTOCHROME P450 KIT)

The CYP450 Protein Assay – Human Induction Kits use an LC/MS workflow to enable direct measurement of protein expression changes of individual CYP450 isoforms with high specificity, sensitivity, and accuracy.

These kits have been developed to employ MRM analysis to quantify the protein levels of seven key CYP450 protein isoforms for induction studies: 1A2, 2B6, 2C9, 2C19, 2E1, 3A4, and 3A5. Both four isoform (1A2, 2B6, 3A4, and 3A5) and seven isoform (1A2, 2B6, 2C9, 2C19, 2E1, 3A4, and 3A5) kits are available.

Benefits

- Allows for direct measurement of CYP450 induction at the protein level
- Specific, sensitive, and accurate – measures individual CYP450 isoforms
- Easy-to-use kits – method employs a common MRM workflow
- Gives equivalent results to traditional mRNA or activity assays

Cat. No.	Description
4445252	P450 Human Induction 100 Assay Kit
4445494	P450 Human Induction Starter Kit
4465863	CYP450 Peptide Standards Extended Panel Human Induction 100 Assay Kit
4466004	CYP450 Peptide Standards Extended Panel Human Induction Starter Kit

AMPLIFEX™ REAGENTS

The Amplifex Reagents are designed for derivatization and mass spectrometry analysis of small molecule biomarkers that are otherwise very difficult to study by MS. Amplifex treatment forms positively charged derivatives of the target molecules with strongly improved ionization efficiency and fragmentation. This greatly lowers the limits of target detection and quantitation.

- The Amplifex Diene Reagent reacts with any molecule with a cis-diene group, such as Vitamin D3, Vitamin D2, and analogs of each
- The Amplifex Keto Reagent reacts with the carbonyl groups in keto-or aldehyde-containing species, such as ketosteroids

Benefits

- Greatly enhanced sensitivity and signal strength
- Substantially reduced sample sizes and analysis times
- Derivatization protocols that are simple (one-step) and fast (< 1 hr)
- Potential to prepare internal standards and to do multiplexing

Cat. No.	Description
5037804	Amplifex Diene Reagent Kit
4465962	Amplifex Keto Reagent Kit

For more information, visit
sigma-aldrich.com/sciex

UNIVERSAL PROTEOMICS STANDARD (UPS)

Standardize Your Proteomics Research

Sigma offers the Universal Proteomics Standard and the Proteomics Dynamic Range Standard as complex, well-defined, well-characterized reference standards for mass spectrometry. Both standards contain the same 48 human proteins ranging in molecular mass from 6,000 to 83,000 Daltons. Each constituent protein has been HPLC purified and AAA quantitated prior to formulation.

UNIVERSAL PROTEOMICS STANDARD

UPS1

Developed in collaboration with the Association of Biomolecular Resource Facilities (ABRF) Proteomics Standards Research Group (sPRG), the Universal Proteomics Standard contains 48 human proteins (5 pmoles of each) ranging in molecular mass from 6,000 to 83,000 Daltons.

PROTEOMICS DYNAMIC RANGE STANDARD

UPS2

This standard is an enhancement of Sigma's original Universal Proteomics Standard (UPS1). The same complex mixture of 48 human proteins has been formulated into a dynamic range of concentration levels, ranging from 50 pmoles to 0.5 fmoles.

- Troubleshoot and optimize your analytical protocol
- Confirm system suitability before analyzing critical samples
- Normalize analytical results day-to-day or lab-to-lab
- Determine your limit of detection

Ordering Information

Cat. No.	Product Name	Package Size
UPS1	Universal Proteomics Standard Set*	1KT
UPS2	Proteomics Dynamic Range Standard Set*	1Set

* Each set contains one vial of Standard and one vial (20 µg) of Proteomics Grade Trypsin.

Criteria Used to Develop and Produce the Universal Proteomics Standards Line of Products

Criteria	Verified By
Proteins	More than 175 proteins were screened by SDS-PAGE and LCMS to be considered suitable for use in the standard
Minimal PTMs	LCMS of the intact proteins to verify homogeneity of the protein population
Diversity	Proteins are of wide-ranging molecular masses, hydrophobicities, isoelectric points, etc.
High Purity	Proteins are purified to be single-banded by SDS-PAGE and then further purified by HPLC
Accurate Quantitation	Amino Acid Analysis in triplicate

To learn more, visit
sigma-aldrich.com/ups

UniProt Accession Number	UniProt Protein Name [Synonyxm]	UPS1 Amount (fmol)	UPS2 Amount (fmol)
P00915	Carbonic anhydrase 1	5,000	50,000
P00918	Carbonic anhydrase 2	5,000	50,000
P01031	Complement C5[Complement C5a]	5,000	50,000
P69905	Hemoglobin alpha chain	5,000	50,000
P68871	Hemoglobin beta chain	5,000	50,000
P41159	Leptin	5,000	50,000
P02768	Serum Albumin	5,000	50,000
P62988	Ubiquitin	5,000	50,000
P04040	Catalase	5,000	5,000
P00167	Cytochrome b_5	5,000	5,000
P01133	Epidermal Growth Factor	5,000	5,000
P02144	Myoglobin C	5,000	5,000
P15559	NAD(P)H dehydrogenase [quinone] 1 [DT Diaphorase] C	5,000	5,000
P62937	Peptidyl-prolyl cis-trans isomerase A [Cyclophilin A]	5,000	5,000
Q06830	Peroxiredoxin 1	5,000	5,000
P63165	Small ubiquitin-related modifier 1 [SUMO-1]	5,000	5,000
P00709	Alpha-lactalbumin	5,000	500
P06732	Creatine kinase M-type [CK-MM]	5,000	500
P12081	Histidyl-tRNA synthetase [Jo-1]	5,000	500
P61626	Lysozyme C	5,000	500
Q15843	Neddylin [Nedd8]	5,000	500
P02753	Retinol-binding protein	5,000	500
P16083	Ribosyldihydronicotinamide dehydrogenase [quinone] [Quinone oxidoreductase 2] [NQO2]	5,000	500
P63279	SUMO-conjugating enzyme UbcH9	5,000	500
P01008	Antithrombin-III	5,000	50
P61769	Beta-2-microglobulin	5,000	50
P55957	BH3 Interacting domain death agonist [BID]	5,000	50
O76070	Gamma-synuclein	5,000	50
P08263	Glutathione S-transferase A1 [GST A1-1]	5,000	50
P01344	Insulin-like growth factor II	5,000	50
P01127	Platelet-derived growth factor B chain	5,000	50
P10599	Thioredoxin	5,000	50
P01112	GTPase HRas	5,000	5
P99999	Gelsolin	5,000	5
P06396	Glutathione S-transferase P [GST]	5,000	5
P09211	GTPase HRas [Ras protein]	5,000	5
P01579	Interferon gamma (IFN-gamma)	5,000	5
P02787	Serotransferrin [Apotransferrin]	5,000	5
O00762	Ubiquitin-conjugating enzyme E2 C [UbcH10]	5,000	5
P51965	Ubiquitin-conjugating enzyme E2 E1 [UbcH6]	5,000	5
P08758	Annexin A 5	5,000	0.5
P02741	C-reactive protein	5,000	0.5
P05413	Fatty acid-binding protein	5,000	0.5
P10145	Interleukin-8	5,000	0.5
P02788	Lactotransferrin	5,000	0.5
P10636	Microtubule-associated protein tau [Tau protein]	5,000	0.5
P00441	Superoxide dismutase [Cu-Zn]	5,000	0.5
P01375	Tumor necrosis factor / Tumor necrosis factor, soluble form	5,000	0.5

MSRT1 – MS RETENTION TIME CALIBRATION MIX

Calibrate LC-MS the Right Way

The MS RT Calibration Mix (**Cat. No. MSRT1**) is an injection-ready mixture of 14 stable isotope-labeled peptides that is designed to assess LC-MS platform performance. MSRT1 enables users to translate retention times between platforms. These peptides span the normal elution profile of complex proteomic samples, with a readily visualized and well-separated series of peptide peaks.

Application

MSRT1 allows you to assess such characteristics as:

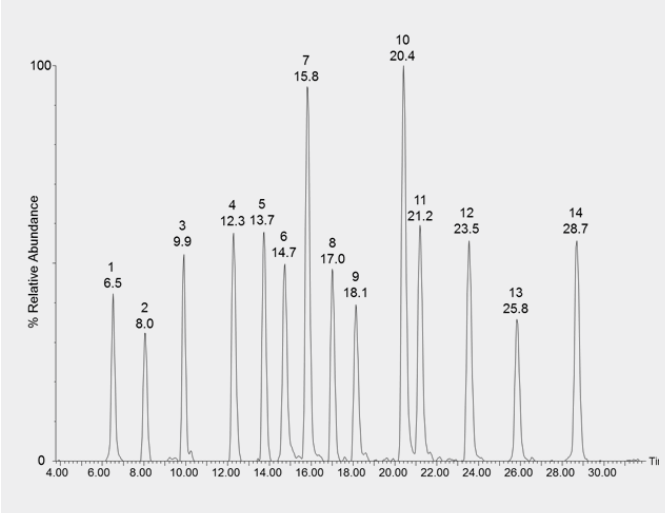
- LC resolution
- Peptide elution profile
- Retention time translation

Features and Benefits

- Well-separated series of peptide peaks in LC-MS analysis
- Easily visualized peaks of comparable intensity
- Injection-ready to save on sample preparation time

Peptide No.	Peptide Sequence (#)	Monoisotopic MW	Retention Factor
1	RGDSPASSP[K]	1008.5080	0.0
2	GLV[K]	423.2937	3.1
3	LGGNETQV[R]	982.5071	13.9
4	AEFAEVS[K]	887.4480	22.7
5	SGFSSVSVS[R]	1021.5068	30.3
6	ADEGISF[R]	903.4325	32.8
7	DISLSDY[K]	947.4691	39.0
8	LVNEVTEFA[K]	1156.6219	45.7
9	DQGGELLSL[R]	1096.5752	49.0
10	GLFIIDD[K]	927.5157	58.9
11	LGEYGFQNA[L]	1117.5517	63.1
12	YWGVASFLQ[K]	1205.6324	75.2
13	TDELFQIEGLKEELAYL[R]	2176.1291	86.7
14	AVQQPDGLAVLGIFL[K]	1675.9752	100.0

(#) Amino acid in [brackets] denotes site of heavy label incorporation.



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. BIOshell A160 Peptide ES C18 column (**Cat. No. 67099-U**) at 90 µL/min, using a linear organic gradient modified with 0.1% formic acid.

For more information, visit
sigma-aldrich.com/msrt

MSRT2 – SIGMAPROT INTACT PROTEIN LC-MS STANDARD FROM SIGMA® LIFE SCIENCE

Proper Protein LC-MS Performance Verification from the Top Down

The SigmaProt Intact Protein LC-MS Standard (Cat. No. MSRT2) is an injection-ready mixture of 9 proteins that is designed to act as an LC-MS platform standard and to assess LC-MS platform performance. These 9 proteins cover a broad range of hydrophobicity and were chosen for ease of electrospray ionization (ESI). MSRT2 can be used as a performance standard for intact protein analysis, such as in top-down proteomics.

Application

MSRT2 allows you to assess such properties as:

- LC resolution
- Protein elution profile
- Electrospray source conditions
- Deconvolution parameters
- Comparison of LC gradients and columns
- Monitor column and system changes

Features and Benefits

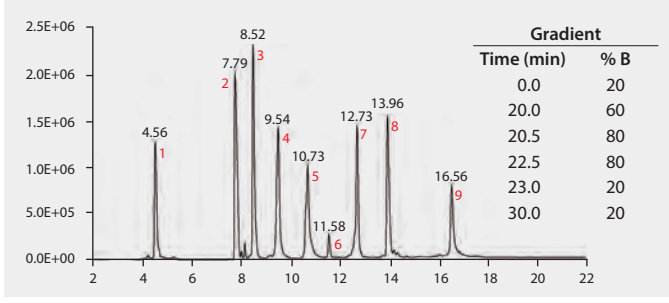
- Well-separated and easily visualized series of protein peaks in LC-MS analysis
- Ready to use after reconstitution, to save on preparation time

Proteins in MSRT2

Protein	RT Order*	Modification Information	Average Mass (Da)*
Ribonuclease B	1	$Man_5GlcNAc_2$	14,899
		$Man_6GlcNAc_2$	15,062
		$Man_7GlcNAc_2$	15,224
		$Man_8GlcNAc_2$	15,386
		$Man_9GlcNAc_2$	15,548
Insulin	2	—	5,808
Lysozyme	3	—	14,305
Transferrin	4	—	79,569
BSA	5	BSA	66,430
		BSA-Cysteinylated	66,549
		BSA-Glycated	66,592
Trypsin inhibitor	6	Mature Sequence	20,091
		C-Terminal Leu Truncation	19,978
β-lactoglobulin A	7	—	18,363
Carbonic anhydrase	8	N-Acetylserine	29,025
Lactic dehydrogenase	9	C Chain	36,160

*Confirmed using ESI mass spectrometry following C4 chromatography as described in the Figure "UV Chromatogram of MSRT2".

UV Chromatogram of MSRT2



UV_{215} chromatogram of MSRT2 using a Waters M-Class Acquity UPLC® and Xevo® G2S mass spectrometer.
Column = Supelco BIOshell® A400 Protein C4, 150 × 1.0 mm, 3.4 µm (Cat. No. 67045-U) at 65 °C.
Flow rate = 70 µL/min with Solvent A = Water, 0.1% Trifluoroacetic Acid;
Solvent B = Acetonitrile, 0.1% Trifluoroacetic Acid.
Injection = 1 µL for column load of 1 µg each protein.

MS PHOSPHOMIX PHOSPHOPEPTIDE STANDARDS

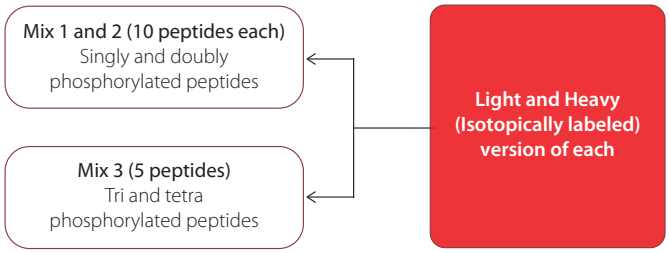
The MS PhosphoMix line of products allows for the testing of the strengths and weaknesses of phosphopeptide sample processing, mass spectrometry analysis, and instrument configurations. The mixes are produced from synthetic phosphopeptides with sequences derived from naturally occurring peptides as identified in HeLa cells.[1] Because the sequences are derived from mammalian cells, many natural phosphorylation motifs, such as those that present an abundance of proline, are represented.[2] Additionally, the phosphopeptide distribution in each mix has been chosen to present a broad range of characteristics, including ionizability, LC retention time, charge state, and isoelectric point. Finally, MS PhosphoMix-1, 2, and 3 were designed in a complementary fashion, as highlighted on the following page. For example, all three mixes contain peptides of the same sequence with different sites of phosphorylation (**Figure 2**).

Each of the three phosphopeptides mixes are available in their naturally occurring isotopic abundances (light) or as stable isotope enriched versions (heavy), making the set of products highly amenable to quantitative analyses, allowing users to compare recovery between workflows or techniques.

Features

- Naturally occurring peptide sequences
- Broad range of peptide characteristics
- Complementary produce designs
- Available in light and heavy versions

MS Phosphomix Product Design



Ordering Information

Cat. No.	Name	Amount/vial	Amount/peptide
MSP1L-1VL	MS PhosphoMix 1 Light	200 pmol	20 pmol/peptide
MSP1H-1VL	MS PhosphoMix 1 Heavy	200 pmol	20 pmol/peptide
MSP2H-1VL	MS PhosphoMix 2 Heavy	200 pmol	20 pmol/peptide
MSP2L-1VL	MS PhosphoMix 2 Light	200 pmol	20 pmol/peptide
MSP3H-1VL	MS PhosphoMix 3 Heavy	200 pmol	40 pmol/peptide
MSP3L-1VL	MS PhosphoMix 3 Light	200 pmol	40 pmol/peptide

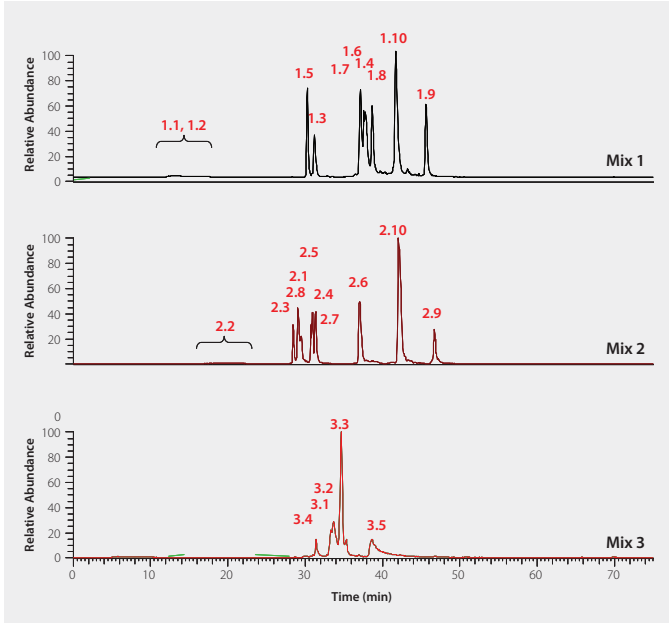


Figure 1. HPLC chromatograms of the 3 phosphopeptide mixtures using reverse phase (C18) stationary phase. The broad range of elution times as well as signal strength following electrospray (shown) or MALDI ionizations were taken into account during product design.

Reference:

1. J. V. Olsen, et al. *Cell*, 2006, **127**: 635-648
2. D. Schwatz, et al. *Nat. Biotech.* 2005, **23**(11): 1391-1398.

Peptide[1]	FASTA Abbreviation[2]	Complementary Peptide	No. of Phosphates	Light MW (Monoisotopic)	Heavy MW (Monoisotopic)	Relative Signal Intensity[3]	No. of Phosphates per amino acid		
							S	T	Y
PhosphoMix-1									
VLHSGpS[R]	1.1	—	1	834.37	844.38	Weak	1	—	—
RSpYpSRS[R]	1.2	2.2	2	1070.41	1080.41	Weak	1	—	1
RDSLGpTYSS[R]	1.3	—	1	1220.52	1230.53	Medium	—	1	—
pTKLIpTQLRDA[K]	1.4	—	2	1445.70	1453.72	Strong	—	2	—
EVQAEQPSSpSSP[R]	1.5	—	1	1480.62	1490.63	Medium	1	—	—
ADEPpSSEESDLEID[K]	1.6	1.7, 2.6, 3.5	1	1742.68	1750.69	Strong	1	—	—
ADEPSpSEEpSDLEID[K]	1.7	1.6, 2.6, 3.5	2	1822.64	1830.66	Medium	2	—	—
FEDEGAGFEESpSETGDYEE[K]	1.8	—	1	2333.84	2341.85	Strong	1	—	—
ELSNpSPLRENSFGpSPLEF[R]	1.9	2.9	2	2338.00	2348.01	Medium	2	—	—
SPTEYHEPVpYANPFYRPTpTPQ[R]	1.10	—	2	2809.19	2819.20	Strong	—	1	1
PhosphoMix-2									
LPQEpTA[R]	2.1	—	1	893.40	903.40	Weak	—	1	—
RSYpSpSRS[R]	2.2	1.2	2	1070.41	1080.41	Weak	2	—	—
EpTQSPEQV[K]	2.3	—	1	1124.48	1132.49	Weak	—	1	—
VIEDNEpYTA[R]	2.4	—	1	1288.53	1298.54	Medium	—	—	1
pSRSPpSSPELNN[K]	2.5	—	2	1474.59	1482.60	Medium	2	—	—
ADEPSSEEpSDLEID[K]	2.6	1.6, 1.7, 3.5	1	1742.68	1750.69	Strong	1	—	—
HQYSDYDpYHSSpSE[K]	2.7	—	2	1904.63	1912.64	Medium	1	—	1
NTPpSQHSHpSIQHSPE[R]	2.8	—	2	2000.79	2010.80	Medium	2	—	—
ELpSNpSPLRENSFGSPLEF[R]	2.9	1.9	2	2338.00	2348.01	Medium	2	—	—
LGPGRPLPTFPpTSE(CAM) TSDVEPDT[R]	2.10	—	1	2708.22	2718.22	Strong	—	1	—
PhosphoMix-3									
SLpSpYpSP[V]ER	3.1	—	3	1276.42	1282.43	Weak	2	—	1
LQGpSGVpS[L]ApSK	3.2	—	3	1285.48	1292.49	Medium	3	—	—
PPpYpSRV[I]pTQR	3.3	—	3	1455.57	1462.59	Strong	1	1	1
pSRS[R]pSYpTPEpYR	3.4	—	4	1720.54	1730.55	Weak	2	1	1
ADEPpSpSEEpSDLE[I]DK	3.5	1.6, 1.7, 2.6	3	1902.61	1909.63	Medium	3	—	—

1. Amino acid in [brackets] denotes site of label incorporation for heavy mixes
2. A FASTA file with all of the phosphopeptide sequences in the PhosphoMix product line is available for free download on the product display page at sigma-aldrich.com
3. As determined using electrospray ionization following standard reverse phase chromatography

Figure 2. MS Phosphomix product design demonstrating the diversity of the three products. In addition to the broad characteristics, several peptides were chosen to present several phosphorylation patterns as shown in the complementary peptide series.

For more information, visit
sigma-aldrich.com/phosphomix

PEPSCREEN® – CUSTOM PEPTIDE LIBRARIES

An Enabling Technology for Rapid Characterization and Selection of MS Compatible Peptides

A Perfect Solution for:

- Qualifying peptides for mass spectrometry suitability regarding chromatographic, ion suppression, and transition states
- Screening multiple proteotyptic peptides quickly and economically
- Identifying the best (isotopically labeled) AQUA™ Peptide candidate for optimal protein quantitation performance using your analytical techniques

Product Specifications

- Quantity: 0.5–2 mg or 2–5 mg
- Length: 6–20 mers
- Modifications Available
- C-Terminal acid or amide
- Format: dried in 96-tube rack format
- Shipped with electronic PDF files of QC data and peptide sequence map
- Minimum order size is 24 peptides

Features and Benefits

- Ideal for identifying the optimal candidate for AQUA peptides for your protein targets using your analytical platform
- Compatible with robotic automation for resuspension and dispensing in screening applications
- Suitable for robotic production of peptide microarrays
- N-Terminal modifications and nonstandard residues available upon request
- Dispatch of product in less than 7 business days allows for faster target identification

Sigma's proprietary peptide synthesis platform enables the fastest and most efficient high-throughput parallel synthesis of small milligram quantities of peptides.

The PEPscreen service provides a solution for screening experiments that were previously prohibitive due to high costs and long delivery time.

To place your order call (800) 234-5362 or visit
sigma-aldrich.com/pepscreen

CUSTOM AQUA™ PEPTIDES

To meet the specific demands of AQUA experimentation, Sigma® has developed a specialized custom peptide offering. Custom AQUA Peptides are synthesized using fully labeled 98 atom % ^{13}C and 98 atom % ^{15}N enriched amino acids (one labeled amino acid per peptide) and are stringently tested to ensure high purity (HPLC), accurate molecular mass (ESI-MS), and specific peptide content.

The AQUA Technology

Sigma's AQUA Peptides enable accurate, efficient mass spectrometric quantitation of protein biomarkers.

- Focus your analysis on significant protein biomarkers
- Accurately quantitate low abundance proteins
- Eliminate costly, time consuming stable isotope labeling steps
- Measure site-specific phosphorylation states
- Validate gene silencing at the protein level

AQUA Specifications

- Length: Up to 30 amino acids
- Amount: 5 x 1 nmol (quantified using AAA)
- Purity: >95%
- Incorporation of one stable isotopically labeled amino acid

Available modifications:

- Phosphorylation (Ser, Thr, Tyr)
- Carboxymethylation (Cys)
- Carbamidomethylation (Cys)
- Hydroxyproline
- N-terminal biotin

Non-Labeled Peptides:

In addition, Sigma-Aldrich offers custom synthesis of non-labeled peptides, with the same general features as the AQUA peptides:

- Length: Up to 30 amino acids
- Amount: 5 × 1 nmol (quantified using AAA)
- Purity: >95%

Ordering Information

Length	Labeled Peptide Price ($)	Non-labeled Peptide Price ($)
Up to 15 aa	500.00	450.00
16-20 aa	700.00	550.00
21-25 aa	1,100.00	900.00
26-30 aa	1,600.00	1,350.00

To place your order, call (800) 234-5362 or visit
sigma-aldrich.com/aquaorder

SILu™MAB AND SILu™LITE

Universal Monoclonal Antibody Standards

SILuMab is a Critical Tool for Assessment of the Pharmacokinetic Properties of Biotherapeutics

SILuMab is a highly purified stable isotope-labeled monoclonal antibody expressed in a proprietary Sigma-Aldrich CHO cell line grown in serum-free $^{13}C_6$ $^{15}N_4$ 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. Due to overlap with the common sequences in the Fc and light chain regions with candidate antibodies, SILuMab provides universal utility, thus eliminating the need for production of candidate-specific internal standards.

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

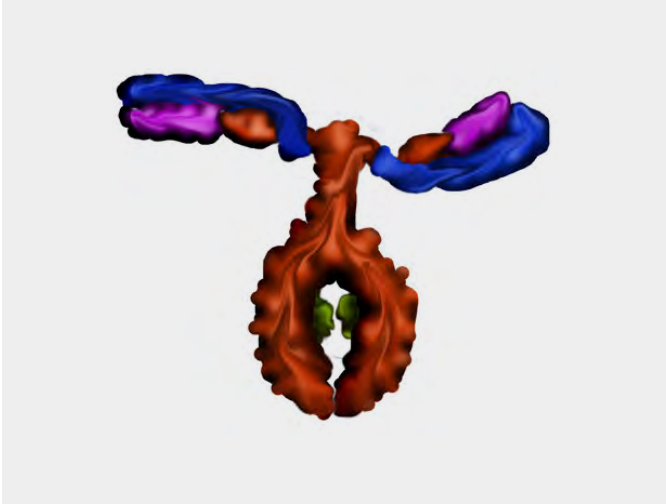
Vertical integration of SILuMab into the LC/MS analytical workflow yields universal stable isotope-labeled tryptic peptides that are utilized as internal standards.

As a full-length protein standard, SILuMab is superior to horizontally-integrated labeled peptide standards in that it reduces errors associated with fractionation, enrichment, and proteolysis.

SILuMab has been validated as an internal standard for quantitation of relevant biotherapeutics in a complex biological matrix by MRM-based LC-MS/MS.

- SILuMab yielded reproducible, linear curves from 0.1 µg/mL to 1,000 µg/mL without enrichment or depletion.
- Excellent agreement was observed between multiple peptides derived from the same target.
- SILuMab has been highly characterized.
- Label incorporation was determined to be >98% by mass spectrometry.
- Sequence was confirmed by peptide mapping and intact mass analysis
- Purity has been determined to be ≥ 90% by SDS-PAGE

Sigma-Aldrich also offers SILuLite, which is the same recombinant monoclonal antibody sequence as SILuMab, in unlabeled form.



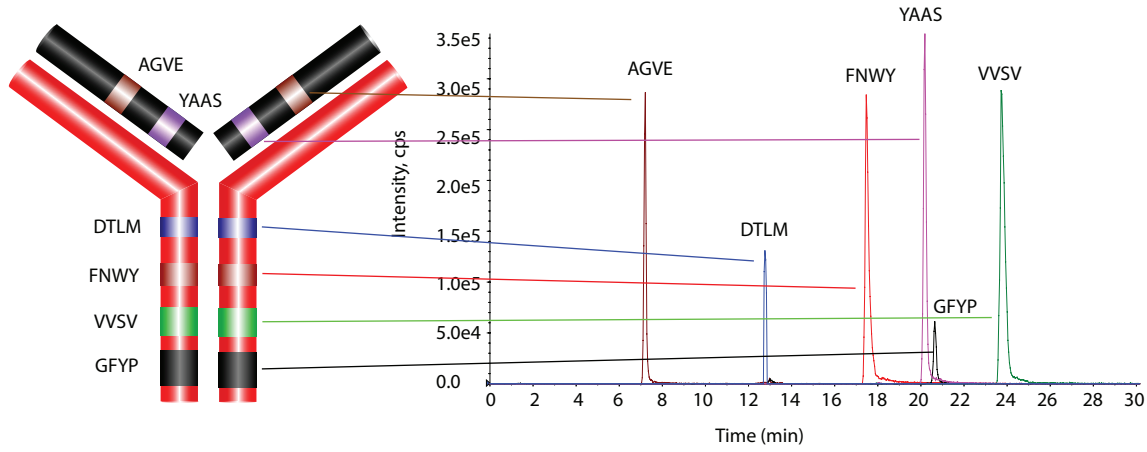
Ordering Information

Product Description	Pk. Size	Cat. No.
SILuMab Stable-Isotope Labeled Universal Monoclonal Antibody Standard	100 ug	MSQC3
SILuLite Monoclonal Antibody Standard (Unlabeled)	1 mg	MSQC4
SILuMab Stable-Isotope Labeled Universal Monoclonal Antibody IgG1 Kappa Standard	100 ug	MSQC6
SILuMab Stable-Isotope Labeled Universal Monoclonal Antibody IgG4 Kappa Standard	100 ug	MSQC7

Inquire about custom packaging

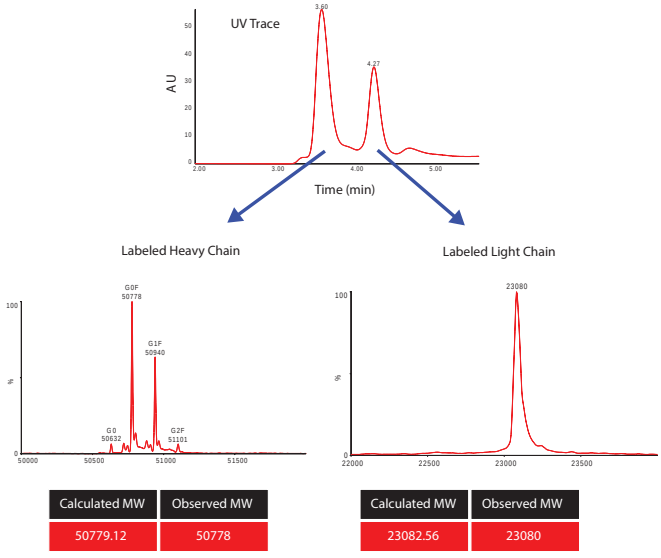
For more information or to place an order, call or contact your Sigma-Aldrich Sales Representative or visit **sigma-aldrich.com/silumab**

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

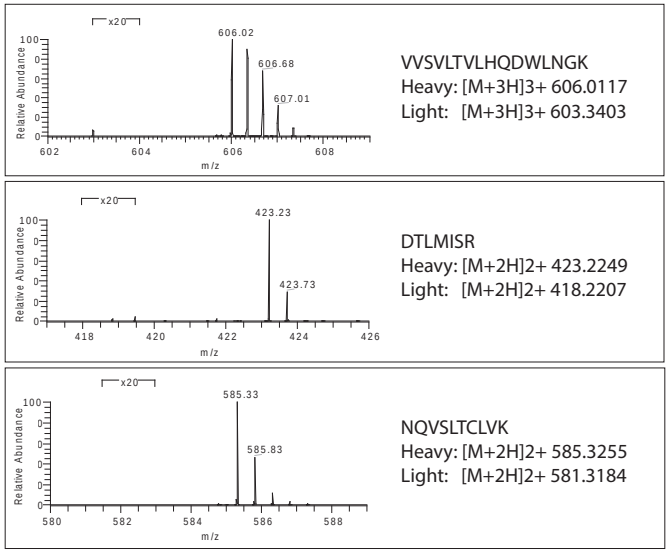


Calculated MW	Observed MW
50779.12	50778

Calculated MW	Observed MW
23082.56	23080

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.

>98% Isotopically Labeled



Incorporation of stable labeled isotopes for representative SILuMab peptides. No unlabeled peptides were detectable. Therefore incorporation was considered to be >98%.

MSQC1 – MS QUAL/QUANT QC MIX

Better than BSA for Standardizing MS Proteomic QC Runs

Experience the newest product available in proteomic analysis. MS Qual/Quant QC Mix (**Cat. No. MSQC1**) allows you to benchmark and monitor the daily performance of both qualitative and quantitative proteomic platforms.

Application

MS Qual/Quant QC Mix is an injection ready standard, optimized to assess platform characteristics including:

- Repeatability between runs
- System stability (drift, chromatography, signal intensity, sensitivity, etc.)
- Inter- and intra-platform and lab comparisons

Features and Benefits

- **Complexity** – defined mixture gives confidence in your instruments analysis
- **Dynamic range** – generate data points that simulate the range of real world conditions
- **Predigested** – eliminate variability
- **Injection ready** – decrease prep time

Qualitative Benefits

Mixture of 6 tryptically digested human proteins

- Consistent, defined mixture
- 25-fold concentration range
- C18 purified

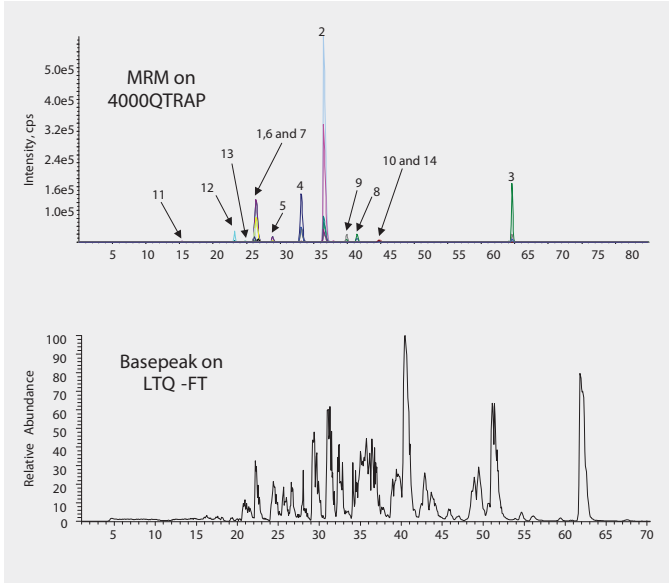
Quantitative Benefits

14 stable isotope labeled (SIL) peptides corresponding to 2–3 tryptic peptides for each protein have been incorporated into the protein digest

- Concentration range greater than three orders of magnitude
- MRM settings and transitions provided
- Light:Heavy ratios from 50:1 to 1:5

Protein	Peptide #	Peptide Sequence*
Carbonic Anhydrase I	1	GGPFSDSY[R]
	2	VLDALQAI[K]
Carbonic Anhydrase II	3	AVQQPDGLAVLGIFL[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



For more information, visit
sigma-aldrich.com/msqc

PROTEOMASS™ SELECTION GUIDE

	ProteoMass Peptide and Protein Calibration Kit	ProteoMass Peptide Calibration Kit	ProteoMass Protein Calibration Kit	ProteoMass vMALDI Calibration Kit	ProteoMass Guanidination Kit
					
Primary Application(s)	Calibration and sensitivity testing of MALDI-MS instruments.	Calibration and sensitivity testing of MALDI-MS instruments.	Calibration and sensitivity testing of MALDI-MS instruments.	Calibration and sensitivity testing of Thermo Scientific Exactive Series MS, LTQ XL and LTQ Hybrids with MALDI ion source	Enhancement of MALDI signal strength and sequence coverage through efficient conversion of C-terminal lysine residues to homoarginine.
Mass Range	757 to 66,000 Daltons	757 to 3,500 Daltons	5,700 to 66,000 Daltons	523 to 3,675 Daltons	—
Cat. No.	MSCAL1	MSCAL2	MSCAL3	MSCAL4	MS0100
Package Size	1 kit	1 kit	1 kit	1 kit	1 kit
Components	**Calibrants** • Bradykinin Fragment 1–7, 10 nmols • Angiotensin II, 10 nmols • P14R, 10 nmols • ACTH Fragment 18–39, 10 nmols • Insulin Oxidized B chain, 10 nmols • Insulin, 10 nmols • Cytochrome c, 10 nmols • Apomyoglobin, 10 nmols • Aldolase, 10 nmols • Albumin, 10 nmols **Matrices** • α-cyano, 4 x 10 mg • sinapinic acid, 4 x 10 mg **Solvents** • 0.1% TFA – 30 mL • 1% TFA – 4 mL • Acetonitrile – 30 mL	**Calibrants** • Bradykinin Fragment 1–7, 2 x 10 nmols • Angiotensin II, 2 x 10 nmols • P14R, 2 x 10 nmols • ACTH Fragment 18–39, 2 x 10 nmols • Insulin Oxidized B chain, 2 x 10 nmols **Matrix** • α-cyano, 8 x 10 mg **Solvents** • 0.1% TFA – 30 mL • 1% TFA – 4 mL • Acetonitrile – 30 mL	**Calibrants** • Insulin, 2 x 10 nmols • Cytochrome c, 2 x 10 nmols • Apomyoglobin, 2 x 10 nmols • Aldolase, 2 x 10 nmols • Albumin, 2 x 10 nmols **Matrix** • sinapinic acid, 8 x 10 mg **Solvents** • 0.1% TFA – 30 mL • 1% TFA – 4 mL • Acetonitrile – 30 mL	**Calibration Mix, Standard Range** • 5 vials, each containing MRFA, Bradykinin 1–7, Angiotensin 1, Neurotensin, Renin Substrate, and Bradykinin **Calibration Mix, High Range** • 5 vials, each containing MRFA, Bradykinin, ACTH 1–16, Melittin, and ACTH 7–38 **Sensitivity Standard** • Angiotensin II – 2 x 500 pmols **Matrix** • α-cyano, 5 x 5 mg **Solvents** • 1% TFA – 4 mL • Acetonitrile – 30 mL • Ethanol, 200 Proof, Molecular Biology Grade – 10 mL	• O-Methylisourea hemisulfate • Base reagent • Stop Solution • Control Peptide

For more information, visit
sigma-aldrich.com/mscal

MALDI MATRICES SELECTION TABLE

Matrix-assisted laser desorption/ionization (MALDI) has expanded MS into the analysis of high molecular mass, non-volatile, and thermally labile compounds, such as intact proteins and oligonucleotides. Moreover, it has become an important technique in proteomics research.[1-3] Further significant applications of MALDI-MS include the analysis of polymers, glycans, lipids, and metabolites.

A typical MALDI matrix substance is an aromatic acid with a chromophore that absorbs strongly at the wavelength of the incident laser. The MALDI technique generally involves mixing the sample with a matrix substance, followed by crystallization by different techniques on the MALDI sample plate. The crystallized sample-matrix mixture is irradiated by laser light, usually UV. As the matrix absorbs the light energy, it vaporizes into the gas phase, resulting in an indirect ionization of the sample molecules.[4-6]

Choosing a suitable matrix of high quality is the key to the success of a MALDI-MS experiment. Organic impurities can lead to extraneous peaks, especially in the low mass range. Trace levels of ions, especially Na^+ and K^+, form adducts with sample molecules. These adducts differ in mass according to the number of positive ions and complicate the MS spectrum. Since the matrix substance is generally applied in large excess to the sample, a very high purity is even more crucial.

The MALDI Matrices Selection Table below facilitates choosing the appropriate matrix for the use in proteomics and metabolomics.

Features and Benefits

- High chemical purity
- Low trace metal content to minimize adduct formation and simplify the resulting MS spectrum
- Ultra pure grades of the most popular matrix substances with extremely strict specifications concerning purity, trace metal content, appearance, and solubility

References

1. Karas, M., *et al.*, Matrix-assisted ultraviolet laser desorption of non-volatile compounds. *Int. J. Mass Spectrom. Ion Proc.,* **78**, 53-68 (1987).
2. Hillenkamp, F., and Peter-Katalinic, J. (eds.), *MALDI MS. A Practical Guide to Instrumentation, Methods and Applications*, Wiley-VCH (2007).
3. Aebersold, R., and Mann, M., Mass spectrometry-based proteomics. *Nature,* **422**, 198-207 (2003).
4. Dreisewerd, K., The desorption process in MALDI. *Chem. Rev.,* **103**, 395-425 (2003).
5. Karas, M., and Krüger, R., Ion formation in MALDI. *Chem. Rev.*, **103**, 427-439 (2003).
6. Knochenmuss, R., and Zenobi, R., MALDI ionization: The role of in-plume processes. *Chem. Rev.,* **103**, 441-452 (2003).

Cat. No.	Description	Purity	Abbreviation	Proteins	Peptides	Glycans	Oligonucleotides	Polymers	Lipids	Other Analytes	Note	Pack Sizes
92817	9-Aminoacridine	≥99.5%	9-AA	—	—	—	—	—	•	Metabolites	—	1 g
89132	Aminopyrazine	≥99.0%	AP	—	—	—	—	—	—	Small carbohydrates	—	10 x10 mg, 1 g
82393	6-Aza-2-thiothymine	≥99.0%	ATT	•	•	•	•	—	—	Non-covalent complexes	—	1 g, 5 g
89063	4-Bromo-α-cyanocinnamic acid	≥95%	BrCCA	—	•	—	—	—	•	Phosphopeptides, phospholipids, chlorinated lipids, drugs, fragile analytes, ionic liquids (quantification), ME-SIMS, CID-MS/MS	—	100 mg
68914	4-Bromo-α-cyanocinnamic acid - 4-Chloro-α-cyanocinnamic acid mixture	≥95%	BrCCA:ClCCA	—	•	—	—	—	•	Phosphopeptides, phospholipids, chlorinated lipids, drugs, fragile analytes, ionic liquids (quantification), ME-SIMS, CID-MS/MS	—	100 mg
55841	4-Bromo-α-cyanocinnamic acid - α-Cyano-2,4-difluorocinnamic acid mixture	≥95%	BrCCA:DiFCCA		•	—	—	—	•	Phosphopeptides, phospholipids, chlorinated lipids, drugs, fragile analytes, ionic liquids (quantification), ME-SIMS, CID-MS/MS	—	100 mg

Cat. No.	Description	Purity	Abbreviation	Proteins	Peptides	Glycans	Oligonucleotides	Polymers	Lipids	Other Analytes	Note	Pack Sizes
60018	Caffeic acid	≥99.0%	—	•	•	—	—	—	—	—	—	1 g, 5 g
94141	4-Chloro-α-cyanocinnamic acid	≥95%	ClCCA	—	•	—	—	—	•	Phosphopeptides, phospholipids, chlorinated lipids, drugs, fragile analytes, ionic liquids (quantification), ME-SIMS, CID-MS/MS	—	100 mg
39379	4-Chloro-α-cyanocinnamic acid - α-Cyano-2,4-difluorocinnamic acid mixture	≥95%	ClCCA:DiFCCA	—	•	—	—	—	•	—	—	100 mg
77646	α-Cyano-2, 4-difluorocinnamic acid	≥95%	DiFCCA	—	•	—	—	—	—	Phosphopeptides, phospholipids, chlorinated lipids, drugs, fragile analytes, ionic liquids (quantification), ME-SIMS, CID-MS/MS	—	100 mg
77081	α-Cyano-4-fluorocinnamic acid	≥95%	FCCA	—	•	—	—	—	—	Phosphopeptides, phospholipids, chlorinated lipids, drugs, fragile analytes, ionic liquids (quantification), ME-SIMS, CID-MS/MS	—	100 mg
70990	α-Cyano-4-hydroxycinnamic acid	≥99.0%	CHCA	•	•	•	—	—	—	—	—	250 mg, 1 g
39468	α-Cyano-4-hydroxycinnamic acid	≥99.5%, Ultra pure	CHCA	•	•	•	—	—	—	—	—	10x10 mg
67336	α-Cyano-4-hydroxycinnamic acid butylamine salt	≥99.0%	BA-CHCA	—	•	—	—	•	—	—	Ionic Liquid Matrix	100 mg, 1 g
94190	α-Cyano-4-hydroxycinnamic acid N-tert-butyl-N-isopropyl-N-methylammonium salt	≥99.0%	IMTBA-CHCA	•	•	—	—	—	—	—	Ionic Liquid Matrix	10x10 mg
03841	α-Cyano-4-hydroxycinnamic acid - α-Cyano-2, 4-difluorocinnamic acid - α-Cyano-2, 3, 4, 5, 6-pentafluorocinnamic acid mixture	≥95%	CHCA:DiFCCA: PentaFCCA	—	•	—	—	—	—	Phosphopeptides, phospholipids, chlorinated lipids, drugs, fragile analytes, ionic liquids (quantification), ME-SIMS, CID-MS/MS	—	100 mg
38419	α-Cyano-2, 3, 4, 5, 6-pentafluorocinnamic acid	≥95%	PentaFCCA	—	•	—	—	—	—	Phosphopeptides, phospholipids, chlorinated lipids, drugs, fragile analytes, ionic liquids (quantification), ME-SIMS, CID-MS/MS	—	100 mg
89759	α-Cyano-4-phenylcinnamic acid	≥99.0%	—	—	—	—	—	—	—	PAHs	—	10x10 mg
56451	1,5-Diamino naphthalene	≥99.0%	1,5-DAN	—	•	—	•	—	—	In-Source-Decay	—	250 mg
89415	2' ,5'-Dihydroxy acetophenone	≥99.5%	2,5-DHAP	•	•	•	—	—	—	—	—	250 mg, 1 g
37468	2' ,6'-Dihydroxy acetophenone	≥99.5%	2,6-DHAP	•	•	•	—	—	•	—	—	1 g, 5 g

Cat. No.	Description	Purity	Abbreviation	Proteins	Peptides	Glycans	Oligonucleotides	Polymers	Lipids	Other Analytes	Note	Pack Sizes
85707	2, 5-Dihydroxybenzoic acid	≥99.0%	DHB	•	•	•	—	•	•	Organic molecules	—	10 mg, 250 mg, 1 g
39319	2, 5-Dihydroxybenzoic acid	≥99.5%, Ultra pure	DHB	•	•	•	—	•	•	Organic molecules	—	10x10 mg
46278	trans-Ferulic acid	≥99.0%	FA	•	•	—	—	—	—	—	—	1 g, 5 g
94155	Ferulic acid N-ethyl-N,N-diisopropylammonium salt	≥98.0%	DIEA-F	—	—	•	—	—	—	—	Ionic Liquid Matrix	10x10 mg
95712	(4-Hydroxybenzylidene) malonitrile BioXtra	≥99.0%	—	—	—	—	—	•	—	—	—	10 × 10 mg, 250 mg
68852	3-Hydroxy-2-naphthoic acid	≥99.5%	—	•	•	—	—	—	—	—	—	1 g
54793	2-(4-Hydroxy phenylazo) benzoic acid	≥99.5%	HABA	•	•	•	—	•	—	—	—	1 g, 5 g
56197	3-Hydroxypicolinic acid	≥99.0%	3-HPA	—	—	—	•	—	—	Oligosaccharides	—	250 mg, 1 g
76154	2-Mercapto benzothiazole	≥99.0%	MBT	•	•	—	—	•	—	—	—	250 mg
72311	Nicotinic acid	≥99.5%	—	•	•	—	•	—	—	—	—	250 mg, 1 g
72681	4-Nitroaniline	≥99.0%	—	•	•	—	—	—	•	—	Liquid Matrix	250 mg, 1 g
73148	3-Nitrobenzyl alcohol	≥99.5%	—	—	—	—	—	—	—	—	—	5 g
80362	3-Nitrobenzonitrile	≥99.0%	3-NBN	—	—	—		—	—	Tissues via MAIV	—	1 g
84228	Salicylamide	≥99.0%	—	—	—	—	•	—	—	—	—	1 g
85429	Sinapic acid	≥99.0%	SA	•	•	—	—	—	—	Dendrimers, Fullerenes	—	1 g, 5 g
49508	Sinapic acid	≥99.5%	SA	•	•	—	—	—	—	Dendrimers, Fullerenes	—	10 × 10 mg
50862	Super-DHB BioReagent	—	Super-DHB	•	•	•	—	—	—	—	—	10 × 10 mg, 1 g, 5 g
91928	2', 4', 6'-Trihydroxy acetophenone monohydrate	≥99.5%	THAP	•	•	•	•	—	—	—	—	1 g, 5 g
64199	N,N,N',N'-Tetramethyl-1, 8-naphthalenediamine	≥99.0%	DMAN	—	—	—	—	—	•	—	—	1 g

SUPEL™-SELECT POLYMERIC SPE PRODUCTS

Key Features and Benefits

- Hydrophilic-modified styrene resin extracts and recovers a broad range of analytes (polar to nonpolar, acidic to basic) using a single sorbent
- Generic methodology saves time, money, and headaches during method development
- Greater capacity allows for smaller bed weights = smaller elution volumes = time savings in sample processing
- Resistant to over-drying allowing for more robust methodology

Versatile and Simple Sample Cleanup by SPE

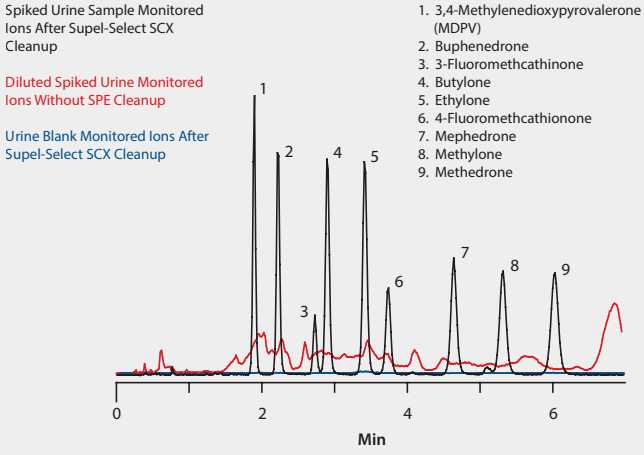
Supel-Select SPE phases are ideal for the solid phase extraction (SPE) of a broad range of compounds from aqueous samples. While reversed-phase interactions dominate retention on the Supel-Select HLB, and the retention mechanisms of the Supel-Select SAX and SCX are predominately based on ion-exchange, the hydrophilic modifications of the styrene-based polymer backbone allow for retention and recovery of more polar compounds.

Supel-Select Properties	
HLB Phase Chemistry	Hydrophilic-modified styrene polymer
SAX Phase Chemistry	Quanternary amine-functionalized hydrophilic-modified styrene polymer
SCX Phase Chemistry	Sulfonic acid-functionalized hydrophilic modified styrene polymer
Suitable for MS Detection?	Yes
pH Compatibility	0 – 14
Particle Size	50 – 70 µm
Surface Area	160 – 420 m^2/g
Pore Volume	0.8 – 1.2 mL/g
Pore Size	80 – 200 Å

Cat. No.	Product Description	Qty.
Supel-Select HLB 96-well SPE		
Inquire	10 mg/well	1
575661-U	30 mg/well	1
575662-U	60 mg/well	1
Supel-Select SAX 96-well SPE		
Inquire	10 mg/well	1
575660-U	30 mg/well	1
575663-U	60 mg/well	1
Supel-Select SCX 96-well SPE		
Inquire	10 mg/well	1
575664-U	30 mg/well	1
575665-U	60 mg/well	1

LC-MS Analysis of Illicit Bath Salts in Urine on Ascentis Express HILIC with and without Supel-Select SCX SPE Cleanup

SPE tube:	Supel-Select SCX, 30 mg/1 mL (54240-U)
column:	Ascentis Express HILIC, 10 cm x 2.1 mm I.D., 2.7 µm (53939-U)
mobile phase:	(A) 5 mM ammonium formate acetonitrile; (B) 5 mM ammonium formate water; (98:2, A:B)
flow rate:	0.6 mL/min
pressure:	127 bar
column temp:	35 °C
detector:	MS, ESI+, 100-1000 m/z
injection:	1 µL
sample:	200 ng/mL in acetonitrile (standards from Cerilliant)



Cat. No.	Product Description	Qty.
Supel-Select HLB SPE		
54181-U	30 mg/1 mL	100
54182-U	60 mg/3 mL	50
54183-U	200 mg/6 mL	30
54184-U	500 mg/12 mL	20
54186-U	1 g/20 mL	20
Supel-Select SAX 96-well SPE		
54231-U	30 mg/1 mL	100
54233-U	60 mg/3 mL	50
54235-U	200 mg/6 mL	30
54236-U	500 mg/12 mL	20
54237-U	1 g/20 mL	20
Supel-Select SAX 96-well SPE		
54240-U	30 mg/1 mL	100
54241-U	60 mg/3 mL	50
54242-U	200 mg/6 mL	30
54243-U	500 mg/12 mL	20
54245-U	1 g/20 mL	20

For more information, visit
sigma-aldrich.com/supel-select

HYBRIDSPE®-PHOSPHOLIPID PRODUCTS FOR CONSISTENT LC-MS IONIZATION

Key Features and Benefits

- Maximize sensitivity by minimizing ion-suppression
- 100% removal of phospholipids and precipitated proteins
- 2-3 step generic procedure
- Ideal for high-throughput pre-clinical and clinical studies

Ion-Suppression and Phospholipid Contamination

When analyzing a compound and its metabolites in biological fluids, such as plasma or serum, one frequently deals with interference from the complex sample matrix. Ion-suppression of the mass spec signal due to contaminants in the matrix often limits our ability to properly identify and quantify the analytes of interest. The presence of phospholipids in biological fluids is one of the major causes of ion-suppression in LC-MS when using positive ion electrospray mode (+ESI). Removing phospholipids with HybridSPE-Phospholipid is a rapid and reliable means to improve identification and quantification of compounds in biological matrices using LC-MS.

How Does HybridSPE-Phospholipid Work?

Sample preparation with HybridSPE-Phospholipid is a very rapid and simple procedure. Proteins in the sample are precipitated by addition of acetonitrile containing 1% formic acid. The sample is then added to the HybridSPE-Phospholipid packed bed, either well plate or tube format. As shown in the accompanying figure, the bed consists of proprietary zirconia-coated silica particles. The zirconia sites exhibit Lewis acid (electron acceptor) properties that will interact strongly with Lewis bases (electron donors).

Phospholipids structurally consist of a polar head group (zwitterionic phosphonate moiety) and a large hydrophobic tail (two hydrophobic fatty acyl groups). The phosphonate group acts as a very strong Lewis base that interacts strongly with zirconia. Formic acid in the precipitation solvent is a critical modifier used to improve the recovery of many analytes of interest (particularly acidic compounds) by preventing analyte retention, while not affecting phospholipid removal.

The HybridSPE-Phospholipid sample preparation products are available in several configurations.

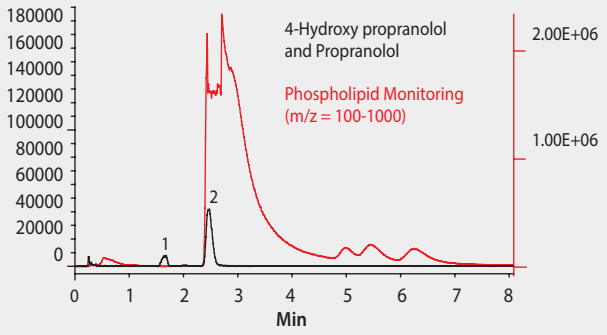
- Two 96-well plate formats for sample volumes of ~100 µL and 20-40 µL. Both formats allow for in-well precipitation.
- Three SPE tube formats; the ultra version allows for in-tube protein precipitation.

For more information and to view a video of HybridSPE-Phospholipid in operation, visit
sigma-aldrich.com/hybridspe-pl

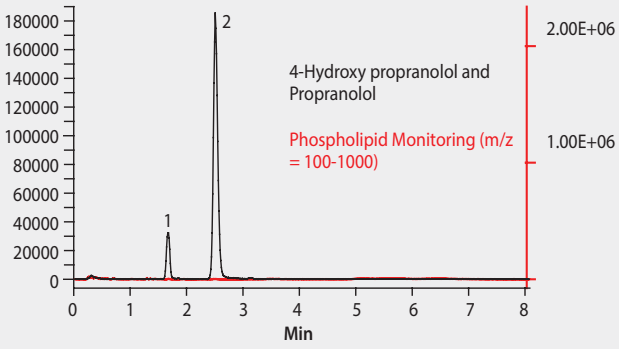
Ion-Suppression from Phospholipids: Standard Protein Precipitation vs. HybridSPE-Phospholipid

sample prep:	standard protein precipitation or HybridSPE-Phospholipid (575656-U)
column:	Ascentis Express F5, 5 cm x 2.1 mm I.D., 2.7 µm (53567-U)
mobile phase:	(A) 2 mM ammonium formate in acetonitrile; (B) 2 mM ammonium formate in water; (90:10, A:B)
flow rate:	0.4 mL/min
pressure:	1073 psi
temp.:	35 °C
detector:	MS, ESI(+) TOF, m/z =100-1000
injection:	2 µL
sample:	each compound, 200 ng/mL in plasma
system:	Agilent 1200SL Rapid Resolution; 6210 Time of Flight (TOF) MS

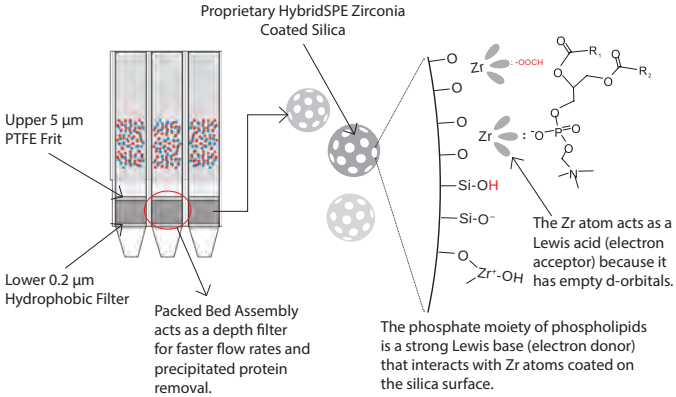
Standard Protein Precipitation Technique
(Note suppression of propranolol signal)



HybridSPE-Phospholipid Technique



Interaction of Phospholipids with HybridSPE-Phospholipid



Featured Products

Cat. No.	Product Description	Qty.
HybridSPE®-Phospholipid		
52794-U	96-well Plate, volume 0.8 mL	1 ea
52798-U	96-well Plate, volume 0.8 mL	20 ea
52818-U	HybridSPE-PLus 96-Well Plate Essentials Kit	—
575659-U	HybridSPE-PLus 96-well Plate, volume 2 mL	1 ea
575673-U	HybridSPE-PLus 96-well Plate, volume 2 mL	20 ea
55261-U	Cartridge, volume 1 mL	100 ea
55276-U	Cartridge, volume 1 mL	200 ea
55267-U	Cartridge, volume 6 mL	30 ea
HybridSPE®-Phospholipid Ultra		
55269-U	Cartridge, volume 1 mL	100 ea

Protein Precipitation

96-Well Protein Precipitation Filter Plate

The 96-well protein precipitation filter plate is ideal for removing precipitated proteins from biological plasma/serum. The plate consists of a 0.2 µm hydrophobic graded filter/frit. Biological plasma is first added to the 96-well plate followed by a protein precipitating agent (e.g., acetonitrile). After a brief mixing step, vacuum is applied to the plate, and the filter/frit removes precipitated proteins from the sample. The resulting filtrate is ready for further processing and/or analysis.

Cat. No.	Product Description	Qty.
55263-U	2 mL	1 ea.

SUPELMIP® MOLECULARLY IMPRINTED POLYMERS

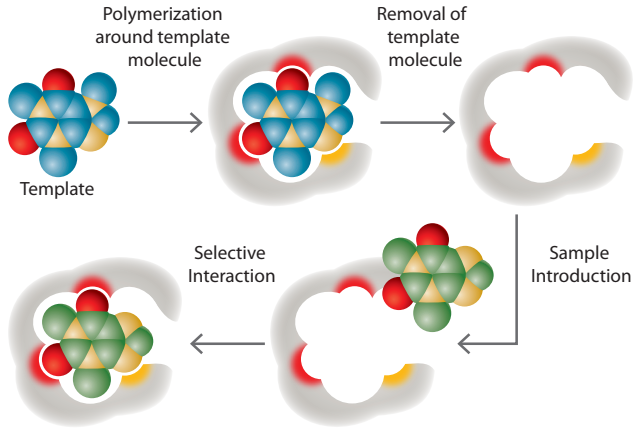
Key Features and Benefits

- Achieve lower detection limits through superior selectivity
- Reduce ion-suppression
- Save time and reduce cost via robust and rapid sample prep methodology
- Minimal to no method development required

Highly Selective Extraction of Trace Analytes from Complex Matrices

Molecularly imprinted polymers (MIPs) are a class of highly cross-linked polymer-based molecular recognition elements engineered to bind one target compound or a class of structurally related target compounds with high selectivity. Selectivity is introduced during MIP synthesis in which a template molecule, designed to mimic the analyte, guides the formation of specific cavities or imprints that are sterically and chemically complementary to the target analyte.

Formation of MIPs



SupelMIPs are available for these analyte and matrix combinations

Analytes	Matrix
Chloramphenicol	Milk, plasma, honey, urine, and shrimp/prawns
Clenbuterol	Urine
Fluoroquinolones	Bovine kidney, honey, and milk
PAHs	Edible oils
Riboflavin (Vitamin B_2)	Milk
β-Agonists and/or β-Blockers	Tissue, urine and wastewater
TSNAs (4 Different Tobacco-Specific Nitrosamines: NNK, NNN, NAB, NAT)	Urine and tobacco
NNAL (4-(Methylnitrosamino)-1-(3-pyridyl)-1-butanol)	Urine

SupelMIP Molecularly Imprinted Polymer SPE Tubes

Cat. No.	Description	Pkg. Size
53225-U	SupelMIP SPE - β-agonists, bed wt. 25 mg, volume 3 mL	50
53202-U	SupelMIP SPE - β-agonists, bed wt. 25 mg, volume 10 mL	50
53209-U	SupelMIP SPE - Chloramphenicol, bed wt. 25 mg, volume 3 mL	50
53210-U	SupelMIP SPE - Chloramphenicol, bed wt. 25 mg, volume 10 mL	50
53201-U	SupelMIP SPE - Clenbuterol, bed wt. 25 mg, volume 10 mL	50
53269-U	SupelMIP SPE - Fluoroquinolones, bed wt. 25 mg, volume 3 mL	50
53224-U	SupelMIP SPE - Full β-receptor (β-blockers and β-agonists), bed wt. 25 mg, volume 3 mL	50
53223-U	SupelMIP SPE - Full β-receptor (β-blockers and β-agonists), bed wt. 25 mg, volume 10 mL	50
53207-U	SupelMIP SPE - Riboflavin (vitamin B_2), bed wt. 25 mg, volume 10 mL	50
53222-U	SupelMIP SPE - TSNAs, bed wt. 50 mg, volume 3 mL	50
53221-U	SupelMIP SPE - TSNAs, bed wt. 50 mg, volume 10 mL	50
53203-U	SupelMIP SPE - NNAL, bed wt. 25 mg, volume 3 mL	50

STABLE ISOTOPE LABELED BIOACTIVE COMPOUNDS

ISOTEC® Products for Use as Internal Standards

Stable isotope labeled compounds are used as internal standards for various MS techniques and within many applications. With chemical and ionization properties nearly identical to their unlabeled counterparts, stable isotope labeled compounds are often considered the top choice for an internal standard. Furthermore, the labeled standard and the analyte of interest can be easily differentiated by the mass shift between the two compounds, which is ideally three or more units.[1]

ISOTEC Stable Isotopes offers a large selection of labeled products suitable for this purpose. Labeled standards have been utilized within numerous applications, including quantification of cholesterol in a clinical setting,[2] vitamin D within baby formula,[3] and B vitamins in human milk.[4] Labeled internal standards have also been employed in research on the diagnosis of Graves disease[5] and hypertension,[6] the study of fatty acid oxidation,[7] and the analysis of androgenic steroids in wastewater.[8]

MS standards from ISOTEC have high chemical and isotopic purities with labeling patterns including ^{13}C, ^{15}N, and deuterium. The ^{13}C and/or ^{15}N labels do not exchange within the mass spectrometer source, providing further advantage.[9]

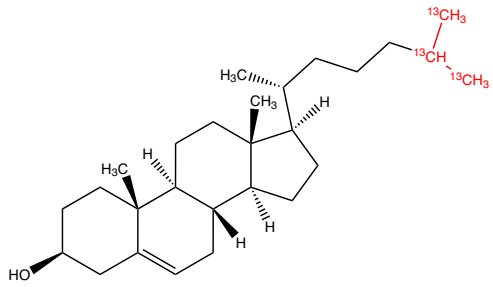
ISOTEC is also able to custom-synthesize labeled compounds upon request. Custom compounds can be designed with specific isotopes in specific locations. Whether a fully labeled or specifically labeled compound is of interest, let our expert team evaluate your needs.

Carbohydrates

Cat. No.	Description	Isotopic Purity	Assay
587621	D-Fructose-$^{13}C_6$	99 atom % ^{13}C	99% (CP)
720127	D-Glucose-1,2,3-$^{13}C_3$	99 atom % ^{13}C	99% (CP)
605492	D-Mannitol-$^{13}C_6$	99 atom % ^{13}C	99% (CP)
605484	D-Ribose-2,3,4,5-$^{13}C_4$	99 atom % ^{13}C	99% (CP)
605514	D-Sorbitol-$^{13}C_6$	99 atom % ^{13}C	99% (CP)
605417	Sucrose-$^{13}C_{12}$	99 atom % ^{13}C	99% (CP)
738921	α,α–Trehalose-$^{13}C_{12}$	99 atom % ^{13}C	99% (CP)
740934	Xylitol-$^{13}C_5$	99 atom % ^{13}C	98% (CP)
666378	D-Xylose-$^{13}C_5$	98 atom % ^{13}C	99% (CP)

References

1. Vogeser, M. and Seger, C., Pitfalls associated with the use of liquid chromatography-tandem mass spectrometry in the clinical laboratory. ***Clin. Chem.***, **56**, 1234-1244 (2010).
2. Edwards, S.H., ***et al.***, Proposed serum cholesterol reference measurement procedure by gas chromatography-isotope dilution mass spectrometry. ***Clin. Chem.***, **57**, 614-622 (2011).
3. Sullivan, D., Infant formula and adult/pediatric nutritional methods approved First Action using the AOAC voluntary consensus standards process. ***J. AOAC Int.***, **95**, 1-4 (2012).
4. Hampel, D., ***et al.***, Ultra-performance liquid chromatography tandem mass-spectrometry (UPLC-MS/MS) for rapid, simultaneous analysis of thiamin, riboflavin, flavin adenine dinucleotide, nicotinamide and pyridoxal in human milk. ***J. Chromatogr. B***, **903**, 7-13 (2012).
5. Higashi, T., ***et al.***, Stable isotope-dilution liquid chromatography/tandem mass spectrometry method for determination of thyroxine in saliva. ***J. Chromatogr. B,*** **879,** 1013-1017 (2011).
6. Taylor, P.J., ***et al.***, Measurement of aldosterone in human plasma by semiautomated HPLC-tandem mass spectrometry. ***Clin. Chem.***, **55**, 1155-1162 (2009).
7. Mohammad, M.A., ***et al.***, Galactose promotes fat mobilization in obese lactating and nonlactating women. ***Am. J. Clin. Nutr.***, **93**, 374-381 (2011).
8. Backe, W.J., ***et al.***, Analysis of androgenic steroids in environmental waters by large-volume injection liquid chromatography tandem mass spectrometry. ***Anal. Chem.***, **83**, 2622-2630 (2011).
9. Ciccimaro, E. and Blair, I.A. Stable-isotope dilution LC-MS for quantitative biomarker analysis. ***Bioanalysis,*** **2(2),** 311-341(2010).



To find addional stable isotope labeled standards, visit **sigma-aldrich.com/isotec**

To inquire about Stable Isotopes pricing and availability, email us at **isosales@sial.com.**

Fatty Acids and Derivatives

Cat. No.	Description
735000	Arachidonic-5,6,8,9,11,12,14,15-d_8 acid
729663	Cholesteryl linoleate-$^{13}C_{18}$
729515	Cholesteryl-26,26,26,27,27,27-d_6 linoleate
729523	Cholesteryl oleate-$^{13}C_{18}$
729671	Cholesteryl-26,26,26,27,27,27-d_6 oleate-1,2,3,7,8,9,10-$^{13}C_7$
616125	Decanoic-10,10,10-d_3 acid
733326	*cis*-4,7,10,13,16,19-Docosahexaenoic-21,21,22,22,22-d_5 acid
734322	*cis*-5,8,11,14,17-Eicosapentaenoic acid-19,19,20,20,20-d_5
793760	*cis*-8,11,14-Eicosatrienoic acid-1-^{13}C
741388	*rac*-Glyceryl-2,3-di(oleate-$^{13}C_{18}$)-1-palmitate
730076	*rac*-Glyceryl-d_5-2,3-dioleate-1-palmitate
730068	*rac*-Glyceryl-d_5-2-linoleate-3-oleate-1-palmitate
741086	Glyceryl 1-oleate-$^{13}C_{18}$-2,3-dioleate
741124	*rac*-Glyceryl-2-oleate-$^{13}C_{18}$-3-oleate-1-palmitate
729507	Glyceryl-d_5 trilinoleate
617121	Glyceryl tri(octanoate-d_{15})
605638	Glyceryl-$^{13}C_3$ trioleate
425907	Glyceryl tri(palmitate-1-^{13}C)
777862	Glyceryl tri(palmitate-1,2,3,4-$^{13}C_4$)
616966	Glyceryl tri(palmitate-d_{31})
606499	Heptanoic-5,6,7-$^{13}C_3$ acid
617040	Heptanoic-d_{13} acid
722774	*trans*-9-Hexadecenoic acid-1,2,3,7,8-$^{13}C_5$
750875	6-Hydroxyhexanoic acid-$^{13}C_6$
451401	Lauric-d_{23} acid
605735	Linoleic acid-$^{13}C_{18}$
730033	2-Linoleoyl-1-palmitoyl-rac-glycero-3-phosphocholine-(trimethyl-d_9)
733148	Methyl heptadecanoate-d_{33}
490865	Myristic acid-1,2-$^{13}C_2$
614165	Myristic acid-13,13,14,14,14-d_5
722847	*trans*-6-Octadecenoic acid-1,2,3,4,5-$^{13}C_5$
722790	*trans*-9-Octadecenoic acid-1,2,3,7,8-$^{13}C_5$
722855	*trans*-11-Octadecenoic acid-1,2,3,9,10-$^{13}C_5$
605727	Octanoic acid-$^{13}C_8$
448214	Octanoic-d_{15} acid
490431	Oleic acid-$^{13}C_{18}$
730041	2-Oleoyl-1-palmitoyl-rac-glycero-3-phosphocholine-(trimethyl-d_9)
605573	Palmitic acid-$^{13}C_{16}$
366897	Palmitic acid-d_{31}
724173	Palmitoleic acid-$^{13}C_{16}$

Additional products and labeling patterns are available.

For a full listing of labeled lipid and fatty acid products, visit
sigma-aldrich.com/lipid

To inquire about Stable Isotopes pricing and availability, email us at **isosales@sial.com.**

Steroids and Hormones

Cat. No.	Description
706035	Aldosterone-2, 2, 4, 6, 6, 21, 21-d_7
802883	Aldosterone-9,11,12,12-d_4 solution
730645	4-Androstene-3, 17-dione-2, 3, 4-$^{13}C_3$ solution
747505	5α-Cholestane-2,2,4,4-d_4
777900	5α-Cholestane-3β-ol-2,2,3,4,4-d_5
749478	Cholesterol-2,3,4-$^{13}C_3$
488577	Cholesterol-2, 2, 3, 4, 4, 6-d_6
707678	Cholesterol-25, 26, 27-$^{13}C_3$
802905	Corticosterone-9,11,12,12-d_4
803146	Cortisol-2, 3, 4-$^{13}C_3$ solution
803154	Cortisone-2, 3, 4-$^{13}C_3$ solution
705586	Cortisone-2, 2, 4, 6, 6, 12, 12-d_7
709549	Dehydroepiandrosterone-2, 2, 3, 4, 4, 6-d_6
723266	Dehydroepiandrosterone-2, 2, 3, 4, 4, 6-d_6 sulfate sodium salt
710784	11-Deoxycortisol-2, 2, 4, 6, 6-d_5
730637	Dihydrotestosterone-2, 3, 4-$^{13}C_3$ solution, 0.1 mg/mL
749001	4,6-Dioxoheptanoic acid-3, 4, 5, 6, 7-$^{13}C_5$
719552	17β-Estradiol-2, 3, 4-$^{13}C_3$
613967	17β-Estradiol-2, 4, 16, 16, 17-d_5
731668	Estriol-2, 3, 4-$^{13}C_3$
719544	Estrone-2, 3, 4-$^{13}C_3$
802921	Estrone-2,3,4-$^{13}C_3$ solution
710806	18-Hydroxycorticosterone
705594	Hydrocortisone-9, 11, 12, 12-d_4
731641	16-α-Hydroxyestrone-2, 3, 4-$^{13}C_3$
803081	17-α-Hydroxypregnenolone-20, 21-$^{13}C_2$-16,16-d_2
738093	17α-Hydroxyprogesterone-2, 3, 4-$^{13}C_3$
705713	4-Methoxy-13C, d_3-estradiol
705829	2-Methoxy-13C, d_3-estradiol
705705	2-Methoxy-^{13}C, d_3-estrone
705691	4-Methoxy-^{13}C, d_3-estrone
739545	Pregnenolone-20, 21-$^{13}C_2$-16, 16-d_2
740985	Pregnenolone-20, 21-$^{13}C_2$-16, 16-d_2 sulfate sodium salt
737143	Progesterone-2, 3, 4-$^{13}C_3$
803065	Progesterone-2, 3, 4-$^{13}C_3$ solution
730610	Testosterone-2, 3, 4-$^{13}C_3$ solution
750026	3α, 5β-Tetrahydroaldosterone
709719	3, 3′, 5′-Triiodothyronine-(diiodophenyl-$^{13}C_6$) hydrochloride
709611	3, 3′, 5-Triiodothyronine-(tyrosine ring-$^{13}C_6$) hydrochloride

For a full listing of labeled vitamins, steroids and hormones, visit
sigma-aldrich.com/sibio

To inquire about Stable Isotopes custom synthesis or pricing and availability, email us at **isosales@sial.com.**

Vitamins

Cat. No.	Name
699004	L-Ascorbic acid-2-^{13}C
699012	L-Ascorbic acid-3-^{13}C
705268	Biotin-(*ring*-6, 6-d_2)
802891	Coenzyme Q10-(*ring*-d_9)
739898	1α, 25-Dihydroxyvitamin D_2 solution
739855 739863 740578	1α, 25-Dihydroxyvitamin D_2 (6, 19, 19-d_3) solution
740551 740543 740578	1α, 25-Dihydroxyvitamin D_3 (6, 19, 19-d_3) solution
705942	1α, 25-Dihydroxyvitamin D_3 (6, 19, 19-d_3)
803162	Folic acid-(*glutamic acid*-$^{13}C_5$,^{15}N)
803049	Folic acid-(*glutamic acid*-$^{13}C_5$)
705993	3-*epi*-25-Hydroxyvitamin D_3
751316	3-*epi*-25-Hydroxyvitamin D_3 (6, 19, 19-d_3)
803030	25-Hydroxyvitamin D_3-(26,26,26,27,27,27-d_6)
802913	(24*R*), 24,25-Dihydroxyvitamin D_3-26,26,26,27,27,27-d_6 solution
803103	25-Hydroxyvitamin D_3-(23-24-25-26-27-$^{13}C_5$) solution
803138	25-Hydroxyvitamin D_3-(6,19,19-d_3) sulfate solution
803111	25-Hydroxyvitamin D_3-(26,26,26,27,27,27-d_6) sulfate solution
740217	25-Hydroxyvitamin D_2 solution
740209 740195 740071	25-Hydroxyvitamin D_2 (6, 19, 19-d_3) solution
705497	25-Hydroxyvitamin D_2 (6, 19, 19-d_3)
752266	25-Hydroxyvitamin D_2 (25, 26, 27-13C_3) solution
739650	25-Hydroxyvitamin D_3 solution
705888	25-Hydroxyvitamin D_3 (6, 19, 19-d_3)
753149	3-*epi*-25-Hydroxyvitamin D_2
762970	Nicotinamide-2, 4, 5, 6-d_4
705187	Pyridoxal-(*methyl*-d_3) hydrochloride
705322	Pyridoxamine-(*methyl*-d_3) dihydrochloride
705292	Riboflavin-dioxopyrimidine-$^{13}C_4$, $^{15}N_2$
731188	Thiamine-(*4-methyl-*^{13}*C-thiazol-5-yl-*$^{13}C_3$) hydrochloride
731234	α-Tocopherol-(*ring*-5, 7-dimethyl-d_6)
705837	Vitamin B_5 (di-β-alanine-$^{13}C_6$, $^{15}N_2$) calcium salt
803170	Vitamin B_{12}-(dimethylbenzimidazole-$^{13}C_7$) solution
740306	Vitamin D_2 solution
705489	Vitamin D_2 (6,19,19-d_3)
739839	Vitamin D_2 (6,19,19-d_3) solution
740292	Vitamin D_3 solution
740284 731285	Vitamin D_3 (6,19,19-d_3) solution
803189	Vitamin D_3-(6,19,19-d_3) sulfate solution
615366	Vitamin E acetate-(*trimethyl*-d_9)
705470	Vitamin K-d_7(5,6,7,8-d_4, 2-*methyl*-d_3)
737836	Vitamin K_3-d_8

Other Bioactive Compounds

Cat. No.	Name
750913	L-Arbrine-(*methyl*-d_3)
733865	Aldicarb-(*N-methyl*-^{13}C,d_3, *carbomoyl*-^{13}C)
733873	Aldicarb-(*N-methyl*-^{13}C,d_3, *carbomoyl*-^{13}C) sulfone
733881	Aldicarb-(*N-methyl*-^{13}C,d_3, *carbomoyl*-^{13}C) sulfoxide
799122	Azo-Resveratrol-$^{15}N_2$
705101	Barbituric acid-$^{13}C_4$,$^{15}N_2$
791938	Carfilzomib-(*morpholine*-d_8)
719579	(±)-Catechin-2,3,4-$^{13}C_3$
614122	Chenodeoxycholic acid-2,2,4,4-d_4
614149	Cholic acid-2,2,4,4-d_4
741833	L-Citrulline-5,5-d_2
614130	Deoxycholic acid-2,2,4,4-d_4
705349	Desethylamodiaquine-(*ethyl*-d_5)
719528	3, 3′-Diiodo-L-thyronine-(phenoxy-$^{13}C_6$) (T2)
719536	3,3′-Diiodo-L-thyronine (T2)
749001	4,6-Dioxoheptanoic acid-3,4,5,6,7-$^{13}C_5$
722820	Ferulic acid-1,2,3-$^{13}C_3$
739723	Glycocholic-2,2,4,4-d_4 acid
762962	Histamine-α, α,β, β-d_4 dihydrochloride
776084	Histamine-1-^{13}C,1-^{15}N dihydrochloride
763993	1′-Hydroxymidazolam-$^{13}C_3$
762997	2-Imidazolidone-(*ethylene*-d_4)
709557	3-Iodothyronamine-(*ethylamino*-1,1,2,2-d_4) hydrochloride
790362	Isorhamnetic-(*phenyl*-$^{13}C_6$)
793477	Kynurenic acid-3,5,6,7,8-d_5
777498	Malathion-(*diethyl*-d_6)
777447	Metobromuron-(*phenyl*-$^{13}C_6$)
750905	Metalaxyl-(*phenyl*-$^{13}C_6$)
749443	L-Ornithine-3-3,4,4,5,5-d_6 hydrochloride
746266	Oxamyl-1-^{13}C
775634	Penconazol-(*propyl*-d_7)
790370	Phloretin-(*hydroxyphenyl*-$^{13}C_6$)
751073	Ricinine-(*methyl*-d_3)
709891	Spermidine-(*butane*-d_8) trihydrochloride
740780	Spermidine-(*butane*-$^{13}C_4$) trihydrochloride
705330	Spermine-(*butane*-d_8) tetrahydrochloride
755524	Stachydrine-(*dimethyl*-$^{13}C_2$) monohydrate
746274	Vinblastine-^{13}C,d_3
731242	Yohimbine-(*methyl*-^{13}C,d_3 ester)
778400	Ziprasidone-(*piperazine*-d_8)

METABOLOMICS ANALYSIS AND THE METLIN METABOLITE DATABASE

Metabolomics is an emerging field in "-omics" research and has been gaining momentum as a discovery platform in pharmaceutical and diagnostic research. In fact, most biomarkers are metabolites and have been used for decades to assess disease or disease risk.[1] Identifying novel metabolite biomarkers and discerning their biological roles are essential to discovering new methods for disease diagnosis as well as identifying new therapeutic targets. With technological advancements in analytical instrumentation and methods, the ability to rapidly measure thousands of metabolites within a single sample has now been realized.

Metabolomics analyses generally employ one of two approaches: targeted or untargeted metabolomics. Targeted metabolomic analysis involves the measurement of specific known metabolites in a sample, usually within a defined pathway or related group of compounds. This approach can be useful to screen for a group of metabolites implicated as signals for disease, such as diabetes, or to screen newborns for inborn errors in metabolism.

Untargeted metabolomic analysis is global in scope and provides an unbiased metabolic profile of both known and unknown metabolites within a sample.[2] This technique is used in a broad range of applications, including nutritional assessments and the investigation into biomarkers for disease and toxicological effects.[3] The untargeted metabolomic method can generate extremely large amounts of data, which require software programs and databases for processing. Using bioinformatics software such as XCMS to detect and align features of the LC/MS data can help simplify the process.[4] Any feature of interest is identified by searching the m/z value of the compound in a database, such as METLIN. A database match should be confirmed by comparison of retention times and MS/MS data to a standard compound.[2]

The METLIN Metabolite Database was created in 2004 through the efforts of Dr. Gary Siuzdak and his lab at the Scripps Center for Metabolomics and Mass Spectrometry. METLIN is a freely accessible, web-based database to assist researchers in metabolite identification by providing metabolite structural information along with high-resolution tandem mass spectrometry (MS/MS) spectra.[5] METLIN currently contains over 64,000 compounds with annotations and structures, with corresponding MS/MS spectra available on >10,000 compounds.

Sigma Life Science is proud to be working together with the Scripps Center for Metabolomics to expand the library of tested metabolites within the METLIN Metabolite Database. The tandem mass spectrometry data generated by Scripps are available in the METLIN Metabolite Database and on Sigma product webpages. METLIN also provides links to Sigma metabolite pages to simplify the identification and ordering process of standard compounds.

For additional information on METLIN and the collaboration between Sigma and Scripps Center for Metabolomics, visit
sigma-aldrich.com/metlin

References

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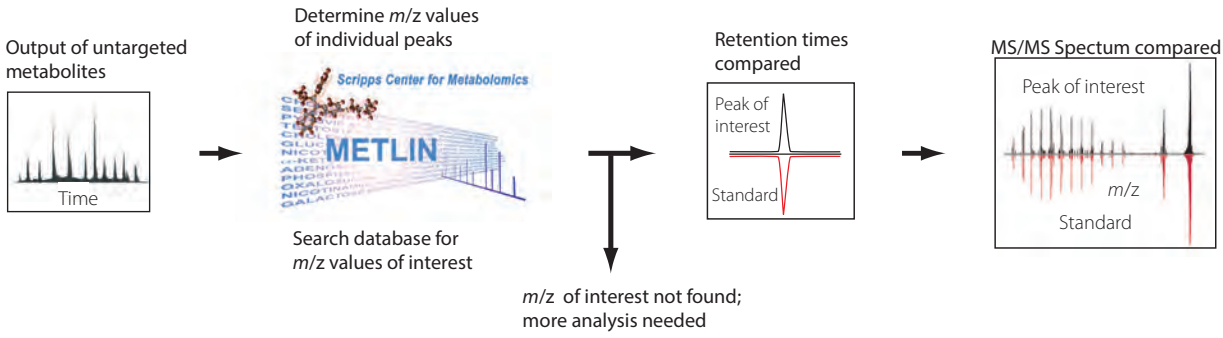

The Untargeted Metabolomic Workflow

The workflow involves determining the ***m/z*** values for peaks within a biological sample, then searching METLIN for the ***m/z*** value of interest. Once the peak of interest is identified, comparison of retention times and tandem MS to a standard compound is required.

MASS SPECTROMETRY METABOLITE LIBRARY OF STANDARDS

Supplied by IROA Technologies

Product Description

MSMLS™ (Mass Spectrometry Metabolite Library of Standards) is a collection of high quality small biochemical molecules that span a broad range of primary metabolism. These are high purity (>95%) compounds supplied in an economical, ready-to-use format. The library of standards are most commonly used to provide retention times and spectra for key metabolic compounds, help optimize mass spectrometry analytical protocols, and qualify and quantify mass spectrometry sensitivity and limit of detection. MSMLS comes with MSMLSDiscovery™, a software tool to support the extraction, manipulation, and storage of the data generated when using our MSMLS Library of authentic metabolomics standards.

Features and Benefits

Compounds

619 unique small molecule metabolites organized in a 96-well format according to solubility:

- Water-soluble
- 40% Aqueous ethanol-soluble
- 100% ethanol-soluble

Broad metabolite spectrum, key primary metabolites and intermediates covering key metabolic pathways, including the following classes of compounds:

- Carboxylic acids, amino acids
- Biogenic amines, polyamines
- Nucleotides, coenzymes and vitamins
- Mono- and disaccharides
- Fatty acids, lipids, steroids, and hormones

Convenient

- High purity metabolites, pre-weighed, solubilized in either water, 40% aqueous ethanol or 100% ethanol and supplied dried
- The library is intended to be used for mass spectrometry metabolomics applications and provides a broad representation of primary metabolites

Formatted

MSMLS contains 619 small molecule metabolites:

- Arrayed in 96-well format
  - 7 polypropylene racks
  - Supplied as 5 µg dried weight
- Rack map provided upon purchase
  - Alphanumeric assigned position
  - Descriptors: Name, Parent CID, molecular formula, molecular weight, CAS, ChEBI, HMDB ID, PubChem Compound and Substance ID
- Suitable for manual and automated work flow

Software

MSMLSDiscovery™ software package is distributed with and is tailored to work with MSMLS. A User Manual and video instructions are provided. The requirements of the program are that:

- The most recent version of Java 7 must be installed and callable
- The computer should have at least 8 GB of RAM
- You are running Windows 7 or 8

Acknowledgements

We gratefully acknowledge usage of the following websites and databases for their publicly accessible information:

Database

- The Human Metabolome Database (HMDB), v 2.5 [1-3] **http://hmdb.ca/**
- Chemical Entities of Biological Interest (ChEBI) [4] **https://www.ebi.ac.uk/chebi/**
- Chemical Abstracts Service (CAS) REGISTRY Database **https://www.cas.org/**
- Kyoto Encyclopedia of Genes and Genomes (KEGG) [5] **http://www.kegg.com/**
- The METLIN Metabolomics Database [6-7] **http://metlin.scripps.edu/index.php**
- The PubChem Compound Database [8] **http://www.ncbi.nlm.nih.gov/pccompound/**

References

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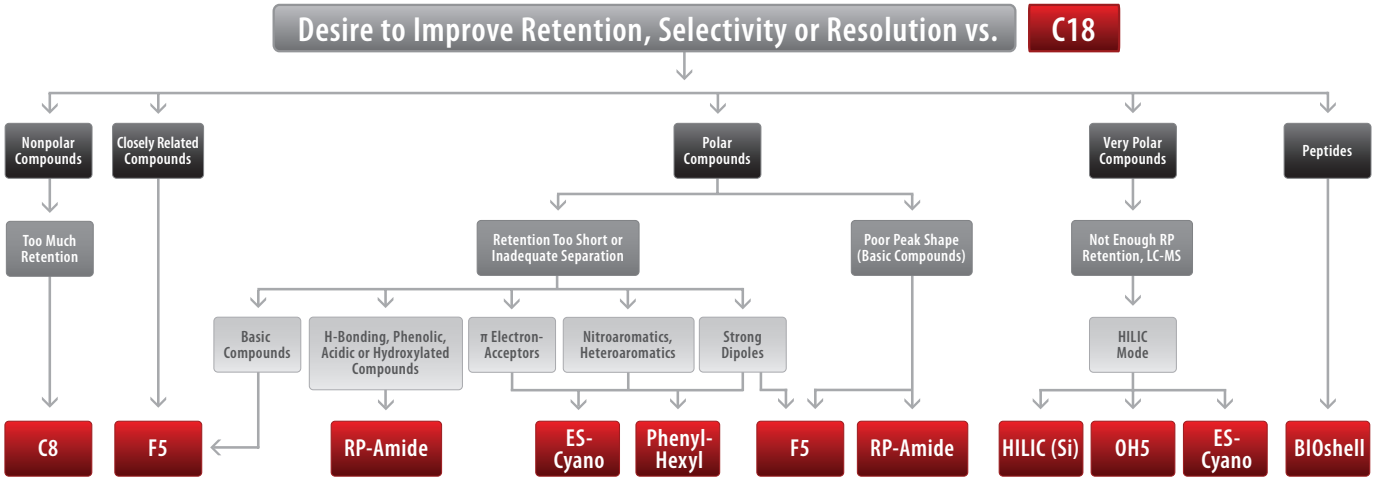
SELECTING THE RIGHT PHASE CHEMISTRY FOR YOUR APPLICATION

C18 column is the standard first choice when starting a new LC-MS method. You can consider selecting another stationary phase when C18 doesn't give the desired separation, or the sample contains compounds difficult to retain or resolve on C18. The Ascentis Express and BIOshell product lines offer a wide range of selectivities for making an effective choice. This decision tree will help you to select an alternative phase based on the particular compound type or separation challenge. All options displayed are relative to the C18 column that started your separation journey. Supelco® provides a wide selection of stationary phase options.



Key product features for LC/MS and (U)HPLC applictions

Primary Application	Product Line	Particle Size (µm)	Pore Size (A)	Surface Area (m2/g)	Max Temperature	Pressure (bar)
Small molecules, metabolites and low molecular weight peptides	Titan	1.9	80	410	60	1,000
	Ascentis Express	2.0	90	120	60	1,000
		2.7	90	150	60	600
		5.0	90	100	60	600
Proteins, Peptides and large Bio-molecules	BIOshell	2.7	160	90	90	600
		3.4	400	15	90	600
		5.0	160	60	90	600

For a complete listing of LC/MS columns, visit
sigma-aldrich.com/hplc

Available in a variety of analytical and capillary column dimensions

	Column Length (cm)						
Column I.D	2	3	5	7.5	10	15	25
75 µm			•			•	
100 µm			•			•	
200 µm			•			•	
2.1 mm	•	•	•	•	•	•	•
3 mm	•	•	•	•	•	•	•
4.6 mm	•	•	•	•	•	•	•

For Part Numbers, visit
sigma-aldrich.com/hplc

LC/MS & (U)HPLC COLUMNS

Ascentis Express & BIOshell™ Fused-Core® U/HPLC & LC/MS Columns

Key Features and Benefits*

- Maximize speed with sharp peaks even at ultra-high flow rates
- Stable low-bleed for LC-MS and LC-UV
- Suitable for all HPLC, UHPLC, and LC-MS instruments
- Achieve UHPLC performance on a traditional HPLC system
- Available in both 2.0, 2.7 and 5 µm particles
- Wide variety of pore sizes, ranging from 90 - 400 Å, for small to large molecules

Ascentis® Express Fused-Core® Columns

Ascentis Express columns provide a breakthrough in (U)HPLC and LC/MS column performance. Based on Fused-Core particle technology, Ascentis Express columns provide the benefits of high speed and high efficiency. The Fused-Core particle consists of a solid core and a porous shell, allowing for a shorter diffusion path compared to conventional fully porous particles. Compared to totally porous particles typically used in HPLC, Ascentis Express Fused-Core particles generate approximately half the backpressure without loss of resolution. This permits for more resolving power, and faster flow rates, for higher throughput.

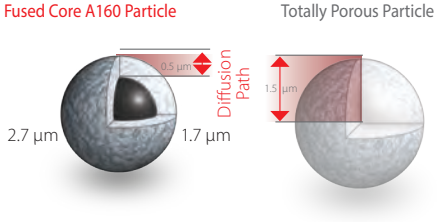
Ascentis Express Fused Core Columns are now available in 2.0, 2.7 and 5 µm particle sizes with 8 different phase chemistries. Available in pore size of 90 Å, Ascentis Express are ideal for LC/MS and (U)HPLC separations of small molecules, metabolites and low molecular weight peptides.

BIOshell™ Fused-Core® Columns

Faster, Better Peptide and Protein Separations

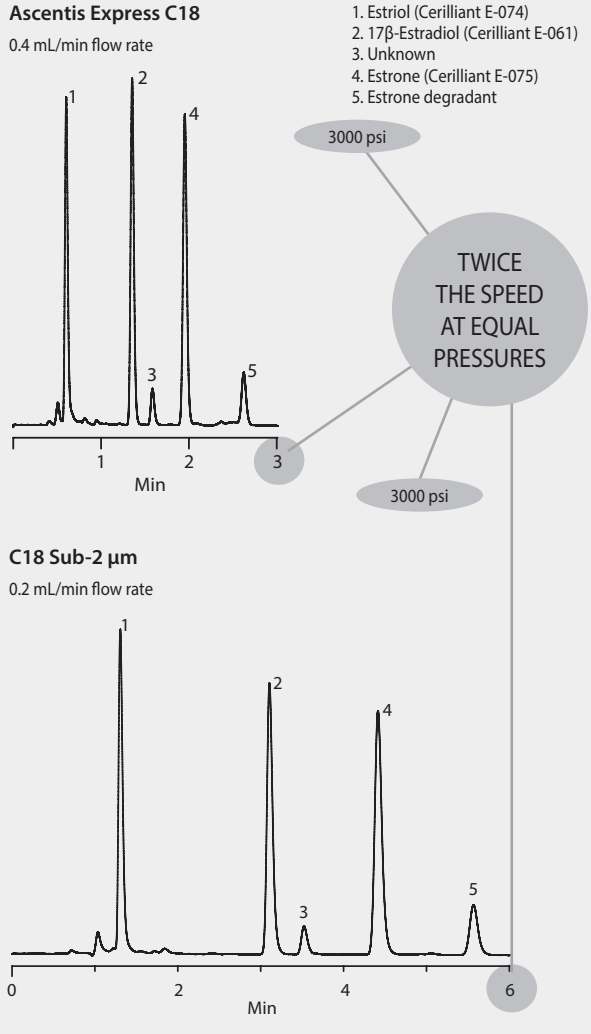
BIOshell columns are the most recent innovation in Fused-Core particle technology: high efficiency reversed-phase columns for protein and peptide separations. BIOshell columns can be operated in HPLC or UHPLC instrumentation equipped with a mass spectrometer or any other detector. BIOshell A160 Peptide columns are packed with either 2.7 or 5 µ particles containing 160 Å pores, and are available with a C18 alkyl or alkyl cyano (CN) bonded phase functionality. BIOshell A400 Protein columns are packed with 3.4 µ particles containing 400 Å pores, and are bonded with C4 alkyl functional groups.

Comparison of Fused-Core and Standard HPLC Particle



Hyper-Fast Separations on Ascentis Express: Twice the Speed at Equivalent Pressure vs. Sub-2 µm

columns: Ascentis Express C18, 10 cm × 2.1 mm I.D., 2.7 µm particles (53823-U) and sub-2 µm particle column (same dimensions)
mobile phase: 49:51 or 55:45, water:acetontrile
flow rate: 0.4 or 0.2 mL/min
column temp: ambient
detector: UV, 200 nm
injection: 1 µL



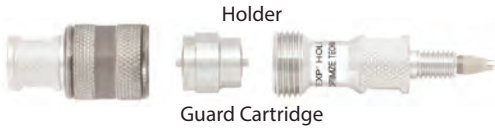
Ascentis® Express, BIOshell™ & Titan Columns for LC/MS & (U)HPLC

Particle Size	I.D.	Length	C18	C8	Peptide C18	OH5
Capillary Dimensions Columns						
2.7 µm	75 µm	5 cm	53982-U	53983-U	67085-U	—
2.7 µm	75 µm	15 cm	54219-U	54229-U	67086-U	—
2.7 µm	100 µm	5 cm	53985-U	53987-U	67087-U	—
2.7 µm	100 µm	15 cm	54256-U	54260-U	67088-U	—
2.7 µm	200 µm	5 cm	53989-U	53991-U	67089-U	—
Ascentis Express Columns						
2.0 µm	2.1 mm	2 cm	50805-U	51652-U	—	50951-U
2.0 µm	2.1 mm	3 cm	50809-U	51654-U	—	50952-U
2.0 µm	2.1 mm	5 cm	50811-U	51656-U	—	50957-U
2.0 µm	2.1 mm	7.5 cm	50812-U	51657-U	—	50958-U
2.0 µm	2.1 mm	10 cm	50813-U	51658-U	—	50959-U
2.0 µm	2.1 mm	15 cm	50814-U	51661-U	—	50962-U
2.0 µm	3.0 mm	3 cm	50815-U	51663-U	—	50963-U
2.0 µm	3.0 mm	5 cm	50816-U	51664-U	—	50964-U
2.0 µm	3.0 mm	7.5 cm	50817-U	51672-U	—	50965-U
2.0 µm	3.0 mm	10 cm	50819-U	51673-U	—	50967-U
2.0 µm	3.0 mm	15 cm	50821-U	51674-U	—	50968-U
2.7 µm	2.1 mm	2 cm	53799-U	53795-U	—	53779-U
2.7 µm	2.1 mm	3 cm	53802-U	53839-U	66901-U	53748-U
2.7 µm	2.1 mm	5 cm	53822-U	53831-U	66902-U	53749-U
2.7 µm	2.1 mm	7.5 cm	53804-U	53843-U	66903-U	53755-U
2.7 µm	2.1 mm	10 cm	53823-U	53832-U	66904-U	53757-U
2.7 µm	2.1 mm	15 cm	53825-U	53834-U	66905-U	53764-U
2.7 µm	3.0 mm	3 cm	53805-U	53844-U	66906-U	53766-U
2.7 µm	3.0 mm	5 cm	53811-U	53848-U	66907-U	53767-U
2.7 µm	3.0 mm	7.5 cm	53812-U	53849-U	53312-U	53768-U
2.7 µm	3.0 mm	10 cm	53814-U	53852-U	66908-U	53769-U
2.7 µm	3.0 mm	15 cm	53816-U	53853-U	66909-U	53771-U
2.7 µm	4.6 mm	3 cm	53818-U	53857-U	53316-U	53772-U
2.7 µm	4.6 mm	5 cm	53826-U	53836-U	66913-U	53774-U
2.7 µm	4.6 mm	7.5 cm	53819-U	53858-U	53323-U	53775-U
2.7 µm	4.6 mm	10 cm	53827-U	53837-U	66915-U	53776-U
2.7 µm	4.6 mm	15 cm	53829-U	53838-U	66917-U	53778-U
5 µm	2.1 mm	10 cm	50517-U	50368-U	67004-U	50322-U
5 µm	2.1 mm	15 cm	50518-U	50372-U	67006-U	50327-U
5 µm	2.1 mm	2 cm	50507-U	50362-U	—	50313-U
5 µm	2.1 mm	25 cm	50521-U	50373-U	—	50328-U
5 µm	2.1 mm	3 cm	50508-U	50363-U	67001-U	50314-U
5 µm	2.1 mm	5 cm	50509-U	50364-Y\U	67002-U	50317-U
5 µm	2.1 mm	7.5 cm	50511-U	50367-U	67003-U	50321-U
5 µm	3.0 mm	10 cm	50526-U	50381-U	67011-U	50338-U
5 µm	3.0 mm	15 cm	50527-U	50382-U	67012-U	50339-U
5 µm	3.0 mm	25 cm	50528-U	50385-U	—	50341-U
5 µm	3.0 mm	3 cm	50522-U	50376-U	67007-U	50329-U
5 µm	3.0 mm	5 cm	50523-U	50377-U	67008-U	50335-U
5 µm	3.0 mm	7.5 cm	50525-U	50378-U	—	50336-U
5 µm	4.6 mm	10 cm	50536-U	50391-U	67014-U	50346-U
5 µm	4.6 mm	15 cm	50537-U	50392-U	67015-U	50347-U
5 µm	4.6 mm	25 cm	50538-U	50394-U	—	50348-U
5 µm	4.6 mm	3 cm	50529-U	50386-U	—	50343-U
5 µm	4.6 mm	5 cm	50530-U	50389-U	67013-U	50344-U
5 µm	4.6 mm	7.5 cm	50533-U	50390-U	—	50345-U
Ascentis Express Guard Cartridges, Package of 3						
2.0 µm	2.1 mm	0.5 cm	50822-U	51676-U	—	—
2.0 µm	3.0 mm	0.5 cm	50823-U	51679-U	—	—
2.7 µm	2.1 mm	—	53501-U	53509-U	66918-U	53780-U
2.7 µm	3.0 mm	—	53504-U	53511-U	66919-U	53781-U
2.7 µm	4.6 mm	—	53508-U	53512-U	66921-U	53782-U
5 µm	2.1 mm	—	50539-U	—	67016-U	—
5 µm	3.0 mm	—	50541-U	—	67017-U	—
5 µm	4.6 mm	—	50542-U	—	67018-U	—

Particle Size	I.D.	Length	C18	C8	Peptide C18	OH5
Titan U/HPLC columns						
1.9 µm	2.1 mm	2 cm	577120-U	—	—	—
1.9 µm	2.1 mm	3 cm	577121-U	—	—	—
1.9 µm	2.1 mm	5 cm	577122-U	—	—	—
1.9 µm	2.1 mm	7.5 cm	577123-U	—	—	—
1.9 µm	2.1 mm	10 cm	577124-U	—	—	—
1.9 µm	3.0 mm	3 cm	577125-U	—	—	—
1.9 µm	3.0 mm	5 cm	577126-U	—	—	—
Titan U/HPLC columns						
1.9 µm	2.1 mm	—	577127-U	—	—	—
1.9 µm	3.0 mm	—	577128-U	—	—	—

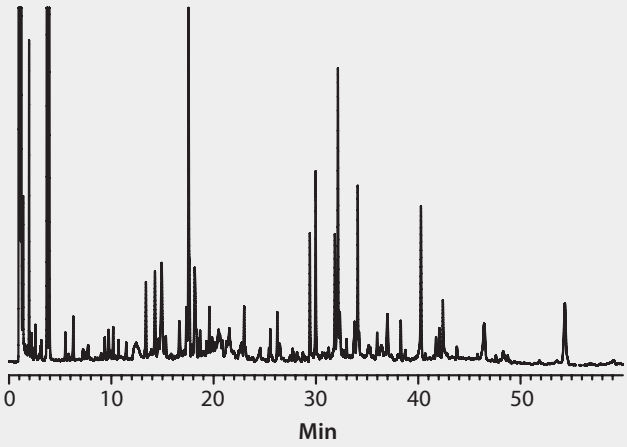
Guard Cartridge Holder

Cat. No.	Description	Pkg. Size
	Universal Guard Holder	
53500-U	Holder w/EXP Titanium Hybrid Ferrule (cartridge not included)	1



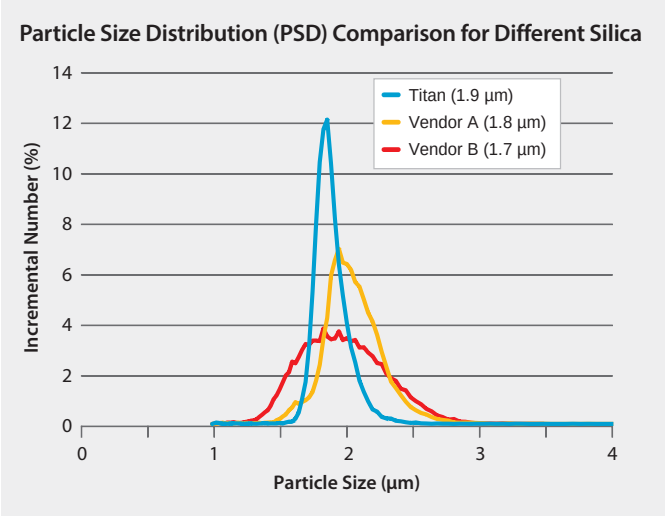
Analysis of Tryptic Digests on BIOshell A160 Peptide ES-C18

column: BIOshell A160 Peptide C18, 10 cm x 4.6 mm I.D. (66915-U)
mobile phase A: 0.1% (w/v) TFA in water
mobile phase B: 0.1% TFA (w/v) in 40:60 water:acetonitrile
gradient: initial = 3% B to 100% B in 53 min.
flow rate: 1.0 mL/min
temp.: 30 °C
det.: UV at 215 nm
injection: 20 µL



Titan UHPLC Columns

Titan C18 is based on a silica particle platform that has the narrowest particle size distribution available of any totally porous particles. This provides performance advantages in the A-term of the van Deemter equation and in the elimination of fines associated with broader particle size distributions. Monodisperse particles, owing to their narrow particle size distributions, are one of the key reasons that core-type particles achieve higher efficiencies than comparative porous particles.



Key Features

These monodisperse particles offer:

- Minimized voiding and channeling in silica bed compared to higher PSD particles
- A positive influence on column permeability, as evident from a Titan UHPLC column's low pressure drop compared to other traditional porous particle columns
- A profound affect on separation impedance or kinetic performance, resulting in more robust and rugged LC/MS columns

TSKGEL® HPLC COLUMNS FOR PROTEIN FRACTIONATION AND PEPTIDE ANALYSIS

- Researchers in metabolomics and proteomics rely heavily on HPLC and UHPLC columns to reduce the complexity of their sample before it enters the mass spec
- Use a TSKgel gel filtration column to pre-fractionate your sample in specific MW fractions
- Perform high speed separations on a non-porous TSKgel cation exchange column in the 1st dimension of your 2D LC system
- Improve sample throughput with the Fused-Core® Ascentis® Express Peptide ES-C18 column whether you operate a traditional HPLC or an UHPLC system

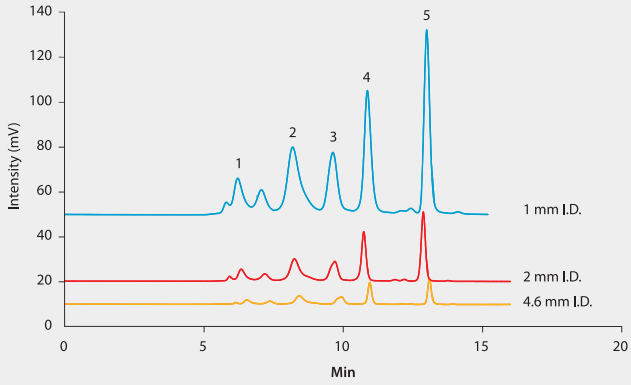
High Resolution TSKgel® Gel Filtration Chromatography Columns

In 1977, Tosoh introduced the TSKgel SW-type product line (10 µm), the first silica-based high performance gel filtration columns for proteins. Since then, TSKgel SW × l (5 µm) and later TSKgel SuperSW columns (4 µm) have become synonymous with analyzing protein molecular mass, first in the emerging field of biotechnology and currently in the development of biotherapeutics. Featuring ultra-efficient 4 µm particles, TSKgel SuperSW2000 and SuperSW3000 provide higher efficiency than 5 µm TSKgel G2000SW × l and G3000SW × l columns. Use narrow bore 2.1 mm or 1.0 mm I.D. columns when you are sample limited, want to reduce buffer consumption, or connect the column to MS. To benefit fully from the high efficiency of 4 µm columns, it is important to minimize the amount of dead volume in the HPLC system. TSKgel SuperSW2000 columns are best suited for peptides and recombinant proteins up to a molecular mass of ~100 kDa. Larger proteins, including monoclonal antibodies and antibody drug conjugates require the larger pore size available in TSKgel SuperSW3000 columns. Depending on the mass of the therapeutic protein, either column can be used successfully to determine protein aggregates.

Cat. No.	Product Name	L (cm)	I.D. (mm)	Pore Diameter (Å)	Particle Size (µm)
818674	TSKgel® SuperSW2000 Size Exclusion HPLC Column	30	4.6	125	4
818675	TSKgel® SuperSW3000 Size Exclusion HPLC Column	30	4.6	250	4
821485	TSKgel® SuperSW3000 Size Exclusion HPLC Column	30	2.0	250	4
821845	TSKgel® SuperSW3000 Size Exclusion HPLC Column	30	1.0	250	4

Effect of Sample Mass on Detection Sensitivity

columns:	TSKgel SuperSW3000, 30 cm × 4.6 mm I.D. TSKgel SuperSW3000, 30 cm × 2 mm I.D. TSKgel SuperSW3000, 30 cm × 1 mm I.D.
eluent:	0.1 mol/L phosphate buffer + 0.1 mol/L Na_2SO_4 + 0.05% NaN_3 (pH 6.7)
flow rate:	0.350 mL/min (4.6 mm I.D.) 0.650 mL/min (2 mm I.D.) 0.016 mL/min (1 mm I.D.)
detection:	UV at 280 nm
detector cell volume:	2 µL (4.6 and 2 mm I.D.) 35 nL (1 mm I.D.)
temperature:	25 °C
injection volume:	1 µL



High Speed TSKgel STAT® Ion Exchange Chromatography Columns

The recently launched TSKgel STAT columns are packed with non-porous particles to which an expanded network of functional groups is grafted to obtain relatively high binding capacity. The matrix in all TSKgel STAT columns is composed of a methacrylate copolymer that is shaped into spherical particles of 5, 7 or 10 micron size. TSKgel Q-STAT and DNA-STAT columns contain strong (quaternary ammonium) anion exchange groups, while TSKgel CM-STAT and SP-STAT contain (weak) carboxymethyl and strong (sulfopropyl) cation exchange groups, respectively.

TSKgel STAT columns are Tosoh's second generation of non-porous particles. In the mid 1990's, Tosoh led the trend towards ultra-efficient HPLC columns by introducing TSKgel NPR columns containing 2.5 micron non-porous poly(methacrylate) particles for the analysis of proteins by reversed phase, hydrophobic interaction and ion exchange chromatography.

Compared to porous particles, nonporous particles show better recoveries at low peptide and protein concentrations. Compared to TSKgel NPR columns, the longer TSKgel STAT columns display similar efficiency, but higher throughput and binding capacity.

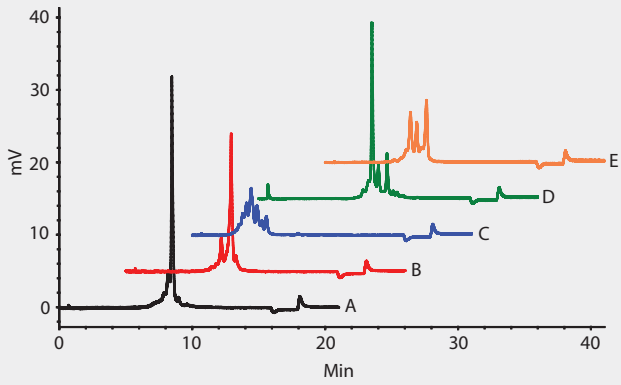
In addition to the analysis of charge variants shown on this page, Separation Report 109 details typical applications for TSKgel STAT columns. The report is available for download at **sigma-aldrich.com/tsk**

Cat. No.	Product Name	L (cm)	I.D. (mm)	Pore Diameter (Å)	Particle Size (µm)
821962	TSKgel DNA-STAT Strong Anion Exchange HPLC Column	10	4.6	Non-porous	5
821961	TSKgel Q-STAT Strong Anion Exchange HPLC Column	10	4.6	Non-porous	7
821960	TSKgel Q-STAT Strong Anion Exchange HPLC Column	3.5	3.0	Non-porous	10
821966	TSKgel CM-STAT Weak Cation Exchange HPLC Column	10	4.6	Non-porous	7
821965	TSKgel CM-STAT Weak Cation Exchange HPLC Column	3.5	3.0	Non-porous	10
821964	TSKgel SP-STAT Strong Cation Exchange HPLC Column	10	4.6	Non-porous	7
821963	TSKgel SP-STAT Strong Cation Exchange HPLC Column	3.5	3.0	Non-porous	10

Fast Analysis of Therapeutic mAbs on a TSKgel STAT Weak Cation Exchange Column

A TSKgel CM-STAT weak cation exchange column was applied to separate charge variants of several monoclonal antibodies. The typical analysis time on conventional 25 cm long WCX columns of about eighty minutes could be significantly reduced when separation was performed on a 10 cm TSKgel CM-STAT column, filled with 7 µm particles. The analysis profiles for five antibodies show that high resolution analysis can be obtained in about 20 minutes analysis time.

Column	TSKgel CM-STAT, 10 cm × 4.6 mm I.D., 7 µm particles (821966)
mobile phase	A: 20mM MES buffer, ph 6.0 B: 0.5 M NaCl in buffer A, pH 6.0 gradient: 10% B (0min.), 30% B (15 min.), 100% B (15.1 min.) 100% B (17.1 min.), 10% B (17 min.), 10% B (21 min.)
flow rate	1 mL/min
column temp.	ambient
detector	UV at 280 nm
injection	20 µL
sample	monoclonal antibodies (mAb A through E)
Application No.	G005458



For a convenient listing of all available TSKgel STAT columns search the Sigma-Aldrich website for TSKgel STAT.

For more information on TSKgel columns, visit
sigma-aldrich.com/tsk

CHEMICAL DERIVATIZATION REAGENTS FOR LC-MS

Modern mass spectrometry techniques such as APCI or ESI are highly successful in providing valuable structural information and allow the detection of very low analyte concentrations in various sample matrices. However, in today's advanced research and analytical areas, such as metabolomics, clinical and forensics analytics, such methods are sometimes insufficiently sensitive to deliver the solution to a particular analytical problem [1].

Therefore, derivatization is used in mass spectrometry to increase ionization efficiency, and thus enhance the sensitivity of the ionization used, to result in lower analyte detectability [2]. The derivatization reagents have functional groups with high proton (cation) affinity that stabilize positive charge. Of similar importance in derivatization is the improvement of qualitative analysis by modifying fragmentation behavior to form unique product ions, and shifting them to a specific, unique mass ("fingerprinting"), as well as precise quantitative analysis to profile comparatively small analyte molecules, particularly in metabolomics.

For more information, visit
sigma-aldrich.com/derivatization

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Cat. No.	Product Name	Analyte Functional Group	Typical Application	Reference
00721	4-(Dimethyl-d_6-amino)benzoyl chloride	Hydroxy	Deuterium mass shift	[3]
03334	Dansylhydrazine	Carbonyl	—	[2c]
03641	Dansyl chloride	Hydroxy	—	[2c]
05022	*N,N*-Dimethylglycine	Hydroxy	Cholesterol	[11]
05689	Diethyl ethoxymethylenemalonate	Amine	Amino acids	[12]
06696	3-Amino-9-ethylcarbazole	Hydroxy	Sugars	[13]
06963	4-(Diethylamino)benzhydrazide	Carbonyl	—	[3]
08843	2-Hydrazinopyridine	Carbonyl	Steroids	[14]
29208	(*N*-Succinimidyloxycarbonylmethyl) tris(2,4,6-trimethoxyphenyl) phosphonium bromide	Amine	Protein sequence analysis	[15]
42579	4-Phenyl-1,2,4-triazoline-3,5-dione	Diene	Vitamin D	[16]
59799	4-(Diethylaminomethyl) benzhydrazide	Carbonyl	—	[3]
61224	*N*-Succinimidyl 4-(dimethylamino) benzoate	Amine	Glycerophosphoethanolamine lipids	[4]
65562	2-Picolylamine	Carbonyl	Steroids	[14]
67954	4-(Dimethylamino) benzoyl chloride	Hydroxy	17β-Estradiol	[3]
69706	6-Bromo-3-pyridinylboronic acid	1,2-Dihydroxy	Brassinosteroids	[5]
72702	3,5-Dinitrobenzoyl chloride	Hydroxy	Tetrahydrocorticosterones	[6]
73177	1-Fluoro-2,4-dinitrobenzene	Amine	Prim./sec. aliphatic amines	[7]
74905	9-Anthracenemethanol	Carboxylic acid, amine, alcohol	—	[17]
75821	1,2-Benzo-3,4-dihydrocarbazole-9-ethyl-*p*-toluenesulfonate	Carboxylic acid	Fatty-/bile acids	[8]
79291	4-[2-(*N,N*-Dimethylamino)ethylaminosulfonyl]-7-(2-aminoethylamino)-2,1,3-benzoxadiazole	Carboxylic acid	Fatty acids	[9]
89397	Girard's reagent T	Carbonyl	Nucleosides	[18]
92989	4-(Dimethylamino)benzohydrazide	Carbonyl	—	[3]
93742	Pentafluorophenylhydrazine	Carbonyl	Oligosaccharides	[10]
94076	{1-[2-(Diethylamino)ethoxy]-2-isothiocyanatoethyl}benzene	Amine	—	[3]
97622	2-Mercaptoethanol	Double bond	Microcystins	[19]

TOOLS FOR METABOLITE ANALYSIS BY GC-MS

Strategies to analyze small biological compounds in a metabolome range from analyzing a particular class of metabolites (targeted analysis) to separating and detecting as many metabolites as possible of a particular developmental stage (metabolite profiling or metabonomics). When gas chromatography (GC) is used as the separation technique, the analyst benefits from the high resolving power of capillary GC, but the task is complex, as not all compounds are volatile and therefore need to be derivatized before analysis.

This and other pages in this publication list selected product options for the analysis of volatile and semi-volatile metabolites, including metabolite standards, derivatization reagents, solid-phase microextraction (SPME), and selected GC columns and accessories. For detailed information, references 1 and 2 look at the role of GC and MS in metabolite analysis, while references 3 and 4 discuss compound identification and sample throughput, respectively.

References

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SLB®-5ms, An MS-Grade Capillary GC Column for Metabolomics Research

The 5% phenyl equivalent phase provides a boiling point elution order with a slight increase in selectivity, especially for aromatic compounds. The low bleed characteristics, inertness, and durable nature make it the column of choice for the analysis of semivolatiles or, in general, any application that requires a low bleed non-polar column. Temp. Limits for ≤0.25 mm I.D. are -60 °C to 340 °C (isothermal) or 360 °C (programmed).

Cat. No.	I.D. (mm)	df (µm)	Length (m)	Beta Value	Qty.
28465-U	0.10	0.10	10	250	1 ea.
28466-U	—	0.10	15	250	1 ea.
28564-U	0.18	0.18	20	250	1 ea.
28566-U	—	0.30	12	150	1 ea.
28575-U	—	0.30	30	150	1 ea.
28576-U	—	0.36	20	125	1 ea.
28513-U	0.20	0.20	30	250	1 ea.
28467-U	0.25	0.10	30	625	1 ea.
28469-U	—	0.25	15	250	1 ea.
28471-U	—	0.25	30	250	1 ea.
28472-U	—	0.25	60	250	1 ea.
28577-U	—	0.50	15	125	1 ea.
28473-U	—	0.50	30	125	1 ea.
28474-U	—	0.50	60	125	1 ea.
28476-U	—	1.00	30	63	1 ea.

Extend the Lifetime of Your Capillary Column

A guard column/retention gap is a short (1-5 m) piece of uncoated deactivated fused silica tubing which is placed in-line between the GC injection port and the capillary column. A guard column/ retention gap consists of two parts: a short length of fused silica tubing and a connector. Match the deactivation of the fused silica tubing with the polarity of the injection solvent. In most cases, it is also recommended to match the I.D. of the capillary column.

For more information about guard column selection, visit
sigma-aldrich.com/gc-guard

SPME, A Unique Sample Preparation Technique

Solid Phase Microextraction is the sample preparation technique of choice for analyzing volatile and semi-volatile metabolites by GC-MS. SPME eliminates most drawbacks to extracting organics by more traditional methods. It requires no solvents or complicated apparatus, and can concentrate volatile and nonvolatile compounds, in both liquid and gaseous samples, for analysis by GC and GC-MS. SPME reduces sample preparation time by 70%, minimizes the use of solvents and their disposal, is cost-effective, can be used with any GC system, and can be automated.

An SPME fiber assembly consists of a length of fused silica fiber coated with a polymer material, in some cases mixed with a solid adsorbent. The fiber is attached to a stainless steel plunger sheathed by a protective needle.

Fiber holders are available for manual injection as well as for use with autosamplers. The holder protects the coated fiber, and controls exposure of the fiber during analyte adsorption and desorption. The holder is reusable indefinitely and accepts the replaceable fiber assembly. First time users must order both a holder and a fiber assembly. Fiber holders for use with an autosampler are also available.

Fiber Holder for Manual Sampling

An adjustable depth guide positions the fiber for sampling and for correct placement in the heated zone of the GC injection port. The fiber can be locked in the exposed position.

Cat. No.	Description	Qty.
57330-U	SPME Fiber Holder, for use with manual sampling	1 ea.

SPME Fiber Assemblies

SPME fiber assemblies can be reused for ≥100 analyses, depending on the application and the care they are given. For reuse, simply condition with heat before and after every analysis. Each assembly has a color-coded or notched hub indicating the type of coating on the fiber. Choose the appropriate assembly for the holder: manual or autosampler. The key to proper SPME performance is fiber selection.

For information on how to select a fiber, visit
sigma-aldrich.com/spme

SPME Fiber Assortment Kit for Volatiles and Semivolatiles

Recommended starter kit for the extraction of volatile and semivolatile metabolites contains one fiber each of 85 µm polyacrylate coating, 100 µm polydimethylsiloxane coating, and 7 µm polydimethylsiloxane coating.

Cat. No.	For Use with	Needle	Qty.
57306	Manual holder	24 ga	1 kit
57307	Autosampler	24 ga	1 kit
57285-U	Autosampler	23 ga	1 kit

Achieve Sharper Peaks with SPME-GC Analyses Using Supelco® Inlet Liners

GC injection port liners are designed for optimal sample introduction for specific injection techniques. When using SPME, a 0.75 mm I.D. inlet liner increases linear velocity, compared to a conventional, larger volume 2 mm I.D. liner, and rapidly introduces analytes onto the column in a narrow band. To minimize sample loss or peak tailing, the inlet liner must be inert to minimize adsorption of active sample components. An inlet liner, in conjunction with efficient, solvent-free, SPME sample introduction, helps to achieve excellent chromatographic results. An inlet liner for several Agilent® GC systems is available.

For Agilent® (5890, 6890, and 7890)

Inlet Liner, Direct (SPME) Type, Straight Design (unpacked)

L × O.D. × I.D. _____ 785 mm × 65 mm × 0.75 mm

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To select the appropriate inlet liner for your GC, visit **sigma-aldrich.com/inletliners**

GC Derivatization Reagents

Gas chromatography does not easily apply to compounds of biomedical interest, particularly to compounds containing functional groups with active hydrogen atoms (-COOH, -OH, -NH, and-SH). These groups are difficult to analyze by GC because they are not sufficiently volatile, show excessive tailing, can be too strongly attracted to the stationary phase or are thermally unstable. Nevertheless, GC coupled with MS has proven to be a highly efficient, sensitive and reproducible method for metabolomics. To render analytes amenable for GC-MS, chemical derivatization is required to make them less polar, but more volatile and thermally stable. Derivatizing with a characteristic moiety can also serve to enhance mass spectrometric properties, by producing either more favorable diagnostic fragmentation patterns of use in structure investigations, or characteristic ions in trace analyses employing selected ion monitoring and related techniques. Most derivatization reactions commonly used for gas chromatography applications fall into three categories: silylation, acylation, alkylation and esterification. Here we briefly mention silyl derivatization. Much more information can be found in the 100 page guide "Derivatization Reagents", which can be requested from the Sigma-Aldrich® website.

Trimethylsilyl (TMS) derivatization reagents are the most common for GC analysis. The TMS group contributes both chemical and thermal stability, and increases analyte volatility for GC and GC-MS applications. *N,O*-Bis(trimethylsilyl) trifluoroacetamide (BSTFA) and *N,O*-Bis(trimethylsilyl)-acetamide) (BSA) are widely used reagents to introduce the TMS group. These are used either as such or in the presence of a catalyst, like Trimethylchlorosilane (TMCS), Trifluoroacetamide (TFA), hydrochloric acid, potassium acetate, piperidine or pyridine. TMCS is often added to reagents to increase the silyl donor strength. Basic catalysts such as potassium acetate can be used to promote silyl enol ether formation.

N-Methyl-*N*-trimethylsilylfluoroacetamide (MSTFA) is also an important TMS reagent. It has similar reactivity as BSA and BSTFA. However, because the reaction byproducts are more volatile, MSTFA is particularly useful for GC analysis of early-eluting compounds that would otherwise be obscured in the chromatogram. Silylation is also valuable for MS applications where introducing the silyl group produces either more interesting diagnostic fragments or particular characteristic ions used for SIM (Selected Ion Monitoring). The product table below features selected silylation reagents for GC derivatization.

Cat. No.	Product Name
43340	1,1,3,3-Tetramethyl-1,3-diphenyldisilazane
69649	4-(Trimethylsiloxy)-3-penten-2-one
14755	Bis(dimethylamino)dimethylsilane
15256	BSA+TMCS
76750	Chlorodimethyl(pentafluorophenyl)silane
90383	Chlorotriethylsilane
89595	Chlorotrimethylsilane
52619	Hexamethyldisilazane
01565	Hexamethyldisiloxane
91566	*N*-(Trimethylsilyl)acetamide
15235	*N,N*-Bis(trimethylsilyl)methylamine
89539	*N,O*-Bis(*tert*-butyldimethylsilyl)trifluoroacetamide
15269	*N,O*-Bis(trimethylsilyl)acetamide
15222	*N,O*-Bis(trimethylsilyl)trifluoroacetamide
15209, 15238	*N,O*-Bis(trimethylsilyl)trifluoroacetamide with trimethylchlorosilane
69479	*N*-Methyl-*N*-(trimethylsilyl)trifluoroacetamide
69478	*N*-Methyl-N-(trimethylsilyl)trifluoroacetamide with 1% trimethylchlorosilane
00942	*N*-*tert*-Butyldimethylsilyl-*N*-methyltrifluoroacetamide with 1% tert-Butyldimethylchlorosilane
33036, 33035-U, 33037-U	BSA Derivatization Grade
33030, 33151, 33031-U	BSA+TMCS+TMSI
33149-U, 33154-U, 33155-U, 33148	BSTFA + TMCS
33024, 33027, 33084	BSTFA, Derivatization Grade
33014	Chlorotrimethylsilane
33350-U	HMDS, Derivatization Grade
33038, 33039	HMDS+TMCS+Pyridine
33175	Silica Column Regeneration Solution
505846	Silylation Sampler Kit
33065-U	Sylon CT
33092-U	*tert*-Butyldimethylsilylimidazole solution
33068-U	TMSI, Derivatization Grade
33156-U, 33159-U	TMSI+Pyridine

To request the 100 page guide "Derivatization Reagents for Selective Response and Detection in Complex Matrices", you can search for T407138.

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