

SupelMIP® Solid Phase Extraction

Molecularly Imprinted Polymers for the
Highly Selective Extraction of Trace Analytes
from Complex Matrices



SupelMIP Phases and Applications

Achieve Lower Detection Limits

Reduce Sample Prep Time

Improve MS-Compatibility

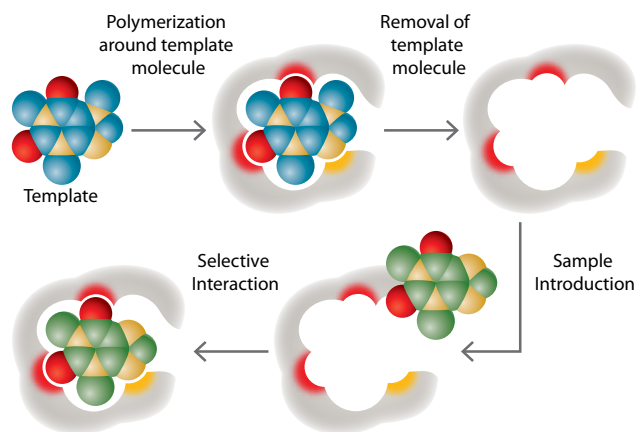
No Method Development Required

What are Molecularly Imprinted Polymers?

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(s).

MIPs are prepared by first mixing a template molecule that consists of a structural analog of the analyte(s) of interest with one or more functional monomers. As illustrated in **Figure 1**, the monomers form spontaneous complexes around the template. Upon complex formation, cross-linking monomers are then added with a suitable porogen (solvent that aids in the role in pore formation) to drive polymerization. An extensive wash procedure is used to remove the template from the polymer, leaving imprints or binding sites that are sterically and chemically complementary to the template.

Figure 1. Formation of MIPs



How is Selectivity Improved Using SupelMIP SPE?

By careful design of the imprinting site, either by molecular modeling, experimental design, or screening methods, the binding cavities can be engineered to offer multiple interactions with the analyte(s) of interest (**Figure 2**). Multiple non-covalent interaction points (ion-exchange, reversed-phase with polymer backbone, and hydrogen bonding) between the MIP phase and analyte functional groups allow for stronger and more specific analyte retention. Improved selectivity is then introduced through the use of harsher wash conditions during sample prep methodology (**Figure 3**). Because extraction selectivity is significantly improved, lower background is observed allowing analysts to achieve lower detection limits relative to other less selective sample prep techniques (**Table 1**).

Figure 2. Visual Depiction of a Typical MIP Binding Site

Ion-exchange, reversed-phase, hydrogen bonding and/or steric interactions at multiple points provide selective and robust retention of the target analyte on the MIP phase.

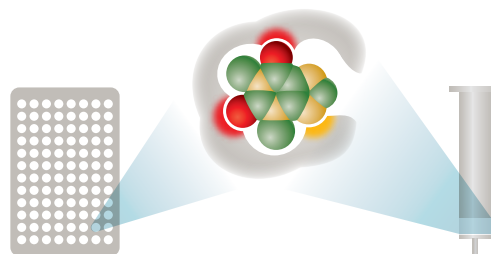


Table 1. Relative Selectivity of Various Sample Prep Techniques

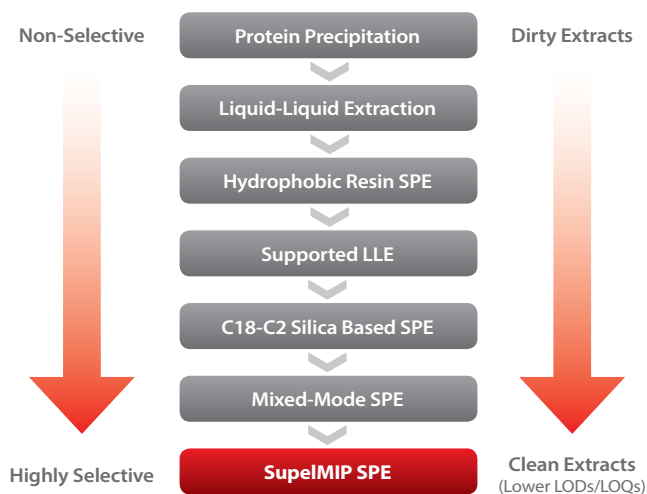
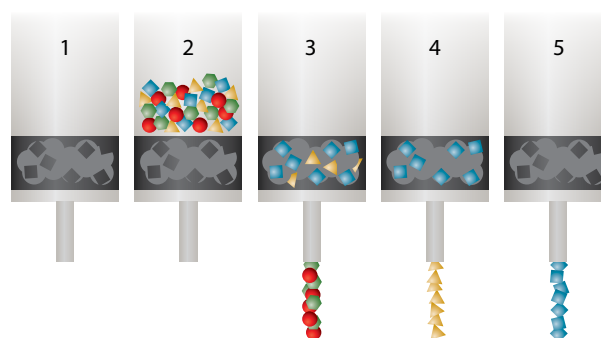


Figure 3. Overview of a Typical SupelMIP SPE Procedure

1. Condition and equilibrate the cartridge
2. Load Sample
- 3-4. Apply vigorous wash steps. Analytes of interest will be retained selectively while interferences will be eluted.
5. Elute the analyte of interest



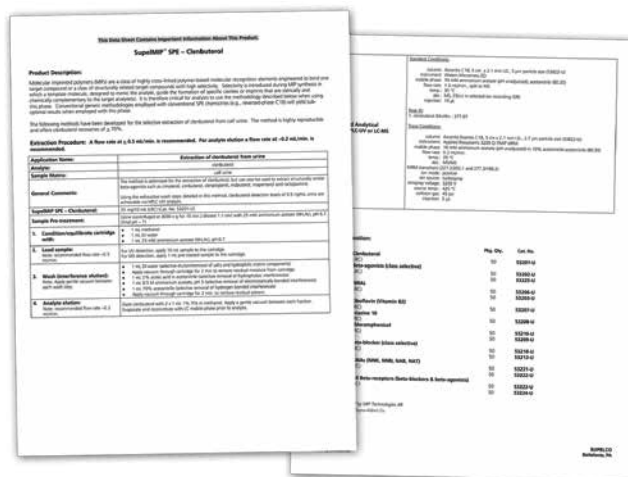
Minimal to No Method Development Required

Sample prep methods are often developed using a variety of schemes such as: referring to published methods of similar/identical applications; implementation of generic methodology; requesting support from a chromatography vendor; screening of techniques, phase chemistries, and method conditions. These approaches are often effective; however, more often than not, a sample prep method can often be frustrating and time consuming.

Unlike many traditional sample prep techniques, SupelMIP is developed and tailored for very specific applications. Therefore, each SupelMIP SPE phase comes with a detailed protocol and analytical technique for its respective application.

Figure 4 depicts a typical data/instruction sheet that is included with each SupelMIP SPE phase.

Figure 4. Example of a Typical Data/Instruction Sheet included with each SupelMIP SPE Phase



High Stability

SupelMIP SPE consists of highly cross-linked polymers that maintain stability when exposed to a broad range of organic solvents, can withstand high temperatures, and can be used over broad pH ranges, without loss of selectivity. Furthermore, they can be stored at room temperatures for prolonged periods of times. This is extremely advantageous over immunoaffinity based products.

SupelMIP Phases and Methods Available for:

- PAHs in edible oil
- Non-steroidal anti-inflammatory drugs (NSAIDs) in wastewater and other sample matrices
- Nitroimidazoles in milk, eggs, and other food matrices
- Fluoroquinolones in bovine kidney, honey, and milk
- Chloramphenicol in milk, plasma, honey, urine and shrimp/prawns
- NNAL in urine
- TSNA in urine and tobacco
- β -agonists in tissue, urine and wastewater
- Clenbuterol in urine
- Riboflavin in milk
- Patulin in fruit matrices
- Aminoglycosides in animal tissue, cell culture, and honey
- Bisphenol A from broth or milk-based matrices

Application: Highly Selective Sample Preparation for the Analysis of Aminoglycoside Antibiotics in Pork Muscle

Aminoglycosides are a microbial resistant class of antibiotics that are routinely monitored in animal-derived foods. Due to the concern of the impact that these compounds may have on human health and development, many countries have instituted regulatory limits for aminoglycosides.

This study focuses on the extraction and analysis of ten aminoglycosides from porcine tissues using molecular imprinted polymer (MIP) solid phase extraction with LC-MS/MS detection.

This study utilizes the unique extraction capabilities of MIPs to successfully quantitate ten aminoglycosides by LC-MS/MS at 100 ng/g (400 ng/g for neomycin) with recoveries $\geq 70\%$. The SPE cleanup procedure, using SupelMIP SPE-Aminoglycosides, as well as the HPLC analysis, using an Ascentis® Express C18 HPLC column, is described in the condition section of **Figure 5**. Quantitation was performed using matrix matched calibration standards, ranging from concentrations of 10 ng/mL to 1000 ng/mL.

Figure 5. LC-MS/MS Analysis of Aminoglycosides after SupelMIP SPE Cleanup

sample/matrix: 3 mL of pork extract (For additional information regarding this application, refer to an article from Supelco Reporter 32.2 available at sigma-aldrich.com/supelmip)
 SPE tube/cartridge: SupelMIP SPE – Aminoglycosides, 50 mg/3 mL (52777-U)
 conditioning: 1 mL of methanol, then 1 mL of 50 mM potassium phosphate in water (pH = 7.8)
 sample addition: 3 mL of pork extract
 washing: 3 mL of water, followed by drying with slight vacuum for 10 seconds
 washing: 1 mL of 50:50 dichloromethane:methanol (v/v), followed by drying with slight vacuum for 10 seconds
 elution: 1 mL of 1% formic acid containing 5 mM heptafluorobutyric acid (HFBA) in 80:20 water:acetonitrile (v/v)
 eluate post-treatment: thoroughly mix via vortex agitation, and transfer to polypropylene HPLC vials
 column: Ascentis Express C18, 10 cm x 2.1 mm I.D., 2.7 μ m (53823-U)
 mobile phase: (A) 5mM heptafluorobutyric in water; (B) 5 mM heptafluorobutyric in acetonitrile
 gradient: 20 to 90% B in 3.0 min; held at 90% B for 1 min; 90 to 20% B in 0.1 min; held at 20% B for 5.9 min
 flow rate: 0.4 mL/min
 temp.: 40 °C
 injection: 10 μ L
 det.: MS/MS, ESI(+), MRM

Analyte	Precursor	Product
Gentamicin C1	478.1	157.2
Streptomycin	582.1	263.2
Neomycin	615.0	161.1
Kanamycin	485.2	163.1
Tobramycin	468.1	163.1
Amikacin	586.2	163.1
Hygromycin B	528.1	177.1
Spectinomycin	351.1	333.1
Dihydrostreptomycin	584.2	263.1
Apramycin	540.2	217.1

1. Spectinomycin
2. Hygromycin B
3. Streptomycin
4. Dihydrostreptomycin
5. Amikacin
6. Kanamycin
7. Apramycin
8. Tobramycin
9. Gentamicin C1
10. Neomycin

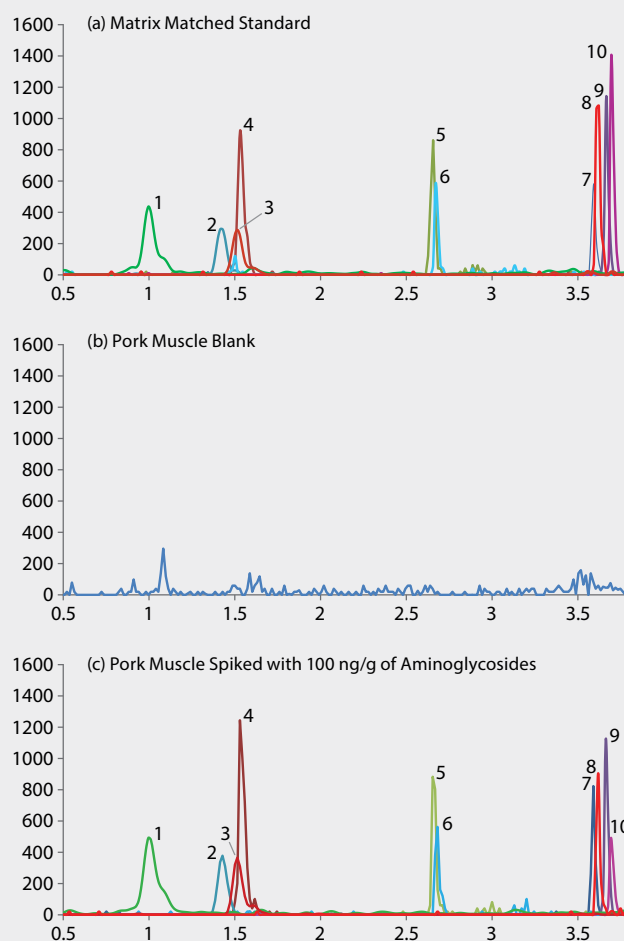


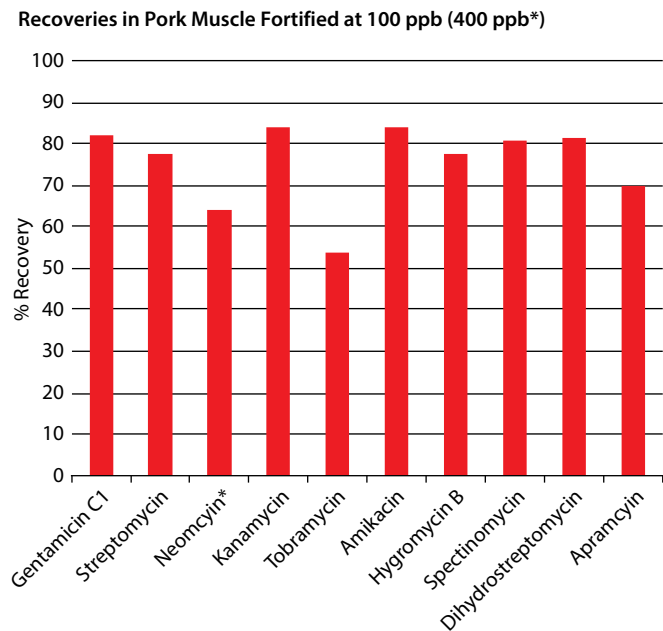
Figure 6. Aminoglycoside Recoveries in Pork Muscle

Figure 5 depicts chromatograms of the analytes in pork muscle extracts. Recoveries for the 10 aminoglycosides are given in Figure 6. Most of the analyte recoveries were $\geq 70\%$, except for neomycin and tobramycin. Low recoveries for neomycin and tobramycin may be attributed to stronger binding of the analytes to the MIP sorbent due to the presence of several amino groups.

Because the MIP material's unique selectivity facilitated the removal of additional matrix interferences prior to eluting the analytes of interest, a simple and sensitive method for the cleanup, analysis and quantification of aminoglycosides in pork muscle has been developed using SupelMIP SPE-Aminoglycosides and LC-MS/MS analysis.

Application: Low Level Quantification of Patulin in Organic Apple Puree for Infants

Patulin is a mycotoxin produced by a number of fungal species. One species, *Penicillium Expansum*, is the primary source of patulin contamination in food products.¹ *P. Expansum* occurs most often in apples and is commonly present in apple juice, and purees.² Because studies have shown that patulin possesses immunotoxic and genotoxic properties, regulatory limits for patulin have been set in 50 countries, including the USA and the European Union.

Historically, analytical methods for patulin have employed liquid-liquid extraction (LLE) followed by HPLC separation with UV detection at 276 nm.^{1,3} Researchers have highlighted problems with these methodologies, including:

- Tedious sample preparation associated with liquid-liquid extraction
- Patulin instability in alkaline conditions resulting from sodium carbonate cleanup
- The requirement of extra cleanup or chromatographic method development to prevent the coelution of patulin and interfering matrix component 5-hydroxymethylfurfural (HMF).^{1,4}

Therefore, a quick, simple and robust sample preparation method for patulin analysis is needed.

The application outlined in Figure 7 demonstrates the effectiveness of the SupelMIP SPE – Patulin cartridge when used to concentrate low levels of patulin in an apple puree matrix. The application uses a Titan™ C18 UHPLC column for the analysis of patulin in a product marketed for consumption by infants. (Please note, this application can be adapted to a variety of apple-containing products.)

As seen in Figure 7, chromatographic analysis demonstrates that no direct matrix interference with patulin analysis was observed. Unlike LLE procedures, the cleanup procedure using SupelMIP SPE – Patulin successfully removed HMF and other common interfering components from the final extract. Sodium bicarbonate was necessarily used for an effective SPE cleanup, so the final extract was acidified to stabilize patulin for analysis. A highly concentrated patulin sample was produced, and patulin was easily detected by LC-UV analysis in apple puree at concentrations of 10 ng/g.

Figure 7. Chromatograms of Apple Puree after SPE Cleanup

sample/matrix: 4 mL of apple puree spiked with patulin at 10 ng/g prepared in the following manner: 10 grams of apple puree spiked with 150 μ L of pectinase and 100 μ L of 1 μ g/mL patulin in 0.1% acetic acid. Dilution with 9.750 mL of deionized water, followed by heating at 40 °C, centrifugation at 4,500 rpm for 5 minutes, and filtration produces the final sample.

SPE tube/cartridge: SupelMIP SPE – Patulin, 100 mg/3 mL (52776-U)

conditioning: 2 mL of acetonitrile, then 1 mL of deionized water at 1 drop/second

sample addition: 4 mL of filtered apple puree supernatant, load and pass through the tubes in 2 mL aliquots at a rate of 1 drop/2 seconds

washing: 4 mL of 1% acetic acid solution, 1 mL of 1% sodium bicarbonate, 3 mL of deionized water at 1 drop/second, followed by additional vacuum for 30 seconds to remove excess water

washing: 500 μ L of diethyl ether at 1 drop/second

elution: 2 mL of ethyl acetate at 1 drop/second

eluate post-treatment: 10 μ L glacial acetic acid, thoroughly mix via vortex agitation, dry under nitrogen at 40 °C, reconstitute in 1.0 mL of 0.1% acetic acid in water

column: Titan™ C18, 10 cm x 2.1 mm I.D., 1.9 μ m particles (577124-U)

mobile phase: (A) 95:5 water:acetonitrile (B) 100% acetonitrile

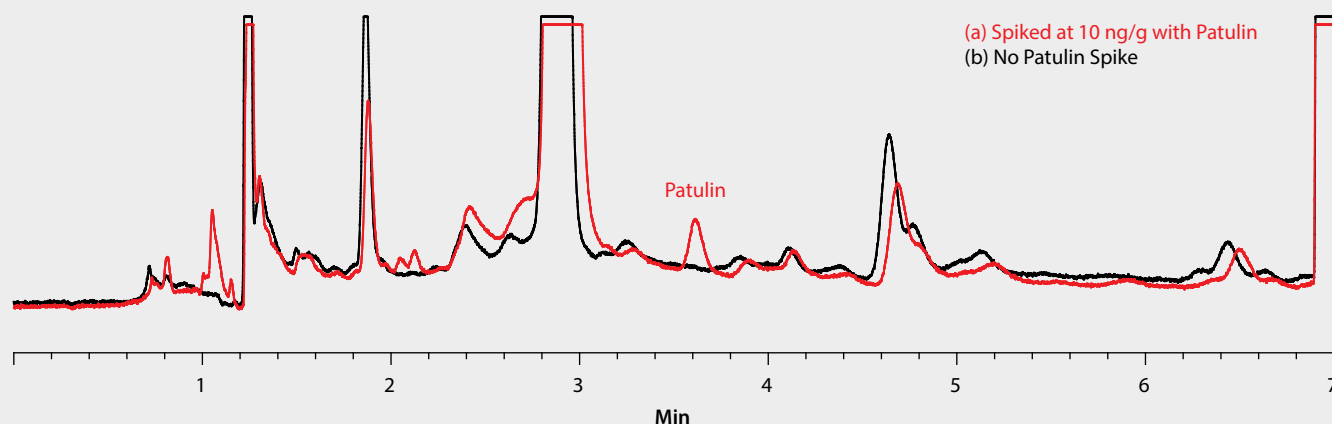
gradient: hold at 100% A for 6 min at 0.3 mL/min; 0% to 80% B in 0.1 min at 0.4 mL/min; hold at 80% B for 1.4 min at 0.4 mL/min, 80% to 0% B in 0.1 min at 0.4 mL/min, hold at 100% A for 1.4 min at 0.4 mL/min

flow rate: 0.3 – 0.4 mL/min

temp.: 35 °C

detector: UV, 276 nm

injection: 15 μ L



This study successfully demonstrates the use of SupelMIP SPE – Patulin for the cleanup and concentration of patulin from apple puree. By selectively extracting patulin with the use of molecularly imprinted polymers and effectively removing interfering matrix compounds during the SPE washing procedure, UHPLC-UV analysis of patulin was made possible. Using this MIP phase, the SPE procedure yielded a high analyte recovery with excellent reproducibility. The average recovery of patulin from the spiked apple puree sample was calculated at 70.2% with a relative standard deviation (RSD) of 2.7% (n=3). No patulin was detected in the unspiked infant organic apple puree sample.

In conclusion, the use of SupelMIP SPE – Patulin for sample cleanup eliminates the aforementioned problems associated with liquid-

liquid extraction and provides a fast, easy and reliable sample preparation method for patulin analysis in apple matrices.

References

- Desmarchelier, A. et al. Analysis of Patulin in Pear- and Apple-Based Food stuffs by Liquid Chromatography Electrospray Ionization Tandem Mass Spectrometry *J. Agric. Food Chem.*, **2011**, 59, 7659-7665.
- Hopmans, E.C. Patulin: a Mycotoxin in Apples *Perishables Handlings Quarterly*, **1997**, 91, 5-6.
- Roach, J. A. et al. HPLC Detection of Patulin in Apple Juice with GC/MS Confirmation of Patulin Identity *Adv. Exp. Med. Biol.*, **2002**, 504, 135-140.
- Sargenti, S. and Almeida, C.A.A. Determination of Patulin in Apple Juice by HPLC Using a Simple and Fast Sample Preparation Method *Ecl. Quím.*, **2010**, 35, 14-21.

Application: Reduced Ion-Suppression for the Analysis of Tobacco Specific Nitrosamines

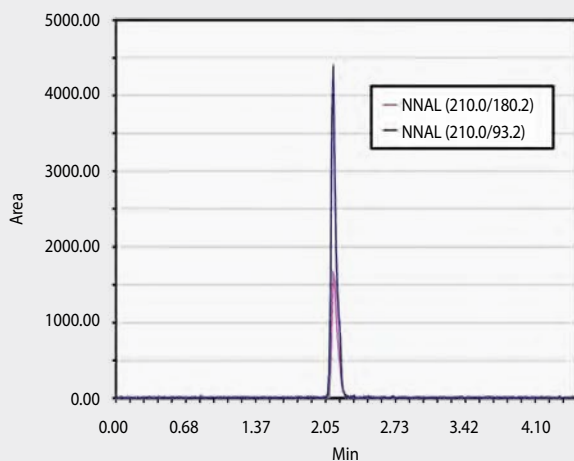
Tobacco Specific Nitrosamines (TSNAs) are highly carcinogenic and derived solely from tobacco products. They are generated from the fermentation, curing, and burning of tobacco. For example, NNAL is a valuable biomarker in human urine to determine exposure to second-hand smoke. Because TSNAs are often found in very low concentrations in difficult biological matrixes, a highly selective and sensitive assay is required for sample preparation and analysis.

SupelMIP SPE – NNAL is designed for the extraction of NNAL, and SupelMIP SPE – TSNA is a class selective phase developed for the extraction of four different tobacco specific nitrosamines: NNK, NNN, NAB, and NAT.

Figures 8 and 9 depict LC-MS-MS chromatograms (MRM) of SupelMIP extracts of human urine spiked with 1 ng/mL NNAL and 25 pg/mL TSNAs, respectively.

Figure 8. Representative LC-MS-MS Chromatogram (MRM) of a SupelMIP SPE – NNAL Extract of Human Urine Spiked with 1 ng/mL NNAL

sample/matrix: human urine, centrifuged at 3000 rpm. Supernatant spiked with 1 ng/mL NNAL and acidified to pH 6 with acetic acid
SPE tube/cartridge: SupelMIP SPE – NNAL, 25 mg/10 mL (53206-U)
conditioning: 1 mL of dichloromethane, 1 mL of methanol, then 1 mL of DI water
sample addition: 5 mL of pre-treated urine sample
washing: 2 x 1 mL DI water, followed by drying with full vacuum for 10 min
washing: 1 mL of toluene, 1 mL of toluene:dichloromethane (9:1, v/v), 1 mL of toluene:dichloromethane (4:1, v/v), followed by drying with full vacuum for 2 min
elution: 2 x 1 mL 10% methanol in dichloromethane. Apply gentle vacuum between each fraction
eluate post-treatment: evaporate and reconstitute in 0.15 – 0.25 mL of LC mobile phase
column: Ascentis® Express C18, 5 cm x 2.1 mm I.D., 2.7 µm (53822-U)
mobile phase: (A) 10 mM ammonium acetate; (B) 10 mM ammonium acetate in acetonitrile
gradient: 10 to 30% B in 1.5 min; held at 30% B for 1.0 min; 30 to 10% B in 0.1 min; held at 10% B for 3.4 min
flow rate: 0.3 mL/min
temp.: 35 °C
injection: 20 µL
det.: MS/MS, ESI(+), MRM transitions (210.2/180.2 and 210.2/93.2 m/z)



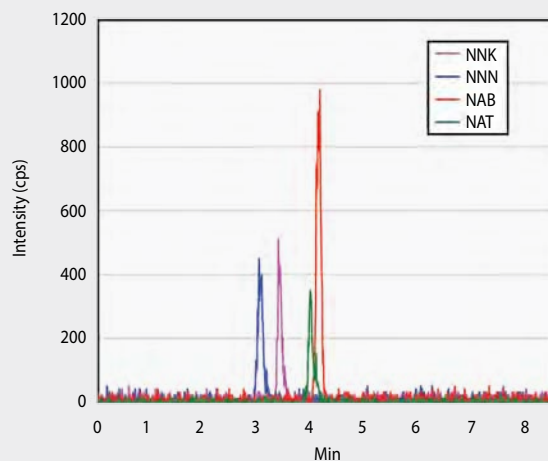
SupelMIP SPE – NNAL:

- Consistent low background
- Recoveries greater than 90%
- Achieve LODs of 5 pg/mL
- Achieve LOQs of 13 pg/mL

For additional information regarding this application, refer to an article from Supelco Reporter 25.3 available at sigma-aldrich.com/supelmip

Figure 9. Representative LC-MS-MS Chromatogram (MRM) of a SupelMIP SPE – TSNA Extract of Human Urine Spiked with 25 pg/mL TSNAs

sample/matrix: human urine, spiked with 25 pg/mL TSNAs, adjusted with acetic acid to pH 5.5
SPE tube/cartridge: SupelMIP SPE – TSNAs, 25 mg/3 mL (53222-U)
conditioning: 1 mL of methanol, then 1 mL of DI water (do not allow cartridge to go dry)
sample addition: 1 mL of pre-treated urine sample
washing: 1 mL 10 mM ammonium acetate, pH 5.5, followed by drying with full vacuum for 10 min
washing: 1 mL of heptane, followed by drying with full vacuum for 5 min
elution: 2 x 1 mL 10% methanol in dichloromethane
eluate post-treatment: evaporate and reconstitute in 100 µL LC mobile phase
column: Ascentis® Express C18, 3 cm x 3.0 mm I.D., 3 µm (581307-U)
mobile phase: (A) 10 mM ammonium formate, pH 6.1 (adjusted with acetic acid); (B) acetonitrile
gradient: 10% B held for 1.0 min; 10 to 40% B in 3.0 min; 40 to 70% B in 1.0 min; held at 70% B for 1.0 min; 70 to 10% B in 0.1 min; held at 10% B for 2.9 min
flow rate: 0.5 mL/min
temp.: ambient
injection: 5 µL
det.: MS/MS, ESI(+), MRM



SupelMIP SPE – TSNAs:

- Consistent low background
- Recoveries greater than 90%
- Achieve LODs of 2.5 pg/mL
- Achieve LOQs of 4 pg/mL

For additional information regarding this application, refer to an article from Supelco Reporter 25.5 available at sigma-aldrich.com/supelmip

NNAL = 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanol
NNK = 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone
NNN = N-nitrosanornicotine

NAB = N'-nitrosoanabasine
NAT = N'-nitrosoanatabine

SupelMIP® Solid Phase Extraction

Ion-suppression or ion-enhancement is caused by one or more interfering components/species that co-elute with the analyte(s) of interest during LC-MS analysis. These co-eluting species can affect droplet formation or ionize concurrently resulting in an erroneous decrease (suppression) or increase (enhancement) in signal response. Ion-suppression often leads to poor assay reproducibility, accuracy, and sensitivity, and such deleterious effects are often most notable at the lower limits of quantitation.

In order to achieve adequate lower limits of quantitation when conducting trace analysis of analytes in complex matrices such as biological fluids, it is absolutely critical to procure adequate selectivity during sample preparation. By virtue of molecularly imprinted polymer technology, SupelMIP SPE offers the necessary selectivity and sample cleanup required for achieving ever-decreasing detection limits that are challenging analysts today.

Blank urine samples were extracted with SupelMIP SPE – NNAL and the resulting SPE (post-SPE) eluate was spiked with NNAL and

analyzed via LC-MS-MS. The resulting chromatogram response (peak area) levels generated were compared against external standards (prepared in buffer). The results (**Figure 10**) show that ion-suppression was nominal (< 4% signal suppression) for the SupelMIP SPE – NNAL urine extract (post-SPE spike) relative to the external standard calibration curve.

In another study, blank urine samples were extracted with SupelMIP SPE Beta-agonists and conventional hydrophilic polymer SPE phases and the resulting SPE eluate was spiked (post-SPE) with metaproterenol at the levels of 0.5, 1, and 5 ng/mL, respectively. **Figure 11** compares the response levels and linear relation of known spike concentrations vs. calculated concentrations determined from the signal responses obtained from blank urine extracts spiked post-extraction using both the SupelMIP SPE – Beta-agonist method and conventional polymer SPE method. Increased levels of ion-suppression were observed for the polymer SPE protocol relative to the SupelMIP procedure.

Figure 10. Response Comparison of NNAL Calibration Curve Generated from SupelMIP SPE – NNAL Urine Extract (post-SPE spike) vs. External Standards

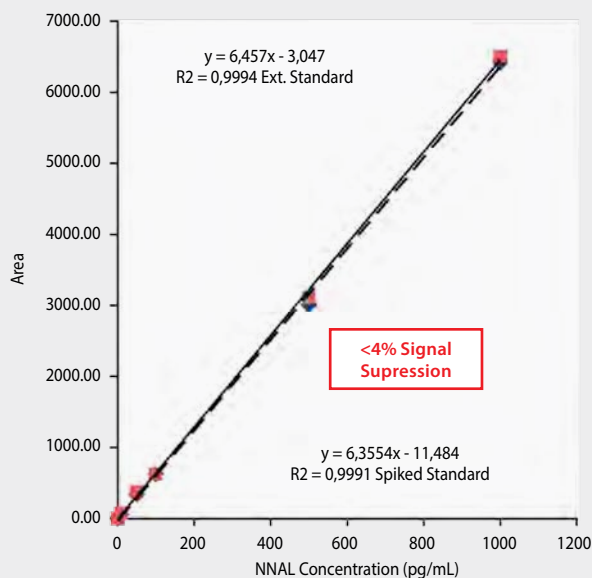
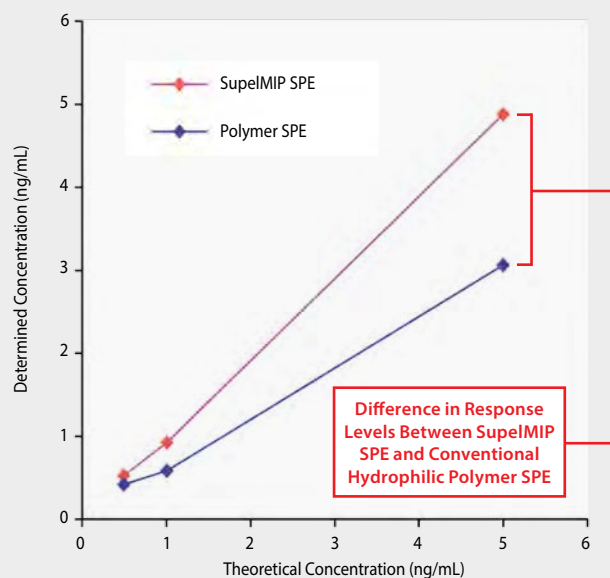


Figure 11. Known Spike Concentration vs. Determined Concentration for SupelMIP SPE Beta-agonist and Polymer SPE for Metaproterenol from Urine (Post-Extraction Spike)



Application: Reduced Background and Improved Recoveries for the Extraction of PAHs from Olive Oil

Polynuclear aromatic hydrocarbons (PAHs), some of which are known to be carcinogenic in nature, reside in the environment as a result of petroleum processing and incomplete combustion of fossil fuels.¹

This study compares SupelMIP SPE-PAHs and two competitor silica gel SPE cartridges in terms of matrix removal and analyte recovery for the extraction of select polycyclic aromatic hydrocarbons (PAHs) from olive oil. Multiple replicates of both unspiked and spiked (20 ng/g with PAHs) oil samples were processed for each SPE cleanup technique. Extracts were then analyzed by GC-MS (SIM mode). Quantitation was performed against a 5-point calibration curve (1-20 ng/mL) prepared in unspiked olive oil extract with naphthalene- d_8 , fluoranthene- d_{10} , perylene- d_{12} internal standards, spiked at 10 ng/mL.

Figure 12 shows the GC-MS (full scan) chromatograms of the extracts after cleanup with SupelMIP SPE-PAHs, Competitor A silica gel SPE, and Competitor B silica gel SPE, respectively. The chromatograms illustrate that SupelMIP SPE-PAHs cleanup produces much lower background than the silica gel SPE cleanup.

As illustrated in Figure 13, the SupelMIP SPE-PAHs samples produced better overall analyte recoveries than those cleaned with the silica SPE cartridges. The reproducibility for all PAHs tested, exhibited by percent relative standard deviation (%RSD), fell within an acceptable range of less than 20% for the SupelMIP SPE-PAHs cleaned samples. Also, SupelMIP SPE-PAHs produced better overall recoveries and removed more problematic matrix interferences than the silica gel SPE cartridges, while maintaining good reproducibility. Thus, the SupelMIP SPE-PAHs provides suitable matrix removal for rugged GC-MS analysis of PAHs in olive oil.

Reference

1. Polynuclear Aromatic Hydrocarbons, US EPA factsheet, January 2008, Office of Solid Waste, Washington DC. (epa.gov/osw)

Figure 12. GC-MS Full Scan Chromatograms of Olive Oil Extract (same y axis)

sample/matrix: 0.5 g oil diluted to 1 mL in cyclohexane
SPE tube/cartridge: SupelMIP SPE – PAHs, 50 mg/3 mL (52773-U)
conditioning: 1 mL cyclohexane
sample addition: 0.5 g oil diluted to 1 mL in cyclohexane
washing: 1 mL cyclohexane
elution: 3 x 1 mL ethyl acetate
eluate post-treatment: Evaporate to less than 1 mL (not dryness) under nitrogen at 40 °C. Adjust final volume to 1 mL with ethyl acetate.

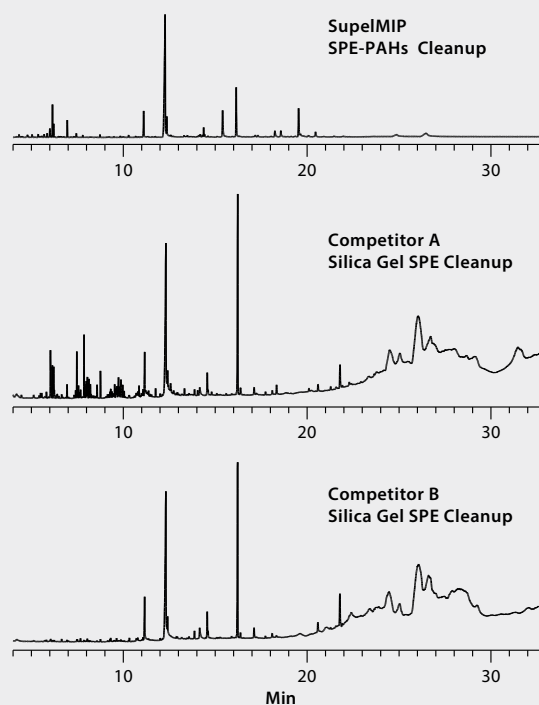
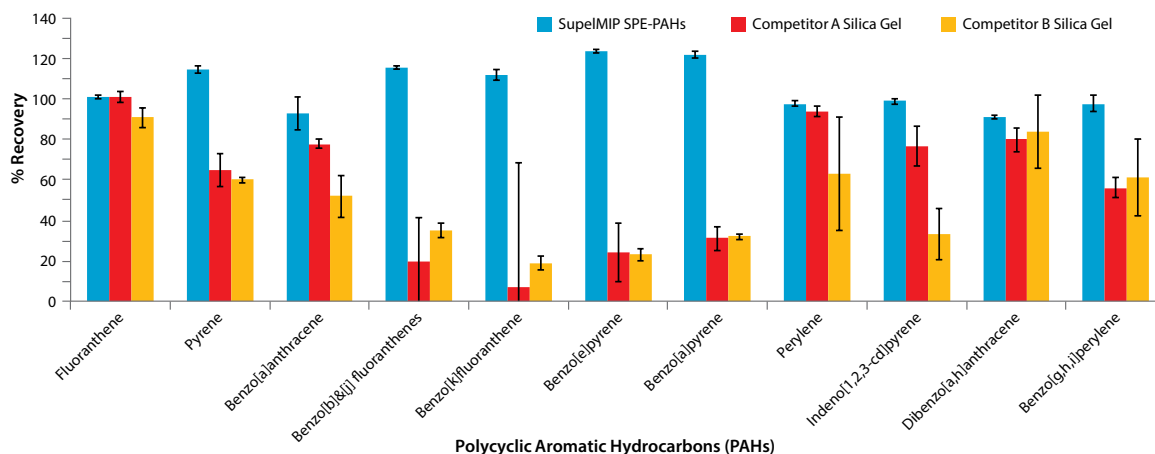


Figure 13. Analyte Recovery of PAHs from Olive Oil Extract (n=3)



Frequently Asked Questions (FAQs):

1. How is sample preparation improved using molecularly imprinted polymer SPE technology?

Because MIPs are tailor-made for individual analytes and analyte classes, analyte retention strength is increased significantly allowing for powerful wash steps within the SPE procedure. This allows for highly selective and simple extractions resulting in lower detection limits and improved MS compatibility (reduced ion-suppression). Each SupelMIP phase also comes with a detailed application specific protocol simplifying the method development process which in turn saves time and cost.

2. Are sample packs available?

Yes. Sample packs are available and can be obtained through the SupelMIP website: sigma-aldrich.com/supelmip. Alternatively, you can also request a sample pack by calling or emailing your local Sigma-Aldrich office and connecting with technical service.

3. There is no MIP phase for my application? How do I develop a MIP protocol for my application?

Within the SupelMIP website, sigma-aldrich.com/supelmip, there is a survey where you can describe your application and needs for

MIP based SPE product/procedure. Scientists will evaluate your application through a short feasibility stage. If your application is prioritized to move through feasibility, the next stages will be development and optimization.

4. Are process scale MIP products available through Supelco?

No. Process scale MIP products are not available through Supelco.

5. Can we use existing or traditional SPE protocols with SupelMIP SPE technology?

No. Existing protocols cannot be used. Every SupelMIP SPE includes a detailed extraction protocol that is analyte and matrix specific. This protocol needs to be used in order to achieve optimal retention during sample load, maximum interference removal during sample wash, and high recoveries during elution.

6. What dimensions are available for SupelMIP SPE?

Currently, our standard product consists of 25 mg, 50 mg, and 100 mg bed weights packed in 3 mL and 10 mL LRC (large reservoir cartridges) SPE tubes. The phases can be custom packed in all other SPE hardware that Supelco offers (other SPE tube dimensions, glass SPE tubes, 96-well plates, etc.).

Ordering Information

SupelMIP SPE Cartridges	Sorbent Mass (mg)	Cartridge Volume (mL)	Cartridge per Box	Cat. No.
PAHs	25	3	50	52773-U
Nitroimidazoles	50	3	50	52734-U
NSAIDs	25	3	50	52769-U
Fluoroquinolones	25	3	50	53269-U
Clenbuterol	25	10	50	53201-U
Beta-agonists (class selective)	25	10	50	53202-U
Beta-agonists (class selective)	25	3	50	53225-U
Full Beta Receptor (Beta-agonists and Beta-blockers)	25	10	50	53223-U
Full Beta Receptor (Beta-agonists and Beta-blockers)	25	3	50	53224-U
Chloramphenicol	25	10	50	53210-U
Chloramphenicol	25	3	50	53209-U
NNAL (4-(methylnitrosamino)-1-(3-pyridyl)-1-butanol)	25	10	50	53206-U
NNAL (4-(methylnitrosamino)-1-(3-pyridyl)-1-butanol)	25	3	50	53203-U
NNAL (4-(methylnitrosamino)-1-(3-pyridyl)-1-butanol)	25 (mg/well)	N/A	1 (96-well plate)	53255-U
TSNAs (4 different Tobacco specific Nitrosamines: NNK, NNN, NAB, NAT)	50	10	50	53221-U
TSNAs (4 different Tobacco specific Nitrosamines: NNK, NNN, NAB, NAT)	50	3	50	53222-U
Riboflavin (vitamin B2)	25	10	50	53207-U
Patulin	100	3	50	52776-U
Aminoglycosides	50	3	50	52777-U
SupelMIP SPE - Bisphenol A (BPA)	100	3	50	52775-U
SupelMIP SPE - Bisphenol A (BPA)	100	6	50	54277-U

For a complete SupelMIP product listing, and to request a SupelMIP sample pack, visit sigma-aldrich.com/supelmip

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