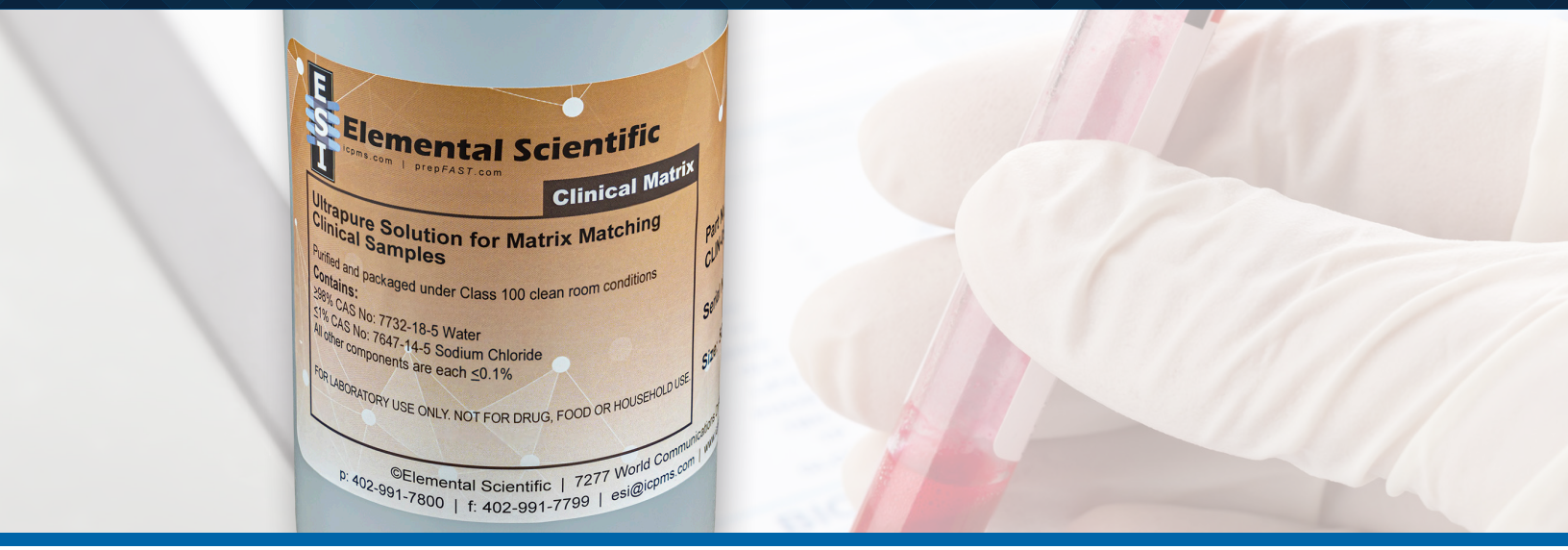

Synthetic Clinical Matrix Solution for ICPMS *(CLIN-0500)*

Brief

CLIN-0500 ICPMS matrix-matching solution improves detection limits up to 20x or more for important elements such as Mn, Se, and Pb while also improving accuracy. Methods were validated by analyzing proficiency testing samples from NYDOH and CTQ programs.

Introduction

Accurate ICPMS determination of trace elements in complex biological matrices, such as urine, whole blood, blood plasma, or serum, is hindered by matrix effects from high total dissolved solids (TDS) and other biological components present in the samples. Traditionally, the best accuracy for the analysis of these types of samples has been achieved by matrix matching calibrations with actual clinical samples (e.g., pooled urine or whole blood). Unfortunately, this technique requires collection, handling, and characterization of large volumes of potentially hazardous biological material and a separate calibration matrix for every type of clinical sample. Furthermore, the elements of interest likely are present in the calibration matrix, which makes it necessary to apply a blank correction to achieve accurate results. CLIN-0500 synthetic matrix solution permits clinical ICPMS labs to easily and automatically prepare low-blank, non-hazardous, matrix-matched calibration standards using either prep*FAST* inline or prep*FAST* DilutionStation offline automation systems.

Features

- Ultrapure, proprietary synthetic mixture designed to mimic biological matrices
  - Whole blood, blood plasma, serum, urine, digested hair and nails
- Low or sub-ppt contamination for most elements on the periodic table
- Improve washout for carryover-prone elements like Hg

CLIN-0500 Specifications

- Purified and packaged under class 100 clean room conditions
- Neutral pH; suitable for matrix matching calibrations for both acidic and basic sample preparations
- 500 mL volume

Applications

Quarles Jr., C. D., et. al., Evaluation of blood and synthetic matrix-matched calibrations using manual and inline sample preparation methods, JAAS, 2022, 37, 1512-1521.

Table 1. Limits of detection (LOD) for the blood matrix-matched manual method, CLIN-0500 synthetic matrix-matched manual method, and CLIN-0500 synthetic matrix-matched inline method. All three calibrations were analyzed using a 50X dilution of blood or synthetic matrix.

			LOD (µg/L)			
Element	Measurement Mode	m/z	Blood Matrix-Matched Calibration Manual Preparation	CLIN-0500 Synthetic Matrix-Matched Calibration Manual Preparation	CLIN-0500 Synthetic Matrix-Matched Calibration Inline Preparation	LOD Improvements with Synthetic Matrix
Mn (MnO)	QQQ (O_2)	71	0.397	0.016	0.019	21X
Se (SeO)	QQQ (O_2)	96	0.335	0.015	0.005	67X
Cd	KED (He)	113	0.015	0.010	0.010	1.5X
Hg	KED (He)	202	0.017	0.010	0.008	2X
Pb	KED (He)	208	0.070 (µg/dL)	0.005 (µg/dL)	0.002 (µg/dL)	35X

Table 2. Overall %BIAS to the target NYDOH PT sample values for the three methods evaluated.

	Overall %BIAS to PT Reference Values		
	Manual Preparation	Manual Preparation	Inline Preparation
Element	Blood Matrix-Matched Calibration	CLIN-0500 Synthetic Matrix-Matched Calibration	CLIN-0500 Synthetic Matrix-Matched Calibration
Pb	7.9	3.1	3.7
Se	22	2.5	2.3
Cd	9.9	6.9	6.9
Hg	9.7	5.0	4.2
Mn	14	3.9	3.0

Quarles Jr., C. D., et. al., Rapid automated total arsenic and arsenic speciation by inductively coupled plasma mass spectrometry, JAAS, 2022, 37, 1512-1521.

Table 3. Comparison of results from the total arsenic measurements to reference values. Reference values provided by NYDOH (UE) and CTQ (QM and PC). n = 3. Matrix-matched calibrations were prepared using ESI's synthetic clinical matrix (CLIN-0500).

Proficiency Testing Sample ID	Reference Value (µg L^{-1} As)	Measured Value (µg L^{-1} As)
UE19-11	3.7 ± 6	4.0 ± 0.2
UE20-08	21 ± 6	20 ± 1
QM-U-Q2014	378 ± 4	362 ± 14
PC-U-S1912	631 ± 95	633 ± 18