



# Contamination Control Report

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## Summary

Witness Coupons were analyzed for amino acids for Contamination Control. Only one foil (#10) had amino acid levels higher than the highest blank foil (#2), but the replicates of that exposure were below the blanks. Overall amino acid exposure was below the requirement.

## Introduction

The purpose of this experiment was to quantify the amount of amino acids on different OSIRIS-REx Contamination Control aluminum foil samples.

## Samples:

Tube Number	Location	Pre-Weight (g)	Post-Weight (g)	Foil Weight sent (g)	Foil Weight analyzed (g)
1	Blank	9.93191	10.17286	0.24095	0.1272
2		10.02337	10.26244	0.23907	0.1272
3		9.89537	10.21257	0.3172	0.1724
4	Flight Sampler Head Integration + Test	9.93919	10.21998	0.28079	0.141
5		9.91805	10.21578	0.29773	0.1583
6		10.07409	10.3528	0.27871	0.1357
7	Launch Container	9.94188	10.20973	0.26785	0.1292
8		10.06036	10.30281	0.24245	0.1212
9		9.86295	10.16596	0.30301	0.581
10	SRC Final Deploy	10.0815	10.36717	0.28567	0.1491
11		10.04641	10.30866	0.26225	0.1223
12		9.84826	10.09581	0.24755	0.1185
13	Qual TAGSAM Head Final Deploy	9.97094	10.33542	0.36448	0.1826
14		9.97566	10.25611	0.28045	0.1516
15		10.03938	10.37022	0.33084	0.1728
16	TAGSAM Deploy/Alignment Test	9.8985	10.19191	0.29341	0.1685
17		10.00748	10.28965	0.28217	0.1292
18		10.02036	10.27781	0.25745	0.147
19	Launch Container/TAGSAM Deploy 3/17-3/22	10.01098	10.28179	0.27081	0.126
20		9.99084	10.28832	0.29748	0.1603
21		9.9625	10.2649	0.3024	0.1602
22	SSB EM 3/16/16-4/1/16	9.95715	10.23883	0.28168	0.1486
23		9.92199	10.1881	0.26611	0.1372
24		10.10219	10.3819	0.27971	0.151
25	SSB EM 3/16/16-4/26/16	9.99083	10.31199	0.32116	0.1624
26		9.94944	10.25421	0.30477	0.1534
27		9.9482	10.26534	0.31714	0.1474

## Procedure

Tubes were opened, and foils were torn in half using clean, baked tweezers. The portion of the foil to be analyzed was weighed and placed in a clean, baked 13 mm test tube. The tubes were flame sealed with 2 mL of 18.2MΩ 3 ppb TOC Millipore water (hereafter water) and extracted at 100°C for 24 hours. The extract was removed and sample tubes rinsed 2x with 500 µL of water and dried via centrifugal evaporation. The samples were hydrolyzed over 6M HCl vapor for 3 hours at 150°C. The samples were dried again. Please note that sample #27 shattered during extraction; no data is reported for this foil.

## Analysis

The dried sample extracts (hydrolyzed and unhydrolyzed) were suspended in 100µL water. Of that 50 µL was dried in a total recovery vial and reconstituted in 10 µL of water, 20 µL of Waters AccQ•Tag derivatizing agent, and 70 µL of borate. Both samples and standards were heated for 10 minutes at 55°C immediately following the addition of the derivatizing agent. The sample was then analyzed via the commercial Waters AccQ•Tag protocol on a Waters LCT Premier time of flight mass spectrometer equipped with an electrospray ionization source (positive ion mode), mass resolution setting of 5,000 m/Δm but without external mass accuracy calibration. Sample was introduced via a Waters Acquity UPLC with fluorescence detector. For UPLC analysis a 250 µL syringe, 50 µL loop, and 30 µL needle were used. The total injection volume was 1µL. A set of 9 calibrators of proteinogenic amino acids (0.25 to 250 µM) was prepared in water and analyzed. A linear least-square model was fit to each analyte. Both mass and fluorescence traces were quantitated; however, sensitivity on the mass detector was lower than the fluorescence detector, and no reliable peaks were detected above background levels. The tables below report only fluorescence. Since only side of the foil was exposed, only one side was used for calculations.

Table 2. Osiris-Rex total amount of amino acids in samples 1 through 15 (ng/cm<sup>2</sup>)

Average	Blank			Flight Sampler Head Integration + Test			Launch Container			SRC Final Deploy			Qual TAGSAM Head Final Deploy		
	O-Rex 1	O-Rex 2	O-Rex 3	O-Rex 4	O-Rex 5	O-Rex 6	O-Rex 7	O-Rex 8	O-Rex 9	O-Rex 10	O-Rex 11	O-Rex 12	O-Rex 13	O-Rex 14	O-Rex 15
His	0.02± 0.03									0.03± 0.01					
Ser	0.15± 0.02	0.22± 0.01	0.04± 0.00	0.10± 0.01	0.04± 0.00	0.10± 0.01	0.04± 0.01	0.04± 0.00	0.01± 0.00	0.22± 0.00		0.02± 0.01	0.02± 0.01	0.05± 0.01	
Arg	0.01± 0.01	0.06± 0.01		0.01± 0.01						0.12± 0.01					
Gly	0.34± 0.05	0.35± 0.03	0.18± 0.06	0.22± 0.08	0.18± 0.09	0.20± 0.10	0.23± 0.06	0.15± 0.00	0.04± 0.01	0.31± 0.20	0.35± 0.26	0.13± 0.01	0.10± 0.01	0.12± 0.03	0.10± 0.06
Asp		0.03± 0.01					0.01± 0.01			0.10± 0.00					
Glu	0.08± 0.01	0.18± 0.02	0.01± 0.00	0.03± 0.01		0.02± 0.02	0.06± 0.02		0.01± 0.00	0.26± 0.01				0.04± 0.01	
Thr	0.01± 0.01	0.03± 0.00								0.06± 0.00					
Ala	0.03± 0.00	0.05± 0.00		0.04± 0.00		0.01± 0.00	0.02± 0.01	0.01± 0.00		0.11± 0.00		0.01± 0.00	0.01± 0.01	0.01± 0.00	
Pro										0.06± 0.03					
Tyr															
Cys															
Lys	0.02± 0.01	0.02± 0.02								0.10± 0.00					
Meth															
L-Val	0.07± 0.01	0.07± 0.01	0.02± 0.00	0.16± 0.01	0.15± 0.00	0.10± 0.00	0.17± 0.02	0.14± 0.01	0.04± 0.00	0.38± 0.01	0.20± 0.02	0.17± 0.02	0.18± 0.01	0.18± 0.01	0.15± 0.00
L-Leu	0.01± 0.01	0.02± 0.00								0.06± 0.00					
L-Ileu	0.06± 0.01	0.08± 0.01		0.03± 0.00			0.03± 0.01			0.15± 0.00					
Phe	0.01± 0.01	0.02± 0.00								0.07± 0.01					
EAC A	0.58± 0.04	0.41± 0.02	0.41± 0.02	0.21± 0.01	0.17± 0.01	0.20± 0.00	0.26± 0.02	0.26± 0.01	0.07± 0.00	0.28± 0.01	0.25± 0.01	0.38± 0.03	0.12± 0.00	0.14± 0.01	0.17± 0.01
<b>Total</b>	1.38± 0.22	1.53± 0.15	0.67± 0.09	0.80± 0.13	0.54± 0.10	0.62± 0.14	0.83± 0.15	0.59± 0.03	0.17± 0.01	2.31± 0.31	0.81± 0.30	0.71± 0.09	0.42± 0.04	0.54± 0.07	0.42± 0.07
<b>Average</b>	1.19			0.65			0.53			1.28			0.46		

Table 3. Osiris-Rex total amount of amino acids in samples 16 through 26 (ng/cm<sup>2</sup>); foil 27 was not able to be quantified due to tube failure during extraction.

Average	TAGSAM Deploy/Alignment Test			Launch Container/TAGSAM Deploy 3/17-3/22			SSB EM 3/16/16-4/1/16			SSB EM 3/16/16-4/26/16		
	O-Rex 16	O-Rex 17	O-Rex 18	O-Rex 19	O-Rex 20	O-Rex 21	O-Rex 22	O-Rex 23	O-Rex 24	O-Rex 25	O-Rex 26	O-Rex 27
His								0.01± 0.01				
Ser	0.02± 0.00	0.01± 0.01	0.02± 0.01	0.09± 0.01	0.01± 0.00	0.04± 0.00	0.01± 0.01			0.05± 0.01		
Arg												
Gly	0.09± 0.04	0.13± 0.03	0.10± 0.01	0.16± 0.06	0.13± 0.04	0.13± 0.00	0.13± 0.00	0.12± 0.00	0.05± 0.01	0.22± 0.00	0.13± 0.00	
Asp												
Glu		0.01± 0.01		0.05± 0.01	0.01± 0.01	0.03± 0.02						
Thr												
Ala		0.01± 0.01		0.01± 0.00						0.01± 0.00	0.01± 0.00	
Pro												
Tyr												
Cys												
Lys												
Meth												
L-Val	0.14± 0.01	0.11± 0.00	0.07± 0.00	0.17± 0.01	0.21± 0.00	0.28± 0.02	0.43± 0.02	0.46± 0.01	0.25± 0.02	0.62± 0.02	0.32± 0.01	
L-Leu												
L-Ileu				0.03± 0.00								
Phe										0.01± 0.00		
EACA	0.19± 0.01	0.28± 0.02	0.24± 0.01	0.18± 0.00	0.21± 0.01	0.21± 0.00	0.09± 0.00	0.06± 0.00	0.04± 0.00	0.05± 0.00	0.07± 0.00	
<b>Total</b>	0.44± 0.06	0.55± 0.07	0.44± 0.04	0.71± 0.11	0.57± 0.06	0.69± 0.05	0.66± 0.03	0.65± 0.03	0.34± 0.03	0.97± 0.05	0.53± 0.02	
<b>Average</b>	0.48			0.66			0.55			0.75		