Certificate of Analysis

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Analytical services

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Verify Results Online

Sample Identification

Sample Name	GHK-Cu 50 mg
Batch Number	2026332
Date Published	2026-07-13 15:09

Results for LYO-0336

Peptides	Result	Unit	Uncertainty	Acceptable Range
GHK-Cu Assay Peptide Screening 0.1% TFA	47.1	*mg*	[± 0.2]	
GHK-Cu Purity Peptide Screening 0.1% TFA	99.3	*%*	[± 0.5]	
GHK-Cu Identification by Spectrum (FTIR) Peptide Screening 0.1% TFA	988		[± 5]	
GHK-Cu Identification by RT Peptide Screening 0.1% TFA	0.986		[± 0.005]	

Microbiology	Result	Unit	Uncertainty	Acceptable Range
Total Aerobic Microbial Count USP <61>/Eur. Ph. 2.6.12. Plate Count Method	0	*CFU/g*	[±]	0 - 1000
Total Yeast and Mold Count USP <61>/Eur. Ph. 2.6.12. Plate Count Method	0	*CFU/g*	[±]	0 - 100
Bacterial Endotoxin Chromgenic USP<85>/ Eur. Ph. 2.6.14. Bacterial Endotoxin Chromgenic Test	< 0.001	*EU/mg*		0 - 0.5

Elemental Impurities	Result	Unit	Uncertainty	Acceptable Range
Arsenic Elemental Impurities screening USP ⟨232⟩ / Ph. Eur. 5.20 / 2.4.20	< 0.001	*ppm*		0 - 1.5
Cadmium Elemental Impurities screening USP ⟨232⟩ / Ph. Eur. 5.20 / 2.4.20	< 0.001	*ppm*		0 - 0.5
Quicksilver Elemental Impurities screening USP ⟨232⟩ / Ph. Eur. 5.20 / 2.4.20	< 0.001	*ppm*		0 - 1.5
Lead Elemental Impurities screening USP ⟨232⟩ / Ph. Eur. 5.20 / 2.4.20	< 0.001	*ppm*		0 - 1.5
Nickel Elemental Impurities screening USP ⟨232⟩ / Ph. Eur. 5.20 / 2.4.20	< 0.001	*ppm*		0 - 25
Vanadium Elemental Impurities screening USP ⟨232⟩ / Ph. Eur. 5.20 / 2.4.20	< 0.001	*ppm*		0 - 25
Cobalt Elemental Impurities screening USP ⟨232⟩ / Ph. Eur. 5.20 / 2.4.20	< 0.001	*ppm*		0 - 25

Mass Spectrometry	Result	Unit	Uncertainty	Acceptable Range
Molecular Ion Mass Identification (MS Deconvolution) Mass Spectrometry Identity	341	*Da*	[± 1]	

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LIQUILABS	Method Specification	
Determination of identity, content and purity of GHK-Cu		
Document number: GHKCu_006_2026	Superseded document: -	Number of pages: 4

1. Content Assesment

1.1. Instrumentation

Module	Name	Serial Number
System Controller	Shimadzu CBM-40 Lite	L221226351398
Degassing Unit	Shimadzu DGU-403	NA
Pump	Shimadzu LC-40B XR	L22146350560
Autosampler	Shimadzu SIL-40C XR	L22216351622
Colum Thermostat	Shimadzu CTO-40S	L22236351602
PDA Detector	Shimadzu SPD-M40	L22276352608
SQ MS Detector	Shimadzu LCMS-2050	012476200760

1.2. Chromatographic conditions

Chromatographic conditions	
Eluent A	0.1% TFA in Water (HPLC, Gradient Grade)
Eluent B	0.1% TFA in Acetonitrile (HPLC, Gradient Grade)
Flow rate	0.4 mL/min
Program	Gradient elution
Injection volume	2 µL
Colum Temperature	60°C
Column	Phenomenex Biozen Peptide Polar C18, 150x2.1mm 3µm
Detection wavelength	225nm

Gradient Program		
Time [min]	A [%]	B [%]
3	100	0
18	45	55
20	1	99
21	1	99
21.01	100	0
26	end	

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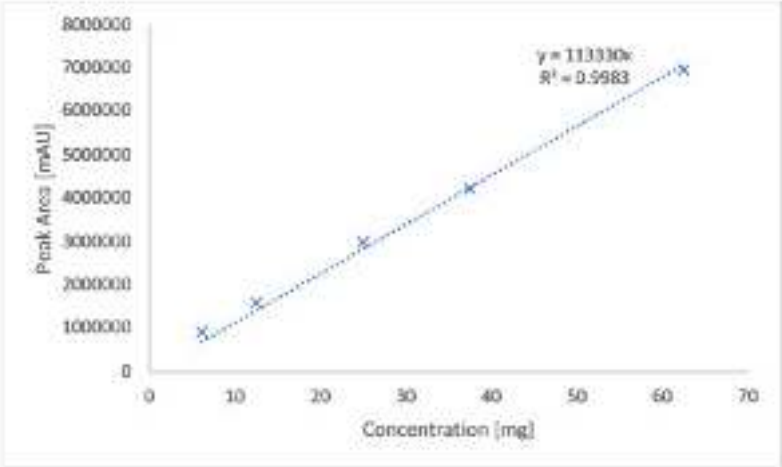
1.3. Sample preparation

Whole amount of container was dissolved in 2mL of water (LCMS Grade). 100 µL of sample was transferred to HPLC vial and diluted by 900 µL water (LCMS Grade) and submitted for analysis.

1.4. Calibration curve

Calibration curve detail	
Quantitative method	External Standard
Calibration Type	Linear
Number of calibration points	5
Force through Zero	Enabled
Weighting Method	None



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2. Purity assessment

2.1 Instrumentation

Module	Name	Serial Number
System Controller	Shimadzu CBM-40 Lite	L221226351396
Degassing Unit	Shimadzu DGU-403	NA
Pump	Shimadzu LC-40B XR	L22146350580
Autosampler	Shimadzu SIL-40C XR	L22216351622
Colum Thermostat	Shimadzu CTO-40S	L22236351602
PDA Detector	Shimadzu SPD-M40	L22276352808
SQ MS Detector	Shimadzu LCMS-2050	D12476200760

2.2 Chromatographic conditions

Chromatographic conditions	
Eluent A	0.1% TFA in Water (HPLC, Gradient Grade)
Eluent B	0.1% TFA in Acetonitrile (HPLC, Gradient Grade)
Flow rate	0.4 mL/min
Program	Gradient elution
Injection volume	2 µL
Colum Temperature	60°C
Column	Phenomenex Biozen Peptide Polar C18, 150x2.1mm 3µm
Detection wavelength	225nm

Gradient Program		
Time [min]	A [%]	B [%]
3	100	0
18	45	55
20	1	99
21	1	99
21.01	100	0
26	end	

2.3 Purity assesment

Purity of compound assesed by area normalization method, comparing area of each peak to sum of area of all peaks detected at wavelenght of 225nm.

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3. Identity Assessment

3.1 Instrumentation

Module	Name	Serial Number
System Controller	Shimadzu CBM-40 Lite	L221226351398
Degassing Unit	Shimadzu DGU-403	NA
Pump	Shimadzu LC-40B XR	L22146350580
Autosampler	Shimadzu SIL-40C XR	L22216351622
Colum Thermostat	Shimadzu CTO-40S	L22236351602
PDA Detector	Shimadzu SPD-M40	L22276352808
SQ MS Detector	Shimadzu LCMS-2050	O12476200760

3.2 Chromatographic conditions

Chromatographic conditions	
Eluent A	0.1% TFA in Water (HPLC, Gradient Grade)
Eluent B	0.1% TFA in Acetonitrile (HPLC, Gradient Grade)
Flow rate	0.4 mL/min
Program	Gradient elution
Injection volume	2 µL
Colum Temperature	60°C
Column	Phenomenex Biozen Peptide Polar C18, 150x2.1mm 3µm
Mass spectrometry	Scan: positive 280-2000 Da

Gradient Program		
Time [min]	A [%]	B [%]
3	100	0
18	45	55
20	1	99
21	1	99
21.01	100	0
26	end	

3.3 Molecular Ion Mass evaluation

Molecular ion mass was determined by deconvolution of multiply charged ESI-MS spectra to calculate the average neutral (zero-charge) molecular mass by equation:

$$M(neutral) = (z_i\{(mz_i) - H\}) - ME$$

Where:
mz_i - Measured mass of charged particle
z_i - charge
H - proton mass (1.0076 Da)
ME – mass error

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Analysis Report

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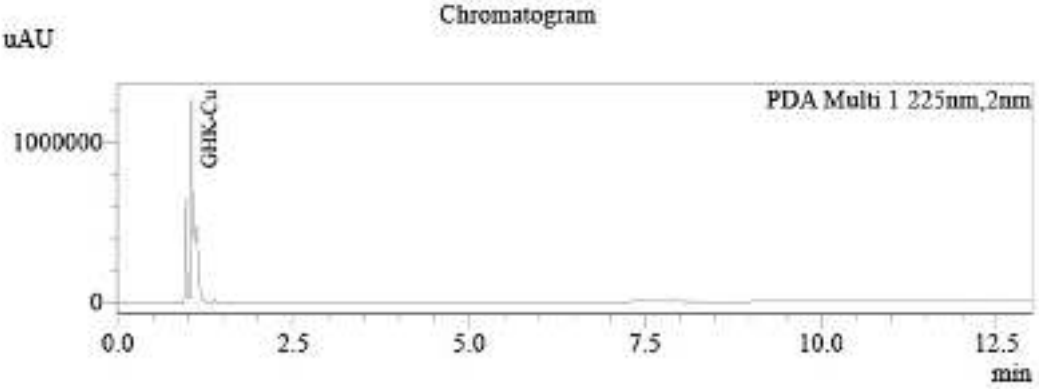
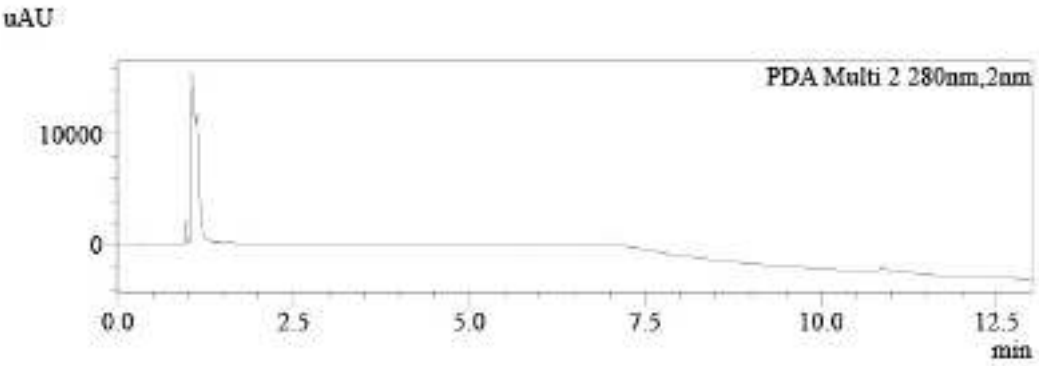
Analysis of quantity and purity of active ingredient by UHPLC with UV detection

Sample Information

Injection Volume	: 2
Data File	: LYO-0336__001.lcd
Method File	: Peptide screening polar_KLOW.lcm
Date Acquired	: 7/13/2026 3:17:44 PM

Chromatogram





Peak Table

PDA Ch1 225nm

Name	Ret. Time	Area	Conc.	Unit	Area%
GHK-Cu	1.045	4830131	47.083	mg	99.321
	1.367	24494	0.000		0.504
	1.502	391	0.000		0.008
	1.604	8144	0.000		0.167
		4863160			100.000

Peak Table

PDA Ch2 280nm

Name	Ret. Time	Area	Conc.	Unit
	0.972	4257	0.000	
	1.053	101669	0.000	
	10.887	2288	0.000	

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Name	Ret. Time	Area	Conc.	Unit
		108214		

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Analysis Report

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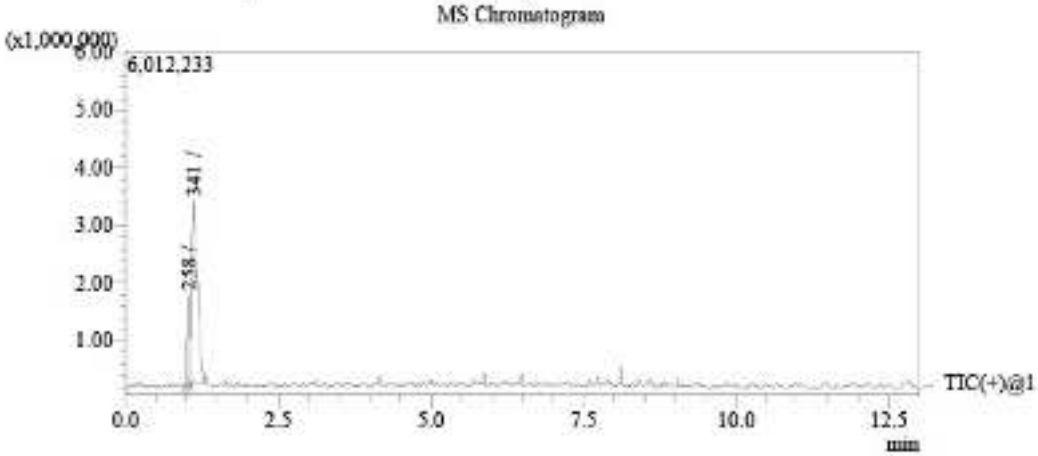
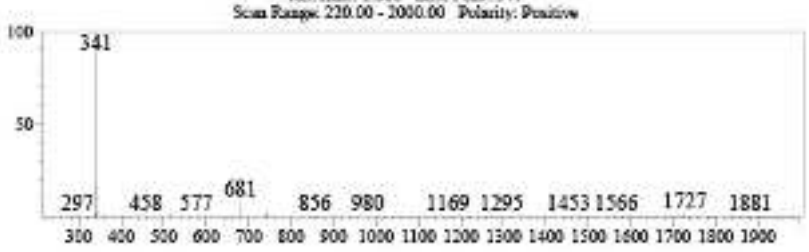
Analysis of identity of active ingredient by UHPLC with mass spectrometric detection

MS Chromatogram

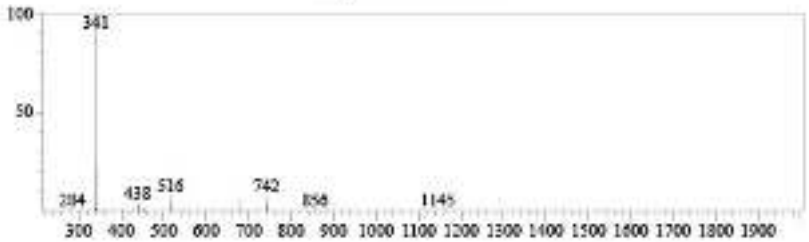


Library Search

Detected compound
Ret.Time: 1.086 Base Peak: 341
Scan Range: 220.00 - 2000.00 Polarity: Positive



Library: Peptide screening lib
Formula: C14H24Cu2N6O4 CAS: 49557-75-7 Mol.Weight: 401 Ref.Index: 0
Compound Name: GHK-Cu



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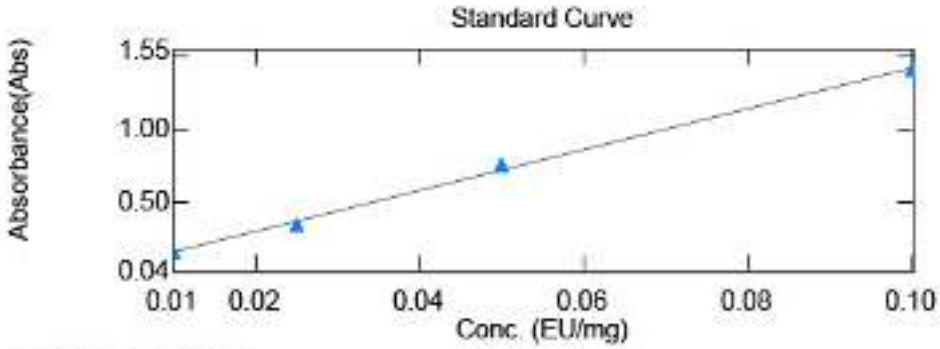
Endotoxin Determination Report

File Information
Filename: C:\UVVis-Data\Data\File_260713_144946.vqud
Date/Time: 07/13/2026 03:28:57 PM

Instrument Information
Instrument Type: UV-1900 Series
Model (S/N): UV-1900i (A12536253123)



y = 13.9884 x + 0.0252453
r2 = 0.99817

	Sample Name	Type	Conc	Result	Dilution Rate
1	LYO-0299	UNK	0.100	0.095	20.00
2	LYO-0300	UNK	0.233	0.189	20.00
3	LYO-0301	UNK	0.798	0.583	20.00
4	LYO-0302	UNK	0.642	0.474	20.00
5	LYO-0303	UNK	3.516	0.517	100.00
6	LYO-0321	UNK	0.116	0.107	20.00
7	LYO-0326	UNK	3.147	2.227	20.00
8	LYO-0327	UNK	0.022	0.041	20.00
9	LYO-0332	UNK	0.043	0.055	20.00
10	LYO-0333	UNK	0.041	0.054	20.00
11	LYO-0334	UNK	0.122	0.111	20.00
12	LYO-0335	UNK	0.264	0.210	20.00
13	LYO-0336	UNK	-0.011	0.017	20.00

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LIQUILABS	Method Specification	
Determination of bioburden of lyophilized samples		
Document number: MIC_001_2025	Superseded document: -	Number of pages: 2

1. Instrumentation and chemicals

1.1. Instruments used

- Sterile Syringe 2mL Luer
- Sterile needles
- Ready made PCA Plate ROTI Aquatest
- Ready made Sab4 Plate ROTI Aquatest

1.2. Chemicals

Sterile physiological solution (0.9% NaCl)

2. Sample preparation and innoculation

2.1 Sample preparation

1. Fresh sterile needle and syringe was used for measuring exactly 2 mL of sterile physiological solution.
2. Needle was changed and by new needle rubber top of peptide containter was penetrated and 2 mL of sterile physiological solution was dispensed.
3. Content of container was completely dissolved and left for 5 minutes to settle potentially created bubbles.
4. This procedure is repeated for two vials.

2.2 Total Aerobic microbial count innoculation and cultivation

1. By sterile needle 1 mL of solution was filled into the sterile syringe.
2. Needle was placed above the flame for few seconds to sterilize.
3. Consequently 1 mL of solution was poured into the ready to use sterile petri dish filled with PCA agar and petri dish was closed.
4. Proces was repeated for two petri dishes.
5. With sterile needle, 1 mL of sterile physiological solution was filled into the sterile needle and was innoculated onto one sterile petri dish filled with PCA agar as negative control sample.
6. Samples and negative control sample were placed in incubator at temperature 37°C for 120h.

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2.3 Total Yeast and Mold count innoculation and cultivation

1. By sterile needle 1 mL of solution was filled into the sterile syringe.
2. Needle was placed above the flame for few seconds to sterilize.
3. Consequently 1 mL of solution was poured into the ready to use sterile petri dish filled with Sab4 agar and petri dish was closed.
4. Proces was repeated for two petri dishes.
5. With sterile needle, 1 mL of sterile physiological solution was filled into the sterile needle and was innoculated onto one sterile petri dish filled with Sab4 agar as negative control sample.
6. Samples and negative control sample were placed in incubator at temperature 25°C for 72h.

3. Evaluation of results

After incubation time, colonies are counted as cfu (colonies forming units) and result per 1g of sample is determined as:

$$CFU_{avg} = \frac{\sum CFU_n}{n}$$

$$CFU_{avg} = average\ CFU\ counted\ form\ n\ innoculations$$
$$CFU_n = CFU\ counted\ per\ innoculation$$
$$n = number\ of\ innoculations$$

$$CFU\ per\ gram = \frac{CFU_{avg}}{m_s} * DF$$

$$CFU_{avg} = Average\ CFU\ counted\ from\ n\ innoculations$$
$$m_s = mass\ of\ sample\ (mg)$$
$$DF = Dilution\ factor$$

If negative control sample is evaluated as positive, process have to be repeated due to possible contamination in the process of innoculation or incubation.

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Responsibles

Mr. Ján Galbavý
CEO

Analysis results relate only to the samples tested.
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