

Certificate of Analysis

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Sample Identification

Sample Name	Glow
Batch Number	GLOW/2026-05-12
Date Published	2026-05-28 15:35

Results for LYO-0165

Peptides	Result	Unit	Uncertainty	Acceptable Range
BPC-157 Assay Peptide Screening 0.1% TFA	11.48	mg	[± 0.06]	
GHK-Cu Assay Peptide Screening 0.1% TFA	60.3	mg	[± 0.3]	
BPC-157 Purity Peptide Screening 0.1% TFA	> 99.8	%		
GHK-Cu Purity Peptide Screening 0.1% TFA	> 99.8	%		
BPC-157 Identification by Spectrum Peptide Screening 0.1% TFA	993		[± 5]	
GHK-Cu Identification by Spectrum Peptide Screening 0.1% TFA	1000		[± 5]	
BPC-157 Identification by RT Peptide Screening 0.1% TFA	0.989		[± 0.005]	
GHK-Cu Identification by RT Peptide Screening 0.1% TFA	0.992		[± 0.005]	
Thymosin Beta 4 (TB-500) Assay Peptide Screening 0.1% TFA	13.53	mg	[± 0.07]	
Thymosin Beta 4 (TB-500) Purity Peptide Screening 0.1% TFA	98.2	%	[± 0.5]	
Thymosin Beta 4 (TB-500) Identification by Spectrum Peptide Screening 0.1% TFA	992		[± 5]	
Thymosin Beta 4 (TB-500) Identification by RT Peptide Screening 0.1% TFA	0.990		[± 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 Chromogenic USP<85>/ Eur. Ph. 2.6.14. Bacterial Endotoxin Chromogenic Test	0.005	EU/mg	[± 0]	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 (BPC-157) Mass Spectrometry Identity	1419	g/mol	[± 1]	

Mass Spectrometry	Result	Unit	Uncertainty	Acceptable Range
Molecular Ion Mass Identification (GHK-Cu) Mass Spectrometry Identity	402	<i>g/mol</i>	[± 1]	
Molecular Ion Mass Identification (TB-500) Mass Spectrometry Identity	4963	<i>g/mol</i>	[± 1]	

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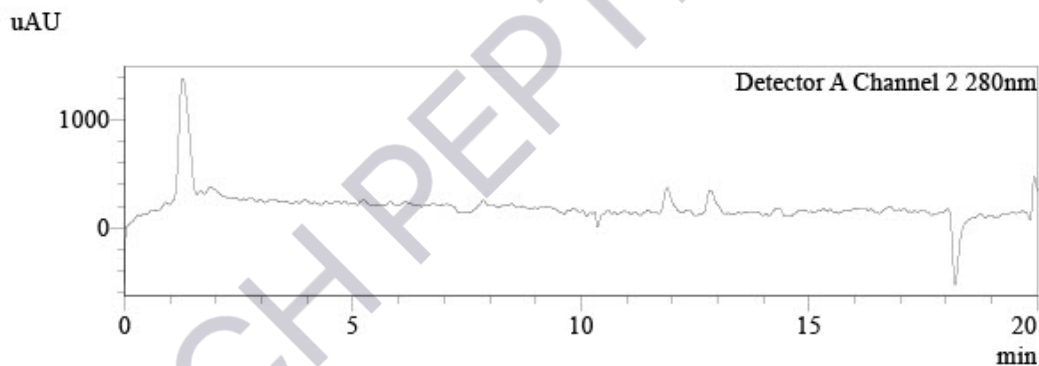
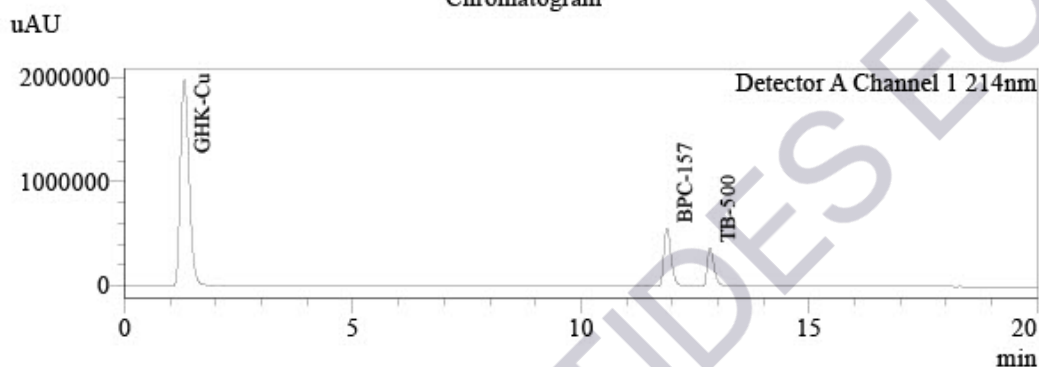
Analysis Report



Sample Information

Injection Volume : 0,5
 Data File : LYO-0165_017.lcd
 Method File : Peptide screening_202602_Polar_Blend A.lcm
 Date Acquired : 18.05.2026 22:59:17

Chromatogram



Peak Table

Detector A Channel 1 214nm					
Peak#	Name	Ret. Time	Conc.	Unit	Area%
1	GHK-Cu	1,307	60,336	mg/L	72,628
2		11,072	0,000		0,023
3		11,551	0,000		0,007
4	BPC-157	11,883	11,477	mg/L	16,671
5		12,358	0,000		0,273
6	TB-500	12,827	13,534	mg/L	10,387
7		13,627	0,000		0,011
Total					100,000

Peak Table

Detector A Channel 2 280nm				
Peak#	Name	Ret. Time	Conc.	Unit
Total				

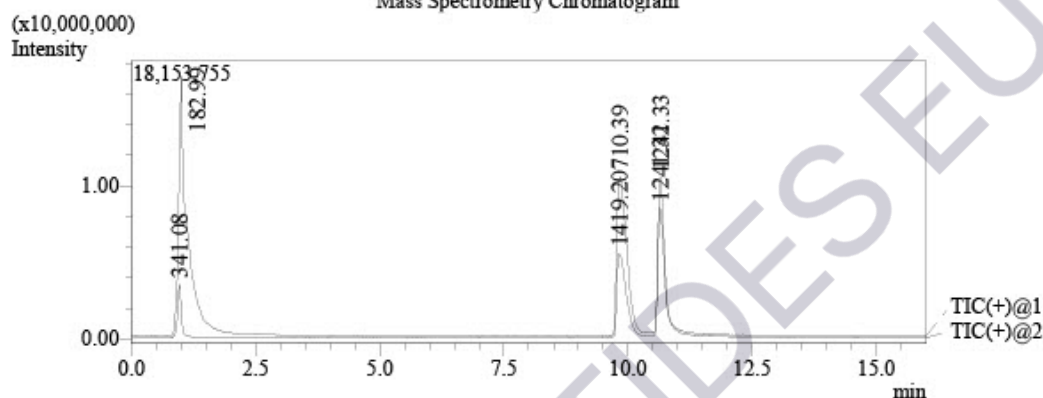
Mass Spectrum Report



Sample Information

Injection Volume : 0.5
Data File : LYO-0165_003.lcd
Method File : Peptide screening_V3_Blend Polar.lcm
Date Acquired : 5/19/2026 3:55:12 PM

Mass Spectrometry Chromatogram



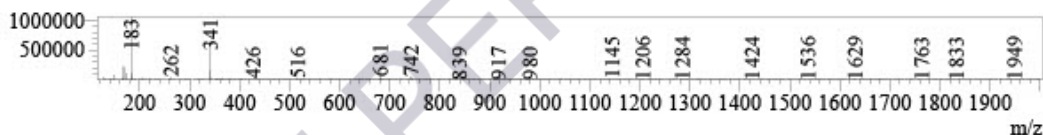
MS Spectrum

Line#:1 R.Time:----(Scan#----)

MassPeaks:2235

Spectrum Mode:Averaged 0.819-1.701(53-109) Base Peak:183(1055404)

BG Mode:Calc Segment 1 - Event 1

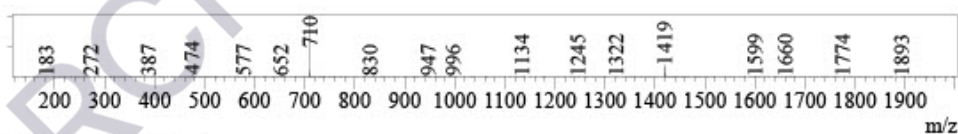


Line#:2 R.Time:----(Scan#----)

MassPeaks:1420

Spectrum Mode:Averaged 9.671-10.301(615-655) Base Peak:710(2032980)

BG Mode:Calc Segment 1 - Event 1

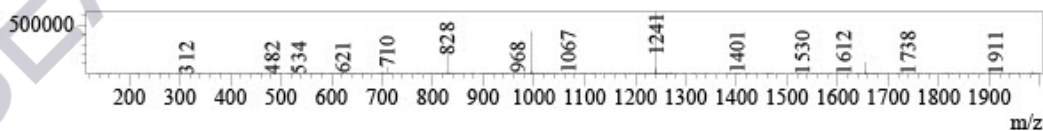


Line#:3 R.Time:----(Scan#----)

MassPeaks:1559

Spectrum Mode:Averaged 10.301-11.088(655-705) Base Peak:1241(634824)

BG Mode:Calc Segment 1 - Event 1



 LIQUILABS Analytical services	Method Specification	
Determination of bacterial endotoxin content of lyophilized samples		
<i>Document number</i> ENDOTOX_0517_2026	<i>Superseded document</i> -	<i>Number of pages</i> 2

1. Chromgenic LAL Assay Determination of Bacterial Endotoxin content of sample

1.1. Instrumentation

- Pipette set 1-1000 µL
- Thermostatically controlled water bath
- UV VIS spectrometer (Shimadzu UV-1601)
- GenScript ToxinSensor Chromgenic LAL Endotoxin Assay kit

1.2. Chemicals

- LAL Reagent water (endotoxin free)
- Limulus Amoebocyte Lysate
- LAL Substrate
- Color Stabilizer #1
- Color Stabilizer #2
- Color Stabilizer #3
- 35% HCl (p.a.)

1.3. Sample preparation

1. Sample container was weighed prior to dissolution and measured weight was marked.
2. Sample was completely dissolved in its container by 2 mL of LAL Reagent water.
3. 100 µL of the sample was aliquoted for analysis.
4. After analysis container was emptied and dried.
5. Dry mass of container was measured and exact weight of dissolved content was determined as:

$$m_{dc} = m_{sample} - m_{container}$$

1.4. Toxin sensor Chromgenic LAL Endotoxin Assay kit preparation

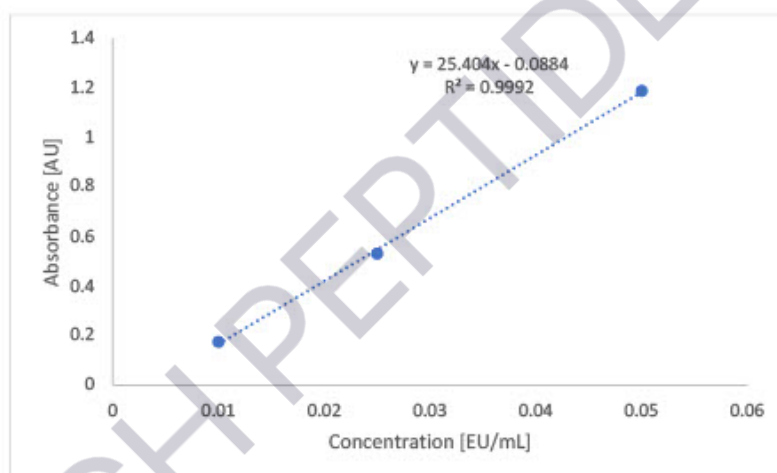
Procedures regarding preparation of reaction solutions possible to find in:

https://www.genscript.com/site2/document/5292_20080806231827.PDF

1.5. Measurement procedure

	Standards	Samples	Blank
Standards (mL)	0.1	-	-
Samples (mL)	-	0.1	-
LAL Reagent Water (mL)	-	-	0.1
LAL Solution (mL)	0.1	0.1	0.1
Mix well and incubate at 37°C for 27 min			
Substrate solution (mL)	0.1	0.1	0.1
Mix well and incubate at 37°C for 6 min			
Color Stabilizer #1 solution	0.5	0.5	0.5
Color Stabilizer #2 solution	0.5	0.5	0.5
Color Stabilizer #3 solution	0.5	0.5	0.5
Mix well and read the absorbance at 545nm			

1.6. Calibration curve



1.7. Calculation of endotoxin content

Endotoxin content of the sample was calculated from the calibration curve as:

$$Endotox[EU/mg] = \frac{\left(\frac{ABS_{sample}}{S_{calib}} \right) * 20}{m_{sample}}$$

ABS_{sample} = Measured absorbance of sample

S_{calib} = Slope of calibration curve

m_{sample} = real measured mass of sample

20 = dilution factor of measured sample

 LIQUILABS Analytical services	Method Specification	
Determination of bioburden of lyophilized samples		
<i>Document number</i> MIC_001_2025	<i>Superseded document</i> -	<i>Number of pages</i> 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 inoculation

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 container 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 inoculation 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. Process was repeated for two petri dishes.
5. With sterile needle, 1 mL of sterile physiological solution was filled into the sterile needle and was inoculated 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.

2.3 Total Yeast and Mold count inoculation 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 inoculated 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 inoculations

CFU_n = CFU counted per inoculation

n = number of inoculations

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

CFU_{avg} = Average CFU counted from n inoculations

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 inoculation or incubation.

Responsibles



Mr. Ján Galbavý
CEO

Analysis results relate only to the samples tested.

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