

Certificate of Analysis

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Sample Identification

| | |
|-----------------------|---------------------------|
| Sample Name | HGH Fragment 175-191 5 mg |
| Batch Number | GF-HGHFR-B241 |
| Date Published | 2026-06-22 17:36 |

Results for LYO-0245

| Peptides | Result | Unit | Uncertainty | Acceptable Range |
|--|---------|-------|-------------|------------------|
| HGH Fragment 176-191 Assay Peptide Screening 0.1% TFA | 3.64 | mg | [± 0.02] | |
| HGH Fragment 176-191 Purity Peptide Screening 0.1% TFA | 99.6 | % | [± 0.5] | |
| HGH Fragment 176-191 Identification by Spectrum (FTIR) Peptide Screening 0.1% TFA | 989 | | [± 5] | |
| HGH Fragment 176-191 Identification by RT Peptide Screening 0.1% TFA | 0.996 | | [± 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 | 1800 | Da | [± 1] | |

| | | |
|---|---------------------------------|-----------------------------|
|  | Method Specification | |
| Determination of identity, content and purity of HGH Fragment 176-191 | | |
| <i>Document number</i> HGFR_006_2026 | <i>Superseded document</i> - | <i>Number of pages</i> 4 |

1. Content Assessment

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 | 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 |

1.2. Chromatographic conditions

| Chromatographic conditions | |
|----------------------------|--|
| Eluent A | 0.05% TFA in Water (HPLC, Gradient Grade) |
| Eluent B | 0.0425% TFA in Acetonitrile (HPLC, Gradient Grade) |
| Flow rate | 0.9 mL/min |
| Program | Gradient elution |
| Injection volume | 2 µL |
| Colum Temperature | 55°C |
| Column | Waters XSelect CSH C18, 100x2.1mm 2.5µm |
| Detection wavelength | 225nm |

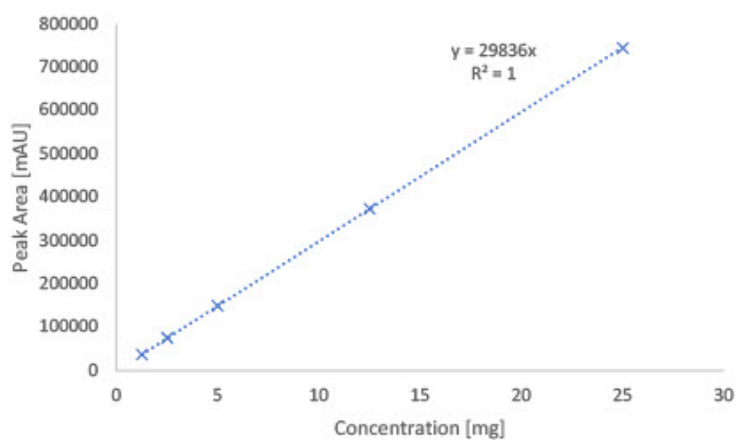
| Gradient Program | | |
|------------------|-------|-------|
| Time [min] | A [%] | B [%] |
| 1.5 | 95 | 5 |
| 13 | 45 | 55 |
| 13.5 | 1 | 99 |
| 14.5 | 1 | 99 |
| 14.51 | 95 | 5 |
| 16 | end | |

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 |



2. Purity assessment

2.1 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 |

2.2 Chromatographic conditions

| Chromatographic conditions | |
|----------------------------|--|
| Eluent A | 0.05% TFA in Water (HPLC, Gradient Grade) |
| Eluent B | 0.0425% TFA in Acetonitrile (HPLC, Gradient Grade) |
| Flow rate | 0.9 mL/min |
| Program | Gradient elution |
| Injection volume | 2 µL |
| Colum Temperature | 55°C |
| Column | Waters XSelect CSH C18, 100x2.1mm 2.5µm |
| Detection wavelength | 225nm |

| Gradient Program | | |
|------------------|-------|-------|
| Time [min] | A [%] | B [%] |
| 1.5 | 95 | 5 |
| 13 | 45 | 55 |
| 13.5 | 1 | 99 |
| 14.5 | 1 | 99 |
| 14.51 | 95 | 5 |
| 16 | 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 214 nm.

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 | 0.05% TFA in Water (HPLC, Gradient Grade) |
| Eluent B | 0.0425% TFA in Acetonitrile (HPLC, Gradient Grade) |
| Flow rate | 0.9 mL/min |
| Program | Gradient elution |
| Injection volume | 2 µL |
| Colum Temperature | 55°C |
| Column | Waters XSelect CSH C18, 100x2.1mm 2.5µm |
| Mass spectrometry | Scan: positive 280-2000 Da |

| Gradient Program | | |
|------------------|-------|-------|
| Time [min] | A [%] | B [%] |
| 1.5 | 95 | 5 |
| 13 | 45 | 55 |
| 13.5 | 1 | 99 |
| 14.5 | 1 | 99 |
| 14.51 | 95 | 5 |
| 16 | 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:

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

Where:

mz_i - Measured mass of charged particle

z_i - charge

H - proton mass (1.0076 Da)

ME - mass error

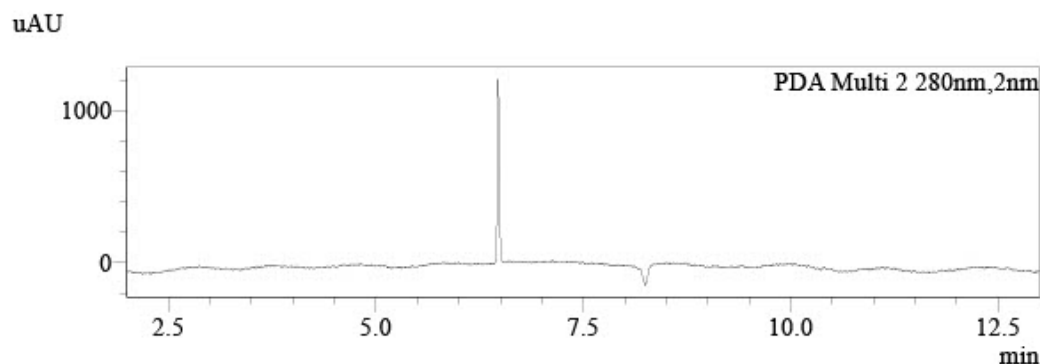
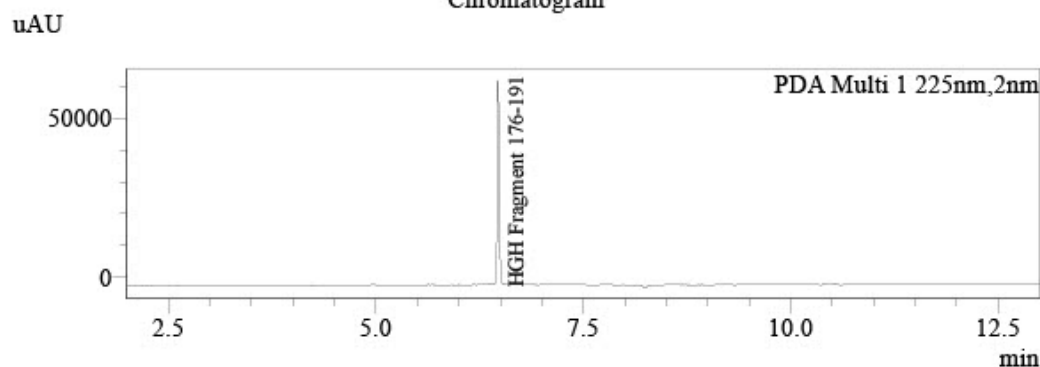
Analysis Report



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

Sample Information
Injection Volume : 2
Data File : LYO-0245_020.lcd
Method File : Peptide screening_V7_Group E.lcm
Date Acquired : 6/19/2026 6:22:50 AM

Chromatogram



Peak Table

PDA Ch1 225nm

| Name | Ret. Time | Area | Conc. | Unit | Area% |
|----------------------|-----------|--------|-------|------|---------|
| | 6.368 | 235 | 0.000 | | 0.216 |
| | 6.406 | 43 | 0.000 | | 0.039 |
| HGH Fragment 176-191 | 6.473 | 108469 | 3.636 | mg | 99.615 |
| | 6.603 | 141 | 0.000 | | 0.130 |
| | | 108888 | | | 100.000 |

Peak Table

PDA Ch2 280nm

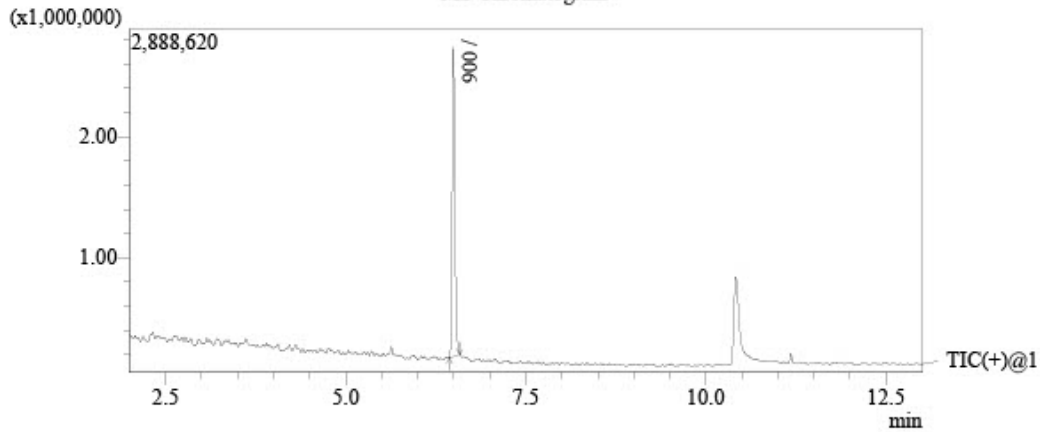
| Name | Ret. Time | Area | Conc. | Unit |
|------|-----------|------|-------|------|
| | 6.473 | 2095 | 0.000 | |
| | | 2095 | | |

Analysis Report



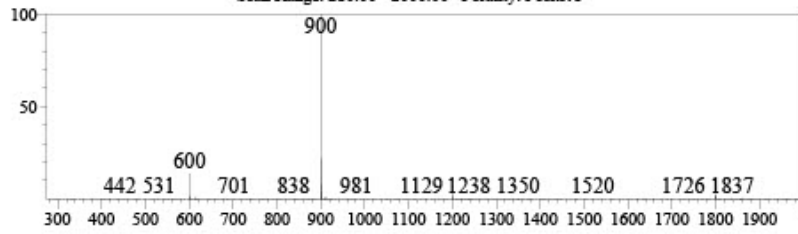
Analysis of identity of active ingredient by UHPLC with mass spectrometric detection

MS Chromatogram



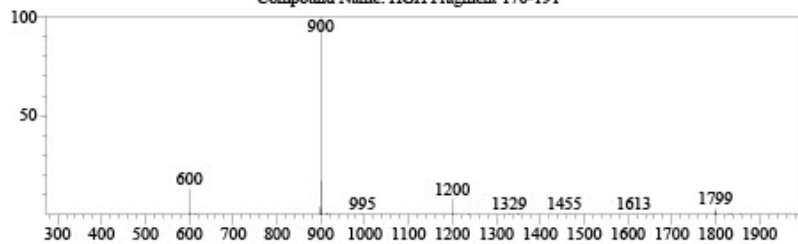
Library Search


Detected compound
Ret. Time: 6.440 Base Peak: 900
Scan Range: 280.00 - 2000.00 Polarity: Positive



Reference

Library: Peptide screening lib
Formula: C78H123N23O22S2 CAS: 66004-57-7 Mol. Weight: 1799 Ret. Index: 0
Compound Name: HGH Fragment 176-191



| | | | |
|---|---------------------------------|-----------------------------|--|
|  | Method Specification | | |
| Determination of bacterial endotoxin content of lyophilized samples | | | |
| <i>Document number</i> ENDOTOX_0616_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

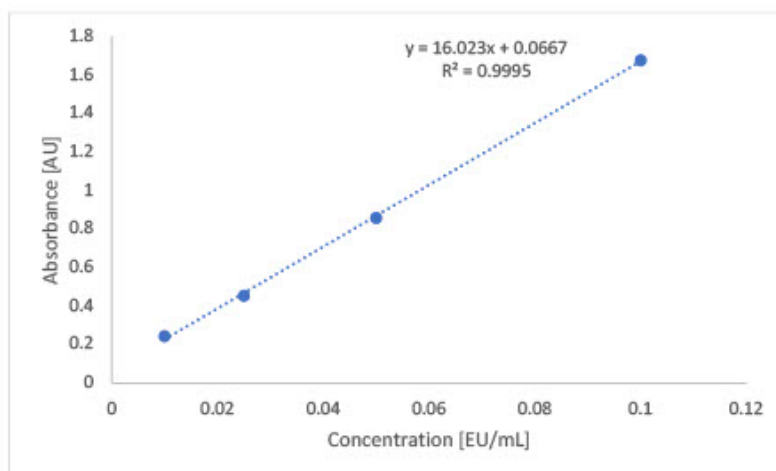
Procedures regarding preparation of reaction solutions possible to find in:

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

| | | | |
|---|---------------------------------|-----------------------------|--|
|  | 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. 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 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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