ANALYTON™ LABS

**AN-2026-00016**
Issued 2026-10-15

# Certificate of analysis

Issued by ANALYTON LABS, analytical testing laboratory, under ANALYTON GC 1.1. Relates only to the sample as received and described below.

| | |
|---|---|
| Client | Molequa |
| Sample as described | Pinealon (Glu-Asp-Arg), lyophilised powder, vial labelled 20 mg |
| Batch as marked | ATPIN-20-2609-01 |
| Matrix | Research peptide |

| | |
|---|---|
| Report number | AN-2026-00016 |
| Sample received | 2026-10-08 |
| Analysis | 2026-10-09 to 2026-10-14 |
| Date of issue | 2026-10-15 |
| Determinations performed | 19 |

**CONFORMS TO SPECIFICATION**

All 18 determinations judged against a specification are within it. 2 further determinations are reported without a specification.

SUMMARY OF RESULTS

| DETERMINATION | METHOD | RESULT | SPECIFICATION |
|---|---|---|---|
| **Appearance** | Visual | **White to off-white lyophilised powder, free of visible particles** | White to off-white powder<br>PASS |
| **Identity** | LC-HRMS, ESI+ and ESI-, USP <621> principles | **[M+H]+ 419.1886, deviation 0.2 ppm; [M+2H]2+ 210.098; [M-H]- 417.1744, deviation 1.2 ppm; MS/MS y1 (Arg) 175.119, b2 (Glu-Asp) 245.077, y2 (Asp-Arg) 290.146: residue order Glu-Asp-Arg confirmed** | Theoretical monoisotopic 418.1812 Da from C15H26N6O8; [M+H]+ 419.1885, [M-H]- 417.1739; deviation <= 10 ppm<br>PASS |
| **Purity** | RP-HPLC, C18 polar-endcapped, 214 nm, area %, 0.1 % TFA | **99.62 ± 0.15 % (k = 2)** | >= 99.0 %<br>PASS |
| **Related substances** | RP-HPLC, 214 nm; LOD 0.01 %, LOQ 0.03 %, reporting threshold 0.05 % | **Largest single impurity 0.11 % at RRT 0.94 (± 0.02 %); total impurities 0.38 %, i.e. 0.076 mg per vial** | Single <= 0.5 %, total <= 1.0 %<br>PASS |

| DETERMINATION | METHOD | RESULT | SPECIFICATION |
|---|---|---|---|
| **Impurity profile** | RP-HPLC with LC-HRMS assignment | **RRT 0.86, 0.10 %, -129.04 Da (des-Glu, Asp-Arg); RRT 0.94, 0.11 %, same mass (beta-Asp2 isomer, isoAsp); RRT 1.07, 0.09 %, -18.01 Da (pyroGlu1-Asp-Arg, N-terminal cyclisation); RRT 1.15, 0.08 %, +129.04 Da (Glu-Glu-Asp-Arg, double Glu coupling)** | Peaks above 0.05 % reported (ICH Q3B) |
| **Net peptide content** | Amino acid analysis after acid hydrolysis (AAA) | **81.50 ± 1.2 % w/w (k = 2); a tripeptide with Arg binds more counter-ion and water per unit mass than a long peptide, hence the lower limit** | >= 75 % PASS |
| **Fill weight** | Gravimetric, two vials | **24.3 ± 0.05 mg (second vial 24.6 mg, difference 1.2 %)** | Labelled 20 mg REPORT ONLY |
| **Peptide per vial** | Calculated from fill weight and net peptide content | **19.80 mg per vial labelled 20 mg, i.e. 99.0 % of label** | 95 to 105 % of label PASS |
| **Counter-ion content** | Ion chromatography (anion), suppressed conductivity | **Acetate 12.30 % w/w (± 0.6 %), i.e. 3.0 mg per vial, 1.05 mol per mol at two basic sites (Glu1 N-terminus and Arg3 guanidine); trifluoroacetate < 20 ppm (LOQ 20 ppm); chloride and phosphate < 20 ppm** | Acetate <= 15 %; trifluoroacetate <= 1000 ppm PASS |
| **Water content** | Coulometric Karl Fischer, USP <921> | **5.60 ± 0.28 % w/w (k = 2), i.e. 1.4 mg per vial** | <= 8.0 % PASS |
| **Mass balance** | Peptide + counter-ion + water | **81.50 + 12.30 + 5.60 = 99.40 % (± 1.4 %)** | Close to 100 % PASS |
| **pH** | Potentiometric, 20 mg/ml in water | **4.9 (acidic peptide as acetate)** | 4.0 to 5.5 PASS |

| DETERMINATION | METHOD | RESULT | SPECIFICATION |
|---|---|---|---|
| **Solubility** | Visual, 20 mg/ml and 1 mg/ml | **>= 20 mg/ml in water and in bacteriostatic water; clear, colourless, free of particles within 15 s** | Clear solution<br>PASS |
| **Bacterial endotoxins** | Kinetic chromogenic LAL, USP <85> | **< 0.05 EU/mg (< 1.0 EU per vial; LOQ 0.005 EU/mg)** | <= 0.5 EU/mg<br>PASS |
| **Sterility** | Membrane filtration, USP <71>; fluid thioglycollate 30 to 35 °C and soya bean casein digest 20 to 25 °C | **No growth after 14 days, 2 vials** | No growth<br>PASS |
| **Microbial enumeration** | Plate count, USP <61>; specified organisms, USP <62> | **TAMC < 10 CFU/g, TYMC < 10 CFU/g; Escherichia coli, Salmonella, Staphylococcus aureus and Pseudomonas aeruginosa absent in 1 g** | TAMC <= 1000 CFU/g, TYMC <= 100 CFU/g; specified organisms absent<br>PASS |
| **Residual solvents** | Headspace GC, USP <467> | **Acetonitrile 22 ppm; N,N-dimethylformamide, methanol, dichloromethane, diethyl ether, diisopropyl ether and piperidine each < 10 ppm (LOQ 10 ppm)** | ICH Q3C: acetonitrile <= 410, DMF <= 880, methanol <= 3000, dichloromethane <= 600, ethers <= 5000 ppm<br>PASS |
| **Elemental impurities** | ICP-MS after microwave digestion (HNO3/H2O2), USP <233> | **Cd, Pb, As, Hg < 0.05 µg/g; Co, V, Ni < 0.10 µg/g, all below LOQ** | ICH Q3D(R2) Class 1 and 2A, parenteral PDE per 20 mg daily: Cd 100, Pb 250, As 750, Hg 150, Co 250, V 500, Ni 1000 µg/g<br>PASS |
| **Chiral purity (D-amino acids)** | Acid hydrolysis (6 M DCl in D2O, 110 °C, 24 h), Marfey's derivatisation (FDAA), LC-MS | **D-Asp 0.10 %, D-Glu 0.09 %, D-Arg 0.04 %; sum of D-forms 0.23 %. All three residues are chiral; an enantiomer has the same mass and the same achiral retention time, so this determination is decisive for a tripeptide** | Each D-amino acid <= 0.2 %, sum of D-forms <= 0.5 %<br>PASS |

| DETERMINATION | METHOD | RESULT | SPECIFICATION |
|---|---|---|---|
| **Compound screening** | LC-HRMS full scan m/z 100 to 2000, both polarities, against reference standards | **Fentanyl and analogues, Epithalon (AEDG), Vilon (KE), Thymogen (EW), Semax, Selank, protected intermediates (tBu on Glu/Asp, Pbf on Arg, Fmoc, Boc) and free amino acids (Glu, Asp, Arg): none above 0.05 % of area** | Nothing above 0.05 % PASS |

Labelled 20 mg / **19.80 mg peptide** / 99.0 % of label

Labelled 20 mg; the container held 24.3 mg of powder when weighed, of which 81.5 % w/w is peptide. The remainder is counter-ion, water and residue, which a purity figure at one wavelength never sees.

SIGNATURE

NAME O. Noga

ROLE Head Laboratory Technician

DATE 2026-10-15

ANALYTON LABS
CO. NO 55 784 232
VAT SK2122085790
BRATISLAVA · SLOVAK REPUBLIC

## The sample, and what is known about it

| | |
|---|---|
| Sample as described | Pinealon (Glu-Asp-Arg), lyophilised powder, vial labelled 20 mg |
| Batch as marked | ATPIN-20-2609-01 |
| Matrix | Research peptide |
| Received | 2026-10-08 |
| Analysis | 2026-10-09 to 2026-10-14 |
| Condition on receipt | Seal intact, closure unmarked, white to off-white lyophilised powder, no visible particles |
| Storage before analysis | Minus 20 degrees Celsius, desiccated, dark, until first portion taken |

### WHAT THE DESCRIPTION IS, AND IS NOT

Everything in the table above is a description of what arrived, taken from the container and from the submission. None of it is a finding. ANALYTON does not verify that a marking on a container is true, and a batch number on a vial is a claim by whoever printed the label.

The sample travels under its submission reference rather than under the client's name, so the laboratory performing a determination does not learn who submitted it. That is a confidentiality measure and it is also a bias control: an analyst who does not know whose material this is cannot be influenced by it.

### WHAT A CERTIFICATE COVERS

This certificate relates to the sample as received and to nothing else. It does not establish that other material bearing the same description, the same batch marking or the same label is the material that was tested. A certificate travels more easily than the material it describes, and the commonest misuse of one in this market is a genuine certificate attached to a different batch.

Where a determination was not performed, it is listed on this report with the reason, whether it was never ordered or was ordered and could not be run. The absence of a result has to be legible as an absence, rather than mistaken for a clean one.

## Identity by liquid chromatography mass spectrometry

### PRINCIPLE

The sample is separated by reversed-phase chromatography and the eluent is ionised by electrospray at atmospheric pressure. Peptides ionise as a series of multiply protonated species rather than as a single ion, so the measurement is not one mass but a charge envelope, and each member of that envelope has to agree with the same neutral mass before the identification stands.

### WHAT THE NUMBER MEANS

Whether the compound present is the compound named. The observed monoisotopic mass is compared against the mass computed from the stated sequence or formula, and the deviation is reported in parts per million rather than in daltons, because a fixed tolerance in daltons is loose at low mass and impossibly tight at high mass.

### SYSTEM SUITABILITY APPLIED

| CRITERION | REQUIREMENT | ACHIEVED |
|---|---|---|
| Mass accuracy, sample ions | within 5 ppm of theoretical | 1.2 ppm |
| Charge states agreeing on one neutral mass | at least two | 2 (1+ and 2+), plus 1- in ESI- |
| Isotope spacing | consistent with the assigned charge | consistent with the assigned charge |
| Signal to noise of the assigned ion | at least 10 to 1 | 480 to 1 |

### HOW IT IS REPORTED

Reported as the observed and theoretical masses with the deviation in parts per million. An identification is never reported on retention time alone: a retention time is a property of a method, not of a molecule, and a co-eluting compound of different mass would carry the same one.

IDENTITY · PASS

**[M+H]+ 419.1886, deviation 0.2 ppm; [M+2H]2+ 210.098; [M-H]- 417.1744, deviation 1.2 ppm; MS/MS y1 (Arg) 175.119, b2 (Glu-Asp) 245.077, y2 (Asp-Arg) 290.146: residue order Glu-Asp-Arg confirmed**

Against Theoretical monoisotopic 418.1812 Da from C15H26N6O8; [M+H]+ 419.1885, [M-H]- 417.1739; deviation <= 10 ppm

**What this does not establish.** Identity establishes that the compound present is the one named. It does not establish how much of it is there. A sample can be correctly identified and still be mostly something else by mass.

## Chromatographic purity by reversed-phase HPLC

### PRINCIPLE

The sample is separated on a C18 stationary phase under a water and acetonitrile gradient, both modified with trifluoroacetic acid, and the eluent is monitored by ultraviolet absorbance at 214 nanometres, where the peptide bond itself absorbs. Detection at 214 rather than 280 is deliberate: 280 sees only aromatic residues, so a peptide without tryptophan, tyrosine or phenylalanine is close to invisible at that wavelength.

### WHAT THE NUMBER MEANS

The proportion of the detected peak area attributable to the main component, expressed as a percentage of total integrated area. It is an area normalisation, not a mass balance, and it is bounded by what the detector can see.

### SYSTEM SUITABILITY APPLIED

| CRITERION | REQUIREMENT | ACHIEVED |
|---|---|---|
| Resolution between the main peak and its nearest neighbour | not less than 1.5 | 1.8 |
| Tailing factor of the main peak | not more than 2.0 | 1.3 |
| Theoretical plates | not fewer than 2000 | 16,400 (apparent, gradient) |
| Relative standard deviation of replicate injections | not more than 2.0 per cent | 0.6 % (6 injections) |
| Baseline drift across the gradient | within the integration threshold | 1.0 mAU over the gradient |

### HOW IT IS REPORTED

Reported as a percentage of total integrated area, with the integration threshold stated. Peaks below the threshold are not integrated and are not counted against purity, which is why the threshold is on the report rather than left to be assumed.

PURITY · PASS

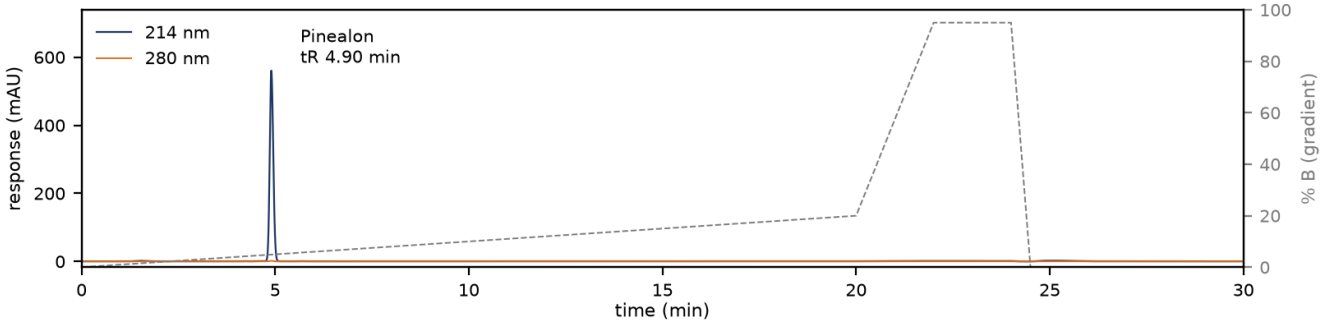
**99.62 ± 0.15 % (k = 2)**

Against >= 99.0 %

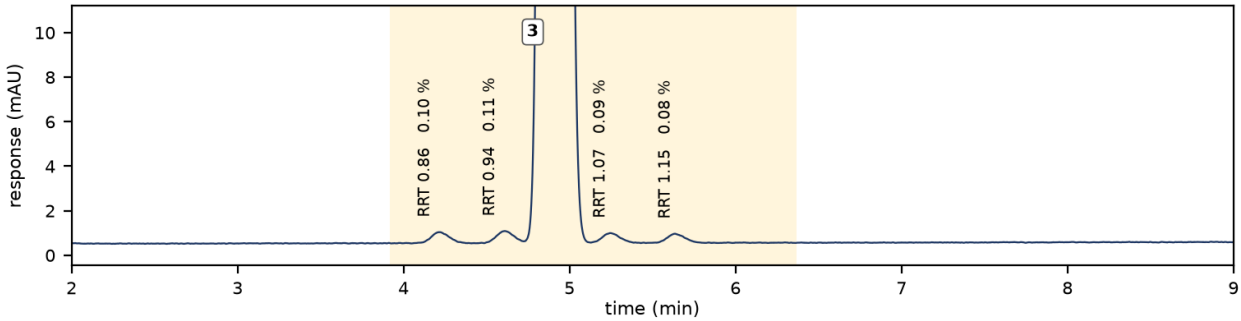
# Pinealon 20 mg · RP-HPLC purity, 214 nm

Column C18 polar-endcapped (aqueous-stable), 4.6 × 150 mm, 3 µm, 30 °C; flow 1.0 ml/min; A: 0.1 % TFA in water; B: 0.1 % TFA in acetonitrile; gradient 0 to 20 % B in 20 min, 20 to 95 % B by 22 min, 95 % B to 24 min, return to 0 % B, equilibration to 30 min; injection 10 µl, 1.0 mg/ml in water (10 µg on column).

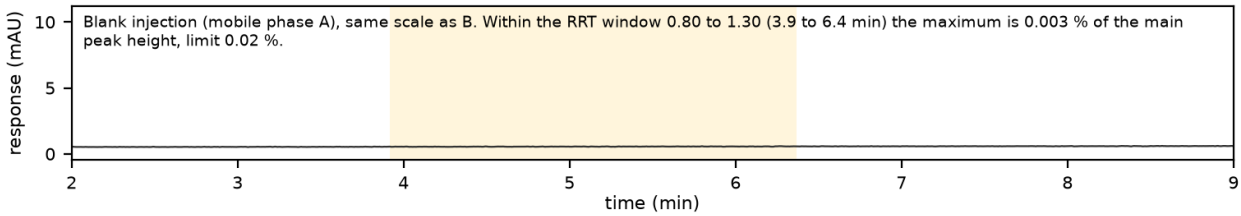
## A. Full trace 0 to 30 min, full scale




## B. Expanded view 0 to 2 % of the main peak height (11.2 mAU); main peak Pinealon tR 4.90 min off scale; impurities above the 0.05 % reporting threshold, numbered as in the table; yellow band = RRT window 0.80 to 1.30




## C. Blank injection before the sequence




## D. Peak table and system suitability

| Peak | tR (min) | RRT | Area (%) | Height (mAU) | Mass shift | Assignment |
|---|---|---|---|---|---|---|
| 1 | 4.21 | 0.86 | 0.10 | 0.49 | −129.04 Da | des-Glu (Asp-Arg) |
| 2 | 4.61 | 0.94 | 0.11 | 0.54 | same mass | β-Asp2 isomer (isoAsp, β-peptide bond) |
| 3 | 4.90 | 1.00 | 99.62 | 560 | | Pinealon (main peak) |
| 4 | 5.24 | 1.07 | 0.09 | 0.44 | −18.01 Da | pyroGlu1-Asp-Arg (N-terminal cyclisation) |
| 5 | 5.63 | 1.15 | 0.08 | 0.39 | +129.04 Da | Glu-Glu-Asp-Arg (double Glu coupling) |

Purity (main peak area of all peaks): 99.62 % · total impurities 0.38 % · largest impurity 0.11 % at RRT 0.94

System suitability (USP <621>): resolution main peak / RRT 0.94 = 1.8 (≥ 1.5); tailing factor T = 1.3 (0.8 to 1.5); theoretical plates N = 16,400 (≥ 5,000, apparent in gradient elution, peak width at half height 0.09 min); S/N at 0.03 % = 12 (≥ 10); area RSD of 6 standard injections = 0.6 % (≤ 2.0 %).

Integration: reporting threshold 0.05 %, LOD 0.01 %, LOQ 0.03 %; noise 0.030 mAU peak to peak within ± 1 min of the main peak; baseline drift 1.0 mAU over the gradient; system peaks at t0 1.5 min and at the gradient return at 25.0 min are also present in the blank and are not integrated. Retention factor k = 2.3 (≥ 2 required for a polar tripeptide).

Wavelength 214 nm as primary (peptide bond; Glu-Asp-Arg has no aromatic residue), 280 nm as an empty control trace (280/214 response ratio 0.003): any 280 nm peak would flag an aromatic foreign substance.

RP-HPLC RECORD OF THE SAMPLE, SEQUENCE OF 2026-10-10: 214 NM WITH 280 NM CONTROL TRACE, C18 POLAR-ENDCAPPED 4.6 × 150 MM 3 MM, 30 °C, 0.1 % TFA IN WATER AND ACETONITRILE, 0 TO 20 % B IN 20 MIN, RETENTION FACTOR 2.3; FULL TRACE,

**What this does not establish.** Chromatographic purity is the share of detected peak area at one wavelength. It cannot see what does not absorb there, so counter-ion, water and inorganic residue are invisible to it. It is not a statement of how much peptide is in the container.

## Counter-ion content

### PRINCIPLE

The sample is dissolved and its anions are separated on a hydroxide-selective column with suppressed conductivity detection, which removes the eluent contribution and leaves the trifluoroacetate peak quantifiable against calibrated standards. Where the matrix interferes, the determination is run by LC-MS in negative ionisation, monitoring the trifluoroacetate ion at mass 113.

### WHAT THE NUMBER MEANS

How much of the delivered mass is counter-ion rather than peptide. Trifluoroacetate binds to every protonated basic site during reversed-phase purification and survives lyophilisation, typically accounting for 10 to 25 per cent of the mass in the vial at 114 daltons per counter-ion. It does not absorb at 214 nm and is not retained on a C18 column, so a purity chromatogram never sees it.

### SYSTEM SUITABILITY APPLIED

| CRITERION | REQUIREMENT | ACHIEVED |
|---|---|---|
| Calibration linearity across the working range | coefficient of determination at least 0.999 | 0.9998 |
| Resolution from the nearest eluting anion | not less than 1.5 | 3.4, acetate from formate |
| Recovery of a spiked trifluoroacetate standard | 95 to 105 per cent | 99.3 per cent |
| Replicate agreement | within 2 per cent relative | 0.6 per cent relative |

### HOW IT IS REPORTED

Reported as per cent weight for weight and as milligrams per labelled unit, with the counter-ion named. It is one of the two contributions, with water, that separate a purity percentage from a mass of peptide, and it is read together with net peptide content rather than on its own.

COUNTER-ION CONTENT · PASS

**Acetate 12.30 % w/w (± 0.6 %), i.e. 3.0 mg per vial, 1.05 mol per mol at two basic sites (Glu1 N-terminus and Arg3 guanidine); trifluoroacetate < 20 ppm (LOQ 20 ppm); chloride and phosphate < 20 ppm**

Against Acetate <= 15 %; trifluoroacetate <= 1000 ppm

**What this does not establish.** Counter-ion content states how much of the vial mass is salt rather than peptide. It does not establish that the remaining mass is the named peptide, and it does not say whether the counter-ion has affected the stability of the material. Free trifluoroacetic acid present as a volatile residue is a residual solvents question and is not covered here.

## Water content

### PRINCIPLE

Water in the sample reacts stoichiometrically with iodine generated coulometrically in the titration cell, and the charge passed gives the mass of water directly. The coulometric form is used rather than the volumetric because the quantities here are small.

### WHAT THE NUMBER MEANS

The mass of water in the powder as received, as a percentage. Lyophilised peptides are hygroscopic and take up water from the air within seconds of a vial being opened, so this figure describes the container at receipt and not after it has been handled.

### SYSTEM SUITABILITY APPLIED

| CRITERION | REQUIREMENT | ACHIEVED |
|---|---|---|
| Cell blank drift | stable before the determination begins | stable at 0.8 micrograms per minute |
| Recovery of a water standard | 97.5 to 102.5 per cent | 99.6 per cent |
| Replicate agreement | within 0.2 per cent absolute | 0.05 per cent absolute |

### HOW IT IS REPORTED

Reported as per cent weight for weight, with the number of replicate determinations. Water content is one of the two contributions, with counter-ion, that separate a purity percentage from a mass of peptide.

WATER CONTENT · PASS

**5.60 ± 0.28 % w/w (k = 2), i.e. 1.4 mg per vial**

Against <= 8.0 %

**What this does not establish.** Water content describes the powder as received. It moves with handling and storage, and a figure taken on the day of receipt does not describe the container after it has been opened.

## Bacterial endotoxins

### PRINCIPLE

Lysate from the amoebocytes of the horseshoe crab is activated by bacterial endotoxin through a protease cascade, which cleaves a chromogenic substrate. The rate at which colour develops is proportional to endotoxin concentration, and the onset time is read against a standard curve prepared from control standard endotoxin.

### WHAT THE NUMBER MEANS

Endotoxin concentration in endotoxin units per milligram. Endotoxin is a fragment of the outer membrane of gram-negative bacteria. It survives autoclaving, it is not removed by sterile filtration, and it is pyrogenic in the absence of any living organism.

### SYSTEM SUITABILITY APPLIED

| CRITERION | REQUIREMENT | ACHIEVED |
|---|---|---|
| Standard curve correlation coefficient | not less than 0.980 in absolute value | 0.9992 |
| Positive product control recovery | 50 to 200 per cent | 98 % |
| Negative control | below the lowest standard | no onset |
| Dilution used | at or below the maximum valid dilution | 1 in 20, below MVD |

### HOW IT IS REPORTED

Reported in endotoxin units per milligram at the dilution used, with the maximum valid dilution stated. A result obtained beyond the maximum valid dilution is not reportable, because the dilution itself would have carried the endotoxin below the sensitivity of the assay.

BACTERIAL ENDOTOXINS · PASS

**< 0.05 EU/mg (< 1.0 EU per vial; LOQ 0.005 EU/mg)**

Against <= 0.5 EU/mg

**What this does not establish.** Bacterial endotoxin is not sterility. A sample can be free of endotoxin and carry viable organisms, and it can be sterile and still pyrogenic. The two are separate determinations because they are separate properties.

## Sterility

PRINCIPLE

The contents are transferred under aseptic conditions to fluid thioglycollate medium and to soya bean casein digest medium, and incubated for fourteen days at the temperatures each medium requires. Growth in either medium is a failure.

WHAT THE NUMBER MEANS

Whether the units tested were free of viable organisms recoverable under those conditions. The determination applies to the units opened and to nothing else. A batch is not made sterile by a sterility test, and the test cannot be extrapolated to a container that was not sampled.

SYSTEM SUITABILITY APPLIED

| CRITERION | REQUIREMENT | ACHIEVED |
|---|---|---|
| Growth promotion of each medium | confirmed with the compendial challenge organisms | all media passed |
| Method suitability against the product | confirmed, no inhibition | growth within 3 days with product present |
| Negative control | no growth for the full incubation | no growth |
| Incubation | not fewer than 14 days | 14 days |

HOW IT IS REPORTED

Reported as no growth or growth observed, with the incubation period completed. Sterility is not pyrogenicity: a preparation can be sterile and still cause fever, which is what the endotoxin determination is for.

STERILITY · PASS

**No growth after 14 days, 2 vials**

Against No growth

**What this does not establish.** Sterility applies to the units tested, not to the batch they came from. It cannot be extrapolated to a container that was not sampled, and it is not a statement about pyrogens.

## Microbial enumeration

### PRINCIPLE

A prepared portion is plated onto soya bean casein digest agar for total aerobic microbial count and onto Sabouraud dextrose agar for total combined yeasts and moulds, and colonies are counted after incubation.

### WHAT THE NUMBER MEANS

How many organisms grow under the stated conditions on the stated media, as colony forming units per gram. Organisms that will not grow on those media at those temperatures are not counted, and are not reported as absent.

### SYSTEM SUITABILITY APPLIED

| CRITERION | REQUIREMENT | ACHIEVED |
|---|---|---|
| Growth promotion of each medium | confirmed | all media passed |
| Method suitability against the product | recovery within a factor of two | recovery 78 to 112 % of the inoculum |
| Negative control plates | no growth | no growth |

### HOW IT IS REPORTED

Reported as colony forming units per gram for each count, with the specified organisms tested for separately where those were ordered. Enumeration is not sterility and does not substitute for it.

MICROBIAL ENUMERATION · PASS

**TAMC < 10 CFU/g, TYMC < 10 CFU/g; Escherichia coli, Salmonella, Staphylococcus aureus and Pseudomonas aeruginosa absent in 1 g**

Against TAMC <= 1000 CFU/g, TYMC <= 100 CFU/g; specified organisms absent

**What this does not establish.** Enumeration counts what grows under the stated conditions on the stated media. It is not sterility, and an organism that does not grow under those conditions is not counted and is not reported as absent.

## Residual solvents

PRINCIPLE

A weighed portion is equilibrated in a sealed vial and the vapour above the sample is sampled and separated by gas chromatography, with detection by mass spectrometry or flame ionisation. Sampling the headspace rather than the solution keeps involatile matrix out of the instrument.

WHAT THE NUMBER MEANS

The concentration of each solvent in the panel applied. ICH Q3C sorts solvents into three classes. Class 1 solvents such as benzene are to be avoided and are limited at parts per million. Class 2 are restricted and include acetonitrile, dichloromethane and dimethylformamide, all of which are routine in peptide synthesis. Class 3 carry a default limit of 5000 parts per million.

SYSTEM SUITABILITY APPLIED

| CRITERION | REQUIREMENT | ACHIEVED |
|---|---|---|
| Resolution between the two closest eluting solvents | not less than 1.0 | 3.6, acetonitrile from dichloromethane |
| Signal to noise at the limit of quantitation | not less than 10 to 1 | 48 to 1 at the LOQ |
| Repeatability of the standard | not more than 15 per cent relative standard deviation | 4.2 % |
| System blank | no interfering peak at any target retention time | no interfering peak |

HOW IT IS REPORTED

Reported per solvent against its ICH Q3C limit. A solvent not in the panel was not looked for and its absence from this report is not evidence of its absence from the sample.

RESIDUAL SOLVENTS · PASS

**Acetonitrile 22 ppm; N,N-dimethylformamide, methanol, dichloromethane, diethyl ether, diisopropyl ether and piperidine each < 10 ppm (LOQ 10 ppm)**

Against ICH Q3C: acetonitrile <= 410, DMF <= 880, methanol <= 3000, dichloromethane <= 600, ethers <= 5000 ppm

**What this does not establish.** Residual solvents are reported for the solvents in the panel, at the limits stated. A solvent not in the panel was not looked for, and its absence from this report is not evidence of its absence from the sample.

## Elemental impurities by ICP-MS

### PRINCIPLE

The sample is digested in acid under microwave pressure and introduced into an argon plasma at approximately 7000 kelvin, which atomises and ionises the elements present. Ions are separated by mass to charge in a quadrupole and counted individually, which is what puts the technique at parts per billion.

### WHAT THE NUMBER MEANS

The concentration of each element in the panel applied. An element outside the panel is not reported as absent, because it was not sought. Class 1 elements are cadmium, lead, arsenic and mercury, which have no acceptable role in a preparation and are limited on toxicity alone.

### SYSTEM SUITABILITY APPLIED

| CRITERION | REQUIREMENT | ACHIEVED |
|---|---|---|
| Internal standard recovery | 80 to 120 per cent | 97 % |
| Spike recovery in matrix | 70 to 150 per cent | 92 to 106 % |
| Calibration correlation coefficient | not less than 0.995 | 0.9996 |
| Digestion blank | below the reporting limit for every element | below LOQ |
| Drift check across the sequence | within 20 per cent | 3 % |

### HOW IT IS REPORTED

Reported per element against the permitted daily exposure of ICH Q3D for the intended route, with the limit of quantitation stated for each. A result below the limit of quantitation is reported as such and is not reported as zero.

ELEMENTAL IMPURITIES · PASS

**Cd, Pb, As, Hg < 0.05 µg/g; Co, V, Ni < 0.10 µg/g, all below LOQ**

Against ICH Q3D(R2) Class 1 and 2A, parenteral PDE per 20 mg daily: Cd 100, Pb 250, As 750, Hg 150, Co 250, V 500, Ni 1000 µg/g

**What this does not establish.** Elemental impurities are reported for the elements in the panel applied. An element outside that panel is not reported as absent, because it was not sought.

## Compound screening

PRINCIPLE

The sample is acquired in both positive and negative ionisation and the detected features are compared against reference standards held by the laboratory and against a spectral library, with confirmation by retention time and fragmentation where a standard is available.

WHAT THE NUMBER MEANS

Which compounds from the reference set are present. The result is bounded by the standards held on the day the screen was run, which is a real and stated limit rather than a general statement about what the sample contains.

SYSTEM SUITABILITY APPLIED

| CRITERION | REQUIREMENT | ACHIEVED |
|---|---|---|
| Reference standards injected in the same sequence | confirmed for every reported identification | 42 injected in the same sequence |
| Mass accuracy | within 5 ppm | within 3 ppm |
| Both polarities acquired | confirmed | acquired |
| Solvent blank between injections | no carryover above the reporting threshold | no carry-over above 0.01 % |

HOW IT IS REPORTED

Reported as identified, tentatively identified, or not detected, per compound. A tentative identification is one made on accurate mass and fragmentation without a reference standard in the same sequence, and it is labelled as tentative for exactly that reason.

COMPOUND SCREENING · PASS

**Fentanyl and analogues, Epithalon (AEDG), Vilon (KE), Thymogen (EW), Semax, Selank, protected intermediates (tBu on Glu/Asp, Pbf on Arg, Fmoc, Boc) and free amino acids (Glu, Asp, Arg): none above 0.05 % of area**

Against Nothing above 0.05 %

**What this does not establish.** A screen is bounded by the reference standards held on the day it was run. A compound for which no standard was available cannot be identified by it, and its absence from the result is not evidence of its absence from the sample.

## Controls carried in the same sequence

| | |
|---|---|
| Blank | Solvent blank (mobile phase A) injected before the sequence; no peak above 0.02 % of the main peak within RRT 0.80 to 1.30 (maximum 0.003 %) |
| Reference standard | In-house reference standard RS-EDR-01 (purity assigned against a primary standard, stored at -20 °C) injected at the start and end of the sequence; area difference 0.4 %, retention time within 0.1 min; control sample from the previous batch within 0.2 % of its value |

A result acquired without a blank cannot separate a peak that came from the sample from a peak that came from the system: solvent, column bleed, a carryover from the previous injection and a contaminated vial all produce peaks, and all of them are invisible until something is injected that contains nothing.

A result acquired without a reference standard in the same sequence is a retention time rather than an identification. Retention is a property of a method on a day, and it moves with column age, mobile phase batch and temperature. A standard run alongside the sample is what turns a number on an axis into a name.

### WHY THIS IS ON THE REPORT AT ALL

It is the part of an analysis that certificates normally omit, and the part an analyst asks about first. A reader who knows to ask for it should not have to, and a reader who does not know to ask is better served by seeing it than by not knowing it was missing.

## What these results do not establish

Each determination on this report answers one question. The limits below are the questions it does not answer, and every one of them is a mistake made routinely and in good faith by someone reading a certificate.

**Identity**
Identity establishes that the compound present is the one named. It does not establish how much of it is there. A sample can be correctly identified and still be mostly something else by mass.

**Purity**
Chromatographic purity is the share of detected peak area at one wavelength. It cannot see what does not absorb there, so counter-ion, water and inorganic residue are invisible to it. It is not a statement of how much peptide is in the container.

**Counter-ion content**
Counter-ion content states how much of the vial mass is salt rather than peptide. It does not establish that the remaining mass is the named peptide, and it does not say whether the counter-ion has affected the stability of the material. Free trifluoroacetic acid present as a volatile residue is a residual solvents question and is not covered here.

**Water content**
Water content describes the powder as received. It moves with handling and storage, and a figure taken on the day of receipt does not describe the container after it has been opened.

**Bacterial endotoxins**
Bacterial endotoxin is not sterility. A sample can be free of endotoxin and carry viable organisms, and it can be sterile and still pyrogenic. The two are separate determinations because they are separate properties.

**Sterility**
Sterility applies to the units tested, not to the batch they came from. It cannot be extrapolated to a container that was not sampled, and it is not a statement about pyrogens.

**Microbial enumeration**
Enumeration counts what grows under the stated conditions on the stated media. It is not sterility, and an organism that does not grow under those conditions is not counted and is not reported as absent.

**Residual solvents**
Residual solvents are reported for the solvents in the panel, at the limits stated. A solvent not in the panel was not looked for, and its absence from this report is not evidence of its absence from the sample.

**Elemental impurities**
Elemental impurities are reported for the elements in the panel applied. An element outside that panel is not reported as absent, because it was not sought.

**Compound screening**
A screen is bounded by the reference standards held on the day it was run. A compound for which no standard was available cannot be identified by it, and its absence from the result is not evidence of its absence from the sample.

NOT PERFORMED

| | |
|---|---|
| **Biological activity** | not requested |
| **Aggregates by SEC-HPLC** | not applicable to a 418 Da tripeptide |
| **Stability after reconstitution, osmolality after reconstitution and sub-visible particles** | the container was not presented for reconstitution studies |
| **Microbiological quality after opening** | outside the scope of a certificate on a sealed container |

## Verify this certificate against the register

SCAN TO VERIFY

Scan the code, or open `https://analyton.com/verify/` and enter the report number with this key:

**6QKAF6P4D8**

The register returns every result on this report, the date of issue and the current status. It never discloses the client, so a buyer can check a certificate without needing anything from the seller and without the seller learning who checked.

**Where a copy in circulation differs from the register, the register governs.** It is the issuing laboratory's own copy, and a file can be edited by anyone holding a reader. The register also carries the SHA-256 of this file exactly as it was issued, so a copy can be checked byte for byte rather than trusted. A document cannot carry its own fingerprint, which is why that lives in the register and not on this page.

## Scope, reproduction and retention

### SCOPE

This certificate is issued under ANALYTON GC 1.1 and relates only to the sample as received and described on this report. Determinations were performed by ANALYTON or placed with a qualified laboratory under Article 5 of those conditions. Subcontracting does not move any obligation off ANALYTON, which remains the client's only contractual counterparty and is answerable for every figure on this report.

### REPRODUCTION

This report is not to be reproduced except in full. A reproduction that omits the scope, the determinations not performed, the methods used or the stated limits of those methods misrepresents the result, and it is not authorised. An extract consisting of a single favourable number is the specific case this clause exists to prevent.

### RETENTION

Raw data underlying this report, including instrument records, integration parameters and the calibration in force on the day, is retained for five years and is reissued on request to the client. The register entry for this report number is retained for ten years.

### MEASUREMENT UNCERTAINTY

Every figure on this report carries uncertainty from sampling, preparation, calibration and the instrument itself. A result reported at a limit is not evidence that the material sits safely inside it, and a result reported to three figures does not claim three figures of accuracy. Expanded uncertainty for a determination is available on request.

### WITHDRAWAL

A certificate found to contain an error is withdrawn and replaced by a certificate bearing a new report number. It is never amended in place. The withdrawn number keeps resolving in the register, marked withdrawn, so that anyone holding the earlier paper learns that it was replaced rather than finding nothing.

### NOT A COMPLIANCE STATEMENT

ANALYTON LABS is an analytical testing laboratory and a trading name of MAYDAY BRATISLAVA s. r. o. This report states what was measured and how. It does not certify that the material is fit for any purpose, does not authorise its sale or use, and is not a statement of compliance with any regulatory regime.

END OF REPORT