

Certificate of Analysis



Grail Formula B.V.

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Sample Identification

Sample Name	DSIP 10 mg
Batch Number	GF-DSIP10-B243
Date Published	2026-09-10 08:22

Results for LYO-0747

Peptides	Result	Unit	Uncertainty	Acceptable Range
DSIP Assay Peptide Screening 0.1% TFA	13.23	mg	[± 0.07]	
DSIP Purity Peptide Screening 0.1% TFA	99.3	%	[± 0.5]	
DSIP Identification by Spectrum (FTIR) Peptide Screening 0.1% TFA	985		[± 5]	
DSIP Identification by RT Peptide Screening 0.1% TFA	0.983		[± 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	0.225	EU/mg	[± 0.004]	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	848	Da	[± 1]	

	Method Specification	
Determination of identity, content and purity of DSIP		
Document number DSIP_008_2026	Superseded document -	Number of pages 4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	0.1% DFA in Water (HPLC, Gradient Grade)
Eluent B	0.1% DFA in Acetonitrile (HPLC, Gradient Grade)
Flow rate	0.8 mL/min
Program	Gradient elution
Injection volume	2 µL
Colum Temperature	60°C
Column	Waters XSelect CSH C18, 100x2.1mm 2.5µm
Detection wavelength	280nm

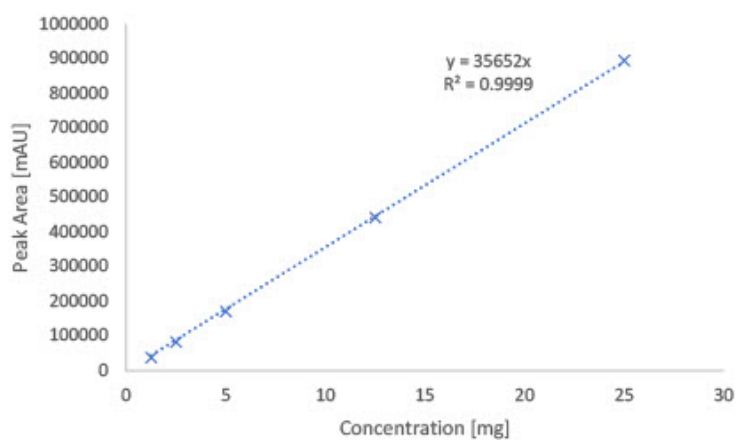
Gradient Program		
Time [min]	A [%]	B [%]
1	98	2
13.99	35	65
14	5	95
15	5	95
15.01	98	2
19	end	

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	0.1% DFA in Water (HPLC, Gradient Grade)
Eluent B	0.1% DFA in Acetonitrile (HPLC, Gradient Grade)
Flow rate	0.8 mL/min
Program	Gradient elution
Injection volume	2 µL
Colum Temperature	60°C
Column	Waters XSelect CSH C18, 100x2.1mm 2.5µm
Detection wavelength	225nm

Gradient Program		
Time [min]	A [%]	B [%]
1	98	2
13.99	35	65
14	5	95
15	5	95
15.01	98	2
19	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 225 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
Column 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% DFA in Water (HPLC, Gradient Grade)
Eluent B	0.1% DFA in Acetonitrile (HPLC, Gradient Grade)
Flow rate	0.8 mL/min
Program	Gradient elution
Injection volume	2 µL
Column Temperature	60°C
Column	Waters XSelect CSH C18, 100x2.1mm 2.5µm
Detection wavelength	280nm

Gradient Program		
Time [min]	A [%]	B [%]
1	98	2
13.99	35	65
14	5	95
15	5	95
15.01	98	2
19	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

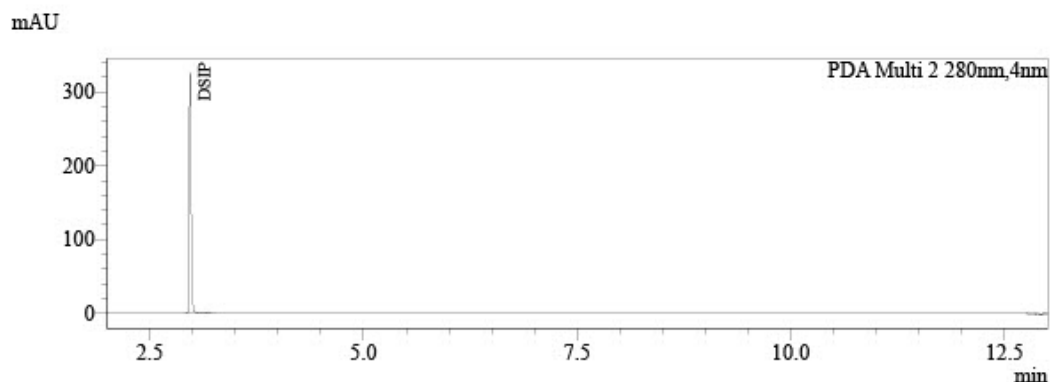
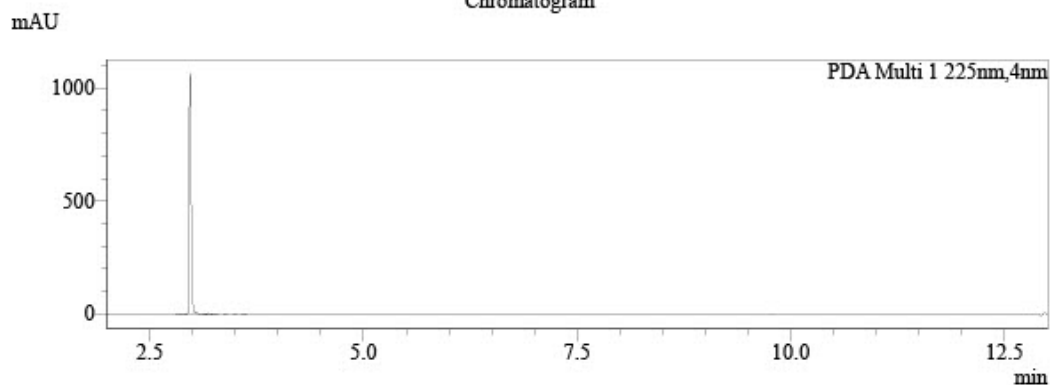


Analysis of quantity of active ingredient by UHPLC with MS detection

Sample Information

Injection Volume : 2
Data File : LYO-0747_015.lcd
Method File : Peptide Screening_DFA_Group D.lcm
Date Acquired : 9/2/2026 2:37:01 PM

Chromatogram



Peak Table

PDA Ch1 225nm

Peak#	Name	Ret. Time	Area	Area%	Conc.	Unit
1		2.854	1711	0.096	0.000	
2		2.968	1762138	99.295	0.000	
3		3.141	43	0.002	0.000	
4		3.192	5992	0.338	0.000	
5		3.240	4231	0.238	0.000	
6		3.385	146	0.008	0.000	
7		3.494	158	0.009	0.000	
8		3.584	224	0.013	0.000	
Total			1774643	100.000		

Peak Table

PDA Ch2 280nm

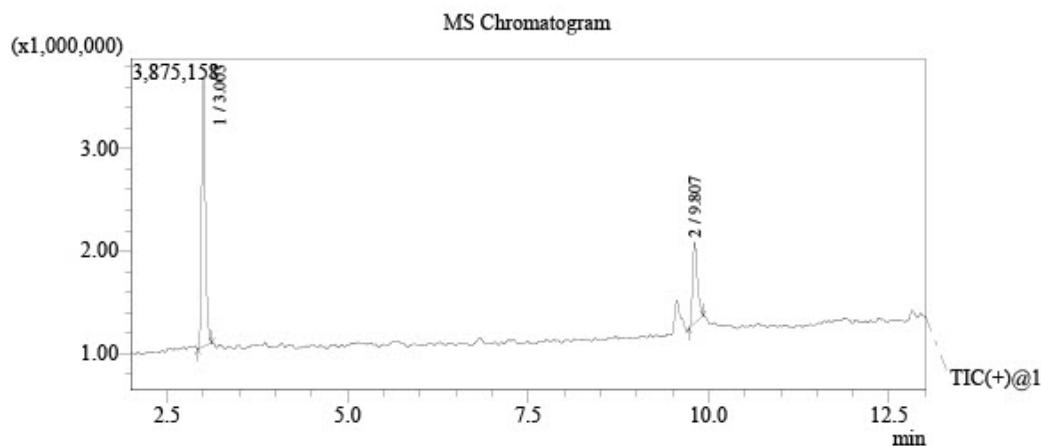
Peak#	Name	Ret. Time	Area	Area%	Conc.	Unit
1	DSIP	2.968	514897	95.666	13.231	mg
2		3.187	1358	0.252	0.000	

Peak#	Name	Ret. Time	Area	Area%	Conc.	Unit
3		12.790	4454	0.827	0.000	
4		12.888	3557	0.661	0.000	
5		12.968	10862	2.018	0.000	
6		14.245	3099	0.576	0.000	
Total			538226	100.000		

Analysis Report



Identification of active ingredient by UHPLC Mass Spectrometry

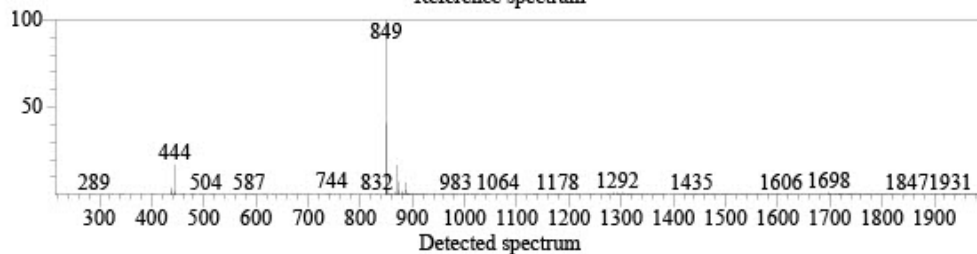


Library Search

Base Peak: 849(1115299)

Scan Range: 220.00 - 2000.00 Polarity: Positive

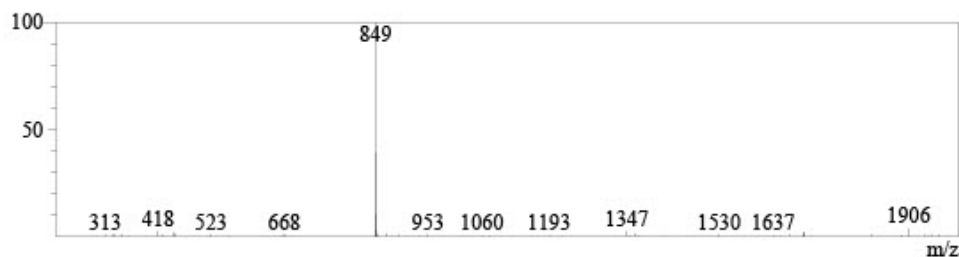
Reference spectrum



Library: Peptide screening.lib

Formula: C₃₅H₄₈N₁₀O₁₅ CAS: 62568-57-4 Mol.Weight: 848(0!=)

Compound Name: DSIP



Endotoxin Determination Report

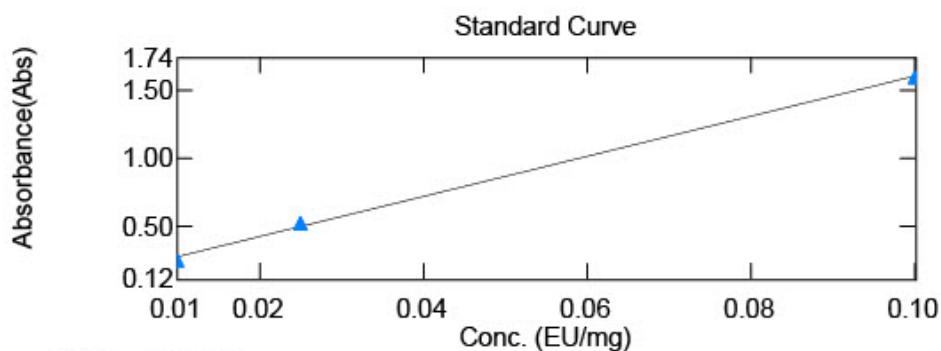


File Information

Filename: C:\UVVis-Data\Data\File_260903_204104.vqud
Date/Time: 09/03/2026 09:40:26 PM

Instrument Information

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



$$y = 14.7148x + 0.132903$$
$$r^2 = 0.99870$$

	Sample Name	Conc	Raw_WL545.0	Dilution Rate
1	LYO-0745	0.055	0.1732	20.00
2	LYO-0746	-0.026	0.1141	20.00
3	LYO-0747	2.977	1.2279	40.00
4	LYO-0748	-0.034	0.1076	20.00
5	LYO-0749	-0.042	0.1268	100.00
6	LYO-0750	-0.083	0.0716	20.00
7	LYO-0752	1.909	0.8353	40.00
8	LYO-0753	0.931	0.8176	20.00
9	LYO-0754	2.152	0.9247	40.00
10	LYO-0755	2.610	1.0929	40.00
11	LYO-0756	-0.025	0.1143	20.00
12	LYO-0757	-0.317	0.0862	100.00
13	LYO-0767	0.152	0.2445	20.00
14	LYO-0768	0.589	0.5665	20.00
15	LYO-0769	3.621	1.4649	40.00
16	LYO-0770	1.007	0.8736	20.00
17	LYO-0771	0.148	0.2419	20.00
18	LYO-0772	3.598	1.4565	40.00
19	LYO-0773	-0.045	0.0999	20.00
20	LYO-0774	3.668	1.4823	40.00

	Sample Name	Conc	Raw_WL545.0	Dilution Rate
21	LYO-0775	3.612	1.4616	40.00
22	LYO-0776	4.197	1.6769	40.00
23	LYO-0777	3.621	1.4648	40.00
24	LYO-0780	0.768	0.6977	20.00
25	LYO-0781	-0.021	0.1171	20.00
26	LYO-0782	-0.025	0.1148	20.00
27	LYO-0783	0.244	0.3121	20.00
28	LYO-0784	0.031	0.1557	20.00
29	LYO-0785	0.000	0.1329	20.00
30	LYO-086	4.729	1.0027	80.00
31	LYO-0787	3.923	1.5759	40.00
32	LYO-0788	0.099	0.2057	20.00
33	LYO-0789	1.454	1.2027	20.00
34	LYO-0790	0.264	0.3270	20.00
35	LYO-0791	1.650	0.7397	40.00
36	LYO-0792	14.164	1.4355	160.00
37	LYO-0793	-0.021	0.1176	20.00
38	LYO-0794	-0.164	0.1088	100.00

 LIQUILABS Analytical services	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 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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