

Certificate of Analysis



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Sample Identification

Sample Name	MOD GRF (1-29) (CJC 1295) 5 mg + Ipamorelin 5 mg
Batch Number	NCI-015
Date Published	2026-08-25 16:01

Results for LYO-0628

Peptides	Result	Unit	Uncertainty	Acceptable Range
Ipamorelin Assay Peptide Screening 0.1% TFA	5.90	mg	[± 0.03]	
MOD GRF (1-29) Assay Peptide Screening 0.1% TFA	5.55	mg	[± 0.03]	
Ipamorelin Purity Peptide Screening 0.1% TFA	99.5	%	[± 0.5]	
MOD GRF (1-29) Purity Peptide Screening 0.1% TFA	98.9	%	[± 0.5]	
Ipamorelin Identification by Spectrum (FTIR) Peptide Screening 0.1% TFA	987		[± 5]	
MOD GRF (1-29) Identification by Spectrum (FTIR) Peptide Screening 0.1% TFA	955		[± 5]	
Ipamorelin Identification by RT Peptide Screening 0.1% TFA	0.999		[± 0.005]	
MOD GRF (1-29) Identification by RT Peptide Screening 0.1% TFA	0.999		[± 0.005]	
Microbiology	Result	Unit	Uncertainty	Acceptable Range
Bacterial Endotoxin Chromgenic USP<85>/ Eur. Ph. 2.6.14. Bacterial Endotoxin Chromgenic Test	0.004	EU/mg	[± 0]	
Elemental Impurities	Result	Unit	Uncertainty	Acceptable Range
Arsenic Elemental Impurities screening USP (232) / Ph. Eur. 5.20 / 2.4.20	< 0.001	ppm		
Cadmium Elemental Impurities screening USP (232) / Ph. Eur. 5.20 / 2.4.20	< 0.001	ppm		
Quicksilver Elemental Impurities screening USP (232) / Ph. Eur. 5.20 / 2.4.20	< 0.001	ppm		
Lead Elemental Impurities screening USP (232) / Ph. Eur. 5.20 / 2.4.20	< 0.001	ppm		
Mass Spectrometry	Result	Unit	Uncertainty	Acceptable Range
Molecular Ion Mass Identification (Ipamorelin) Mass Spectrometry Identity	711	Da	[± 1]	
Molecular Ion Mass Identification (MOD GRF 1-29) Mass Spectrometry Identity	3367	Da	[± 1]	





	Method Specification		
Determination of identity, content and purity of Ipamorelin			
<i>Document number</i> IPA_008_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Superseded document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	0.1% 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

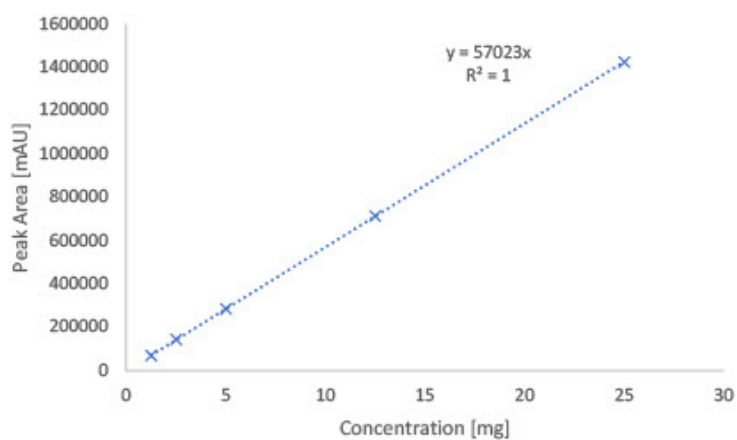
Gradient Program		
Time [min]	A [%]	B [%]
1	98	2
13.99	35	65
14	5	95
15	5	95
15.01	98	2
19	end	

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
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Column	Waters XSelect CSH C18, 100x2.1mm 2.5µm
Detection	MS 220-2000 Da

Gradient Program		
Time [min]	A [%]	B [%]
1	98	2
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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

	Method Specification	
Determination of identity, content and purity of MOD GRF 1-29		
Document number MOD_008_2026	Superseded document -	Number of pages 4

1. Content Assessment

1.1. Instrumentation

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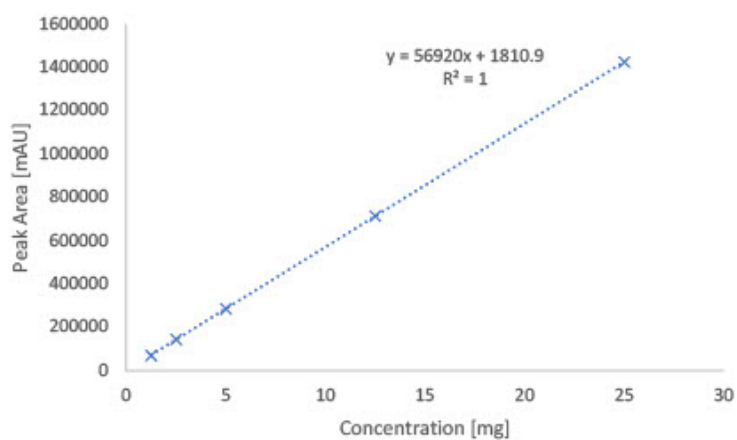
Gradient Program		
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Where:

mz_i - Measured mass of charged particle

z_i - charge

H - proton mass (1.0076 Da)

ME - mass error

Analysis Report

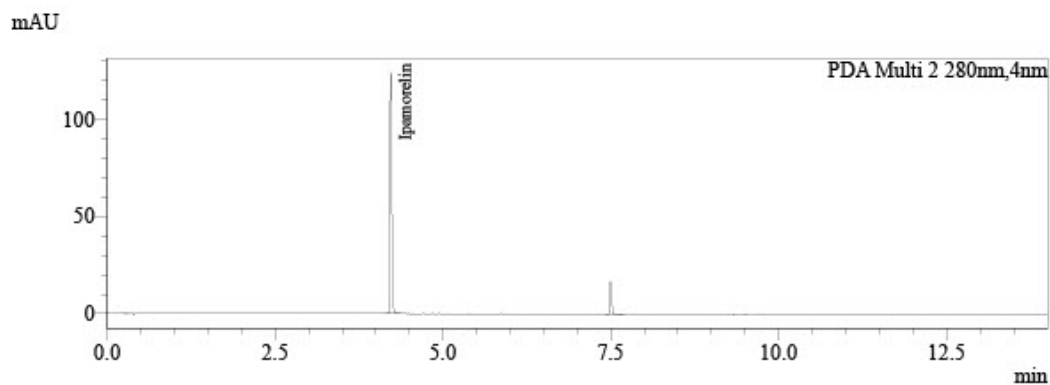
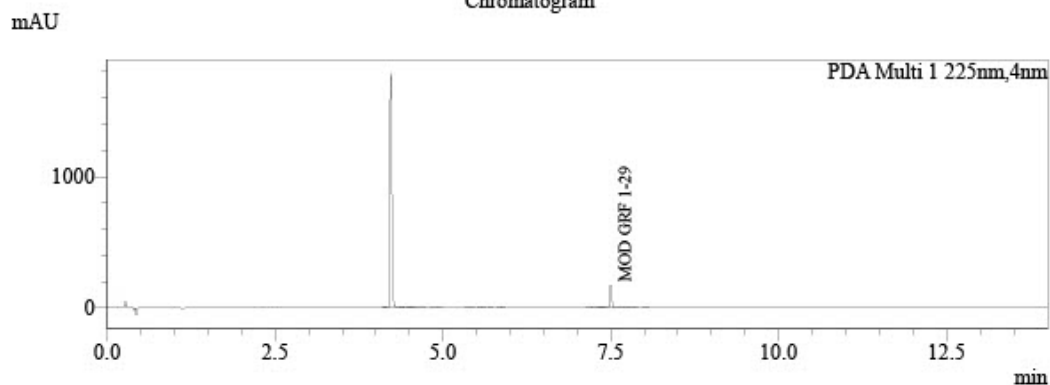


Analysis of quantity of active ingredient by UHPLC with MS detection

Sample Information

Injection Volume : 2
Data File : LYO-0628__012.lcd
Method File : Peptide Screening_DFA_Group B.lcm
Date Acquired : 8/20/2026 8:06:49 PM

Chromatogram



Peak Table

Peak#	Name	Ret. Time	Area	Area%	Conc.	Unit
1		4.135	1279	0.032	0.000	
2		4.223	3649955	91.488	0.000	
3		4.381	1021	0.026	0.000	
4		4.491	549	0.014	0.000	
5		4.547	424	0.011	0.000	
6		4.705	2151	0.054	0.000	
7		4.845	2423	0.061	0.000	
8		4.941	1713	0.043	0.000	
9		5.376	2844	0.071	0.000	
10		5.543	604	0.015	0.000	
11		5.605	77	0.002	0.000	
12		5.705	120	0.003	0.000	
13		5.863	5027	0.126	0.000	
14		7.189	893	0.022	0.000	
15		7.231	827	0.021	0.000	
16		7.358	518	0.013	0.000	

Peak#	Name	Ret. Time	Area	Area%	Conc.	Unit
17		7.406	216	0.005	0.000	
18	MOD GRF 1-29	7.497	317755	7.965	5.551	mg
19		7.721	218	0.005	0.000	
20		7.790	195	0.005	0.000	
21		7.883	140	0.003	0.000	
22		8.003	609	0.015	0.000	
Total			3989557	100.000		

Peak Table

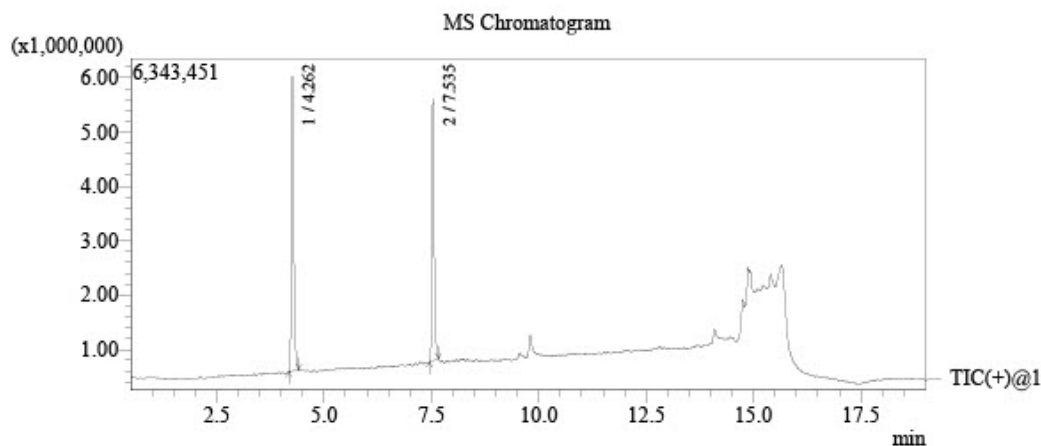
PDA Ch2 280nm

Peak#	Name	Ret. Time	Area	Area%	Conc.	Unit
1	Ipamorelin	4.222	235316	87.756	5.899	mg
2		7.497	30875	11.514	0.000	
3		14.239	1958	0.730	0.000	
Total			268150	100.000		

Analysis Report



Identification of active ingredient by UHPLC Mass Spectrometry

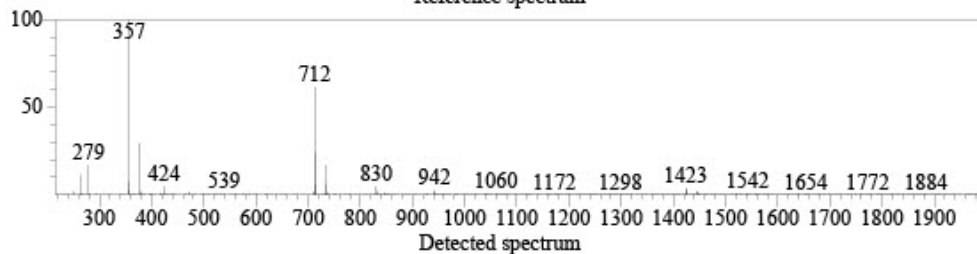


Library Search

Base Peak: 357(1609474)

Scan Range: 220.00 - 2000.00 Polarity: Positive

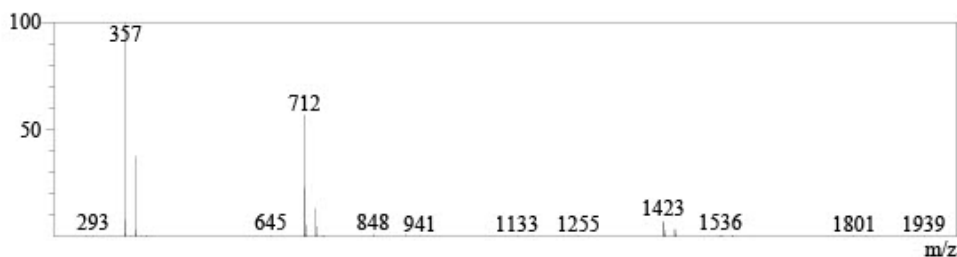
Reference spectrum



Library: Peptide screening.lib

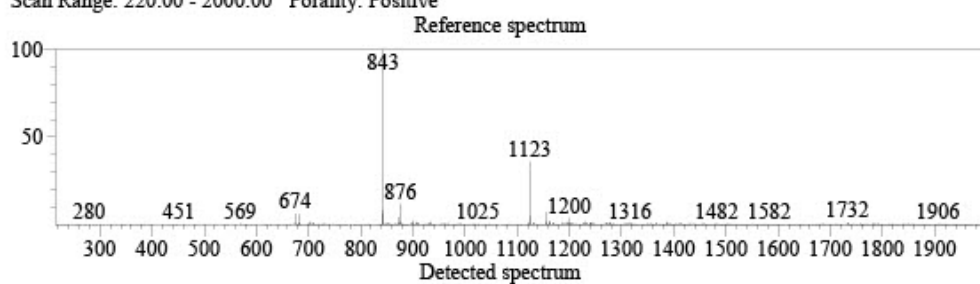
Formula: C₃₈H₄₉N₉O₅ CAS: 170851-70-4 Mol.Weight: 711(0!=)

Compound Name: Ipamorelin



Base Peak: 843(1800751)

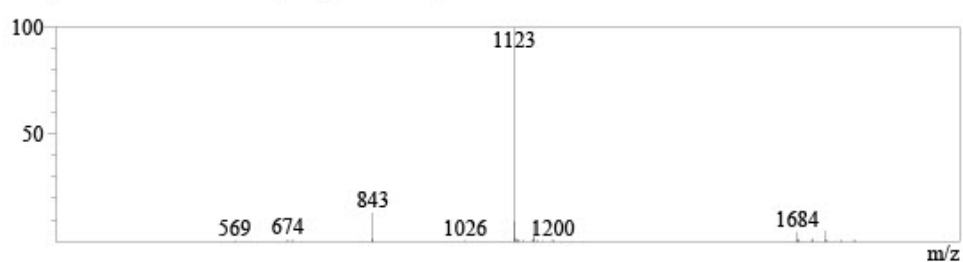
Scan Range: 220.00 - 2000.00 Polarity: Positive



Library: Peptide screening.lib

Formula: C₁₅₂H₂₅₂N₄₄O₄₂ CAS: 863288-34-0 Mol.Weight: 3367(0!=)

Compound Name: MOD GRF (1-29) (CJC-1295)



Responsibles



Mr. Ján Galbavý
CEO

Analysis results relate only to the samples tested.

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