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Certificate of Analysis

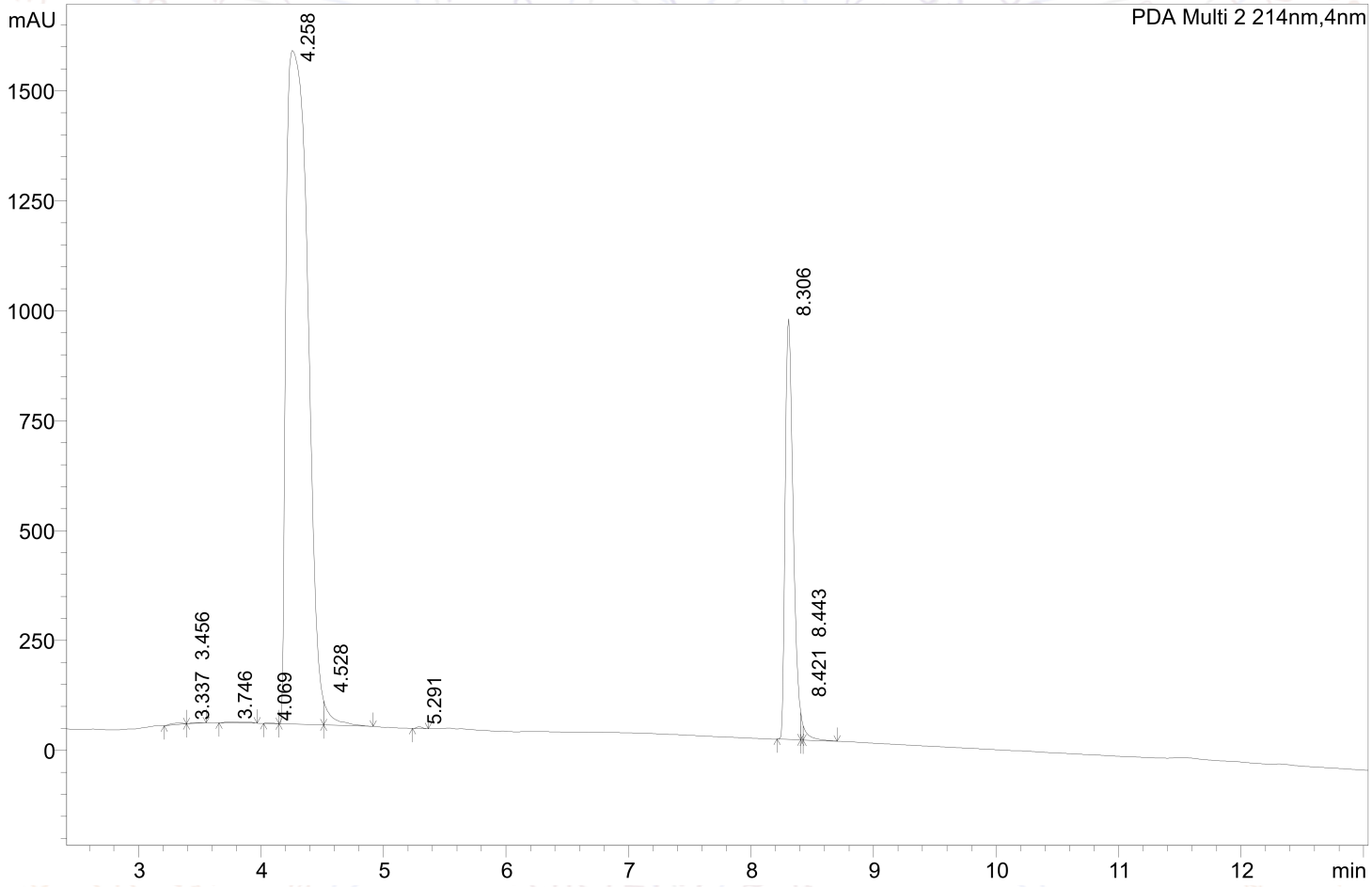
CJC-1295 + Ipamorelin 5mg / 5mg

Compound : CJC-1295 + Ipamorelin
Lot Number : 12/11/2026
Analysis date : 17/11/2026
Method : UPLC-MS/MS
Verification : OZ-HPLCMS-7Q6D
Purity : **98.17%**

Net Content : Ipamorelin: 4.22mg
CJC-1295 No DAC: 7.51mg
Client : PeptiGenix



Ultra Performance Liquid Chromatography (UPLC-UV) Chromatogram



PEAK LIST

Peaks Detected: 10

#	Time (min)	Area	%Area	Assignments
1	3.337	22999	0.098	
2	3.456	9060	0.039	
3	3.746	31896	0.136	
4	4.069	3667	0.016	
5	4.258	18709174	79.614	Ipamorelin
6	4.528	217419	0.925	
7	5.291	13497	0.057	
8	8.306	4360585	18.556	CJC-1295 No DAC
9	8.421	49110	0.209	
10	8.443	82509	0.351	

Analysis by Ibrahim A. Ozcan,
Lead Chemist Ozcanium Analytics
Signature

Report Compiled by Zein S. Sabini
18/11/2026

Note: Sample may contain salts and sugars, as standard additives. These are not considered impurities and are not included in the peak list

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Ipamorelin

CAS Number : 170851-70-4 PubChem CID : 9831659

Liquid Chromatography Mass Spectrometry (LC-MS) Identity Analysis

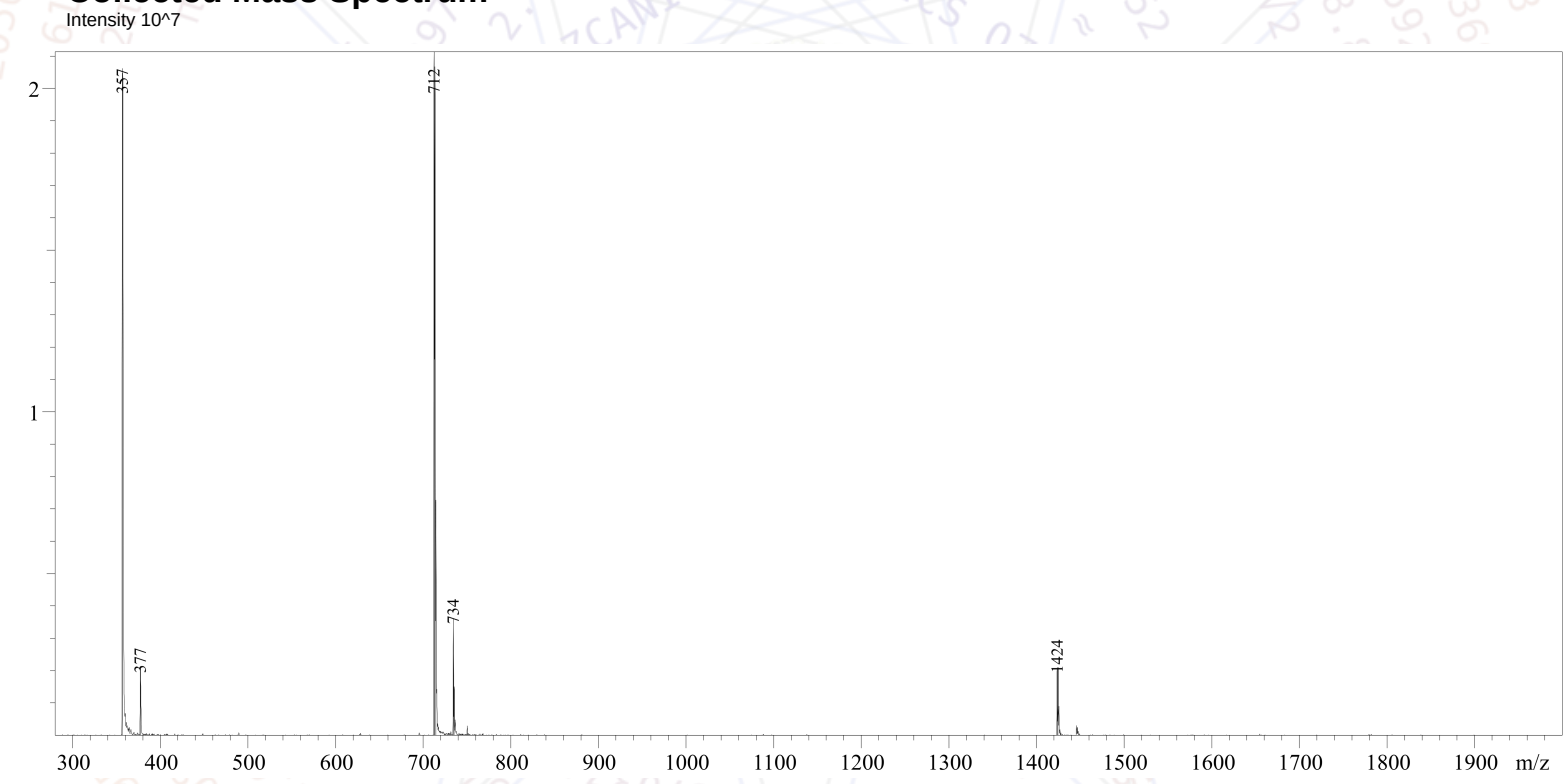
Identity confirmation with SIM **Analysis date** : 17/11/2026

Monitored Ion Channels (SIM):

Monitored (m/z):	Detected (m/z):
356.9	357.15
712.9	712.45
734.9	734.35

Detection Assignment: Ipamorelin

Collected Mass Spectrum



Note : Monoisotopic m/z values are not easily seen in full spectrum view for larger molecules and peptides.

The recorded fragmentation pattern may differ between systems, and vary based on method.

Analysis by Ibrahim A. Ozcan,
Lead Chemist Ozcanium Analytics
Signature

Report Compiled by Zein S. Sabini
18/11/2026

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CJC-1295 No DAC

CAS Number : 446036-97-1 PubChem CID : 91976842

Liquid Chromatography Mass Spectrometry (LC-MS) Identity Analysis

Identity confirmation with SIM **Analysis date** : 17/11/2026

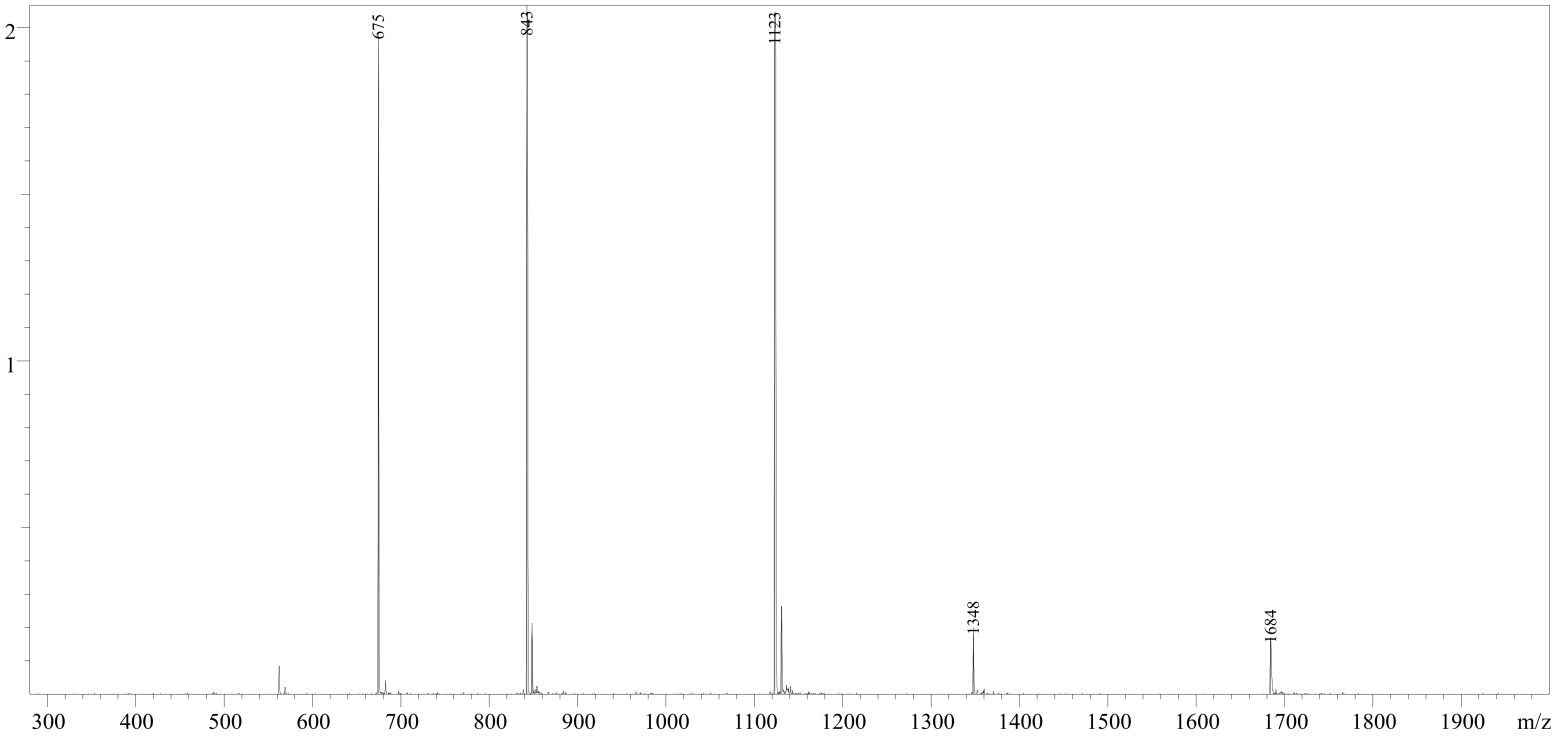
Monitored Ion Channels (SIM):

Monitored (m/z):	Detected (m/z):
842	842.75
854	854.25
1123	1123.10

Detection Assignment: **CJC-1295 No DAC**

Collected Mass Spectrum

Intensity 10^7



Note : Monoisotopic m/z values are not easily seen in full spectrum view for larger molecules and peptides.

The recorded fragmentation pattern may differ between systems, and vary based on method.

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