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CERTIFICATE OF ANALYSIS

Purity, Identity & NPC

COA ID: XESJVKC9

PRODUCT NAME	CLIENT	LOT ID
BPC-157 (Body Protection Compound-157)	Cosmic Peptides	26084

MOLECULAR FORMULA	MOLECULAR WEIGHT	DISSOLUTION
$C_{62}H_{98}N_{16}O_{22}$	1419.54 g/mol	3% HAc + 25% ACN + 72% H_2O

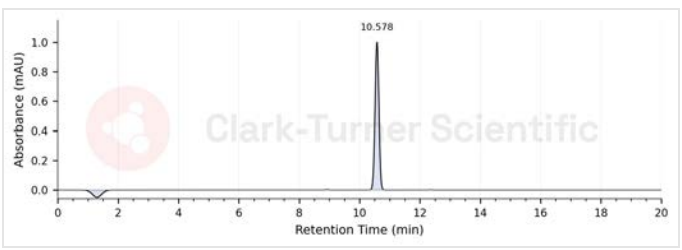
TEST RESULTS



02/07/2026 XESJVKC9

TEST	SPECIFICATION	RESULT	STATUS
Appearance	White to off-white powder	Lyophilized White Powder	✓ CONFORMS
Purity (HPLC)	≥ 98.0%	99.57%	✓ CONFORMS
Net Peptide Content	Report result	10.73 mg	✓ CONFORMS
Identity (MS)	710.78 ± 2.0 Da $[M+2H]^{2+}$	708.85 Da	✓ CONFORMS
Total Impurities	≤ 2.0%	0.43%	✓ CONFORMS

HPLC CHROMATOGRAM



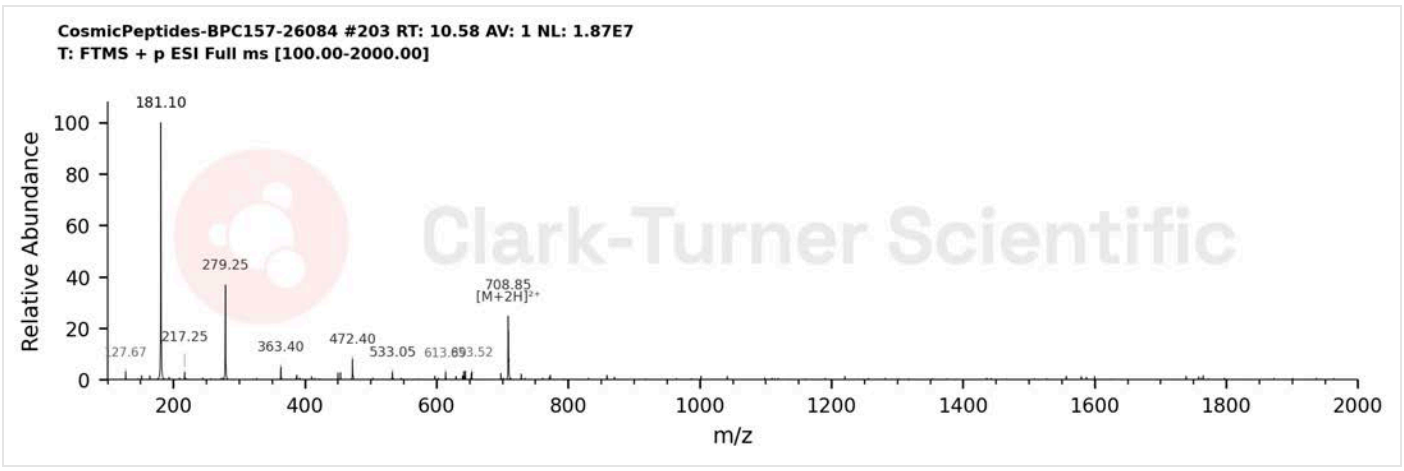
PEAK #	RT (MIN)	AREA %
1	10.578	99.57

TEST PARAMETERS

Pump A	0.1% TFA in 100% water
Pump B	0.1% TFA in 100% acetonitrile
Total Flow	1.0 mL/min
Wavelength	220 nm
Analytical Column	Agilent ZORBAX StableBond 5µm C18 (4.6 × 250 mm)
Dissolution Method	3% HAc + 25% ACN + 72% H_2O
Injection Volume	20 µL
Analysis Date	February 7, 2026

Reversed-phase HPLC analysis of BPC-157 was performed using a C18 stationary phase with a TFA-modified water/acetonitrile gradient and detection at 220 nm. The analyte eluted as a single well-resolved peak at 10.578 minutes, accounting for 99.57% of total integrated peak area. The moderate retention time is consistent with the amphiphilic character of this pentadecapeptide: the proline-rich N-terminal region (three consecutive Pro residues) and the C-terminal Leu-Val dipeptide provide substantial hydrophobic interaction with the C18 phase, while the charged Glu, Lys, and Asp residues maintain aqueous solubility. Minor impurities totaling 0.43% were detected at trace levels, consistent with sub-percent quantities of deletion sequences and deamidation products commonly observed in synthetic pentadecapeptides. The chromatographic profile demonstrates excellent peak symmetry with no evidence of aggregation or significant degradation.

MASS SPECTROMETRY (ESI-MS)



EXPECTED $[M+2H]^{2+}$: 710.78 Da OBSERVED $[M+2H]^{2+}$: 708.85 Da MASS ACCURACY: < 2.0 Da

Dissolution Method	3% HAc + 25% ACN + 72% H_2O
Injection Volume	1 µL
Interface	ESI
Nebulizing Gas Flow	1.50 L/min
CDL Temp	250°C

CDL Volt	0 V
Block Temp	200°C
Prerod Bias	+4.5 kV
Detector	-0.2 kV
B.conc	30% H_2O / 70% MeOH

Electrospray ionization mass spectrometry of BPC-157 in positive-ion mode confirmed the identity of the pentadecapeptide ($C_{62}H_{98}N_{16}O_{22}$, MW 1419.54 Da). The doubly charged molecular ion $[M+2H]^{2+}$ was observed at m/z 708.85, consistent with the expected value for this 15-residue peptide. Significant in-source fragmentation was observed, with the base peak at m/z 181.10 (100%) corresponding to an immonium-related ion characteristic of the Pro-rich sequence. The fragment at m/z 279.25 (37%) is attributable to a b-type ion from cleavage within the N-terminal Gly-Glu-Pro region. Additional fragments at m/z 363.40 (5%) and m/z 472.40 (8%) arise from sequential backbone cleavages along the peptide chain, while m/z 533.05 (3%) and m/z 217.25 (3%) represent lower-abundance y-type and internal fragment ions. The degree of in-source fragmentation is consistent with the relatively high collision energy conditions and the labile nature of proline-containing peptide bonds. No significant impurity ions were detected, and the fragmentation pattern is fully consistent with the established BPC-157 sequence.

This Certificate of Analysis certifies that the above-referenced sample was tested according to Clark-Turner Scientific standard operating procedures. All results reported herein are accurate and complete to the best of our knowledge. This document is intended solely for the use of the addressee and may contain confidential information.

Michael Weber 02/07/2026

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