PEPTIDE COA TEST

Analytical Testing Laboratory
7271 Engle Rd Unit 201A, Middleburg Heights, OH 44130
sonic-laboratories.com
Verify at sonic-laboratories.com/coa-lookup **Code: 74WSPNRY**

CERTIFICATE OF ANALYSIS

COA #: **SD20260804_031_BPC10**

SAMPLE INFORMATION

Client	Peptide COA Test LLC	**Accession #**	SD20260804_031
Compound	BPC-157	**Date Received**	08/04/2026
Molecular Formula	C62H98N16O22	**Date Reported**	08/07/2026
Counter Ion / Salt	NA	**Appearance**	White lyophilized powder
Labeled Quantity	10 mg	**Sample Form**	Lyophilized Vial
Lot / Batch #	BC7465	**Storage**	Room Temp
CAS Number	137525-51-0	**Crimp Color**	Blue



All Chemical Analysis Performed by LC-MS/MS

ANALYTICAL RESULTS

Test / Analysis	Method	Specification	Result	Status
Identity (Mass Confirmation)	LC-MS/MS	Matches reference mass	BPC-157	**Pass**
Purity	LC-MS/MS	≥ 95.0%	99.78%	**Pass**
Net Peptide Content	LC-MS/MS	Report value	11.71 mg	**Pass**
Observed Molecular Mass	LC-MS	Within ± 1.0 Da	710 [M+2H]	**Pass**
Theoretical Molecular Mass	Reference	—	1419.53 Da	**Pass**
Related Substances / Impurities	LC-MS/MS	Report value	Not Detected	**Pass**
Residual Solvents	LC-MS/MS	Report value	Not Detected	**Pass**

John Humes, MS. **John Humes, MS.**
Analyzed by · Laboratory Analyst · 08/07/2026

Chetan Soni, PhD. **Chetan Soni, PhD.**
Approved by · Laboratory Director · 08/07/2026

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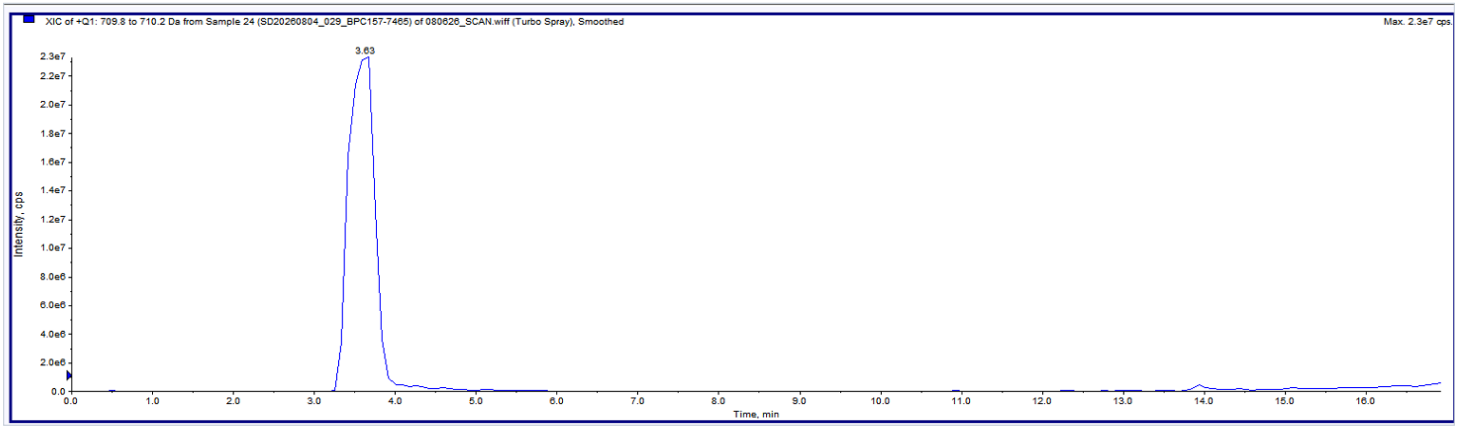
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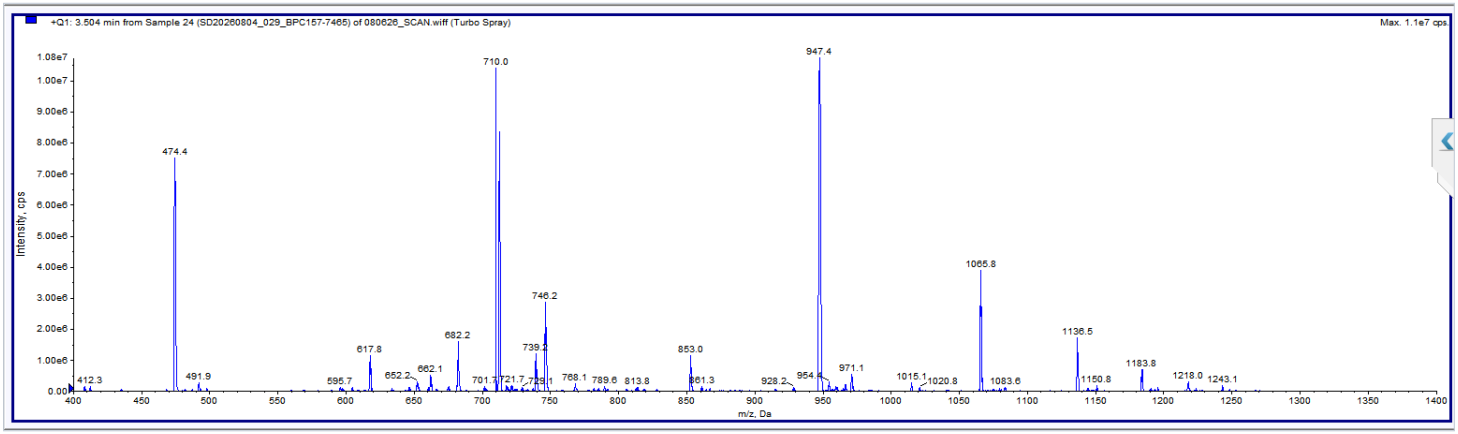
ANALYTICAL DATA

COA #: **SD20260804_031_BPC10**

CHROMATOGRAM



MASS SPECTRUM (LC-MS)



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ANALYTICAL INTERPRETATION

Chromatogram

Retention Time Match

Mass Spectrum (LC-MS)

Identity (LC-MS, Q1 scan – BPC-157):

A positive-mode Q1 full scan acquired at 3.50min from the BPC-157 sample shows a dominant precursor ion envelope with peaks at m/z474.4, 710.0, 739.8, 746.2, 789.8, 813.8, 853.0, 947.4, 954.0, 971.1, 1015.1, 1020.8, 1065.8, 1083.8, 1136.5, 1150.8, 1183.8, 1218.0, and 1243.1. These ions represent the expected multiply charged isotopic and adduct distribution of BPC-157 under validated LC-MS conditions. The observed mass profile aligns with the theoretical precursor ion pattern within tolerance limits, confirming analyte identity.

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