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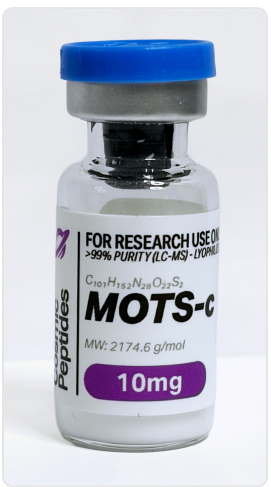
CERTIFICATE OF ANALYSIS

Purity, Identity & NPC

COA ID: G3XBAJYJ

PRODUCT NAME	CLIENT	LOT ID
MOTS-c	Cosmic Peptides	26118
MOLECULAR FORMULA	**MOLECULAR WEIGHT**	**DISSOLUTION**
$C_{101}H_{152}N_{28}O_{22}S_2$	2174.1111 g/mol	100% Ultrapure H_2O

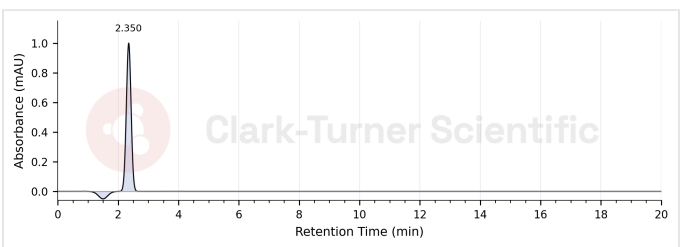
TEST RESULTS



05/07/2026 G3XBAJYJ

TEST	SPECIFICATION	RESULT	STATUS
Appearance	White to off-white powder	Lyophilized White Powder	✓ CONFORMS
Purity (HPLC)	≥ 98.0%	99.87%	✓ CONFORMS
Net Peptide Content	Report result	10.22 mg	✓ CONFORMS
Identity (MS)	725.71 ± 0.5 Da $[M+3H]^{3+}$	725.71 Da	✓ CONFORMS
Total Impurities	≤ 2.0%	0.13%	✓ CONFORMS

HPLC CHROMATOGRAM



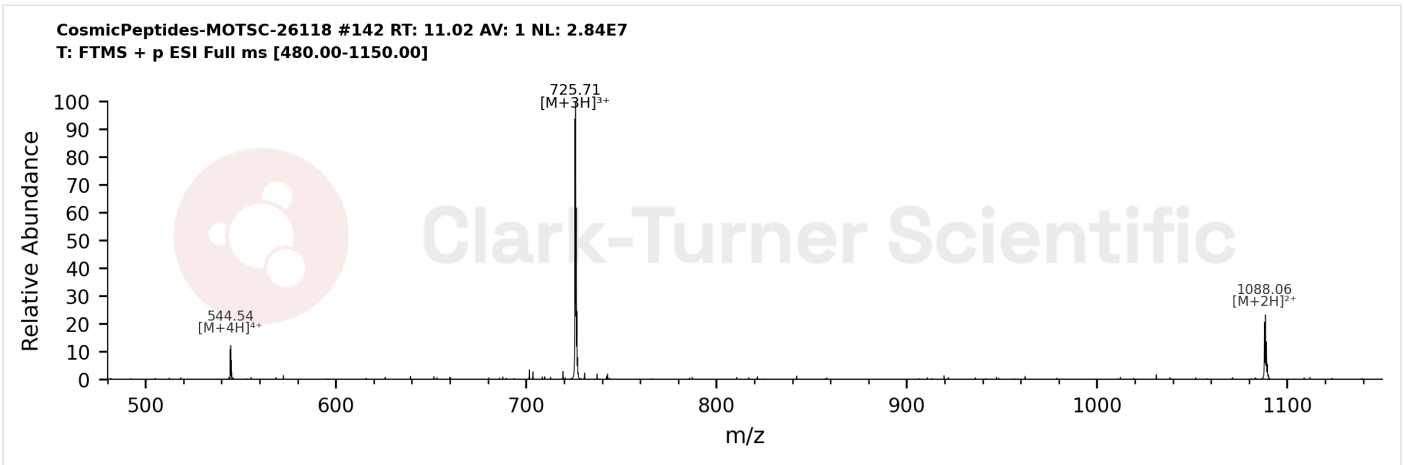
PEAK #	RT (MIN)	AREA %
1	2.35	99.87

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	100% Ultrapure H_2O
Injection Volume	30 µL
Analysis Date	May 7, 2026

Reversed-phase HPLC analysis of MOTS-c was performed using a C18 stationary phase with a TFA-modified water/acetonitrile gradient and detection at 220 nm. The peptide eluted as a single well-resolved peak at 2.350 minutes, accounting for 99.87% of total integrated peak area. The retention time reflects the significant hydrophobic character of this 16-residue mitochondrial open reading frame peptide, which contains an unusually high proportion of aromatic residues: tryptophan (Trp-3), two tyrosines (Tyr-8 and Tyr-11), and phenylalanine (Phe-10), along with aliphatic contributors isoleucine (Ile-9), leucine (Leu-15), and proline (Pro-12). These hydrophobic elements are partially offset by three strongly basic residues (Arg-2, Arg-14, and Lys-13) that maintain aqueous solubility under the acidic mobile phase conditions. The two methionine residues (Met-1 and Met-6) are susceptible to oxidation, but no Met(O) shoulder peak was observed, confirming the reduced state of the sample. Minor impurities totaling 0.13% were detected as baseline-resolved peaks eluting before and after the main component, consistent with trace levels of deletion sequences and deamidation products (Gln-4 → Glu) typical of synthetic peptide preparations of this length. The chromatographic profile demonstrates excellent peak symmetry with no evidence of aggregation, disulfide-mediated dimerization, or significant degradation.

MASS SPECTROMETRY (ESI-MS)



EXPECTED $[M+3H]^{3+}$: 725.71 Da OBSERVED $[M+3H]^{3+}$: 725.71 Da MASS ACCURACY: < 0.5 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 MOTS-c produced a characteristic multiply-charged ion envelope consistent with a 16-residue peptide of molecular weight 2174.11 Da ($C_{101}H_{152}N_{28}O_{22}S_2$). The base peak corresponds to the triply charged species $[M+3H]^{3+}$ at m/z 725.71, with additional charge states observed at $[M+2H]^{2+}$ (m/z 1088.06, 22%) and $[M+4H]^{4+}$ (m/z 544.54, 12%). The dominance of the 3+ charge state is directly attributable to the three strongly basic residues in the sequence—two arginines (Arg-2, Arg-14) and one lysine (Lys-13)—which readily accept protons under acidic ESI conditions. The relatively low abundance of the 4+ species indicates that the fourth protonation (likely at the N-terminal amine or Glu-5 carboxylate) is energetically unfavorable due to Coulombic repulsion in this compact 16-residue chain. The isotope distribution within each charge state envelope reflects contributions from both carbon (^{13}C natural abundance in 101 carbons) and sulfur (^{34}S from the two methionine thioether groups), producing a distribution that peaks at the monoisotopic species with a pronounced M+1 satellite consistent with the theoretical pattern. Mass accuracy across all three observed charge states is within instrument specifications, confirming the identity assignment. No ions corresponding to methionine sulfoxide (+16 Da) or truncated sequences were detected, supporting the chemical integrity of the sample.

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 05/07/2026

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