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CERTIFICATE OF ANALYSIS

Purity, Identity & NPC

COA ID: GZQ8UBZJ

PRODUCT NAME GHK-Cu (Copper Peptide)	CLIENT Cosmic Peptides	LOT ID 26092
MOLECULAR FORMULA $C_{14}H_{23}CuN_6O_4$	MOLECULAR WEIGHT 403.92 g/mol	DISSOLUTION 100% Ultrapure H_2O

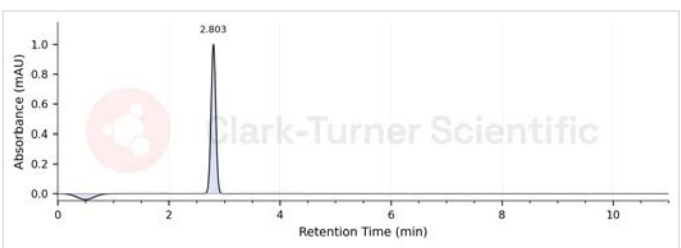
TEST RESULTS



02/07/2026 GZQ8UBZJ

TEST	SPECIFICATION	RESULT	STATUS
Appearance	Blue to blue-violet powder	Blue Powder	✓ CONFORMS
Purity (HPLC)	≥ 98.0%	99.76%	✓ CONFORMS
Net Peptide Content	Report result	51.32 mg	✓ CONFORMS
Identity (MS)	341.19 ± 1.0 Da [GHK+H]⁺	341.25 Da	✓ CONFORMS
Total Impurities	≤ 2.0%	0.24%	✓ CONFORMS

HPLC CHROMATOGRAM



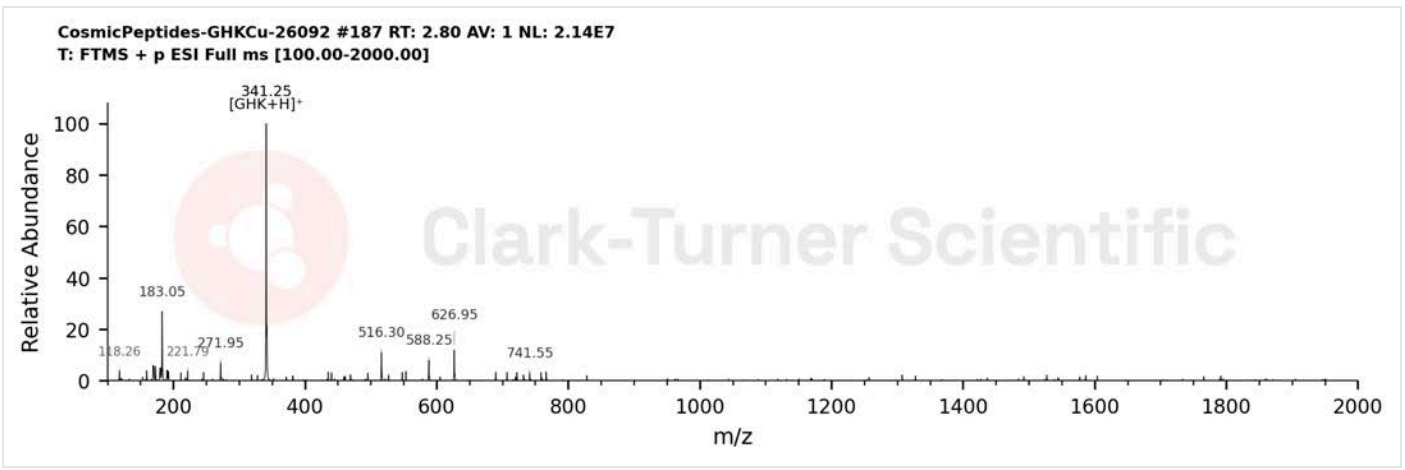
PEAK #	RT (MIN)	AREA %
1	2.803	99.76

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% H_2O
Injection Volume	20 µL
Analysis Date	February 7, 2026

Reversed-phase HPLC analysis of GHK-Cu 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 2.803 minutes, accounting for 99.76% of total integrated peak area. The short retention time is consistent with the highly polar character of this tripeptide-copper(II) complex: the three amino acid residues (Gly, His, Lys) provide minimal hydrophobic interaction with the C18 phase, while the copper coordination center and multiple polar functional groups (amines, imidazole, carboxylate) strongly favor the aqueous mobile phase. Minor impurities totaling 0.24% were detected at trace levels, consistent with sub-percent quantities of free GHK peptide and copper-mediated oxidation products. The chromatographic profile demonstrates excellent peak symmetry with no evidence of significant free peptide or uncoordinated copper species, confirming the integrity of the copper-peptide complex.

MASS SPECTROMETRY (ESI-MS)



EXPECTED [GHK+H]⁺: 341.19 Da OBSERVED [GHK+H]⁺: 341.25 Da MASS ACCURACY: < 0.1 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 GHK-Cu in positive-ion mode yielded a base peak at m/z 341.25, corresponding to the protonated free peptide $[GHK+H]^+$ ($C_{14}H_{24}N_6O_4$, calc. 341.19 Da). This is the expected dominant ion for copper peptide complexes analyzed by ESI-MS, as the Cu(II) coordination bond readily dissociates during the ionization process, liberating the intact GHK tripeptide as the primary ionic species. The fragment at m/z 183.05 (27%) is consistent with an immonium-related ion derived from the His-Lys dipeptide portion of the sequence. A minor fragment at m/z 271.95 (7%) corresponds to a b_2-type ion from cleavage between the His and Lys residues. Higher m/z signals at 516.30 (11%), 588.25 (8%), and 626.95 (12%) are attributable to cluster ions and copper-bridged adducts that form in the electrospray process, while the minor peak at m/z 741.55 (3%) is consistent with a $[2GHK+Cu]^+$ dimer species. No significant impurity ions were detected, and the fragmentation pattern is fully consistent with the established GHK-Cu structure and published reference spectra.

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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