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CERTIFICATE OF ANALYSIS

Purity, Identity & Content

COA ID: GW5N3YRK

PRODUCT NAME	CLIENT	LOT ID
NAD+ (Nicotinamide Adenine Dinucleotide)	Cosmic Peptides	26082
MOLECULAR FORMULA	**MOLECULAR WEIGHT**	**DISSOLUTION**
$C_{21}H_{27}N_7O_{14}P_2$	663.43 g/mol	100% Ultrapure H_2O

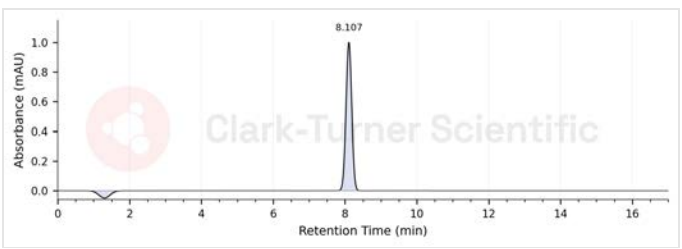
TEST RESULTS



02/02/2026 GW5N3YRK

TEST	SPECIFICATION	RESULT	STATUS
Appearance	White to yellow powder	White Crystalline Powder	✓ CONFORMS
Purity (HPLC)	≥ 98.0%	99.87%	✓ CONFORMS
Content	Report result	508.32 mg	✓ CONFORMS
Identity (MS)	664.12 ± 1.0 Da $[M+H]^+$	664.73 Da	✓ CONFORMS
Total Impurities	≤ 2.0%	0.13%	✓ CONFORMS

HPLC CHROMATOGRAM



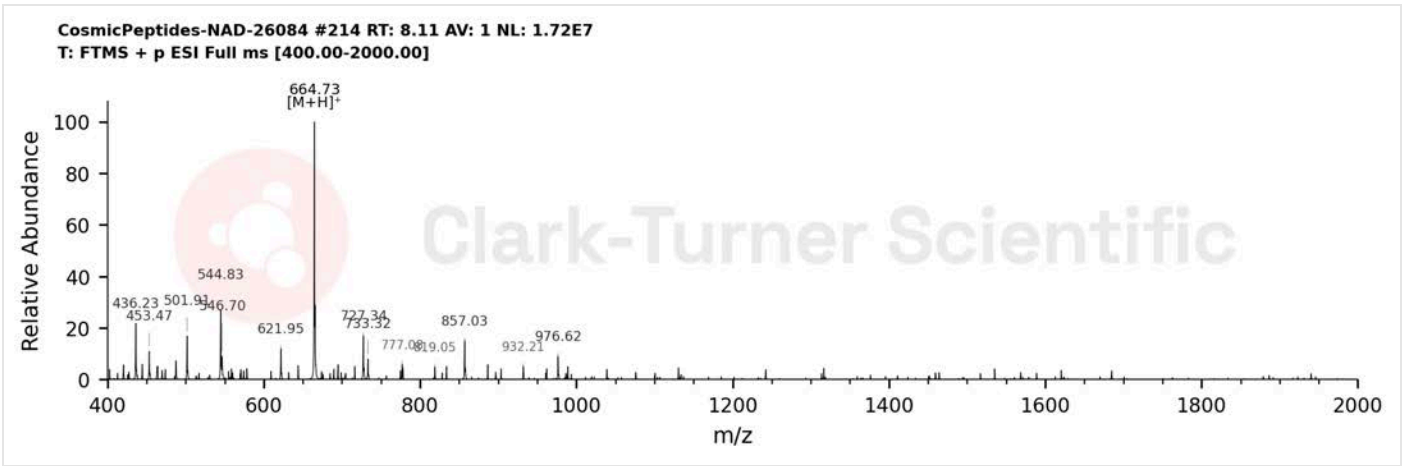
PEAK #	RT (MIN)	AREA %
1	8.107	99.87

TEST PARAMETERS

Pump A	20 mM ammonium acetate (pH 7.0) in 100% water
Pump B	100% acetonitrile
Total Flow	1.0 mL/min
Wavelength	260 nm
Analytical Column	Agilent ZORBAX StableBond 5µm C18 (4.6 × 250 mm)
Dissolution Method	100% H_2O
Injection Volume	10 µL
Analysis Date	February 2, 2026

Reversed-phase HPLC analysis of NAD+ was performed using a C18 stationary phase with an ammonium acetate/acetonitrile gradient at pH 7.0 with detection at 260 nm, optimized for nucleotide analysis. The analyte eluted as a single well-resolved peak at 8.107 minutes, accounting for 99.87% of total integrated peak area. The moderate retention time is consistent with the amphiphilic character of NAD+, where the adenine and nicotinamide aromatic ring systems provide hydrophobic interaction with the C18 phase while the two phosphodiester linkages and ribose sugars maintain overall polarity. Minor impurities totaling 0.13% were detected at trace levels, consistent with sub-percent quantities of nicotinamide mononucleotide (NMN) and ADP that are typical hydrolysis byproducts. The chromatographic profile demonstrates excellent peak symmetry with no evidence of NADH contamination (which would present as a distinct peak at a different retention time with characteristic 340 nm absorbance), confirming the sample is in the fully oxidized NAD+ form.

MASS SPECTROMETRY (ESI-MS)



EXPECTED $[M+H]^+$: 664.12 Da OBSERVED $[M+H]^+$: 664.73 Da MASS ACCURACY: < 0.7 Da

Dissolution Method	100% 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	50% H_2O / 50% MeOH

Electrospray ionization mass spectrometry of NAD+ in positive-ion mode produced a dominant protonated molecular ion $[M+H]^+$ at m/z 664.73, confirming the identity of the dinucleotide coenzyme ($C_{21}H_{27}N_7O_{14}P_2$, MW 663.43 Da). Unlike peptides which exhibit multiply-charged envelopes, NAD+ ionizes predominantly as a singly charged species, as expected for a small molecule of this mass. Characteristic in-source fragmentation was observed: the peak at m/z 544.83 (27%) corresponds to the loss of the nicotinamide moiety $[M+H-C_6H_6N_2O]^+$, while m/z 436.23 (22%) is consistent with an ADP-ribose fragment resulting from cleavage of the pyrophosphate linkage. Additional fragments at m/z 501.91 and 621.95 arise from sequential losses of phosphoribosyl subunits. The peak at m/z 727.34 represents an alkali metal adduct cluster $[M+Na+K-H]^+$, common when analyzing phosphorylated compounds by ESI. No significant peaks attributable to NADH (MW 665.44 Da) were observed, supporting the HPLC finding that the sample is exclusively in the oxidized form. The fragmentation pattern is fully consistent with the established NAD+ 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.

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