ANALYSED BY AN INDEPENDENT UK LABORATORY PARTNER USING ESTABLISHED HPLC & LC-MS METHODS.

CERTIFICATE ID	PREPARED FOR	SAMPLE	EXPECTED MW
PV-E8B4E0-ASNN-D5	Lumina Biologics	NAD+	663.40 Da
SERVICE TIER	**BATCH / LOT**	**ANALYSIS DATE**	**INSTRUMENT**
Combined · HPLC + LC-MS	Not provided	17/08/2026 17:20	Shimadzu LCMS-8040 · PDA
METHOD	**DETECTION**	**MS IONIZATION**	**ACQUISITION**
HPLC + ESI-MS	UV 215 nm (±4)	ESI+	Single injection · UV and MS in line

00 ASSESSMENT

SAMPLE AS RECEIVED

PURITY — HPLC	**99.63%**	Main-peak Area % of the integrated UV signal. 2 peaks resolved. *What this means: 99.63% is the reported purity figure for this sample.*
IDENTITY — LC-MS	● **Confirmed**	Detected intact mass 663.1 Da vs expected 663.40 Da; charge states agree and base peak matches. *What this means: the detected molecular weight matches the declared peptide within method tolerance.*

⊕ SAMPLE DESCRIPTION & LAB NOTES

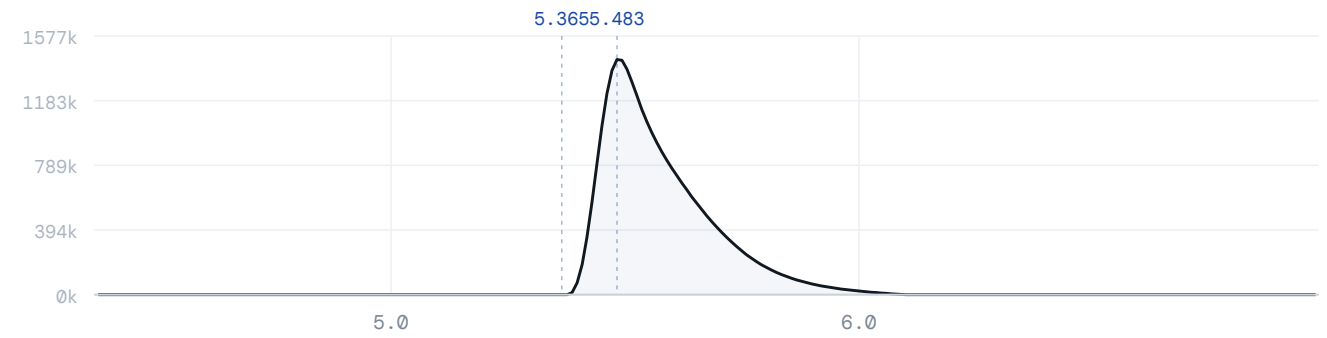
RECORDED ON RECEIPT

FORM	COLOUR	CONDITION	OBSERVED RT	MS / IDENTITY MATCH
Lyophilized powder	White	As Expected	5.48 min	As Expected

01 HPLC — CHROMATOGRAM

HPLC · PDA · 215 NM

CHROMATOGRAM — DISPLAY WINDOW 4.4-7.0 MIN · FULL RUN 0.0-30.0 MIN



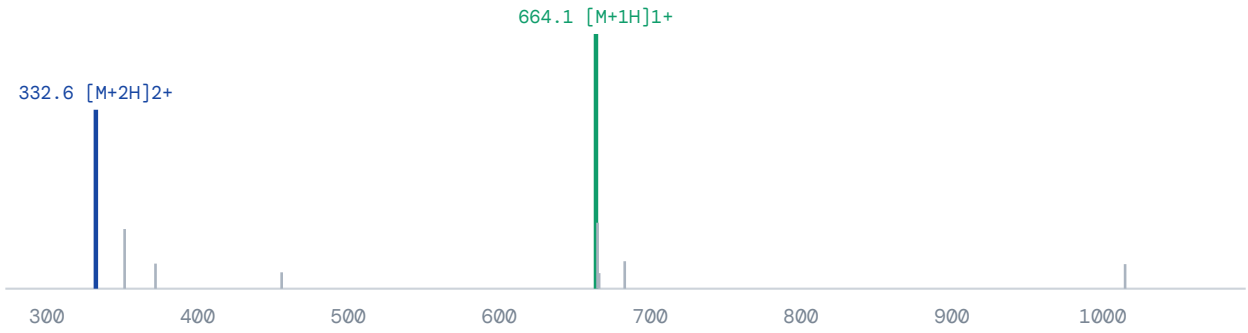
PEAK	RT / MIN	AREA	AREA %	PPI %	TAILING	PLATES N	RES (USP)
1	5.365	71,505	0.37	—	—	—	—
2	5.483	19,223,903	99.63	—	3.00	4,970	—

Area % = the main peak's share of total UV area — the reported purity figure for a multi-peak sample. **PPI %** = Peak Purity Index (spectral homogeneity), per peak. Tailing = peak symmetry; Plates N = column efficiency; Res = USP resolution from the adjacent peak (≥ 1.5 = baseline-separated).

02 LC-MS — IDENTITY

ESI · INTACT-MASS DECONVOLUTION

ESI-MS SPECTRUM — DETECTED IONS · CHARGE-MATCHED HIGHLIGHTED



CHARGE STATE	EXP. M/Z	OBS. M/Z	Δ (DA)	CALC. MW	INTENSITY	MATCH
[M+1H]1+	664.12	664.10	-0.02	663.1	5,012,391	MATCH
[M+2H]2+	332.56	332.60	+0.04	663.2	3,522,007	MATCH

Expected m/z is quoted on the monoisotopic mass scale, matching what the instrument reports at each charge state. Δ is the difference between the observed and expected ion. Identity is assessed against an absolute mass window of approximately ±1 Da, appropriate to a unit-resolution quadrupole, together with the requirement that the ion dominates the spectrum and its isotope spacing fits the assigned charge. This method is not specified to parts-per-million mass accuracy.

Identity: Confirmed. 2 independent charge states ([M+1H]1+, [M+2H]2+) deconvolute to the same intact mass (≈ 663.1 Da), matching NAD+ within the method's unit-resolution tolerance. Base peak corresponds to the expected dominant charge state.

03 SYSTEM SUITABILITY

PARAMETER	RESULT	LIMIT	OUTCOME
Tailing factor (T) — main peak	3.00	≤ 3.5	PASS
Theoretical plates (N)	4,970	—	HILIC · N/A
Detector / wavelength	PDA	215 nm	PASS

HILIC method — this polar compound is separated by hydrophilic-interaction chromatography, where peaks are inherently broad. Reverse-phase plate-count and resolution limits do not apply; identity is established by LC-MS intact mass.

04 VERIFICATION

TAMPER-EVIDENT RECORD

● INDEPENDENTLY VERIFIABLE

peptideverify.co.uk/verify/PV-E8B4E0-ASNN-D5

INTEGRITY SHA-256 · 4c156cc0…7a0aaf24
SOURCE DATA · 20260814 Batch 1_PV-E8B4E0_ASNN-D5_003.lcd
Scan or visit the URL to confirm this certificate against PeptideVerify's source record.

AUTHORISED BY

C Bray

CHRISTOPHER BRAY · PEPTIDEVERIFY · 17/08/2026