



DOC PV-COA
REPORT PV-670171-XLNM
ISSUED 23/09/2026

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

00 ASSESSMENT

PURITY – HPLC

98.95%

Peak Purity Index (PPI) of the integrated UV signal. Single integrated peak.
What this means: 98.95% is the reported purity figure for this sample.

IDENTITY - LC-MS

- **Confirmed**

Detected intact mass 4,730.5 Da vs expected 4,731.41 Da; 2 charge states agree and the base peak matches.

What this means: the detected molecular weight matches the declared peptide within method tolerance.

⊕ SAMPLE DESCRIPTION & LAB NOTES RECORDED ON RECEIPT

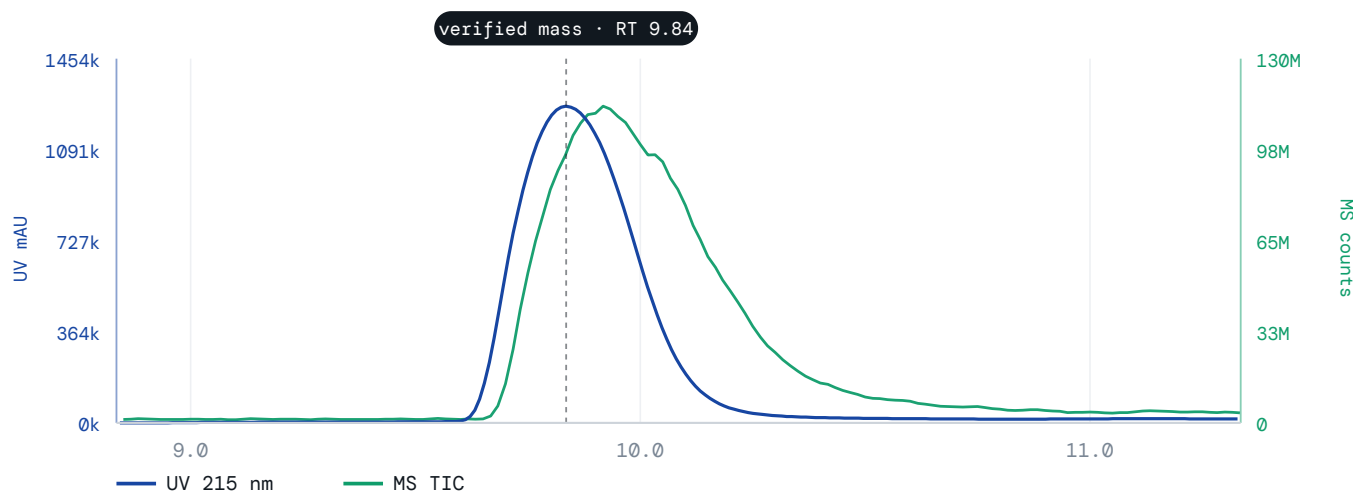
FORM	COLOUR	CONDITION	OBSERVED RT	MS / IDENTITY MATCH
Lyophilized powder	White	As Expected	9.84 min	As Expected



SAMPLE AS RECEIVED

01 HPLC + LC-MS - CO-ELUTION PDA 215 NM · ESI TIC

UV PURITY PEAK (BLUE, LEFT AXIS) AND LC-MS TOTAL-ION RESPONSE (GREEN, RIGHT AXIS) ON ONE RETENTION-TIME AXIS - THE VERIFIED MASS CO-ELUTES WITH THE UV PEAK - WINDOW 8.8-11.3 MIN.



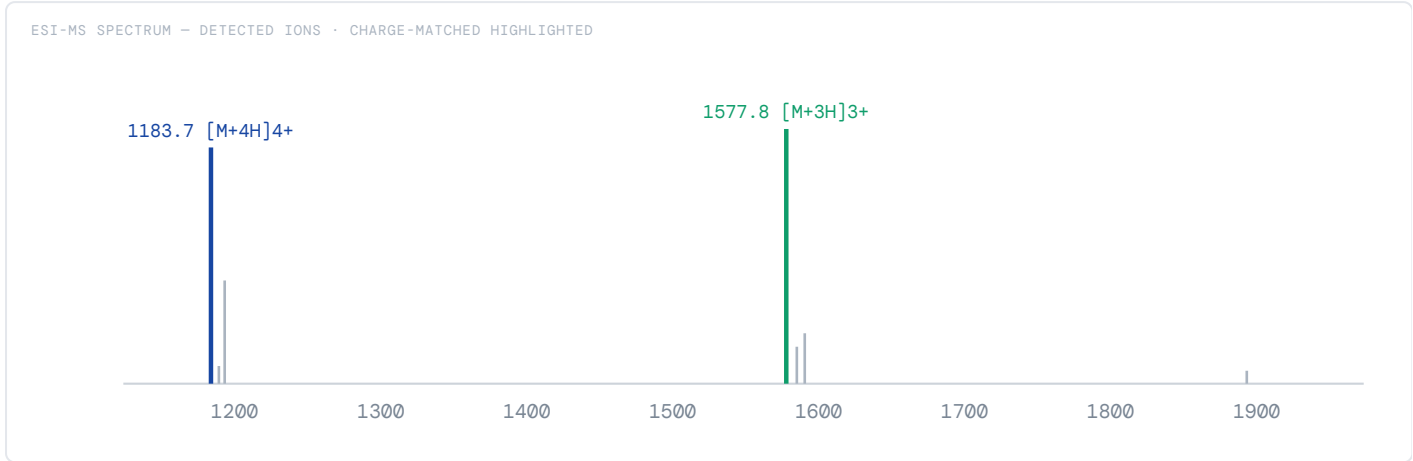
PEAK	RT / MIN	AREA	AREA %	PPI %	TAILING	PLATES N
1	9.835	22.719.973	100.00	99.0	1.35	6.994

PPI % = Peak Purity Index – the reported purity (spectral homogeneity). **Area %** = this peak's share of total UV area, not a purity claim. Tailing = peak symmetry; Plates N = column efficiency.



02 LC-MS – IDENTITY

ESI · INTACT-MASS DECONVOLUTION



CHARGE STATE	EXP. M/Z	OBS. M/Z	Δ (DA)	CALC. MW	INTENSITY	MATCH
[M+3H]3+	1578.12	1577.80	-0.32	4730.4	7,365,712	MATCH
[M+4H]4+	1183.84	1183.65	-0.19	4730.6	6,830,041	MATCH

Expected m/z is quoted on the average 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+3H]3+, [M+4H]4+) deconvolute to the same intact mass (≈ 4,730.5 Da), matching Retatrutide 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	1.35	≤ 3.5	PASS
Theoretical plates (N)	6,994	≥ 600	PASS
Detector / wavelength	PDA	215 nm	PASS

04 VERIFICATION

TAMPER-EVIDENT RECORD

● INDEPENDENTLY VERIFIABLE

peptideverify.co.uk/verify/PV-670171-XLNW

INTEGRITY SHA-256 · 93fbc331_ea1718eb

SOURCE DATA · 20260922 batch 4_PV-670171_XLNW_017.lcd

Scan or visit the URL to confirm this certificate against PeptideVerify's source record.

AUTHORISED BY

C Bray

CHRISTOPHER BRAY · PEPTIDEVERIFY · 23/09/2026

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