



DOC PV-COA
REPORT PV-82D8C6-XTFK
ISSUED 06/08/2026

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

CERTIFICATE ID	PREPARED FOR	SAMPLE	EXPECTED MW
PV-82D8C6-XTFK	BRITISH PEPTIDE LABS	Retatrutide	4,731.41 Da
SERVICE TIER	BATCH / LOT	ANALYSIS DATE	INSTRUMENT
Combined · HPLC + LC-MS	Not provided	06/08/2026 15:04	Shimadzu LCMS-8040 · PDA
METHOD	DETECTION	MS IONIZATION	ACQUISITION
HPLC + ESI-MS	UV 215 nm (±4)	ESI+	Single injection · UV and MS in line

SAMPLE AS RECEIVED

PURITY – HPLC

98.93%

Main-peak Area % of the integrated UV signal. 2 peaks resolved.

What this means: 98.93% is the reported purity figure for this sample.

IDENTITY - LC-MS

- **Confirmed**

Detected intact mass 4,730.2 Da vs expected 4,731.41 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

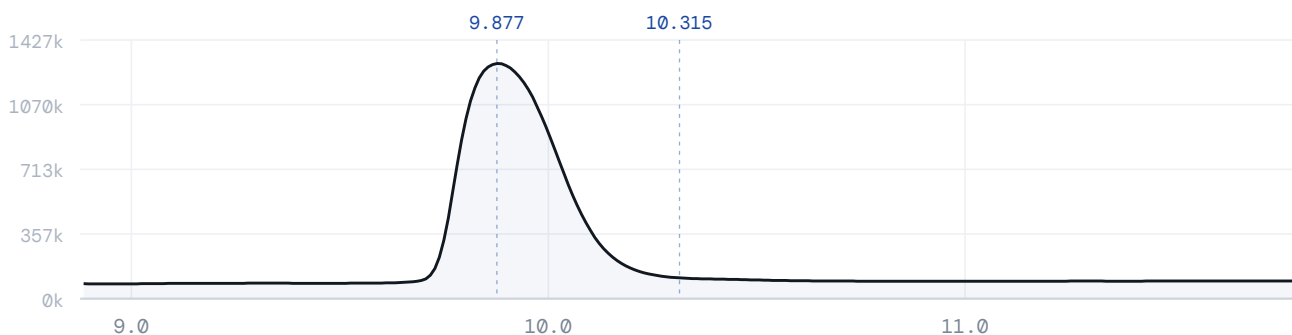
RECORDED ON RECEIPT

FORM	COLOUR	CONDITION	OBSERVED RT	MS / IDENTITY MATCH
Lyophilized powder	White	As Expected	9.88 min	As Expected

01 HPLC – CHROMATOGRAM

HPLC · PDA · 215 NM

CHROMATOGRAM - DISPLAY WINDOW 8.9-11.8 MIN · FULL RUN 0.0-20.0 MIN



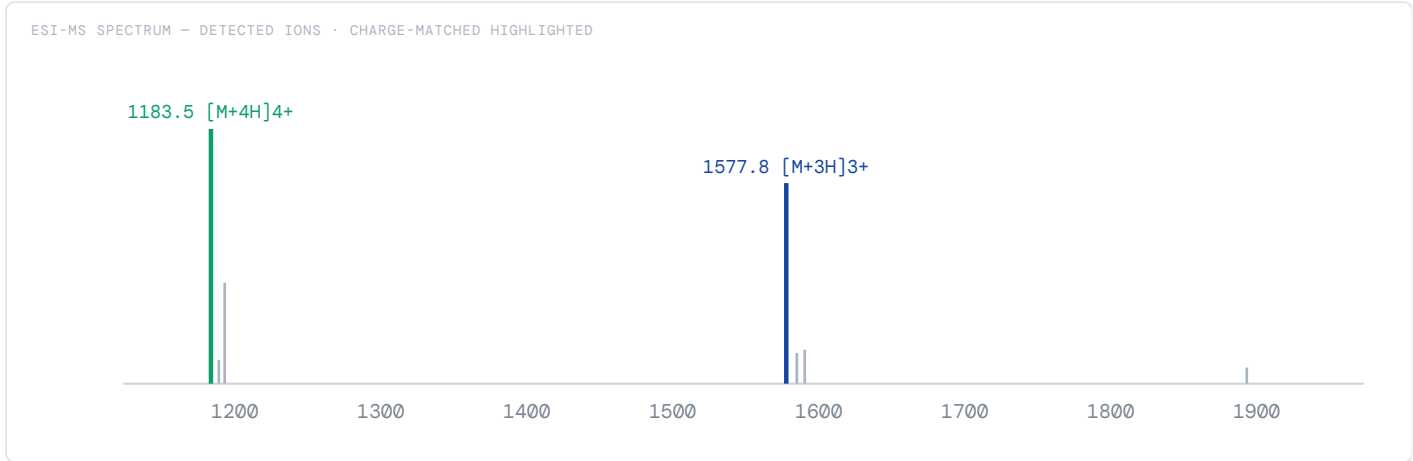
PEAK	RT / MIN	AREA	AREA %	PPI %	TAILING	PLATES N	RES (USP)
1	9.877	19,539,415	98.93	99.0	1.60	9,135	—
2	10.315	211,035	1.07	99.7	—	15,847	1.18

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



CHARGE STATE	EXP. M/Z	OBS. M/Z	Δ (DA)	CALC. MW	INTENSITY	MATCH
[M+3H]3+	1578.12	1577.75	-0.37	4730.2	6,999,713	MATCH
[M+4H]4+	1183.84	1183.55	-0.29	4730.2	8,888,703	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 (≈ 4,730.2 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	1.60	≤ 3.5	PASS
Theoretical plates (N)	9,135	≥ 600	PASS
Resolution (Rs, USP) – min	1.18	≥ 1.5	CHECK
Detector / wavelength	PDA	215 nm	PASS

04 VERIFICATION

TAMPER-EVIDENT RECORD

● INDEPENDENTLY VERIFIABLE

peptideverify.co.uk/verify/PV-82D8C6-XTFK

INTEGRITY SHA-256 · 32f771b8_1d697702

SOURCE DATA · 20260803 batch_PV-82D8C6_XTFK_081.lcd

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

AUTHORISED BY

C Bray

CHRISTOPHER BRAY · PEPTIDEVERIFY · 06/08/2026

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