

PEPTIDEVERIFY · INDEPENDENT VERIFICATION · PEPTIDEVERIFY · INDEPENDENT VERIFICATION · PEPTIDEVERIFY · INDEPENDENT VERIFICATION · PEPTIDEVERIFY · INDEPENDENT VERIFICATION · PEPTIDEVERIFY · INDEPENDENT VERIFICATION · PEPTIDEVERIFY · INDEPENDENT VERIFICATION · PEPTIDE

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

CERTIFICATE ID	PREPARED FOR	SAMPLE	EXPECTED MW
PV-F01FF8-WRWI	BioSupplyUK	Retatrutide	4,731.41 Da
SERVICE TIER	BATCH / LOT	ANALYSIS DATE	INSTRUMENT
Combined · HPLC + LC-MS	BSUK003	21/07/2026 15:31	Shimadzu LCMS-8040 · PDA
METHOD	DETECTION	MS IONIZATION	
HPLC + ESI-MS	UV 215 nm (±4)	ESI+	

00 ASSESSMENT

SAMPLE AS RECEIVED

PURITY — HPLC

99.0%

Main-peak Area % of the integrated UV signal. 2 peaks resolved.
What this means: 99.0% is the reported purity figure for this sample.

IDENTITY — LC-MS

Confirmed

Detected intact mass 4,730.3 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.

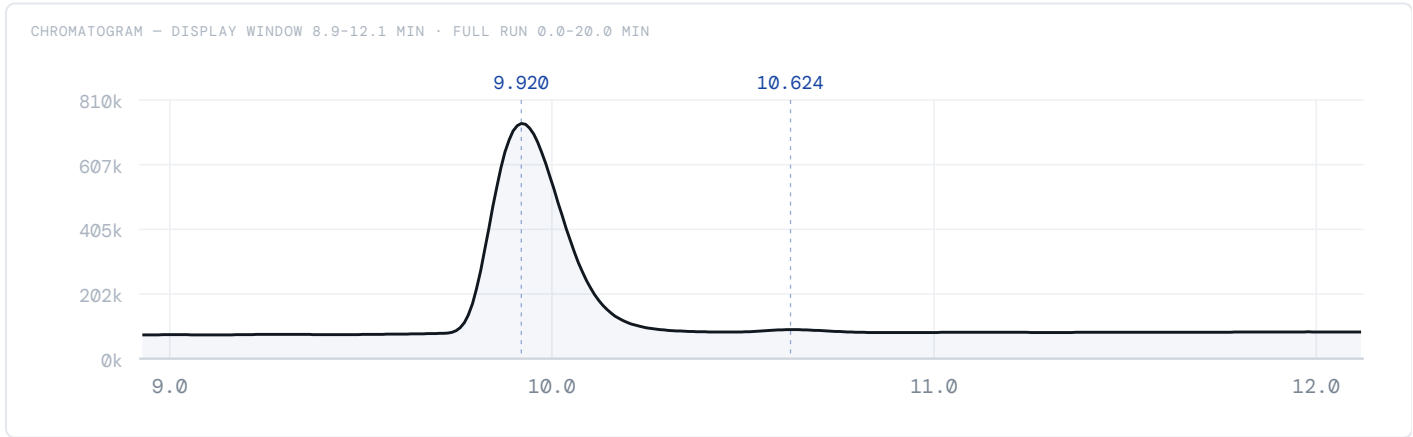
⊕ SAMPLE DESCRIPTION & LAB NOTES

RECORDED ON RECEIPT

FORM	COLOUR	CONDITION	OBSERVED RT	MS / IDENTITY MATCH
Lyophilized powder	White	As Expected	9.92 min	As Expected

01 HPLC — CHROMATOGRAM

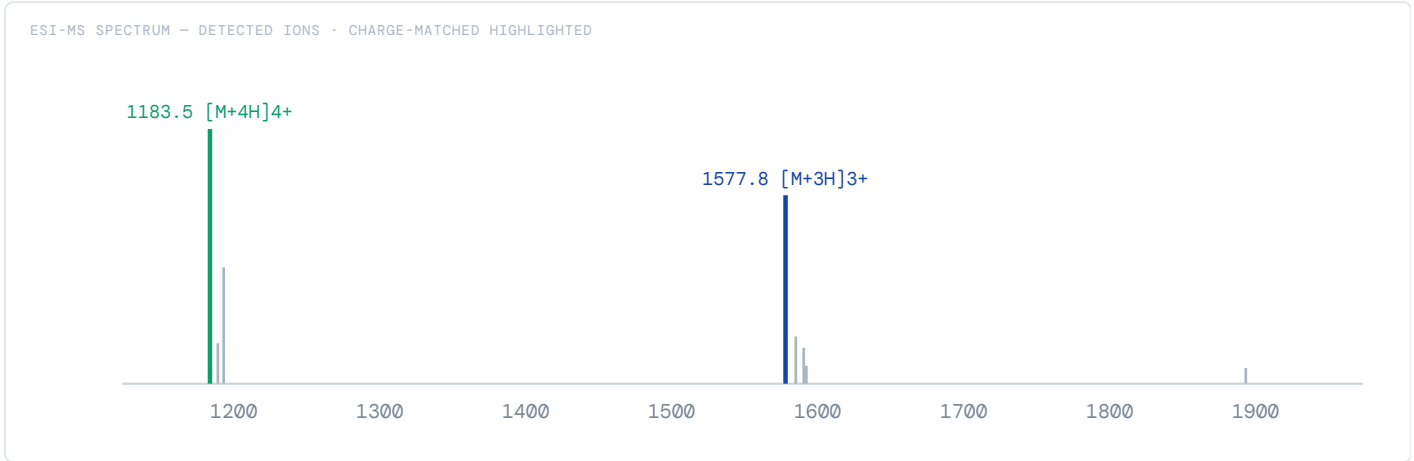
HPLC · PDA · 215 NM



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	CALC. MW	INTENSITY	MATCH
[M+3H]3+	1578.12	1577.80	4730.4	2,794,397	MATCH
[M+4H]4+	1183.84	1183.55	4730.2	3,779,011	MATCH

Identity: Confirmed. 2 independent charge states ([M+3H]3+, [M+4H]4+) deconvolute to the same intact mass (≈ 4,730.3 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	1.42	≤ 3.5	PASS
Theoretical plates (N)	13,055	≥ 600	PASS
Resolution (Rs, USP) – min	2.18	≥ 1.5	PASS
Detector / wavelength	PDA	215 nm	PASS

04 VERIFICATION

TAMPER-EVIDENT RECORD



● INDEPENDENTLY VERIFIABLE

peptideverify.co.uk/verify/PV-F01FF8-WRWI

INTEGRITY SHA-256 · f2d3d59f...b62a2d16

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

AUTHORISED BY

C Bray

CHRISTOPHER BRAY · PEPTIDEVERIFY · 21/07/2026

TERMS This certificate reports analysis of the sample as received. It is not a guarantee of other units or batches, and is not an endorsement of any product, seller or vendor. For research use only – not for human consumption, and not a safety assessment or medical advice. Confirm authenticity at peptideverify.co.uk/verify.