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

CERTIFICATE ID	PREPARED FOR	SAMPLE	EXPECTED MW
PV-143F3D-CFOP-33	BioSupplyUK	PT-141 (Bremelanotide)	1,025.18 Da
SERVICE TIER	**BATCH / LOT**	**ANALYSIS DATE**	**INSTRUMENT**
Combined · HPLC + LC-MS	BSUK003	17/11/2026	Shimadzu LCMS-8040 · PDA
METHOD	**DETECTION**	**MS IONIZATION**	**ACQUISITION**
HPLC + ESI-MS	UV 215 nm (±4)	ESI+	Single injection · UV and MS in line
COLUMN	**MOBILE PHASE**	**FLOW RATE**	
Zorbax Extend C18, 4.6 x 150 mm	0.1% Formic Acid in Water / 0.1% Formic Acid in Acetonitrile	0.5ml/min	

00 ASSESSMENT

SAMPLE AS RECEIVED

PURITY — HPLC	**99.36%**	Peak Purity Index (PPI) of the integrated UV signal. Single integrated peak. *What this means: 99.36% is the reported purity figure for this sample.*
IDENTITY — LC-MS	● **Confirmed**	Detected intact mass 1,024.9 Da vs expected 1,025.18 Da; mass agrees within method tolerance. *What this means: the detected molecular weight matches the declared peptide within method tolerance.*

⊕ SAMPLE DESCRIPTION & LAB NOTES

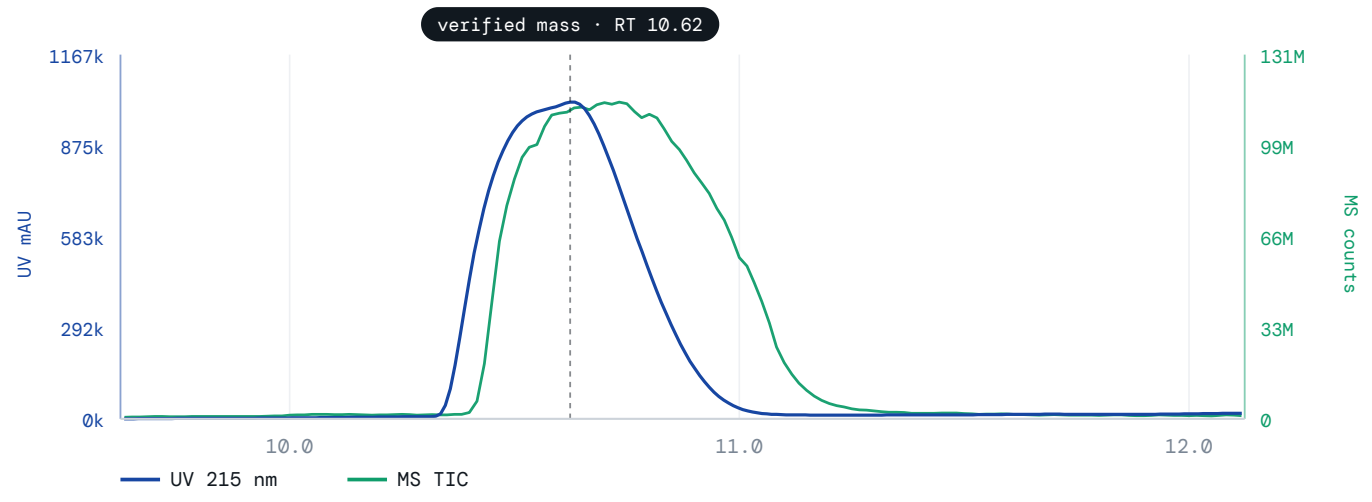
RECORDED ON RECEIPT

FORM	COLOUR	CONDITION	OBSERVED RT	MS / IDENTITY MATCH
Lyophilized powder	White	As Expected	10.62 min	As Expected

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 9.6-12.1 MIN.



PEAK	RT / MIN	AREA	AREA %	PPI %	TAILING	PLATES N	UV MAX / NM
1	10.624	22,965,294	100.00	99.4	1.12	5,588	203 / 280

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; UV max = wavelengths at which the peak absorbs most strongly.

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+2H]2+	513.27	513.45	+0.18	1024.9	15,797,275	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. The detected mass (≈ 1,024.9 Da), matching PT-141 (Bremelanotide) 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	1.12	≤ 3.5	PASS
Theoretical plates (N)	5,588	≥ 600	PASS
Detector / wavelength	PDA	215 nm	PASS

04 VERIFICATION

TAMPER-EVIDENT RECORD

● INDEPENDENTLY VERIFIABLE

peptideverify.co.uk/verify/PV-143F3D-CFOP-33

INTEGRITY SHA-256 · 07b6a548…69177fcb
SOURCE DATA · 20261117 batch 2_PV-143F3D_CFOP-33_005.lcd
Scan or visit the URL to confirm this certificate against PeptideVerify's source record.

AUTHORISED BY

C Bray

CHRISTOPHER BRAY · PEPTIDEVERIFY · 18/11/2026

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.