Analytical Evidence Report

HPLC-DAD results for the submitted Retatrutide sample

REPORT NUMBER
WB-RETA-20-092126

GENERATED
September 30, 2026

Retatrutide

Results and chromatograms

Sample 6026_0146 | Client report WB-RETA-20-092126

Laboratory Analysis: LAB-CA-01

Laboratory identity and applicable credentials are maintained by Testides and are available to regulatory authorities where required by law.

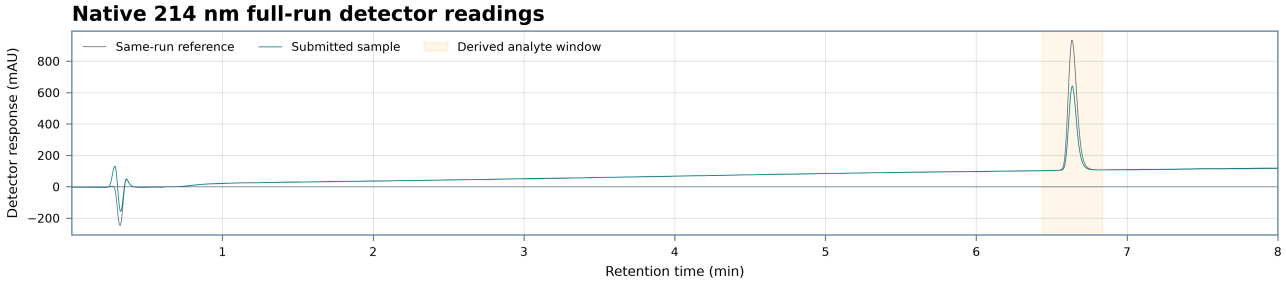
VIAL PHOTOGRAPH	SAMPLE INFORMATION		ANALYSIS		RUN DETAILS	
	Peptide:	**Retatrutide**	Method:	**HPLC-DAD**	Run date:	**Sep 26, 2026**
	Sample ID:	**6026_0146**	Channels:	**214 / 280 nm + spectra**	First acquired:	**20:12:59 UTC**
	Client ID:	**WB-RETA-20-092126**	Area metric:	**214 nm blank-excluded**	Last acquired:	**00:27:50 UTC**
	Label claim:	**20 mg**	Comparison:	**Reference aligned**	Run time:	**8.00 min / acquisition**

RESULTS AT A GLANCE

PROJECTED AMOUNT	HPLC PURITY	CONTENT VS. LABEL	REFERENCE ALIGNMENT
24.72 mg†	**99.54%**	**123.6%**	**Observed**
BASED ON SAMPLE PREPARATION	214 NM AREA PERCENT, LIMIT 0.458%	24.72 MG OF 20 MG CLAIMED	RETENTION TIME + UV PROFILE**

CHROMATOGRAM

Complete run - 214 nm detector response



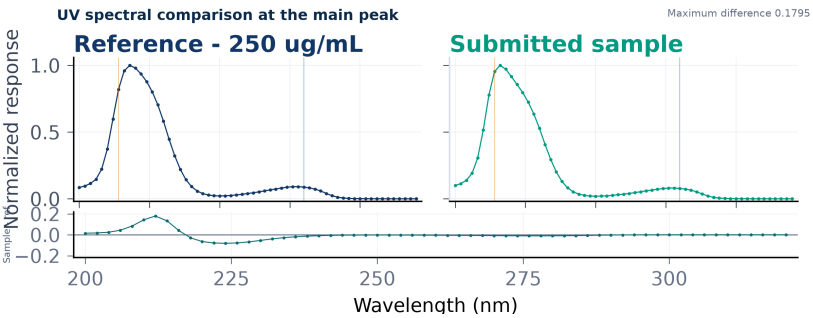
HPLC PURITY (214 NM)

Peptide + related	Main peak area %	Reporting limit	UV match
99.54%	**99.54%**	**0.458%**	**1.00000**
Main peak and UV-matched forms	1 injection(s)	Smallest reportable peak	Sample vs. reference

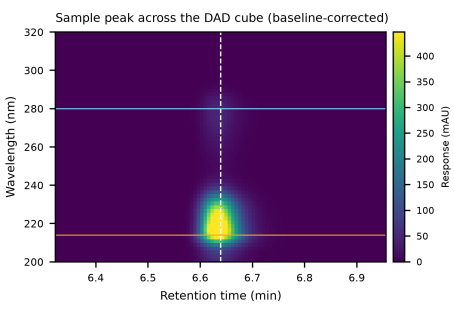
Purity is the main peak's share of the total integrated peak area at 214 nm, measured from the native detector readings. Peaks below 0.458% of total area cannot be resolved from this run's baseline and are not counted. No impurity was detected above the reporting limit; the smallest impurity this run could resolve is that limit. This result rests on a single injection; no duplicate was run.

UV SPECTRAL COMPARISON

Native wavelength samples - baseline-corrected, normalized; no smoothing



UV response through the sample peak



The complete acquisition is shown without smoothing or resampling: 1,200 native readings on the 214 nm channel.

* HPLC purity is the main peak's share of total integrated peak area at 214 nm. Peaks below 0.458% of total area are not resolvable from this run's baseline; every peak is itemised on page 3.

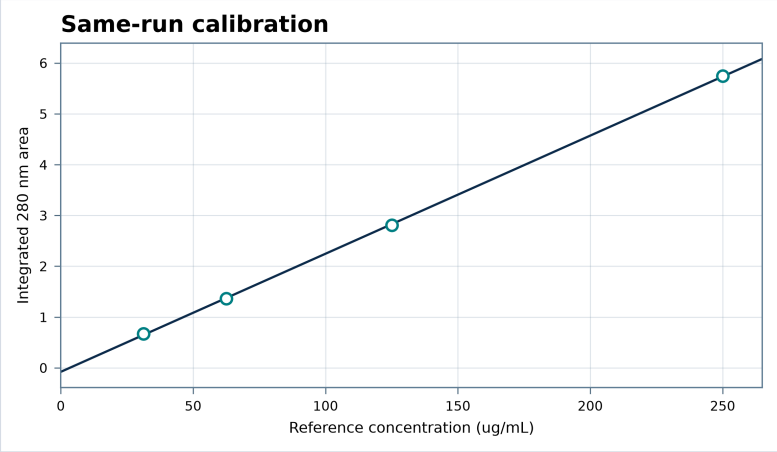
** Reference alignment: retention time within the same-run standards' range or within ±5% of their mean, and a UV match (220-300 nm cosine) at or above the standards' lowest or 0.999.

Retatrutide

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Reference comparison and calculation

CONCENTRATION CALIBRATION - 280 NM



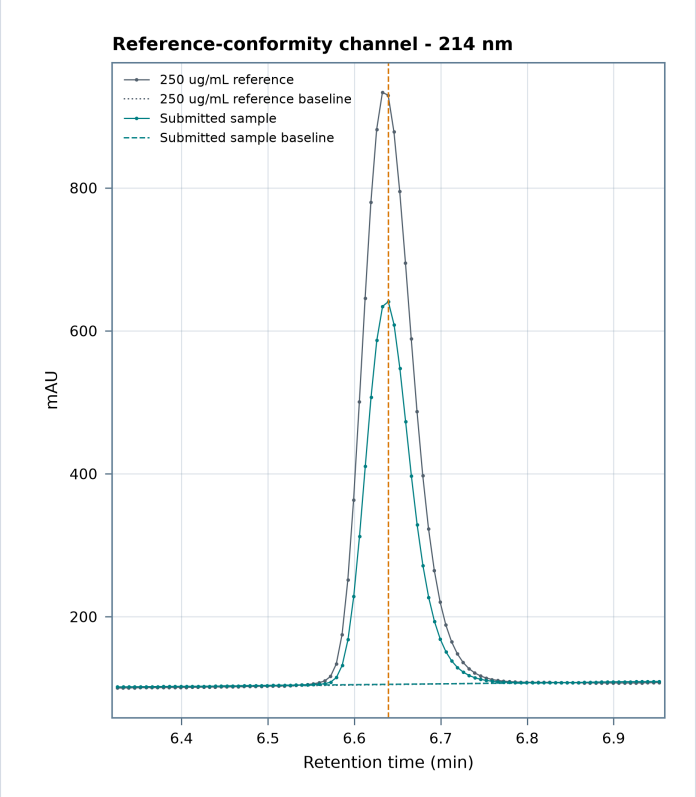
ug/mL	Area	Recovery
31.25	0.67261	103.35%
62.5	1.36097	99.05%
125	2.80575	99.24%
250	5.74511	100.20%

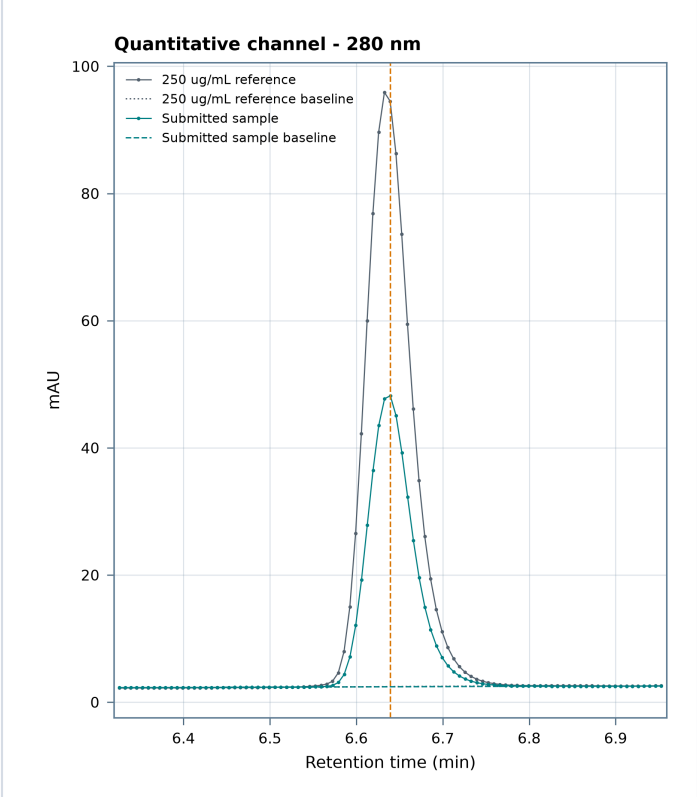
Area = 0.02324788C -0.07824888
Unweighted OLS | R2 0.9999080
Sample area 2.7956 = 123.62 ug/mL x 2 mL x 100 / 1000 = 24.72 mg

UV spectra were recorded from 190-400 nm across the run

The integration method and the full peak table are on page 3.

MAIN PEAK COMPARED WITH THE SAME-RUN REFERENCE





Native acquisition points with the exact quantitative baselines; the dashed line marks the reference retention-time centre.
** Reference alignment: retention time within the same-run standards' range or within ±5% of their mean, and a UV match (220-300 nm cosine) at or above the standards' lowest or 0.999.

Retatrutide

Definitions, calculation detail, and scope

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HOW TO READ THIS REPORT

Start with the result on page 1. Pages 2 and 3 show the comparisons, calculations, and limits behind it.

01 **Complete chromatogram**

Shows the main peak in the context of the full detector run.

02 **Integrated peak table**

Lists every peak counted towards the purity result, and every peak not.

03 **UV comparison**

Compares the peak's UV pattern with the same-run reference.

WHAT THE UV COMPARISON ADDS

What diode-array detection adds to the comparison

What it adds

Retention time tells us when the peak left the column; DAD records its UV fingerprint across many wavelengths. Alignment requires both: retention time within the same-run standards' range or ±5% of their mean, and a UV match at or above the standards' lowest or 0.999.

What it can reveal

A UV fingerprint that changes across the peak can indicate hidden co-elution. Here, apex cosine similarity is 0.999998 and minimum within-peak cosine is 0.999991, supporting close reference alignment and spectral uniformity.

Identity: retention time and UV spectrum are both compared with the reference standards.

HOW THE PURITY RESULT WAS MEASURED

214 nm area percent, measured from the native detector readings

The run's blank injections give the baseline and the detection floor. Each injection is corrected against the blanks bracketing it in time, every peak is integrated to a valley-to-valley baseline, and purity is the main peak's share of the total counted area.

Purity (%) = main peak area / total counted peak area x 100

RT (min)	Area	Area %	Classification	UV vs main	Counted
6.639	34.1034	99.542	Main peak	-	Counted

Reporting limit 0.458% of total area | counted peaks 0 | injections 1

Area percent assumes every peak absorbs at 214 nm like the main peak.

Content vs. label: Recovered mass is calculated from the same-run calibration and the sample preparation recorded for this vial, against reference material at its stated concentration. The bracketing quality-control injections verify that calibration held across the run; the vial's reconstitution and dilution are recorded by the laboratory and are not independently measured here.

WHAT THIS REPORT CAN AND CANNOT TELL YOU

The report explains the measurement; it does not decide how a material should be used

Observed evidence

Chromatograms, reference and blank comparisons, and classified peaks.

Calculated results

Area-percent purity, concentration, projected amount, and calibration trace.

Method context

Retention time (standards' range or ±5%) and UV match (standards' lowest or 0.999).

Safety and regulatory status

No conclusion on safety, efficacy, fitness for use, or regulatory status.

This analytical record does not authorize or endorse manufacture, sale, marketing, distribution, or use of the material.