



Retatrutide

Results and chromatograms

Sample 6026_0149 | Client report JSOS-RETA-10-091326

Laboratory Analysis: LAB-CA-01

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

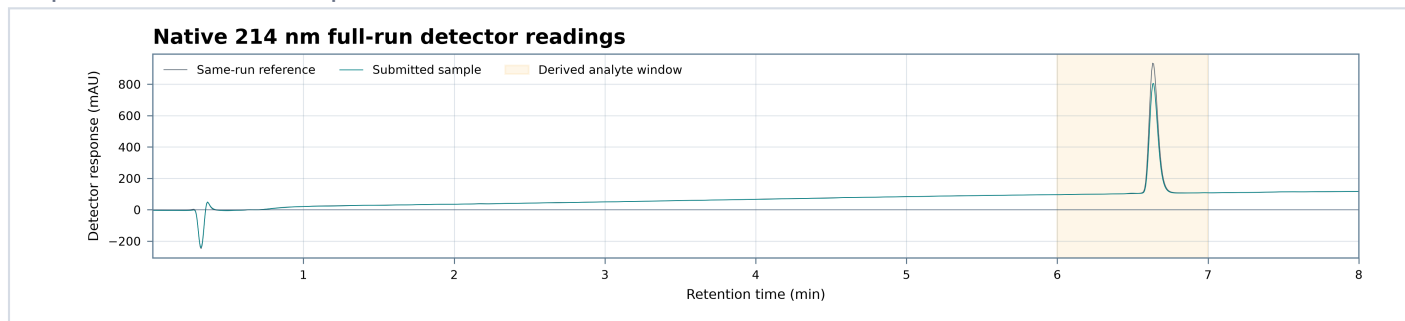
VIAL PHOTOGRAPH	SAMPLE INFORMATION	ANALYSIS	RUN DETAILS
	Peptide: Retatrutide Sample ID: 6026_0149 Client ID: JSOS-RETA-10-091326 Label claim: 10 mg	Method: HPLC-DAD Channels: 214 / 280 nm + spectra Area metric: 214 nm blank-excluded Comparison: Reference aligned	Run date: Sep 26, 2026 First acquired: 20:12:59 UTC Last acquired: 02:04:12 UTC Run time: 8.00 min / acquisition

RESULTS AT A GLANCE

PROJECTED AMOUNT 18.31 mg† BASED ON SAMPLE PREPARATION	HPLC PURITY 98.72% 214 NM AREA PERCENT, LIMIT 0.053%	CONTENT VS. LABEL 183.1% 18.31 MG OF 10 MG CLAIMED	REFERENCE ALIGNMENT Observed RETENTION TIME + UV PROFILE**
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CHROMATOGRAM

Complete run - 214 nm detector response



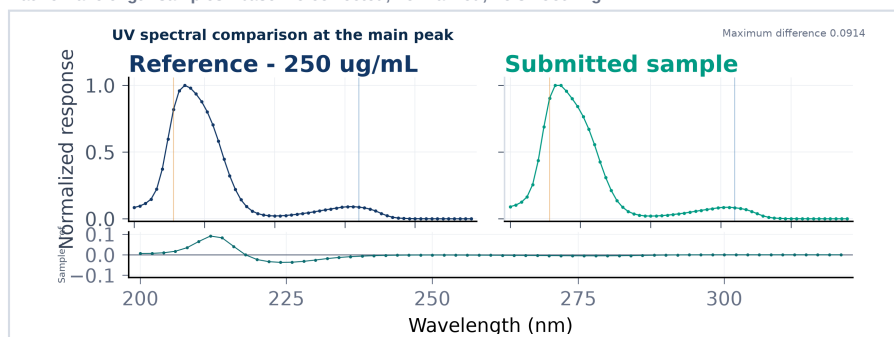
HPLC PURITY (214 NM)

Peptide + related 98.72% Main peak and UV-matched forms	Main peak area % 98.72% 1 injection(s)	Reporting limit 0.053% Smallest reportable peak	UV match 0.99999 Sample vs. reference
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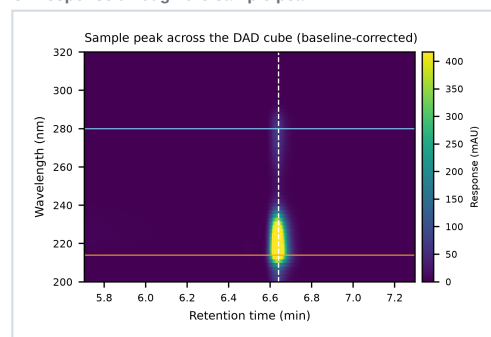
Purity is the main peak's share of the total integrated peak area at 214 nm, measured from the native detector readings. Peaks below 0.053% of total area cannot be resolved from this run's baseline and are not counted. This result rests on a single injection; no duplicate was run.

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 0.053% 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 $\pm 5\%$ of their mean, and a UV match (220-300 nm cosine) at or above the standards' lowest or 0.999.

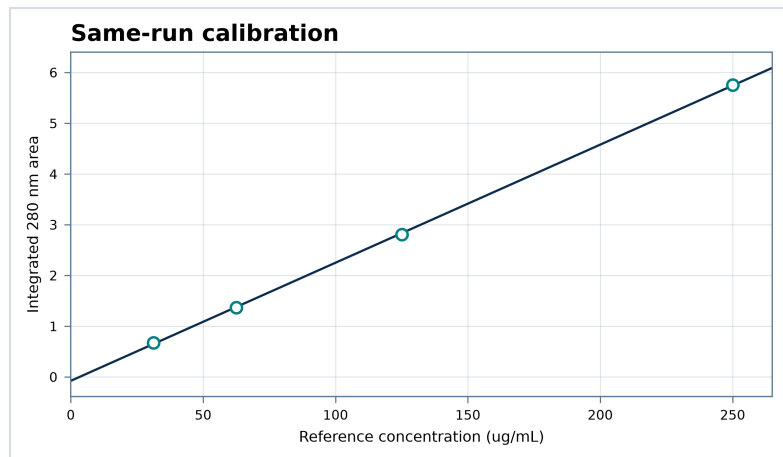


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Reference comparison and calculation

CONCENTRATION CALIBRATION - 280 NM

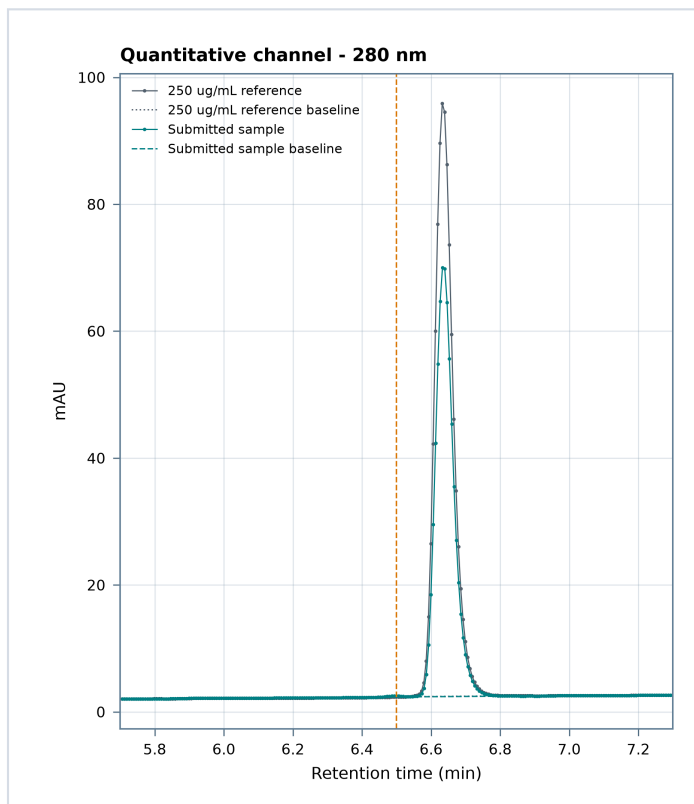
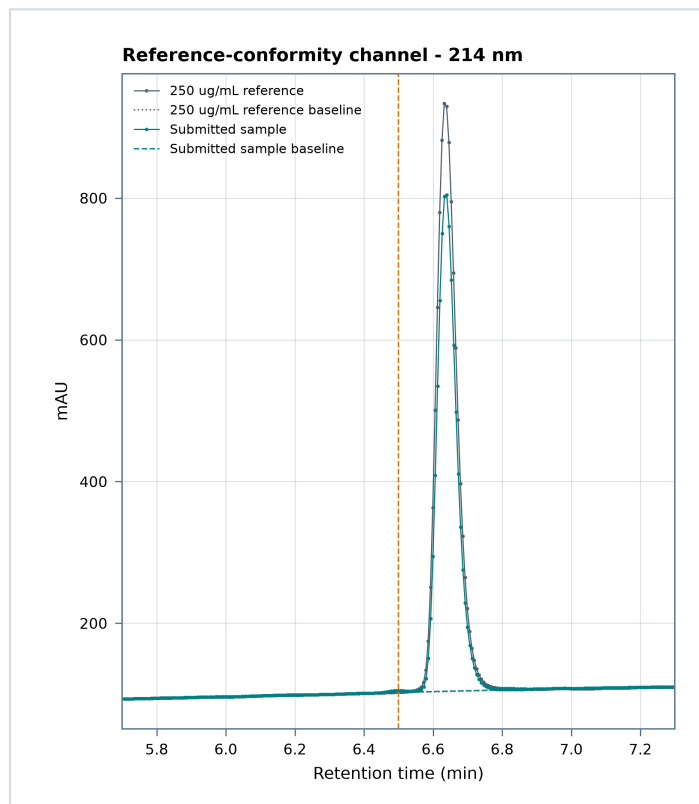


ug/mL	Area	Recovery
31.25	0.67036	102.85%
62.5	1.36908	99.44%
125	2.80807	99.17%
250	5.75401	100.20%

Area = 0.02328173C - 0.07794911
Unweighted OLS | R2 0.9999202
Sample area 4.1842 = 183.07 ug/mL x 2 mL x 50 / 1000 = 18.31 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 $\pm 5\%$ of their mean, and a UV match (220-300 nm cosine) at or above the standards' lowest or 0.999.



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Definitions, calculation detail, and scope

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.
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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 $\pm 5\%$ 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 0.999889 and minimum within-peak cosine is 0.999973, 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
6.640	46.6451	98.717	Main peak	-	Counted
4.599	0.2582	0.555	impurity	0.959	Counted
0.632	0.2029	0.436	impurity	0.953	Counted
1.372	0.1357	0.292	impurity	0.976	Counted
and 6 further peak(s), each smaller than those listed; the complete peak table is in the evidence record					
Reporting limit 0.053% of total area counted peaks 3 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 $\pm 5\%$) 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.	