



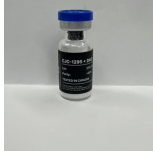
CJC-1295 DAC

Sample 6026_0057 | Client report SYNA-CJCD-10-090826

Results and chromatograms

Laboratory Analysis: LAB-CA-01

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

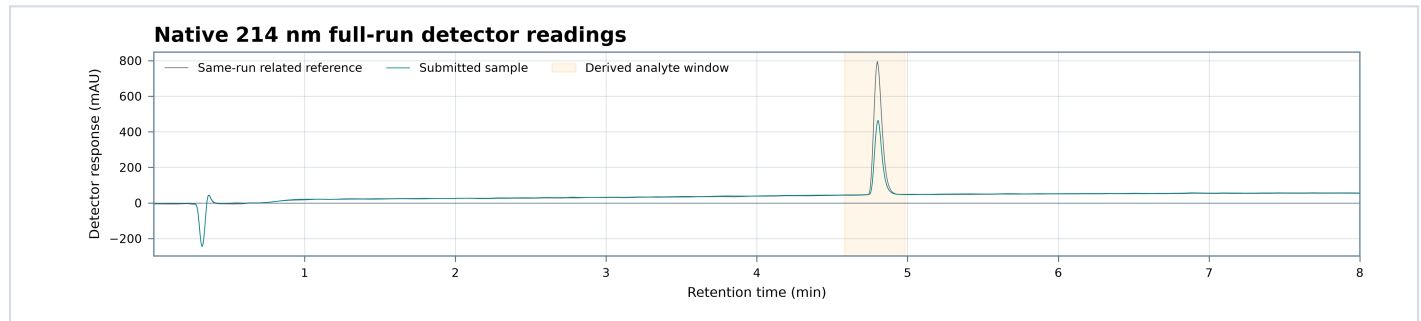
VIAL PHOTOGRAPH	SAMPLE INFORMATION	ANALYSIS	RUN DETAILS
	Peptide: CJC-1295 DAC Sample ID: 6026_0057 Client ID: SYNA-CJCD-10-090826 Label claim: 10 mg	Method: HPLC-DAD Channels: 214 / 280 nm + spectra Area metric: 214 nm blank-excluded Comparison: Not assessed	Run date: Sep 23, 2026 First acquired: 15:23:01 UTC Last acquired: 19:12:18 UTC Run time: 8.00 min / acquisition

RESULTS AT A GLANCE

PROJECTED AMOUNT 12.21 mg† BASED ON SAMPLE PREPARATION	HPLC PURITY 99.17% MAIN PEAK 98.55% + RELATED	CONTENT VS. LABEL 122.1% 12.21 MG OF 10 MG CLAIMED	REFERENCE ALIGNMENT Not assessed NO SAME-RUN STANDARD
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CHROMATOGRAM

Complete run - 214 nm detector response



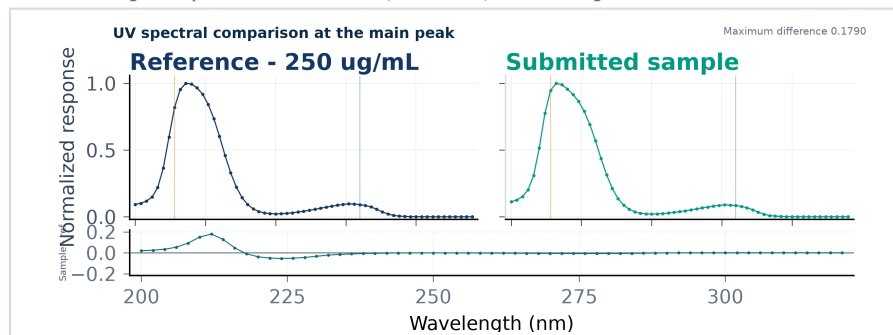
HPLC PURITY (214 NM)

Peptide + related 99.17% Main peak and UV-matched forms	Main peak area % 98.55% 1 injection(s)	Reporting limit 0.130% Smallest reportable peak	UV match 0.99982 Sample vs. reference
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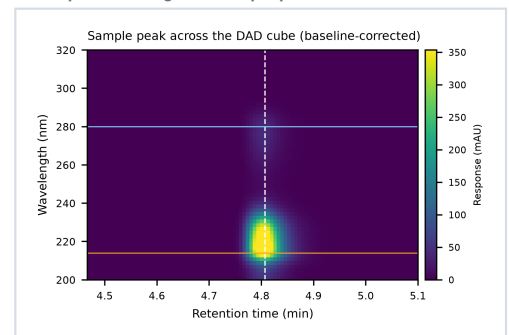
Purity is the main peak's share of the total integrated peak area at 214 nm, measured from the native detector readings. Peaks below 0.130% of total area cannot be resolved from this run's baseline and are not counted. Peaks sharing the main peak's UV spectrum total 0.62% and are reported together with it as peptide and related variants. UV spectral similarity to the main peak over 220-300 nm. UV cannot distinguish one peptide from another of similar composition; related peaks are not mass-confirmed. 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: 1,201 native readings on the 214 nm channel.

* HPLC purity is the main peak plus peaks matching its UV spectrum, as a share of total integrated area at 214 nm. The main peak alone is 98.55%; 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.

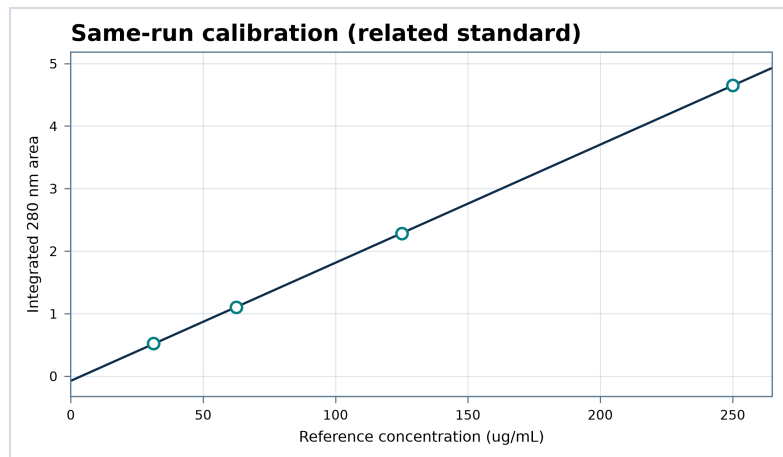


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Reference comparison and calculation

CONCENTRATION CALIBRATION - 280 NM



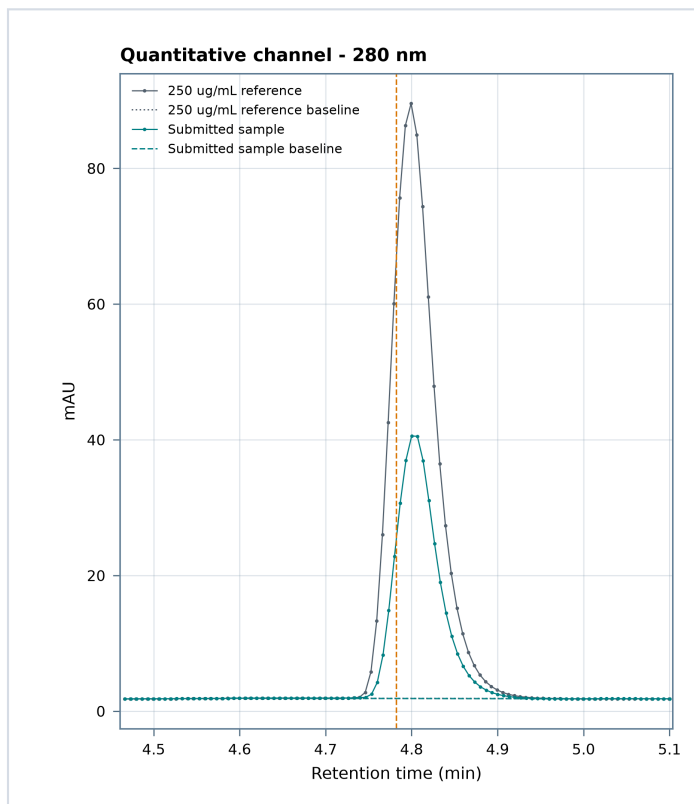
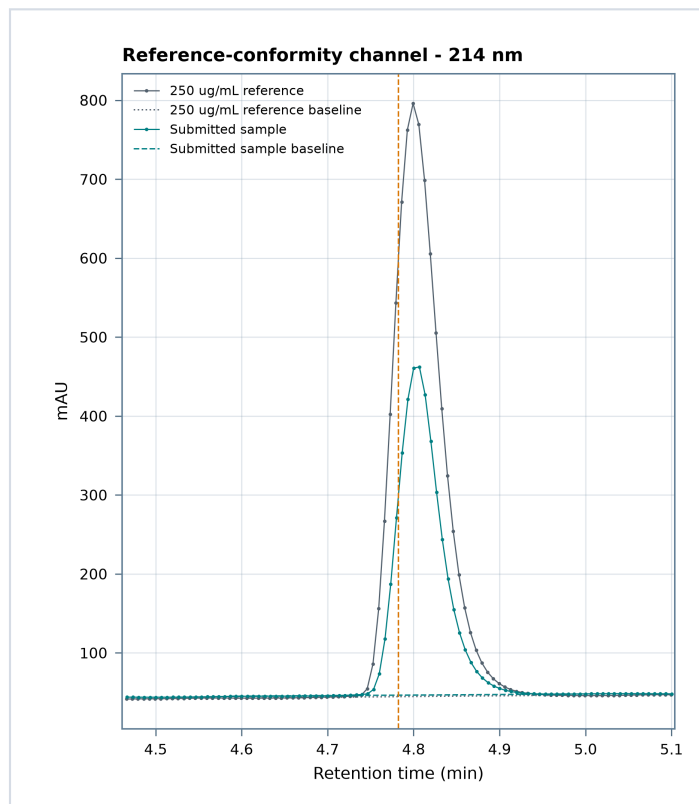
ug/mL	Area	Recovery
31.25	0.52361	101.35%
62.5	1.10123	99.60%
125	2.27976	99.71%
250	4.65132	100.08%

Area = 0.01888943C - 0.07462584
Unweighted OLS | R2 0.9999856
Sample area 2.2310 = 122.06 ug/mL x 2 mL x 50 / 1000 = 12.21 mg

No standard of this peptide in the run: amount read by peak area

Curve: CJC no DAC (4.78 min); identity not compared

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.



CJC-1295 DAC

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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 ±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 0.999817 and minimum within-peak cosine is 0.999994, supporting spectral uniformity. The run holds no standard of this peptide, so the similarity is to a related reference and is not an identity match.
Scope: the UV comparison supports method-specific reference alignment. It does not establish definitive molecular identity, absolute purity, safety, or efficacy.	

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
4.807	24.4910	98.550	Main peak	-	Counted
2.780	0.1528	0.618	related variant	0.989	Counted
3.060	0.1277	0.517	impurity	0.970	Counted
1.793	0.0777	0.315	impurity	0.978	Counted
0.540	0.2824	-	non peptide	0.876	Excluded
Reporting limit 0.130% of total area counted peaks 3 injections 1					
Area percent assumes every peak absorbs at 214 nm like the main peak. UV cannot establish identity; a related peak is matched by spectrum, not by mass.					
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.	Identity and composition No definitive identity or absolute purity unless separately supported.
Calculated results Area-percent purity, concentration, projected amount, and calibration trace.	Safety and performance No conclusion on safety, sterility, efficacy, fitness for purpose, or suitability.
Method context Retention time (standards' range or ±5%) and UV match (standards' lowest or 0.999).	Regulatory status No regulatory compliance finding, approval, or authorization to manufacture, sell, or use.
This analytical record does not authorize or endorse manufacture, sale, marketing, distribution, or use of the material.	