



CJC/lpamorelin

Results and chromatograms

Sample 6026_0056 | Client report SYNA-CJCI-10-090826

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/lpamorelin	Method: HPLC-DAD, by component	Run date: Sep 23, 2026
	Sample ID: 6026_0056	Components: 2 listed, 2 found	First acquired: 19:00:13 UTC
	Client ID: SYNA-CJCI-10-090826	Injections: 1 method(s)	Last acquired: 19:00:13 UTC
	Label claim: 10 mg	Identity: All confirmed	Run time: per method / acquisition

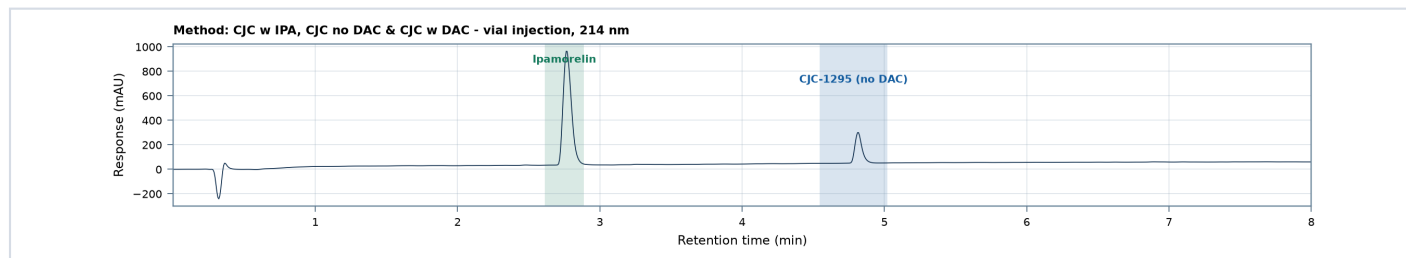
RESULTS AT A GLANCE

AMOUNT FOUND 13.09 mg SUM OF AMOUNTS STATED BELOW	COMPONENTS FOUND 2 of 2 EACH AT ITS OWN PEAK	LOWEST COMPONENT PURITY 94.98% 214 NM AREA PERCENT	LABEL CLAIM 10 mg SUBMITTED INFORMATION
--	---	---	--

COMPONENTS

Component	RT (min)	Located by	Amount	Label share	Content	Purity	Identity	Pages
CJC-1295 (no DAC)	4.78	its standard	6.98 mg	Not recorded	-	94.98%	Supported	2-4
Ipamorelin	2.75	combined standard	6.10 mg	Not recorded	-	98.61%	Supported	5-7

CHROMATOGRAMS



Each component is measured in the vial's injection on the method that runs it, at its own retention time, against that method's same-run standards, with the preparation the laboratory lists for it. The amount found is the sum of the components measured.

CJC-1295 (no DAC): purity from a single injection; the blend's composition is not recorded, so no content is stated.

Ipamorelin: purity from a single injection; the standards' own purity disagrees with the sample's; the blend's composition is not recorded, so no content is stated.

* Amounts marked * are read against a related standard or outside the calibration range.



CJC-1295 (no DAC) in CJC/Ipamorelin

Results and chromatograms

Sample 6026_0056 | Client report SYNA-CJCI-10-090826

Laboratory Analysis: LAB-CA-01

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

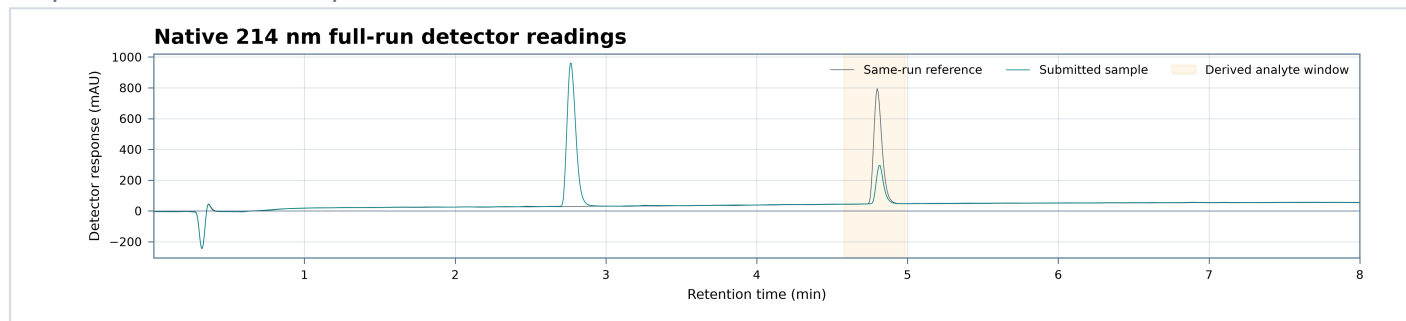
VIAL PHOTOGRAPH	SAMPLE INFORMATION	ANALYSIS	RUN DETAILS
	Peptide: CJC-1295 (no DAC) in CJC/Ipamo... Sample ID: 6026_0056 Client ID: SYNA-CJCI-10-090826 Label claim: Not recorded	Method: HPLC-DAD Channels: 214 / 280 nm + spectra Area metric: 214 nm blank-excluded Comparison: Reference aligned	Run date: Sep 23, 2026 First acquired: 15:23:01 UTC Last acquired: 19:00:13 UTC Run time: 8.00 min / acquisition

RESULTS AT A GLANCE

PROJECTED AMOUNT 6.98 mg† BASED ON SAMPLE PREPARATION	HPLC PURITY 94.98% 214 NM AREA PERCENT, LIMIT 0.050%	LABEL AMOUNT Not recorded SUBMITTED INFORMATION	REFERENCE ALIGNMENT Observed RETENTION TIME + UV PROFILE**
--	---	--	---

CHROMATOGRAM

Complete run - 214 nm detector response



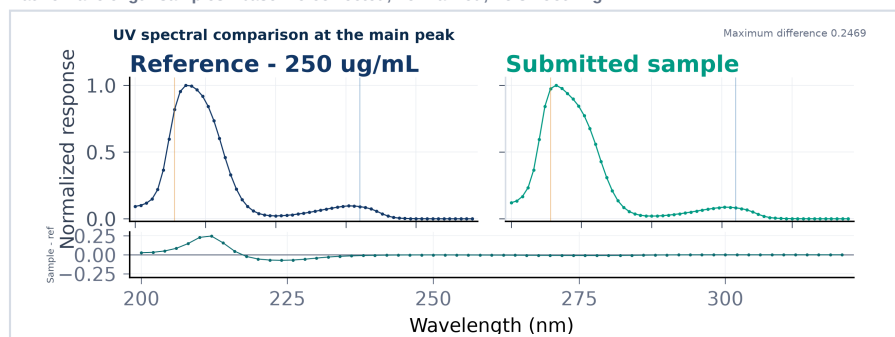
HPLC PURITY (214 NM)

Peptide + related 94.98% Main peak and UV-matched forms	Main peak area % 94.98% 1 injection(s)	Reporting limit 0.050% Smallest reportable peak	UV match 0.99981 Sample vs. reference
--	---	--	--

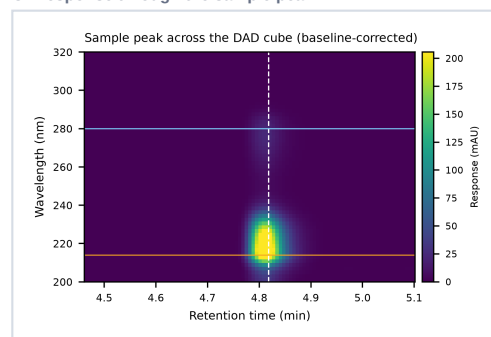
Purity is the main peak's share of the total integrated peak area at 214 nm, measured from the native detector readings. Peaks below 0.050% of total area cannot be resolved from this run's baseline and are not counted. This result rests on a single injection; no duplicate was run.

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 0.050% 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.

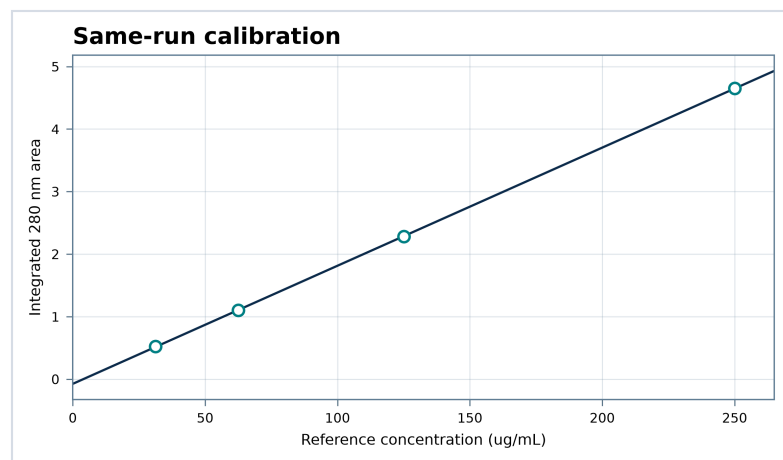


CJC-1295 (no DAC) in CJC/lpamorelin

Sample 6026_0056 | Client report SYNA-CJCI-10-090826

Reference comparison and calculation

CONCENTRATION CALIBRATION - 280 NM

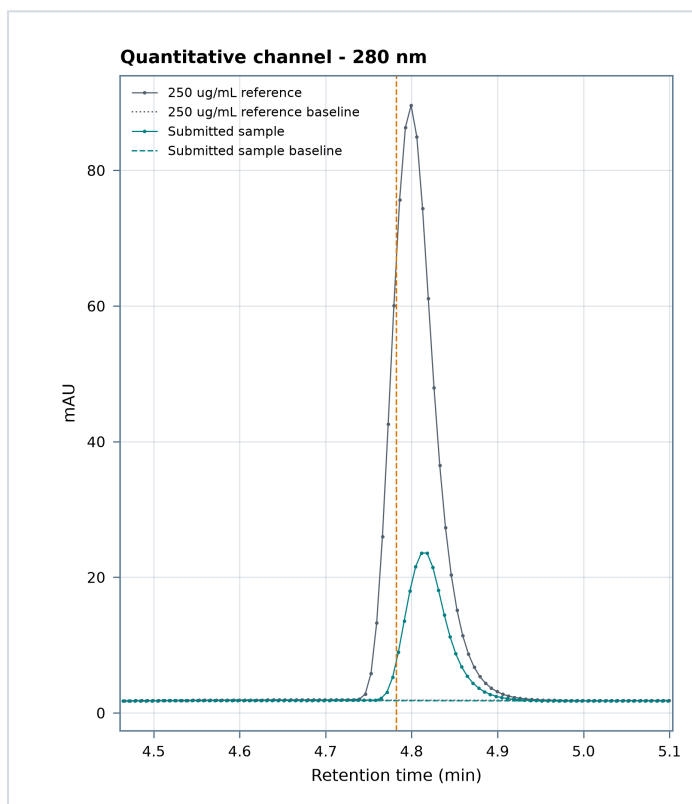
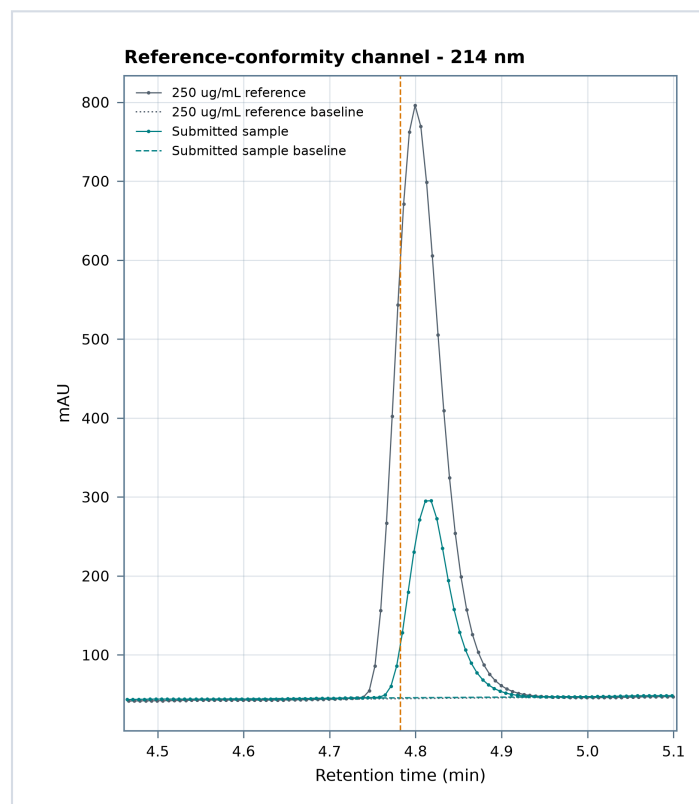


ug/mL	Area	Recovery
31.25	0.52361	101.35%
62.5	1.10123	99.60%
125	2.27976	99.71%
250	4.65132	100.08%

Area = 0.01888943C - 0.07462584
Unweighted OLS | R2 0.9999856
Sample area 1.2446 = 69.84 ug/mL x 2 mL x 50 / 1000 = 6.98 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.



CJC-1295 (no DAC) in CJC/lpamorelin

Sample 6026_0056 | Client report SYNA-CJCI-10-090826

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.
-----------	--	-----------	---	-----------	---

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 0.999809 and minimum within-peak cosine is 0.999998, supporting close reference alignment and spectral uniformity.
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
4.818	14.3548	94.979	Main peak	-	Counted
1.603	0.4475	2.978	impurity	0.973	Counted
2.330	0.1177	0.783	impurity	0.975	Counted
2.483	0.0819	0.545	impurity	0.972	Counted
6.619	0.0579	0.385	impurity	0.976	Counted
3.851	0.0494	0.329	impurity	0.942	Counted
2.770	61.9683	-	blend component	0.985	Excluded
Reporting limit 0.050% of total area counted peaks 5 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.					

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 $\pm 5\%$) 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.	



Ipamorelin in CJC/Ipamorelin

Results and chromatograms

Sample 6026_0056 | Client report SYNA-CJCI-10-090826

Laboratory Analysis: LAB-CA-01

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

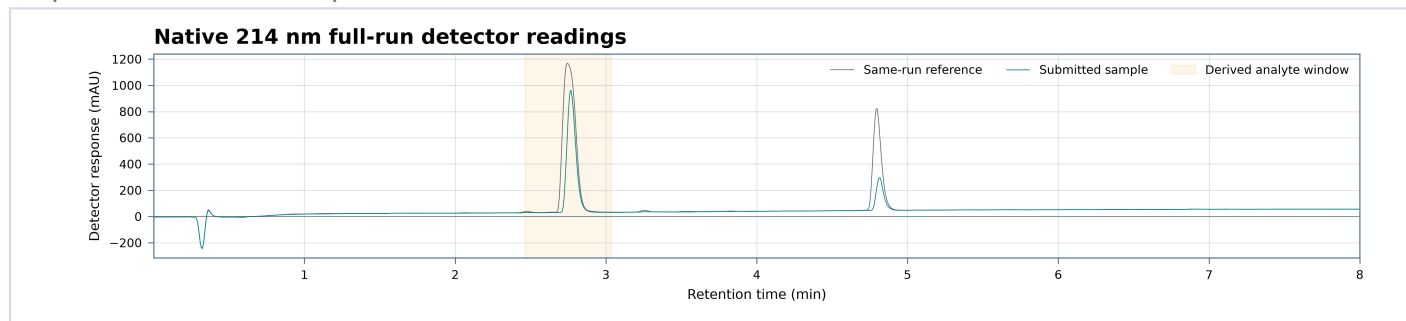
VIAL PHOTOGRAPH	SAMPLE INFORMATION	ANALYSIS	RUN DETAILS
	Peptide: Ipamorelin in CJC/Ipamorelin Sample ID: 6026_0056 Client ID: SYNA-CJCI-10-090826 Label claim: Not recorded	Method: HPLC-DAD Channels: 214 / 280 nm + spectra Area metric: 214 nm blank-excluded Comparison: Reference aligned	Run date: Sep 23, 2026 First acquired: 13:46:23 UTC Last acquired: 19:00:13 UTC Run time: 8.00 min / acquisition

RESULTS AT A GLANCE

PROJECTED AMOUNT 6.10 mg† BASED ON SAMPLE PREPARATION	HPLC PURITY 98.61% 214 NM AREA PERCENT, LIMIT 0.050%	LABEL AMOUNT Not recorded SUBMITTED INFORMATION	REFERENCE ALIGNMENT Observed RETENTION TIME + UV PROFILE**
--	---	--	---

CHROMATOGRAM

Complete run - 214 nm detector response



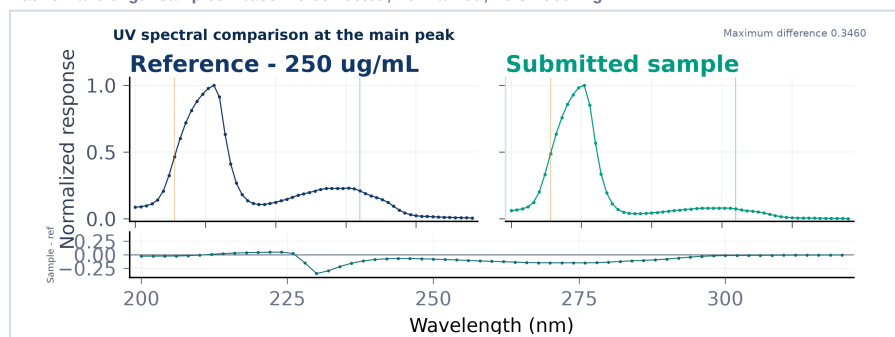
HPLC PURITY (214 NM)

Peptide + related 98.61% Main peak and UV-matched forms	Main peak area % 98.61% 1 injection(s)	Reporting limit 0.050% Smallest reportable peak	UV match 0.99511 Sample vs. reference
--	---	--	--

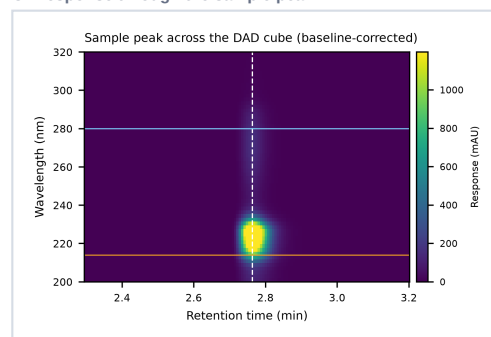
Purity is the main peak's share of the total integrated peak area at 214 nm, measured from the native detector readings. Peaks below 0.050% of total area cannot be resolved from this run's baseline and are not counted. This result rests on a single injection; no duplicate was run.

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 0.050% 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.

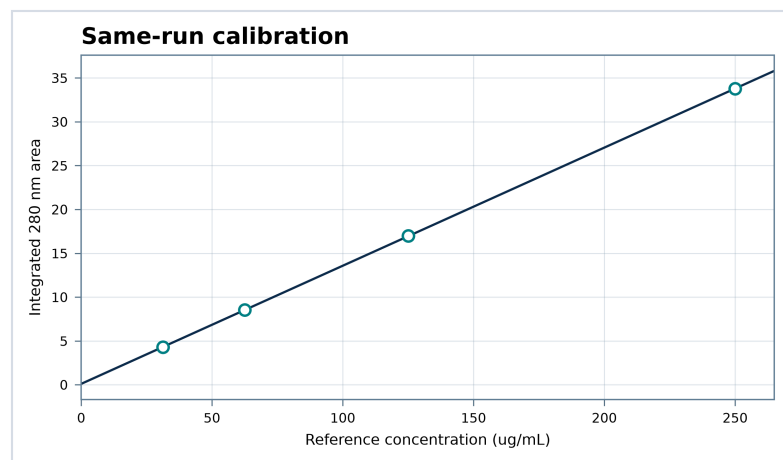


Ipamorelin in CJC/Ipamorelin

Sample 6026_0056 | Client report SYNA-CJCI-10-090826

Reference comparison and calculation

CONCENTRATION CALIBRATION - 280 NM



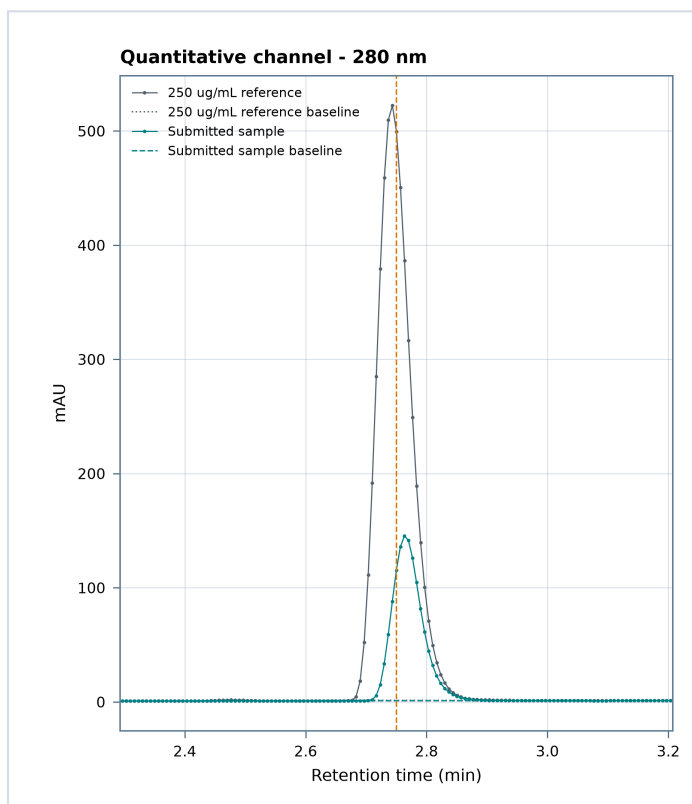
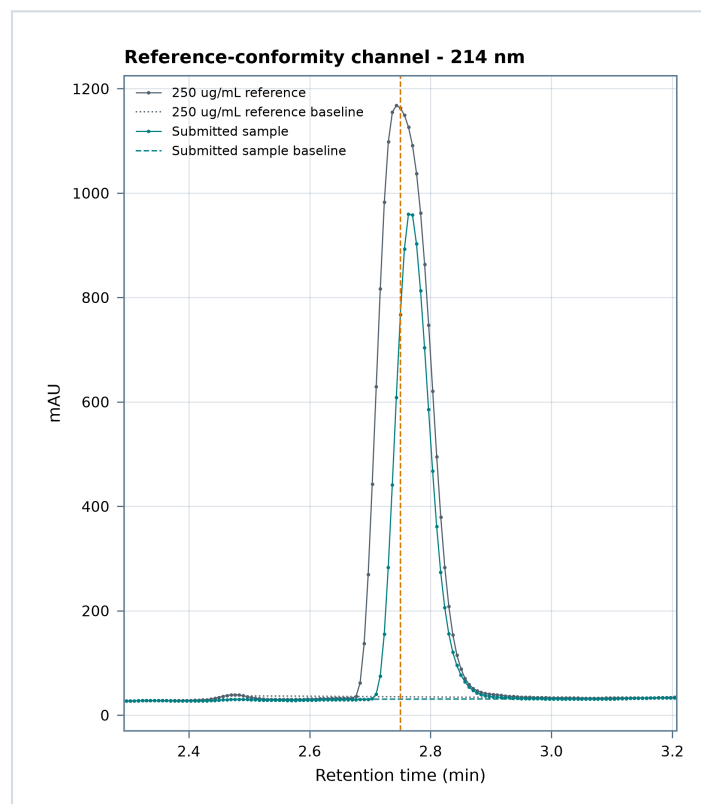
ug/mL	Area	Recovery
31.25	4.27853	99.16%
62.5	8.52766	100.03%
125	17.00487	100.34%
250	33.76648	99.93%

Area = 0.13475548C + 0.10272802
Unweighted OLS | R2 0.9999898
Sample area 8.3272 = 61.03 ug/mL x 2 mL x 50 / 1000 = 6.10 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.



Ipamorelin in CJC/Ipamorelin

Sample 6026_0056 | Client report SYNA-CJCI-10-090826

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.
-----------	--	-----------	---	-----------	---

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 0.995106 and minimum within-peak cosine is 0.998710, supporting close reference alignment and spectral uniformity.
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
2.763	62.6723	98.612	Main peak	-	Counted
1.603	0.3436	0.545	impurity	0.948	Counted
1.229	0.2408	0.382	impurity	0.945	Counted
2.330	0.1136	0.180	impurity	0.946	Counted
3.851	0.1135	0.180	impurity	0.905	Counted
6.619	0.0625	0.099	impurity	0.946	Counted
and 2 further peak(s), each smaller than those listed; the complete peak table is in the evidence record					
Reporting limit 0.050% of total area counted peaks 5 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.					

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 $\pm 5\%$) 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.	