



5-Amino-1MQ

Results and chromatograms

Sample vial 4, injection 1 | Client report CBI-5AM-10-091826

Laboratory Analysis: LAB-CA-02

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

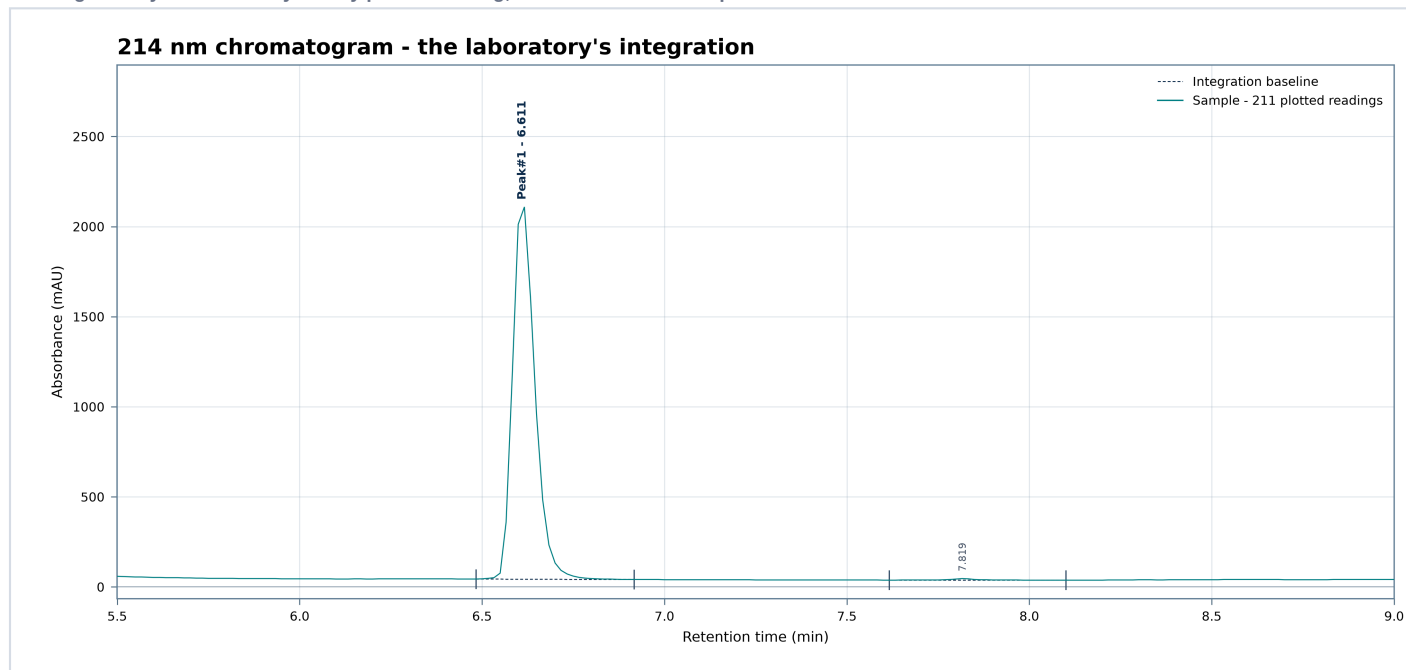
VIAL PHOTOGRAPH	SAMPLE INFORMATION	ANALYSIS	RUN DETAILS
	Peptide: 5-Amino-1MQ	Method: HPLC-UV	Run date: Sep 23, 2026
	Client ID: CBI-5AM-10-091826	Channel: 214 nm	Acquired: 18:14:39 UTC
	Label claim: 10 mg	Integration: Laboratory	Run time: 15 min
	Injection: 10 uL, 214 nm	Identity: Lab-assigned peak	Instrument: HPLC 02

RESULTS AT A GLANCE

PROJECTED AMOUNT 10.91 mg† BASED ON SAMPLE PREPARATION	HPLC PURITY 99.53% 214 NM AREA PERCENT*	CONTENT VS. LABEL 109.1% 10.91 MG OF 10 MG CLAIMED	IDENTITY Assigned LAB-ASSIGNED PEAK**
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CHROMATOGRAM

As integrated by the laboratory - every plotted reading, with its baselines and peak marks



HPLC PURITY (214 NM)

Main peak area % 99.53% Laboratory integration	Integrated peaks 2 Counted in the total	Smallest peak integrated 0.47% Of total area	Recovered chromatogram ±0.30% Area vs. laboratory table
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Purity is the laboratory-assigned peak's share of the total peak area the laboratory integrated at 214 nm. The smallest peak it integrated was 0.47% of the total; the laboratory does not state a reporting threshold, so peaks below the ones it integrated are not counted. Integrating the chromatogram recovered from the laboratory's report reproduces its main-peak area to within 0.30%. This result rests on a single injection.

The chromatogram is recovered point for point from the laboratory's report: 211 plotted readings from 5.50 to 9.00 min, joined as drawn; nothing is smoothed or resampled.

* HPLC purity is the laboratory-assigned peak's share of all peak area the laboratory integrated; every peak is itemised on page 3.

** Identity: the laboratory's processing method names the analyte's peak. The sample ran on a different method from the reference standard, so retention times are not compared.

LAB ID: D

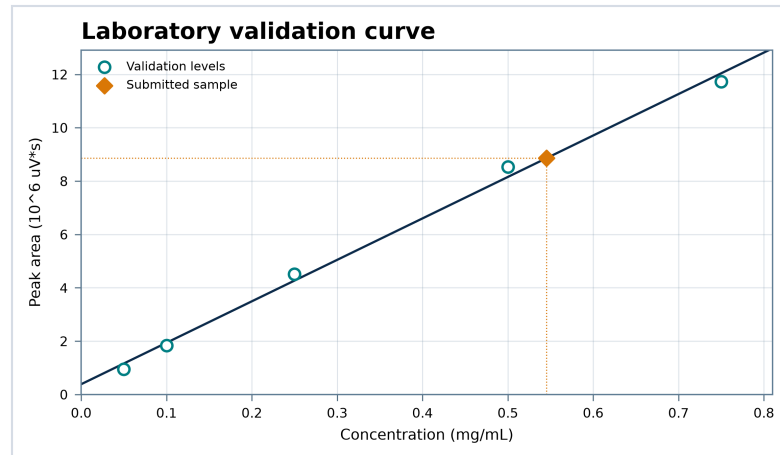


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Reference comparison and calculation

CONCENTRATION CALIBRATION - 214 NM (LABORATORY VALIDATION CURVE)



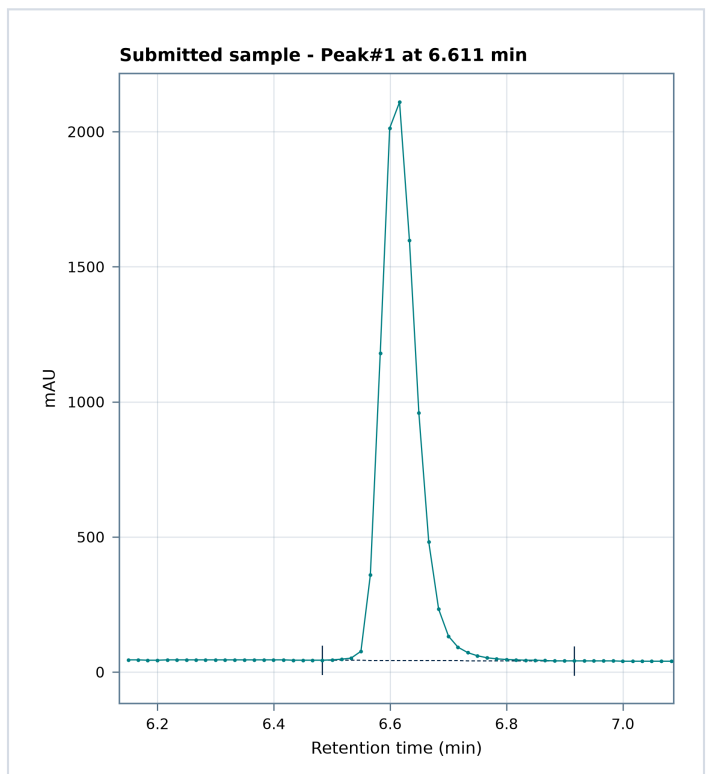
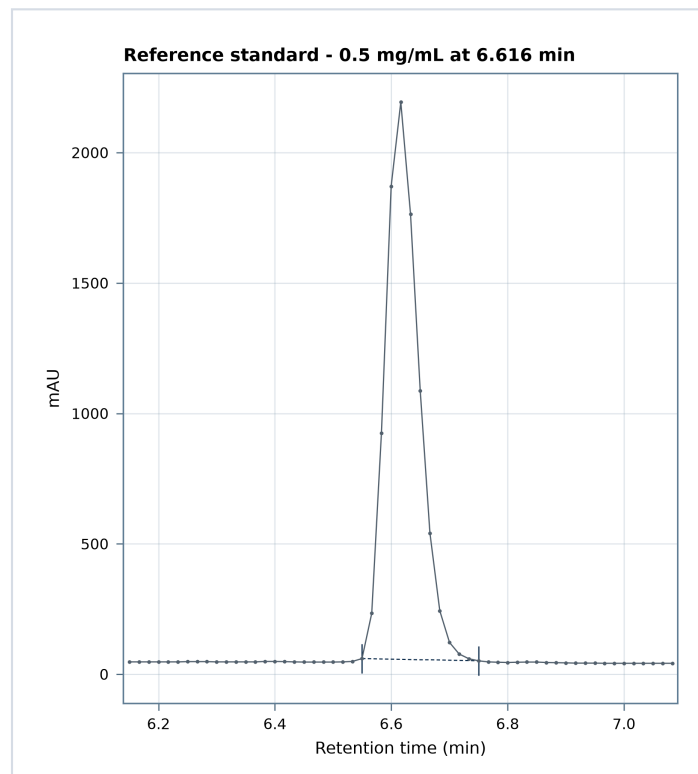
mg/mL	Area (uV*s)	Recovery
0.75	11,734,306	97.37%
0.5	8,536,695	104.90%
0.25	4,509,488	106.14%
0.1	1,842,556	93.72%
0.05	947,191	72.21%

Area = 15,539,027 C + 386,168
Unweighted OLS through 5 levels | R2 0.99577
Sample area 8,859,650 = 0.5453 mg/mL
x 2 mL x 10 = 10.91 mg

† Prepared at the laboratory's working 0.5 mg/mL of label claim

Validated 2026-08-21 | HPLC 02 | injector RSD 0.52% (n=6) | reference 99.1% pure

MAIN PEAK COMPARED WITH THE LABORATORY'S REFERENCE STANDARD



Native plotted readings with the laboratory's integration baselines and peak marks; nothing is smoothed or resampled.

Reference standard injected 2026-08-20 during the laboratory's validation of this curve on another method than the sample's (LC02_Peptide15min_AD_Jul15_26), so retention times differ.



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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 curve, comparison, and peaks behind it.

01	Recovered chromatogram The laboratory's trace, read back point for point from its report.	02	Integrated peak table Every peak the laboratory integrated, and which one is the analyte.	03	Validation curve Converts the peak area to a concentration for this analyte.
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WHAT THE RECOVERED CHROMATOGRAM ADDS

How the chromatogram on this report was obtained	
How it was recovered The laboratory's data system draws the chromatogram in its report as vector data. Every vertex it drew was read back - 211 readings - and both axes were calibrated from the report's own tick marks. Integrating the recovered trace over the laboratory's baselines and peak marks reproduces the area in its peak table to within 0.30%.	What it can and cannot show It shows every peak, shoulder and baseline the laboratory integrated, at the resolution the laboratory printed. It carries a single wavelength and no UV spectrum, so it cannot reveal a co-eluting compound the way diode-array data can.
Scope: the recovered chromatogram reproduces the laboratory's report. It does not re-measure the sample.	

HOW THE PURITY RESULT WAS MEASURED

214 nm area percent, from the laboratory's own integration							
The laboratory integrated each peak to its own baseline and named the analyte's peak in its processing method. Purity is that peak's share of the total integrated area; the shares below are recomputed from the areas, and each peak's area is checked against the recovered chromatogram.							
Purity (%) = assigned peak area / total integrated peak area x 100							
Peak	RT (min)	Area (uV*s)	Area %	Tailing	Plates	Role	Recovered
1	6.611	8,859,650	99.53	1.26	50,386	Peak#1 - main	8,885,909 (+0.30%)
2	7.819	41,655	0.47	1.21	69,559	impurity	-
Integrated peaks 2 smallest 0.47% of total injections 1							
Area percent assumes every peak absorbs at 214 nm like the main peak; the analyte's peak is the one the laboratory's method names. Recovered areas are compared for the analyte's peaks of 1% or more.							

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 The laboratory's chromatogram, its integration, and its validation curve.	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 Laboratory peak assignment; retention against its reference standard where methods match.	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.	