



Understanding the CJC-1295 (with DAC) Certificate of Analysis

When reviewing the independent laboratory certificate for our CJC-1295 (with DAC) batch, you may notice that the Mass Spectrometry (MS) is marked as "✓ **Confirmed**", whilst a Quality Control note mentions a mass tolerance error. Here is a clear explanation of these results:

- **Exceptional Purity:** The HPLC analysis confirms this batch is exceptionally pure at 99%, showing a single, clean peak.
- **The Automated Lab Note:** The testing equipment expected a molecular weight of 3647.3 Da. The detected weight was slightly lighter at 3646.5 Da. Because the lab's software was looking for the standard "Free Acid" form, this slight difference triggered an automated mass tolerance note.
- **Why it is "Confirmed":** The laboratory ultimately passed and confirmed the peptide's identity because this specific weight difference (~0.8 Daltons) perfectly matches the **Amidated** version of CJC-1295 (with DAC).
- **The Benefit:** Amidation is a deliberate, premium manufacturing process used to significantly increase a peptide's stability and shelf-life.

In short, the laboratory has verified that this is a highly pure (99%), amidated, and highly stable batch of CJC-1295 (with DAC).



PeptideVerify | Certificate of Analysis

INDEPENDENT THIRD-PARTY PEPTIDE VERIFICATION

PREMIUM

Report PV-F21A6E-SZKC-CB

| | | | |
|--|---------------------------------|--|---------------------------------------|
| CERTIFICATE ID PV-F21A6E-SZKC-CB | ISSUE DATE 09/03/2026 | BATCH/LOT LOT-2026-JW | CUSTOMER Amino Peptides Ltd |
| SAMPLE DESCRIPTION CJC-1295 (with DAC) | EXPECTED MW 3647.3 Da | ANALYSIS DATE 05/03/2026 14:10 | INSTRUMENT LCMS Line 1 |

VERIFICATION SUMMARY

Purity (HPLC)

99%

Single peak (PPI)

Mass Match

Expected MW: **3647.3 Da**

Detected MW: **3646.5 Da ✓**

MW calculated from m/z 912.65 [M+4H]⁴⁺

ANALYTICAL RESULTS

VERIFIED PURITY

99%

HPLC Analysis - Single Peak

MAIN PEAK

#1 @ 6.347 min

TOTAL PEAKS

1

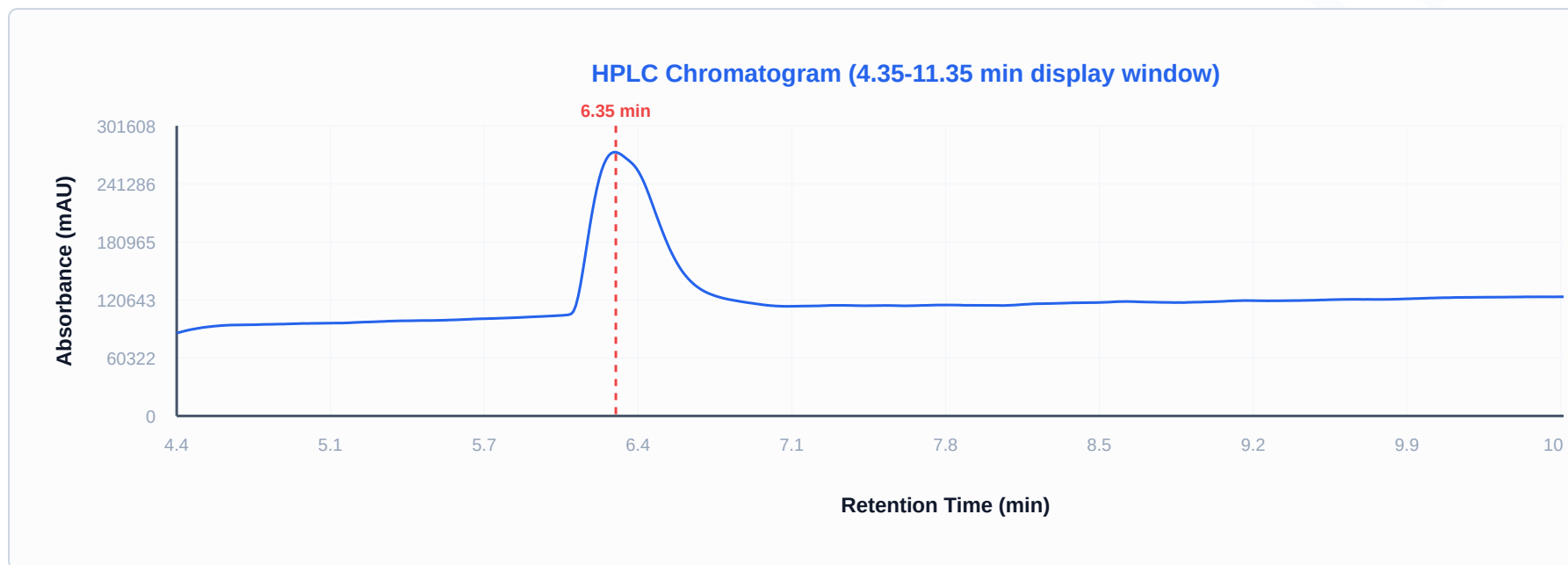
MS VERIFICATION

✓ Confirmed

DETECTION

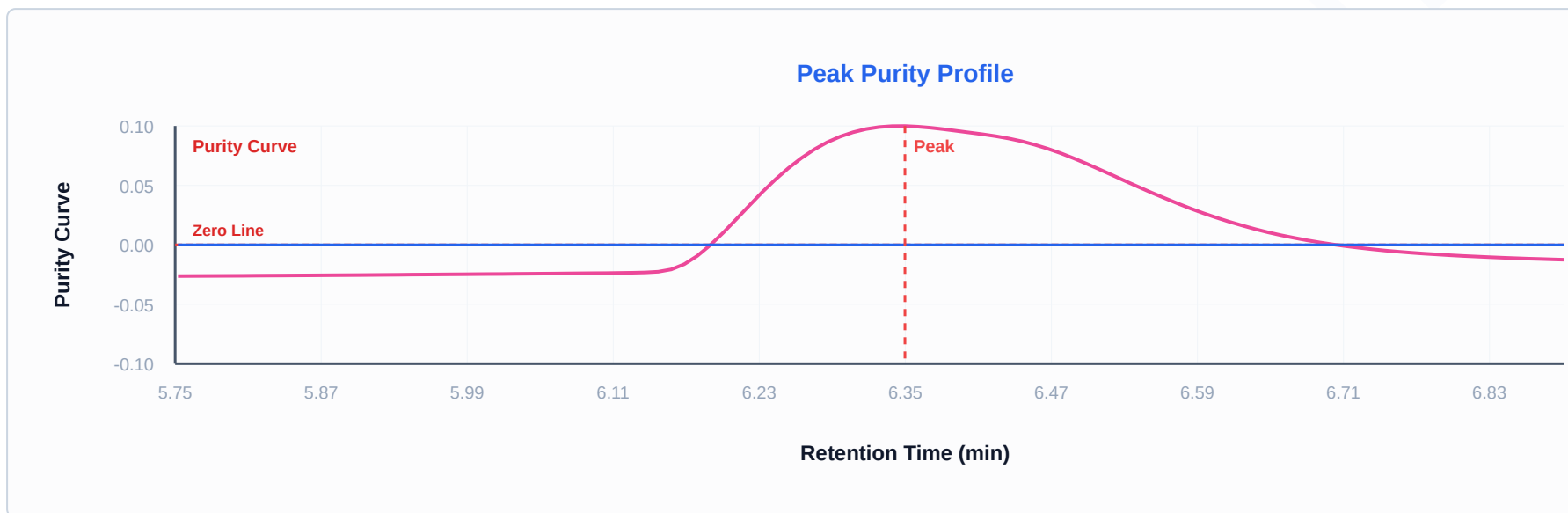
215 nm (± 4)

HPLC CHROMATOGRAM



Detection: 215 nm (± 4 nm)

PEAK PURITY PROFILE



PEAK INTEGRATION DATA

| PEAK # | RETENTION (MIN) | AREA | HEIGHT | AREA % | WIDTH (MIN) | RESOLUTION (RS) | TAILING | PLATES (N) |
|--------|-----------------|-----------|--------|--------|-------------|-----------------|---------|------------|
| 1 | 6.347 | 3,605,182 | N/A | 99.00% | — | — | 1.97 | 2,300 |

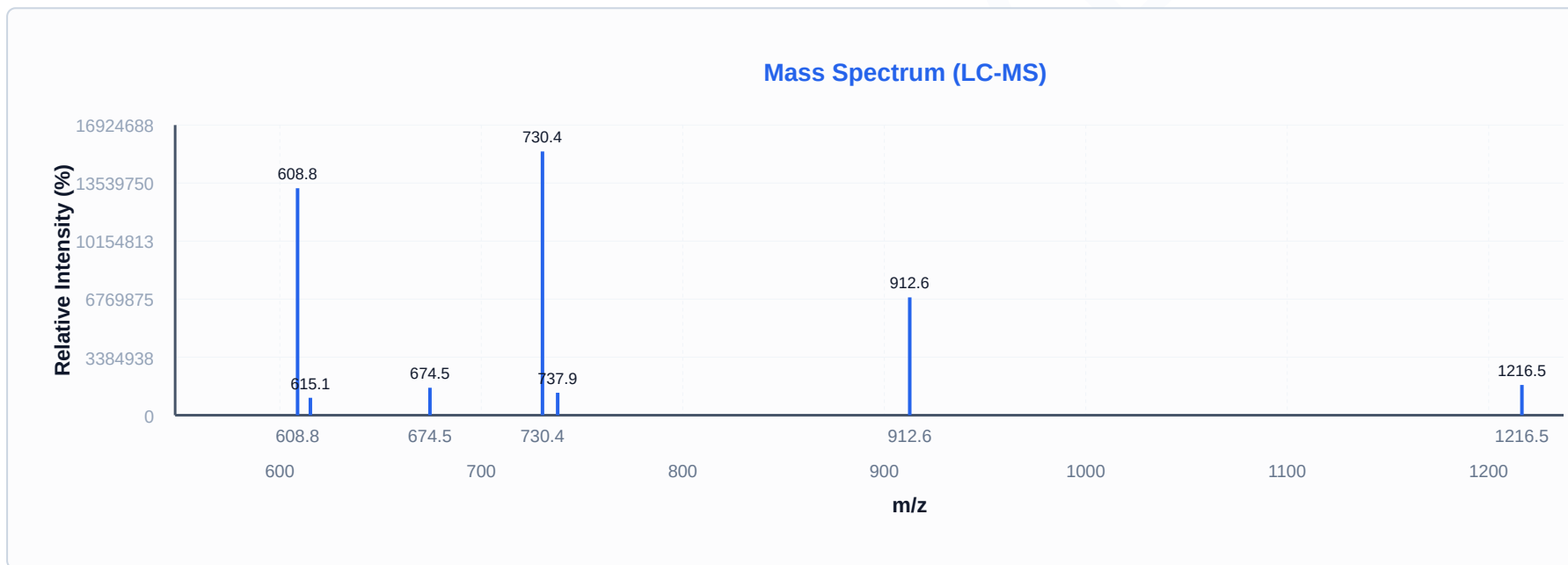
Resolution color-coded: Green ($R_s \geq 2.0$ or N/A for single peak), Yellow ($R_s \geq 1.0$), Red ($R_s < 1.0$). Values calculated from instrument data or derived from peak widths (USP <621>).

MASS SPECTROMETRY ANALYSIS (ESI+)

| | | | |
|--|--|---|---------------------------------------|
| EXPECTED MW 3647.3 Da | DETECTED MW 3646.5 Da | MASS MATCH ✓ | BASE PEAK m/z 730.35 |
|--|--|---|---------------------------------------|

Predicted charge states:

- z=2+ → m/z 1824.65
- z=3+ → m/z 1216.77
- z=4+ → m/z 912.83
- z=5+ → m/z 730.46
- z=6+ → m/z 608.89



| DETECTED M/Z | ASSIGNMENT | INTENSITY | RELATIVE % |
|--------------|----------------------|------------|------------|
| 730.35 | — | 15,386,080 | 100.0% |
| 608.80 | — | 13,240,135 | 86.1% |
| 912.65 | [M+4H] ⁴⁺ | 6,873,264 | 44.7% |
| 1216.50 | [M+3H] ³⁺ | 1,765,251 | 11.5% |

| DETECTED M/Z | ASSIGNMENT | INTENSITY | RELATIVE % |
|--------------|------------|-----------|------------|
| 674.50 | — | 1,601,024 | 10.4% |
| 737.90 | — | 1,310,441 | 8.5% |
| 615.15 | — | 1,015,492 | 6.6% |

QUALITY CONTROL NOTES

Mass error -214 ppm exceeds typical tolerance. Review recommended.

METHOD INFORMATION

| | |
|---------------|----------------------|
| Instrument | LCMS Line 1 |
| Software | LabSolutions 5.97 |
| Analyst | System Administrator |
| Method | HPLC-MS |
| Detection | 215 nm (± 4 nm) |
| MS Ionization | Electrospray (ESI+) |

ANALYST NOTES

Lab Observations: Form: Lyophilized powder Color: White Condition: As expected - no issues

Purity Calculation Method: Purity is calculated in accordance with laboratory practice. Where a single chromatographic peak is present, purity is derived from the Peak Purity Index (PPI) — a measure of spectral homogeneity. Where multiple peaks are detected, purity is calculated as the chromatographic area percentage of the main peak multiplied by its Peak Purity Index (Area% ×

PPI).



 **CERTIFICATE VERIFICATION**

INDEPENDENTLY VERIFIED

peptideverify.co.uk/verify/PV-F21A6E-SZKC-CB

Scan QR code or visit the URL above to verify this certificate's authenticity and view detailed analysis data.

IMPORTANT NOTE

Sample Composition reflects UV-detectable compounds only. Non-UV excipients (mannitol, sugars, salts) are not measured by this method.

PeptideVerify — Independent Third-Party Peptide Verification

Analysis performed under controlled laboratory conditions by GLP-compliant analytical facilities.

Certificate ID: PV-F21A6E-SZKC-CB | Batch/Lot: LOT-2026-JW | Customer: Amino Peptides Ltd | Generated: 09 Mar 2026, 22:56