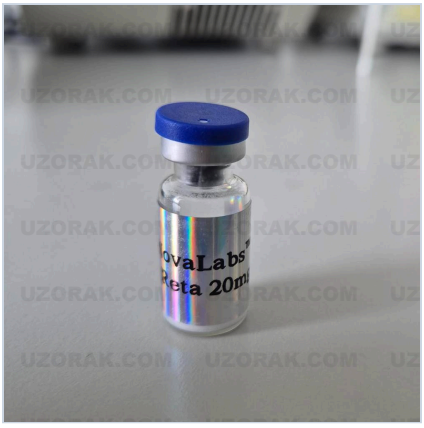
ANALYSIS REPORT YVS-RTM

Report Generated
APR 4, 2026

Analysis	**Standard Mass / Purity** (HPLC-UV) **+ Advanced HRLC-MS Package**
Client	NovaLabs



Sample

Retatrutide 20mg

BATCH April 2026

SELLER NovaLabs

RESULTS

MASS / PURITY RESULTS (HPLC-UV)

PURITY
99.73%

AMOUNT
21.43 mg

Meets or exceeds label

HRLC-MS RESULTS ADVANCED

MS PURITY
99.42%

IMPURITIES

Variants / Degradation	VERY LOW
Process Impurities	NOT DETECTED
Contaminants	NOT DETECTED

PEPTIDE

Identity	CONFIRMED
Sequence	MATCH
Fingerprint	MATCH

COMMENT
Excellent sample. No contamination, High purity under UHPLC-MS.

ANALYSIS CONDUCTED
3 APR 2026
ZAGREB, CROATIA (EU)

Alex Mihaljcic
DIRECTOR

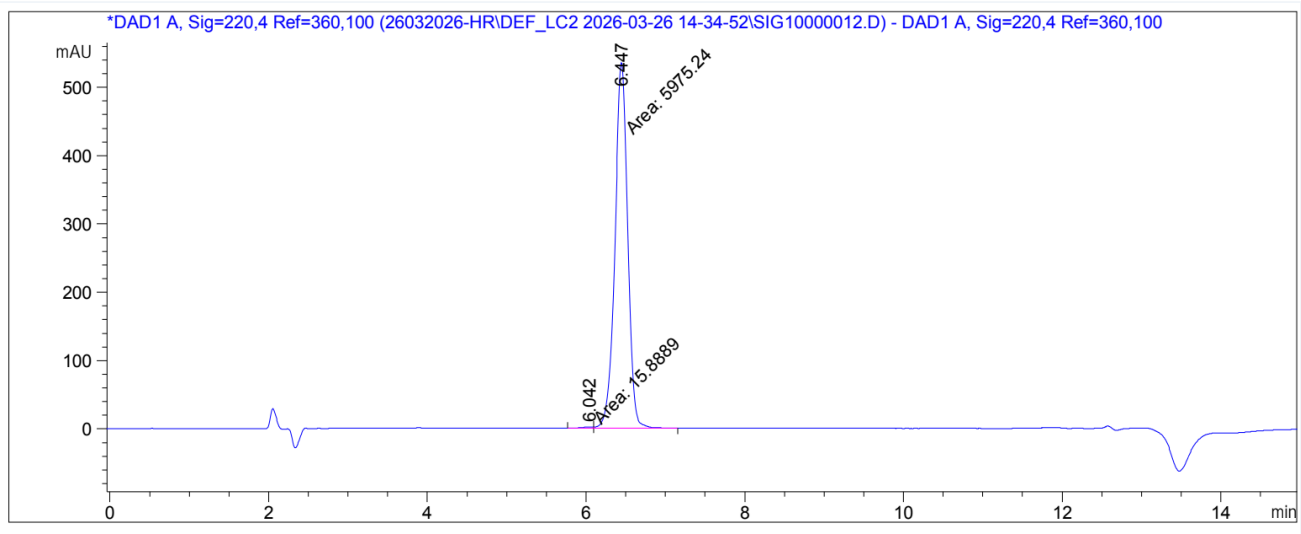
MASS / PURITY RESULTS HPLC-UV

PURITY

UV Diode-Array (DAD) at 220 nm (Reference 360 nm)

99.73%

PURITY CHROMATOGRAM — DAD1 A, SIG=220,4 REF=360,100



Purity determined by area percent method using UV diode-array detection at 220 nm. The principal peak area is expressed as a percentage of total integrated peak area.

PEPTIDE AMOUNT

UV Quantification — External Standard Method

21.43 mg

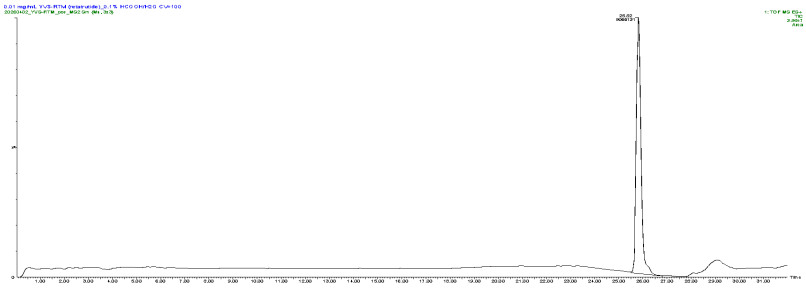
INDIVIDUAL MEASUREMENTS

TEST	MEASURED	VS LABEL
1	**21.6 mg**	108.2%
2	**21.3 mg**	106.6%
3	**21.3 mg**	106.7%
Average	**21.43 mg**	**107.1%**

Peptide content determined by comparing sample UV peak area (220 nm) against a certified reference standard of known concentration. Three independent preparations ensure measurement reproducibility (RSD: 0.8%).

REFERENCE STANDARD

SAMPLE CHROMATOGRAM



IMPURITIES HRMS ADVANCED

MS ANALYSIS SUMMARY

MS PURITY

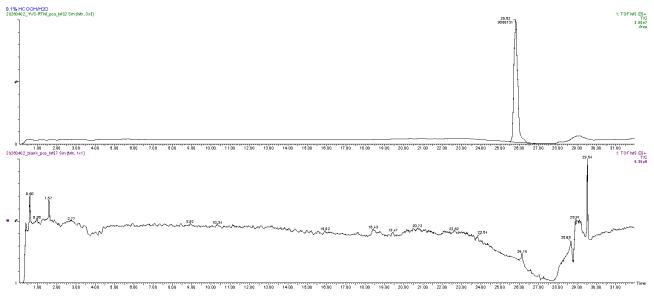
99.42%

TOTAL IMPURITIES

0.58%

BASELINE SYSTEM CONFIRMATION

Sample vs Blank



VARIANTS / DEGRADATION

IMPURITY	MASS SHIFT	%	RISK LEVEL
Mono-Oxidation	+16.00 Da	0.02%	VERY LOW
Di-Oxidation	+31.99 Da	0.01%	VERY LOW
Methylation	+14.02 Da	0.01%	VERY LOW
Deamidation	+0.98 Da	–	NOT DETECTED
Acetylation	+42.01 Da	0.49%	VERY LOW
Hydrolysis	−18.01 Da	–	NOT DETECTED
Cleavage	−17.03 Da	–	NOT DETECTED

PROCESS IMPURITIES

IMPURITY	MASS SHIFT	%	RISK LEVEL
TFA (salts / solvents)	+113.99 Da	–	NOT DETECTED
Fmoc (protecting group)	+222.07 Da	–	NOT DETECTED
tBu (protecting group)	+56.06 Da	–	NOT DETECTED

OTHERS

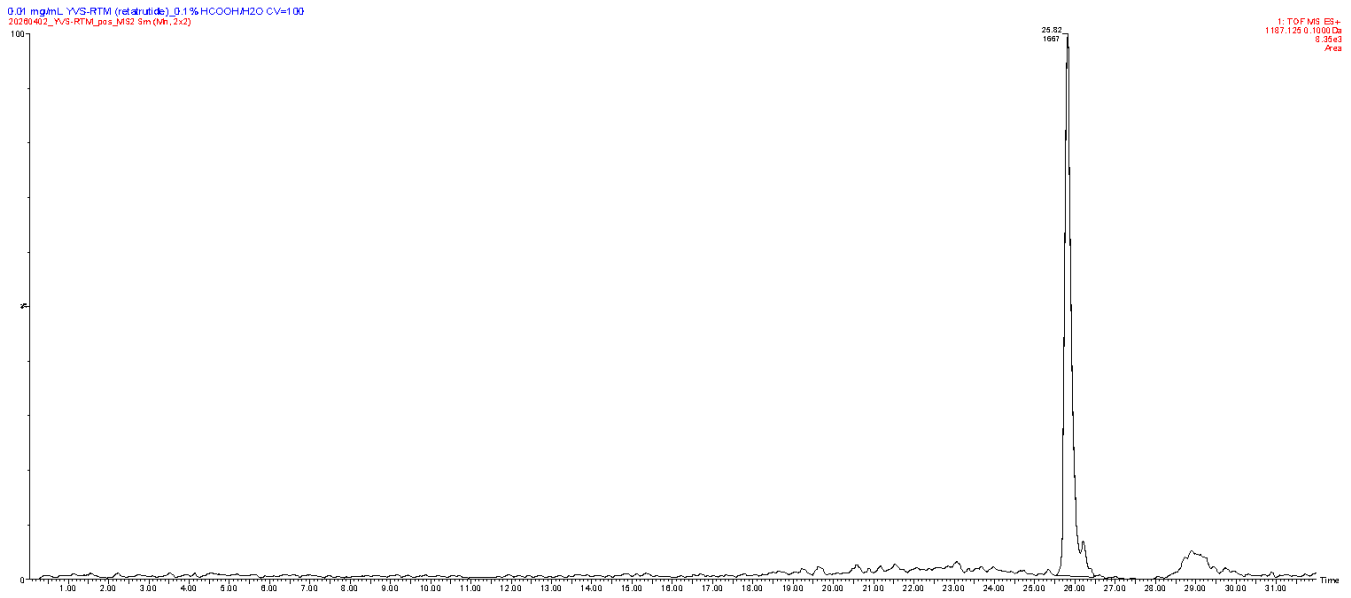
IMPURITY	MASS SHIFT	%	RISK LEVEL
F-met	+27.99 Da	0.06%	VERY LOW

CONTAMINANTS

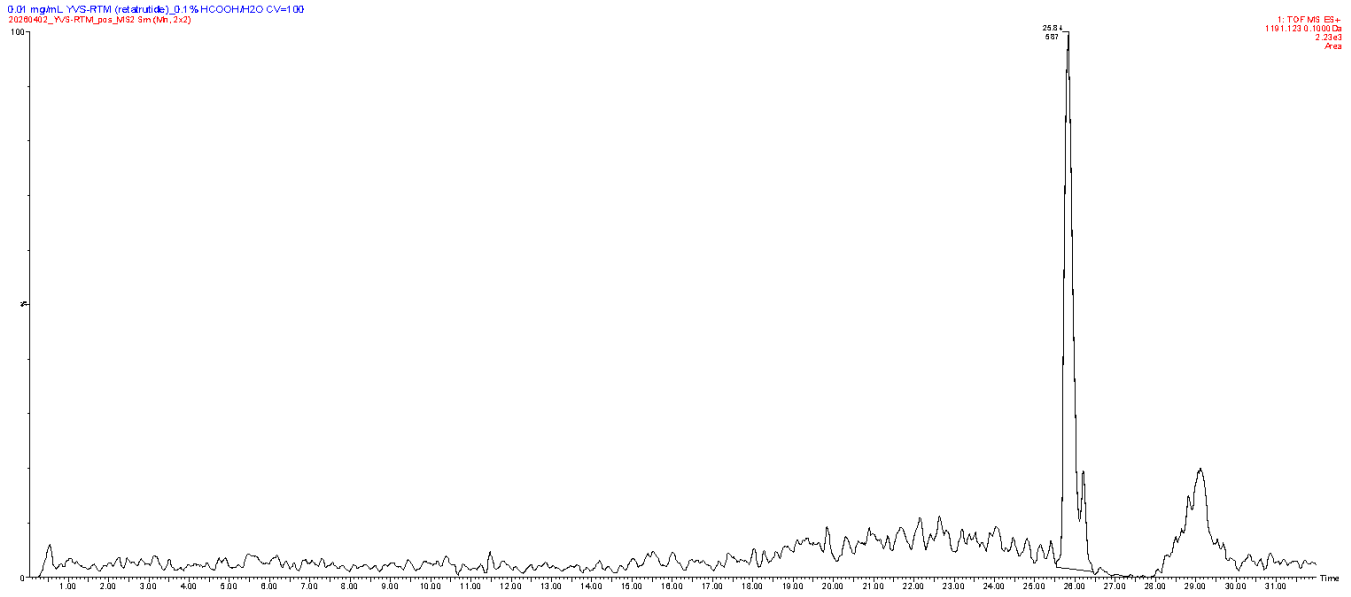
IMPURITY	RISK LEVEL
None	

High-resolution LC-MS analysis, ESI+ ionization, mass accuracy <5 ppm. Impurities identified by exact mass shift from principal peptide peak.

Mono-Oxidation 0.02%



Di-Oxidation 0.01%



Extracted ion chromatograms (EIC) for each detected impurity. Mass accuracy <5 ppm. Chromatographic separation confirms impurity identity by retention time and exact mass.

Acetylation 0.49%

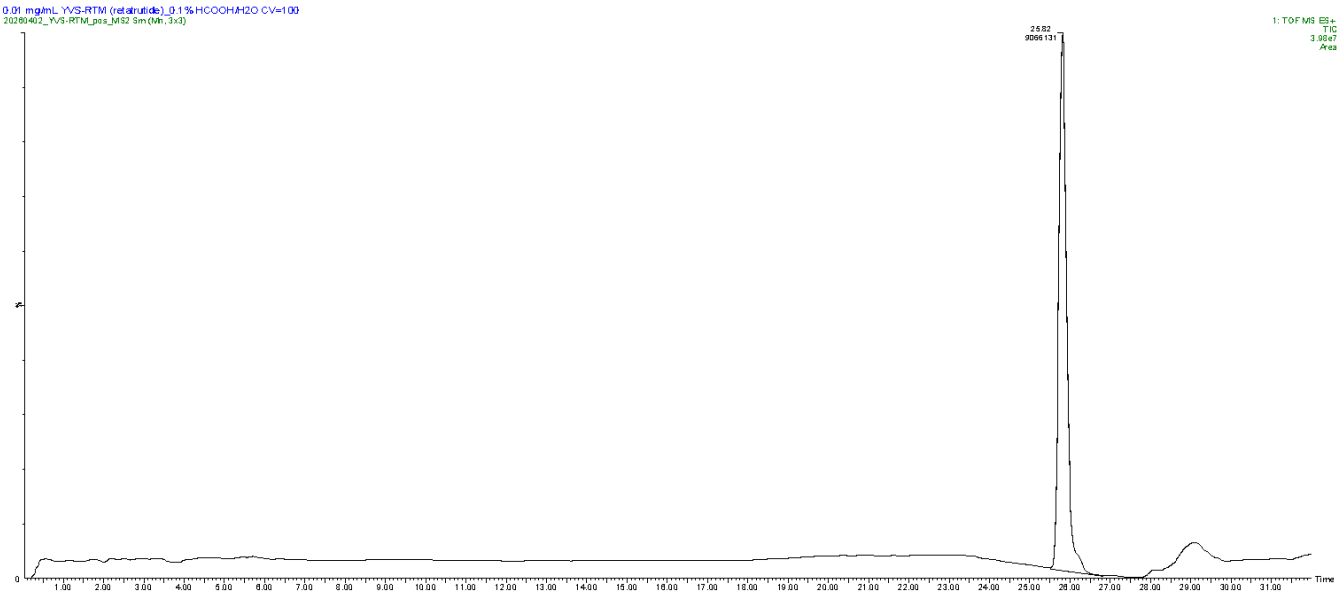
F-met 0.06%

Extracted ion chromatograms (EIC) for each detected impurity. Mass accuracy <5 ppm. Chromatographic separation confirms impurity identity by retention time and exact mass.

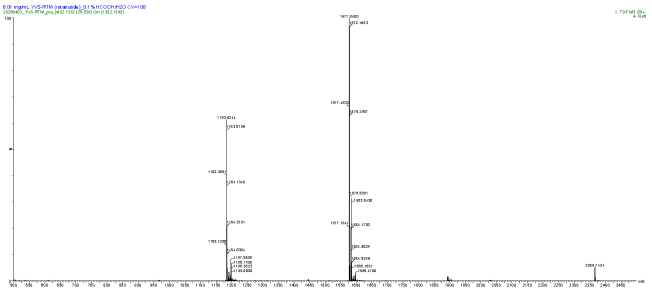
MS IDENTITY CONFIRMATION	CONFIRMED
Theoretical Mass	4729.4790 Da
Measured Mass	4729.4834 Da
Mass Error	0.9 ppm
Acceptance Limit	≤ 5 ppm
Molecular Formula	C221H342N46O68

MASS SPECTRA

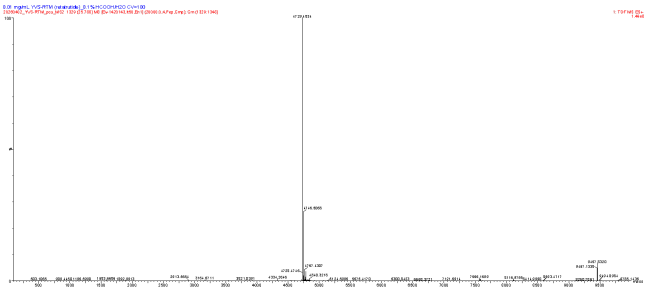
MS1 — FULL SCAN MASS SPECTRUM



MS2 — CHARGE ENVELOPE



MS3 — FRAGMENTATION

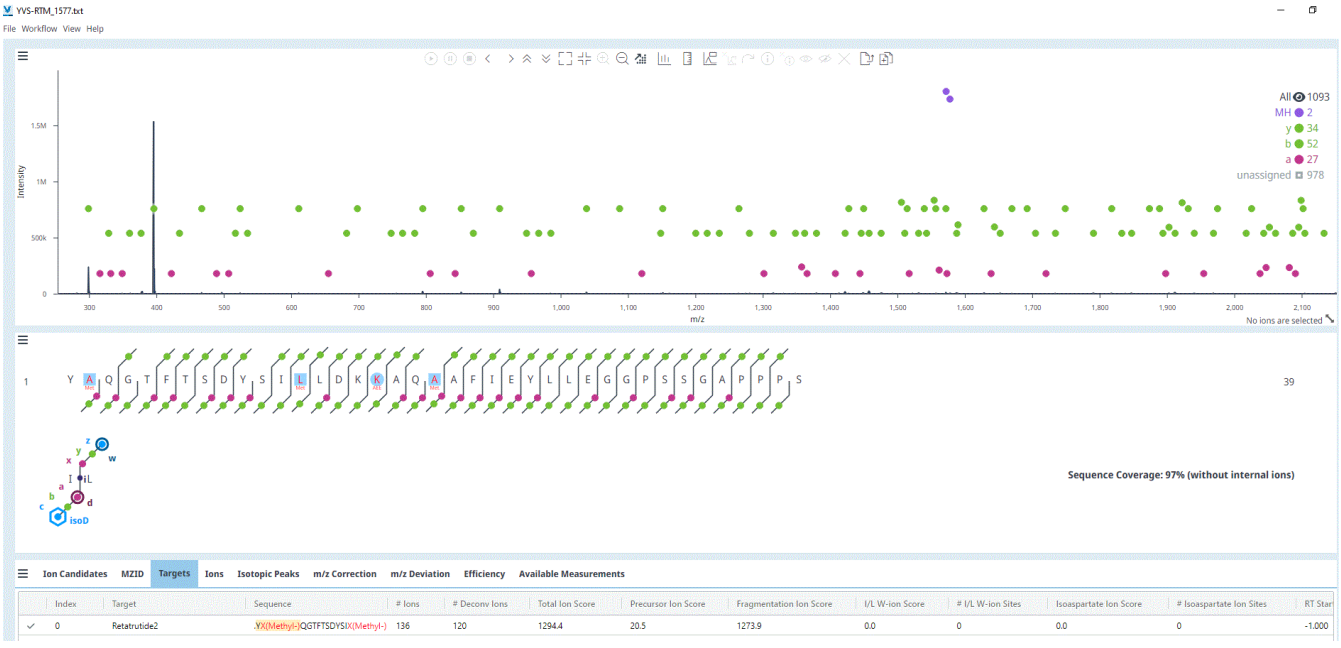


Identity confirmed by accurate mass measurement (ESI-QTOF). Molecular ion detected, charge states deconvoluted, and monoisotopic mass compared to theoretical within ≤5 ppm acceptance criteria.

SEQUENCE ANALYSIS

MATCH

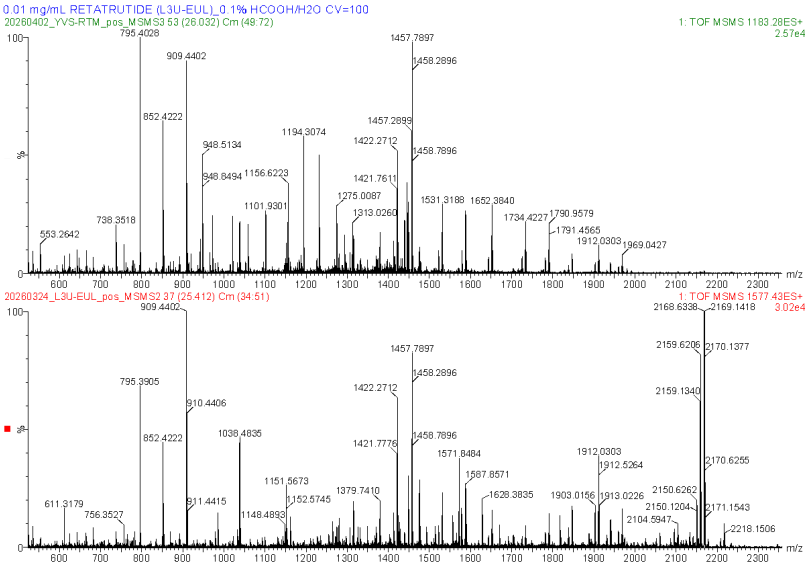
Sequence Coverage	97%
Acceptance Limit	≥ 80%
Amino Acid Match	100%



TANDEM MS FINGERPRINT

MATCH

Fingerprint Similarity	99.6%
Acceptance Limit	≥ 99.0%



Sequence verified by MS/MS fragmentation analysis (≥80% coverage required). Structural integrity assessed by tandem MS fingerprint comparison against certified reference standard (≥99.0% similarity required).

REFERENCE

EQUIPMENT & METHODOLOGY

YVS-RTM

ANALYSIS METHODS

TEST	METHOD	DESCRIPTION
Purity	HPLC–UV	UV Diode-Array (DAD) at 220 nm, Reference 360 nm
Mass (Peptide Amount)	HPLC–UV	Peak area integration, external standard, 3 replicates
Identity	HR–MS	Accurate mass ESI-QTOF, ≤5 ppm acceptance
Sequence	MS/MS	Fragmentation analysis, ≥80% coverage required
Fingerprint	Tandem MS	Spectral comparison vs certified reference standard
Impurities	HR–MS	Exact mass shift screening, ESI+ ionization

INSTRUMENTATION

Mass Spectrometer	Agilent 6545 QTOF
UHPLC System	Agilent 1290 Infinity II
Ionization	Electrospray (ESI+)
Mass Accuracy	< 2 ppm
Software	MassHunter Qualitative Analysis

STANDARDS & COMPLIANCE

Reference Standards

USP-grade certified reference standards used for all quantitative comparisons. Reference materials sourced from accredited suppliers and handled per manufacturer specifications.

Quality System

Analysis performed under controlled laboratory conditions. Instrument calibration verified prior to each analytical run. System suitability checks confirm method performance.

Data Integrity

All raw data electronically archived. Results processed using validated software workflows. Each report includes a unique verification ID for authenticity confirmation.

REFERENCE

THRESHOLDS & CRITERIA

YVS-RTM

VARIANT / DEGRADATION RISK LEVELS

IMPURITY	ND	VERY LOW	LOW	MEDIUM	HIGH
Mono-Oxidation +16 Da	= 0	< 0.5%	< 1.5%	< 3.0%	**≥ 3.0%**
Di-Oxidation +32 Da	= 0	< 0.3%	< 0.8%	< 2.0%	**≥ 2.0%**
Methylation +14 Da	= 0	< 0.3%	< 0.5%	< 1.5%	**≥ 1.5%**
Deamidation +1 Da	= 0	< 0.3%	< 0.5%	< 2.0%	**≥ 2.0%**
Hydrolysis −18 Da	= 0	—	< 0.2%	< 1.0%	**≥ 1.0%**
Cleavage −17 Da	= 0	—	< 0.2%	< 1.0%	**≥ 1.0%**

PROCESS IMPURITY THRESHOLDS

IMPURITY	ND	LOW	MEDIUM	DETECTED
TFA +114 Da	= 0	< 0.1%	< 0.5%	**≥ 0.5%**
Fmoc +222 Da	< 0.05%	—	—	**≥ 0.05%**
tBu +56 Da	< 0.05%	—	—	**≥ 0.05%**

ACCEPTANCE CRITERIA

TEST	PASS	FAIL
Identity (Mass Error)	≤ 5 ppm	> 5 ppm
Sequence Coverage	≥ 80%	< 80%
Fingerprint Similarity	≥ 99.0%	< 99.0%
Detection Limit	0.01%	—
Mass Accuracy	< 2 ppm	—

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