

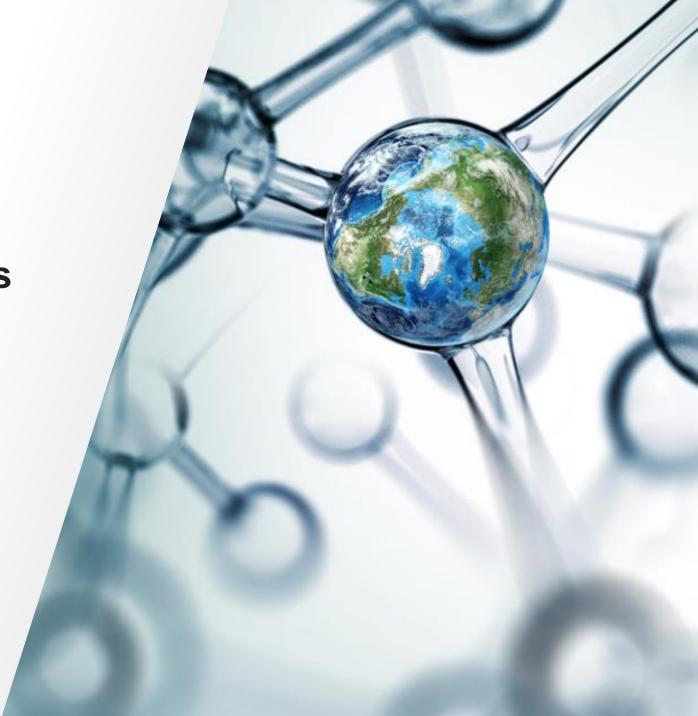
Nitrosamine impurities analysis using Thermo Scientific™ Orbitrap Exploris™ 120 MS

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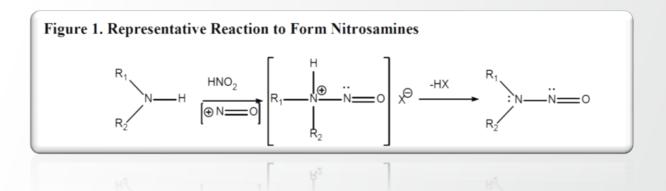


Liquid chromatography high resolution mass spectrometry (LC-HRMS) method for NAs detection and quantitation

- Nitrosamines (NAs) in APIs and drug products
 - Classified as genotoxic impurities, proven as probable human carcinogen
 - Detected elevated levels of NDMA and other impurities in several drug products, announced several recalls
 - US FDA published validated GC/LC-MS/MS and GC/LC-HRAM methods, and interim acceptable limits for several NAs
 - US FDA recently released guidance for industry to 1) conduct risk assessments on approved or marketed drugs and pending applications, and 2) implement control strategy to reduce and prevent formation of NAs in all API and drug products

Goals

- 1 single LC-HRMS method for detection and quantitation of 9 NAs
- High selectivity and sensitivity
- Robustness and reproducibility
- Compliant software for data collection and processing





- Thermo Scientific™
 Vanquish™ LC and Acclaim
 Polar Advantage II column,
 2.1 x 100mm, 2.2µm
 - Excellent retention time and injection reproducibility
 - Good peak shape for target NAs
 - No carryover for target NAs, except NDBA



- Thermo Scientific[™]
 Orbitrap Exploris[™] 120 MS
 - Max 120K resolution at m/z 200
 - Sub ppm mass accuracy with EASY-IC
 - LLOQ ≤ 0.017 ppm for target NAs, in APCI mode for both neat and excipient standards



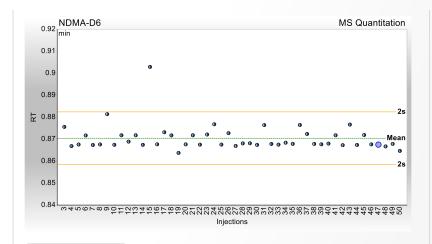
- Thermo Scientific[™]
 Chromeleon[™] CDS 7.2.10
 - Single platform for MS and chromatography
 - Fully integrated with instrument control, data collection, processing and reporting
 - 21 CFR Part 11 compliant ready with full instrument and data audit trail

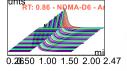


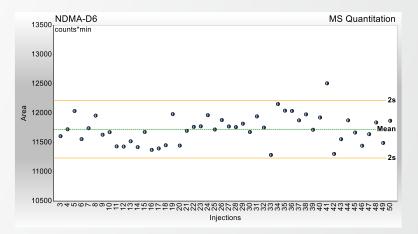
Robust and reproducible injections



- Vanquish LC and Acclaim
 Polar Advantage II column,
 2.1 x 100mm, 2.2µm
 - Excellent retention time and injection reproducibility
 - Good peak shape across all NAs
 - No carryover for target NAs, except NDBA







N = 50, Neat, APCI

Average RT: 0.87 min

RT reproducibility: 0.69%

Average Peak area: 11700

Peak area reproducibility: 2.1%



Good separation with minimal carryover for excipient standards























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 - Minimum carryover for target NAs, except NDBA

Carryover, Excipient, APCI



















XIC of NAs at 50ng/ml, Excipient, APCI

High sensitivity, could achieve LLOQ ≤ 0.017 ppm for target NAs in both neat and excipient matrix



Orbitrap Exploris 120 MS

- Max 120K resolution at m/z 200
- Sub ppm mass accuracy with Thermo Scientific™ EASY-IC™ ion source
- LLOQ ≤ 0.017 ppm for target
 NAs, in APCI mode for both neat
 and excipient standards

	Matrix	LOD (ng/ml)	LLOQ (ng/ml)	PPM*	Linearity
NDMA	Neat	0.2	0.2	0.0068	0.2 – 50
	Excipient	0.2	0.2	0.0068	0.2 - 50
NMEA	Neat	0.2	0.2	0.0068	0.2 - 50
INIVIEA	Excipient	0.2	0.2	0.0068	0.2 - 50
NPYR	Neat	0.1	0.2	0.0068	0.2 - 50
NEIK	Excipient	0.2	0.2	0.0068	0.2 - 50
NDEA	Neat	0.1	0.1	0.0034	0.1 - 50
NDEA	Excipient	0.1	0.1	0.0034	0.1 - 50
NDID	Neat	0.1	0.1	0.0034	0.1 - 50
NPIP	Excipient	0.2	0.2	0.0034	0.1 - 50
NEIPA	Neat	0.5	0.5	0.017	0.5 - 50
	Excipient	0.5	0.5	0.017	0.5 - 50
NDIPA	Neat	0.1	0.1	0.0034	0.1 - 50
	Excipient	0.1	0.1	0.0034	0.1 - 50
NDPA	Neat	0.1	0.1	0.0034	0.1 - 50
	Excipient	0.1	0.1	0.0034	0.1 - 50
NDBA	Neat	0.1	0.5	0.017	0.5 - 50
	Excipient	0.1	0.5	0.017	0.5 – 50

^{*} PPM is calculated based on 30mg/ml of drug substance and product extract



Accuracy and precision for excipient standards at 0.017 ppm



Orbitrap Exploris 120 MS

- Max 120K resolution at m/z 200
- Sub ppm mass accuracy with EASY-IC ion source
- LLOQ ≤ 0.017 ppm for target
 NAs, in APCI mode for both neat
 and excipient standards

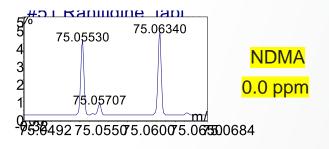
	% Diff	Precision
NDMA	0.7	7.0
NMEA	-5.2	4.2
NPYR	-7.7	2.7
NDEA	-5.4	3.4
NPIP	-2.2	5.1
NEIPA	-6.7	7.8
NDIPA	-3.8	2.9
NDPA	-4.3	3.0
NDBA	-3.3	4.1

^{*} Accuracy and precision based on 5 replicate injections, data were processed by linear with offset, 1/x weighting



High selectivity can be achieved with maximum 120K resolution and sub ppm mass accuracy





DMF, 13C isotope

0.0 ppm

Orbitrap Exploris 120 MS

- Max 120K resolution at m/z 200
- Sub ppm mass accuracy with EASY-IC ion source
- LLOQ ≤ 0.017 ppm for target
 NAs, in APCI mode for both neat
 and excipient standards

DMF, 15N isotope 0.4 ppm

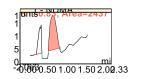
N,N-dimethylformamide (DMF)15N isotope and NDMA are baseline resolved at 120K resolution

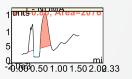




High selectivity can be achieved with maximum 120K resolution and sub ppm mass accuracy







Orbitrap Exploris 120 MS

- Max 120K resolution at m/z 200
- Sub ppm mass accuracy with EASY-IC ion source
- LLOQ ≤ 0.017 ppm for target
 NAs, in APCI mode for both neat
 and excipient standards

NDMA with 25ppm mass tolerance

Measured: 2.8 ng/ml or 0.093ppm

NDMA with 3ppm mass tolerance

Measured: 2.4 ng/ml or 0.08ppm

With inadequate mass tolerance setting, the presence of DMF in Ranitidine tablet extract could cause overestimation of NDMA

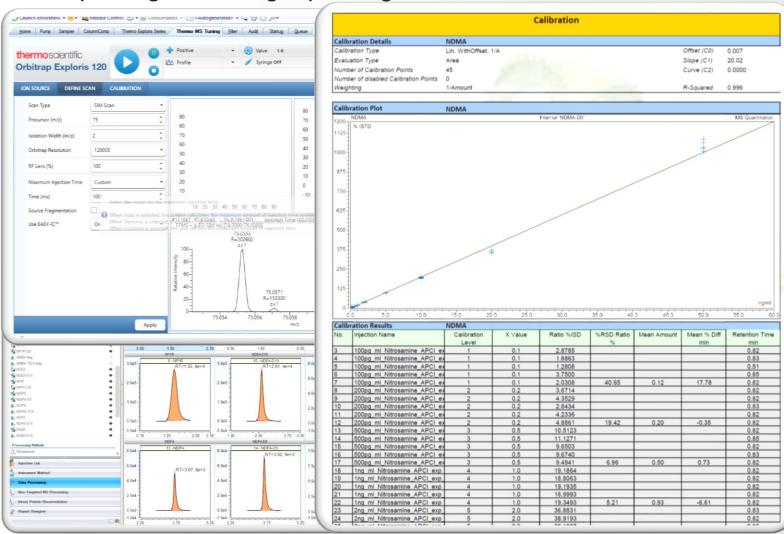


Instrument control, data processing, and reporting all in single package



Chromeleon CDS 7.2.10

- Single platform for MS and chromatography
- Fully integrated with instrument control, data collection, processing and reporting
- 21 CFR Part 11 compliant ready with full instrument and data audit trail





A complete Thermo Fisher Scientific solution

- A robust and reproducible LC-HRMS method for detection and quantitation of 9 NAs in Ranitidine tablet
- High resolution, minimum of 60K, is required to separate DMF isotope interferent peaks to avoid potential isobaric interferences
- Adequate mass accuracy and tolerance setting is essential for reliable and accurate quantitation of NDMA in presence of co-eluting DMF in tablet extract
- Achieved superior sensitivity with APCI, LLOQ ≤ 0.017 ppm for all NAs tested (FDA proposed limit is 0.03 ppm)
- Demonstrated the use of Chromeleon 7.2.10 compliant ready CDS software for instrument control, data acquisition, processing, and reporting

Backup slides



- Recovery and reproducibility of NAs from extraction process
- LLOQ of NAs using HESI mode for both neat and excipient standards
- LLOQ comparison between HESI vs APCI mode for target NAs



NAs recovery and reproducibility from the extraction process

Crush tablet and extract with methanol to give target concentration of 30mg/ml API

Mechanical shaker for 40 minutes

Centrifuge @ 4500 rpm for 15 minutes

Filter the supernatant with 0.22 µm PVDF filter

	2ng/	ml	5ng/ml		
	% Recovery	% RSD	% Recovery	% RSD	
NDMA	99	8.4	97	7.2	
NMEA	93	9.0	97	4.5	
NPYR	101	3.6	99	5.3	
NMBA	94	13.3	94	8.8	
NDEA	95	3.0	97	3.4	
NPIP	97	1.6	96	3.8	
NEIPA	116	10.5	98	7.0	
NDIPA	95	3.1	100	2.9	
NDPA	105	2.2	104	1.8	
NDBA	101	2.8	100	4.9	

High sensitivity, LLOQ ≤ 0.068 ppm for target NAs for both neat and excipient standards, HESI mode



Orbitrap Exploris 120 MS

- Max 120K resolution at m/z 200
- Sub ppm mass accuracy with EASY-IC ion source
- LLOQ ≤ 0.068 ppm for target
 NAs in HESI mode for both neat
 and excipient standards

We can achieve less than 0.017 ppm for all NAs except NEIPA in HESI mode

	Matrix	LOD (ng/ml)	LLOQ (ng/ml)	PPM*	Linearity
NDMA	Neat	0.2	0.5	0.017	0.5 – 50
	Excipient	0.5	0.5	0.017	0.5 - 50
NMEA	Neat	0.5	0.5	0.017	0.5 - 50
	Excipient	0.5	0.5	0.017	0.5 - 50
NPYR	Neat	0.1	0.1	0.0034	0.1 – 50
NPYR	Excipient	0.1	0.2	0.0068	0.2 - 50
NDEA	Neat	0.2	0.5	0.017	0.5 - 50
	Excipient	0.5	0.5	0.017	0.5 - 50
NPIP	Neat	0.2	0.2	0.0068	0.2 - 50
	Excipient	0.2	0.2	0.0068	0.2 - 50
NEIPA	Neat	1	2	0.068	2 – 50
	Excipient	2	2	0.068	2 – 50
NDIPA	Neat	0.2	0.5	0.017	0.5 - 50
	Excipient	0.2	0.5	0.017	0.5 - 50
NDPA	Neat	0.2	0.2	0.0068	0.2 - 50
	Excipient	0.2	0.2	0.0068	0.2 - 50
NDBA	Neat	0.1	0.5	0.017	0.5 - 50
NUDA	Excipient	0.1	0.5	0.017	0.5 – 50

^{*} PPM is calculated based on 30mg/ml of drug substance and product extract

LLOQ comparison between HESI and APCI for all NAs (Neat only)



Orbitrap Exploris 120 MS

- Max 120K resolution at m/z 200
- Sub ppm mass accuracy with EASY-IC ion source
- Superior sensitivity can be achieved using both HESI and APCI mode

	Mode	LOD (ng/ml)	LLOQ (ng/ml)	PPM*	Factor
NDMA	HESI	0.2	0.5	0.017	-
	APCI	0.2	0.2	0.0068	2.5x
NMEA	HESI	0.5	0.5	0.017	-
INIVIEA	APCI	0.2	0.2	0.0068	2.5x
NPYR	HESI	0.1	0.1	0.0034	-
NPYR	APCI	0.1	0.2	0.0068	1/2x
NDEA	HESI	0.2	0.5	0.017	-
NDEA	APCI	0.1	0.1	0.0034	5x
NDID	HESI	0.2	0.2	0.0068	-
NPIP	APCI	0.1	0.1	0.0034	2x
NEIDA	HESI	1	2	0.068	-
NEIPA	APCI	0.5	0.5	0.017	4x
NIDIDA	HESI	0.2	0.5	0.017	-
NDIPA	APCI	0.1	0.1	0.0034	5x
NDDA	HESI	0.2	0.2	0.0068	-
NDPA	APCI	0.1	0.1	0.0034	2x
NDDA	HESI	0.1	0.5	0.017	-
NDBA	APCI	0.1	0.5	0.017	1x

^{*} PPM is calculated based on 30mg/ml of drug substance and product extract