

# Effective Workflow for Pharmaceutical API Impurity Analysis using HR- LCMS and Compound Discoverer

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## Overview

**Purpose:** Demonstrate an effective workflow for pharmaceutical impurity identification using Thermo Scientific™ Orbitrap Elite™ mass spectrometer and novel node-based small molecule structure ID software Thermo Scientific™ Compound Discoverer™ software.

**Methods:** LC-HRMS and Compound Discoverer software for Fexofenadine API impurity analysis.

**Results:** The Fexofenadine API impurity profile was quickly obtained.

## Introduction

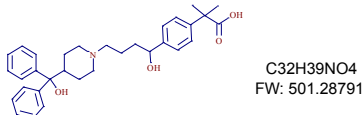
Pharmaceutical impurity analysis is crucial for drug R&D, production, and post-marketing surveillance. LCMS is routinely used for impurity analysis because of its speed and sensitivity. For rapid, accurate, and confident impurity ID, very high resolution mass spectrometer and effective data processing software are essential.

This study demonstrates an effective workflow for pharmaceutical impurity identification using very high resolution mass spectrometer and node-based small molecule structure ID software: Compound Discoverer software.

## Methods

### Sample Preparation

The commercial compound Fexofenadine (Sigma-Aldrich F9427-10MG, cas# 83799-24-0) was dissolved in 1:1 ACN/Water at a concentration of 0.3 µg/mL.



### Liquid Chromatography

HPLC system: Thermo Scientific™ Accela™ 1250 pump, Open Accela Autosampler and PDA

Column: Thermo Scientific™ Accucore™ C18 2.1x 150 columns, 2.6 µm. Injection volume: 5 µl

Mobile phases:	A - H <sub>2</sub> O				
	B - Acetonitrile				
	C - H <sub>2</sub> O with 0.05% Ammonium Hydroxide pH 9				
Gradient :	Time (min.)	A%	B%	C%	ul/min
	0	60	15	25	400
	0.5	60	15	25	400
	14.0	25	50	25	400
	19.0	5.0	70	25	400
	19.1	60	15	25	400
	24.0	60	15	25	400

### Mass Spectrometry

The high resolution accurate mass (HRAM) analysis was conducted on an Orbitrap Elite mass spectrometer equipped with a HESI II ion source. Full scan MS and top3 data-dependent MS/MS data were collected at resolutions of 120,000 and 15,000 respectively.

Ionization mode: ESI positive  
Scan range: 160-1500 amu  
Sheath gas flow rate (N<sub>2</sub>): 45  
Auxiliary gas flow rate (N<sub>2</sub>): 10  
Spray voltage (KV): +4.0 for positive  
Capillary temp (°C): 300  
S-lens RF level: 60.0  
Heater temp (°C): 450



Thermo Scientific™  
Orbitrap Elite™ mass spectrometer

# Data Processing

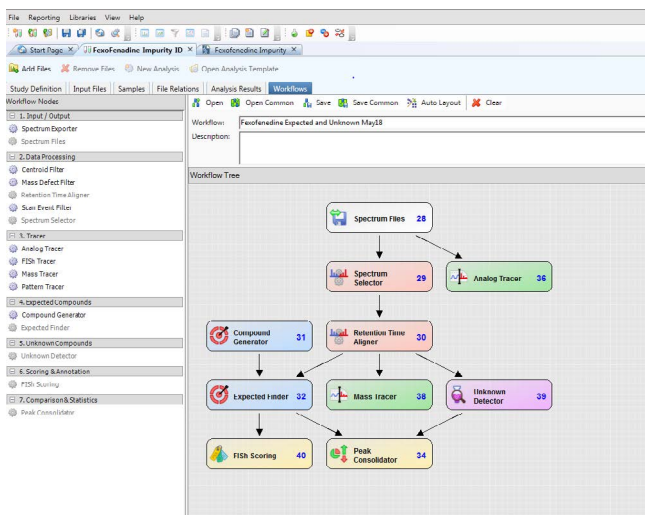
## Node Based Processing Workflow in Compound Discoverer

The HRAM full scan and HCD ms/ms data acquired on an Orbitrap Elite MS was processed using Compound Discoverer (CD) software for Fexofenadine API impurity profiling.

Compound Discoverer (CD) software provides flexible processing workflows which are assembled from a suite of advanced algorithms (nodes). The drag-and-drop workflow editor allows greater control and visibility in terms of how data should be processed.

Most API impurities are structurally related to the API, but unrelated unknowns do occur. In this study, the CD processing workflow included the following nodes to ensure complete impurity identification: Using "Expected Finder" to get an expected ions list from "Compound Generator" node and detect expected compounds. Using "FISH Scoring" node for fragment ion matching and fragment structure annotations on spectra. "Unknown Detector" node was added to detect structurally unrelated impurities. "Peak Consolidator" node grouped the peaks detected from both expected and unknown mechanisms for quick comparison and more confident identification. See Figure 1.

FIGURE 1. Node Based Processing Workflow



## Results

FIGURE 2. Base Peak Chromatogram of Fexofenadine in CD "Specialized Traces"

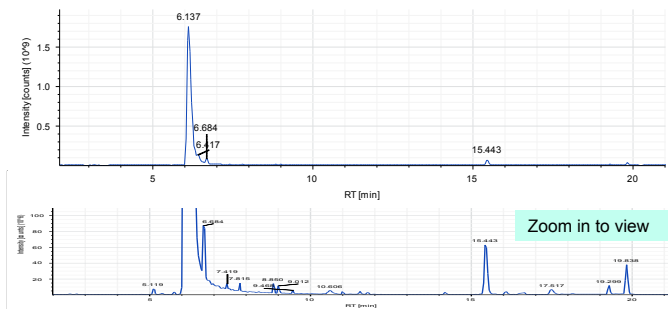
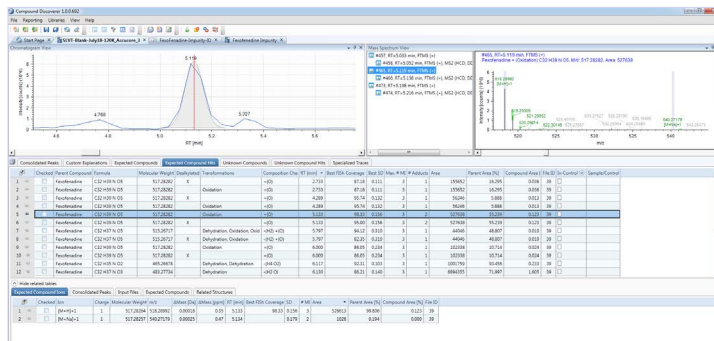


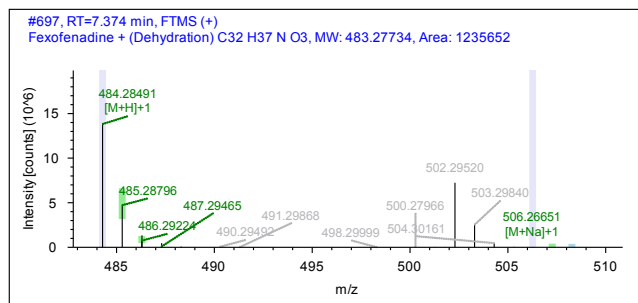
FIGURE 3. Results Review



## Structure Characterization for Expected Compound Hits

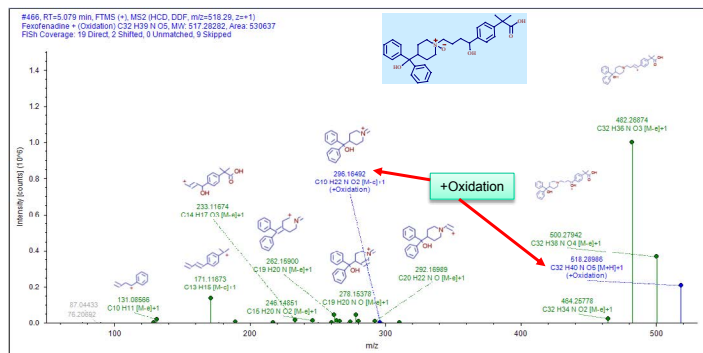
The detailed and comprehensive processing results are shown in Figure 3. It includes "Expected Compound Hits" and "Unknown Compound Hits" from Expected Finder node and Unknown Detector node respectively. An example of fine isotopic pattern confirmation of elemental formula assignment for "Expected Compound Hits" is shown in Figure 4. Color coding of isotopic fidelity gave greater confidence in elemental composition assignment from CD. Automatic adduct grouping reduced false positive hits.

FIGURE 4. Isotope Pattern Fidelity for Assigned Elemental Composition.



For each expected impurity hit, FISH Scoring automatically searched the fragmentation spectra, and annotated matching fragment structures directly on the spectra. The annotations are color-coded to visually indicate the transformation shifted ones for transformation localization, see Figure 5.

FIGURE 5. Expected Compound Hit with Automatically FISH Fragment Annotations



For unknown compound hits, "Mass Spectrum View" showed the HRAM mass and corresponding ms/ms spectrum. The interested unknown compound **s** were added to a custom explanation table. Based on the HRAM fragmentation data, putative structures were propose in "Custom Explanation Editor" (Figure 7), followed by "FiSh Scoring" on the fly, the unknown component ms/ms spectra were automatically annotated with matching fragment structures (Figure 6). "FiSh Coverage" score indicated the percentage of fragment ion matching between experimental data and theoretical predictions from Mass Frontier™ Fragmentation Libraries™.

#222 RT=2.388 min. FTMS (+) MS2 (HCD, DDF, m/z=426.26, z=+1)  
m/z C26 H35 N O4, MW: 425.2661, Area: 299533  
FISH Coverage: 11 Direct, 3 Unmatched, 5 Skipped

Mass spectrum plot showing intensity (counts) versus m/z. The x-axis ranges from 100 to 450 m/z, and the y-axis ranges from 0 to 250 intensity units. The base peak is at m/z 408.26302. Other significant peaks are labeled with their m/z values and chemical structures.

m/z	Chemical Structure
68.49943	<chem>C1=CC=C(C=C1)O</chem>
67.04454	<chem>C1=CC=C(C=C1)O</chem>
131.08530	<chem>C1=CC=C(C=C1)O</chem>
130.11111 [M-e]1	<chem>C1=CC=C(C=C1)O</chem>
174.12787	<chem>C1=CC=C(C=C1)O</chem>
C12 H16 N [M-e]1	<chem>C1=CC=C(C=C1)O</chem>
189.12758	<chem>C1=CC=C(C=C1)O</chem>
C13 H17 O [M-e]1	<chem>C1=CC=C(C=C1)O</chem>
171.11673	<chem>C1=CC=C(C=C1)O</chem>
C13 H15 [M-e]1	<chem>C1=CC=C(C=C1)O</chem>
182.1381	<chem>C1=CC=C(C=C1)O</chem>
204.13789	<chem>C1=CC=C(C=C1)O</chem>
C13 H15 N O [M-e]1	<chem>C1=CC=C(C=C1)O</chem>
233.11691	<chem>C1=CC=C(C=C1)O</chem>
C14 H17 O3 [M-e]1	<chem>C1=CC=C(C=C1)O</chem>
384.63077	<chem>C1=CC=C(C=C1)O</chem>
390.24262	<chem>C1=CC=C(C=C1)O</chem>
C26 H32 N O2 [M-e]1	<chem>C1=CC=C(C=C1)O</chem>
426.26361	<chem>C1=CC=C(C=C1)O</chem>
C26 H36 N O4 [M+H]1	<chem>C1=CC=C(C=C1)O</chem>
426.37256	<chem>C1=CC=C(C=C1)O</chem>
408.26302	<chem>C1=CC=C(C=C1)O</chem>
C26 H34 N O3 [M-e]1	<chem>C1=CC=C(C=C1)O</chem>

The screenshot shows the Chem3D software interface. At the top, a menu bar includes 'File', 'Edit', 'Build', 'View', 'Tools', 'Window', and 'Help'. Below the menu is a toolbar with icons for file operations, editing, and visualization. The main window displays a 3D ball-and-stick model of a complex organic molecule. A yellow callout box with the text 'FISH Scoring' points to the 'FISH Scoring' tab in the bottom-left panel. The bottom-right panel contains several input fields: 'Molecular weight (original)' with the value '425.25661', 'Formula' with 'C28 H35 N O4', 'Name' (empty), and 'Resonance/Impurity P1' (empty). The bottom-left panel has a 'Comments' text area and a 'Composition change' checkbox. At the bottom right, there are 'Save' and 'Cancel' buttons.

**FIGURE 8. Result Filters**

The screenshot shows the 'Result Filters' dialog box with the 'Inspected Compound Hits' section selected. The filters are as follows:

Filter	Value	Unit
Area	greater than	1400.00
RT min	is between	2.00 and 21.00
Best FIDN Coverage	is greater than	75
Best S/N	is less than	0.25

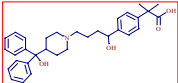
The 'Load' button is highlighted in the bottom left corner.

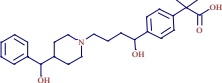
The result was reported in the Expected and Custom explanation formats. For each identified impurity, it's isotope pattern, annotated ms/ms spectrum, transformation, Fish coverage, spectral distance, and others were included in the report, see Figure 9.

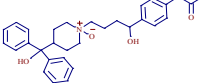
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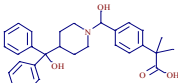
Expected Compound Hits									
G202015 12 18 AM									
Peak Number	Molecular Weight	Transformation	Chemical Change	Mass Change	Retention Time	Score	Rank	Area	Compound Name
1	300.17			-0.04 g/mol	9.77 min	6.575	4.756	4305215.5	1
2	419.22	Dehydration	-H2O	0.0 g/mol	6.649	6.00	6.228	2	680055
3	419.22	Dehydration	-H2O	0.0 g/mol	6.649	9.50	6.228	2	680055
4	419.22	Dehydration	-H2O	0.0 g/mol	6.649	9.50	6.228	2	680055
5	419.22	Dehydration	-H2O	0.0 g/mol	6.649	9.50	6.228	2	680055
6	419.22	Dehydration	-H2O	0.0 g/mol	6.649	9.50	6.228	2	680055
7	419.22	Dehydration	-H2O	0.0 g/mol	6.649	9.50	6.228	2	680055
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18	419.22	Dehydration	-H2O	0.0 g/mol	6.649	9.50	6.228	2	680055
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25	419.22	Dehydration	-H2O	0.0 g/mol	6.649	9.50	6.228	2	680055
26	419.22	Dehydration	-H2O	0.0 g/mol	6.649	9.50	6.228	2	680055
27	419.22	Dehydration	-H2O	0.0 g/mol	6.649	9.50	6.228	2	680055
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32	419.22	Dehydration	-H2O	0.0 g/mol	6.649	9.50	6.228	2	680055
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36	419.22	Dehydration	-H2O	0.0 g/mol	6.649	9.50	6.228	2	680055
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38	419.22	Dehydration	-						

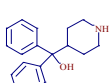
**Fexofenadine**

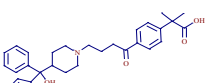
  
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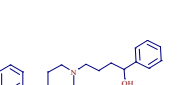
  
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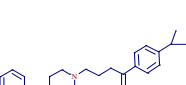
  
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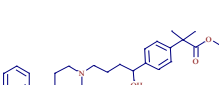
  
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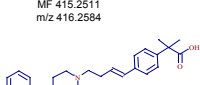
  
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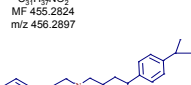
  
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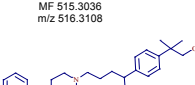
  
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 $C_{25}H_{29}NO_3$   
MF 515.3036  
m/z 516.3108

  
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 $C_{25}H_{29}NO_2$   
MF 457.2981  
m/z 458.3054

  
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 $C_{25}H_{29}NO_3$   
MF 487.3064  
m/z 488.3159

▪Effective and confident impurity analysis was achieved using very high resolution LCMS from the Orbitrap Elite mass spectrometer and Compound Discoverer software.

- Powerful workflow options in Compound Discoverer software detect components with targeted and untargeted mechanisms, and utilize very high resolution to quickly perform fine isotope searches. The determination of the structures of impurities is simplified with automatic FISH (fragment ion search) annotations.



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