

•
•
•
•
•
•
•

DATA ANALYSIS IN MASS SPECTROMETRY BASED METABOLOMICS

Pavel Aronov

Stanford Mass Spectrometry
Users' Meeting
September 26, 2011





Presented at the 2011 Stanford Mass Spectrometry Users' Meeting

**For personal use only.
Please do not reuse or reproduce
without the author's permission.**



Types of Experiments in Metabolomics

targeted

non-targeted

quantitative

semi-quantitative

- Number of analyzed metabolites is limited by the number of available **standards**

- **Absolute quantitation** of metabolites (nM, mg/mL)

- Number of analyzed metabolites is limited by the number of available **library spectra**

- **Relative quantitation** of metabolites (fold)

- Number of analyzed metabolites is limited by capacity of **analytical instrumentation**

- **Relative quantitation** of metabolites (fold)



Targeted LC/MS metabolomics

- Absolute quantitation of metabolites using triple quadrupole instruments
 - SUMS: Quattro Premier (Waters) and TSQ Vantage (Thermo)
- Chemical standards of metabolites are required, internal standards (isotopically labeled metabolites, ^{13}C or ^2H) are desired
- Custom methods; amino acid method is available (~30 amino acids)
 - SUMS contact: Karolina Krasinska



Untargeted GC/MS based metabolomics

- Agilent 5795 single quadrupole GC/MS
- Metabolomics method based on Kind T. et al 2009, Anal Chem 81(24)
- Identification based on Agilent MSRI library (~700 metabolites, mostly primary metabolism)

For general overview: SUMS 2010 users' meeting workshop presentation



Untargeted GC/MS based metabolomics

- Service began: Summer 2011
- Sample requirements: dry or non-aqueous solvent
- Samples tested: tissue, bacterial cells, urine, plasma
- Metabolites identified: ~30-120
- Metabolites detected: ~200-500
- Data output: AMDIS IDs, non-targeted and pathway analysis is under development



Untargeted LC/MS based metabolomics

Sample prep

Blood Plasma: protein precipitation with 4 v of Acetonitrile, evaporation, reconst in 5 % ACN

LC

Reversed Phase Chromatography

Aqueous Normal Phase Chromatography



MS

Thermo Exactive: +ESI and -ESI, R =50,000
m/z 70-800 (+APCI if necessary)

Data Analysis

MZmine 2.2
accurate mass database search (HMDB)

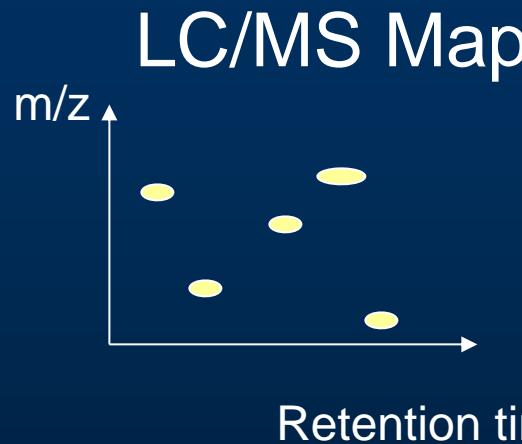
Identification

Stanford U
MASS SPECT

structure elucidation (Orbitrap Velos),
data interpretation (Mass Frontier)



Data Processing Workflow



Peak ID (m/z, t_R) | Area

Peak ID (m/z, t_R)	Area
0001	3500
0002	6000
0003	9000
0004	700
0005	1200

	Sample1	Sample2	SampleN
Peak ID	Area	Area	Area
0001	3500	2300	300
0002	6000	7800	5600
0003	9000	5100	9700
0004	700	1300	1200
0005	1200	400	900

Peak annotation
and statistical analysis



File Format Conversion

Universal MS data formats:

- netCDF (*.cdf)

All MS manufacturers provide tools for conversion into netCDF

- XMLs (mzXML, mzML)

Less common in metabolomics



Data Processing Software

- Proprietary

MarkerLynx (Waters), SIEVE (Thermo),
MarkerView (Sciex), Mass Profiler
Professional (Agilent)

- Open Source

XCMS (<http://metlin.scripps.edu/xcms/>)

and

MZmine (<http://mzmine.sourceforge.net/>)

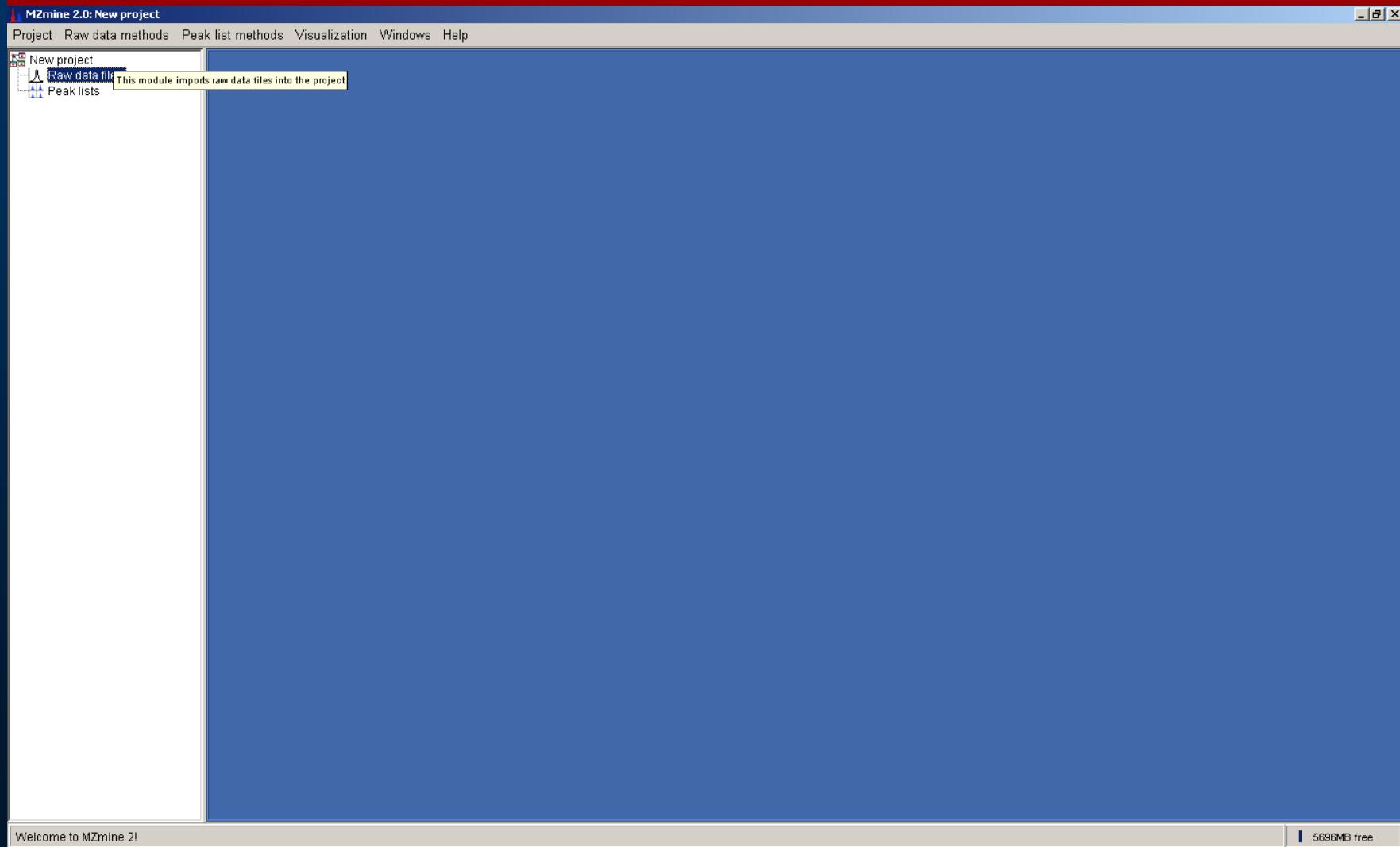


MZmine: Hardware considerations

- Multi-processor systems
- Server CPU are expensive (Xeon, Opteron), Desktop processors are ok (Phenom, Core i7)
- 64-bit OS with Java and CPUs to address more than 4 GB memory
- At least 8 GB memory (high resolution profile data)



MZmine: main window





MZmine: supported file formats

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project
Raw data files
Peak lists

Raw data import

Look in: April2010

File name:

Files of type:

- All raw data files
- All Files
- NetCDF files
- mzData files
- mzML files
- XCalibur RAW files
- mzXML files
- All XML files
- All raw data files

Welcome to MZmine 2!

5273MB free

Start MZmine screenshots.ppt... Shortcut to startMZmine... MZmine 2.0: New proj...

8:11 PM

The screenshot displays the MZmine 2.0 software interface. At the top, there's a red header bar with the title 'MZmine: supported file formats'. Below it is a standard Windows-style menu bar with options like 'Project', 'Raw data methods', 'Peak list methods', 'Visualization', 'Windows', and 'Help'. On the left, a sidebar shows a tree structure: 'New project' is expanded, showing 'Raw data files' and 'Peak lists'. The main area is a large blue workspace. A 'Raw data import' dialog box is open in the center. It has a 'Look in:' dropdown set to 'April2010'. The left pane of the dialog shows a file tree with 'My Recent Documents', 'Desktop', 'My Documents', 'My Computer', and 'My Network'. The right pane lists numerous raw data files, each with a small icon and a file name like 'MeyerT_100422_sample0047.raw'. Below the list is a 'File name:' input field and a 'Files of type:' dropdown menu. The 'Files of type:' menu is open, showing a list of supported file formats: 'All raw data files', 'All Files', 'NetCDF files', 'mzData files', 'mzML files', 'XCalibur RAW files', 'mzXML files', 'All XML files', and 'All raw data files'. The 'All raw data files' option is highlighted with a dark blue background. At the bottom of the screen, there's a taskbar with icons for 'Start', 'MZmine screenshots.ppt...', 'Shortcut to startMZmine...', and 'MZmine 2.0: New proj...'. The system tray shows the date and time as '8:11 PM'.



MZmine: use of multiple CPU cores

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project
Raw data files
Peak lists

Tasks in progress...

Item	Priority	Status	% done
Opening file E:\Aronov\April2010\MeyerT_100422_sample0047.raw	NORMAL	PROCESSING	[progress bar] 36%
Opening file E:\Aronov\April2010\MeyerT_100422_sample0048.raw	NORMAL	PROCESSING	[progress bar] 36%
Opening file E:\Aronov\April2010\MeyerT_100422_sample0049.raw	NORMAL	PROCESSING	[progress bar] 35%
Opening file E:\Aronov\April2010\MeyerT_100422_sample0050.raw	NORMAL	PROCESSING	[progress bar] 38%
Opening file E:\Aronov\April2010\MeyerT_100422_sample0051.raw	NORMAL	PROCESSING	[progress bar] 37%
Opening file E:\Aronov\April2010\MeyerT_100422_sample0052.raw	NORMAL	PROCESSING	[progress bar] 35%

6:25:38 PM: Started parsing file E:\Aronov\April2010\MeyerT_100422_sample0050.raw

Start C:\WINDOWS\system32... MZmine 2.0: New proj... Untitled 1 - OpenOffice... 6:25 PM



MZmine: inspection of raw data

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project

- Raw data files
 - MeyerT_100422_sample0051.raw
 - MeyerT_100422_sample0050.raw
 - MeyerT_100422_sample0048.raw**
 - MeyerT_100422_sample0047.raw
 - MeyerT_100422_sample0049.raw
 - MeyerT_100422_sample0052.raw
- Peak lists
 - MeyerT_100422_sample0050.raw peak list5000
 - MeyerT_100422_sample0052.raw peak list5000
 - MeyerT_100422_sample0047.raw peak list5000
 - MeyerT_100422_sample0048.raw peak list5000
 - MeyerT_100422_sample0051.raw peak list5000
 - MeyerT_100422_sample0049.raw peak list5000
 - MeyerT_100422_sample0052.raw peak list5000 resolved
 - MeyerT_100422_sample0050.raw peak list5000 resolved
 - MeyerT_100422_sample0047.raw peak list5000 resolved
 - MeyerT_100422_sample0048.raw peak list5000 resolved
 - MeyerT_100422_sample0051.raw peak list5000 resolved
 - MeyerT_100422_sample0049.raw peak list5000 resolved
 - MeyerT_100422_sample0052.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0050.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0047.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0051.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0048.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0049.raw peak list5000 resolved deisotoped

Please set parameter values for TIC/XIC visualizer

Raw data files

- MeyerT_100422_sample0051.raw
- MeyerT_100422_sample0050.raw
- MeyerT_100422_sample0048.raw
- MeyerT_100422_sample0047.raw
- MeyerT_100422_sample0049.raw
- MeyerT_100422_sample0052.raw

MS level 1

Plot type TIC

Retention time 1:00 - 49:59

m/z range 212.000 - 213.000 m/z

Selected peaks

OK Cancel Set automatically Help

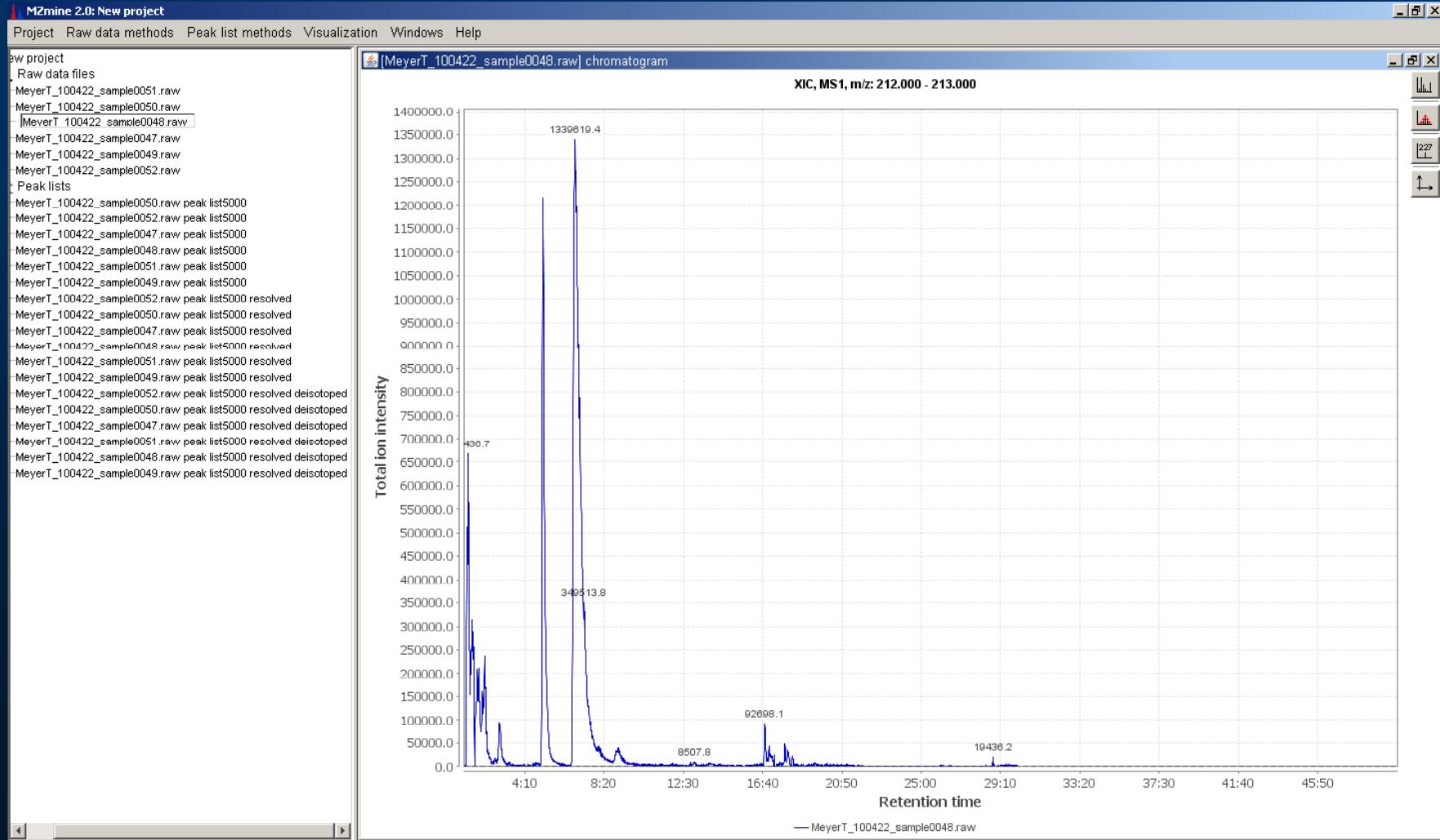
[6:39:04 PM] Finished isotopic peak grouper on MeyerT_100422_sample0049.raw peak list5000 resolved

5350MB free

Start C:\WINDOWS\system32... MZmine 2.0: New proj... Untitled 1 - OpenOffice....



MZmine: raw data SIC



[6:39:04 PM]: Finished isotopic peak grouper on MeyerT_100422_sample0049.raw peak list5000 resolved

5647MB free



MZmine: peak picking

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project

Raw data files

- + MeyerT_100422_sample0051.raw
- + MeyerT_100422_sample0050.raw
- + MeyerT_100422_sample0049.raw
- + MeyerT_100422_sample0047.raw
- + MeyerT_100422_sample0049.raw
- + MeyerT_100422_sample0052.raw

Peak lists

Please set parameter values for Chromatogram builder

Filename suffix: peak list5000

Mass detection: Exact mass Set parameters

Filtering: FTML_shoulders filter Set parameters

Chromatogram construction: Highest data point Set parameters

OK Cancel Help

[6:25:59 PM]: Finished parsing E:\AronowApril2010\MeyerT_100422_sample0052.raw, parsed 2732 scans

5839MB free

Start C:\WINDOWS\system32... MZmine 2.0: New proj... Untitled 1 - OpenOffice....



MZmine: preview of parameters

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project

Raw data files

- + MeyerT_100422_sample0051.raw
- + MeyerT_100422_sample0050.raw
- + MeyerT_100422_sample0049.raw
- + MeyerT_100422_sample0047.raw
- + MeyerT_100422_sample0049.raw
- + MeyerT_100422_sample0052.raw

Peak lists

Please set parameter values for Chromatogram builder

Exact mass's parameter setup dialog

Filename suffix:

Mass detector: Noise level: 5000.0 absolute

Filtering: Show preview

Chromatogram construction:

OK Cancel Help

parameters

parameters

parameters

[6:25:59 PM]: Finished parsing E:\AronowApril2010\MeyerT_100422_sample0052.raw, parsed 2732 scans

5720MB free

Start C:\WINDOWS\system32... MZmine 2.0: New proj... Untitled 1 - OpenOffice....



MZmine: estimating the noise level

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project

Raw data files

- MeyerT_100422_sample0051.raw
- MeyerT_100422_sample0050.raw
- MeyerT_100422_sample0048.raw
- MeyerT_100422_sample0047.raw
- MeyerT_100422_sample0049.raw
- MeyerT_100422_sample0052.raw

Peak lists

Exact mass's parameter setup dialog

Noise level: 5000.0 (absolute) Intensities less than this value are interpreted as noise.

Show preview:

Data file: MeyerT_100422_sample0051.raw

Scan number: 1457

[MeyerT_100422_sample0051.raw] scan #1457
MS1, RT 14:38, base peak: 89.023 m/z (362766.2)

Intensity

m/z

Scan #1457 ■ Detected peaks

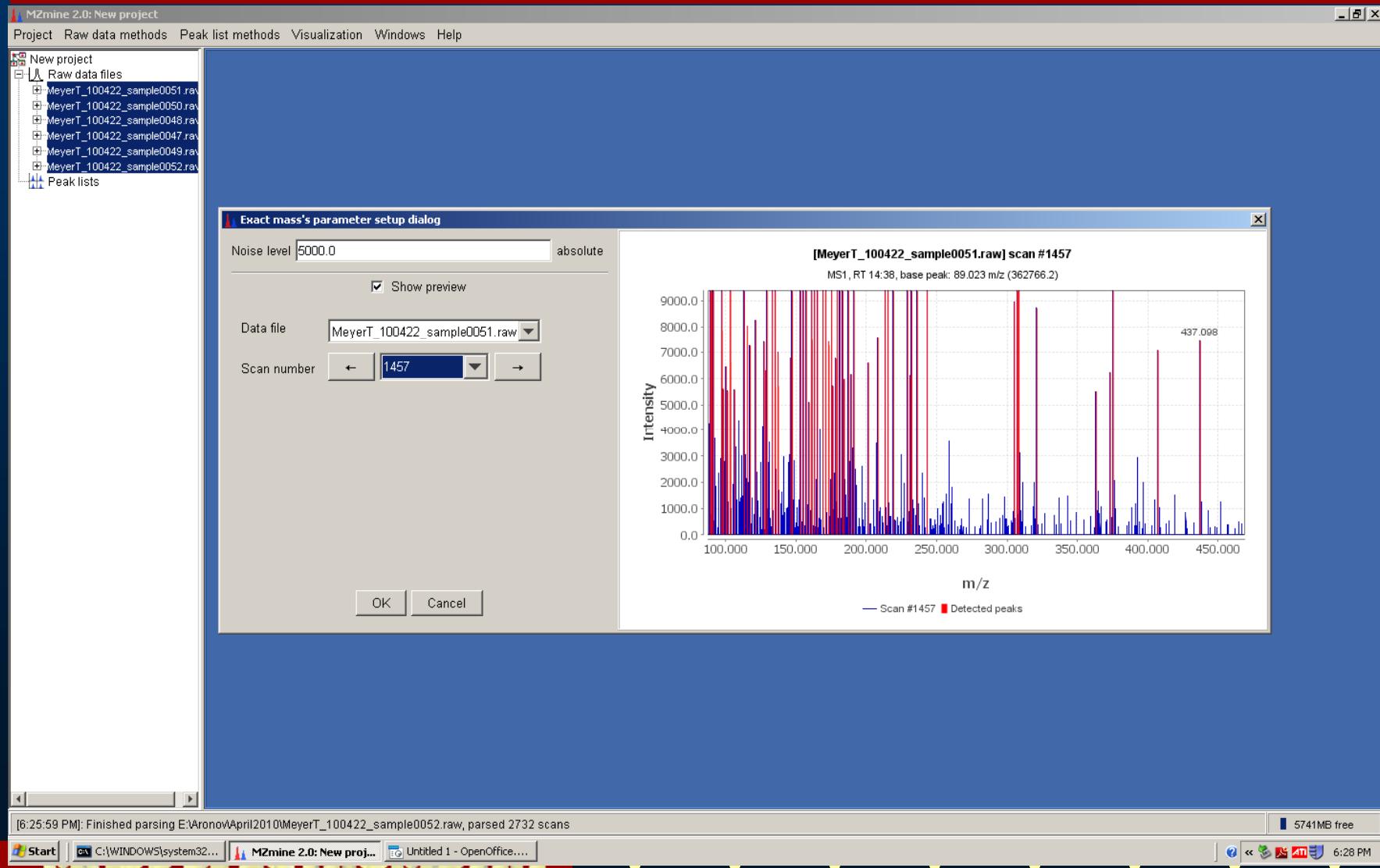
[6:25:59 PM]: Finished parsing E:\Aronov\April2010\MeyerT_100422_sample0052.raw, parsed 2732 scans

5774MB free

Start C:\WINDOWS\system32... MZmine 2.0: New proj... Untitled 1 - OpenOffice....



MZmine: zooming into noise





MZmine: chromatogram construction

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project

Raw data files

- MeyerT_100422_sample0051.raw
- MeyerT_100422_sample0050.raw
- MeyerT_100422_sample0049.raw
- MeyerT_100422_sample0047.raw
- MeyerT_100422_sample0049.raw
- MeyerT_100422_sample0052.raw

Peak lists

Please set parameter values for Chromatogram builder

Filename suffix: peak list5000

Mass detection: Exact mass Set parameters

Filtering: FTML shoulder peaks filter Set parameters

Chromatogram construction: Highest data point Set parameters

Highest data point's parameter setup

Min time span: 0:15

Min height: 10000.0

m/z tolerance: 0.003 m/z

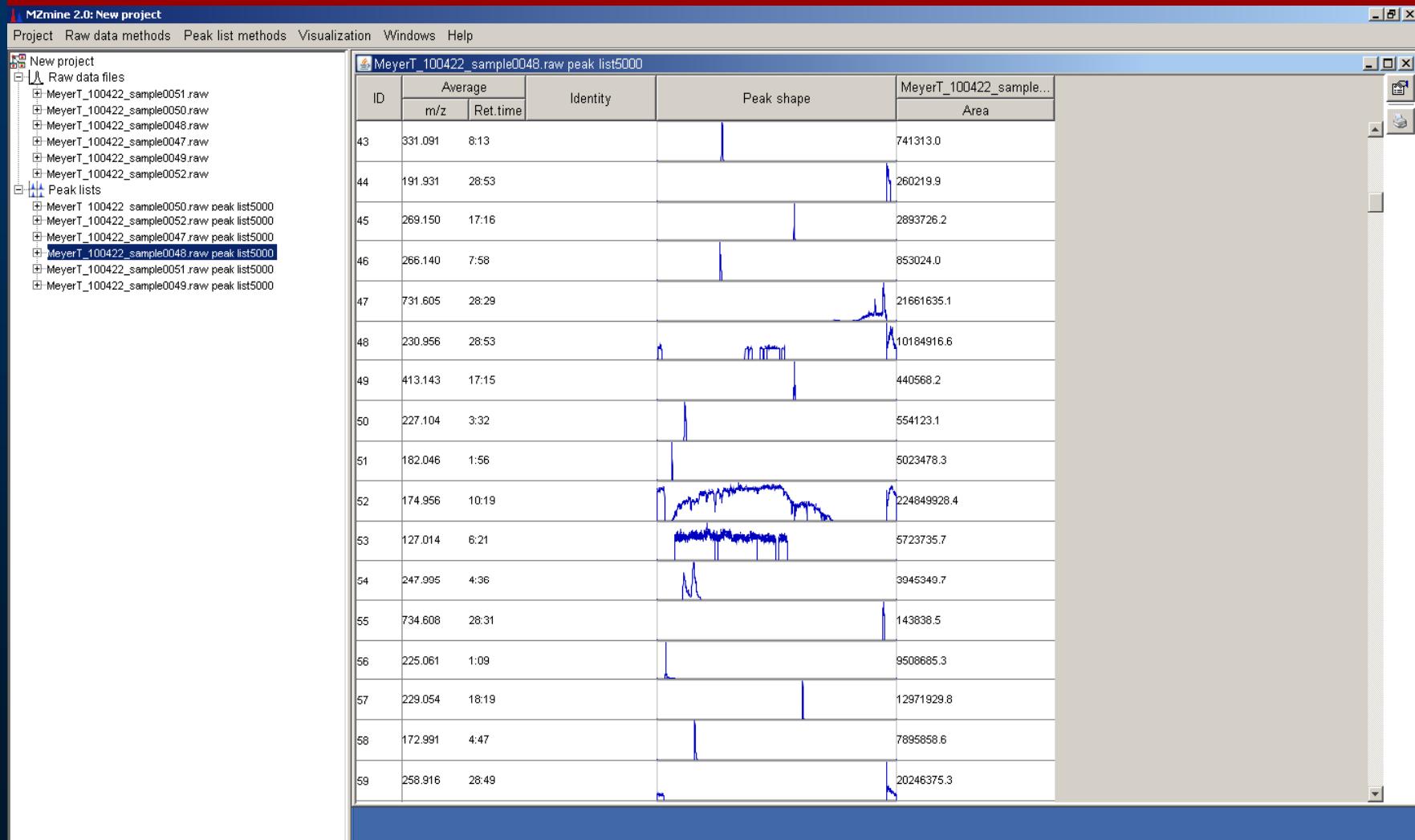
[6:25:59 PM] Finished parsing E:\Aronow\April2010\MeyerT_100422_sample0052.raw, parsed 2732 scans

5716MB free

Start C:\WINDOWS\system32... MZmine 2.0: New proj... Untitled 1 - OpenOffice....



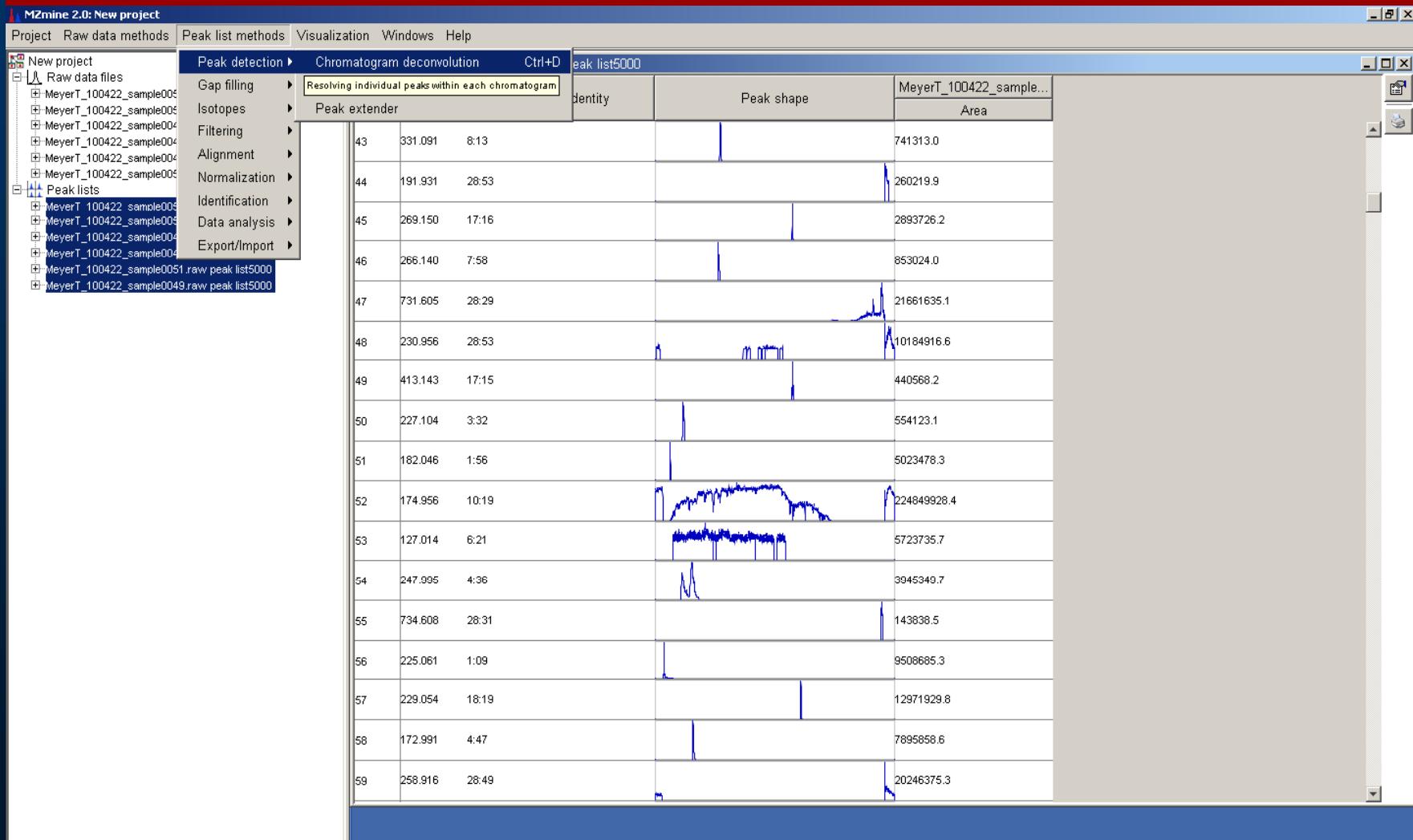
MZmine: peak picking results



[6:32:09 PM]: Finished chromatogram builder on MeyerT_100422_sample0049.raw

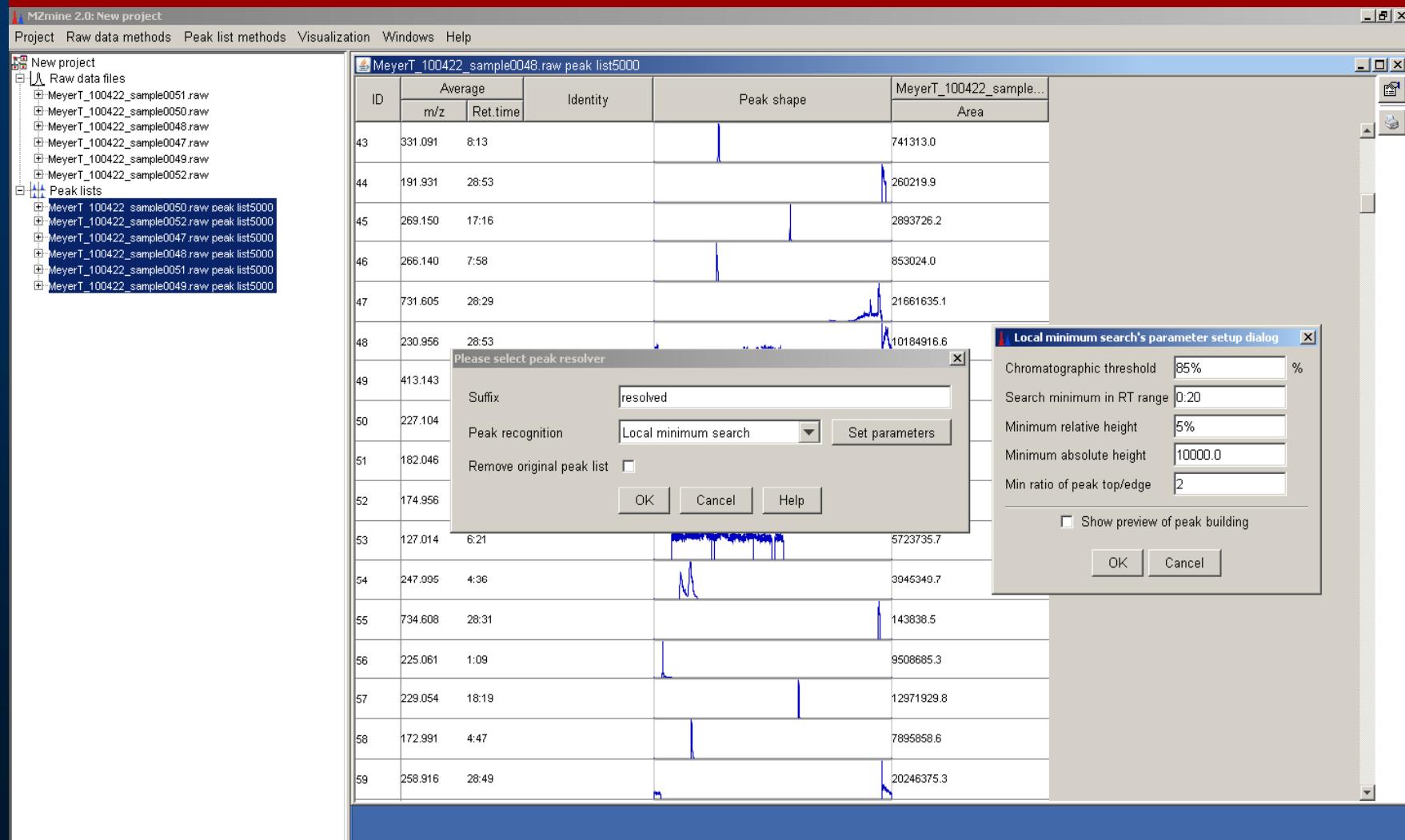


MZmine: deconvolution





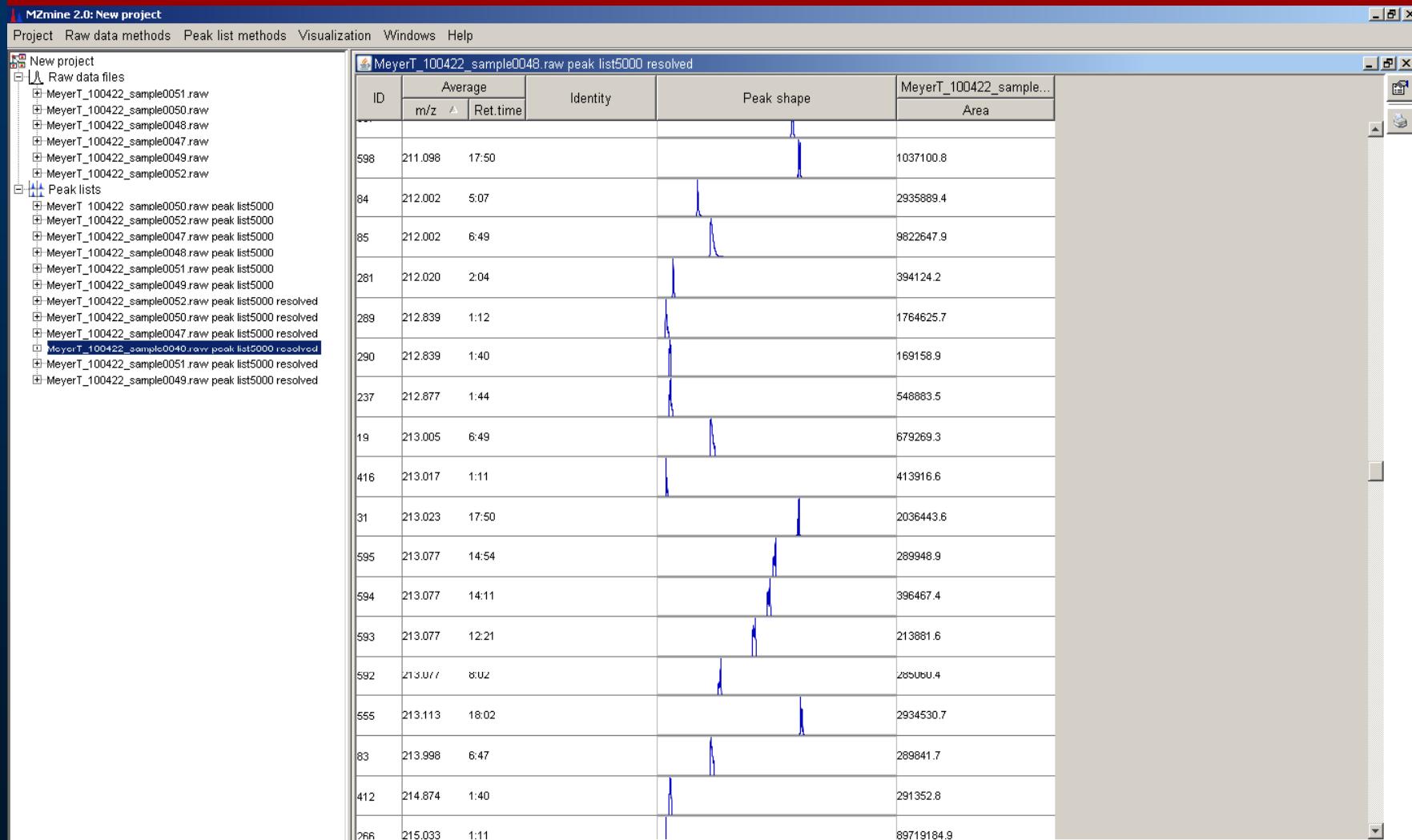
MZmine: deconvolution parameters



[6:32:09 PM]: Finished chromatogram builder on MeyerT_100422_sample0049.raw

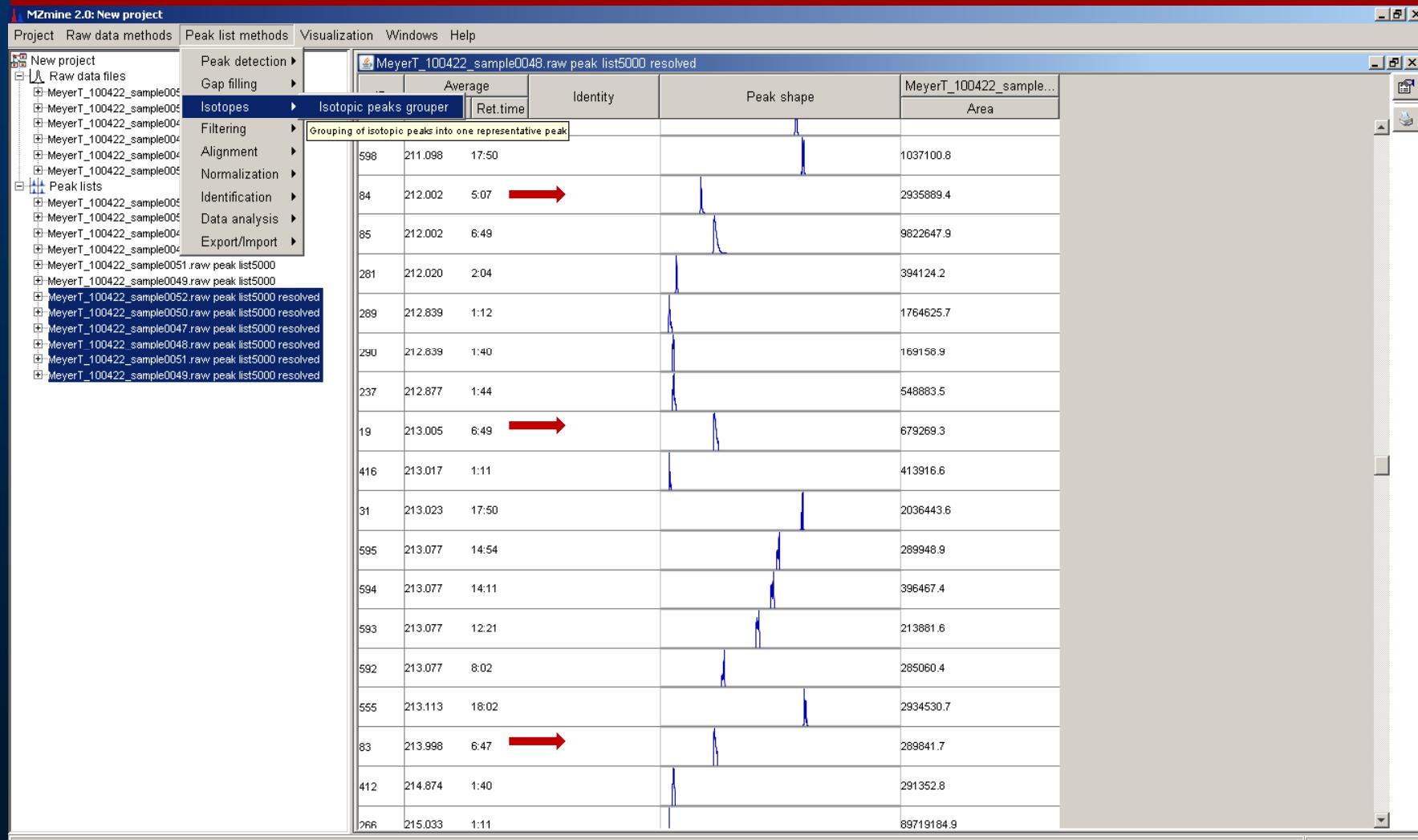


MZmine: deconvolution results





MZmine: deisotoping





MZmine: deisotoping parameters

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project

Raw data files

- MeyerT_100422_sample0051.raw
- MeyerT_100422_sample0050.raw
- MeyerT_100422_sample0048.raw
- MeyerT_100422_sample0047.raw
- MeyerT_100422_sample0049.raw
- MeyerT_100422_sample0052.raw

Peak lists

- MeyerT_100422_sample0050.raw peak list5000
- MeyerT_100422_sample0052.raw peak list5000
- MeyerT_100422_sample0047.raw peak list5000
- MeyerT_100422_sample0048.raw peak list5000
- MeyerT_100422_sample0051.raw peak list5000
- MeyerT_100422_sample0049.raw peak list5000
- MeyerT_100422_sample0052.raw peak list5000 resolved
- MeyerT_100422_sample0050.raw peak list5000 resolved
- MeyerT_100422_sample0047.raw peak list5000 resolved
- MeyerT_100422_sample0048.raw peak list5000 resolved
- MeyerT_100422_sample0051.raw peak list5000 resolved
- MeyerT_100422_sample0049.raw peak list5000 resolved

MeyerT_100422_sample0048.raw peak list5000 resolved

ID	Average	Identity	Peak shape	MeyerT_100422_sample... Area
	m/z			
598	211.098	17:50		1037100.8
84	212.002	5:07		2935889.4
85	212.002	6:49		9822647.9
281	212.020	2:04		394124.2
289	212.839	1:12		1764625.7
290	212.839	1:40		169158.9
237	212.877	1:44		548883.5
19	213.005	6:49		679269.3
416	213.017	1:11		413916.6
31	213.023	17:50		2036443.6
595	213.077	14:54		289948.9
594	213.077	14:11		396467.4
593	213.077	12:21		213881.6
592	213.077	8:02		285060.4
555	213.113	18:02		2934530.7
83	213.998	6:47		289841.7
412	214.874	1:40		291352.8
266	215.033	1:11		89719184.9

Please set parameter values for Isotopic peak...

Name suffix: deisotoped

m/z tolerance: 0.030 m/z

RT tolerance: 0:10

Monotonic shape:

Maximum charge: 3

Remove original peaklist:

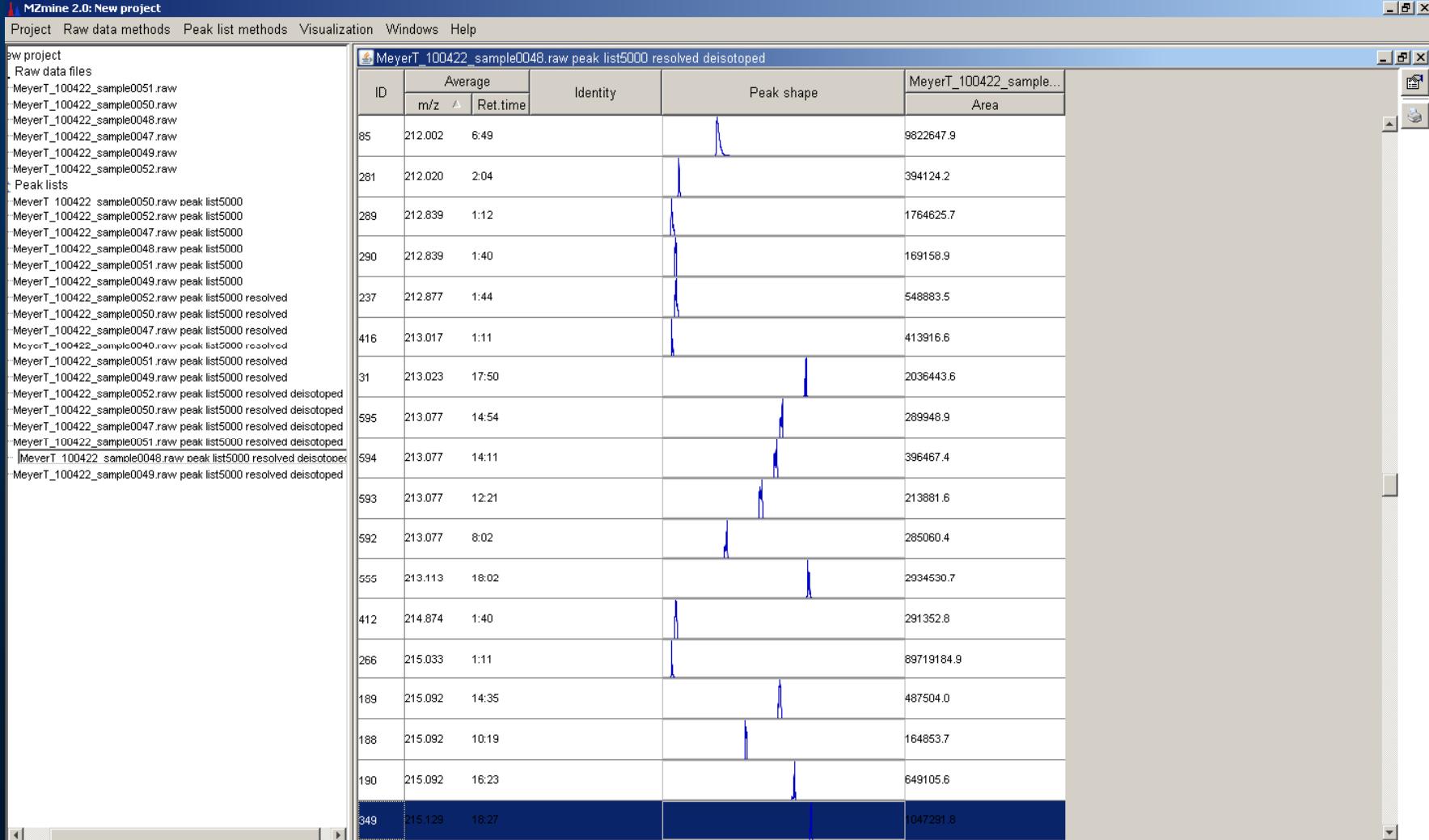
OK Cancel Help

[6:34:40 PM]: Finished peak recognition on MeyerT_100422_sample0049.raw peak list5000

19MB free



MZmine: deisotoping results



[6:39:04 PM]: Finished Isotopic peak grouper on MeyerT_100422_sample0049.raw peak list5000 resolved



MZmine: alignment

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project
Raw data files
MeyerT_100422_sample0051.raw
MeyerT_100422_sample0050.raw
MeyerT_100422_sample0040.raw
MeyerT_100422_sample0047.raw
MeyerT_100422_sample0049.raw
MeyerT_100422_sample0052.raw
Peak lists
MeyerT_100422_sample0050.raw
MeyerT_100422_sample0052.raw
MeyerT_100422_sample0047.raw
MeyerT_100422_sample0048.raw
MeyerT_100422_sample0051.raw peak list5000
MeyerT_100422_sample0049.raw peak list5000
MeyerT_100422_sample0052.raw peak list5000 resolved
MeyerT_100422_sample0050.raw peak list5000 resolved
MeyerT_100422_sample0047.raw peak list5000 resolved
MeyerT_100422_sample0048.raw peak list5000 resolved
MeyerT_100422_sample0051.raw peak list5000 resolved
MeyerT_100422_sample0049.raw peak list5000 resolved
MeyerT_100422_sample0052.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0050.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0047.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0051.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0048.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0049.raw peak list5000 resolved deisotoped

Peak detection ▾
Gap filling ▾
Isotopes ▾
Filtering ▾
Alignment ▾ Join aligner
Normalization ▾ RANSAC aligner
Identification ▾
Data analysis ▾
Export/Import ▾

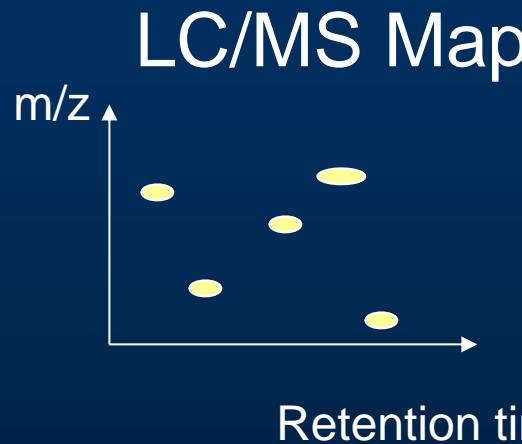
[6:39:04 PM] Finished isotopic peak grouper on MeyerT_100422_sample0049.raw peak list5000 resolved

5642MB free

Start C:\WINDOWS\system32... MZmine 2.0: New proj... Untitled 1 - OpenOffice...



Data Processing Workflow



Peak ID (m/z, t_R) | Area

Peak ID (m/z, t_R)	Area
0001	3500
0002	6000
0003	9000
0004	700
0005	1200

	Sample1	Sample2	SampleN
Peak ID	Area	Area	Area
0001	3500	2300	300
0002	6000	7800	5600
0003	9000	5100	9700
0004	700	1300	1200
0005	1200	400	900

Peak annotation
and statistical analysis



MZmine: alignment parameters

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project

- Raw data files
 - MeyerT_100422_sample0051.raw
 - MeyerT_100422_sample0050.raw
 - MeyerT_100422_sample0048.raw
 - MeyerT_100422_sample0047.raw
 - MeyerT_100422_sample0049.raw
 - MeyerT_100422_sample0052.raw
- Peak lists
 - MeyerT_100422_sample0050.raw peak list5000
 - MeyerT_100422_sample0052.raw peak list5000
 - MeyerT_100422_sample0047.raw peak list5000
 - MeyerT_100422_sample0048.raw peak list5000
 - MeyerT_100422_sample0051.raw peak list5000
 - MeyerT_100422_sample0049.raw peak list5000
 - MeyerT_100422_sample0052.raw peak list5000 resolved
 - MeyerT_100422_sample0050.raw peak list5000 resolved
 - MeyerT_100422_sample0047.raw peak list5000 resolved
 - MeyerT_100422_sample0048.raw peak list5000 resolved
 - MeyerT_100422_sample0051.raw peak list5000 resolved
 - MeyerT_100422_sample0049.raw peak list5000 resolved
 - MeyerT_100422_sample0052.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0050.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0047.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0051.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0048.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0049.raw peak list5000 resolved deisotoped

Please set parameter values for Join aligner

Peak list name	test10000-30sec
m/z tolerance	0.003
Weight for m/z	10
Retention time tolerance type	Absolute
Absolute RT tolerance	0:30
Relative RT tolerance	15%
Weight for RT	10
Require same charge state	<input type="checkbox"/>
Require same ID	<input type="checkbox"/>
Compare isotope pattern	<input type="checkbox"/>
Isotope pattern score threshold level	65%

[6:39:04 PM]: Finished isotopic peak grouper on MeyerT_100422_sample0049.raw peak list5000 resolved

Start C:\WINDOWS\system32... MZmine 2.0: New proj... Untitled 1 - OpenOffice....



MZmine: alignment is computationally intense

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project

- Raw data files
 - MeyerT_100422_sample0051.raw
 - MeyerT_100422_sample0050.raw
 - MeyerT_100422_sample0048.raw
 - MeyerT_100422_sample0047.raw
 - MeyerT_100422_sample0049.raw
 - MeyerT_100422_sample0052.raw
- Peak lists
 - MeyerT_100422_sample0050.raw peak list5000
 - MeyerT_100422_sample0052.raw peak list5000
 - MeyerT_100422_sample0047.raw peak list5000
 - MeyerT_100422_sample0048.raw peak list5000
 - MeyerT_100422_sample0051.raw peak list5000
 - MeyerT_100422_sample0049.raw peak list5000
 - MeyerT_100422_sample0052.raw peak list5000 resolved
 - MeyerT_100422_sample0050.raw peak list5000 resolved
 - MeyerT_100422_sample0047.raw peak list5000 resolved
 - MeyerT_100422_sample0048.raw peak list5000 resolved
 - MeyerT_100422_sample0051.raw peak list5000 resolved
 - MeyerT_100422_sample0049.raw peak list5000 resolved
 - MeyerT_100422_sample0052.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0050.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0047.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0051.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0048.raw peak list5000 resolved deisotoped
 - MeyerT_100422_sample0049.raw peak list5000 resolved deisotoped

test10000-30sec

Tasks in progress...

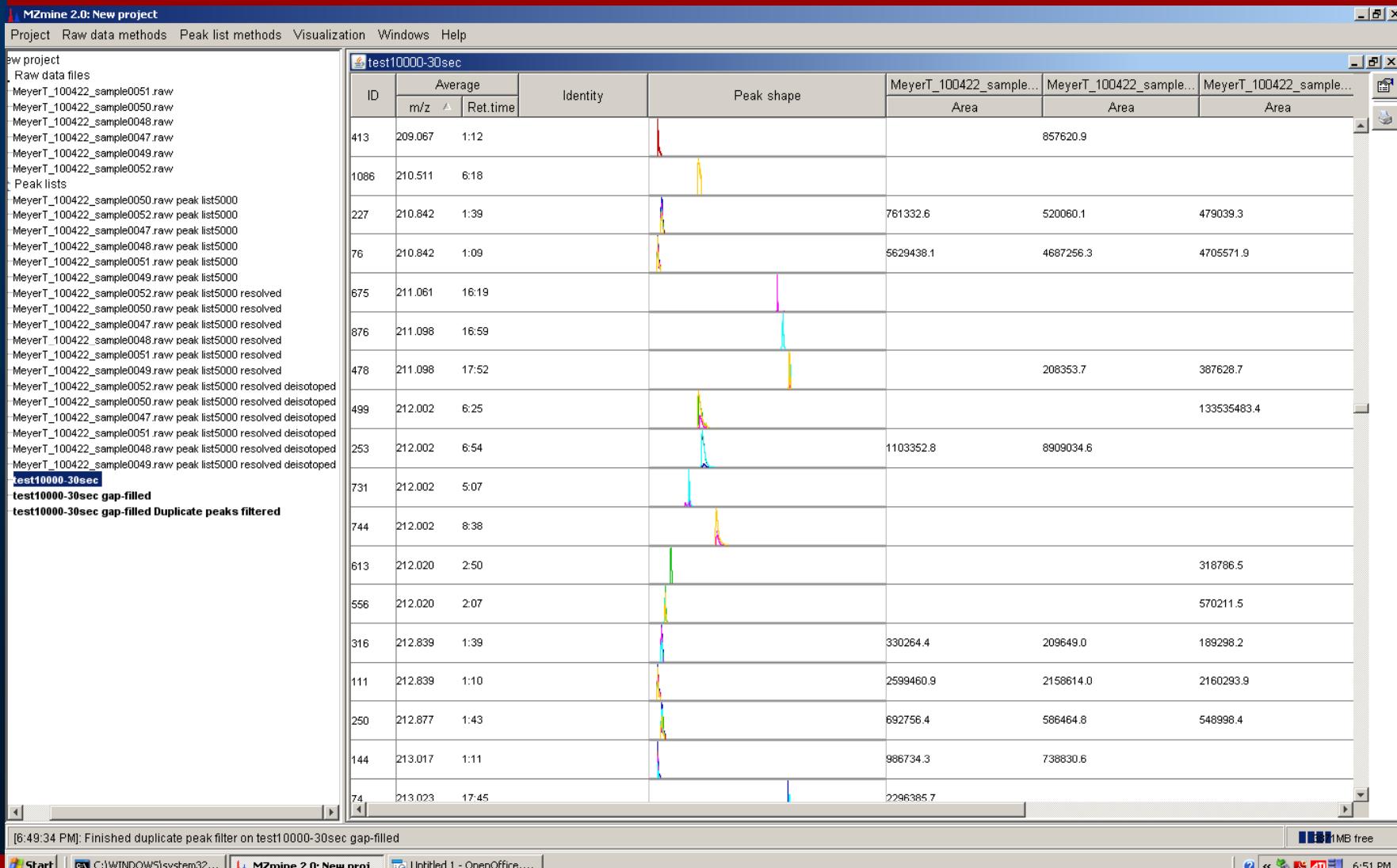
Item	Priority	Status	% done
Cap filling test10000-30sec	NORMAL	PROCESSING	5%

[6:46:15 PM]: Running gap filler on test1 0000-30sec

Start C:\WINDOWS\system32... MZmine 2.0: New proj... Untitled 1 - OpenOffice....

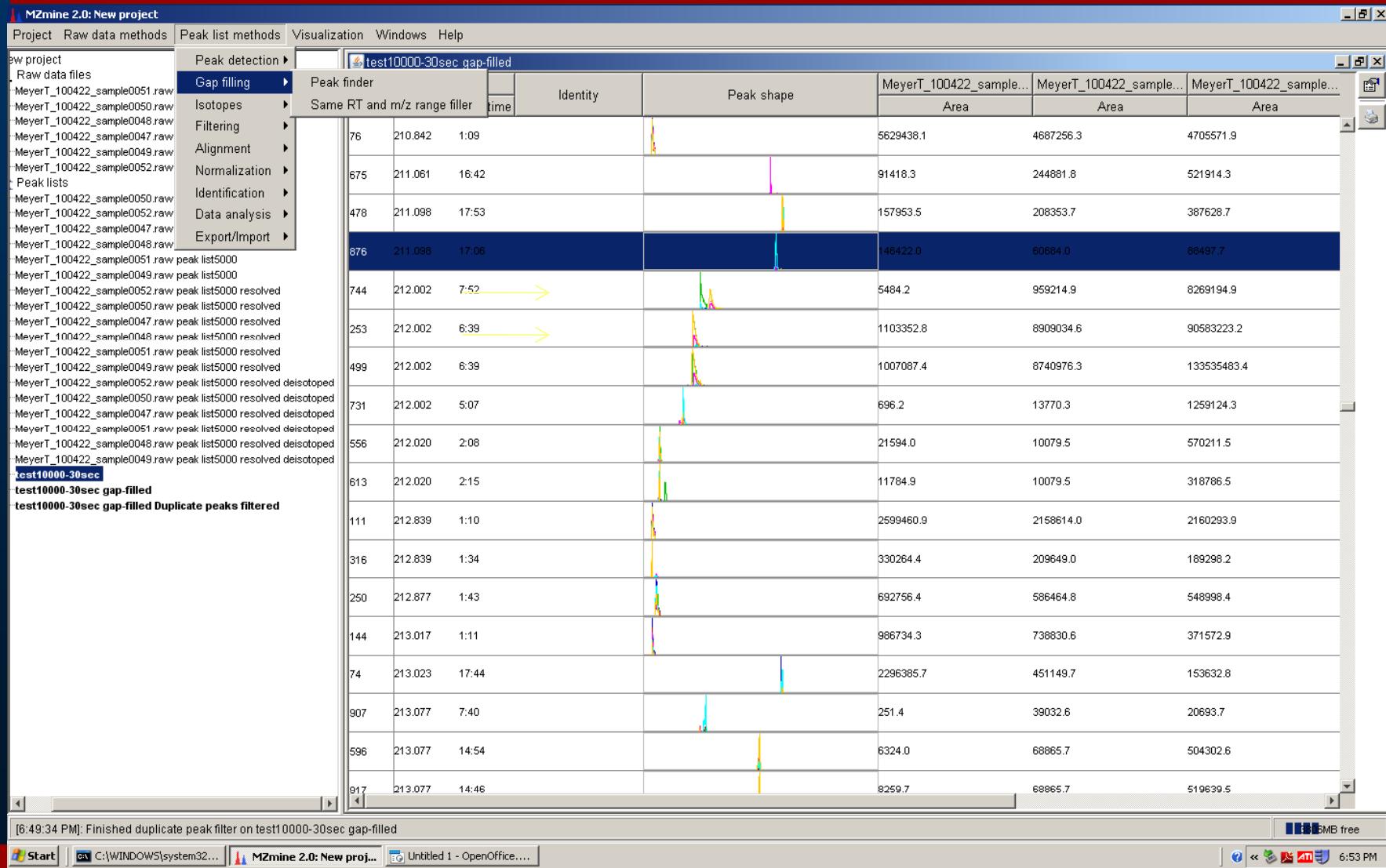


MZmine: alignment results





MZmine: gap filling





MZmine: removal of duplicates

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project Raw data files MeyerT_100422_sample0051.raw MeyerT_100422_sample0050.raw MeyerT_100422_sample0048.raw MeyerT_100422_sample0047.raw MeyerT_100422_sample0049.raw MeyerT_100422_sample0052.raw Peak lists MeyerT_100422_sample0050.raw MeyerT_100422_sample0052.raw MeyerT_100422_sample0047.raw MeyerT_100422_sample0048.raw MeyerT_100422_sample0051.raw peak list5000 MeyerT_100422_sample0049.raw peak list5000 MeyerT_100422_sample0052.raw peak list5000 resolved MeyerT_100422_sample0050.raw peak list5000 resolved MeyerT_100422_sample0047.raw peak list5000 resolved MeyerT_100422_sample0048.raw peak list5000 resolved MeyerT_100422_sample0051.raw peak list5000 resolved MeyerT_100422_sample0049.raw peak list5000 resolved MeyerT_100422_sample0052.raw peak list5000 resolved deisotoped MeyerT_100422_sample0050.raw peak list5000 resolved deisotoped MeyerT_100422_sample0047.raw peak list5000 resolved deisotoped MeyerT_100422_sample0051.raw peak list5000 resolved deisotoped MeyerT_100422_sample0048.raw peak list5000 resolved deisotoped MeyerT_100422_sample0049.raw peak list5000 resolved deisotoped test10000-30sec test10000-30sec gap-filled test10000-30sec gap-filled Duplicate peaks filtered

Peak detection > Gap filling > Isotopes > Filtering > Alignment > Normalization > Identification > Data analysis > Export/Import

test10000-30sec gap-filled Duplicate peaks filtered

ID	Average m/z	Identity	Peak shape	MeyerT_100422_sample... Area	MeyerT_100422_sample... Area	MeyerT_100422_sample... Area
478	211.098	17:53		157953.5	208353.7	387628.7
876	211.098	17:06		146422.0	60684.0	68497.7
744	212.002	7:52		5484.2	959214.9	8269194.9
499	212.002	6:39		1007087.4	8740976.3	133535483.4
731	212.002	5:07		696.2	13770.3	1259124.3
556	212.020	2:08		21594.0	10079.5	570211.5
111	212.839	1:10		2599460.9	2158614.0	2160293.9
250	212.877	1:43		692756.4	586464.8	548998.4
144	213.017	1:11		986734.3	738830.6	371572.9
74	213.023	17:44		2296385.7	451149.7	153632.8
907	213.077	7:40		251.4	39032.6	20693.7
917	213.077	14:46		8259.7	68865.7	519639.5
945	213.077	12:07		1125.9	30266.0	39073.6
212	213.113	18:02		503510.6	1162807.6	1918710.3
620	214.005	6:38		401.1	10621.0	693328.5
598	214.837	1:10		327047.0	202366.4	430162.6
303	214.874	1:41		410872.2	347242.2	290299.1

[6:49:34 PM]: Finished duplicate peak filter on test10000-30sec gap-filled

Start C:\WINDOWS\system32... MZmine 2.0: New proj... Untitled 1 - OpenOffice....

6:54 PM



MZmine: normalization options

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project Raw data files MeyerT_100422_sample0051.raw MeyerT_100422_sample0050.raw MeyerT_100422_sample0048.raw MeyerT_100422_sample0047.raw MeyerT_100422_sample0049.raw MeyerT_100422_sample0052.raw Peak lists MeyerT_100422_sample0050.raw MeyerT_100422_sample0052.raw MeyerT_100422_sample0047.raw MeyerT_100422_sample0048.raw MeyerT_100422_sample0051.raw peak list5000 MeyerT_100422_sample0049.raw peak list5000 MeyerT_100422_sample0052.raw peak list5000 resolved MeyerT_100422_sample0050.raw peak list5000 resolved MeyerT_100422_sample0047.raw peak list5000 resolved MeyerT_100422_sample0048.raw peak list5000 resolved MeyerT_100422_sample0051.raw peak list5000 resolved MeyerT_100422_sample0049.raw peak list5000 resolved MeyerT_100422_sample0052.raw peak list5000 resolved deisotoped MeyerT_100422_sample0050.raw peak list5000 resolved deisotoped MeyerT_100422_sample0047.raw peak list5000 resolved deisotoped MeyerT_100422_sample0051.raw peak list5000 resolved deisotoped MeyerT_100422_sample0048.raw peak list5000 resolved deisotoped MeyerT_100422_sample0049.raw peak list5000 resolved deisotoped test10000-30sec test10000-30sec gap-filled test10000-30sec gap-filled Duplicate peaks filtered

Peak detection > Gap filling > Isotopes > Filtering > Alignment > Normalization > Identification > Data analysis > Export/Import

test10000-30sec gap-filled Duplicate peaks filtered

ID	Average		Identity	Peak shape	MeyerT_100422_sample...	MeyerT_100422_sample...	MeyerT_100422_sample...
	m/z	Ret.time			Area	Area	Area
675	211.061	16:42			91418.3	244881.8	521914.3
744	212.002	7:52			5484.2	959214.9	8269194.9
499	212.002	6:39			1007087.4	8740976.3	133535483.4
731	212.002	5:07			696.2	13770.3	1259124.3
556	212.020	2:08			21594.0	10079.5	570211.5
111	212.839	1:10			2599460.9	2158614.0	2160293.9
250	212.877	1:43			692756.4	586464.8	548998.4
144	213.017	1:11			986734.3	738830.6	371572.9
74	213.023	17:44			2296385.7	451149.7	153632.8
907	213.077	7:40			251.4	39032.6	20693.7
917	213.077	14:46			8259.7	68865.7	519639.5
945	213.077	12:07			1125.9	30266.0	39073.6
212	213.113	18:02			503510.6	1162807.6	1918710.3
620	214.005	6:38			401.1	10621.0	693328.5
598	214.837	1:10			327047.0	202366.4	430162.6
303	214.874	1:41			410872.2	347242.2	290299.1

[6:49:34 PM]: Finished duplicate peak filter on test10000-30sec gap-filled

Start C:\WINDOWS\system32... MZmine 2.0: New proj... Untitled 1 - OpenOffice....



MZmine: identification options

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project
Raw data files
MeyerT_100422_sample0051.raw
MeyerT_100422_sample0050.raw
MeyerT_100422_sample0049.raw
MeyerT_100422_sample0047.raw
MeyerT_100422_sample0049.raw
MeyerT_100422_sample0052.raw
Peak lists
MeyerT_100422_sample0050.raw
MeyerT_100422_sample0052.raw
MeyerT_100422_sample0047.raw
MeyerT_100422_sample0048.raw
MeyerT_100422_sample0051.raw peak list5000
MeyerT_100422_sample0049.raw peak list5000
MeyerT_100422_sample0052.raw peak list5000 resolved
MeyerT_100422_sample0050.raw peak list5000 resolved
MeyerT_100422_sample0047.raw peak list5000 resolved
MeyerT_100422_sample0048.raw peak list5000 resolved
MeyerT_100422_sample0051.raw peak list5000 resolved
MeyerT_100422_sample0049.raw peak list5000 resolved
MeyerT_100422_sample0052.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0050.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0047.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0051.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0048.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0049.raw peak list5000 resolved deisotoped
test10000-30sec
test10000-30sec gap-filled
test10000-30sec gap-filled Duplicate peaks filtered

Peak detection >
Gap filling >
Isotopes >
Filtering >
Alignment >
Normalization >
Identification > Custom database search
Data analysis >
Export/Import >

test10000-30sec gap-filled Duplicate peaks filtered

test10000-30sec gap-filled Duplicate peaks filtered							
ID	Average m/z	Ret.time	Identity	Peak shape	MeyerT_100422_sample... Area	MeyerT_100422_sample... Area	MeyerT_100422_sample... Area
675	211.061	16:42			91418.3	244881.8	521914.3
478	211.098	17:53			157953.5	208353.7	387628.7
					146422.0	60664.0	88497.7
					5484.2	959214.9	8269194.9
					1007087.4	8740976.3	133535483.4
					696.2	13770.3	1259124.3
556	212.020	2:08			21594.0	10079.5	570211.5
111	212.839	1:10			2599460.9	2158614.0	2160293.9
250	212.877	1:43			692756.4	586464.8	548998.4
144	213.017	1:11			986734.3	738830.6	371572.9
74	213.023	17:44			2296385.7	451149.7	153632.8
907	213.077	7:40			251.4	39032.6	20693.7
917	213.077	14:46			8259.7	68865.7	519639.5
945	213.077	12:07			1125.9	30266.0	39073.6
212	213.113	18:02			503510.6	1162807.6	1918710.3
620	214.005	6:38			401.1	10621.0	693328.5
598	214.837	1:10			327047.0	202366.4	430162.6
303	214.874	1:41			410872.2	347242.2	290299.1

[6:49:34 PM]: Finished duplicate peak filter on test1 0000-30sec gap-filled



MZmine: accurate mass online search

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project

- Raw data files
- MeyerT_100422_sample0051.raw
- MeyerT_100422_sample0050.raw
- MeyerT_100422_sample0048.raw
- MeyerT_100422_sample0047.raw
- MeyerT_100422_sample0049.raw
- MeyerT_100422_sample0052.raw
- Peak lists
- MeyerT_100422_sample0050.raw peak list5000
- MeyerT_100422_sample0052.raw peak list5000
- MeyerT_100422_sample0047.raw peak list5000
- MeyerT_100422_sample0048.raw peak list5000
- MeyerT_100422_sample0051.raw peak list5000
- MeyerT_100422_sample0049.raw peak list5000
- MeyerT_100422_sample0052.raw peak list5000 resolved
- MeyerT_100422_sample0050.raw peak list5000 resolved
- MeyerT_100422_sample0047.raw peak list5000 resolved
- MeyerT_100422_sample0048.raw peak list5000 resolved
- MeyerT_100422_sample0051.raw peak list5000 resolved
- MeyerT_100422_sample0049.raw peak list5000 resolved
- MeyerT_100422_sample0052.raw peak list5000 resolved deisotoped
- MeyerT_100422_sample0050.raw peak list5000 resolved deisotoped
- MeyerT_100422_sample0047.raw peak list5000 resolved deisotoped
- MeyerT_100422_sample0048.raw peak list5000 resolved deisotoped
- MeyerT_100422_sample0051.raw peak list5000 resolved deisotoped
- MeyerT_100422_sample0049.raw peak list5000 resolved deisotoped

test10000-30sec

test10000-30sec gap-filled

test10000-30sec gap-filled Duplicate peaks filtered

Online database search setup dialog

ID	Average m/z	Identity Ret.time	Peak shape	MeyerT_100422_sample... Area	MeyerT_100422_sample... Area	MeyerT_100422_sample... Area
675	211.061	16:42		91418.3	244881.8	521914.3
478	211.098	17:53		157953.5	208353.7	387628.7
876	211.098	17:06		146422.0	60684.0	88497.7
744	212.002	7:52		5484.2	959214.9	8269194.9
499	212.002	6:35	Database	Human Metabolome Database	8740976.3	133535483.4
731	212.002	5:07	Peak m/z	832.052	13770.3	1259124.3
556	212.020	2:08	Charge	1	10079.5	570211.5
111	212.839	1:10	Ionization method	-H	2158614.0	2160293.9
250	212.877	1:43	Neutral mass	1.008	586464.8	548998.4
144	213.017	1:11	Number of results	5	738830.6	371572.9
74	213.023	17:4	Mass tolerance	0.003	451149.7	153632.8
907	213.077	7:40	Isotope pattern filter	<input checked="" type="checkbox"/>	39032.6	20693.7
917	213.077	14:46	Isotope pattern score threshold	65%	68865.7	519639.5
945	213.077	12:07		8259.7	30266.0	39073.6
212	213.113	18:02		1125.9	1162807.6	1918710.3
620	214.005	6:38		503510.6	10621.0	693328.5
598	214.837	1:10		401.1	327047.0	202366.4
303	214.874	1:41		410872.2	347242.2	430162.6

[6:49:34 PM]: Finished duplicate peak filter on test10000-30sec gap-filled

Start C:\WINDOWS\system32... MZmine 2.0: New proj... Untitled 1 - OpenOffice....

5MB free 6:58 PM



Metabolomics Databases

- Human Metabolome Database:
<http://www.hmdb.ca/>
- BioCyc: <http://biocyc.org/>
- Metlin: <http://metlin.scripps.edu/>
- KEGG: <http://www.genome.jp/kegg/>
- PubChem (not biology specific):
<http://pubchem.ncbi.nlm.nih.gov/>



MS/MS databases

- Metlin

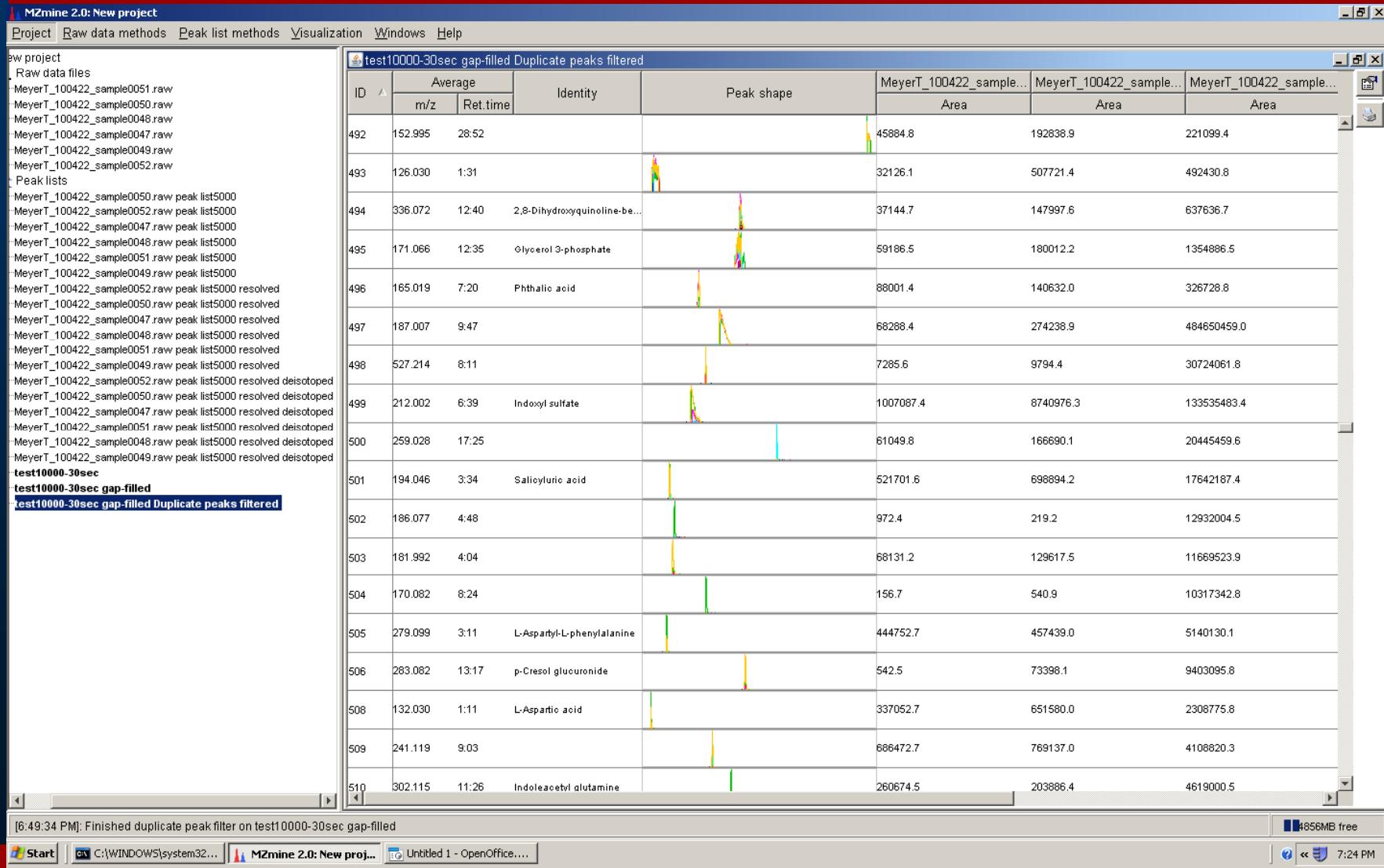
<http://metlin.scripps.edu/>

- MassBank (not only metabolites)

<http://www.massbank.jp/?lang=en>



MZmine: identification results





Monoisotopic vs Average Mass

Two stable isotopes important in biochemistry

Carbon-12 (100 %) and Carbon-13 (~1.1 %)

Sulfur-32 (100 %) and Sulfur-34 (4.4 %)

Tryptophan statistically can contain:

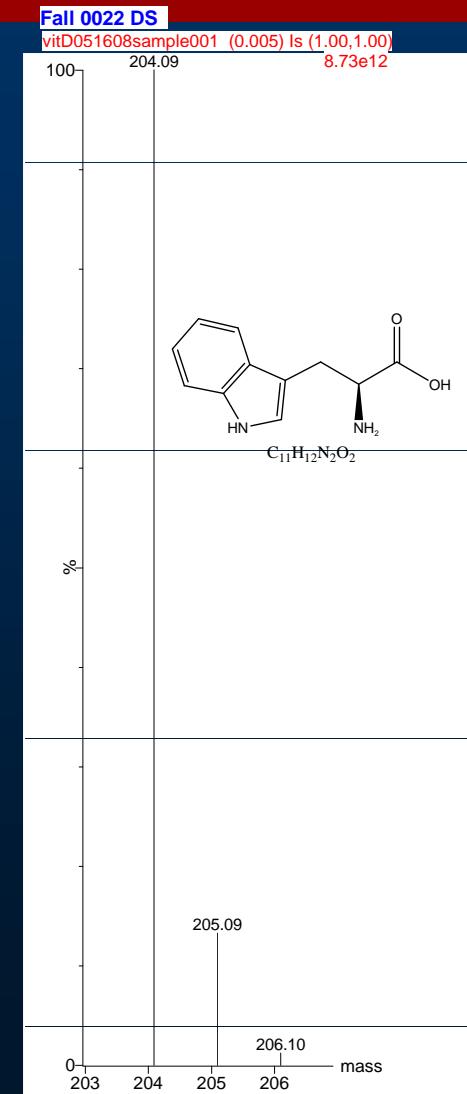
no carbon-13 (M): 204.09 Da (100 %)

one carbon-13 (M+1): 205.09 Da (11.9 %)

two carbons-13 (M+2): 206.09 Da (1.4 %)

These are monoisotopic masses

Average mass = $(204.09 * 100 + 205.09 * 11.9 + 206.09 * 1.4) / 113.2 = 204.22$ (molecular weight, g/mol)





Elemental composition from accurate mass

^1H	1.0078 u
^{12}C	12.0000 u
^{14}N	14.0031 u
^{16}O	15.9949 u

What is 28 u?

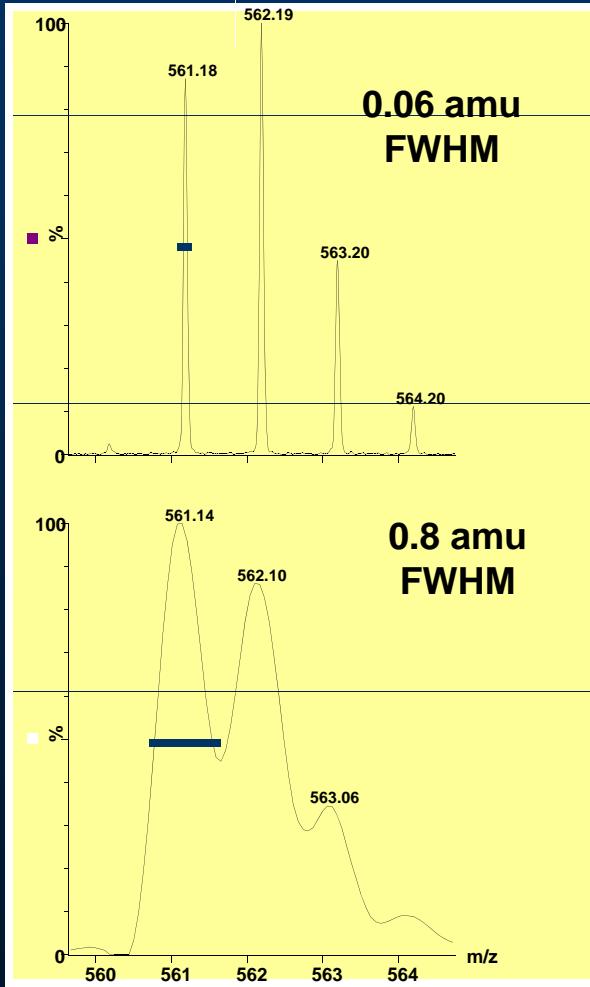
N_2 (2×14 u), CO (12 u + 16 u) or C_2H_4 (2×12 u + 4×1 u)?

What is 28.0313 u? [high accuracy]

C_2H_4 (2×12.0000 u + 4×1.0078 u)



High Resolution



High Resolution: $R = 561/0.06 \sim 9,000$

TOF: 7,000-50,000
Orbitrap: 10^4 - 10^5
FT ICR: 10^5 - 10^6

Nominal Mass Resolution
(<1000)
 $R = 561/0.8 \sim 700$

Accurate mass measurement is possible without high resolution.
High resolution improves precision
of mass measurement.



Mass of an electron becomes important at high accuracies

Even Electron (EE) Ions

Typically generated by chemical ionization techniques and electrospray

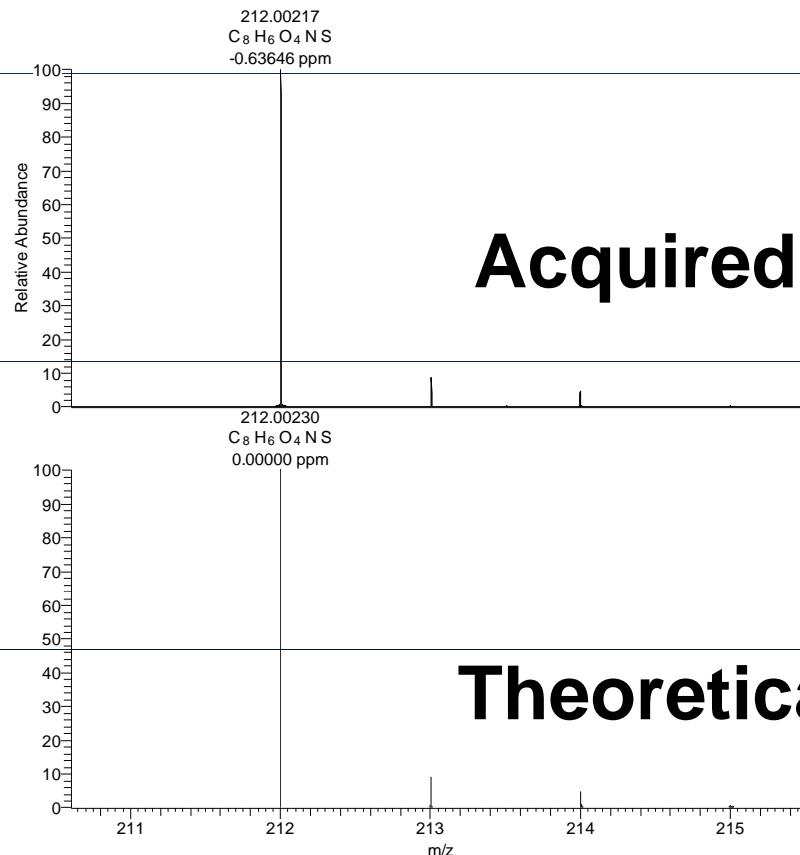


Orbitrap can achieve < 1 ppm accuracy



Identification based on accurate mass

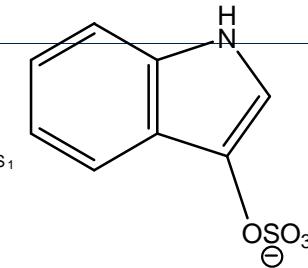
Matching accurate mass
and isotopic peak ratio



Acquired spectrum

NL:
6.95E6
MeyerT_100422_sampl
e0062#636 RT: 6.29
AV: 1 T: FTMS {1,1} - p
ESI Full ms
[70.00-800.00]

NL:
8.59E5
C₈H₆O₄NS:
C₈H₆O₄N₁S₁
pa Chrg -1



Theoretical spectrum

$$\text{Error} = -0.00013 \text{ Da}/212.0023 \text{ Da} * 1000,000 = 0.6 \text{ parts per million (ppm)}$$



MZmine: data export options

MZmine 2.0: New project

Project Raw data methods Peak list methods Visualization Windows Help

New project
Raw data files
MeyerT_100422_sample0051.raw
MeyerT_100422_sample0050.raw
MeyerT_100422_sample0048.raw
MeyerT_100422_sample0047.raw
MeyerT_100422_sample0049.raw
MeyerT_100422_sample0052.raw
Peak lists
MeyerT_100422_sample0050.raw
MeyerT_100422_sample0052.raw
MeyerT_100422_sample0047.raw
MeyerT_100422_sample0048.raw
MeyerT_100422_sample0051.raw peak list5000
MeyerT_100422_sample0049.raw peak list5000
MeyerT_100422_sample0052.raw peak list5000 resolved
MeyerT_100422_sample0050.raw peak list5000 resolved
MeyerT_100422_sample0047.raw peak list5000 resolved
MeyerT_100422_sample0048.raw peak list5000 resolved
MeyerT_100422_sample0051.raw peak list5000 resolved
MeyerT_100422_sample0049.raw peak list5000 resolved
MeyerT_100422_sample0052.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0050.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0047.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0048.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0051.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0049.raw peak list5000 resolved deisotoped
MeyerT_100422_sample0052.raw peak list5000 resolved deisotoped
test10000-30sec
test10000-30sec gap-filled
test10000-30sec gap-filled Duplicate peaks filtered

Peak detection >
Gap filling >
Isotopes >
Filtering >
Alignment >
Normalization >
Identification >
Data analysis >
Export/Import >

Export to CSV file Ctrl+C
Export to XML file Ctrl+X
Import from XML file Ctrl+I

test10000-30sec gap-filled Duplicate peaks filtered

test10000-30sec gap-filled Duplicate peaks filtered					
ID	Average		Identity	Peak shape	
	m/z	Ret.time			
492	152.995	28:52			45884.8 192638.9 221099.4
493	126.030	1:31	Glycerol 3-phosphate		32126.1 507721.4 492430.8
494	336.072	12:40	2,8-Dihydroxyquinoline-be...		37144.7 147997.6 637636.7
			Phthalic acid		88001.4 140632.0 326728.8
497	187.007	9:47			68288.4 274238.9 484650459.0
498	527.214	8:11			7285.6 9794.4 30724061.8
499	212.002	6:39	Indoxyl sulfate		1007087.4 8740976.3 133535483.4
500	259.028	17:25			61049.8 166690.1 20445459.6
501	194.046	3:34	Salicyluric acid		521701.6 698894.2 17642187.4
502	186.077	4:48			972.4 219.2 12932004.5
503	181.992	4:04			68131.2 129617.5 11669523.9
504	170.082	8:24			156.7 540.9 10317342.8
505	279.099	3:11	L-Aspartyl-L-phenylalanine		444752.7 457439.0 5140130.1
506	283.082	13:17	p-Cresol glucuronide		542.5 73398.1 9403095.8
508	132.030	1:11	L-Aspartic acid		337052.7 651580.0 2308775.8
509	241.119	9:03			686472.7 769137.0 4108820.3
510	302.115	11:26	Indoleacetyl glutamine		260674.5 203886.4 4619000.5

[6:49:34 PM]: Finished duplicate peak filter on test1 0000-30sec gap-filled

808MB free

Start C:\WINDOWS\system32... MZmine 2.0: New proj... Untitled 1 - OpenOffice....

7:24 PM



Manual Revision of Metabolomics Data

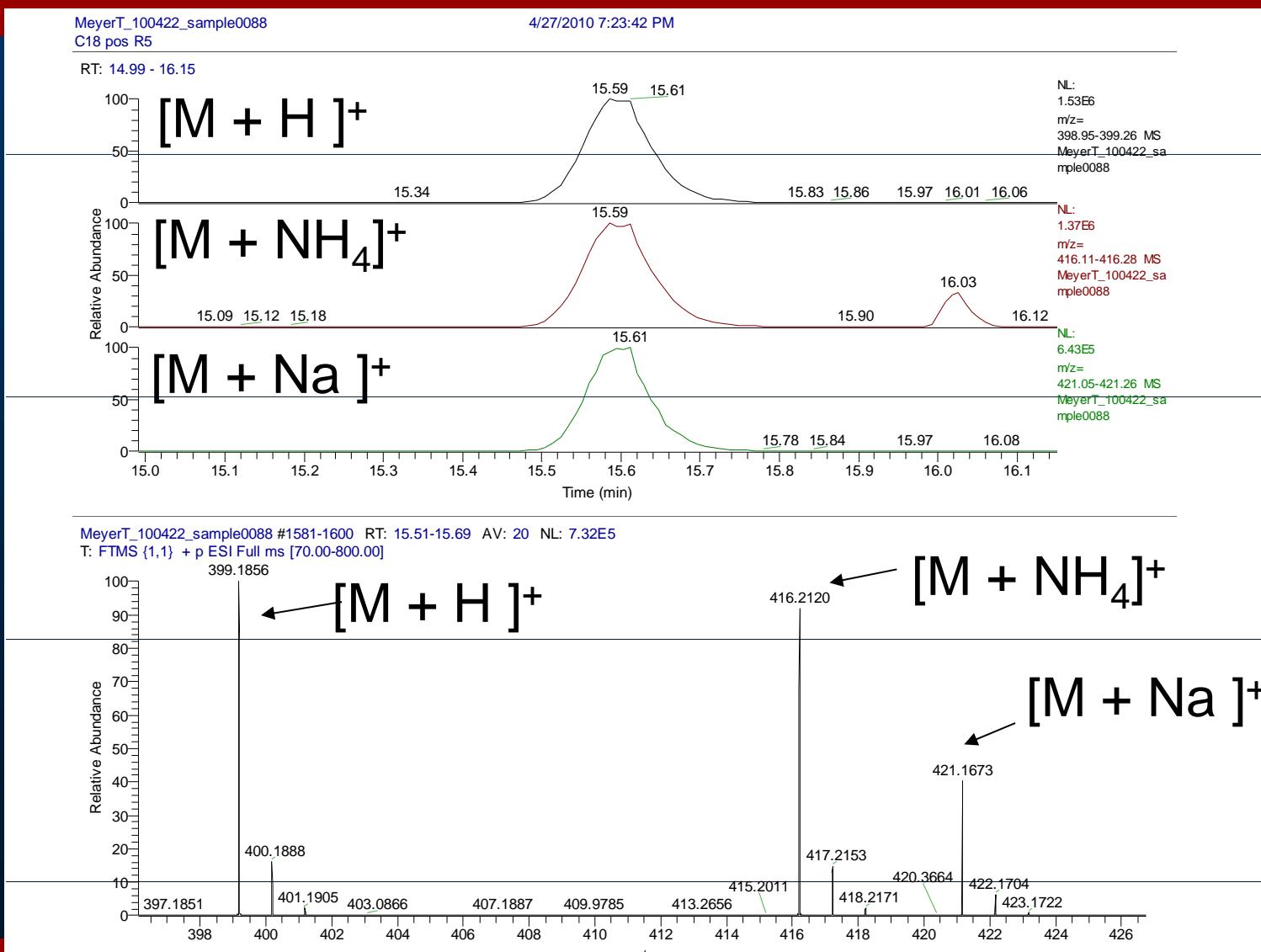
**Many software tools can't remove some artifacts:
unusual adducts, fragments**

*A majority of detected features may
be isotopes, adducts, fragments
and/or impurities*

Baran R et al 2010, Anal Chem

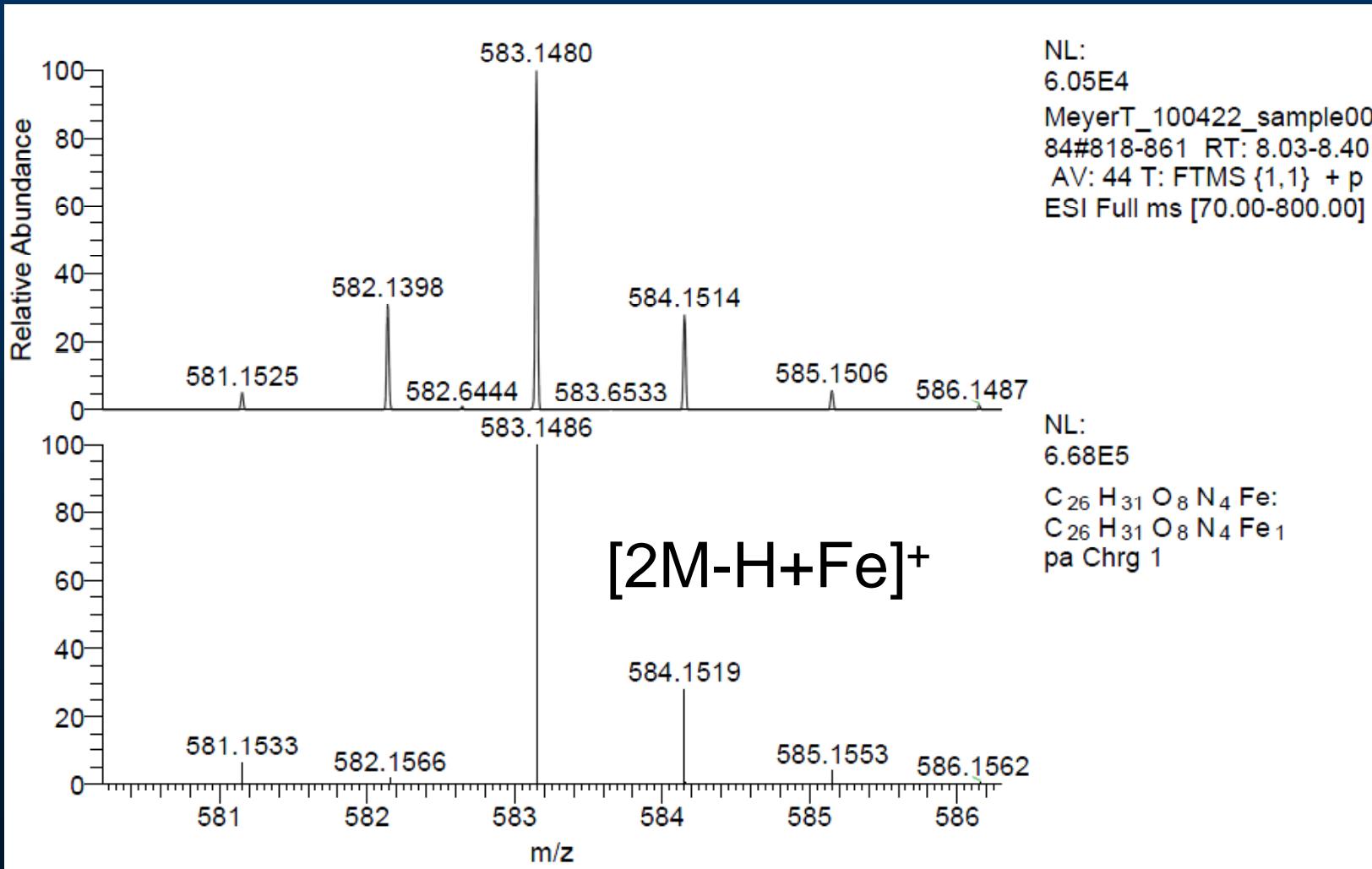


ESI-MS Adducts



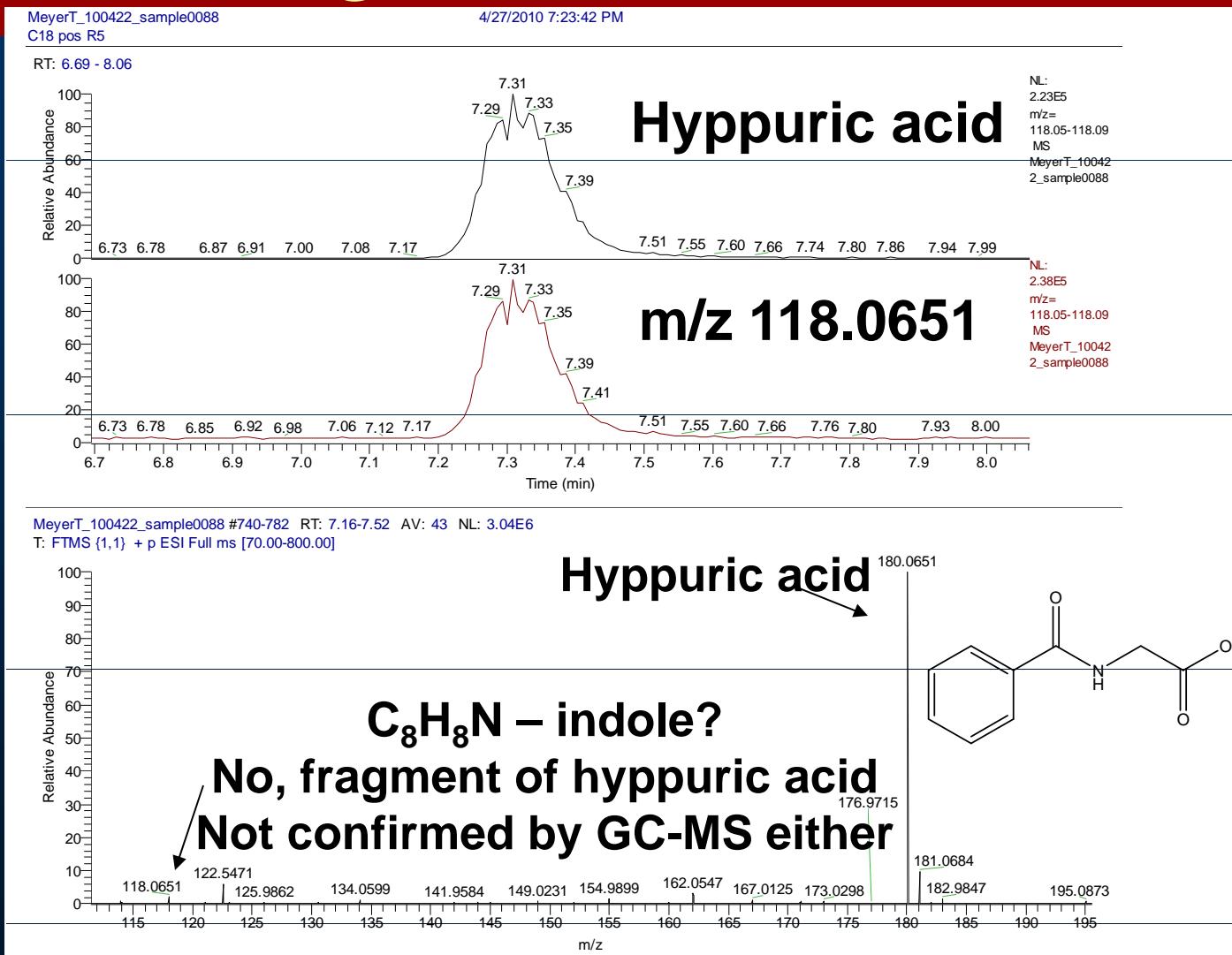


Unusual LC-ESI-MS Adducts





Fragments in LC-MS



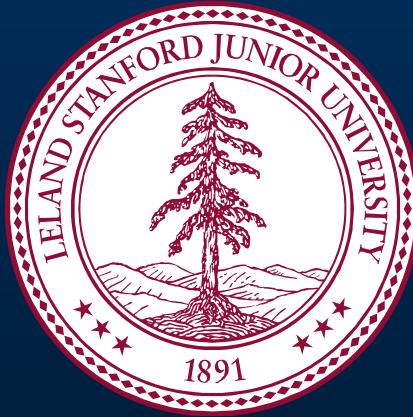


Conclusions

- Open source MZmine software is capable to perform automated peak extraction, alignment and annotation from high resolution LC/MS metabolomics and proteomics data
- Manual curation of the results is required to rule out fragments, some adducts and isotopes



Acknowledgements



- Allis Chien
- Theresa McLaughlin
- Karolina Krasinska
- Chris Adams
- Anna Okumu

- Tim Meyer
- Natalie Plummer
- Tammy Sirich

- Angela Marcobal
- Justin Sonneburg

- Mike Snyder