

Overview of METLIN and MassBank libraries

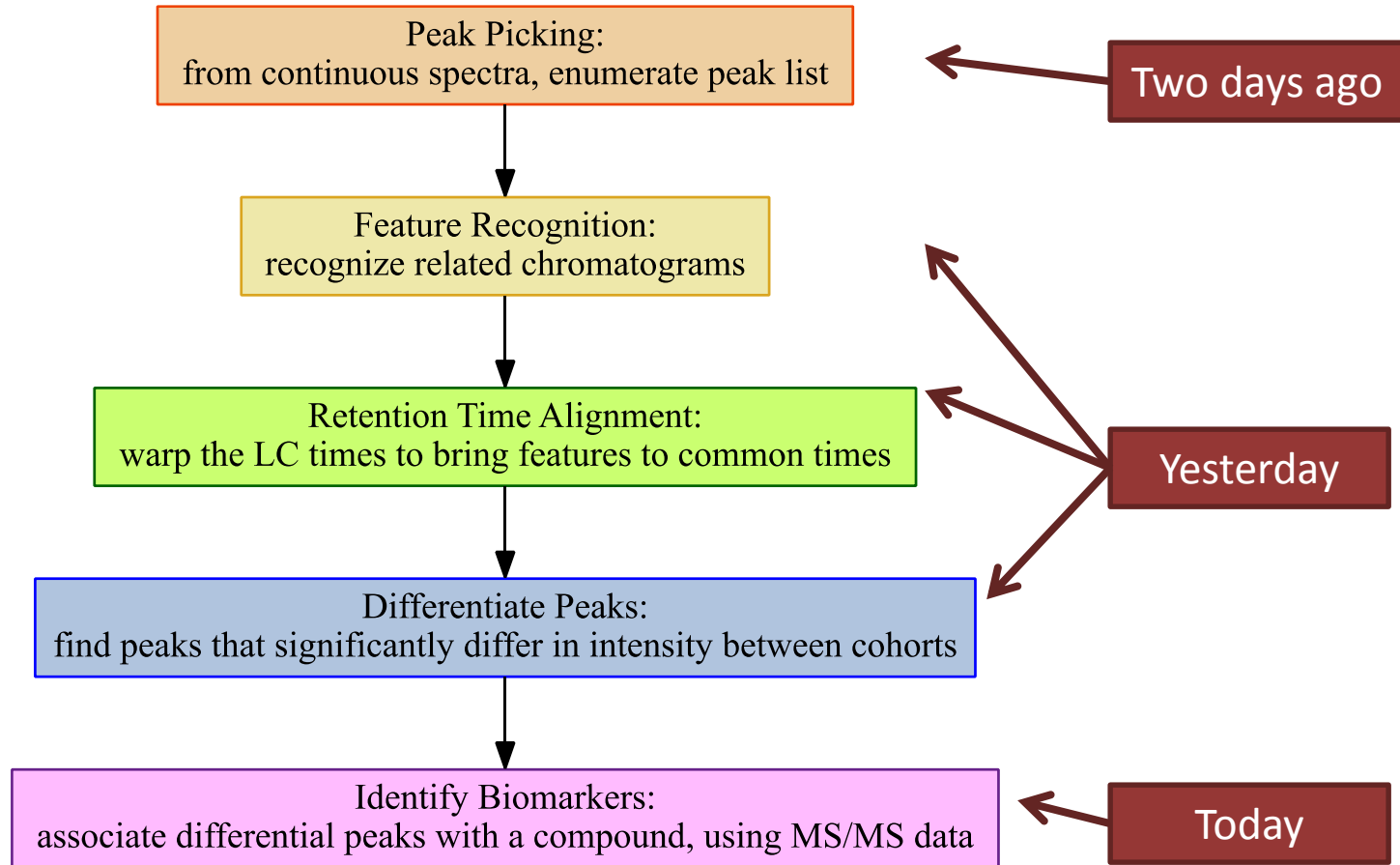
David L. Tabb, Ph.D.

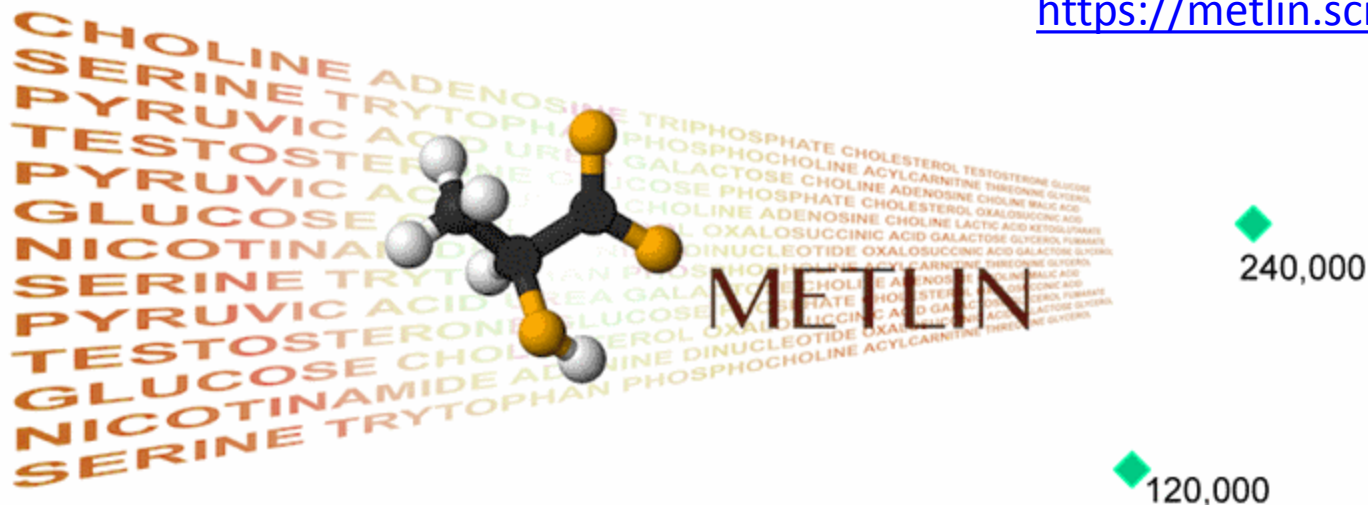
dtabb1973@gmail.com

Overview

- Investigating search types available within the METLIN database at Scripps Research Institute
- Examining the international federated database at MassBank

Metabolome informatics

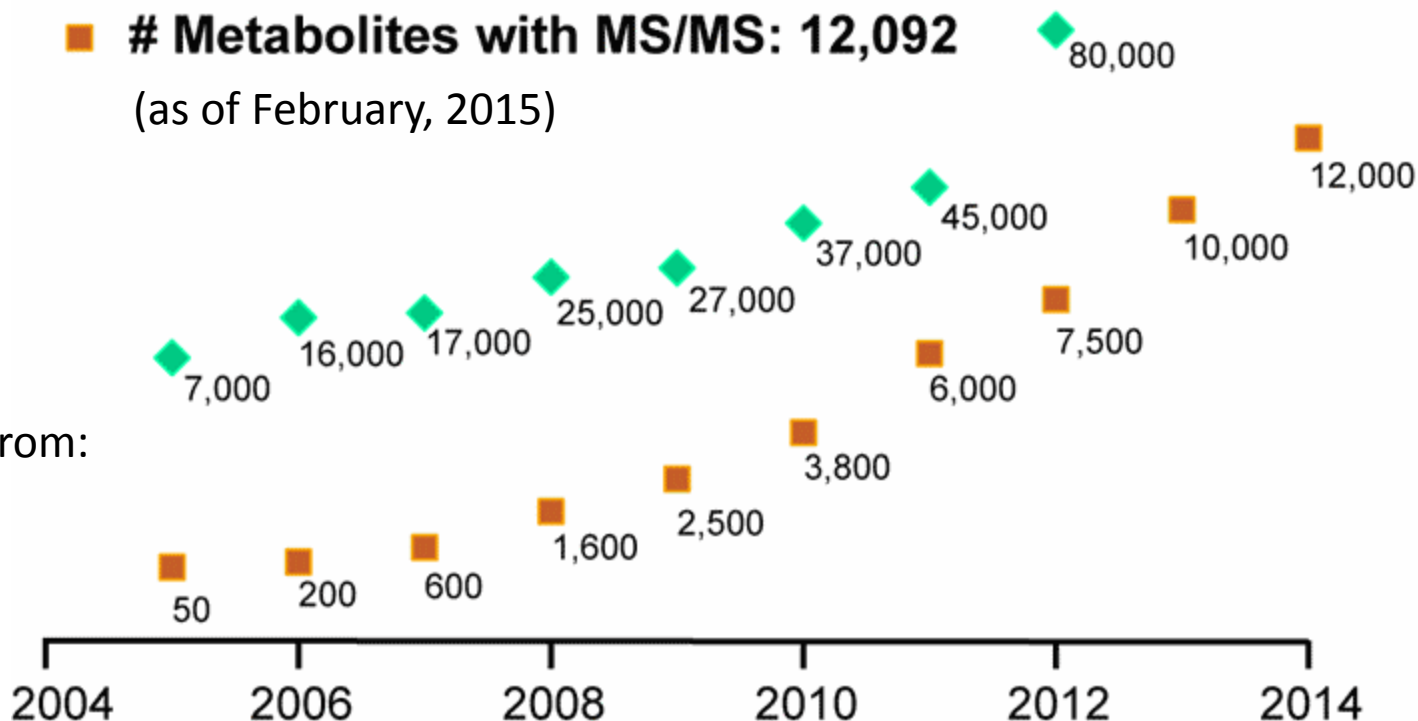




◆ # Metabolites: 240,528

■ # Metabolites with MS/MS: 12,092

(as of February, 2015)



Chemicals from:

Agilent

SIGMA

Cayman

Cambridge

Chromadex

METLIN origins


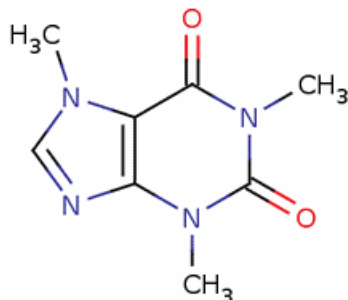
Its name derives from “Metabolite Link,” connecting information from these sources:

- Structural and physical data
- FTMS data from reference samples
- MS/MS data from reference samples
- LC-MS profiles from human and other samples

Where did these spectra come from?

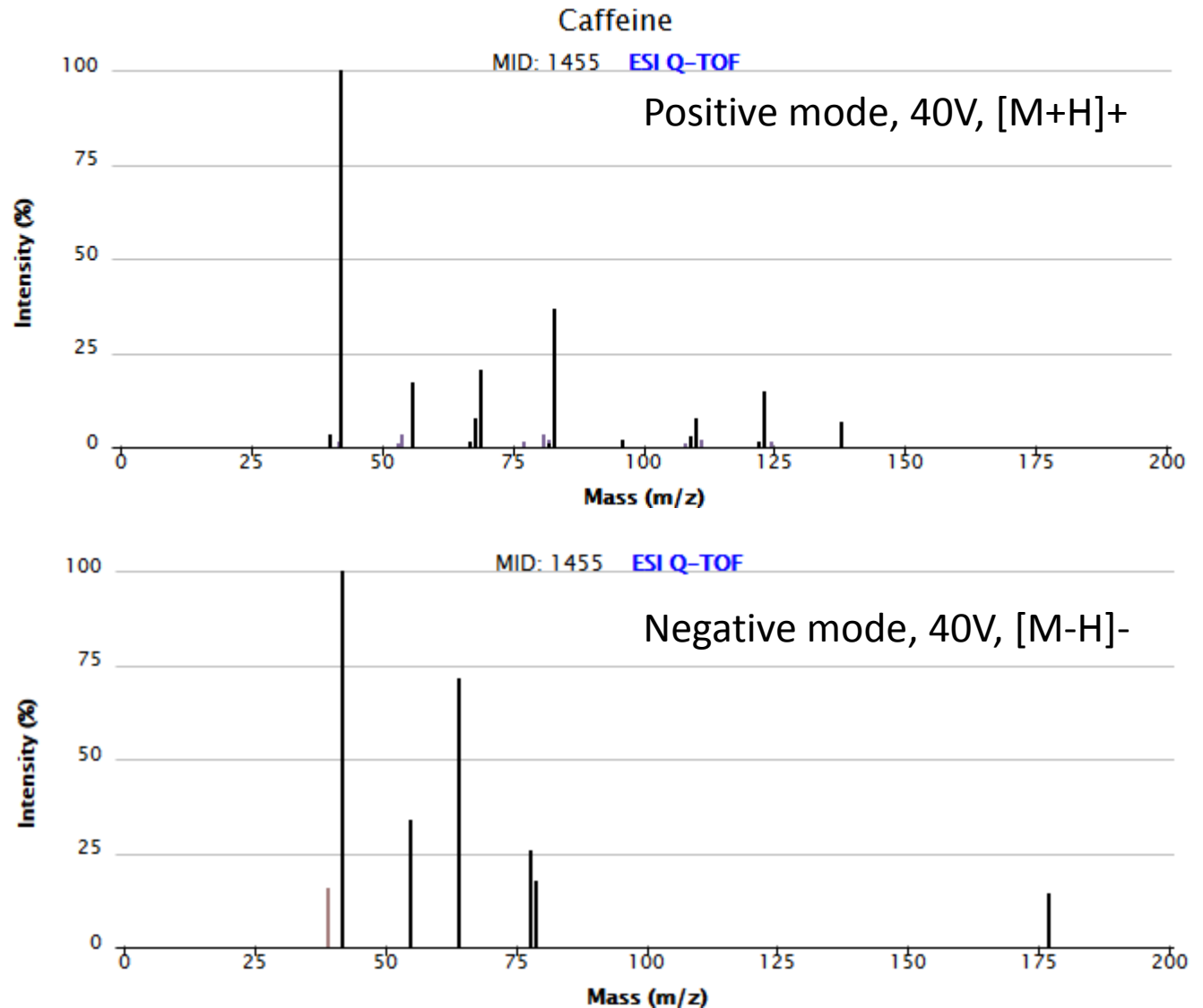
- Siuzdak Lab formed partnerships with chemical companies, who provided reference compounds to his team.
- At Scripps, these samples were subjected to multiple collision energies in both polarities to produce MS/MS scans and high-resolution FTMS scans.
- The library is accessed only via website.

An entry for our friend

MID	1455		
Mass	194.080376	<input type="button" value="m/z calculator"/>	
Name	Caffeine		
Synonym	1,3,7-Trimethylxanthine; 7-methyl Theophylline; Thein; 1-methyl-Theobromine; Methylxanthine theophylline; 1,3,7-Trimethyl-3,7-dihydro-1H-purine-2,6-dione; Lanorinal; 1,3,7-Trimethyl-2,6-dioxopurine; 3,7-Dihydro-1,3,7-trimethyl-1H-purine-2,6-dione; Methyltheobromide; Guanine; Anhydrous caffeine (JP15); Monohydrate Caffeine		
Systematic Name	1,3,7-trimethylpurine-2,6-dione		
Formula	C ₈ H ₁₀ N ₄ O ₂		
CAS	58-08-2		
Purchase Option	Sigma-Aldrich: C1778 SIGMA-ALDRICH Chromadex: ASB-00003032-010  ChromaDex		
LMID			
KEGG	C07481		
HMDB	HMDB01847		
PubChem	2519		
Notes	naturally occurring alkaloid Dollery, Colin Therapeutic Drugs, 2nd Ed. 1999 p. C4		
Updated	2014-07-29 15:58:37		
Drug	N		
Structure	<div></div> <div><input type="button" value="Structure View"/></div>		

Visualizing MS/MS

In both positive and negative ion mode, energies from 0 to 40V are available for display.



Search possibilities

Simple

Mass:
Tolerance (\pm): ppm
Charge:

Neutral	M+H
Positive	M+NH ₄
Negative	M+Na
	M+H-2H ₂ O
	M+H-H ₂ O
	M+K
	M+ACN+H
	M+ACN+Na
	M+2Na-H
	M+2H
	M+3H
	M+H+Na
	M+2H+Na
	M+2Na
	M+2Na+H
	M+Li
	M+CH ₃ OH+H

Remove peptides from search: ☐

Advanced

MID:
Mass: -
Name:
Formula:
CAS:
KEGG:
Search only the MS/MS data ☐
Remove peptides from search ☐
Remove drug from search ☐

Working from your data

Batch

Masses:

Charge:

Neutral	M-H
Positive	M-H ₂ O-H
Negative	M+Na-2H
	M+Cl
	M+K-2H
	M+FA-H
	M-2H
	M-3H
	M+CH ₃ COO
	M+F

Accuracy (ppm):

Display Structure:

☐

Remove peptides from search:

☐

Find Metabolites

Reset

Fragment

Fragment m/z:
(Maximum Number of m/z: 5)

Tolerance (±):

 ppm

Mode:

Filter out fragments with
intensity less than:

 %

Order by:

☐ Δppm ☒ intensity

Fragments with Structure Only

☐

Precursor m/z (optional)

☐

Find Fragment

Reset

Highly specific matches by MS/MS

MS/MS Spectrum Match

Peaks:
(MAX: 30 peaks)

<i>m/z</i>	<i>intensity</i>
177.040	956
79.029	569
78.022	520
178.047	441
121.028	308
64.007	128

Mode:

Positive
Negative

M-H
M-H2O-H
M+Na-2H
M+Cl
M+K-2H
M+FA-H
M-2H
M-3H
M+CH3COO
M+F

*To select multiple Adducts:
Hit Ctrl + Adducts
Hit Command + Adducts

Collision Energy (eV): 20eV

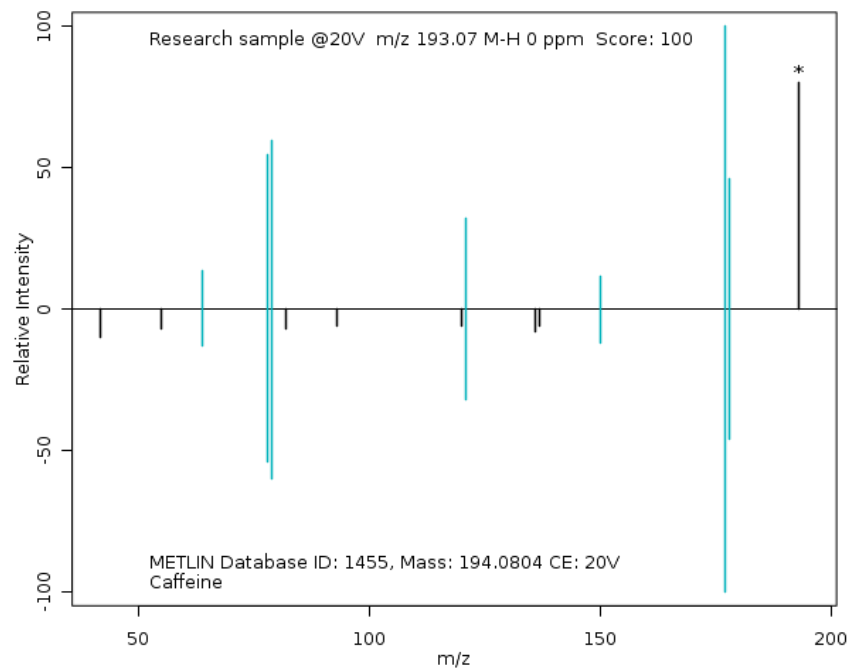
Tolerance MS/MS (Da): 0.01

Tolerance Precursor (ppm): 20

Precursor m/z: 193.0731

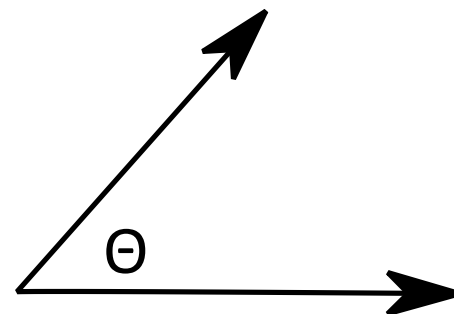
Find Metabolites Reset

Response to query



Dot products: MS/MS comparison

- Computes a similarity score between spectra:
 - Each spectrum becomes a vector in n dimensions, where n is the number of m/z values included. The intensity values are the coordinates.
 - Comparing two spectra computes the cosine of angle between the two corresponding vectors.
- To emphasize minor peaks, many systems use square root of intensity instead.





Database Service



Statistics



Publications



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Japanese Site



News

- Feb 23, 2015 [Java applets were updated with Code Signing.](#) **new**
- Feb 05, 2015 [For updating CodeSigning, MassBank Java applets are unavailable few days.](#) **new**
- Dec 22, 2014 [MassBank service will stop 0:00 – 7:00, 27 Dec \(UTC\) for electricity maintenance.](#) **new**
- Oct 16, 2014 [MassBank service will stop 9:00, 17 Oct - 0:00, 20 Oct \(GMT\) for maintenance.](#)
- Oct 03, 2014 [MassBank service will stop on Oct. 18-19 \(UTC+9\) for electricity maintenance.](#)

[All news](#)<<About the security checks of Java blocked MassBank applets>> **fixed**

To all the MassBank users who installed **Java 7 Update 51**, we apologize for their inconvenience that mass spectra are not displayed because the security checks of Java blocked MassBank applets.

[See more details](#)

Database Service

→ Spectrum Search

→ Quick Search

→ Peak Search

→ Substructure Search

→ Metabolite Prediction

→ Spectral Browser

→ Batch Service

→ Browse Page

→ Record Index

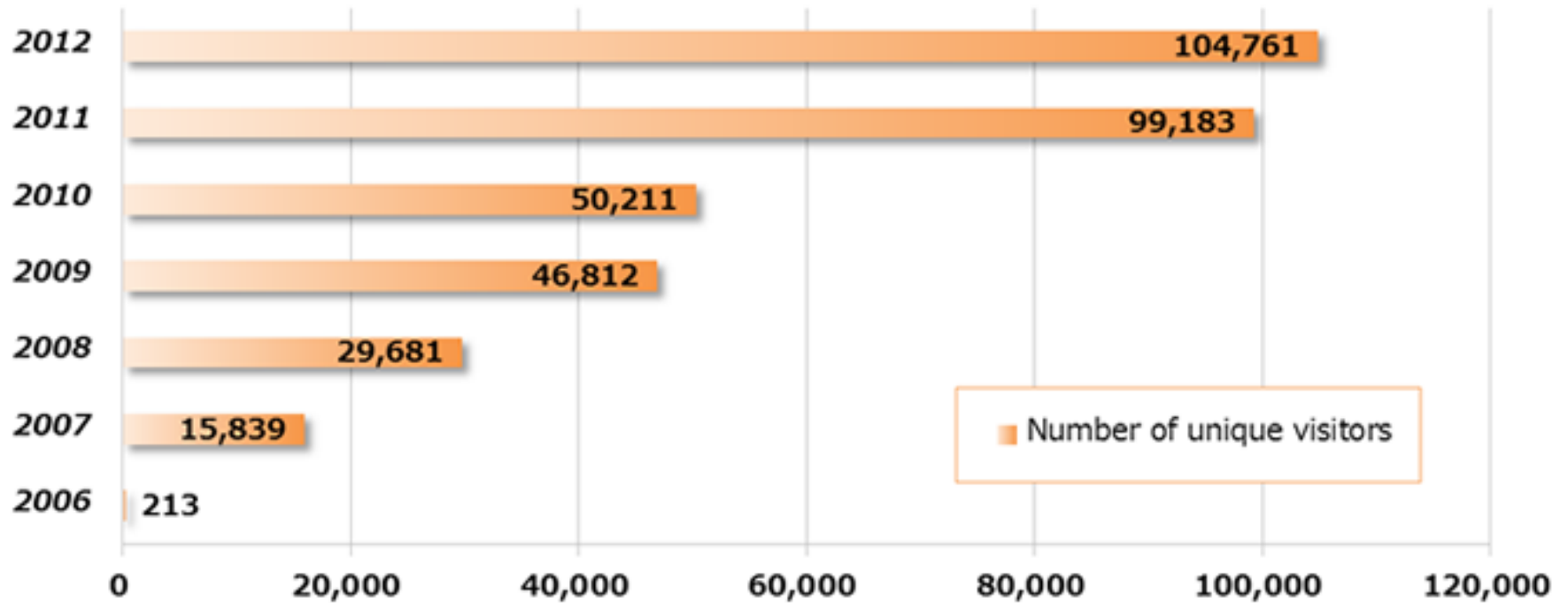
MassBank is financially supported from [National Bioscience Database Center, Japan Science and Technology Agency](#) (2011-2013).

[The Mass Spectrometry Society of Japan](#) officially supports MassBank.

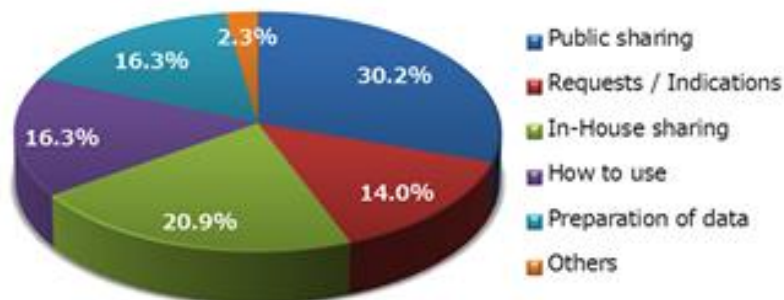
Please cite the article ([DOI](#)) when using MassBank.

<http://www.massbank.jp/>

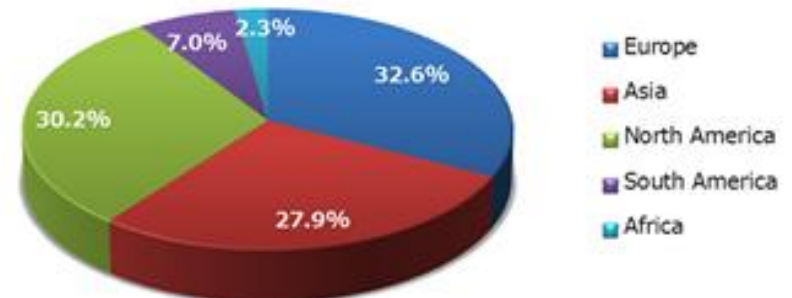
The number of unique visitors to MassBank



The contents of the inquiry



Contact by Region



MassBank origins

- MassBank is a distributed database, with twenty-eight research groups contributing data through local servers.
- The Institute for Advanced Biosciences led publications, and the School of Engineering at the University of Tokyo has contributed EI spectra for more than 11,000 compounds.
- MassBank collates spectra rather than collecting them.

Database services

Spectrum Search

- Retrieves spectra similar to user's spectrum in terms of the m/z value. This search is helpful to identify chemical compound by comparing similar spectra on a 3D-display.



Substructure Search

- Retrieves chemical compounds for which the chemical structure contains the substructures specified by users and displays their spectra.



MassBank Batch Service

Query File
 No file selected.
[sample file](#) [sample archive](#)

Mail Address

Batch Service conducts a batch spectrum search, and emails you the results.
Use this in such cases as when you would like to search for a large number of spectra.

Instrument Type

<input type="checkbox"/> EI	<input type="checkbox"/> EI-B
	<input type="checkbox"/> EI-EBEB
	<input type="checkbox"/> GC-EI-QQ
	<input type="checkbox"/> GC-EI-TOF
<hr/>	
<input checked="" type="checkbox"/> ESI	<input checked="" type="checkbox"/> CE-ESI-TOF
	<input checked="" type="checkbox"/> ESI-ITFT
	<input checked="" type="checkbox"/> ESI-ITTOF
	<input checked="" type="checkbox"/> LC-ESI-IT

MS Type

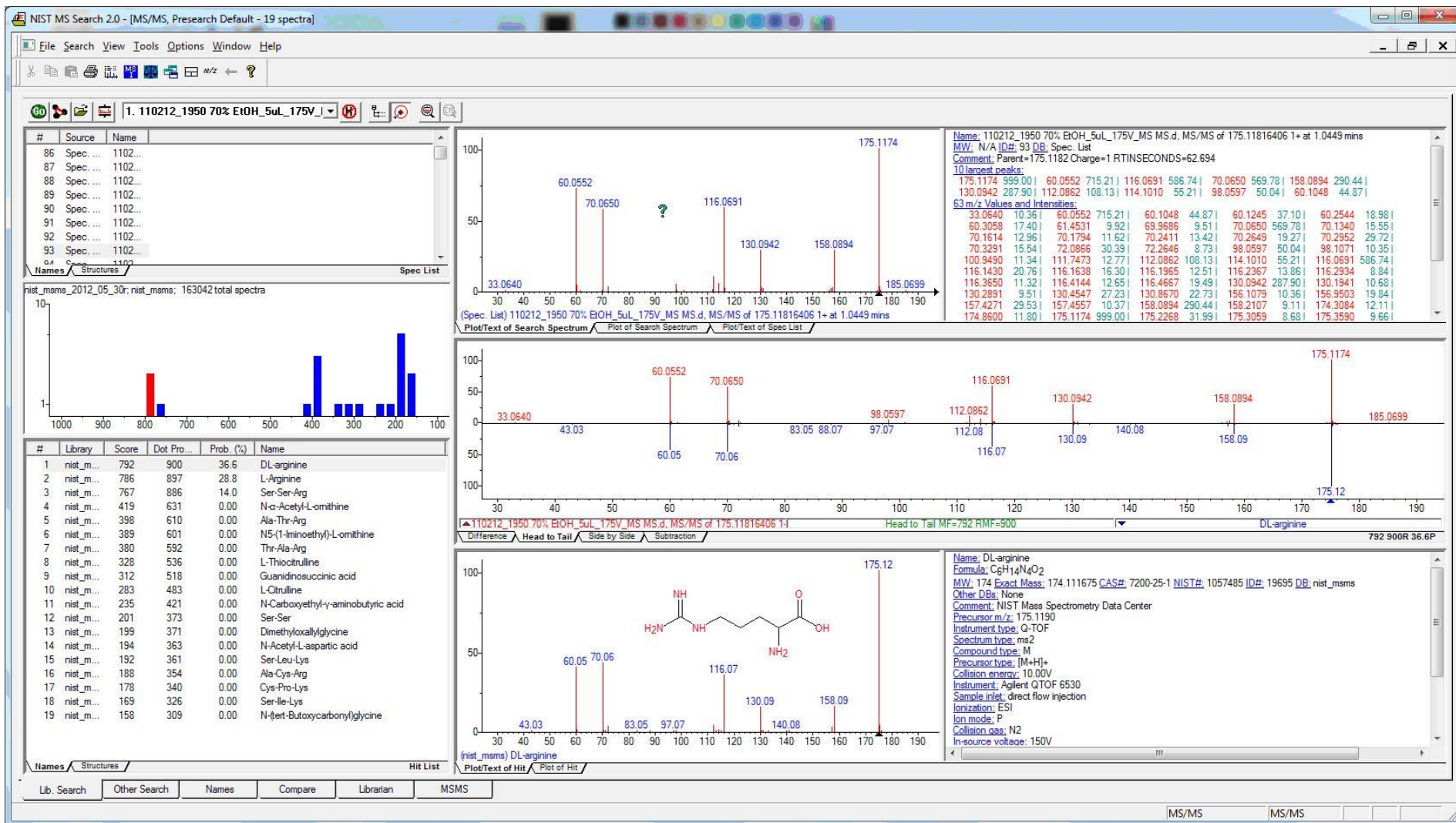
<input checked="" type="checkbox"/> All	<input checked="" type="checkbox"/> MS	<input checked="" type="checkbox"/> MS2	<input checked="" type="checkbox"/> MS3	<input checked="" type="checkbox"/> MS4
---	--	---	---	---

Ion Mode

<input checked="" type="radio"/> Positive	<input type="radio"/> Negative	<input type="radio"/> Both
---	--------------------------------	----------------------------

Text report includes only best 20 hits. HTML report can include larger number of analytes, and it contains links to KEGG for context.

NIST 12 MS/MS Database and Search Program



Current NIST contents

Database Contents:

6,999	Compounds
15,180	Precursor Ions
121,586	Spectra
~90%	Positive Ion Spectra
~10%	Negative Ion Spectra

Instrument Type	Precursor Ions
Ion Trap	12,047
Collision Cell (QTOF and QQQ)	9,232

Takeaway messages

- Repositories for EI and ESI spectra have become a major effort during the last decade.
- If an unknown compound appears in many contexts, its MS/MS may already be available.
- Library matching generally makes use of the dot product strategy.